Analytical and Bioanalyical Chemistry

Electronic Supplementary Material

Optimization of Parameters for Coverage of Low Molecular Weight Proteins

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FigureS1: Simulated 2D-PAGE of the LMW proteins identified in our study (red) and the LMW proteins of *E. coli* included in the SwissProt protein database (black).

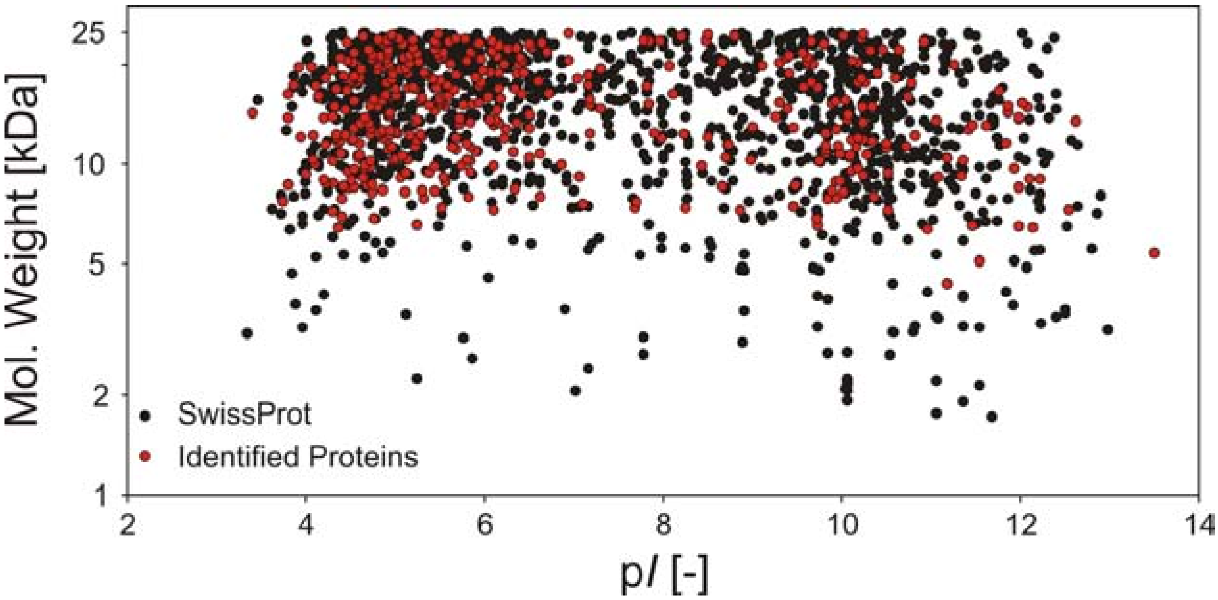
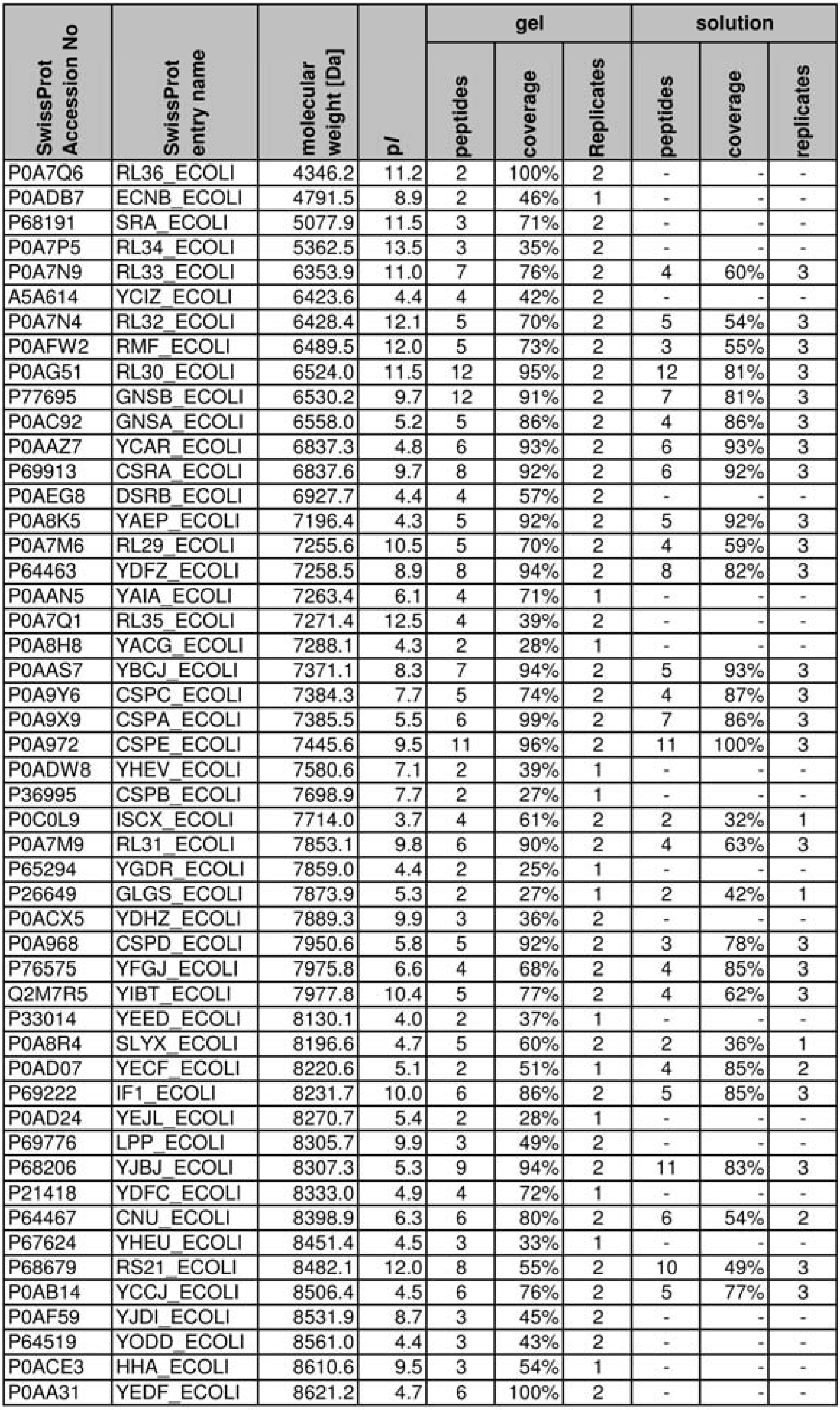


Table S1: List of 54 fully sequenced species from GenBank used as input for the multiz alignment *E. coli* str. K-12 substr. MG1655 is used as reference species.

Accession Number	Species
NC_011833.1	Buchnera aphidicola str. 5A (Acyrthosiphon pisum), complete genome
NC_008513.1	Buchnera aphidicola str. Cc (Cinara cedri), complete genome
NC_004545.1	Buchnera aphidicola str. Bp (Baizongia pistaciae), complete genome
NC_004061.1	Buchnera aphidicola str. Sg (Schizaphis graminum), complete genome
NC_011834.1	Buchnera aphidicola str. Tuc7 (Acyrthosiphon pisum), complete genome
NC_002528.1	Buchnera aphidicola str. APS (Acyrthosiphon pisum), complete genome
NC_009792.1	Citrobacter koseri ATCC BAA-895, complete genome
NC_000913.2	Escherichia coli str. K-12 substr. MG1655, complete genome
NC_009436.1	Enterobacter sp. 638, complete genome
NC_004547.2	Erwinia carotovora subsp. atroseptica SCRI1043, complete genome
NC_011740.1	Escherichia fergusonii ATCC 35469, complete genome
NC_009778.1	Enterobacter sakazakii ATCC BAA-894, complete genome
NC_010694.1	Erwinia tasmaniensis Et1/99, complete genome
NC_011283.1	Klebsiella pneumoniae 342, complete genome
NC_009648.1	Klebsiella pneumoniae MGH 78578, complete genome
NC_005126.1	Photorhabdus luminescens subsp. laumondii str. TT01, complete genome
NC_010554.1	Proteus mirabilis HI4320, complete genome
NC_010658.1	Shigella boydii CDC 3083-94, complete genome
NC_007613.1	Shigella boydii Sb227, complete genome
NC_007606.1	Shigella dysenteriae Sd197, complete genome
NC_010067.1	Salmonella enterica subsp. arizonae serovar 62:z4,z23:□, complete genome
NC_006905.1	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome
NC_006511.1	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150, complete genome
NC_004337.1	Shigella flexneri 2a str. 301, complete genome
NC_008258.1	Shigella flexneri 5 str. 8401, complete genome
NC_007384.1	Shigella sonnei Ss046, complete genome
NC_007712.1	Sodalis glossinidius str. □morsitans□, complete genome
NC_009832.1	Serratia proteamaculans 568, complete genome
NC_011149.1	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome
NC_010102.1	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome
NC_012125.1	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome
NC_011205.1	Salmonella enterica subsp. enterica serovar Dublin str. CT 02021853, complete genome
NC_011294.1	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109, complete genome
NC_011274.1	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91, complete genome
NC_011083.1	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome
NC_011080.1	Salmonella enterica subsp. enterica serovar Newport str. SL254, complete genome
NC_011147.1	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU 12601, complete genome
NC_011094.1	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome
NC_004631.1	Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome
NC_003197.1	Salmonella typhimurium LT2, complete genome
NC_003198.1	Salmonella enterica subsp. enterica serovar Typhi str. CT18, complete genome
NC_004344.2	Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis, complete genome
NC_008800.1	Yersinia enterocolitica subsp. enterocolitica 8081, complete genome
NC_010634.1	Yersinia pseudotuberculosis PB1/+, complete genome
NC_006155.1	Yersinia pseudotuberculosis IP 32953, complete genome
NC_010159.1	Yersinia pestis Angola, complete genome
NC_005810.1	Yersinia pestis biovar microtus str. 91001, complete genome
NC_003143.1	Yersinia pestis CO92, complete genome
NC_008149.1	Yersinia pestis Nepal516, complete genome
NC_009708.1	Yersinia pseudotuberculosis IP 31758, complete genome
NC_004088.1	Yersinia pestis KIM, complete genome
NC_008150.1	Yersinia pestis Antiqua, complete genome
NC_009381.1	Yersinia pestis Pestoides F, complete genome
NC_010465.1	Yersinia pseudotuberculosis YPIII, complete genome

Table S2: Protein identification table.



SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P0A7Q6	RL36_ECOLI	4346.2	11.2	2	100%	2	-	-	-
P0ADB7	ECNB_ECOLI	4791.5	8.9	2	46%	1	-	-	-
P68191	SRA_ECOLI	5077.9	11.5	3	71%	2	-	-	-
P0A7P5	RL34_ECOLI	5362.5	13.5	3	35%	2	-	-	-
P0A7N9	RL33_ECOLI	6353.9	11.0	7	76%	2	4	60%	3
A5A614	YCIZ_ECOLI	6423.6	4.4	4	42%	2	-	-	-
P0A7N4	RL32_ECOLI	6428.4	12.1	5	70%	2	5	54%	3
P0AFW2	RMF_ECOLI	6489.5	12.0	5	73%	2	3	55%	3
P0AG51	RL30_ECOLI	6524.0	11.5	12	95%	2	12	81%	3
P77695	GNSB_ECOLI	6530.2	9.7	12	91%	2	7	81%	3
P0AC92	GNSA_ECOLI	6558.0	5.2	5	86%	2	4	86%	3
P0AAZ7	YCAR_ECOLI	6837.3	4.8	6	93%	2	6	93%	3
P69913	CSRA_ECOLI	6837.6	9.7	8	92%	2	6	92%	3
P0AEG8	DSRB_ECOLI	6927.7	4.4	4	57%	2	-	-	-
P0A8K5	YAEP_ECOLI	7196.4	4.3	5	92%	2	5	92%	3
P0A7M6	RL29_ECOLI	7255.6	10.5	5	70%	2	4	59%	3
P64463	YDFZ_ECOLI	7258.5	8.9	8	94%	2	8	82%	3
P0AAN5	YAIA_ECOLI	7263.4	6.1	4	71%	1	-	-	-
P0A7Q1	RL35_ECOLI	7271.4	12.5	4	39%	2	-	-	-
P0A8H8	YACG_ECOLI	7288.1	4.3	2	28%	1	-	-	-
P0AAS7	YBCJ_ECOLI	7371.1	8.3	7	94%	2	5	93%	3
P0A9Y6	CSPC_ECOLI	7384.3	7.7	5	74%	2	4	87%	3
P0A9X9	CSPA_ECOLI	7385.5	5.5	6	99%	2	7	86%	3
P0A972	CSPE_ECOLI	7445.6	9.5	11	96%	2	11	100%	3
P0ADW8	YHEV_ECOLI	7580.6	7.1	2	39%	1	-	-	-
P36995	CSPB_ECOLI	7698.9	7.7	2	27%	1	-	-	-
P0C0L9	ISCX_ECOLI	7714.0	3.7	4	61%	2	2	32%	1
P0A7M9	RL31_ECOLI	7853.1	9.8	6	90%	2	4	63%	3
P65294	YGDR_ECOLI	7859.0	4.4	2	25%	1	-	-	-
P26649	GLGS_ECOLI	7873.9	5.3	2	27%	1	2	42%	1
P0ACX5	YDHZ_ECOLI	7889.3	9.9	3	36%	2	-	-	-
P0A968	CSPD_ECOLI	7950.6	5.8	5	92%	2	3	78%	3
P76575	YFGJ_ECOLI	7975.8	6.6	4	68%	2	4	85%	3
Q2M7R5	YIBT_ECOLI	7977.8	10.4	5	77%	2	4	62%	3
P33014	YEED_ECOLI	8130.1	4.0	2	37%	1	-	-	-
P0A8R4	SLYX_ECOLI	8196.6	4.7	5	60%	2	2	36%	1
P0AD07	YECF_ECOLI	8220.6	5.1	2	51%	1	4	85%	2
P69222	IF1_ECOLI	8231.7	10.0	6	86%	2	5	85%	3
P0AD24	YEJL_ECOLI	8270.7	5.4	2	28%	1	-	-	-
P69776	LPP_ECOLI	8305.7	9.9	3	49%	2	-	-	-
P68206	YJBJ_ECOLI	8307.3	5.3	9	94%	2	11	83%	3
P21418	YDFC_ECOLI	8333.0	4.9	4	72%	1	-	-	-
P64467	CNU_ECOLI	8398.9	6.3	6	80%	2	6	54%	2
P67624	YHEU_ECOLI	8451.4	4.5	3	33%	1	-	-	-
P68679	RS21_ECOLI	8482.1	12.0	8	55%	2	10	49%	3
P0AB14	YCCJ_ECOLI	8506.4	4.5	6	76%	2	5	77%	3
P0AF59	YJDI_ECOLI	8531.9	8.7	3	45%	2	-	-	-
P64519	YODD_ECOLI	8561.0	4.4	3	43%	2	-	-	-
P0ACE3	HHA_ECOLI	8610.6	9.5	3	54%	1	-	-	-
P0AA31	YEDF_ECOLI	8621.2	4.7	6	100%	2	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P0A6A8	ACP_ECOLI	8621.4	3.8	6	45%	2	2	41%	3
P31992	PPTA_ECOLI	8655.4	4.7	3	38%	2	-	-	-
P64503	YEBV_ECOLI	8735.1	4.3	5	67%	2	2	41%	2
P30748	MOAD_ECOLI	8739.8	4.2	2	36%	2	2	36%	3
P64455	YDCY_ECOLI	8782.0	5.6	8	53%	2	4	71%	3
P0ABS8	HOLE_ECOLI	8828.5	9.9	2	38%	2	-	-	-
P0ACW6	YDCH_ECOLI	8860.7	10.0	8	66%	2	2	26%	1
P0ABR1	DINI_ECOLI	8931.2	4.5	3	59%	1	-	-	-
P0A8G9	EX7S_ECOLI	8934.1	4.2	3	43%	1	2	35%	1
P0A7T7	RS18_ECOLI	8969.0	12.2	9	64%	2	7	57%	3
P0A7M2	RL28_ECOLI	8988.5	12.1	14	82%	2	13	77%	3
P0C079	RELB_ECOLI	9054.0	4.6	3	42%	1	3	54%	2
P0A890	TUSA_ECOLI	9076.9	5.1	2	31%	1	4	85%	2
P0AA04	PTHP_ECOLI	9101.2	5.5	7	88%	2	4	85%	3
P0AD10	YECJ_ECOLI	9104.5	4.7	2	25%	1	-	-	-
P0A7L8	RL27_ECOLI	9106.6	11.1	9	62%	2	4	52%	3
P0AC62	GLRX3_ECOLI	9119.9	7.1	6	78%	2	3	58%	3
P0A7T3	RS16_ECOLI	9172.6	11.3	12	85%	2	6	66%	3
P0ACF4	DBHB_ECOLI	9208.0	10.2	10	80%	2	6	72%	3
P0ACV8	YMJA_ECOLI	9303.5	4.0	-	-	-	2	42%	1
P0AE60	CEDA_ECOLI	9358.8	10.5	2	25%	2	2	25%	1
P0AB61	YCIN_ECOLI	9367.8	5.4	9	100%	2	9	100%	3
Q47150	DINJ_ECOLI	9388.4	5.1	3	36%	1	-	-	-
P0A9W6	YRBA_ECOLI	9433.6	5.8	6	92%	2	3	31%	3
P0AFW8	ROF_ECOLI	9461.7	4.5	5	69%	2	4	42%	3
P0ACF0	DBHA_ECOLI	9517.2	10.1	8	96%	2	10	92%	3
P0AF36	ZAPB_ECOLI	9616.6	4.5	5	67%	2	4	59%	3
P68688	GLRX1_ECOLI	9666.8	4.7	6	86%	2	2	33%	1
P0A7U7	RS20_ECOLI	9666.9	11.9	8	53%	1	7	63%	2
P0AG63	RS17_ECOLI	9686.3	10.2	10	88%	2	10	74%	3
P52102	YFHL_ECOLI	9773.1	4.7	2	42%	1	-	-	-
P0A9N0	PTSO_ECOLI	9792.3	4.1	2	40%	1	-	-	-
P0A8J4	YBED_ECOLI	9809.2	5.4	5	63%	2	4	58%	3
P0ABF4	EUTM_ECOLI	9847.4	6.1	3	37%	2	-	-	-
P37590	PMRD_ECOLI	9852.4	8.4	5	65%	2	4	57%	2
P75694	YAHO_ECOLI	9877.8	5.7	8	68%	2	2	24%	1
P0AAN9	IRAP_ECOLI	9919.9	4.7	5	64%	2	6	97%	2
P76227	YNJH_ECOLI	9929.1	6.9	2	22%	1	-	-	-
P64540	YFCL_ECOLI	9982.2	4.1	3	53%	2	-	-	-
P64530	RCNR_ECOLI	10115.9	9.4	2	19%	1	-	-	-
P37188	PTKB_ECOLI	10204.2	5.8	3	64%	2	6	97%	3
P0A9L5	PPIC_ECOLI	10214.4	9.8	9	66%	2	6	74%	3
P0C037	YAIE_ECOLI	10216.1	4.3	3	26%	2	-	-	-
P0A734	MINE_ECOLI	10217.4	5.0	9	93%	2	7	63%	3
P0A800	RPOZ_ECOLI	10218.3	4.7	8	77%	2	7	93%	3
P0ADZ4	RS15_ECOLI	10251.0	11.4	9	75%	2	13	78%	3
P0ADP9	YIHD_ECOLI	10255.7	5.0	6	76%	2	6	82%	3
P0AB65	ACYP_ECOLI	10281.5	9.0	5	42%	2	2	26%	1
P0AD33	YFCZ_ECOLI	10299.6	4.1	8	99%	2	6	75%	3
P0AAP3	FRMR_ECOLI	10299.8	5.8	5	57%	2	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P0AEM4	FLGM_ECOLI	10322.9	5.1	3	42%	1	-	-	-
P0A6F9	CH10_ECOLI	10369.0	5.0	8	89%	2	9	94%	3
P0A7U3	RS19_ECOLI	10412.6	11.2	6	59%	2	5	49%	3
P64476	YDIH_ECOLI	10436.5	6.5	2	15%	1	-	-	-
P52060	YGGU_ECOLI	10438.2	10.1	3	35%	1	3	44%	3
P39274	YJDJ_ECOLI	10450.4	8.7	2	33%	1	2	48%	1
P76172	YNFD_ECOLI	10458.5	4.6	6	69%	2	-	-	-
P64559	YGFY_ECOLI	10529.7	5.2	2	23%	1	-	-	-
P0AB55	YCII_ECOLI	10584.1	5.1	6	66%	2	3	37%	3
P0A6Y1	IHFB_ECOLI	10633.4	10.1	9	79%	2	5	66%	3
P64602	MLAB_ECOLI	10662.7	4.6	3	41%	1	2	29%	3
P68919	RL25_ECOLI	10675.6	10.3	14	85%	2	10	84%	3
P0AFX0	RP5M_ECOLI	10732.3	6.6	5	67%	2	5	38%	3
P32162	YIIS_ECOLI	10758.6	4.4	5	53%	2	4	67%	2
P0AGK4	YHBY_ECOLI	10765.8	10.0	6	49%	2	5	79%	3
P52119	YFJF_ECOLI	10771.7	9.8	9	70%	2	-	-	-
P64479	YDIZ_ECOLI	10847.3	4.1	2	16%	1	-	-	-
P69822	ULAB_ECOLI	10877.5	6.3	2	25%	1	2	37%	1
P0A8P3	FETP_ECOLI	10934.8	5.9	16	97%	2	11	88%	3
P64581	YQJD_ECOLI	11033.7	9.8	3	28%	2	-	-	-
Q2M7X4	YICS_ECOLI	11052.1	4.9	4	32%	1	-	-	-
P0ADF8	ILVN_ECOLI	11087.6	5.7	2	18%	1	2	32%	1
P0ADZ0	RL23_ECOLI	11180.9	10.5	12	61%	2	5	48%	3
P0A6R3	FIS_ECOLI	11221.9	10.2	3	28%	1	-	-	-
P64461	LSRG_ECOLI	11236.6	5.6	2	27%	1	-	-	-
Q46868	YQIC_ECOLI	11258.3	5.8	10	73%	2	5	50%	3
P0ACX3	YDHR_ECOLI	11270.1	5.0	8	59%	2	7	59%	3
P0AEH5	ELAB_ECOLI	11288.0	5.2	4	47%	2	-	-	-
P60624	RL24_ECOLI	11298.3	10.7	16	89%	2	18	81%	3
P0A6X7	IHFA_ECOLI	11336.5	10.0	4	29%	1	6	58%	3
P08245	YCIH_ECOLI	11378.6	9.8	3	35%	1	-	-	-
P0AF61	YJDK_ECOLI	11450.8	4.2	2	43%	1	-	-	-
P23857	PSPE_ECOLI	11457.2	8.7	6	58%	2	-	-	-
P0ADU2	YGIN_ECOLI	11514.1	5.8	8	80%	2	4	40%	3
P0AAC8	ISCA_ECOLI	11537.9	4.6	5	48%	2	9	50%	2
P0AG48	RL21_ECOLI	11545.9	10.5	10	52%	2	9	50%	3
P0AG59	RS14_ECOLI	11563.0	11.8	8	63%	2	8	58%	3
P0AAT6	YBEB_ECOLI	11564.2	4.4	3	31%	1	-	-	-
P0A7R5	RS10_ECOLI	11717.8	10.3	16	79%	2	12	82%	3
P0AB20	HSPQ_ECOLI	11761.1	4.4	4	41%	1	-	-	-
P0AA25	THIO_ECOLI	11789.4	4.5	11	95%	2	8	85%	3
P0AB46	YMGD_ECOLI	11834.1	5.2	7	73%	1	2	29%	1
P0AES9	HDEA_ECOLI	11839.6	4.9	14	75%	2	-	-	-
P76076	YDBL_ECOLI	11860.0	10.1	3	31%	1	-	-	-
P0ADZ7	YAJC_ECOLI	11869.6	10.2	2	22%	1	-	-	-
P67603	YQFB_ECOLI	11887.7	4.5	7	64%	2	7	80%	3
P0ABE2	BOLA_ECOLI	11975.6	6.2	2	27%	2	3	42%	3
P75734	YBFN_ECOLI	11980.5	7.7	2	35%	1	-	-	-
P0A8B5	YBAB_ECOLI	11996.9	4.9	5	55%	2	10	84%	2
P0ADB1	OSME_ECOLI	12002.5	8.0	3	36%	2	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P76402	YEGP_ECOLI	12006.6	10.2	10	88%	2	10	84%	3
P0AET2	HDEB_ECOLI	12025.1	5.7	10	68%	2	3	44%	3
P0A6V5	GLPE_ECOLI	12064.2	4.3	4	55%	2	-	-	-
P0AE70	CHPA_ECOLI	12079.9	8.5	2	27%	1	-	-	-
P0ACC3	ERPA_ECOLI	12082.6	3.9	4	35%	2	3	27%	3
P0A8U6	METJ_ECOLI	12123.1	5.3	10	78%	1	4	61%	3
P61175	RL22_ECOLI	12208.6	10.8	12	68%	2	15	76%	3
P27838	CYAY_ECOLI	12213.7	4.1	6	74%	2	2	39%	3
P32156	RHAM_ECOLI	12246.7	5.2	2	32%	1	-	-	-
P0A9I8	NIRD_ECOLI	12266.1	4.9	5	45%	1	2	31%	1
P0A7K2	RL7_ECOLI	12277.0	4.4	9	82%	2	7	57%	3
P0A9R4	FER_ECOLI	12312.7	4.3	5	56%	2	4	53%	2
P69488	CUTA_ECOLI	12313.1	4.7	2	35%	1	-	-	-
P0AFJ1	PHNA_ECOLI	12327.5	4.8	7	57%	2	3	36%	3
P0A881	TRPR_ECOLI	12337.6	5.3	2	17%	2	-	-	-
P64506	YEBY_ECOLI	12360.8	8.2	5	66%	2	6	57%	2
P0AB18	TUSE_ECOLI	12392.8	7.2	3	25%	1	-	-	-
P0AB43	YCGL_ECOLI	12397.1	9.8	5	62%	2	6	57%	2
P0A9Z1	GLNB_ECOLI	12407.7	5.0	9	77%	2	5	30%	3
P64534	YOHN_ECOLI	12449.0	7.9	7	65%	2	4	51%	3
P0AEB7	YOAB_ECOLI	12475.2	4.8	7	55%	2	2	18%	1
P0ADS2	ZAPA_ECOLI	12576.4	5.0	6	54%	2	9	72%	2
P0AB52	YCHN_ECOLI	12675.2	4.9	2	29%	1	-	-	-
P0A703	HYBF_ECOLI	12678.4	4.9	2	20%	1	-	-	-
P0C018	RL18_ECOLI	12751.7	11.4	11	79%	2	10	72%	3
P0A8M6	YEEX_ECOLI	12760.6	9.9	6	66%	2	6	60%	3
P0AD49	RAIA_ECOLI	12766.7	6.2	7	84%	2	5	54%	3
P0AE48	YTFP_ECOLI	12848.8	6.5	3	29%	2	4	50%	3
P0AC69	GLRX4_ECOLI	12861.1	4.5	6	58%	2	7	62%	3
P38521	YGGL_ECOLI	12862.8	4.7	2	24%	2	-	-	-
P76170	YNFB_ECOLI	12891.0	9.5	3	43%	1	-	-	-
P33219	YEBF_ECOLI	12943.6	9.0	11	68%	2	5	43%	3
P0A7S9	RS13_ECOLI	13082.1	11.6	15	77%	2	14	75%	3
P0A7K6	RL19_ECOLI	13115.0	11.5	16	83%	2	11	75%	3
P0ADN2	YIFE_ECOLI	13115.7	6.1	9	68%	2	13	75%	3
P0ACE7	HINT_ECOLI	13223.7	5.7	8	95%	2	4	55%	3
P77667	SUFA_ECOLI	13282.0	4.7	3	30%	2	-	-	-
P0AAQ6	YBAA_ECOLI	13300.4	4.6	2	26%	1	-	-	-
P0AAQ2	YAJD_ECOLI	13346.2	6.2	6	43%	1	3	21%	1
P76243	YEAO_ECOLI	13368.7	6.4	9	70%	2	4	54%	3
P76569	YFGD_ECOLI	13381.0	5.8	4	35%	1	-	-	-
P0AA57	YOBA_ECOLI	13392.1	10.2	2	16%	1	-	-	-
P76001	YCGJ_ECOLI	13396.7	5.2	8	69%	2	2	32%	1
P0A7L3	RL20_ECOLI	13479.6	12.6	10	48%	2	4	31%	3
P0AF50	YJBR_ECOLI	13501.4	6.1	5	67%	2	4	52%	3
P0ADY3	RL14_ECOLI	13523.2	11.1	9	68%	2	9	63%	3
P24178	YFFB_ECOLI	13583.4	6.1	4	34%	2	5	34%	3
P0AF93	YJGF_ECOLI	13593.4	**5.2**	15	99%	2	8	80%	3
P64488	YEAR_ECOLI	13593.5	6.1	4	35%	1	2	21%	1
P76364	YEEU_ECOLI	13666.0	5.6	2	23%	1	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P0ADK8	YIBL_ECOLI	13678.4	10.1	4	36%	2	4	43%	1
P0AEQ1	GLCG_ECOLI	13718.6	5.7	3	33%	2	-	-	-
P0A7S3	RS12_ECOLI	13718.7	12.0	9	41%	2	7	59%	3
P09996	YIDB_ECOLI	13769.0	4.2	2	19%	1	-	-	-
P0A6T9	GCSH_ECOLI	13793.2	3.8	6	61%	2	-	-	-
P0A7R9	RS11_ECOLI	13827.0	12.0	11	72%	2	11	75%	3
P0ACD4	NIFU_ECOLI	13830.9	4.7	12	81%	2	7	73%	3
P42616	YQJC_ECOLI	13888.3	9.3	2	24%	1	-	-	-
P0A8E5	YACL_ECOLI	13923.0	4.3	2	12%	1	-	-	-
P0AGL2	TDCF_ECOLI	13989.0	4.9	2	20%	1	-	-	-
P0ADU5	YGIW_ECOLI	13992.4	4.9	6	49%	2	3	20%	3
P31130	YDEI_ECOLI	14103.3	6.5	8	67%	2	2	25%	1
P0A7W7	RS8_ECOLI	14108.9	10.1	7	55%	2	7	70%	3
P25738	MSYB_ECOLI	14241.1	3.4	3	21%	1	-	-	-
P68066	GRCA_ECOLI	14266.0	4.9	17	91%	2	14	87%	3
P0AG44	RL17_ECOLI	14347.2	11.9	14	74%	2	11	57%	3
P0ADX1	YHFA_ECOLI	14498.4	5.4	2	18%	1	-	-	-
P76549	YFFR_ECOLI	14535.9	6.1	2	17%	1	-	-	-
P39332	YJGH_ECOLI	14572.2	4.4	3	21%	1	-	-	-
P75874	YCCU_ECOLI	14683.3	7.3	4	55%	2	4	61%	3
Q46864	YGIT_ECOLI	14685.1	9.4	2	21%	1	2	21%	1
P0A7X3	RS9_ECOLI	14838.6	12.1	14	76%	2	15	72%	3
P0A7J7	RL11_ECOLI	14857.5	10.2	6	49%	2	7	46%	3
P76002	YCGK_ECOLI	14888.6	10.3	10	68%	2	6	68%	3
P0AC81	LGUL_ECOLI	14902.2	4.8	4	23%	1	-	-	-
P0AFW4	RNK_ECOLI	14909.3	4.3	8	65%	2	-	-	-
P0ADW3	YHCB_ECOLI	14943.3	5.6	3	34%	1	-	-	-
P02413	RL15_ECOLI	14963.1	11.9	13	72%	2	8	62%	3
P31063	YEDD_ECOLI	14965.5	4.7	4	42%	2	2	27%	1
P0A6E6	ATPE_ECOLI	15050.4	5.4	7	69%	2	3	44%	3
P0C0L2	OSMC_ECOLI	15070.5	5.5	12	62%	2	9	48%	3
P0A6Z6	NIKR_ECOLI	15075.5	5.8	3	36%	1	-	-	-
P62768	YAEH_ECOLI	15079.0	7.2	21	91%	2	11	81%	3
P0A7G2	RBFA_ECOLI	15136.8	5.9	6	54%	2	5	42%	3
P0A8I1	RUVX_ECOLI	15168.9	7.8	2	16%	1	-	-	-
P0AAA9	ZRAP_ECOLI	15181.5	9.9	4	35%	1	-	-	-
P0ADY7	RL16_ECOLI	15263.6	12.0	11	63%	2	10	62%	3
P04982	RBSD_ECOLI	15274.2	5.9	6	58%	2	4	43%	2
P0ACG1	STPA_ECOLI	15330.0	9.3	5	49%	1	6	60%	3
P0ABV6	TOLR_ECOLI	15365.0	5.3	2	19%	1	-	-	-
P0A746	MSRB_ECOLI	15433.2	5.5	7	58%	2	4	53%	3
P76341	HIUH_ECOLI	15441.9	9.9	-	-	-	2	23%	1
P0A763	NDK_ECOLI	15445.6	5.5	5	46%	2	6	55%	3
P0AEN8	FUCM_ECOLI	15456.0	5.5	2	24%	1	-	-	-
P0ACG8	HSLR_ECOLI	15478.4	10.6	3	31%	1	-	-	-
P0ABV2	EXBD_ECOLI	15509.3	4.5	2	9%	1	-	-	-
P0ACF8	HNS_ECOLI	15522.0	5.3	16	80%	2	12	75%	3
P0AGG4	THIO2_ECOLI	15536.9	4.9	3	26%	2	-	-	-
P0A905	SLYB_ECOLI	15582.6	10.0	6	39%	2	2	31%	1
P0A780	NUSB_ECOLI	15671.5	7.2	4	36%	1	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P02358	RS6_ECOLI	15685.3	4.8	13	87%	2	9	83%	3
P0A7R1	RL9_ECOLI	15750.7	6.2	17	82%	2	15	85%	3
P0C054	IBPA_ECOLI	15756.2	5.5	4	22%	1	2	29%	3
P03817	MIOC_ECOLI	15790.5	4.1	4	43%	1	2	29%	1
P0AB96	ARSC_ECOLI	15836.0	5.3	2	28%	1	-	-	-
P39177	USPG_ECOLI	15916.8	6.0	14	98%	2	11	89%	3
P37903	USPF_ECOLI	15998.9	5.6	8	45%	2	4	53%	3
P0AA10	RL13_ECOLI	16000.7	10.7	20	94%	2	18	80%	3
P0ADE6	YGAU_ECOLI	16045.4	5.6	12	89%	2	10	74%	3
P0AED0	USPA_ECOLI	16048.5	5.0	9	70%	2	5	70%	3
P0AEM0	FKBX_ECOLI	16063.5	4.1	2	22%	2	3	22%	2
P06968	DUT_ECOLI	16137.8	4.9	5	44%	2	3	22%	1
P61714	RISB_ECOLI	16138.9	5.0	6	48%	1	2	22%	2
P16681	PHNB_ECOLI	16153.6	4.9	7	69%	2	-	-	-
P65367	YQCA_ECOLI	16256.3	3.8	4	42%	1	-	-	-
P0AAB8	USPD_ECOLI	16276.2	6.4	7	56%	2	-	-	-
P0ABL3	NAPB_ECOLI	16277.9	8.1	3	13%	1	-	-	-
P0A8W2	SLYA_ECOLI	16335.9	6.7	6	46%	2	-	-	-
P0ADX7	YHHA_ECOLI	16605.9	11.8	5	37%	2	-	-	-
P0ABD8	BCCP_ECOLI	16669.0	4.5	4	39%	2	2	11%	1
P0A9A9	FUR_ECOLI	16776.9	5.7	9	81%	2	6	32%	3
P0AF67	YJEE_ECOLI	16835.4	4.3	2	20%	1	-	-	-
P0AF96	YJGK_ECOLI	16847.5	5.2	-	-	-	2	23%	1
P0AD59	IVY_ECOLI	16854.5	6.3	9	72%	2	8	69%	3
P69828	PTKA_ECOLI	16889.7	5.0	5	28%	1	2	22%	1
P0A731	MGSA_ECOLI	16900.8	6.2	3	15%	2	2	36%	2
P0A8D3	YAII_ECOLI	16951.8	5.4	2	20%	2	-	-	-
P0A9M5	XGPT_ECOLI	16952.7	5.5	4	40%	1	-	-	-
P30749	MOAE_ECOLI	16962.7	5.1	4	47%	1	2	36%	1
P12994	YBHB_ECOLI	17067.0	5.2	3	24%	1	2	23%	1
P0AAR3	YBAK_ECOLI	17075.5	9.7	3	21%	1	-	-	-
P0AE91	CREA_ECOLI	17090.1	9.6	5	36%	2	3	37%	1
P0A8D0	NRDR_ECOLI	17210.8	7.8	8	59%	1	-	-	-
P0ABA0	ATPF_ECOLI	17246.5	5.9	2	12%	1	2	19%	1
P0AG86	SECB_ECOLI	17259.1	4.1	-	-	-	2	32%	1
P0AGK8	ISCR_ECOLI	17318.7	7.2	2	20%	1	5	54%	2
P18390	YJJA_ECOLI	17335.3	5.6	8	68%	2	-	-	-
P0A8R0	RRAA_ECOLI	17342.4	3.9	4	20%	1	-	-	-
P0ABS1	DKSA_ECOLI	17510.1	4.9	12	82%	2	6	54%	3
P0A6G3	YGAD_ECOLI	17563.3	4.9	2	15%	1	-	-	-
P0A7W1	RS5_ECOLI	17585.0	10.8	13	70%	2	14	84%	3
P0AE52	BCP_ECOLI	17616.2	4.9	11	76%	2	6	47%	3
P0A9F1	MNTR_ECOLI	17622.0	6.4	2	19%	1	-	-	-
P0A6W5	GREA_ECOLI	17623.1	4.6	9	66%	2	7	52%	3
P0AGD1	SODC_ECOLI	17663.0	6.0	11	67%	2	-	-	-
P0AEU7	SKP_ECOLI	17670.4	10.3	7	55%	2	8	53%	3
P0A8N0	YCBG_ECOLI	17675.8	10.2	4	18%	1	-	-	-
P0A7J3	RL10_ECOLI	17693.8	9.7	12	75%	2	7	56%	3
P37182	HYBD_ECOLI	17733.4	4.5	5	30%	1	-	-	-
P0A862	TPX_ECOLI	17817.2	4.6	11	99%	2	12	99%	3

SwissProt Accession No	**SwissProt entry name**	**molecular weight [Da]**	***pI***	**gel**			**solution**		
				peptides	**coverage**	**Replicates**	**peptides**	**coverage**	**replicates**
P64483	YEAK_ECOLI	17832.8	6.6	4	26%	1	-	-	-
P69829	PTSN_ECOLI	17942.0	5.5	8	56%	1	-	-	-
P33012	GYRI_ECOLI	18063.0	4.5	6	36%	2	3	28%	2
P04128	FIMA1_ECOLI	18092.8	5.0	5	45%	2	4	29%	2
P76270	YEBR_ECOLI	18103.8	4.5	8	67%	2	-	-	-
P23869	PPIB_ECOLI	18135.2	5.4	6	45%	2	8	59%	3
P23827	ECOT_ECOLI	18174.2	7.0	10	51%	2	7	57%	3
P77754	SPY_ECOLI	18181.8	10.2	8	30%	1	-	-	-
P69783	PTGA_ECOLI	18233.5	4.6	9	69%	2	11	72%	3
P0AFZ3	SSPB_ECOLI	18244.4	4.2	2	12%	1	-	-	-
P0A832	SSRP_ECOLI	18251.5	10.6	2	13%	1	2	9%	1
P31131	YDEJ_ECOLI	18303.1	4.6	4	27%	1	-	-	-
P0A8E7	YAJQ_ECOLI	18326.2	5.9	17	85%	2	7	52%	3
P0ABD3	BFR_ECOLI	18478.1	4.5	9	61%	1	-	-	-
P63417	YHBS_ECOLI	18515.9	4.4	5	40%	1	-	-	-
P0AFD1	NUOE_ECOLI	18571.9	5.3	4	28%	2	3	33%	2
P21362	YCIF_ECOLI	18579.7	5.4	2	16%	1	-	-	-
P0A917	OMPX_ECOLI	18585.0	7.2	-	-	-	8	57%	2
P0AEZ9	MOAB_ECOLI	18647.1	5.7	9	64%	1	-	-	-
P0ABT2	DPS_ECOLI	18678.1	5.7	18	90%	2	8	57%	3
P0AAT9	YBEL_ECOLI	18778.9	5.0	10	69%	2	6	59%	3
P0A912	PAL_ECOLI	18806.5	6.4	4	26%	1	-	-	-
P45470	YHBO_ECOLI	18840.9	5.1	2	14%	1	-	-	-
P0A8D6	YMDB_ECOLI	18861.9	5.3	3	24%	2	-	-	-
P62395	SECM_ECOLI	18862.0	11.3	2	16%	1	-	-	-
P0ACJ0	LRP_ECOLI	18869.3	9.4	6	34%	2	4	24%	1
P0AG55	RL6_ECOLI	18885.5	10.4	17	86%	2	17	89%	3
P0AE85	CPXP_ECOLI	18946.5	6.4	8	55%	1	-	-	-
P0A6Q3	FABA_ECOLI	18951.6	6.2	2	23%	2	-	-	-
P0AGE0	SSB_ECOLI	18956.4	5.3	5	28%	1	2	14%	3
P75818	YBJP_ECOLI	18973.8	6.1	3	19%	1	-	-	-
P0A7B8	HSLV_ECOLI	19075.3	6.0	2	17%	1	-	-	-
P0AC51	ZUR_ECOLI	19235.7	6.0	4	34%	1	-	-	-
P0AB28	YCED_ECOLI	19296.3	4.3	2	13%	1	2	9%	1
P0A6K3	DEF_ECOLI	19310.9	5.1	6	36%	1	3	20%	2
P0ABA4	ATPD_ECOLI	19314.3	4.8	9	57%	2	2	15%	1
P45578	LUXS_ECOLI	19398.2	5.1	8	70%	2	5	49%	3
P0A998	FTNA_ECOLI	19406.6	4.6	8	58%	1	3	26%	2
P0A8J2	DNAT_ECOLI	19436.9	5.0	2	16%	1	-	-	-
P77368	YBCL_ECOLI	19457.8	7.3	2	14%	1	-	-	-
P0A6D7	AROK_ECOLI	19520.1	5.1	7	53%	2	-	-	-
P0ABY4	FLAW_ECOLI	19683.0	3.9	2	14%	1	-	-	-
P0A7A9	IPYR_ECOLI	19685.9	4.9	10	47%	2	3	19%	2
P61949	FLAV_ECOLI	19719.7	4.1	6	52%	2	5	46%	3
P0AEE1	DCRB_ECOLI	19769.7	4.9	3	24%	1	-	-	-
P45771	YRDD_ECOLI	19852.6	8.1	2	9%	1	3	29%	3
P51024	YAIL_ECOLI	19905.5	9.1	6	27%	1	2	14%	1
P0ABZ4	KDSC_ECOLI	19979.9	4.8	2	14%	1	-	-	-
P02359	RS7_ECOLI	20001.3	11.3	20	82%	2	17	70%	3
P64596	YRAP_ECOLI	20009.7	9.6	5	30%	2	3	18%	2

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P0ACY1	YDJA_ECOLI	20041.1	6.4	9	62%	1	5	15%	3
P77791	MAA_ECOLI	20078.0	6.2	3	27%	1	-	-	-
P0A9M2	HPRT_ECOLI	20097.9	4.9	7	43%	1	-	-	-
P67095	YFCE_ECOLI	20104.0	5.6	3	16%	1	-	-	-
P0ADV1	LPTA_ECOLI	20108.7	9.7	12	61%	2	2	13%	3
P0A6L9	HSCB_ECOLI	20120.4	4.9	2	12%	1	-	-	-
P0A9W9	YRDA_ECOLI	20227.0	5.2	2	15%	1	-	-	-
P62399	RL5_ECOLI	20284.6	10.2	17	78%	2	10	46%	3
P0AFY8	SEQA_ECOLI	20297.8	9.3	4	28%	1	-	-	-
P65556	YFCD_ECOLI	20357.3	4.5	4	30%	1	-	-	-
P39187	YTFJ_ECOLI	20402.9	8.7	7	48%	2	7	47%	2
P0AFL3	PPIA_ECOLI	20413.3	9.6	9	70%	2	8	66%	3
P0ADI7	YECD_ECOLI	20434.5	5.3	3	22%	1	-	-	-
P0AFG0	NUSG_ECOLI	20513.0	6.4	10	74%	2	5	32%	3
P0ACR9	MPRA_ECOLI	20546.1	5.8	4	21%	1	-	-	-
P0A707	IF3_ECOLI	20546.4	10.1	15	74%	2	6	39%	3
P0A6N4	EFP_ECOLI	20573.5	4.7	5	39%	2	2	11%	1
P0A7X6	RIMM_ECOLI	20587.5	4.5	3	19%	1	-	-	-
P0A805	RRF_ECOLI	20621.3	6.9	19	88%	2	8	32%	3
P0AE08	AHPC_ECOLI	20743.9	4.9	18	91%	2	17	95%	3
P45748	RIMN_ECOLI	20749.8	4.8	2	13%	1	-	-	-
P63224	GMHA_ECOLI	20797.4	6.0	3	19%	2	2	27%	1
P0A784	ORN_ECOLI	20798.4	4.8	3	23%	1	-	-	-
P0A8G6	WRBA_ECOLI	20827.4	5.5	8	48%	1	3	38%	2
P0A9K9	SLYD_ECOLI	20833.0	4.7	3	23%	2	3	23%	3
P76537	YFEY_ECOLI	20879.9	5.1	2	10%	1	-	-	-
P0A8X2	YCEI_ECOLI	20895.3	5.5	8	45%	2	7	29%	2
P0ADA5	YAJG_ECOLI	20932.4	9.4	5	22%	2	-	-	-
P63020	NFUA_ECOLI	20979.9	4.4	6	33%	2	5	12%	2
P0A8B2	YFCN_ECOLI	20995.4	8.5	2	20%	1	-	-	-
P52061	RDGB_ECOLI	21021.2	5.1	5	39%	1	-	-	-
P0AFH8	OSMY_ECOLI	21055.1	6.4	18	83%	2	5	39%	2
P0A7D1	PTH_ECOLI	21065.1	9.6	2	14%	2	-	-	-
P0AF03	MOG_ECOLI	21204.4	4.8	5	36%	1	-	-	-
P0A8E1	YCFP_ECOLI	21208.8	6.1	6	35%	1	-	-	-
P0A8C4	YGFB_ECOLI	21211.9	4.0	2	14%	1	-	-	-
P0AGD3	SODF_ECOLI	21248.2	5.5	14	95%	2	2	13%	1
P63228	GMHB_ECOLI	21276.2	4.8	2	15%	2	2	23%	1
P0ADC1	LPTE_ECOLI	21339.2	9.4	4	28%	2	-	-	-
P0A8X0	YJGA_ECOLI	21342.5	5.2	2	12%	1	-	-	-
P25536	YHDE_ECOLI	21497.4	5.5	2	16%	1	-	-	-
P0A6N8	EFPL_ECOLI	21515.4	4.7	6	36%	2	3	20%	2
P41407	AZOR_ECOLI	21640.4	4.9	2	13%	2	-	-	-
P0A729	YCEF_ECOLI	21673.5	5.9	3	12%	1	-	-	-
P0AGB6	RPOE_ECOLI	21678.1	5.2	2	14%	1	-	-	-
P32160	YIIQ_ECOLI	21746.1	9.6	2	11%	1	-	-	-
P09372	GRPE_ECOLI	21779.8	4.5	4	17%	1	3	28%	1
P0A7I7	RIBA_ECOLI	21818.4	5.5	2	13%	1	-	-	-
P0AEY5	MDAB_ECOLI	21873.2	5.8	3	12%	1	-	-	-
P77285	RNFG_ECOLI	21894.3	6.7	9	41%	2	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P0A9H5	BTUR_ECOLI	21980.4	6.1	2	12%	1	-	-	-
P60723	RL4_ECOLI	22068.6	10.3	18	82%	2	10	50%	3
P76576	YFGM_ECOLI	22158.4	4.9	2	13%	1	-	-	-
P37665	YIAD_ECOLI	22179.6	10.6	4	27%	1	-	-	-
P0A9L3	FKBB_ECOLI	22198.1	4.7	9	39%	1	2	12%	1
P60438	RL3_ECOLI	22224.8	10.5	18	68%	2	13	66%	3
P0A955	ALKH_ECOLI	22266.3	5.4	5	37%	1	-	-	-
P0A7C2	LEXA_ECOLI	22339.8	6.3	3	15%	1	-	-	-
P61316	LOLA_ECOLI	22479.1	6.4	11	63%	2	4	37%	3
P0AB38	YCFM_ECOLI	22497.2	6.5	4	30%	2	-	-	-
P0A8F0	UPP_ECOLI	22515.8	5.2	6	34%	1	-	-	-
P0ACA1	YIBF_ECOLI	22527.6	5.0	2	8%	1	-	-	-
P0A8Y3	YIHX_ECOLI	22714.2	5.1	2	12%	1	-	-	-
P0A7Z0	RPIA_ECOLI	22842.5	5.1	10	39%	2	4	26%	3
P18776	DMSB_ECOLI	22850.6	6.2	2	11%	1	-	-	-
P0A9D2	GST_ECOLI	22851.3	5.8	2	13%	1	-	-	-
P43340	YCAK_ECOLI	23018.2	5.1	2	12%	1	-	-	-
P0ADT8	YGIM_ECOLI	23058.8	9.8	2	17%	1	-	-	-
P00448	SODM_ECOLI	23079.8	6.5	7	26%	2	6	47%	2
P21367	YCAC_ECOLI	23082.9	5.1	5	37%	1	-	-	-
P0AEG4	DSBA_ECOLI	23086.3	5.9	16	65%	2	3	9%	2
P0A6G7	CLPP_ECOLI	23169.3	5.5	3	30%	1	-	-	-
P0AFR4	YCIO_ECOLI	23194.4	5.9	6	35%	2	3	16%	3
P0A7A5	PIMT_ECOLI	23239.6	6.6	4	18%	1	-	-	-
P0A744	MSRA_ECOLI	23296.9	4.9	2	14%	2	2	19%	1
P21369	PNCA_ECOLI	23343.7	4.5	3	16%	2	-	-	-
P0AFU8	RISA_ECOLI	23426.8	5.6	2	9%	1	-	-	-
P0A7V8	RS4_ECOLI	23451.7	10.9	21	71%	2	16	56%	3
P39310	YTFB_ECOLI	23487.1	4.9	2	13%	1	-	-	-
P61320	LOLB_ECOLI	23533.6	9.7	2	9%	1	-	-	-
P0A6P7	ENGB_ECOLI	23543.2	7.8	2	12%	1	-	-	-
P69441	KAD_ECOLI	23568.4	5.4	6	35%	2	7	43%	3
P60546	KGUA_ECOLI	23575.2	6.1	4	30%	1	-	-	-
P0ADA1	TESA_ECOLI	23605.0	8.0	5	26%	2	-	-	-
P0ACJ8	CRP_ECOLI	23622.9	8.5	11	44%	2	3	11%	2
P69407	RCSB_ECOLI	23654.2	7.8	4	16%	2	-	-	-
P33218	YEBE_ECOLI	23669.7	5.2	3	14%	1	-	-	-
P0ACA7	YLIJ_ECOLI	23696.0	4.9	8	38%	1	-	-	-
P0A720	KTHY_ECOLI	23765.5	5.2	2	13%	1	-	-	-
P75849	YCBL_ECOLI	23766.4	4.8	4	23%	2	2	15%	1
P0AED5	UVRY_ECOLI	23874.9	6.6	2	10%	1	-	-	-
P38489	NFNB_ECOLI	23887.3	5.8	14	71%	2	5	28%	3
P0AF28	NARL_ECOLI	23909.5	5.7	3	20%	1	3	17%	3
P0AAV4	YBGJ_ECOLI	23928.4	5.0	2	10%	1	-	-	-
P0ADV7	MLAC_ECOLI	23945.5	10.2	20	78%	2	6	12%	3
P77247	YNIC_ECOLI	24312.9	4.6	2	9%	1	-	-	-
P0AC59	GLRX2_ECOLI	24333.7	8.2	8	45%	2	-	-	-
P0AF12	MTNN_ECOLI	24336.1	5.0	3	16%	2	-	-	-
P64451	YDCL_ECOLI	24409.3	8.8	-	-	-	2	19%	1
P0A9R7	FTSE_ECOLI	24422.0	10.0	3	12%	1	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	gel			solution		
				peptides	coverage	Replicates	peptides	coverage	replicates
P0AG07	RPE_ECOLI	24536.9	5.0	3	17%	1	-	-	-
P68739	NFI_ECOLI	24655.0	8.5	-	-	-	2	10%	1
P0A7L0	RL1_ECOLI	24711.4	10.2	8	44%	2	10	52%	3
P0A6I0	KCY_ECOLI	24728.6	5.5	4	23%	2	-	-	-
P0A6T5	GCH1_ECOLI	24813.0	6.9	2	8%	1	-	-	-

Table S3: Peptide identification table digestion: G- *in-gel* approach, S- *in-solution* approach; lysis: U- Urea, T- TFA; protease: A- AspN, T- trypsin; replicate A or B or C.

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7Q6	4346.2	G	U	A	A	CID	LIT	2	100.0	DGVIRVICSAEPKHKQRQG	2178.2	R	-	3.4	0.4	72.8	13.4
P0A7Q6	4346.2	G	U	A	A	CID	LIT	2	100.0	MKVRASVKKLCRNCKIVKR	2374.4	-	D	3.5	0.0	15.0	9.0
P0A7Q6	4346.2	G	U	T	B	CID	LIT	2	36.8	RDGVIR	715.4	K	V	2.4	0.2	20.6	14.8
P0A7Q6	4346.2	G	U	T	B	CID	LIT	2	36.8	VICSAEPK	903.5	R	H	2.4	0.0	38.4	9.0
P68191	5077.9	G	U	A	A	CID	LIT	2	71.1	DHKISNQRKIVTEG	1624.9	L	D	3.7	0.0	30.0	13.8
P68191	5077.9	G	U	A	A	CID	LIT	2	71.1	DKSSVVNNPTGRKRPAEK	1983.1	G	-	2.3	0.5	14.1	12.6
P68191	5077.9	G	U	T	B	CID	LIT	3	55.6	HILGLDHK	932.5	R	I	2.9	0.0	22.2	12.3
P68191	5077.9	G	U	T	B	CID	LIT	3	55.6	IVTEGDKSSVVNNPTGR	1772.9	K	K	4.0	0.0	42.4	12.0
P68191	5077.9	G	U	T	B	CID	LIT	3	55.6	SSVVNNPTGR	1030.5	K	K	3.1	0.5	54.0	13.2
P0A7P5	5362.5	G	U	T	A	CID	LIT	3	34.8	NRSHGFR	873.4	R	A	2.4	0.2	29.9	13.8
P0A7P5	5362.5	G	U	T	A	CID	LIT	3	34.8	TFQPSVLK	919.5	R	R	2.2	0.5	11.2	13.2
P0A7P5	5362.5	G	U	T	A	CID	LIT	3	34.8	TFQPSVLKR	1075.6	R	N	1.6	0.7	29.4	12.3
P0A7P5	5362.5	G	T	T	A	CID	LIT	3	30.4	SHGFR	603.3	R	A	1.6	0.6	15.4	11.8
P0A7P5	5362.5	G	T	T	A	CID	LIT	3	30.4	TFQPSVLK	919.5	R	R	1.5	0.5	10.7	13.6
P0A7P5	5362.5	G	T	T	A	CID	LIT	3	30.4	TFQPSVLKR	1075.6	R	N	1.9	0.6	19.6	12.3
P0A7P5	5362.5	G	U	T	B	CID	LIT	2	19.6	TFQPSVLK	919.5	R	R	1.9	0.6	17.0	13.6
P0A7P5	5362.5	G	U	T	B	CID	LIT	2	19.6	TFQPSVLKR	1075.6	R	N	1.8	0.7	29.6	12.3
P0A7N9	6353.9	G	U	T	A	CID	LIT	7	76.4	FDPVVR	732.4	K	Q	1.5	0.3	19.8	13.0
P0A7N9	6353.9	G	U	T	A	CID	LIT	7	76.4	IKLVSSAGTGHFYTTTK	1811.0	K	N	5.1	0.7	46.9	10.4
P0A7N9	6353.9	G	U	T	A	CID	LIT	7	76.4	KFDPVVR	860.5	K	Q	2.7	0.6	41.3	14.0
P0A7N9	6353.9	G	U	T	A	CID	LIT	7	76.4	LVSSAGTGHFYTTTK	1569.8	K	N	4.1	0.8	51.6	13.4
P0A7N9	6353.9	G	U	T	A	CID	LIT	7	76.4	QHVIYK	787.4	R	E	1.8	0.4	6.3	16.4
P0A7N9	6353.9	G	U	T	A	CID	LIT	7	76.4	QHVIYKEAK	1115.6	R	I	3.0	0.8	12.8	13.2
P0A7N9	6353.9	G	U	T	A	CID	LIT	7	76.4	TKPEKLELK	1085.7	R	K	2.0	0.5	12.1	8.5
P0A7N9	6353.9	G	T	T	A	CID	LIT	6	76.4	IKLVSSAGTGHFYTTTK	1811.0	K	N	4.7	0.7	50.0	10.4
P0A7N9	6353.9	G	T	T	A	CID	LIT	6	76.4	KFDPVVR	860.5	K	Q	2.8	0.4	32.3	14.0
P0A7N9	6353.9	G	T	T	A	CID	LIT	6	76.4	LVSSAGTGHFYTTTK	1569.8	K	N	4.3	0.8	65.7	14.1
P0A7N9	6353.9	G	T	T	A	CID	LIT	6	76.4	QHVIYK	787.4	R	E	1.8	0.4	20.6	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7N9	6353.9	G	T	T	A	CID	LIT	6	76.4	QHVIYKEAK	1115.6	R	I	2.6	0.8	13.8	13.2
P0A7N9	6353.9	G	T	T	A	CID	LIT	6	76.4	TKPEKLELK	1085.7	R	K	2.0	0.4	19.0	8.5
P0A7N9	6353.9	G	T	A	A	CID	LIT	2	29.1	DPVVRQHVIYK	1353.8	F	E	2.3	0.7	13.4	10.4
P0A7N9	6353.9	G	T	A	A	CID	LIT	2	29.1	DPVVRQHVIYKEAKIK	1923.1	F	-	3.2	0.0	21.3	4.8
P0A7N9	6353.9	G	U	T	B	CID	LIT	5	70.9	IKLVSSAGTGHFYTTTK	1811.0	K	N	4.2	0.0	83.6	10.4
P0A7N9	6353.9	G	U	T	B	CID	LIT	5	70.9	KFDPVVR	860.5	K	Q	2.7	0.6	35.2	14.0
P0A7N9	6353.9	G	U	T	B	CID	LIT	5	70.9	LVSSAGTGHFYTTTK	1569.8	K	N	4.3	0.7	73.5	14.0
P0A7N9	6353.9	G	U	T	B	CID	LIT	5	70.9	QHVIYK	787.4	R	E	2.0	0.3	15.3	17.2
P0A7N9	6353.9	G	U	T	B	CID	LIT	5	70.9	TKPEKLELK	1085.7	R	K	1.9	0.0	27.8	8.5
P0A7N9	6353.9	S	U	T	C	CID	LIT	4	60.0	IKLVSSAGTGHFYTTTK	1811.0	K	N	5.1	0.7	78.7	16.2
P0A7N9	6353.9	S	U	T	C	CID	LIT	4	60.0	LVSSAGTGHFYTTTK	1569.8	K	N	3.2	0.6	17.6	16.8
P0A7N9	6353.9	S	U	T	C	CID	LIT	4	60.0	QHVIYK	787.4	R	E	2.0	0.6	23.2	19.2
P0A7N9	6353.9	S	U	T	C	CID	LIT	4	60.0	RTKPEKLELK	1241.8	K	K	3.5	0.4	32.6	12.6
P0A7N9	6353.9	S	U	T	B	ETD	LIT	2	45.5	LVSSAGTGHFYTTTK	1569.8	K	N	3.0	0.7	41.2	16.9
P0A7N9	6353.9	S	U	T	B	ETD	LIT	2	45.5	RTKPEKLELK	1241.8	K	K	3.7	0.4	17.4	12.6
P0A7N9	6353.9	S	U	T	C	ETD	LIT	3	49.1	IKLVSSAGTGHFYTTTK	1811.0	K	N	1.6	0.3	14.4	17.0
P0A7N9	6353.9	S	U	T	C	ETD	LIT	3	49.1	LVSSAGTGHFYTTTK	1569.8	K	N	1.9	0.6	35.8	16.7
P0A7N9	6353.9	S	U	T	C	ETD	LIT	3	49.1	RTKPEKLELK	1241.8	K	K	3.6	0.3	30.6	12.6
P0A7N9	6353.9	S	U	T	A	ETD+CID	LIT	2	29.1	QHVIYK	787.4	R	E	1.7	0.4	9.5	19.2
P0A7N9	6353.9	S	U	T	A	ETD+CID	LIT	2	29.1	RTKPEKLELK	1241.8	K	K	2.8	0.4	22.3	12.6
P0A7N9	6353.9	S	U	T	B	ETD+CID	LIT	2	29.1	QHVIYK	787.4	R	E	1.8	0.5	11.2	19.2
P0A7N9	6353.9	S	U	T	B	ETD+CID	LIT	2	29.1	RTKPEKLELK	1241.8	K	K	3.3	0.4	29.5	12.3
P0A7N9	6353.9	S	U	T	C	ETD+CID	LIT	3	60.0	IKLVSSAGTGHFYTTTK	1811.0	K	N	5.2	0.7	84.6	16.2
P0A7N9	6353.9	S	U	T	C	ETD+CID	LIT	3	60.0	QHVIYK	787.4	R	E	1.9	0.5	11.2	19.2
P0A7N9	6353.9	S	U	T	C	ETD+CID	LIT	3	60.0	RTKPEKLELK	1241.8	K	K	2.9	0.4	33.0	12.6
A5A614	6423.6	G	U	T	A	CID	LIT	3	42.1	MSEFDAQR	983.4	-	V	2.3	0.7	23.7	7.8
A5A614	6423.6	G	U	T	A	CID	LIT	3	42.1	QVAESTPDIPK	1184.6	R	A	2.2	0.7	16.0	10.4
A5A614	6423.6	G	U	T	A	CID	LIT	3	42.1	QVAESTPDIPKAPWEI	1780.9	R	-	3.3	0.3	23.3	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
A5A614	6423.6	G	U	T	B	CID	LIT	4	42.1	MSEFDAQR	983.4	-	V	2.6	0.4	41.7	7.8
A5A614	6423.6	G	U	T	B	CID	LIT	4	42.1	QVAESTPDIPK	1184.6	R	A	2.7	0.0	27.3	10.0
A5A614	6423.6	G	U	T	B	CID	LIT	4	42.1	QVAESTPDIPKAPWEI	1780.9	R	-	3.6	0.6	45.8	12.0
A5A614	6423.6	G	U	T	B	CID	LIT	4	42.1	SEFDAQR	852.4	M	V	0.0	0.0	33.9	9.0
P0A7N4	6428.4	G	U	T	A	CID	LIT	5	70.2	AVQQNKPTR	1041.6	M	S	0.0	0.0	37.1	10.8
P0A7N4	6428.4	G	U	T	A	CID	LIT	5	70.2	HHITADGYYR	1232.6	R	G	4.0	0.6	43.1	10.8
P0A7N4	6428.4	G	U	T	A	CID	LIT	5	70.2	RSHDALTAVTSLSVDK	1699.9	R	T	4.5	0.9	61.0	13.8
P0A7N4	6428.4	G	U	T	A	CID	LIT	5	70.2	SHDALTAVTSLSVDK	1543.8	R	T	5.7	0.7	74.9	14.1
P0A7N4	6428.4	G	U	T	A	CID	LIT	5	70.2	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	1.8	0.6	14.4	10.8
P0A7N4	6428.4	G	T	T	A	CID	LIT	4	54.4	HHITADGYYR	1232.6	R	G	2.8	0.0	21.9	10.8
P0A7N4	6428.4	G	T	T	A	CID	LIT	4	54.4	RSHDALTAVTSLSVDK	1699.9	R	T	3.8	0.0	39.4	13.4
P0A7N4	6428.4	G	T	T	A	CID	LIT	4	54.4	SHDALTAVTSLSVDK	1543.8	R	T	5.5	0.0	74.7	13.4
P0A7N4	6428.4	G	T	T	A	CID	LIT	4	54.4	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	6.7	0.8	109.0	9.0
P0A7N4	6428.4	G	U	A	A	CID	LIT	3	66.7	DALTAVTSLSVDKTSGEKHLRHHITA	2787.5	H	D	3.4	0.0	57.5	15.4
P0A7N4	6428.4	G	U	A	A	CID	LIT	3	66.7	DGYYRGRKVIAK	1425.8	A	-	2.3	0.5	8.1	12.3
P0A7N4	6428.4	G	U	A	A	CID	LIT	3	66.7	DKTSGEKHLRHHITA	1729.9	V	D	2.3	0.7	15.6	15.8
P0A7N4	6428.4	G	U	T	B	CID	LIT	4	68.4	AVQQNKPTR	1041.6	M	S	0.0	0.0	37.1	10.8
P0A7N4	6428.4	G	U	T	B	CID	LIT	4	68.4	HHITADGYYR	1232.6	R	G	3.1	0.5	38.0	10.8
P0A7N4	6428.4	G	U	T	B	CID	LIT	4	68.4	SHDALTAVTSLSVDK	1543.8	R	T	5.5	0.0	81.6	14.0
P0A7N4	6428.4	G	U	T	B	CID	LIT	4	68.4	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	3.4	0.9	33.5	9.0
P0A7N4	6428.4	G	U	A	B	CID	LIT	3	45.6	DALTAVTSLSV	1076.6	H	D	2.3	0.5	12.5	12.8
P0A7N4	6428.4	G	U	A	B	CID	LIT	3	45.6	DALTAVTSLSVDKTSGEKHLRHHITA	2787.5	H	D	2.5	0.8	7.6	15.1
P0A7N4	6428.4	G	U	A	B	CID	LIT	3	45.6	DKTSGEKHLRHHITA	1729.9	V	D	3.3	0.4	18.2	16.0
P0A7N4	6428.4	S	U	T	A	CID	LIT	3	52.6	HHITADGYYR	1232.6	R	G	3.2	0.4	34.8	13.2
P0A7N4	6428.4	S	U	T	A	CID	LIT	3	52.6	SHDALTAVTSLSVDK	1543.8	R	T	3.3	0.5	19.8	16.6
P0A7N4	6428.4	S	U	T	A	CID	LIT	3	52.6	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	7.4	0.7	99.6	18.3
P0A7N4	6428.4	S	U	T	B	CID	LIT	4	54.4	HHITADGYYR	1232.6	R	G	3.0	0.2	26.6	12.3
P0A7N4	6428.4	S	U	T	B	CID	LIT	4	54.4	RSHDALTAVTSLSVDKTSGEK	2202.1	R	H	6.9	0.7	71.6	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7N4	6428.4	S	U	T	B	CID	LIT	4	54.4	SHDALTAVTSLSVDK	1543.8	R	T	4.8	0.6	47.6	16.6
P0A7N4	6428.4	S	U	T	B	CID	LIT	4	54.4	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	7.0	0.7	93.5	18.0
P0A7N4	6428.4	S	U	T	C	CID	LIT	5	54.4	HHITADGYYR	1232.6	R	G	3.5	0.5	19.9	13.2
P0A7N4	6428.4	S	U	T	C	CID	LIT	5	54.4	RSHDALTAVTSLSVDK	1699.9	R	T	3.5	0.5	21.1	17.4
P0A7N4	6428.4	S	U	T	C	CID	LIT	5	54.4	RSHDALTAVTSLSVDKTSGEK	2202.1	R	H	5.6	0.6	73.2	18.4
P0A7N4	6428.4	S	U	T	C	CID	LIT	5	54.4	SHDALTAVTSLSVDK	1543.8	R	T	4.3	0.6	38.8	16.6
P0A7N4	6428.4	S	U	T	C	CID	LIT	5	54.4	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	7.4	0.7	106.0	17.9
P0A7N4	6428.4	S	U	T	C	ETD	LIT	4	54.4	HHITADGYYR	1232.6	R	G	2.9	0.8	0.0	0.0
P0A7N4	6428.4	S	U	T	C	ETD	LIT	4	54.4	RSHDALTAVTSLSVDKTSGEK	2202.1	R	H	6.6	0.0	90.4	17.8
P0A7N4	6428.4	S	U	T	C	ETD	LIT	4	54.4	SHDALTAVTSLSVDK	1543.8	R	T	2.1	0.6	16.6	16.8
P0A7N4	6428.4	S	U	T	C	ETD	LIT	4	54.4	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	7.8	0.7	70.1	18.1
P0A7N4	6428.4	S	U	T	C	ETD	FT	2	54.4	HHITADGYYR	1232.6	R	G	1.3	0.0	36.0	13.8
P0A7N4	6428.4	S	U	T	C	ETD	FT	2	54.4	RSHDALTAVTSLSVDKTSGEK	2202.1	R	H	3.0	0.0	34.4	17.7
P0A7N4	6428.4	S	U	T	B	ETD+CID	LIT	2	43.9	HHITADGYYR	1232.6	R	G	3.0	0.2	30.7	13.2
P0A7N4	6428.4	S	U	T	B	ETD+CID	LIT	2	43.9	SHDALTAVTSLSVDK	1543.8	R	T	3.2	0.4	7.5	16.8
P0A7N4	6428.4	S	U	T	C	ETD+CID	LIT	4	54.4	HHITADGYYR	1232.6	R	G	2.8	0.7	0.0	0.0
P0A7N4	6428.4	S	U	T	C	ETD+CID	LIT	4	54.4	RSHDALTAVTSLSVDKTSGEK	2202.1	R	H	4.3	0.6	31.9	18.2
P0A7N4	6428.4	S	U	T	C	ETD+CID	LIT	4	54.4	SHDALTAVTSLSVDK	1543.8	R	T	3.7	0.5	31.6	16.6
P0A7N4	6428.4	S	U	T	C	ETD+CID	LIT	4	54.4	SHDALTAVTSLSVDKTSGEK	2046.0	R	H	5.9	0.7	75.6	18.1
P0AFW2	6489.5	G	U	T	A	CID	LIT	3	54.5	GYQAGIAGR	892.5	R	S	2.7	0.4	21.5	13.4
P0AFW2	6489.5	G	U	T	A	CID	LIT	3	54.5	SKEMCPYQTLNQR	1654.8	R	S	4.1	0.6	61.7	11.8
P0AFW2	6489.5	G	U	T	A	CID	LIT	3	54.5	SQWLGGWR	989.5	R	E	1.7	0.7	11.4	8.5
P0AFW2	6489.5	G	T	T	A	CID	LIT	5	72.7	EAMADRVVMA	1124.5	R	-	2.7	0.0	40.9	8.5
P0AFW2	6489.5	G	T	T	A	CID	LIT	5	72.7	EMCPYQTLNQR	1439.6	K	S	3.2	0.8	48.9	8.5
P0AFW2	6489.5	G	T	T	A	CID	LIT	5	72.7	GYQAGIAGR	892.5	R	S	3.5	0.0	52.8	13.0
P0AFW2	6489.5	G	T	T	A	CID	LIT	5	72.7	SKEMCPYQTLNQR	1654.8	R	S	4.5	0.6	88.3	11.8
P0AFW2	6489.5	G	T	T	A	CID	LIT	5	72.7	SQWLGGWR	989.5	R	E	2.5	0.8	20.8	9.0
P0AFW2	6489.5	G	U	T	B	CID	LIT	3	40.0	EMCPYQTLNQR	1439.6	K	S	3.0	0.0	28.5	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFW2	6489.5	G	U	T	B	CID	LIT	3	40.0	GYQAGIAGR	892.5	R	S	3.4	0.8	46.8	13.4
P0AFW2	6489.5	G	U	T	B	CID	LIT	3	40.0	SKEMCPYQTLNQR	1654.8	R	S	3.6	0.9	28.9	10.4
P0AFW2	6489.5	S	U	T	B	CID	LIT	2	30.9	GYQAGIAGR	892.5	R	S	2.3	0.5	21.5	15.9
P0AFW2	6489.5	S	U	T	B	CID	LIT	2	30.9	SQWLGGWR	989.5	R	E	2.4	0.4	9.8	17.0
P0AFW2	6489.5	S	U	T	B	ETD	LIT	2	40.0	GYQAGIAGR	892.5	R	S	2.0	0.2	30.9	16.4
P0AFW2	6489.5	S	U	T	B	ETD	LIT	2	40.0	SKEMCPYQTLNQR	1654.8	R	S	0.0	0.0	23.0	14.1
P0AFW2	6489.5	S	U	T	C	ETD	LIT	2	38.2	SKEMCPYQTLNQR	1654.8	R	S	2.1	0.5	0.0	0.0
P0AFW2	6489.5	S	U	T	C	ETD	LIT	2	38.2	SQWLGGWR	989.5	R	E	1.8	0.0	25.6	12.3
P0AFW2	6489.5	S	U	T	A	ETD+CID	LIT	2	30.9	GYQAGIAGR	892.5	R	S	2.6	0.6	27.1	15.6
P0AFW2	6489.5	S	U	T	A	ETD+CID	LIT	2	30.9	SQWLGGWR	989.5	R	E	2.6	0.5	20.3	17.0
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	ATLLGLGLR	913.6	K	R	2.7	0.7	44.1	14.0
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	ATLLGLGLRR	1069.7	K	I	2.1	0.4	20.9	6.0
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	EDTPAIR	801.4	R	G	2.3	0.2	42.8	10.4
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	GMINAVSFMVK	1228.6	R	V	3.5	0.8	49.7	11.8
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	GMINAVSFMVKVEE	1553.8	R	-	3.3	0.7	31.8	11.1
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	HKATLLGLGLR	1178.7	K	R	2.7	0.8	41.6	4.8
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	IGHTVER	811.4	R	E	1.8	0.7	22.7	10.8
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	IGHTVEREDTPAIR	1593.8	R	G	4.0	0.6	37.2	12.6
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	ITQTR	618.4	K	S	1.5	0.4	18.5	17.0
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	RIGHTVER	967.5	R	E	2.8	0.6	33.5	11.8
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	SAIGRLPK	841.5	R	H	2.3	0.6	37.0	10.8
P0AG51	6524.0	G	U	T	A	CID	LIT	12	94.9	TIKITQTR	960.6	K	S	1.9	0.7	16.8	7.8
P0AG51	6524.0	G	T	T	A	CID	LIT	5	76.3	GMINAVSFMVK	1196.6	R	V	2.7	0.8	33.6	10.4
P0AG51	6524.0	G	T	T	A	CID	LIT	5	76.3	HKATLLGLGLR	1178.7	K	R	2.8	0.0	50.5	4.8
P0AG51	6524.0	G	T	T	A	CID	LIT	5	76.3	IGHTVEREDTPAIR	1593.8	R	G	3.4	0.8	28.0	12.6
P0AG51	6524.0	G	T	T	A	CID	LIT	5	76.3	RIGHTVER	967.5	R	E	2.3	0.5	22.1	10.4
P0AG51	6524.0	G	T	T	A	CID	LIT	5	76.3	SAIGRLPK	841.5	R	H	2.6	0.0	37.0	10.8
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	ATLLGLGLR	913.6	K	R	3.1	0.8	50.0	14.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	ATLLGLGLRR	1069.7	K	I	1.8	0.6	37.7	6.0
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	EDTPAIR	801.4	R	G	2.1	0.1	29.9	10.4
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	GMINAVSFMVK	1196.6	R	V	3.9	0.8	58.5	10.4
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	HKATLLGLGLR	1178.7	K	R	2.9	0.0	57.9	4.8
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	IGHTVER	811.4	R	E	1.8	0.0	29.5	10.8
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	IGHTVEREDTPAIR	1593.8	R	G	2.1	0.7	37.1	13.4
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	ITQTR	618.4	K	S	1.5	0.2	13.7	17.0
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	RIGHTVER	967.5	R	E	1.9	0.5	0.0	0.0
P0AG51	6524.0	G	U	T	B	CID	LIT	10	84.7	SAIGRLPK	841.5	R	H	2.1	0.6	15.4	10.8
P0AG51	6524.0	S	U	T	A	CID	LIT	7	81.4	ATLLGLGLR	913.6	K	R	3.0	0.7	57.6	14.5
P0AG51	6524.0	S	U	T	A	CID	LIT	7	81.4	ATLLGLGLRR	1069.7	K	I	2.1	0.3	18.8	12.0
P0AG51	6524.0	S	U	T	A	CID	LIT	7	81.4	GMINAVSFMVKVEE	1553.8	R	-	3.4	0.6	44.6	16.2
P0AG51	6524.0	S	U	T	A	CID	LIT	7	81.4	HKATLLGLGLR	1178.7	K	R	3.5	0.0	51.6	4.8
P0AG51	6524.0	S	U	T	A	CID	LIT	7	81.4	RIGHTVER	967.5	R	E	2.4	0.6	36.5	12.0
P0AG51	6524.0	S	U	T	A	CID	LIT	7	81.4	RIGHTVEREDTPAIR	1749.9	R	G	2.7	0.7	16.8	15.6
P0AG51	6524.0	S	U	T	A	CID	LIT	7	81.4	SAIGRLPK	841.5	R	H	2.0	0.0	23.7	11.5
P0AG51	6524.0	S	U	T	B	CID	LIT	7	67.8	ATLLGLGLR	913.6	K	R	3.0	0.7	49.2	14.5
P0AG51	6524.0	S	U	T	B	CID	LIT	7	67.8	ATLLGLGLRR	1069.7	K	I	1.6	0.3	14.8	12.0
P0AG51	6524.0	S	U	T	B	CID	LIT	7	67.8	GMINAVSFMVK	1196.6	R	V	3.9	0.0	51.2	14.0
P0AG51	6524.0	S	U	T	B	CID	LIT	7	67.8	GMINAVSFMVKVEE	1553.8	R	-	3.2	0.4	35.3	16.2
P0AG51	6524.0	S	U	T	B	CID	LIT	7	67.8	HKATLLGLGLR	1178.7	K	R	3.1	0.0	58.4	4.8
P0AG51	6524.0	S	U	T	B	CID	LIT	7	67.8	IGHTVEREDTPAIR	1593.8	R	G	3.8	0.6	35.0	16.4
P0AG51	6524.0	S	U	T	B	CID	LIT	7	67.8	RIGHTVER	967.5	R	E	2.4	0.7	17.6	12.0
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	ATLLGLGLR	913.6	K	R	2.5	0.5	24.6	14.5
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	ATLLGLGLRR	1069.7	K	I	2.0	0.2	18.0	12.0
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	GMINAVSFMVK	1196.6	R	V	3.5	0.9	47.4	13.8
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	GMINAVSFMVKVEE	1553.8	R	-	4.0	0.4	49.4	16.4
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	HKATLLGLGLR	1178.7	K	R	3.4	0.0	57.4	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	IGHTVER	811.4	R	E	1.9	0.5	21.7	12.3
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	IGHTVEREDTPAIR	1593.8	R	G	1.7	0.6	19.0	16.8
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	RIGHTVER	967.5	R	E	2.6	0.6	23.8	13.4
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	RIGHTVEREDTPAIR	1749.9	R	G	4.4	0.0	18.3	15.6
P0AG51	6524.0	S	U	T	C	CID	LIT	10	81.4	SAIGRLPK	841.5	R	H	2.3	0.0	24.6	11.5
P0AG51	6524.0	S	U	T	A	CID	FT	2	18.6	ATLLGLGLR	913.6	K	R	2.8	0.0	35.5	14.5
P0AG51	6524.0	S	U	T	A	CID	FT	2	18.6	HKATLLGLGLR	1178.7	K	R	2.9	0.0	26.6	4.8
P0AG51	6524.0	S	U	T	B	CID	FT	2	20.3	ATLLGLGLRR	1069.7	K	I	1.4	0.0	22.3	12.0
P0AG51	6524.0	S	U	T	B	CID	FT	2	20.3	HKATLLGLGLR	1178.7	K	R	2.5	0.0	28.3	6.0
P0AG51	6524.0	S	U	T	C	CID	FT	2	20.3	ATLLGLGLRR	1069.7	K	I	1.6	0.0	26.8	12.0
P0AG51	6524.0	S	U	T	C	CID	FT	2	20.3	HKATLLGLGLR	1178.7	K	R	3.3	0.0	30.4	4.8
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	ATLLGLGLR	913.6	K	R	3.0	0.5	0.0	0.0
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	ATLLGLGLRR	1069.7	K	I	4.3	0.5	53.0	12.0
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	GMINAVSFMVKVEE	1553.8	R	-	2.9	0.6	0.0	0.0
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	HKATLLGLGLR	1178.7	K	R	0.0	0.0	54.4	4.8
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	HKATLLGLGLRR	1334.8	K	I	2.6	0.0	32.8	0.0
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	IGHTVER	811.4	R	E	1.6	0.0	22.6	12.0
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	RIGHTVER	967.5	R	E	2.9	0.0	20.5	12.0
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	RIGHTVEREDTPAIR	1749.9	R	G	6.6	0.6	72.9	15.6
P0AG51	6524.0	S	U	T	A	ETD	LIT	9	81.4	SAIGRLPK	841.5	R	H	2.0	0.0	27.5	11.5
P0AG51	6524.0	S	U	T	B	ETD	LIT	7	67.8	ATLLGLGLR	913.6	K	R	3.2	0.5	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD	LIT	7	67.8	ATLLGLGLRR	1069.7	K	I	2.3	0.6	52.8	12.0
P0AG51	6524.0	S	U	T	B	ETD	LIT	7	67.8	GMINAVSFMVK	1196.6	R	V	1.8	0.6	19.1	13.8
P0AG51	6524.0	S	U	T	B	ETD	LIT	7	67.8	GMINAVSFMVKVEE	1553.8	R	-	2.8	0.7	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD	LIT	7	67.8	HKATLLGLGLR	1178.7	K	R	0.0	0.0	75.0	4.8
P0AG51	6524.0	S	U	T	B	ETD	LIT	7	67.8	IGHTVEREDTPAIR	1593.8	R	G	5.3	0.7	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD	LIT	7	67.8	RIGHTVEREDTPAIR	1749.9	R	G	6.5	0.6	92.8	15.7
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	ATLLGLGLR	913.6	K	R	2.5	0.4	82.5	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	ATLLGLGLRR	1069.7	K	I	2.3	0.7	40.0	12.0
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	EDTPAIR	801.4	R	G	1.8	0.6	32.6	12.6
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	GMINAVSFMVK	1196.6	R	V	2.3	0.0	50.5	13.4
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	GMINAVSFMVKVEE	1553.8	R	-	3.3	0.5	0.0	0.0
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	HKATLLGLGLR	1178.7	K	R	4.4	0.0	63.3	4.8
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	HKATLLGLGLRR	1334.8	K	I	5.0	0.0	65.8	0.0
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	IGHTVER	811.4	R	E	1.9	0.4	20.5	12.0
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	IGHTVEREDTPAIR	1593.8	R	G	5.2	0.7	50.3	15.3
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	RIGHTVER	967.5	R	E	2.5	0.5	30.4	13.4
P0AG51	6524.0	S	U	T	C	ETD	LIT	11	67.8	RIGHTVEREDTPAIR	1749.9	R	G	6.6	0.7	85.4	17.0
P0AG51	6524.0	S	U	T	A	ETD	FT	2	44.1	HKATLLGLGLRR	1334.8	K	I	4.0	0.0	63.1	0.0
P0AG51	6524.0	S	U	T	A	ETD	FT	2	44.1	RIGHTVEREDTPAIR	1749.9	R	G	3.6	0.0	40.8	14.6
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	2	25.4	RIGHTVER	967.5	R	E	0.0	0.0	32.3	13.4
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	2	25.4	RIGHTVEREDTPAIR	1749.9	R	G	0.0	0.0	33.5	17.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	ATLLGLGLR	913.6	K	R	0.0	0.0	45.3	14.5
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	EDTPAIR	801.4	R	G	0.0	0.0	23.6	12.6
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	GMINAVSFMVK	1196.6	R	V	0.0	0.0	52.1	14.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	GMINAVSFMVKVEE	1553.8	R	-	0.0	0.0	30.9	16.4
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	HKATLLGLGLR	1178.7	K	R	0.0	0.0	47.1	4.8
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	IGHTVER	811.4	R	E	0.0	0.0	25.4	12.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	RIGHTVER	967.5	R	E	0.0	0.0	32.3	13.4
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	RIGHTVEREDTPAIR	1749.9	R	G	0.0	0.0	33.5	17.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	9	81.4	SAIGRLPK	841.5	R	H	0.0	0.0	32.2	11.1
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	ATLLGLGLR	913.6	K	R	2.4	0.8	54.7	14.5
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	ATLLGLGLRR	1069.7	K	I	2.0	0.5	27.0	12.0
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	EDTPAIR	801.4	R	G	1.8	0.0	29.3	13.4
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	GMINAVSFMVKVEE	1553.8	R	-	3.0	0.4	0.0	0.0
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	HKATLLGLGLR	1178.7	K	R	2.2	0.0	29.0	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	IGHTVER	811.4	R	E	1.8	0.4	23.4	12.0
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	RIGHTVER	967.5	R	E	3.1	0.4	22.8	12.0
P0AG51	6524.0	S	U	T	A	ETD+CID	LIT	8	67.8	RIGHTVEREDTPAIR	1749.9	R	G	2.8	0.4	11.0	14.6
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	2	39.0	ATLLGLGLR	913.6	K	R	2.9	0.7	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	2	39.0	GMINAVSFMVKVEE	1553.8	R	-	3.5	0.5	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	ATLLGLGLR	913.6	K	R	2.9	0.7	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	EDTPAIR	801.4	R	G	0.0	0.0	23.6	12.6
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	GMINAVSFMVK	1196.6	R	V	3.8	0.8	52.1	14.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	GMINAVSFMVKVEE	1553.8	R	-	2.0	0.6	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	HKATLLGLGLR	1178.7	K	R	3.1	0.0	47.1	4.8
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	IGHTVER	811.4	R	E	1.9	0.0	25.4	12.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	IGHTVEREDTPAIR	1593.8	R	G	2.5	0.7	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	RIGHTVER	967.5	R	E	2.5	0.8	32.3	13.4
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	RIGHTVEREDTPAIR	1749.9	R	G	3.4	0.3	0.0	0.0
P0AG51	6524.0	S	U	T	B	ETD+CID	LIT	10	81.4	SAIGRLPK	841.5	R	H	2.1	0.0	32.2	11.1
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	ATLLGLGLR	913.6	K	R	2.4	0.5	15.1	14.5
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	ATLLGLGLRR	1069.7	K	I	2.2	0.3	23.4	12.0
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	EDTPAIR	801.4	R	G	1.8	0.0	23.5	12.6
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	GMINAVSFMVK	1196.6	R	V	4.0	0.8	54.7	12.8
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	GMINAVSFMVKVEE	1553.8	R	-	3.4	0.5	0.0	0.0
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	HKATLLGLGLR	1178.7	K	R	0.0	0.0	65.1	4.8
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	RIGHTVER	967.5	R	E	2.4	0.7	26.3	13.4
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	RIGHTVEREDTPAIR	1749.9	R	G	3.1	0.8	21.9	16.4
P0AG51	6524.0	S	U	T	C	ETD+CID	LIT	9	81.4	SAIGRLPK	841.5	R	H	2.1	0.7	35.7	11.1
P0AG51	6524.0	S	U	T	B	HCD	FT	7	79.7	ATLLGLGLR	913.6	K	R	0.0	0.0	45.3	14.5
P0AG51	6524.0	S	U	T	B	HCD	FT	7	79.7	EDTPAIR	801.4	R	G	0.0	0.0	23.6	12.6
P0AG51	6524.0	S	U	T	B	HCD	FT	7	79.7	GMINAVSFMVK	1196.6	R	V	0.0	0.0	52.1	14.0
P0AG51	6524.0	S	U	T	B	HCD	FT	7	79.7	GMINAVSFMVKVEE	1553.8	R	-	0.0	0.0	30.9	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG51	6524.0	S	U	T	B	HCD	FT	7	79.7	HKATLLGLGLR	1178.7	K	R	0.0	0.0	47.1	4.8
P0AG51	6524.0	S	U	T	B	HCD	FT	7	79.7	IGHTVER	811.4	R	E	0.0	0.0	25.4	12.0
P0AG51	6524.0	S	U	T	B	HCD	FT	7	79.7	SAIGRLPK	841.5	R	H	0.0	0.0	32.2	11.1
P0AG51	6524.0	S	U	T	A	HCD	FT	3	20.3	ATLLGLGLR	913.6	K	R	2.0	0.0	43.6	14.5
P0AG51	6524.0	S	U	T	A	HCD	FT	3	20.3	ATLLGLGLRR	1069.7	K	I	2.0	0.0	25.3	12.0
P0AG51	6524.0	S	U	T	A	HCD	FT	3	20.3	HKATLLGLGLR	1178.7	K	R	3.3	0.0	33.8	4.8
P0AG51	6524.0	S	U	T	B	HCD	FT	2	16.9	ATLLGLGLR	913.6	K	R	2.1	0.8	43.1	14.5
P0AG51	6524.0	S	U	T	B	HCD	FT	2	16.9	ATLLGLGLRR	1069.7	K	I	2.4	0.0	15.0	12.0
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	AEADISEYITK	1239.6	K	K	3.1	0.8	37.3	10.8
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	AEADISEYITKK	1367.7	K	I	3.3	0.8	38.1	10.4
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	EKMTGLESYDVK	1415.7	R	I	3.7	0.7	57.1	11.5
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	EVTSIQFTAR	1151.6	K	E	3.3	0.7	60.0	12.0
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	IIELK	615.4	K	K	1.2	0.6	11.8	11.5
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	IIELKK	743.5	K	K	1.6	0.4	16.2	10.4
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	KIIELK	743.5	K	K	2.2	0.3	18.2	10.4
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	MNIENLK	861.5	-	T	2.7	0.5	36.1	13.2
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	MNIENLKTK	1106.6	-	A	0.0	0.0	43.0	14.0
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	MTGLESYDVK	1142.5	K	I	3.3	0.5	22.5	9.5
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	TGKEVTSIQFTAR	1437.8	K	E	4.2	0.6	66.4	10.4
P77695	6530.2	G	U	T	A	CID	LIT	12	91.2	TKAEADISEYITK	1468.8	K	K	4.6	0.7	57.0	10.0
P77695	6530.2	G	T	T	A	CID	LIT	2	43.9	EKMTGLESYDVK	1415.7	R	I	3.6	0.5	21.6	11.5
P77695	6530.2	G	T	T	A	CID	LIT	2	43.9	TKAEADISEYITK	1468.8	K	K	4.0	0.7	27.2	10.0
P77695	6530.2	G	U	A	A	CID	LIT	3	33.3	DVKINLI	814.5	Y	-	2.6	0.2	22.0	14.3
P77695	6530.2	G	U	A	A	CID	LIT	3	33.3	MNIENLKTKAEA	1361.7	-	D	4.4	0.5	56.0	15.8
P77695	6530.2	G	U	A	A	CID	LIT	3	33.3	NIENLKTKAEA	1230.7	M	D	0.0	0.0	35.2	15.4
P77695	6530.2	G	T	T	B	CID	LIT	2	38.6	EKMTGLESYDVK	1399.7	R	I	2.9	0.7	16.4	13.2
P77695	6530.2	G	T	T	B	CID	LIT	2	38.6	EVTSIQFTAR	1151.6	K	E	1.9	0.4	0.0	0.0
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	AEADISEYITK	1239.6	K	K	3.5	0.8	48.9	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	AEADISEYITKK	1367.7	K	I	2.4	0.8	25.4	12.3
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	EKMTGLESYDVK	1399.7	R	I	3.5	0.5	44.1	11.5
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	EVTSIQFTAR	1151.6	K	E	3.3	0.8	59.8	13.2
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	IIELK	615.4	K	K	1.3	0.5	17.1	11.5
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	KIIELK	743.5	K	K	2.2	0.2	30.3	10.4
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	MNIENLK	861.5	-	T	2.8	0.5	42.2	14.0
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	MTGLESYDVK	1142.5	K	I	3.6	0.5	55.4	10.4
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	TGKEVTSIQFTAR	1437.8	K	E	3.3	0.5	61.4	10.0
P77695	6530.2	G	U	T	B	CID	LIT	10	89.5	TKAEADISEYITK	1468.8	K	K	4.5	0.7	60.7	9.5
P77695	6530.2	G	T	A	B	CID	LIT	2	33.3	DVKINLI	814.5	Y	-	2.5	0.2	23.2	14.3
P77695	6530.2	G	T	A	B	CID	LIT	2	33.3	MNIENLKTKAEA	1361.7	-	D	4.3	0.5	59.7	16.3
P77695	6530.2	G	U	A	B	CID	LIT	4	49.1	DVKINLI	814.5	Y	-	2.4	0.2	20.8	14.3
P77695	6530.2	G	U	A	B	CID	LIT	4	49.1	EKMTGLESY	1057.5	R	D	1.7	0.6	20.0	14.0
P77695	6530.2	G	U	A	B	CID	LIT	4	49.1	MNIENLKTKAEA	1361.7	-	D	4.2	0.5	46.2	16.5
P77695	6530.2	G	U	A	B	CID	LIT	4	49.1	NIENLKTKAEA	1230.7	M	D	0.0	0.0	33.6	15.7
P77695	6530.2	S	U	T	A	CID	LIT	5	68.4	EKMTGLESYDVK	1399.7	R	I	3.7	0.0	53.0	16.9
P77695	6530.2	S	U	T	A	CID	LIT	5	68.4	EVTSIQFTAR	1151.6	K	E	3.0	0.7	43.2	14.9
P77695	6530.2	S	U	T	A	CID	LIT	5	68.4	TGKEVTSIQFTAR	1437.8	K	E	2.3	0.3	12.2	14.0
P77695	6530.2	S	U	T	A	CID	LIT	5	68.4	TKAEADISEYITK	1468.8	K	K	3.2	0.6	42.8	13.6
P77695	6530.2	S	U	T	A	CID	LIT	5	68.4	TKAEADISEYITKK	1596.8	K	I	4.3	0.6	41.6	16.4
P77695	6530.2	S	U	T	B	CID	LIT	5	68.4	EKMTGLESYDVK	1399.7	R	I	4.1	0.8	61.7	16.9
P77695	6530.2	S	U	T	B	CID	LIT	5	68.4	EVTSIQFTAR	1151.6	K	E	2.8	0.8	43.9	14.9
P77695	6530.2	S	U	T	B	CID	LIT	5	68.4	TGKEVTSIQFTAR	1437.8	K	E	3.9	0.5	42.9	14.8
P77695	6530.2	S	U	T	B	CID	LIT	5	68.4	TKAEADISEYITK	1468.8	K	K	4.5	0.6	43.0	13.6
P77695	6530.2	S	U	T	B	CID	LIT	5	68.4	TKAEADISEYITKK	1596.8	K	I	2.1	0.7	0.0	0.0
P77695	6530.2	S	U	T	C	CID	LIT	7	68.4	AEADISEYITKK	1367.7	K	I	2.4	0.6	38.2	15.3
P77695	6530.2	S	U	T	C	CID	LIT	7	68.4	EKMTGLESYDVK	1399.7	R	I	4.2	0.7	56.2	16.3
P77695	6530.2	S	U	T	C	CID	LIT	7	68.4	EVTSIQFTAR	1151.6	K	E	3.0	0.8	43.5	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P77695	6530.2	S	U	T	C	CID	LIT	7	68.4	MTGLESYDVK	1142.5	K	I	2.7	0.7	29.5	12.6
P77695	6530.2	S	U	T	C	CID	LIT	7	68.4	TGKEVTSIQFTAR	1437.8	K	E	2.5	0.7	15.8	13.8
P77695	6530.2	S	U	T	C	CID	LIT	7	68.4	TKAEADISEYITK	1468.8	K	K	2.5	0.6	0.0	0.0
P77695	6530.2	S	U	T	C	CID	LIT	7	68.4	TKAEADISEYITKK	1596.8	K	I	2.7	0.6	33.9	15.6
P77695	6530.2	S	U	T	C	CID	FT	3	52.6	MNIENLK	861.5	-	T	2.1	0.0	40.3	16.4
P77695	6530.2	S	U	T	C	CID	FT	3	52.6	MTGLESYDVK	1142.5	K	I	2.8	0.0	48.0	13.6
P77695	6530.2	S	U	T	C	CID	FT	3	52.6	TKAEADISEYITK	1468.8	K	K	3.2	0.0	42.0	13.0
P77695	6530.2	S	U	T	A	ETD	LIT	5	68.4	EKMTGLESYDVK	1399.7	R	I	2.7	0.6	30.6	16.2
P77695	6530.2	S	U	T	A	ETD	LIT	5	68.4	EVTSIQFTAR	1151.6	K	E	1.7	0.5	0.0	0.0
P77695	6530.2	S	U	T	A	ETD	LIT	5	68.4	TGKEVTSIQFTAR	1437.8	K	E	2.2	0.8	5.2	14.0
P77695	6530.2	S	U	T	A	ETD	LIT	5	68.4	TKAEADISEYITK	1468.8	K	K	2.4	0.4	0.0	0.0
P77695	6530.2	S	U	T	A	ETD	LIT	5	68.4	TKAEADISEYITKK	1596.8	K	I	3.9	0.6	35.6	15.6
P77695	6530.2	S	U	T	B	ETD	LIT	4	68.4	EKMTGLESYDVK	1399.7	R	I	4.5	0.7	69.2	16.2
P77695	6530.2	S	U	T	B	ETD	LIT	4	68.4	TGKEVTSIQFTAR	1437.8	K	E	2.6	0.8	50.9	14.0
P77695	6530.2	S	U	T	B	ETD	LIT	4	68.4	TKAEADISEYITK	1468.8	K	K	3.1	0.5	43.8	15.2
P77695	6530.2	S	U	T	B	ETD	LIT	4	68.4	TKAEADISEYITKK	1596.8	K	I	4.6	0.7	38.9	15.6
P77695	6530.2	S	U	T	C	ETD	LIT	7	68.4	AEADISEYITKK	1367.7	K	I	2.3	0.4	37.1	14.3
P77695	6530.2	S	U	T	C	ETD	LIT	7	68.4	EKMTGLESYDVK	1399.7	R	I	3.3	0.6	36.5	16.9
P77695	6530.2	S	U	T	C	ETD	LIT	7	68.4	EVTSIQFTAR	1151.6	K	E	2.0	0.6	24.5	14.9
P77695	6530.2	S	U	T	C	ETD	LIT	7	68.4	MTGLESYDVK	1142.5	K	I	2.3	0.7	30.3	12.6
P77695	6530.2	S	U	T	C	ETD	LIT	7	68.4	TGKEVTSIQFTAR	1437.8	K	E	3.2	0.7	41.2	14.0
P77695	6530.2	S	U	T	C	ETD	LIT	7	68.4	TKAEADISEYITK	1468.8	K	K	2.5	0.4	12.2	15.4
P77695	6530.2	S	U	T	C	ETD	LIT	7	68.4	TKAEADISEYITKK	1596.8	K	I	4.2	0.6	46.0	16.4
P77695	6530.2	S	U	T	B	ETD	FT	2	43.9	EKMTGLESYDVK	1399.7	R	I	2.0	0.0	33.4	16.2
P77695	6530.2	S	U	T	B	ETD	FT	2	43.9	TGKEVTSIQFTAR	1437.8	K	E	1.1	0.0	48.8	15.1
P77695	6530.2	S	U	T	C	ETD	FT	4	45.6	AEADISEYITKK	1367.7	K	I	1.5	0.0	33.0	14.3
P77695	6530.2	S	U	T	C	ETD	FT	4	45.6	EKMTGLESYDVK	1399.7	R	I	2.1	0.0	34.8	16.9
P77695	6530.2	S	U	T	C	ETD	FT	4	45.6	MTGLESYDVK	1142.5	K	I	1.1	0.0	35.4	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P77695	6530.2	S	U	T	C	ETD	FT	4	45.6	TKAEADISEYITKK	1596.8	K	I	1.5	0.0	46.2	15.6
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	42.1	EVTSIQFTAR	1151.6	K	E	0.0	0.0	30.7	14.9
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	42.1	TKAEADISEYITK	1468.8	K	K	0.0	0.0	43.5	13.8
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	42.1	TKAEADISEYITKK	1596.8	K	I	0.0	0.0	34.3	16.4
P77695	6530.2	S	U	T	A	ETD+CID	LIT	2	42.1	EVTSIQFTAR	1151.6	K	E	3.1	0.7	43.2	15.7
P77695	6530.2	S	U	T	A	ETD+CID	LIT	2	42.1	TKAEADISEYITK	1468.8	K	K	2.8	0.7	0.0	0.0
P77695	6530.2	S	U	T	A	ETD+CID	LIT	2	42.1	TKAEADISEYITKK	1596.8	K	I	3.4	0.8	0.0	0.0
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	47.4	EVTSIQFTAR	1151.6	K	E	3.1	0.8	30.7	14.9
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	47.4	TGKEVTSIQFTAR	1437.8	K	E	2.6	0.5	7.5	13.2
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	47.4	TKAEADISEYITK	1468.8	K	K	4.0	0.6	0.0	0.0
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	47.4	TKAEADISEYITKK	1596.8	K	I	4.3	0.6	0.0	0.0
P77695	6530.2	S	U	T	B	ETD+CID	LIT	2	47.4	VDGAVETR	846.4	-	-	0.7	-0.1	28.0	18.5
P77695	6530.2	S	U	T	C	ETD+CID	LIT	2	47.4	EVTSIQFTAR	1151.6	K	E	2.9	0.8	0.0	0.0
P77695	6530.2	S	U	T	C	ETD+CID	LIT	2	47.4	TGKEVTSIQFTAR	1437.8	K	E	2.1	0.2	14.4	14.0
P77695	6530.2	S	U	T	C	ETD+CID	LIT	2	47.4	TKAEADISEYITK	1468.8	K	K	3.9	0.5	0.0	0.0
P77695	6530.2	S	U	T	C	ETD+CID	LIT	2	47.4	TKAEADISEYITKK	1596.8	K	I	4.5	0.6	53.5	16.4
P77695	6530.2	S	U	T	B	HCD	FT	2	42.1	EVTSIQFTAR	1151.6	K	E	0.0	0.0	30.7	14.9
P77695	6530.2	S	U	T	B	HCD	FT	2	42.1	TKAEADISEYITK	1468.8	K	K	0.0	0.0	43.5	13.8
P77695	6530.2	S	U	T	B	HCD	FT	2	42.1	TKAEADISEYITKK	1596.8	K	I	0.0	0.0	34.3	16.4
P77695	6530.2	S	U	T	C	HCD	FT	2	24.6	AEADISEYITKK	1367.7	K	I	2.8	0.0	39.7	16.3
P77695	6530.2	S	U	T	C	HCD	FT	2	24.6	TKAEADISEYITKK	1596.8	K	I	3.8	0.0	30.7	15.2
P0AC92	6558.0	G	U	T	A	CID	LIT	4	86.0	EKMTGLESYDVK	1415.7	R	I	3.7	0.7	57.1	11.5
P0AC92	6558.0	G	U	T	A	CID	LIT	4	86.0	IAELNKNTGK	1087.6	K	E	3.1	0.7	46.4	14.6
P0AC92	6558.0	G	U	T	A	CID	LIT	4	86.0	MNIEELKK	1004.5	-	Q	2.4	0.5	24.5	12.6
P0AC92	6558.0	G	U	T	A	CID	LIT	4	86.0	MTGLESYDVK	1142.5	K	I	3.3	0.5	22.5	9.5
P0AC92	6558.0	G	U	T	A	CID	LIT	4	86.0	NTGKEVSEIR	1132.6	K	F	3.6	0.5	60.3	13.0
P0AC92	6558.0	G	U	T	A	CID	LIT	4	86.0	QAETEIADFIAQK	1463.7	K	I	4.1	0.7	78.9	11.8
P0AC92	6558.0	G	T	T	B	CID	LIT	2	49.1	EKMTGLESYDVK	1399.7	R	I	2.9	0.7	16.4	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AC92	6558.0	G	T	T	B	CID	LIT	2	49.1	IAELNKNTGK	1087.6	K	E	3.2	0.3	48.4	14.5
P0AC92	6558.0	G	T	T	B	CID	LIT	2	49.1	NTGKEVSEIR	1132.6	K	F	3.5	0.5	64.7	13.2
P0AC92	6558.0	G	U	T	B	CID	LIT	4	86.0	EKMTGLESYDVK	1399.7	R	I	3.5	0.5	44.1	11.5
P0AC92	6558.0	G	U	T	B	CID	LIT	4	86.0	IAELNKNTGK	1087.6	K	E	3.2	0.5	42.5	14.1
P0AC92	6558.0	G	U	T	B	CID	LIT	4	86.0	MNIEELKK	1004.5	-	Q	2.8	0.4	37.9	12.0
P0AC92	6558.0	G	U	T	B	CID	LIT	4	86.0	MTGLESYDVK	1142.5	K	I	3.6	0.5	55.4	10.4
P0AC92	6558.0	G	U	T	B	CID	LIT	4	86.0	NTGKEVSEIR	1132.6	K	F	3.4	0.6	57.0	13.2
P0AC92	6558.0	G	U	T	B	CID	LIT	4	86.0	QAETEIADFIAQK	1463.7	K	I	4.1	0.6	79.3	12.6
P0AC92	6558.0	G	T	A	B	CID	LIT	5	63.2	DFIAQKIA	905.5	A	E	2.0	0.0	19.3	13.2
P0AC92	6558.0	G	T	A	B	CID	LIT	5	63.2	DFIAQKIAELNKNTGKEVS	2105.1	A	E	3.4	0.7	14.2	13.4
P0AC92	6558.0	G	T	A	B	CID	LIT	5	63.2	DVKIKIM	846.5	Y	-	2.1	0.6	37.3	9.5
P0AC92	6558.0	G	T	A	B	CID	LIT	5	63.2	ELNKNTGKEVS	1218.6	A	E	2.2	0.5	9.3	15.2
P0AC92	6558.0	G	T	A	B	CID	LIT	5	63.2	MNIEELKKQA	1203.6	-	E	2.7	0.4	36.1	16.2
P0AC92	6558.0	G	U	A	B	CID	LIT	3	61.4	DFIAQKIA	905.5	A	E	2.4	0.4	19.7	13.2
P0AC92	6558.0	G	U	A	B	CID	LIT	3	61.4	DVKIKIM	846.5	Y	-	1.9	0.6	14.0	9.5
P0AC92	6558.0	G	U	A	B	CID	LIT	3	61.4	EKMTGLESY	1057.5	R	D	1.7	0.6	20.0	14.0
P0AC92	6558.0	G	U	A	B	CID	LIT	3	61.4	ELNKNTGKEVS	1218.6	A	E	2.0	0.6	0.0	0.0
P0AC92	6558.0	S	U	T	A	CID	LIT	2	49.1	EKMTGLESYDVK	1399.7	R	I	3.7	0.0	53.0	16.9
P0AC92	6558.0	S	U	T	A	CID	LIT	2	49.1	IAELNKNTGK	1087.6	K	E	2.4	0.4	16.7	17.7
P0AC92	6558.0	S	U	T	A	CID	LIT	2	49.1	NTGKEVSEIR	1132.6	K	F	2.6	0.4	24.5	17.1
P0AC92	6558.0	S	U	T	C	CID	LIT	3	73.7	EKMTGLESYDVK	1399.7	R	I	4.2	0.7	56.2	16.3
P0AC92	6558.0	S	U	T	C	CID	LIT	3	73.7	IAELNKNTGKEVSEIR	1801.0	K	F	4.4	0.6	67.3	14.6
P0AC92	6558.0	S	U	T	C	CID	LIT	3	73.7	KQAETEIADFIAQK	1591.8	K	I	4.7	0.5	87.1	16.8
P0AC92	6558.0	S	U	T	C	CID	LIT	3	73.7	MTGLESYDVK	1142.5	K	I	2.7	0.7	29.5	12.6
P0AC92	6558.0	S	U	T	C	CID	LIT	3	73.7	QAETEIADFIAQK	1463.7	K	I	3.2	0.5	45.8	17.1
P0AC92	6558.0	S	U	T	A	ETD	LIT	2	71.9	EKMTGLESYDVK	1399.7	R	I	2.7	0.6	30.6	16.2
P0AC92	6558.0	S	U	T	A	ETD	LIT	2	71.9	IAELNKNTGKEVSEIR	1801.0	K	F	5.6	0.3	52.2	14.6
P0AC92	6558.0	S	U	T	A	ETD	LIT	2	71.9	QAETEIADFIAQK	1463.7	K	I	2.5	0.3	36.5	17.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AC92	6558.0	S	U	T	B	ETD	LIT	2	57.9	EKMTGLESYDVK	1399.7	R	I	4.5	0.7	69.2	16.2
P0AC92	6558.0	S	U	T	B	ETD	LIT	2	57.9	MNIEELKK	1004.5	-	Q	2.4	0.2	21.2	16.3
P0AC92	6558.0	S	U	T	B	ETD	LIT	2	57.9	QAETEIADFIAQK	1463.7	K	I	3.0	0.2	12.7	17.1
P0AC92	6558.0	S	U	T	C	ETD	LIT	2	71.9	EKMTGLESYDVK	1399.7	R	I	3.3	0.6	36.5	16.9
P0AC92	6558.0	S	U	T	C	ETD	LIT	2	71.9	IAELNKNTGKEVSEIR	1801.0	K	F	6.1	0.4	65.2	14.5
P0AC92	6558.0	S	U	T	C	ETD	LIT	2	71.9	MTGLESYDVK	1142.5	K	I	2.3	0.7	30.3	12.6
P0AC92	6558.0	S	U	T	C	ETD	LIT	2	71.9	QAETEIADFIAQK	1463.7	K	I	3.4	0.4	61.3	17.1
P0AC92	6558.0	S	U	T	C	ETD+CID	LIT	3	52.6	IAELNKNTGKEVSEIR	1801.0	K	F	5.3	0.6	57.1	14.6
P0AC92	6558.0	S	U	T	C	ETD+CID	LIT	3	52.6	KQAETEIADFIAQK	1591.8	K	I	4.8	0.6	68.8	16.8
P0AC92	6558.0	S	U	T	C	ETD+CID	LIT	3	52.6	QAETEIADFIAQK	1463.7	K	I	3.3	0.5	35.5	16.9
P0AAZ7	6837.3	G	U	T	A	CID	LIT	6	93.3	DGIPVLLETEAR	1312.7	R	V	3.5	0.8	52.4	8.5
P0AAZ7	6837.3	G	U	T	A	CID	LIT	6	93.3	LDNLAFPLR	1058.6	K	D	3.2	0.5	43.2	15.7
P0AAZ7	6837.3	G	U	T	A	CID	LIT	6	93.3	LDNLAFPLRDGIPVLLETEAR	2352.3	K	V	3.8	0.0	29.0	4.8
P0AAZ7	6837.3	G	U	T	A	CID	LIT	6	93.3	LLEIIACPVCNGK	1486.8	R	L	4.8	0.6	61.7	12.8
P0AAZ7	6837.3	G	U	T	A	CID	LIT	6	93.3	LWYNQEKQELICK	1751.9	K	L	4.3	0.6	58.9	11.1
P0AAZ7	6837.3	G	U	T	A	CID	LIT	6	93.3	VLTADESKS	949.5	R	-	2.7	0.8	39.1	9.5
P0AAZ7	6837.3	G	T	T	A	CID	LIT	4	60.0	DGIPVLLETEAR	1312.7	R	V	2.0	0.6	19.7	8.5
P0AAZ7	6837.3	G	T	T	A	CID	LIT	4	60.0	LDNLAFPLR	1058.6	K	D	2.0	0.7	0.0	0.0
P0AAZ7	6837.3	G	T	T	A	CID	LIT	4	60.0	QELICK	790.4	K	L	2.1	0.2	25.4	14.0
P0AAZ7	6837.3	G	T	T	A	CID	LIT	4	60.0	VLTADESKS	949.5	R	-	2.6	0.8	40.8	10.4
P0AAZ7	6837.3	G	U	A	A	CID	LIT	3	48.3	DGIPVLLETEARVLTA	1696.9	R	D	2.9	0.8	28.3	11.1
P0AAZ7	6837.3	G	U	A	A	CID	LIT	3	48.3	DHRLL	653.4	M	E	1.5	0.5	13.1	12.8
P0AAZ7	6837.3	G	U	A	A	CID	LIT	3	48.3	DNLAFPLR	945.5	L	D	2.4	0.8	41.3	14.0
P0AAZ7	6837.3	G	T	A	A	CID	LIT	2	40.0	DGIPVLLETEARVLTA	1696.9	R	D	3.1	0.9	32.6	10.0
P0AAZ7	6837.3	G	T	A	A	CID	LIT	2	40.0	DNLAFPLR	945.5	L	D	3.0	0.7	30.3	14.0
P0AAZ7	6837.3	G	U	T	B	CID	LIT	6	71.7	DGIPVLLETEAR	1312.7	R	V	3.1	0.8	51.7	12.0
P0AAZ7	6837.3	G	U	T	B	CID	LIT	6	71.7	LDNLAFPLR	1058.6	K	D	3.4	0.4	43.4	15.7
P0AAZ7	6837.3	G	U	T	B	CID	LIT	6	71.7	LDNLAFPLRDGIPVLLETEAR	2352.3	K	V	4.2	0.0	28.3	6.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAZ7	6837.3	G	U	T	B	CID	LIT	6	71.7	LLEIIACPVCNGK	1486.8	R	L	3.7	0.0	64.7	13.0
P0AAZ7	6837.3	G	U	T	B	CID	LIT	6	71.7	VLTADESK	862.5	R	-	2.1	0.6	16.4	10.4
P0AAZ7	6837.3	G	U	T	B	CID	LIT	6	71.7	VLTADESKS	949.5	R	-	2.6	0.0	37.2	9.5
P0AAZ7	6837.3	G	T	A	B	CID	LIT	2	40.0	DGIPVLLETEARVLTA	1696.9	R	D	3.7	0.8	48.3	11.1
P0AAZ7	6837.3	G	T	A	B	CID	LIT	2	40.0	DNLAFPLR	945.5	L	D	2.8	0.4	21.6	13.0
P0AAZ7	6837.3	G	U	A	B	CID	LIT	5	58.3	DGIPVLLETEARVLTA	1696.9	R	D	4.1	0.0	32.5	10.0
P0AAZ7	6837.3	G	U	A	B	CID	LIT	5	58.3	DHRLL	653.4	M	E	1.4	0.4	11.0	12.8
P0AAZ7	6837.3	G	U	A	B	CID	LIT	5	58.3	DNLAFPLR	945.5	L	D	2.9	0.7	33.1	14.0
P0AAZ7	6837.3	G	U	A	B	CID	LIT	5	58.3	ELICKL	775.4	Q	D	2.0	0.0	28.7	14.3
P0AAZ7	6837.3	G	U	A	B	CID	LIT	5	58.3	ETEARVLTA	989.5	L	D	1.8	0.0	22.0	14.1
P0AAZ7	6837.3	S	U	T	A	CID	LIT	5	58.3	LLEIIACPVCNGK	1487.8	R	L	2.4	0.5	18.6	17.5
P0AAZ7	6837.3	S	U	T	A	CID	LIT	5	58.3	LLEIIACPVCNGKLWYNQEK	2449.2	R	Q	2.8	0.4	11.2	18.5
P0AAZ7	6837.3	S	U	T	A	CID	LIT	5	58.3	LLEIIACPVCNGKLWYNQEKQELICK	3220.6	R	L	5.5	0.6	25.8	19.4
P0AAZ7	6837.3	S	U	T	A	CID	LIT	5	58.3	LWYNQEKQELICK	1751.9	K	L	4.2	0.6	37.7	16.4
P0AAZ7	6837.3	S	U	T	A	CID	LIT	5	58.3	VLTADESKS	949.5	R	-	2.4	0.8	36.6	15.1
P0AAZ7	6837.3	S	U	T	B	CID	LIT	4	78.3	DGIPVLLETEAR	1312.7	R	V	2.7	0.7	28.9	12.8
P0AAZ7	6837.3	S	U	T	B	CID	LIT	4	78.3	LLEIIACPVCNGK	1487.8	R	L	4.5	0.8	69.1	15.2
P0AAZ7	6837.3	S	U	T	B	CID	LIT	4	78.3	LWYNQEKQELICK	1751.9	K	L	4.7	0.5	35.0	16.4
P0AAZ7	6837.3	S	U	T	B	CID	LIT	4	78.3	VLTADESKS	949.5	R	-	2.3	0.0	37.8	15.1
P0AAZ7	6837.3	S	U	T	C	CID	LIT	6	73.3	LDNLAFPLR	1058.6	K	D	2.3	0.6	21.2	15.9
P0AAZ7	6837.3	S	U	T	C	CID	LIT	6	73.3	LLEIIACPVCNGK	1486.8	R	L	3.8	0.6	29.4	17.0
P0AAZ7	6837.3	S	U	T	C	CID	LIT	6	73.3	LLEIIACPVCNGKLWYNQEK	2449.2	R	Q	3.0	0.4	18.9	18.8
P0AAZ7	6837.3	S	U	T	C	CID	LIT	6	73.3	LLEIIACPVCNGKLWYNQEKQELICK	3220.6	R	L	5.1	0.0	31.7	19.2
P0AAZ7	6837.3	S	U	T	C	CID	LIT	6	73.3	LWYNQEKQELICK	1751.9	K	L	4.4	0.6	25.1	16.8
P0AAZ7	6837.3	S	U	T	C	CID	LIT	6	73.3	VLTADESKS	949.5	R	-	2.0	0.6	24.5	15.1
P0AAZ7	6837.3	S	U	T	B	CID	FT	3	58.3	LLEIIACPVCNGK	1487.8	R	L	3.6	0.0	69.5	15.2
P0AAZ7	6837.3	S	U	T	B	CID	FT	3	58.3	LWYNQEKQELICK	1751.9	K	L	4.2	0.6	66.3	16.7
P0AAZ7	6837.3	S	U	T	B	CID	FT	3	58.3	VLTADESKS	949.5	R	-	1.9	0.0	30.4	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAZ7	6837.3	S	U	T	A	ETD	LIT	2	36.7	LDNLAFPLR	1058.6	K	D	2.3	0.2	0.0	0.0
P0AAZ7	6837.3	S	U	T	A	ETD	LIT	2	36.7	LWYNQEKQELICK	1751.9	K	L	1.7	0.0	29.0	16.8
P0AAZ7	6837.3	S	U	T	B	ETD	LIT	3	51.7	LDNLAFPLR	1058.6	K	D	0.0	0.0	24.6	18.3
P0AAZ7	6837.3	S	U	T	B	ETD	LIT	3	51.7	LWYNQEKQELICK	1751.9	K	L	2.4	0.1	32.6	16.8
P0AAZ7	6837.3	S	U	T	B	ETD	LIT	3	51.7	VLTADESKS	949.5	R	-	1.9	0.7	32.3	15.1
P0AAZ7	6837.3	S	U	T	C	ETD	LIT	3	58.3	LLEIIACPVCNGKLWYNQEK	2449.2	R	Q	3.8	0.0	23.7	18.7
P0AAZ7	6837.3	S	U	T	C	ETD	LIT	3	58.3	LWYNQEKQELICK	1751.9	K	L	2.7	0.1	20.2	16.4
P0AAZ7	6837.3	S	U	T	C	ETD	LIT	3	58.3	VLTADESKS	949.5	R	-	2.1	0.2	24.4	12.8
P0AAZ7	6837.3	S	U	T	B	ETD+CID	LIT	3	63.3	DGIPVLLETEAR	1312.7	R	V	0.0	0.0	26.2	12.8
P0AAZ7	6837.3	S	U	T	B	ETD+CID	LIT	3	63.3	LLEIIACPVCNGK	1487.8	R	L	0.0	0.0	68.5	17.4
P0AAZ7	6837.3	S	U	T	B	ETD+CID	LIT	3	63.3	LLEIIACPVCNGKLWYNQEKQELICK	3220.6	R	L	0.0	0.0	20.9	19.2
P0AAZ7	6837.3	S	U	T	A	ETD+CID	LIT	3	73.3	LDNLAFPLR	1058.6	K	D	3.3	0.5	41.7	18.3
P0AAZ7	6837.3	S	U	T	A	ETD+CID	LIT	3	73.3	LLEIIACPVCNGKLWYNQEKQELICK	3220.6	R	L	4.8	0.0	23.1	19.2
P0AAZ7	6837.3	S	U	T	A	ETD+CID	LIT	3	73.3	VLTADESKS	949.5	R	-	2.1	0.6	16.9	15.1
P0AAZ7	6837.3	S	U	T	B	ETD+CID	LIT	3	63.3	DGIPVLLETEAR	1312.7	R	V	2.4	0.7	26.2	12.8
P0AAZ7	6837.3	S	U	T	B	ETD+CID	LIT	3	63.3	LLEIIACPVCNGK	1487.8	R	L	4.2	0.8	68.5	17.4
P0AAZ7	6837.3	S	U	T	B	ETD+CID	LIT	3	63.3	LLEIIACPVCNGKLWYNQEKQELICK	3220.6	R	L	4.2	0.0	20.9	19.2
P0AAZ7	6837.3	S	U	T	C	ETD+CID	LIT	5	73.3	LDNLAFPLR	1058.6	K	D	3.4	0.5	49.5	18.3
P0AAZ7	6837.3	S	U	T	C	ETD+CID	LIT	5	73.3	LLEIIACPVCNGK	1486.8	R	L	3.0	0.5	24.9	17.2
P0AAZ7	6837.3	S	U	T	C	ETD+CID	LIT	5	73.3	LLEIIACPVCNGKLWYNQEK	2449.2	R	Q	3.8	0.6	26.8	18.6
P0AAZ7	6837.3	S	U	T	C	ETD+CID	LIT	5	73.3	LLEIIACPVCNGKLWYNQEKQELICK	3220.6	R	L	3.5	0.0	27.2	19.5
P0AAZ7	6837.3	S	U	T	C	ETD+CID	LIT	5	73.3	VLTADESKS	949.5	R	-	2.2	0.6	13.1	15.1
P0AAZ7	6837.3	S	U	T	B	HCD	FT	3	63.3	DGIPVLLETEAR	1312.7	R	V	0.0	0.0	26.2	12.8
P0AAZ7	6837.3	S	U	T	B	HCD	FT	3	63.3	LLEIIACPVCNGK	1487.8	R	L	0.0	0.0	68.5	17.4
P0AAZ7	6837.3	S	U	T	B	HCD	FT	3	63.3	LLEIIACPVCNGKLWYNQEKQELICK	3220.6	R	L	0.0	0.0	20.9	19.2
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	EEIYQR	837.4	R	I	1.5	0.7	25.8	14.3
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	EVSVHR	726.4	K	E	1.7	0.6	20.3	13.4
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	EVSVHREEIYQR	1544.8	K	I	2.9	0.6	33.9	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	IGVNAPK	698.4	R	E	2.4	0.5	37.1	12.8
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	IGVNAPKEVSVHR	1405.8	R	E	2.3	0.7	23.5	6.0
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	IQAEKSQQSSY	1268.6	R	-	3.8	0.7	48.8	11.8
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	RVGETLMIGDEVTVTVLGVK	2116.2	R	G	4.6	0.7	73.1	11.1
P69913	6837.6	G	U	T	A	CID	LIT	8	82.0	VGETLMIGDEVTVTVLGVK	1960.1	R	G	5.2	0.9	64.6	4.8
P69913	6837.6	G	T	T	A	CID	LIT	2	31.1	EVSVHREEIYQR	1544.8	K	I	2.2	0.7	19.5	12.0
P69913	6837.6	G	T	T	A	CID	LIT	2	31.1	IGVNAPK	698.4	R	E	2.4	0.6	36.3	12.8
P69913	6837.6	G	U	A	A	CID	LIT	2	27.9	EEIYQRIQAEKSQQSSY	2087.0	R	-	4.8	0.6	38.0	13.0
P69913	6837.6	G	U	A	A	CID	LIT	2	27.9	EIYQRIQAEKSQQSSY	1958.0	E	-	4.0	0.4	50.9	14.8
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	EEIYQR	837.4	R	I	1.6	0.7	28.6	14.3
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	EVSVHR	726.4	K	E	1.8	0.6	17.9	13.4
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	EVSVHREEIYQR	1544.8	K	I	2.4	0.6	43.3	12.6
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	IGVNAPK	698.4	R	E	2.4	0.6	40.9	12.8
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	IQAEKSQQSSY	1268.6	R	-	3.0	0.0	17.1	10.8
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	MLILTR	746.5	-	R	2.0	0.0	25.1	4.8
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	RVGETLMIGDEVTVTVLGVK	2116.2	R	G	4.3	0.6	29.4	10.4
P69913	6837.6	G	U	T	B	CID	LIT	8	91.8	VGETLMIGDEVTVTVLGVK	1960.1	R	G	5.4	0.0	77.2	4.8
P69913	6837.6	G	U	A	B	CID	LIT	3	75.4	DEVTVTVLGVKGNQVRIGVNAPKEVSVHR	3100.7	G	E	3.0	0.4	0.0	0.0
P69913	6837.6	G	U	A	B	CID	LIT	3	75.4	EEIYQRIQAEKSQQSSY	2087.0	R	-	2.5	0.7	0.0	0.0
P69913	6837.6	G	U	A	B	CID	LIT	3	75.4	EIYQRIQAEKSQQSSY	1958.0	E	-	4.0	0.6	0.0	0.0
P69913	6837.6	S	U	T	A	CID	LIT	5	72.1	IGVNAPK	698.4	R	E	2.2	0.4	32.5	13.8
P69913	6837.6	S	U	T	A	CID	LIT	5	72.1	IQAEKSQQSSY	1268.6	R	-	3.4	0.0	46.9	15.4
P69913	6837.6	S	U	T	A	CID	LIT	5	72.1	MLILTR	746.5	-	R	0.7	0.0	30.3	10.8
P69913	6837.6	S	U	T	A	CID	LIT	5	72.1	RVGETLMIGDEVTVTVLGVK	2132.2	R	G	4.7	0.6	50.5	14.5
P69913	6837.6	S	U	T	A	CID	LIT	5	72.1	VGETLMIGDEVTVTVLGVK	1960.1	R	G	5.0	0.6	71.9	13.0
P69913	6837.6	S	U	T	B	CID	LIT	3	42.6	MLILTR	746.5	-	R	1.5	0.0	29.0	10.8
P69913	6837.6	S	U	T	B	CID	LIT	3	42.6	RVGETLMIGDEVTVTVLGVK	2116.2	R	G	4.1	0.5	48.8	15.1
P69913	6837.6	S	U	T	B	CID	LIT	3	42.6	VGETLMIGDEVTVTVLGVK	1960.1	R	G	3.9	0.7	79.8	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69913	6837.6	S	U	T	C	CID	LIT	4	70.5	EVSVHREEIYQR	1544.8	K	I	2.2	0.3	10.2	16.4
P69913	6837.6	S	U	T	C	CID	LIT	4	70.5	IQAEKSQQSSY	1268.6	R	-	4.4	0.7	49.8	15.4
P69913	6837.6	S	U	T	C	CID	LIT	4	70.5	RVGETLMIGDEVTVTVLGVK	2116.2	R	G	3.8	0.3	45.0	15.1
P69913	6837.6	S	U	T	C	CID	LIT	4	70.5	VGETLMIGDEVTVTVLGVK	1960.1	R	G	5.1	0.7	89.3	13.2
P69913	6837.6	S	U	T	A	ETD	LIT	5	62.3	EVSVHR	726.4	K	E	1.4	0.3	14.6	13.2
P69913	6837.6	S	U	T	A	ETD	LIT	5	62.3	EVSVHREEIYQR	1544.8	K	I	0.0	0.0	21.2	16.4
P69913	6837.6	S	U	T	A	ETD	LIT	5	62.3	MLILTR	746.5	-	R	2.2	0.0	40.2	10.8
P69913	6837.6	S	U	T	A	ETD	LIT	5	62.3	RVGETLMIGDEVTVTVLGVK	2116.2	R	G	0.0	0.0	81.9	15.1
P69913	6837.6	S	U	T	A	ETD	LIT	5	62.3	VGETLMIGDEVTVTVLGVK	1960.1	R	G	4.1	0.7	0.0	0.0
P69913	6837.6	S	U	T	B	ETD	LIT	5	80.3	EVSVHREEIYQR	1544.8	K	I	6.0	0.5	55.9	17.6
P69913	6837.6	S	U	T	B	ETD	LIT	5	80.3	IQAEKSQQSSY	1268.6	R	-	2.5	0.0	21.9	14.8
P69913	6837.6	S	U	T	B	ETD	LIT	5	80.3	MLILTR	746.5	-	R	2.0	0.7	0.0	0.0
P69913	6837.6	S	U	T	B	ETD	LIT	5	80.3	RVGETLMIGDEVTVTVLGVK	2116.2	R	G	4.5	0.6	80.8	15.1
P69913	6837.6	S	U	T	B	ETD	LIT	5	80.3	VGETLMIGDEVTVTVLGVK	1960.1	R	G	3.6	0.6	46.8	12.3
P69913	6837.6	S	U	T	C	ETD	LIT	5	80.3	EVSVHREEIYQR	1544.8	K	I	6.2	0.6	53.0	16.2
P69913	6837.6	S	U	T	C	ETD	LIT	5	80.3	IQAEKSQQSSY	1268.6	R	-	3.0	0.0	29.2	14.8
P69913	6837.6	S	U	T	C	ETD	LIT	5	80.3	MLILTR	746.5	-	R	2.3	0.8	0.0	0.0
P69913	6837.6	S	U	T	C	ETD	LIT	5	80.3	RVGETLMIGDEVTVTVLGVK	2116.2	R	G	6.1	0.6	93.7	15.1
P69913	6837.6	S	U	T	C	ETD	LIT	5	80.3	VGETLMIGDEVTVTVLGVK	1960.1	R	G	3.0	0.7	0.0	0.0
P69913	6837.6	S	U	T	A	ETD	FT	2	21.3	IGVNAPK	698.4	R	E	0.0	0.0	25.9	13.8
P69913	6837.6	S	U	T	A	ETD	FT	2	21.3	MLILTR	746.5	-	R	0.0	0.0	32.4	10.8
P69913	6837.6	S	U	T	B	ETD+CID	LIT	2	50.8	IQAEKSQQSSY	1268.6	R	-	0.0	0.0	46.6	15.3
P69913	6837.6	S	U	T	B	ETD+CID	LIT	2	50.8	RVGETLMIGDEVTVTVLGVK	2132.2	R	G	0.0	0.0	49.4	14.8
P69913	6837.6	S	U	T	B	ETD+CID	LIT	2	50.8	VGETLMIGDEVTVTVLGVK	1960.1	R	G	0.0	0.0	84.1	12.3
P69913	6837.6	S	U	T	A	ETD+CID	LIT	2	50.8	IQAEKSQQSSY	1268.6	R	-	4.2	0.6	61.2	15.3
P69913	6837.6	S	U	T	A	ETD+CID	LIT	2	50.8	RVGETLMIGDEVTVTVLGVK	2132.2	R	G	5.8	0.6	48.5	14.8
P69913	6837.6	S	U	T	A	ETD+CID	LIT	2	50.8	VGETLMIGDEVTVTVLGVK	1960.1	R	G	4.0	0.5	50.3	12.3
P69913	6837.6	S	U	T	B	ETD+CID	LIT	2	50.8	IQAEKSQQSSY	1268.6	R	-	4.3	0.0	46.6	15.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69913	6837.6	S	U	T	B	ETD+CID	LIT	2	50.8	RVGETLMIGDEVTVTVLGVK	2132.2	R	G	5.4	0.6	0.0	0.0
P69913	6837.6	S	U	T	B	ETD+CID	LIT	2	50.8	VGETLMIGDEVTVTVLGVK	1960.1	R	G	5.6	0.6	0.0	0.0
P69913	6837.6	S	U	T	C	ETD+CID	LIT	5	91.8	EVSVHR	726.4	K	E	1.7	0.7	21.0	14.0
P69913	6837.6	S	U	T	C	ETD+CID	LIT	5	91.8	IGVNAPKEVSVHREEIYQR	2224.2	R	I	1.5	0.7	17.7	17.4
P69913	6837.6	S	U	T	C	ETD+CID	LIT	5	91.8	IQAEKSQQSSY	1268.6	R	-	3.5	-0.1	50.6	15.4
P69913	6837.6	S	U	T	C	ETD+CID	LIT	5	91.8	KLLEQEMVNFLFEGK	1825.9	-	-	3.5	0.7	56.9	16.9
P69913	6837.6	S	U	T	C	ETD+CID	LIT	5	91.8	MLILTR	746.5	-	R	0.0	0.0	23.5	10.8
P69913	6837.6	S	U	T	C	ETD+CID	LIT	5	91.8	RVGETLMIGDEVTVTVLGVK	2132.2	R	G	5.3	0.6	38.2	14.8
P69913	6837.6	S	U	T	C	ETD+CID	LIT	5	91.8	VGETLMIGDEVTVTVLGVK	1960.1	R	G	5.5	0.6	81.9	12.8
P69913	6837.6	S	U	T	B	HCD	FT	2	50.8	IQAEKSQQSSY	1268.6	R	-	0.0	0.0	46.6	15.3
P69913	6837.6	S	U	T	B	HCD	FT	2	50.8	RVGETLMIGDEVTVTVLGVK	2132.2	R	G	0.0	0.0	49.4	14.8
P69913	6837.6	S	U	T	B	HCD	FT	2	50.8	VGETLMIGDEVTVTVLGVK	1960.1	R	G	0.0	0.0	84.1	12.3
P0AEG8	6927.7	G	U	T	A	CID	LIT	2	22.6	VNDRVTVK	930.5	K	T	2.3	0.6	16.2	14.3
P0AEG8	6927.7	G	U	T	A	CID	LIT	2	22.6	VTVKTDGGPR	1029.6	R	R	2.7	0.0	45.2	16.3
P0AEG8	6927.7	G	U	A	A	CID	LIT	4	56.5	DGIFVEKAE	1007.5	Q	-	3.2	0.8	46.2	17.1
P0AEG8	6927.7	G	U	A	A	CID	LIT	4	56.5	DRVTVKT	818.5	N	D	1.6	0.4	13.7	10.0
P0AEG8	6927.7	G	U	A	A	CID	LIT	4	56.5	DYPLGIWFFNEAGHQ	1793.8	E	D	3.7	0.8	57.7	11.8
P0AEG8	6927.7	G	U	A	A	CID	LIT	4	56.5	MKVNDRVTVKT	1290.7	-	D	1.9	0.2	28.1	14.9
P0AEG8	6927.7	G	U	T	B	CID	LIT	2	16.1	MKVNDR	762.4	-	V	1.9	0.2	25.4	12.8
P0AEG8	6927.7	G	U	T	B	CID	LIT	2	16.1	VNDRVTVK	930.5	K	T	1.9	0.4	11.5	15.1
P0AEG8	6927.7	G	U	A	B	CID	LIT	2	38.7	DGIFVEKAE	1007.5	Q	-	3.2	0.8	45.2	17.1
P0AEG8	6927.7	G	U	A	B	CID	LIT	2	38.7	DYPLGIWFFNEAGHQ	1793.8	E	D	4.0	0.0	50.3	11.8
P0A8K5	7196.4	G	U	T	A	CID	LIT	4	89.4	AAYAAANLLVSDYVNE	1683.8	K	-	3.3	0.5	33.8	13.0
P0A8K5	7196.4	G	U	T	A	CID	LIT	4	89.4	VLNEMAADDALSEAVR	1719.8	K	E	3.0	0.8	52.8	12.0
P0A8K5	7196.4	G	U	T	A	CID	LIT	4	89.4	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	5.1	0.5	60.1	13.6
P0A8K5	7196.4	G	U	T	A	CID	LIT	4	89.4	YCELIR	853.4	K	K	1.9	0.8	12.6	12.3
P0A8K5	7196.4	G	U	T	B	CID	LIT	5	92.4	AAYAAANLLVSDYVNE	1683.8	K	-	3.9	0.7	66.8	13.4
P0A8K5	7196.4	G	U	T	B	CID	LIT	5	92.4	EKAAYAAANLLVSDYVNE	1941.0	R	-	3.8	0.5	24.8	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8K5	7196.4	G	U	T	B	CID	LIT	5	92.4	VLNEMAADDALSEAVR	1703.8	K	E	4.6	0.8	75.8	12.3
P0A8K5	7196.4	G	U	T	B	CID	LIT	5	92.4	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	4.6	0.8	55.8	13.6
P0A8K5	7196.4	G	U	T	B	CID	LIT	5	92.4	YCELIR	853.4	K	K	1.9	0.8	20.7	12.0
P0A8K5	7196.4	G	T	A	B	CID	LIT	2	33.3	DDALSEAVR	975.5	A	E	2.1	0.0	27.8	17.6
P0A8K5	7196.4	G	T	A	B	CID	LIT	2	33.3	EKAAYAAANLLVS	1320.7	R	D	1.8	0.4	0.0	0.0
P0A8K5	7196.4	G	U	A	B	CID	LIT	2	33.3	DDALSEAVR	975.5	A	E	3.1	0.4	29.0	16.5
P0A8K5	7196.4	G	U	A	B	CID	LIT	2	33.3	EKAAYAAANLLVS	1320.7	R	D	2.7	0.7	21.9	13.6
P0A8K5	7196.4	S	U	T	A	CID	LIT	4	83.3	AAYAAANLLVSDYVNE	1683.8	K	-	2.5	0.6	2.6	17.9
P0A8K5	7196.4	S	U	T	A	CID	LIT	4	83.3	VLNEMAADDALSEAVR	1703.8	K	E	3.6	0.2	37.9	16.8
P0A8K5	7196.4	S	U	T	A	CID	LIT	4	83.3	VLNEMAADDALSEAVREK	1961.0	K	A	2.8	0.3	0.0	0.0
P0A8K5	7196.4	S	U	T	A	CID	LIT	4	83.3	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	5.8	0.0	91.5	18.8
P0A8K5	7196.4	S	U	T	B	CID	LIT	3	59.1	VLNEMAADDALSEAVR	1703.8	K	E	3.4	0.2	22.3	17.2
P0A8K5	7196.4	S	U	T	B	CID	LIT	3	59.1	VLNEMAADDALSEAVREK	1961.0	K	A	5.0	0.4	89.8	18.3
P0A8K5	7196.4	S	U	T	B	CID	LIT	3	59.1	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	6.9	0.8	95.9	18.9
P0A8K5	7196.4	S	U	T	C	CID	LIT	4	83.3	AAYAAANLLVSDYVNE	1683.8	K	-	2.1	0.5	0.0	0.0
P0A8K5	7196.4	S	U	T	C	CID	LIT	4	83.3	VLNEMAADDALSEAVR	1703.8	K	E	4.5	0.6	66.1	17.4
P0A8K5	7196.4	S	U	T	C	CID	LIT	4	83.3	VLNEMAADDALSEAVREK	1961.0	K	A	5.0	0.6	60.8	18.1
P0A8K5	7196.4	S	U	T	C	CID	LIT	4	83.3	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	4.8	0.0	77.0	18.5
P0A8K5	7196.4	S	U	T	B	ETD+CID	LIT	3	59.1	VLNEMAADDALSEAVR	1703.8	K	E	0.0	0.0	82.3	17.4
P0A8K5	7196.4	S	U	T	B	ETD+CID	LIT	3	59.1	VLNEMAADDALSEAVREK	1961.0	K	A	0.0	0.0	97.7	18.1
P0A8K5	7196.4	S	U	T	B	ETD+CID	LIT	3	59.1	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	0.0	0.0	75.4	18.5
P0A8K5	7196.4	S	U	T	A	ETD+CID	LIT	4	83.3	AAYAAANLLVSDYVNE	1683.8	K	-	2.2	0.3	0.0	0.0
P0A8K5	7196.4	S	U	T	A	ETD+CID	LIT	4	83.3	VLNEMAADDALSEAVR	1703.8	K	E	3.0	0.3	39.5	17.2
P0A8K5	7196.4	S	U	T	A	ETD+CID	LIT	4	83.3	VLNEMAADDALSEAVREK	1961.0	K	A	4.4	0.4	36.3	18.4
P0A8K5	7196.4	S	U	T	A	ETD+CID	LIT	4	83.3	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	0.0	0.0	43.6	18.6
P0A8K5	7196.4	S	U	T	B	ETD+CID	LIT	4	83.3	AAYAAANLLVSDYVNE	1683.8	K	-	2.2	0.6	0.0	0.0
P0A8K5	7196.4	S	U	T	B	ETD+CID	LIT	4	83.3	VLNEMAADDALSEAVR	1703.8	K	E	4.6	0.5	0.0	0.0
P0A8K5	7196.4	S	U	T	B	ETD+CID	LIT	4	83.3	VLNEMAADDALSEAVREK	1961.0	K	A	4.7	0.6	97.7	18.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8K5	7196.4	S	U	T	B	ETD+CID	LIT	4	83.3	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	5.4	0.8	75.4	18.5
P0A8K5	7196.4	S	U	T	C	ETD+CID	LIT	3	51.5	AAYAAANLLVSDYVNE	1683.8	K	-	2.9	0.7	11.6	17.9
P0A8K5	7196.4	S	U	T	C	ETD+CID	LIT	3	51.5	VLNEMAADDALSEAVR	1703.8	K	E	4.9	0.5	68.7	17.5
P0A8K5	7196.4	S	U	T	C	ETD+CID	LIT	3	51.5	VLNEMAADDALSEAVREK	1961.0	K	A	4.8	0.5	48.0	18.3
P0A8K5	7196.4	S	U	T	B	HCD	FT	3	59.1	VLNEMAADDALSEAVR	1703.8	K	E	0.0	0.0	82.3	17.4
P0A8K5	7196.4	S	U	T	B	HCD	FT	3	59.1	VLNEMAADDALSEAVREK	1961.0	K	A	0.0	0.0	97.7	18.1
P0A8K5	7196.4	S	U	T	B	HCD	FT	3	59.1	YAEIASGDLGYVPDALGCVLK	2211.1	R	V	0.0	0.0	75.4	18.5
P0A7M6	7255.6	G	U	T	A	CID	LIT	5	66.7	EKSVEELNTELLNLLR	1900.0	R	E	4.0	0.5	90.3	11.5
P0A7M6	7255.6	G	U	T	A	CID	LIT	5	66.7	MQAASGQLQQSHLLK	1639.9	R	Q	5.0	0.7	96.3	12.8
P0A7M6	7255.6	G	U	T	A	CID	LIT	5	66.7	SVEELNTELLNLLR	1642.9	K	E	4.3	0.6	101.0	12.0
P0A7M6	7255.6	G	U	T	A	CID	LIT	5	66.7	TLLNEKAGA	916.5	K	-	2.3	0.5	10.7	14.6
P0A7M6	7255.6	G	U	T	A	CID	LIT	5	66.7	VKTLLNEK	944.6	R	A	2.7	0.7	43.6	11.1
P0A7M6	7255.6	G	T	T	A	CID	LIT	4	61.9	EKSVEELNTELLNLLR	1900.0	R	E	3.2	0.4	6.0	11.8
P0A7M6	7255.6	G	T	T	A	CID	LIT	4	61.9	MQAASGQLQQSHLLK	1639.9	R	Q	5.0	0.7	94.0	12.8
P0A7M6	7255.6	G	T	T	A	CID	LIT	4	61.9	SVEELNTELLNLLR	1642.9	K	E	5.2	0.6	70.3	12.0
P0A7M6	7255.6	G	T	T	A	CID	LIT	4	61.9	VKTLLNEK	944.6	R	A	2.8	0.8	47.1	11.1
P0A7M6	7255.6	G	T	T	B	CID	LIT	2	46.0	MQAASGQLQQSHLLK	1639.9	R	Q	3.2	0.8	28.2	12.6
P0A7M6	7255.6	G	T	T	B	CID	LIT	2	46.0	SVEELNTELLNLLR	1642.9	K	E	2.3	0.2	33.2	13.2
P0A7M6	7255.6	G	U	T	B	CID	LIT	5	69.8	EKSVEELNTELLNLLR	1900.0	R	E	2.8	0.0	20.1	11.5
P0A7M6	7255.6	G	U	T	B	CID	LIT	5	69.8	MQAASGQLQQSHLLK	1639.9	R	Q	5.0	0.6	92.3	12.8
P0A7M6	7255.6	G	U	T	B	CID	LIT	5	69.8	RDVAR	616.4	R	V	2.0	0.2	16.1	13.2
P0A7M6	7255.6	G	U	T	B	CID	LIT	5	69.8	SVEELNTELLNLLR	1642.9	K	E	4.8	0.5	87.6	12.8
P0A7M6	7255.6	G	U	T	B	CID	LIT	5	69.8	VKTLLNEK	944.6	R	A	1.7	0.6	17.2	11.1
P0A7M6	7255.6	S	U	T	A	CID	LIT	2	34.9	EKSVEELNTELLNLLR	1900.0	R	E	4.2	0.5	107.0	16.8
P0A7M6	7255.6	S	U	T	A	CID	LIT	2	34.9	SVEELNTELLNLLREQFNLR	2430.3	K	M	2.2	0.0	26.2	16.0
P0A7M6	7255.6	S	U	T	B	CID	LIT	2	49.2	EKSVEELNTELLNLLR	1900.0	R	E	3.2	0.6	46.6	16.8
P0A7M6	7255.6	S	U	T	B	CID	LIT	2	49.2	MQAASGQLQQSHLLK	1640.8	R	Q	4.8	0.5	79.5	17.0
P0A7M6	7255.6	S	U	T	C	CID	LIT	2	46.0	MQAASGQLQQSHLLK	1639.9	R	Q	5.3	0.6	84.5	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7M6	7255.6	S	U	T	C	CID	LIT	2	46.0	SVEELNTELLNLLR	1642.9	K	E	2.0	0.2	0.0	0.0
P0A7M6	7255.6	S	U	T	A	ETD	LIT	4	58.7	EKSVEELNTELLNLLR	1900.0	R	E	2.7	0.4	37.3	16.3
P0A7M6	7255.6	S	U	T	A	ETD	LIT	4	58.7	EKSVEELNTELLNLLREQFNLR	2687.4	R	M	4.2	0.0	34.9	15.3
P0A7M6	7255.6	S	U	T	A	ETD	LIT	4	58.7	MQAASGQLQQSHLLK	1639.9	R	Q	6.1	0.7	69.1	17.9
P0A7M6	7255.6	S	U	T	A	ETD	LIT	4	58.7	SVEELNTELLNLLR	1642.9	K	E	1.9	0.6	0.0	0.0
P0A7M6	7255.6	S	U	T	B	ETD	LIT	3	58.7	EKSVEELNTELLNLLR	1900.0	R	E	6.4	0.0	59.8	16.9
P0A7M6	7255.6	S	U	T	B	ETD	LIT	3	58.7	EKSVEELNTELLNLLREQFNLR	2687.4	R	M	2.9	0.4	27.6	15.3
P0A7M6	7255.6	S	U	T	B	ETD	LIT	3	58.7	MQAASGQLQQSHLLK	1639.9	R	Q	6.6	0.7	64.5	17.2
P0A7M6	7255.6	S	U	T	C	ETD	LIT	3	58.7	EKSVEELNTELLNLLREQFNLR	2687.4	R	M	2.4	0.0	36.8	15.7
P0A7M6	7255.6	S	U	T	C	ETD	LIT	3	58.7	MQAASGQLQQSHLLK	1639.9	R	Q	2.6	0.7	50.8	17.6
P0A7M6	7255.6	S	U	T	C	ETD	LIT	3	58.7	SVEELNTELLNLLR	1642.9	K	E	0.0	0.0	28.2	17.4
P0A7M6	7255.6	S	U	T	A	ETD+CID	LIT	2	34.9	EKSVEELNTELLNLLR	1900.0	R	E	0.0	0.0	46.1	16.7
P0A7M6	7255.6	S	U	T	A	ETD+CID	LIT	2	34.9	EKSVEELNTELLNLLREQFNLR	2687.4	R	M	2.0	0.4	25.0	15.6
P64463	7258.5	G	U	T	A	CID	LIT	6	70.1	GKTVVVEGCEEK	1334.7	R	L	4.3	0.7	58.9	10.4
P64463	7258.5	G	U	T	A	CID	LIT	6	70.1	ILSIDTEGLTAEQIR	1658.9	K	R	4.5	0.6	91.3	12.3
P64463	7258.5	G	U	T	A	CID	LIT	6	70.1	ILSIDTEGLTAEQIRR	1815.0	K	G	1.4	0.6	13.6	11.1
P64463	7258.5	G	U	T	A	CID	LIT	6	70.1	LAPLDLIR	910.6	K	L	1.5	0.0	48.7	7.0
P64463	7258.5	G	U	T	A	CID	LIT	6	70.1	TVVVEGCEEK	1149.5	K	L	3.0	0.7	39.4	11.5
P64463	7258.5	G	U	T	A	CID	LIT	6	70.1	VMVSGTGHTGK	1073.5	R	I	3.3	0.5	55.9	13.6
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	GKTVVVEGCEEK	1334.7	R	L	4.0	0.8	65.4	8.5
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	ILSIDTEGLTAEQIR	1658.9	K	R	4.9	0.7	101.0	12.6
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	ILSIDTEGLTAEQIRR	1815.0	K	G	2.7	0.7	20.9	11.1
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	LAPLDLIR	910.6	K	L	2.1	0.0	24.9	7.0
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	MTTYDRNR	1056.5	-	N	1.8	0.2	9.4	9.5
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	NAITTGSR	819.4	R	V	1.7	0.7	24.4	11.5
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	TVVVEGCEEK	1149.5	K	L	2.6	0.8	45.7	11.5
P64463	7258.5	G	T	T	A	CID	LIT	8	94.0	VMVSGTGHTGK	1073.5	R	I	3.2	0.6	60.0	10.4
P64463	7258.5	G	U	T	B	CID	LIT	5	68.7	GKTVVVEGCEEK	1334.7	R	L	4.1	0.0	53.0	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64463	7258.5	G	U	T	B	CID	LIT	5	68.7	ILSIDTEGLTAEQIR	1658.9	K	R	3.2	0.7	64.2	12.3
P64463	7258.5	G	U	T	B	CID	LIT	5	68.7	NAITTGSR	819.4	R	V	1.8	0.7	31.8	11.5
P64463	7258.5	G	U	T	B	CID	LIT	5	68.7	TVVVEGCEEK	1149.5	K	L	3.0	0.0	35.7	11.5
P64463	7258.5	G	U	T	B	CID	LIT	5	68.7	VMVSGTGHTGK	1089.5	R	I	1.7	0.7	0.0	0.0
P64463	7258.5	S	U	T	A	CID	LIT	6	82.1	GKTVVVEGCEEK	1334.7	R	L	3.0	0.7	27.8	16.2
P64463	7258.5	S	U	T	A	CID	LIT	6	82.1	ILSIDTEGLTAEQIR	1658.9	K	R	4.9	0.7	87.6	17.8
P64463	7258.5	S	U	T	A	CID	LIT	6	82.1	ILSIDTEGLTAEQIRR	1815.0	K	G	2.3	0.6	3.9	15.1
P64463	7258.5	S	U	T	A	CID	LIT	6	82.1	NAITTGSR	819.4	R	V	1.7	0.7	17.8	14.1
P64463	7258.5	S	U	T	A	CID	LIT	6	82.1	TVVVEGCEEKLAPLDLIR	2041.1	K	L	4.5	0.5	36.6	16.5
P64463	7258.5	S	U	T	A	CID	LIT	6	82.1	VMVSGTGHTGK	1073.5	R	I	2.3	0.8	19.4	14.8
P64463	7258.5	S	U	T	B	CID	LIT	3	56.7	GKTVVVEGCEEK	1334.7	R	L	3.9	0.0	65.8	15.8
P64463	7258.5	S	U	T	B	CID	LIT	3	56.7	ILSIDTEGLTAEQIR	1658.9	K	R	4.2	0.6	62.8	17.8
P64463	7258.5	S	U	T	B	CID	LIT	3	56.7	VMVSGTGHTGK	1073.5	R	I	2.0	0.3	22.1	14.8
P64463	7258.5	S	U	T	C	CID	LIT	5	70.1	GKTVVVEGCEEK	1334.7	R	L	3.8	0.0	65.7	15.9
P64463	7258.5	S	U	T	C	CID	LIT	5	70.1	ILSIDTEGLTAEQIR	1658.9	K	R	4.2	0.6	69.6	17.8
P64463	7258.5	S	U	T	C	CID	LIT	5	70.1	ILSIDTEGLTAEQIRR	1815.0	K	G	1.7	0.1	29.6	15.1
P64463	7258.5	S	U	T	C	CID	LIT	5	70.1	NAITTGSR	819.4	R	V	1.9	0.7	6.3	14.0
P64463	7258.5	S	U	T	C	CID	LIT	5	70.1	VMVSGTGHTGK	1073.5	R	I	2.8	0.8	30.8	14.8
P64463	7258.5	S	U	T	A	ETD	LIT	6	70.1	GKTVVVEGCEEK	1334.7	R	L	2.2	0.6	16.6	16.1
P64463	7258.5	S	U	T	A	ETD	LIT	6	70.1	ILSIDTEGLTAEQIR	1658.9	K	R	2.8	0.4	79.1	17.6
P64463	7258.5	S	U	T	A	ETD	LIT	6	70.1	ILSIDTEGLTAEQIRR	1815.0	K	G	4.2	0.5	68.5	15.1
P64463	7258.5	S	U	T	A	ETD	LIT	6	70.1	NAITTGSR	819.4	R	V	2.1	0.5	41.0	14.1
P64463	7258.5	S	U	T	A	ETD	LIT	6	70.1	TVVVEGCEEK	1149.5	K	L	1.7	0.4	0.0	0.0
P64463	7258.5	S	U	T	A	ETD	LIT	6	70.1	VMVSGTGHTGK	1073.5	R	I	4.5	0.7	61.8	14.8
P64463	7258.5	S	U	T	B	ETD	LIT	5	70.1	GKTVVVEGCEEK	1334.7	R	L	4.6	0.4	53.6	16.2
P64463	7258.5	S	U	T	B	ETD	LIT	5	70.1	ILSIDTEGLTAEQIR	1658.9	K	R	2.4	0.4	69.2	17.9
P64463	7258.5	S	U	T	B	ETD	LIT	5	70.1	ILSIDTEGLTAEQIRR	1815.0	K	G	1.7	0.0	53.6	15.8
P64463	7258.5	S	U	T	B	ETD	LIT	5	70.1	NAITTGSR	819.4	R	V	1.6	0.0	34.3	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64463	7258.5	S	U	T	B	ETD	LIT	5	70.1	VMVSGTGHTGK	1073.5	R	I	2.0	0.6	41.8	14.8
P64463	7258.5	S	U	T	C	ETD	LIT	4	52.2	ILSIDTEGLTAEQIR	1658.9	K	R	2.5	0.4	54.2	18.1
P64463	7258.5	S	U	T	C	ETD	LIT	4	52.2	ILSIDTEGLTAEQIRR	1815.0	K	G	2.6	0.3	48.2	15.3
P64463	7258.5	S	U	T	C	ETD	LIT	4	52.2	NAITTGSR	819.4	R	V	1.5	0.0	23.5	14.0
P64463	7258.5	S	U	T	C	ETD	LIT	4	52.2	VMVSGTGHTGK	1073.5	R	I	3.9	0.8	51.8	14.8
P64463	7258.5	S	U	T	A	ETD	FT	2	34.3	GKTVVVEGCEEK	1334.7	R	L	1.6	0.0	29.4	15.8
P64463	7258.5	S	U	T	A	ETD	FT	2	34.3	VMVSGTGHTGK	1073.5	R	I	2.9	0.0	66.3	14.8
P64463	7258.5	S	U	T	B	ETD+CID	LIT	2	40.3	GKTVVVEGCEEK	1334.7	R	L	0.0	0.0	66.1	16.2
P64463	7258.5	S	U	T	B	ETD+CID	LIT	2	40.3	ILSIDTEGLTAEQIR	1658.9	K	R	0.0	0.0	77.3	17.6
P64463	7258.5	S	U	T	A	ETD+CID	LIT	5	70.1	GKTVVVEGCEEK	1334.7	R	L	3.9	0.8	65.8	16.4
P64463	7258.5	S	U	T	A	ETD+CID	LIT	5	70.1	ILSIDTEGLTAEQIR	1658.9	K	R	5.0	0.7	83.1	17.3
P64463	7258.5	S	U	T	A	ETD+CID	LIT	5	70.1	ILSIDTEGLTAEQIRR	1815.0	K	G	2.9	0.4	10.8	15.6
P64463	7258.5	S	U	T	A	ETD+CID	LIT	5	70.1	NAITTGSR	819.4	R	V	1.5	0.4	11.9	14.1
P64463	7258.5	S	U	T	A	ETD+CID	LIT	5	70.1	VMVSGTGHTGK	1073.5	R	I	3.7	0.7	39.0	14.8
P64463	7258.5	S	U	T	B	ETD+CID	LIT	4	58.2	GKTVVVEGCEEK	1334.7	R	L	3.6	0.8	66.1	16.2
P64463	7258.5	S	U	T	B	ETD+CID	LIT	4	58.2	ILSIDTEGLTAEQIR	1658.9	K	R	4.3	0.6	77.3	17.6
P64463	7258.5	S	U	T	B	ETD+CID	LIT	4	58.2	ILSIDTEGLTAEQIRR	1815.0	K	G	2.1	0.6	7.3	15.3
P64463	7258.5	S	U	T	B	ETD+CID	LIT	4	58.2	VMVSGTGHTGK	1073.5	R	I	2.2	0.3	10.3	14.8
P64463	7258.5	S	U	T	C	ETD+CID	LIT	4	58.2	GKTVVVEGCEEK	1334.7	R	L	3.7	0.7	65.4	15.8
P64463	7258.5	S	U	T	C	ETD+CID	LIT	4	58.2	ILSIDTEGLTAEQIR	1658.9	K	R	4.7	0.6	63.0	17.8
P64463	7258.5	S	U	T	C	ETD+CID	LIT	4	58.2	ILSIDTEGLTAEQIRR	1815.0	K	G	5.2	0.4	77.1	15.6
P64463	7258.5	S	U	T	C	ETD+CID	LIT	4	58.2	VMVSGTGHTGK	1073.5	R	I	3.7	0.6	56.1	14.8
P64463	7258.5	S	U	T	B	HCD	FT	2	40.3	GKTVVVEGCEEK	1334.7	R	L	0.0	0.0	66.1	16.2
P64463	7258.5	S	U	T	B	HCD	FT	2	40.3	ILSIDTEGLTAEQIR	1658.9	K	R	0.0	0.0	77.3	17.6
P0AAN5	7263.4	G	T	T	A	CID	LIT	4	71.4	ADHPKPDSLISEHPTAQEAMDAK	2488.2	R	K	4.9	0.8	36.8	10.4
P0AAN5	7263.4	G	T	T	A	CID	LIT	4	71.4	ADHPKPDSLISEHPTAQEAMDAKK	2616.3	R	R	6.2	0.0	41.3	11.8
P0AAN5	7263.4	G	T	T	A	CID	LIT	4	71.4	GKPGQTVTWYQLR	1533.8	K	A	4.4	0.9	34.6	12.8
P0AAN5	7263.4	G	T	T	A	CID	LIT	4	71.4	PTKPPYPR	955.5	M	E	0.0	0.0	29.4	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7Q1	7271.4	G	T	T	A	CID	LIT	4	38.5	AMVSKGDLGLVIACLPYA	1894.0	K	-	4.1	0.0	32.7	11.8
P0A7Q1	7271.4	G	T	T	A	CID	LIT	4	38.5	GDLGLVIACLPYA	1361.7	K	-	3.5	0.0	38.2	15.2
P0A7Q1	7271.4	G	T	T	A	CID	LIT	4	38.5	HANLR	610.3	K	H	1.5	0.6	10.9	12.0
P0A7Q1	7271.4	G	T	T	A	CID	LIT	4	38.5	HKHANLR	875.5	K	H	1.8	0.6	14.0	13.6
P0A7Q1	7271.4	G	U	T	B	CID	LIT	2	27.7	GDLGLVIACLPYA	1361.7	K	-	2.2	0.7	23.5	13.0
P0A7Q1	7271.4	G	U	T	B	CID	LIT	2	27.7	HILTK	611.4	R	K	1.8	0.6	22.6	8.5
P0AAS7	7371.1	G	U	T	A	CID	LIT	7	92.9	ATFSLGKHPHVELCDLLK	2065.1	M	L	0.0	0.0	52.9	11.5
P0AAS7	7371.1	G	U	T	A	CID	LIT	7	92.9	HPHVELCDLLK	1360.7	K	L	4.5	0.6	39.5	13.8
P0AAS7	7371.1	G	U	T	A	CID	LIT	7	92.9	IAIAEGQVK	928.5	K	V	2.8	0.7	27.8	13.2
P0AAS7	7371.1	G	U	T	A	CID	LIT	7	92.9	IAIAEGQVKVDGAVETR	1756.0	K	K	4.8	0.8	84.6	11.5
P0AAS7	7371.1	G	U	T	A	CID	LIT	7	92.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	3.1	0.0	23.9	12.3
P0AAS7	7371.1	G	U	T	A	CID	LIT	7	92.9	LEGWSESGAQAK	1262.6	K	I	4.2	0.8	56.2	11.8
P0AAS7	7371.1	G	U	T	A	CID	LIT	7	92.9	VDGAVETR	846.4	K	K	2.3	0.6	28.2	15.3
P0AAS7	7371.1	G	T	T	A	CID	LIT	2	30.0	IAIAEGQVK	928.5	K	V	2.6	0.6	29.4	13.4
P0AAS7	7371.1	G	T	T	A	CID	LIT	2	30.0	LEGWSESGAQAK	1262.6	K	I	3.1	0.6	32.1	12.3
P0AAS7	7371.1	G	U	T	B	CID	LIT	7	94.3	ATFSLGK	723.4	M	H	0.0	0.0	29.1	13.8
P0AAS7	7371.1	G	U	T	B	CID	LIT	7	94.3	HPHVELCDLLK	1360.7	K	L	4.0	0.7	53.4	13.8
P0AAS7	7371.1	G	U	T	B	CID	LIT	7	94.3	IAIAEGQVK	928.5	K	V	3.1	0.8	36.5	13.4
P0AAS7	7371.1	G	U	T	B	CID	LIT	7	94.3	IVAGQTVSFAGHSVQVVA	1770.0	K	-	3.1	0.0	32.4	11.8
P0AAS7	7371.1	G	U	T	B	CID	LIT	7	94.3	LEGWSESGAQAK	1262.6	K	I	4.1	0.8	59.0	12.0
P0AAS7	7371.1	G	U	T	B	CID	LIT	7	94.3	VDGAVETR	846.4	K	K	2.9	0.6	52.8	15.3
P0AAS7	7371.1	G	U	T	B	CID	LIT	7	94.3	VDGAVETRK	974.5	K	R	2.2	0.7	33.1	14.1
P0AAS7	7371.1	S	U	T	A	CID	LIT	4	82.9	HPHVELCDLLKLEGWSESGAQAK	2604.3	K	I	3.0	0.4	21.1	18.7
P0AAS7	7371.1	S	U	T	A	CID	LIT	4	82.9	IAIAEGQVKVDGAVETR	1756.0	K	K	1.9	0.7	13.1	15.7
P0AAS7	7371.1	S	U	T	A	CID	LIT	4	82.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	3.2	0.6	28.7	17.1
P0AAS7	7371.1	S	U	T	A	CID	LIT	4	82.9	VDGAVETR	846.4	K	K	2.3	0.5	27.6	18.5
P0AAS7	7371.1	S	U	T	B	CID	LIT	6	92.9	ATFSLGKHPHVELCDLLK	2065.1	M	L	0.0	0.0	21.5	17.8
P0AAS7	7371.1	S	U	T	B	CID	LIT	6	92.9	HPHVELCDLLK	1360.7	K	L	3.6	0.5	20.2	18.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAS7	7371.1	S	U	T	B	CID	LIT	6	92.9	HPHVELCDLLKLEGWSESGAQAK	2604.3	K	I	3.5	0.8	26.7	18.5
P0AAS7	7371.1	S	U	T	B	CID	LIT	6	92.9	IAIAEGQVKVDGAVETR	1756.0	K	K	2.6	0.5	24.7	16.1
P0AAS7	7371.1	S	U	T	B	CID	LIT	6	92.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	2.9	0.4	12.8	17.1
P0AAS7	7371.1	S	U	T	B	CID	LIT	6	92.9	VDGAVETR	846.4	K	K	2.4	0.6	39.2	18.9
P0AAS7	7371.1	S	U	T	C	CID	LIT	6	82.9	HPHVELCDLLK	1360.7	K	L	3.9	0.7	50.8	17.3
P0AAS7	7371.1	S	U	T	C	CID	LIT	6	82.9	HPHVELCDLLKLEGWSESGAQAK	2604.3	K	I	3.6	0.0	19.5	18.3
P0AAS7	7371.1	S	U	T	C	CID	LIT	6	82.9	IAIAEGQVKVDGAVETR	1756.0	K	K	2.7	0.4	0.0	0.0
P0AAS7	7371.1	S	U	T	C	CID	LIT	6	82.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	2.8	0.4	9.7	17.1
P0AAS7	7371.1	S	U	T	C	CID	LIT	6	82.9	LEGWSESGAQAK	1262.6	K	I	4.1	0.7	33.2	15.3
P0AAS7	7371.1	S	U	T	C	CID	LIT	6	82.9	VDGAVETR	846.4	K	K	2.5	0.3	25.0	18.5
P0AAS7	7371.1	S	U	T	A	ETD	LIT	5	92.9	ATFSLGKHPHVELCDLLK	2065.1	M	L	0.0	0.0	23.1	16.9
P0AAS7	7371.1	S	U	T	A	ETD	LIT	5	92.9	IAIAEGQVKVDGAVETR	1756.0	K	K	3.9	0.1	0.0	0.0
P0AAS7	7371.1	S	U	T	A	ETD	LIT	5	92.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	4.4	0.4	67.2	16.9
P0AAS7	7371.1	S	U	T	A	ETD	LIT	5	92.9	LEGWSESGAQAK	1262.6	K	I	2.9	0.2	46.2	15.1
P0AAS7	7371.1	S	U	T	A	ETD	LIT	5	92.9	VDGAVETR	846.4	K	K	2.1	0.0	55.7	18.9
P0AAS7	7371.1	S	U	T	B	ETD	LIT	6	92.9	ATFSLGKHPHVELCDLLK	2065.1	M	L	0.0	0.0	34.2	17.5
P0AAS7	7371.1	S	U	T	B	ETD	LIT	6	92.9	IAIAEGQVK	928.5	K	V	2.3	0.3	43.1	16.8
P0AAS7	7371.1	S	U	T	B	ETD	LIT	6	92.9	IAIAEGQVKVDGAVETR	1756.0	K	K	3.0	0.3	0.0	0.0
P0AAS7	7371.1	S	U	T	B	ETD	LIT	6	92.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	3.8	0.4	0.0	0.0
P0AAS7	7371.1	S	U	T	B	ETD	LIT	6	92.9	LEGWSESGAQAK	1262.6	K	I	2.3	0.1	20.3	15.4
P0AAS7	7371.1	S	U	T	B	ETD	LIT	6	92.9	VDGAVETR	846.4	K	K	1.6	0.3	32.8	18.9
P0AAS7	7371.1	S	U	T	C	ETD	LIT	5	92.9	ATFSLGKHPHVELCDLLK	2065.1	M	L	0.0	0.0	53.9	17.2
P0AAS7	7371.1	S	U	T	C	ETD	LIT	5	92.9	IAIAEGQVK	928.5	K	V	2.2	0.1	41.4	14.6
P0AAS7	7371.1	S	U	T	C	ETD	LIT	5	92.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	3.6	0.4	51.0	17.1
P0AAS7	7371.1	S	U	T	C	ETD	LIT	5	92.9	LEGWSESGAQAK	1262.6	K	I	3.1	0.1	47.5	15.1
P0AAS7	7371.1	S	U	T	C	ETD	LIT	5	92.9	VDGAVETR	846.4	K	K	2.2	0.3	44.4	18.9
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	2	67.1	ATFSLGKHPHVELCDLLKLEGWSESGAQAK	3308.7	M	I	0.0	0.0	14.7	18.4
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	2	67.1	HPHVELCDLLKLEGWSESGAQAK	2604.3	K	I	0.0	0.0	45.6	18.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	2	67.1	IAIAEGQVKVDGAVETR	1756.0	K	K	0.0	0.0	28.6	16.3
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	2	67.1	VDGAVETR	846.4	K	K	0.0	0.0	28.0	18.5
P0AAS7	7371.1	S	U	T	A	ETD+CID	LIT	2	82.9	HPHVELCDLLKLEGWSESGAQAK	2604.3	K	I	3.8	0.4	34.5	18.4
P0AAS7	7371.1	S	U	T	A	ETD+CID	LIT	2	82.9	IAIAEGQVKVDGAVETR	1756.0	K	K	2.7	0.8	27.6	16.3
P0AAS7	7371.1	S	U	T	A	ETD+CID	LIT	2	82.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	3.5	0.6	35.2	16.6
P0AAS7	7371.1	S	U	T	A	ETD+CID	LIT	2	82.9	SHQTGVNGENNSVR	1500.7	-	-	3.8	-0.4	57.8	14.3
P0AAS7	7371.1	S	U	T	A	ETD+CID	LIT	2	82.9	VDGAVETR	846.4	K	K	1.9	0.2	8.7	18.9
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	3	92.9	ATFSLGKHPHVELCDLLKLEGWSESGAQAK	3308.7	M	I	0.0	0.0	14.7	18.4
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	3	92.9	HPHVELCDLLKLEGWSESGAQAK	2604.3	K	I	5.2	0.8	45.6	18.2
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	3	92.9	IAIAEGQVKVDGAVETR	1756.0	K	K	2.3	0.7	28.6	16.3
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	3	92.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	2.6	0.3	0.0	0.0
P0AAS7	7371.1	S	U	T	B	ETD+CID	LIT	3	92.9	VDGAVETR	846.4	K	K	0.7	-0.1	28.0	18.5
P0AAS7	7371.1	S	U	T	C	ETD+CID	LIT	5	92.9	ATFSLGKHPHVELCDLLK	2065.1	M	L	0.0	0.0	38.7	17.5
P0AAS7	7371.1	S	U	T	C	ETD+CID	LIT	5	92.9	HPHVELCDLLKLEGWSESGAQAK	2604.3	K	I	4.9	0.5	43.9	18.3
P0AAS7	7371.1	S	U	T	C	ETD+CID	LIT	5	92.9	IAIAEGQVKVDGAVETR	1756.0	K	K	3.1	0.6	21.5	17.2
P0AAS7	7371.1	S	U	T	C	ETD+CID	LIT	5	92.9	IVAGQTVSFAGHSVQVVA	1770.0	K	-	2.8	0.5	0.0	0.0
P0AAS7	7371.1	S	U	T	C	ETD+CID	LIT	5	92.9	LEGWSESGAQAK	1262.6	K	I	3.7	0.5	40.7	16.4
P0AAS7	7371.1	S	U	T	C	ETD+CID	LIT	5	92.9	TAMGEPGPDGR	1087.5	-	-	1.8	0.3	0.0	0.0
P0AAS7	7371.1	S	U	T	C	ETD+CID	LIT	5	92.9	VDGAVETR	846.4	K	K	1.7	0.5	15.9	18.9
P0A9Y6	7384.3	G	U	T	A	CID	LIT	5	73.9	GFGFITPADGSK	1196.6	K	D	3.7	0.9	46.7	10.0
P0A9Y6	7384.3	G	U	T	A	CID	LIT	5	73.9	GPAAVNVTAI	912.5	K	-	1.8	0.5	16.0	12.0
P0A9Y6	7384.3	G	U	T	A	CID	LIT	5	73.9	IKGQVK	672.4	K	W	1.9	0.6	8.5	15.4
P0A9Y6	7384.3	G	U	T	A	CID	LIT	5	73.9	TLAEGQNVEFEIQDGQK	1905.9	K	G	4.8	0.8	90.8	14.0
P0A9Y6	7384.3	G	U	T	A	CID	LIT	5	73.9	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	4.8	0.0	51.8	11.1
P0A9Y6	7384.3	G	U	T	A	CID	LIT	5	73.9	WFNESK	810.4	K	G	2.2	0.5	15.4	10.4
P0A9Y6	7384.3	G	T	T	A	CID	LIT	2	50.7	GFGFITPADGSK	1196.6	K	D	2.3	0.7	2.3	10.4
P0A9Y6	7384.3	G	T	T	A	CID	LIT	2	50.7	TLAEGQNVEFEIQDGQK	1905.9	K	G	4.4	0.6	72.6	12.8
P0A9Y6	7384.3	G	T	T	A	CID	LIT	2	50.7	WFNESK	810.4	K	G	2.1	0.5	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9Y6	7384.3	G	U	A	A	CID	LIT	3	58.0	AKIKGQVKWFNESKGFGFITPADGSK	2840.5	M	D	0.0	0.0	29.1	12.3
P0A9Y6	7384.3	G	U	A	A	CID	LIT	3	58.0	DGQKGPAAVNVTAI	1340.7	Q	-	3.4	0.5	43.0	13.4
P0A9Y6	7384.3	G	U	A	A	CID	LIT	3	58.0	ESKGFGFITPADGSK	1540.8	N	D	3.0	0.5	10.6	15.8
P0A9Y6	7384.3	G	T	T	B	CID	LIT	3	56.5	GFGFITPADGSK	1196.6	K	D	2.6	0.6	5.5	9.0
P0A9Y6	7384.3	G	T	T	B	CID	LIT	3	56.5	TLAEGQNVEFEIQDGQK	1905.9	K	G	5.2	0.6	68.3	12.8
P0A9Y6	7384.3	G	T	T	B	CID	LIT	3	56.5	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	4.2	0.0	26.4	11.8
P0A9Y6	7384.3	G	U	T	B	CID	LIT	3	65.2	GFGFITPADGSK	1196.6	K	D	3.7	0.0	42.1	9.0
P0A9Y6	7384.3	G	U	T	B	CID	LIT	3	65.2	TLAEGQNVEFEIQDGQK	1905.9	K	G	4.6	0.0	94.1	14.1
P0A9Y6	7384.3	G	U	T	B	CID	LIT	3	65.2	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	3.4	0.0	65.6	10.8
P0A9Y6	7384.3	G	U	T	B	CID	LIT	3	65.2	WFNESK	810.4	K	G	2.2	0.0	13.3	9.5
P0A9Y6	7384.3	S	U	T	A	CID	LIT	5	78.3	DVFVHFSAIQGNGFK	1666.8	K	T	4.6	0.7	52.0	17.6
P0A9Y6	7384.3	S	U	T	A	CID	LIT	5	78.3	GFGFITPADGSK	1196.6	K	D	3.7	0.0	36.0	13.4
P0A9Y6	7384.3	S	U	T	A	CID	LIT	5	78.3	GFGFITPADGSKDVFVHFSAIQGNGFK	2844.4	K	T	4.7	0.0	26.6	18.5
P0A9Y6	7384.3	S	U	T	A	CID	LIT	5	78.3	TLAEGQNVEFEIQDGQK	1905.9	K	G	4.9	0.6	81.6	17.7
P0A9Y6	7384.3	S	U	T	A	CID	LIT	5	78.3	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	5.6	0.6	46.8	18.8
P0A9Y6	7384.3	S	U	T	B	CID	LIT	4	87.0	DVFVHFSAIQGNGFK	1666.8	K	T	4.0	0.4	34.7	17.6
P0A9Y6	7384.3	S	U	T	B	CID	LIT	4	87.0	GFGFITPADGSK	1196.6	K	D	3.6	0.8	32.6	14.6
P0A9Y6	7384.3	S	U	T	B	CID	LIT	4	87.0	TLAEGQNVEFEIQDGQK	1905.9	K	G	5.4	0.6	86.0	18.4
P0A9Y6	7384.3	S	U	T	B	CID	LIT	4	87.0	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	5.3	0.0	45.8	18.9
P0A9Y6	7384.3	S	U	T	B	CID	LIT	4	87.0	WFNESK	810.4	K	G	1.7	0.5	1.3	11.1
P0A9Y6	7384.3	S	U	T	C	CID	LIT	5	87.0	DVFVHFSAIQGNGFK	1666.8	K	T	4.7	0.7	52.2	17.2
P0A9Y6	7384.3	S	U	T	C	CID	LIT	5	87.0	GFGFITPADGSK	1196.6	K	D	3.6	0.6	38.2	13.4
P0A9Y6	7384.3	S	U	T	C	CID	LIT	5	87.0	GFGFITPADGSKDVFVHFSAIQGNGFK	2844.4	K	T	5.4	0.7	24.6	18.3
P0A9Y6	7384.3	S	U	T	C	CID	LIT	5	87.0	TLAEGQNVEFEIQDGQK	1905.9	K	G	4.7	0.6	93.4	17.6
P0A9Y6	7384.3	S	U	T	C	CID	LIT	5	87.0	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	5.8	0.6	38.8	18.7
P0A9Y6	7384.3	S	U	T	C	CID	LIT	5	87.0	WFNESK	810.4	K	G	1.7	0.4	0.0	0.0
P0A9Y6	7384.3	S	U	T	A	ETD	LIT	3	63.8	DVFVHFSAIQGNGFK	1666.8	K	T	5.6	0.6	0.0	0.0
P0A9Y6	7384.3	S	U	T	A	ETD	LIT	3	63.8	GFGFITPADGSK	1196.6	K	D	3.5	0.5	14.4	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9Y6	7384.3	S	U	T	A	ETD	LIT	3	63.8	TLAEGQNVEFEIQDGQK	1905.9	K	G	2.4	0.3	50.5	18.2
P0A9Y6	7384.3	S	U	T	B	ETD	LIT	3	63.8	DVFVHFSAIQGNGFK	1666.8	K	T	5.7	0.5	54.6	17.3
P0A9Y6	7384.3	S	U	T	B	ETD	LIT	3	63.8	GFGFITPADGSK	1196.6	K	D	3.4	0.5	25.0	13.4
P0A9Y6	7384.3	S	U	T	B	ETD	LIT	3	63.8	TLAEGQNVEFEIQDGQK	1905.9	K	G	2.8	0.0	46.0	18.3
P0A9Y6	7384.3	S	U	T	C	ETD	LIT	3	72.5	DVFVHFSAIQGNGFK	1666.8	K	T	5.7	0.5	68.3	17.6
P0A9Y6	7384.3	S	U	T	C	ETD	LIT	3	72.5	GFGFITPADGSK	1196.6	K	D	3.1	0.5	16.5	14.1
P0A9Y6	7384.3	S	U	T	C	ETD	LIT	3	72.5	TLAEGQNVEFEIQDGQK	1905.9	K	G	2.3	0.6	0.0	0.0
P0A9Y6	7384.3	S	U	T	C	ETD	LIT	3	72.5	WFNESK	810.4	K	G	1.5	0.6	16.9	11.1
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	DVFVHFSAIQGNGFK	1666.8	K	T	0.0	0.0	66.4	17.7
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	GFGFITPADGSK	1196.6	K	D	0.0	0.0	35.1	13.4
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQK	1905.9	K	G	0.0	0.0	82.7	18.0
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	0.0	0.0	44.7	18.6
P0A9Y6	7384.3	S	U	T	A	ETD+CID	LIT	3	78.3	DVFVHFSAIQGNGFK	1666.8	K	T	4.4	0.7	51.5	17.6
P0A9Y6	7384.3	S	U	T	A	ETD+CID	LIT	3	78.3	GFGFITPADGSK	1196.6	K	D	3.3	0.5	31.5	14.5
P0A9Y6	7384.3	S	U	T	A	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQK	1905.9	K	G	4.9	0.6	81.0	18.4
P0A9Y6	7384.3	S	U	T	A	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	5.3	0.6	0.0	0.0
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	DVFVHFSAIQGNGFK	1666.8	K	T	4.5	0.5	53.4	17.6
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	GFGFITPADGSK	1196.6	K	D	3.4	0.6	35.1	13.4
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQK	1905.9	K	G	5.5	0.6	82.7	18.0
P0A9Y6	7384.3	S	U	T	B	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	5.4	0.5	44.7	18.6
P0A9Y6	7384.3	S	U	T	C	ETD+CID	LIT	3	78.3	DVFVHFSAIQGNGFK	1666.8	K	T	4.8	0.7	66.4	17.6
P0A9Y6	7384.3	S	U	T	C	ETD+CID	LIT	3	78.3	GFGFITPADGSK	1196.6	K	D	3.5	0.8	0.0	0.0
P0A9Y6	7384.3	S	U	T	C	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQK	1905.9	K	G	5.1	0.6	81.2	17.9
P0A9Y6	7384.3	S	U	T	C	ETD+CID	LIT	3	78.3	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	5.6	0.5	44.5	18.8
P0A9Y6	7384.3	S	U	T	B	HCD	FT	3	78.3	DVFVHFSAIQGNGFK	1666.8	K	T	0.0	0.0	53.4	17.6
P0A9Y6	7384.3	S	U	T	B	HCD	FT	3	78.3	GFGFITPADGSK	1196.6	K	D	0.0	0.0	35.1	13.4
P0A9Y6	7384.3	S	U	T	B	HCD	FT	3	78.3	TLAEGQNVEFEIQDGQK	1905.9	K	G	0.0	0.0	82.7	18.0
P0A9Y6	7384.3	S	U	T	B	HCD	FT	3	78.3	TLAEGQNVEFEIQDGQKGPAAVNVTAI	2799.4	K	-	0.0	0.0	44.7	18.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9Y6	7384.3	S	U	T	C	HCD	FT	2	46.4	DVFVHFSAIQGNGFK	1666.8	K	T	3.1	0.0	26.6	17.6
P0A9Y6	7384.3	S	U	T	C	HCD	FT	2	46.4	TLAEGQNVEFEIQDGQK	1905.9	K	G	1.7	0.0	27.8	18.4
P0A9X9	7385.5	G	U	T	A	CID	LIT	6	85.7	DVFVHFSAIQNDGYK	1739.8	K	S	4.5	0.7	54.7	12.6
P0A9X9	7385.5	G	U	T	A	CID	LIT	6	85.7	GPAAGNVTSL	886.5	K	-	1.8	0.6	12.8	10.0
P0A9X9	7385.5	G	U	T	A	CID	LIT	6	85.7	SLDEGQKVSFTIESGAK	1795.9	K	G	4.9	0.7	66.4	13.0
P0A9X9	7385.5	G	U	T	A	CID	LIT	6	85.7	VSFTIESGAK	1038.5	K	G	2.8	0.4	24.3	12.0
P0A9X9	7385.5	G	U	T	A	CID	LIT	6	85.7	WFNADK	780.4	K	G	1.8	0.7	14.6	11.5
P0A9X9	7385.5	G	U	T	A	CID	LIT	6	85.7	WFNADKGFGFITPDDGSK	2001.9	K	D	3.5	0.0	15.1	9.0
P0A9X9	7385.5	G	T	T	A	CID	LIT	4	62.9	DVFVHFSAIQNDGYK	1739.8	K	S	3.3	0.0	19.2	12.8
P0A9X9	7385.5	G	T	T	A	CID	LIT	4	62.9	GFGFITPDDGSK	1240.6	K	D	2.5	0.5	23.6	11.8
P0A9X9	7385.5	G	T	T	A	CID	LIT	4	62.9	SLDEGQKVSFTIESGAK	1795.9	K	G	5.4	0.7	58.2	13.0
P0A9X9	7385.5	G	T	T	A	CID	LIT	4	62.9	VSFTIESGAK	1038.5	K	G	2.9	0.3	28.5	13.4
P0A9X9	7385.5	G	U	A	A	CID	LIT	5	80.0	DEGQKVSFTIESGAKGPAAGNVTSL	2463.2	L	-	5.1	0.0	59.8	14.5
P0A9X9	7385.5	G	U	A	A	CID	LIT	5	80.0	DGYKSL	682.3	N	D	2.1	0.8	13.0	11.8
P0A9X9	7385.5	G	U	A	A	CID	LIT	5	80.0	DKGFGFITPDDGSK	1483.7	A	D	4.5	0.6	69.6	14.0
P0A9X9	7385.5	G	U	A	A	CID	LIT	5	80.0	DVFVHFSAIQN	1276.6	K	D	2.6	0.8	28.3	15.8
P0A9X9	7385.5	G	U	A	A	CID	LIT	5	80.0	DVFVHFSAIQNDGYKSL	1940.0	K	D	3.0	0.4	11.1	15.7
P0A9X9	7385.5	G	U	T	B	CID	LIT	6	77.1	DVFVHFSAIQNDGYK	1739.8	K	S	4.0	0.0	42.7	12.3
P0A9X9	7385.5	G	U	T	B	CID	LIT	6	77.1	GFGFITPDDGSK	1240.6	K	D	2.5	0.5	23.9	11.8
P0A9X9	7385.5	G	U	T	B	CID	LIT	6	77.1	GPAAGNVTSL	886.5	K	-	2.9	0.0	41.9	10.8
P0A9X9	7385.5	G	U	T	B	CID	LIT	6	77.1	SLDEGQK	776.4	K	V	1.7	0.5	15.4	12.3
P0A9X9	7385.5	G	U	T	B	CID	LIT	6	77.1	SLDEGQKVSFTIESGAK	1795.9	K	G	2.9	0.0	24.1	13.0
P0A9X9	7385.5	G	U	T	B	CID	LIT	6	77.1	VSFTIESGAK	1038.5	K	G	3.0	0.3	43.3	12.0
P0A9X9	7385.5	G	T	A	B	CID	LIT	3	71.4	DEGQKVSFTIESGAKGPAAGNVTSL	2463.2	L	-	3.6	0.0	28.3	13.4
P0A9X9	7385.5	G	T	A	B	CID	LIT	3	71.4	DKGFGFITPDDGSK	1483.7	A	D	3.7	0.0	41.3	14.9
P0A9X9	7385.5	G	T	A	B	CID	LIT	3	71.4	DVFVHFSAIQN	1276.6	K	D	2.2	0.5	13.3	15.8
P0A9X9	7385.5	G	U	A	B	CID	LIT	6	98.6	DEGQKVSFTIESGAKGPAAGNVTSL	2463.2	L	-	5.0	0.8	72.1	13.4
P0A9X9	7385.5	G	U	A	B	CID	LIT	6	98.6	DGYKSL	682.3	N	D	2.1	0.7	13.8	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9X9	7385.5	G	U	A	B	CID	LIT	6	98.6	DKGFGFITP	981.5	A	D	2.4	0.8	26.8	13.4
P0A9X9	7385.5	G	U	A	B	CID	LIT	6	98.6	DKGFGFITPDDGSK	1483.7	A	D	4.7	0.7	69.2	14.9
P0A9X9	7385.5	G	U	A	B	CID	LIT	6	98.6	DVFVHFSAIQN	1276.6	K	D	2.5	0.5	39.8	16.3
P0A9X9	7385.5	G	U	A	B	CID	LIT	6	98.6	SGKMTGIVKWFNA	1438.8	M	D	0.0	0.0	41.7	13.2
P0A9X9	7385.5	S	U	T	A	CID	LIT	4	47.1	DVFVHFSAIQNDGYK	1739.8	K	S	3.9	0.6	26.2	17.1
P0A9X9	7385.5	S	U	T	A	CID	LIT	4	47.1	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	4.4	0.5	34.2	18.5
P0A9X9	7385.5	S	U	T	A	CID	LIT	4	47.1	WFNADKGFGFITPDDGSK	2001.9	K	D	5.0	0.4	44.3	16.7
P0A9X9	7385.5	S	U	T	A	CID	LIT	4	47.1	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	4.7	0.0	40.4	17.2
P0A9X9	7385.5	S	U	T	B	CID	LIT	2	47.1	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	5.0	0.7	56.5	18.7
P0A9X9	7385.5	S	U	T	B	CID	LIT	2	47.1	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	4.5	0.0	29.9	17.0
P0A9X9	7385.5	S	U	T	C	CID	LIT	5	71.4	DVFVHFSAIQNDGYK	1739.8	K	S	5.0	0.6	40.3	17.2
P0A9X9	7385.5	S	U	T	C	CID	LIT	5	71.4	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	4.0	0.5	50.3	18.9
P0A9X9	7385.5	S	U	T	C	CID	LIT	5	71.4	SLDEGQKVSFTIESGAK	1795.9	K	G	5.4	0.5	63.6	15.7
P0A9X9	7385.5	S	U	T	C	CID	LIT	5	71.4	WFNADKGFGFITPDDGSK	2001.9	K	D	4.6	0.5	39.3	16.5
P0A9X9	7385.5	S	U	T	C	CID	LIT	5	71.4	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	5.7	0.7	54.5	17.2
P0A9X9	7385.5	S	U	T	A	ETD	LIT	2	47.1	WFNADKGFGFITPDDGSK	2001.9	K	D	3.0	0.5	18.0	15.6
P0A9X9	7385.5	S	U	T	A	ETD	LIT	2	47.1	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	0.0	0.0	29.9	17.5
P0A9X9	7385.5	S	U	T	B	ETD	LIT	2	47.1	WFNADKGFGFITPDDGSK	2001.9	K	D	4.7	0.5	52.4	16.0
P0A9X9	7385.5	S	U	T	B	ETD	LIT	2	47.1	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	5.5	0.0	53.5	17.3
P0A9X9	7385.5	S	U	T	C	ETD	LIT	4	61.4	DVFVHFSAIQNDGYK	1739.8	K	S	4.8	0.6	28.1	16.5
P0A9X9	7385.5	S	U	T	C	ETD	LIT	4	61.4	VSFTIESGAK	1038.5	K	G	0.0	0.0	30.2	15.8
P0A9X9	7385.5	S	U	T	C	ETD	LIT	4	61.4	WFNADKGFGFITPDDGSK	2001.9	K	D	4.8	0.0	44.5	15.4
P0A9X9	7385.5	S	U	T	C	ETD	LIT	4	61.4	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	0.0	0.0	75.1	18.0
P0A9X9	7385.5	S	U	T	B	ETD+CID	LIT	3	47.1	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	0.0	0.0	54.9	18.6
P0A9X9	7385.5	S	U	T	B	ETD+CID	LIT	3	47.1	WFNADKGFGFITPDDGSK	2001.9	K	D	0.0	0.0	37.7	16.6
P0A9X9	7385.5	S	U	T	B	ETD+CID	LIT	3	47.1	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	0.0	0.0	46.1	17.5
P0A9X9	7385.5	S	U	T	A	ETD+CID	LIT	4	47.1	DVFVHFSAIQNDGYK	1739.8	K	S	3.6	0.7	28.8	16.5
P0A9X9	7385.5	S	U	T	A	ETD+CID	LIT	4	47.1	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	6.3	0.7	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9X9	7385.5	S	U	T	A	ETD+CID	LIT	4	47.1	WFNADKGFGFITPDDGSK	2001.9	K	D	5.8	0.5	61.5	16.7
P0A9X9	7385.5	S	U	T	A	ETD+CID	LIT	4	47.1	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	6.6	0.0	61.0	17.1
P0A9X9	7385.5	S	U	T	B	ETD+CID	LIT	4	47.1	DVFVHFSAIQNDGYK	1739.8	K	S	2.7	0.4	5.0	17.0
P0A9X9	7385.5	S	U	T	B	ETD+CID	LIT	4	47.1	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	4.9	0.6	54.9	18.6
P0A9X9	7385.5	S	U	T	B	ETD+CID	LIT	4	47.1	WFNADKGFGFITPDDGSK	2001.9	K	D	4.2	0.4	37.7	16.6
P0A9X9	7385.5	S	U	T	B	ETD+CID	LIT	4	47.1	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	0.0	0.0	46.1	17.5
P0A9X9	7385.5	S	U	T	C	ETD+CID	LIT	7	85.7	DVFVHFSAIQNDGYK	1739.8	K	S	4.4	0.7	49.5	17.2
P0A9X9	7385.5	S	U	T	C	ETD+CID	LIT	7	85.7	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	5.6	0.7	0.0	0.0
P0A9X9	7385.5	S	U	T	C	ETD+CID	LIT	7	85.7	GPAAGNVTSL	886.5	K	-	2.8	0.7	48.2	13.0
P0A9X9	7385.5	S	U	T	C	ETD+CID	LIT	7	85.7	SLDEGQKVSFTIESGAK	1795.9	K	G	5.6	0.6	61.4	16.9
P0A9X9	7385.5	S	U	T	C	ETD+CID	LIT	7	85.7	VSFTIESGAK	1038.5	K	G	2.8	0.3	12.6	14.3
P0A9X9	7385.5	S	U	T	C	ETD+CID	LIT	7	85.7	WFNADKGFGFITPDDGSK	2001.9	K	D	5.0	0.5	20.1	16.8
P0A9X9	7385.5	S	U	T	C	ETD+CID	LIT	7	85.7	WFNADKGFGFITPDDGSKDVFVHFSAIQNDGYK	3722.8	K	S	0.0	0.0	56.6	17.2
P0A9X9	7385.5	S	U	T	B	HCD	FT	2	47.1	GFGFITPDDGSKDVFVHFSAIQNDGYK	2961.4	K	S	0.0	0.0	54.9	18.6
P0A9X9	7385.5	S	U	T	B	HCD	FT	2	47.1	WFNADKGFGFITPDDGSK	2001.9	K	D	0.0	0.0	37.7	16.6
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	DVFVHFSAIQTNGFK	1709.9	K	T	4.3	0.6	56.6	13.8
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	GFGFITPEDGSK	1254.6	K	D	3.3	0.8	42.3	12.0
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	GNVKWFNESK	1208.6	K	G	2.8	0.8	29.2	13.6
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	GPSAANVIAL	912.5	K	-	3.0	0.6	50.0	12.0
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	IKGNVK	658.4	K	W	1.9	0.1	19.5	18.8
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	TLAEGQR	774.4	K	V	2.4	0.3	39.1	16.7
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	TLAEGQRVEFEITNGAK	1863.0	K	G	4.8	0.7	31.5	11.1
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	VEFEITNGAK	1107.6	R	G	2.6	0.5	14.5	13.8
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	VEFEITNGAKGPSAANVIAL	2001.1	R	-	4.2	0.0	38.1	10.4
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	WFNESK	810.4	K	G	2.2	0.5	15.4	10.4
P0A972	7445.6	G	U	T	A	CID	LIT	11	95.7	WFNESKGFGFITPEDGSK	2046.0	K	D	4.9	0.0	52.1	8.5
P0A972	7445.6	G	T	T	A	CID	LIT	4	50.7	GFGFITPEDGSK	1254.6	K	D	3.3	0.0	36.9	11.1
P0A972	7445.6	G	T	T	A	CID	LIT	4	50.7	GPSAANVIAL	912.5	K	-	2.5	0.4	13.6	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A972	7445.6	G	T	T	A	CID	LIT	4	50.7	TLAEGQR	774.4	K	V	2.2	0.2	29.2	16.7
P0A972	7445.6	G	T	T	A	CID	LIT	4	50.7	WFNESK	810.4	K	G	2.1	0.5	0.0	0.0
P0A972	7445.6	G	U	A	A	CID	LIT	4	72.5	EGQRVEFEITNGAKGPSAANVIAL	2471.3	A	-	2.1	0.6	35.3	15.7
P0A972	7445.6	G	U	A	A	CID	LIT	4	72.5	EITNGAKGPSAANVIAL	1625.9	F	-	3.2	0.5	18.5	12.8
P0A972	7445.6	G	U	A	A	CID	LIT	4	72.5	ESKGFGFITPEDGSK	1598.8	N	D	2.2	0.7	7.7	14.0
P0A972	7445.6	G	U	A	A	CID	LIT	4	72.5	SKIKGNVKWFNESKGFGFITPE	2513.3	M	D	0.0	0.0	28.1	14.9
P0A972	7445.6	G	T	T	B	CID	LIT	4	56.5	GFGFITPEDGSK	1254.6	K	D	2.3	0.2	0.0	0.0
P0A972	7445.6	G	T	T	B	CID	LIT	4	56.5	GPSAANVIAL	912.5	K	-	2.0	0.3	10.1	12.0
P0A972	7445.6	G	T	T	B	CID	LIT	4	56.5	TLAEGQRVEFEITNGAK	1863.0	K	G	4.6	0.6	32.8	11.5
P0A972	7445.6	G	T	T	B	CID	LIT	4	56.5	VEFEITNGAK	1107.6	R	G	2.6	0.4	18.4	13.8
P0A972	7445.6	G	U	T	B	CID	LIT	7	71.0	GFGFITPEDGSK	1254.6	K	D	3.1	0.8	41.9	11.5
P0A972	7445.6	G	U	T	B	CID	LIT	7	71.0	GNVKWFNESK	1208.6	K	G	1.9	0.4	8.5	13.6
P0A972	7445.6	G	U	T	B	CID	LIT	7	71.0	GPSAANVIAL	912.5	K	-	3.3	0.6	43.4	11.8
P0A972	7445.6	G	U	T	B	CID	LIT	7	71.0	TLAEGQR	774.4	K	V	2.2	0.3	33.1	16.7
P0A972	7445.6	G	U	T	B	CID	LIT	7	71.0	TLAEGQRVEFEITNGAK	1863.0	K	G	4.7	0.7	52.8	11.5
P0A972	7445.6	G	U	T	B	CID	LIT	7	71.0	VEFEITNGAK	1107.6	R	G	2.6	0.6	44.1	13.6
P0A972	7445.6	G	U	T	B	CID	LIT	7	71.0	WFNESK	810.4	K	G	2.2	0.0	13.3	9.5
P0A972	7445.6	G	U	A	B	CID	LIT	4	56.5	EGQRVEF	864.4	A	E	1.4	0.3	28.8	16.6
P0A972	7445.6	G	U	A	B	CID	LIT	4	56.5	EGQRVEFEITNGAKGPSAANVIAL	2471.3	A	-	4.4	0.9	31.2	15.6
P0A972	7445.6	G	U	A	B	CID	LIT	4	56.5	EITNGAKGPSAANVIAL	1625.9	F	-	4.4	0.6	34.6	12.6
P0A972	7445.6	G	U	A	B	CID	LIT	4	56.5	ESKGFGFITPEDGSK	1598.8	N	D	2.3	0.7	12.6	14.5
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	DVFVHFSAIQTNGFK	1710.8	K	T	4.8	0.6	75.1	16.5
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	GFGFITPEDGSK	1254.6	K	D	1.9	0.6	7.4	14.1
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	GFGFITPEDGSKDVFVHFSAIQTNGFK	2946.4	K	T	5.4	0.5	65.2	18.3
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	GPSAANVIAL	912.5	K	-	3.1	0.6	44.3	13.8
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	TLAEGQRVEFEITNGAK	1863.9	K	G	5.1	0.6	67.8	17.4
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	3.8	0.8	52.4	17.1
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	VEFEITNGAK	1108.6	R	G	3.3	0.7	53.6	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	VEFEITNGAKGPSAANVIAL	2001.1	R	-	3.7	0.4	19.3	16.6
P0A972	7445.6	S	U	T	A	CID	LIT	9	87.0	WFNESKGFGFITPEDGSK	2046.0	K	D	4.3	0.6	18.2	15.8
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	DVFVHFSAIQTNGFK	1710.8	K	T	4.9	0.6	69.2	16.9
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	GFGFITPEDGSK	1254.6	K	D	3.4	0.8	43.3	14.6
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	GFGFITPEDGSKDVFVHFSAIQTNGFK	2945.4	K	T	5.5	0.5	70.6	18.8
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	GPSAANVIAL	912.5	K	-	3.0	0.6	50.1	13.4
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	TLAEGQRVEFEITNGAK	1863.9	K	G	5.4	0.6	65.6	17.3
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	4.1	0.8	41.2	17.1
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	VEFEITNGAK	1108.6	R	G	3.2	0.7	49.5	15.6
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	VEFEITNGAKGPSAANVIAL	2002.0	R	-	4.7	0.5	34.5	18.0
P0A972	7445.6	S	U	T	B	CID	LIT	9	87.0	WFNESK	810.4	K	G	1.7	0.5	1.3	11.1
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	DVFVHFSAIQTNGFK	1710.8	K	T	5.1	0.6	71.1	16.9
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	GFGFITPEDGSK	1254.6	K	D	3.5	0.8	43.3	14.5
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	GFGFITPEDGSKDVFVHFSAIQTNGFK	2945.4	K	T	5.7	0.5	80.7	18.9
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	GPSAANVIAL	912.5	K	-	3.1	0.6	50.1	13.4
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	TLAEGQRVEFEITNGAK	1863.9	K	G	5.1	0.5	68.7	17.4
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	3.6	0.5	41.4	17.4
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	VEFEITNGAK	1107.6	R	G	2.6	0.6	42.6	15.9
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	VEFEITNGAKGPSAANVIAL	2002.0	R	-	4.3	0.6	26.4	18.1
P0A972	7445.6	S	U	T	C	CID	LIT	9	87.0	WFNESK	810.4	K	G	1.7	0.4	0.0	0.0
P0A972	7445.6	S	U	T	A	CID	FT	5	78.3	DVFVHFSAIQTNGFK	1710.8	K	T	3.2	0.0	54.2	16.4
P0A972	7445.6	S	U	T	A	CID	FT	5	78.3	GFGFITPEDGSK	1254.6	K	D	2.2	0.0	24.1	14.0
P0A972	7445.6	S	U	T	A	CID	FT	5	78.3	GPSAANVIAL	912.5	K	-	2.8	0.0	46.7	14.1
P0A972	7445.6	S	U	T	A	CID	FT	5	78.3	TLAEGQRVEFEITNGAK	1863.0	K	G	4.3	0.0	45.5	17.3
P0A972	7445.6	S	U	T	A	CID	FT	5	78.3	VEFEITNGAK	1107.6	R	G	2.2	0.0	29.9	15.9
P0A972	7445.6	S	U	T	B	CID	FT	2	46.4	DVFVHFSAIQTNGFK	1709.9	K	T	2.9	0.0	51.5	16.8
P0A972	7445.6	S	U	T	B	CID	FT	2	46.4	TLAEGQRVEFEITNGAK	1863.9	K	G	5.0	0.0	55.2	16.9
P0A972	7445.6	S	U	T	C	CID	FT	5	78.3	DVFVHFSAIQTNGFK	1710.8	K	T	2.6	0.0	49.3	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A972	7445.6	S	U	T	C	CID	FT	5	78.3	GFGFITPEDGSK	1254.6	K	D	3.8	0.0	42.6	14.6
P0A972	7445.6	S	U	T	C	CID	FT	5	78.3	TLAEGQRVEFEITNGAK	1863.9	K	G	5.7	0.0	67.5	17.2
P0A972	7445.6	S	U	T	C	CID	FT	5	78.3	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	5.4	0.0	20.9	18.1
P0A972	7445.6	S	U	T	C	CID	FT	5	78.3	VEFEITNGAK	1108.6	R	G	2.8	0.0	58.1	15.6
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	DVFVHFSAIQTNGFK	1710.8	K	T	7.4	0.6	76.9	16.9
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	GFGFITPEDGSK	1254.6	K	D	0.0	0.0	31.2	14.6
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	GFGFITPEDGSKDVFVHFSAIQTNGFK	2946.4	K	T	8.9	0.0	61.7	19.2
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	GPSAANVIAL	912.5	K	-	2.2	0.5	0.0	0.0
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	TLAEGQR	774.4	K	V	2.5	0.2	48.7	18.4
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	TLAEGQRVEFEITNGAK	1863.9	K	G	7.8	0.6	98.2	18.0
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	4.5	0.6	0.0	0.0
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	VEFEITNGAK	1108.6	R	G	2.8	0.6	0.0	0.0
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	VEFEITNGAKGPSAANVIAL	2001.1	R	-	2.1	0.2	8.3	17.1
P0A972	7445.6	S	U	T	A	ETD	LIT	10	87.0	WFNESKGFGFITPEDGSK	2046.0	K	D	3.7	0.4	18.3	16.0
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	DVFVHFSAIQTNGFK	1710.8	K	T	6.8	0.6	65.9	17.1
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	GFGFITPEDGSK	1254.6	K	D	3.0	0.5	0.0	0.0
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	GFGFITPEDGSKDVFVHFSAIQTNGFK	2946.4	K	T	0.0	0.0	65.2	19.0
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	GPSAANVIAL	912.5	K	-	2.2	0.6	0.0	0.0
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	TLAEGQRVEFEITNGAK	1863.9	K	G	7.9	0.6	116.0	17.9
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	5.3	0.0	37.8	17.2
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	VEFEITNGAK	1107.6	R	G	2.8	0.4	45.1	15.9
P0A972	7445.6	S	U	T	B	ETD	LIT	8	78.3	VEFEITNGAKGPSAANVIAL	2002.0	R	-	2.8	0.4	17.2	18.2
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	DVFVHFSAIQTNGFK	1710.8	K	T	6.9	0.7	74.8	17.1
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	GFGFITPEDGSK	1254.6	K	D	2.2	0.4	10.1	14.9
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	GFGFITPEDGSKDVFVHFSAIQTNGFK	2945.4	K	T	7.6	0.0	62.2	18.9
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	GPSAANVIAL	912.5	K	-	2.2	0.6	0.0	0.0
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	TLAEGQR	774.4	K	V	2.5	0.2	59.6	18.5
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	TLAEGQRVEFEITNGAK	1863.9	K	G	8.0	0.6	106.0	17.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	4.4	0.0	32.7	17.2
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	VEFEITNGAK	1108.6	R	G	3.1	0.5	0.0	0.0
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	VEFEITNGAKGPSAANVIAL	2002.0	R	-	2.1	0.2	10.1	18.3
P0A972	7445.6	S	U	T	C	ETD	LIT	10	87.0	WFNESK	810.4	K	G	1.5	0.6	16.9	11.1
P0A972	7445.6	S	U	T	B	ETD	FT	4	63.8	DVFVHFSAIQTNGFK	1710.8	K	T	3.7	0.0	58.4	16.4
P0A972	7445.6	S	U	T	B	ETD	FT	4	63.8	GFGFITPEDGSK	1254.6	K	D	1.8	0.0	25.8	14.9
P0A972	7445.6	S	U	T	B	ETD	FT	4	63.8	TLAEGQRVEFEITNGAK	1863.9	K	G	4.9	0.6	49.2	17.0
P0A972	7445.6	S	U	T	B	ETD	FT	4	63.8	VEFEITNGAK	1108.6	R	G	0.0	0.0	37.7	15.6
P0A972	7445.6	S	U	T	C	ETD	FT	4	60.9	DVFVHFSAIQTNGFK	1710.8	K	T	4.8	0.5	67.7	17.0
P0A972	7445.6	S	U	T	C	ETD	FT	4	60.9	TLAEGQRVEFEITNGAK	1863.0	K	G	5.2	0.6	51.5	17.9
P0A972	7445.6	S	U	T	C	ETD	FT	4	60.9	VEFEITNGAK	1108.6	R	G	0.8	0.1	31.0	15.6
P0A972	7445.6	S	U	T	C	ETD	FT	4	60.9	VEFEITNGAKGPSAANVIAL	2002.0	R	-	2.2	0.0	58.1	18.5
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	DVFVHFSAIQTNGFK	1710.8	K	T	0.0	0.0	86.5	16.9
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	GFGFITPEDGSK	1254.6	K	D	0.0	0.0	26.8	14.6
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	GFGFITPEDGSKDVFVHFSAIQTNGFK	2946.4	K	T	0.0	0.0	64.4	18.5
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	GPSAANVIAL	912.5	K	-	0.0	0.0	50.2	14.1
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	TLAEGQR	774.4	K	V	0.0	0.0	27.2	18.4
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	TLAEGQRVEFEITNGAK	1863.9	K	G	0.0	0.0	111.0	17.9
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	0.0	0.0	42.0	17.4
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	VEFEITNGAK	1108.6	R	G	0.0	0.0	40.9	15.3
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	7	78.3	VEFEITNGAKGPSAANVIAL	2001.1	R	-	0.0	0.0	24.1	16.9
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	DVFVHFSAIQTNGFK	1710.8	K	T	8.1	0.8	74.2	17.1
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	GFGFITPEDGSK	1254.6	K	D	3.6	0.8	0.0	0.0
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	GFGFITPEDGSKDVFVHFSAIQTNGFK	2946.4	K	T	0.0	0.0	69.6	18.6
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	GPSAANVIAL	912.5	K	-	2.9	0.6	0.0	0.0
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	SHQTGVNGENNSVR	1500.7	-	-	2.9	0.5	21.4	14.9
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	TLAEGQR	774.4	K	V	2.2	0.1	27.1	18.4
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	TLAEGQRVEFEITNGAK	1863.9	K	G	8.3	0.6	98.0	17.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	4.4	0.7	44.9	19.1
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	VEFEITNGAK	1108.6	R	G	3.0	0.7	0.0	0.0
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	VEFEITNGAKGPSAANVIAL	2001.1	R	-	4.6	0.5	27.3	17.1
P0A972	7445.6	S	U	T	A	ETD+CID	LIT	8	87.0	WFNESKGFGFITPEDGSK	2046.0	K	D	5.4	0.6	0.0	0.0
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	DVFVHFSAIQTNGFK	1710.8	K	T	3.7	0.4	80.8	17.1
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	GFGFITPEDGSK	1254.6	K	D	3.1	0.8	26.8	14.6
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	GFGFITPEDGSKDVFVHFSAIQTNGFK	2946.4	K	T	5.6	0.5	51.8	18.4
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	GPSAANVIAL	912.5	K	-	3.0	0.6	0.0	0.0
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	MSKIKGNVK	1004.6	-	W	1.7	0.5	0.0	0.0
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	SATDAANAAQNR	1189.6	-	-	3.3	0.2	55.1	13.6
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	TLAEGQR	774.4	K	V	1.7	0.4	27.2	18.4
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	TLAEGQRVEFEITNGAK	1863.9	K	G	8.0	0.9	111.0	17.9
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	4.6	0.9	0.0	0.0
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	VEFEITNGAK	1108.6	R	G	3.3	0.7	40.9	15.3
P0A972	7445.6	S	U	T	B	ETD+CID	LIT	8	91.3	VEFEITNGAKGPSAANVIAL	2001.1	R	-	4.1	0.5	24.1	16.9
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	DVFVHFSAIQTNGFK	1710.8	K	T	7.2	0.6	77.0	16.6
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	GFGFITPEDGSK	1254.6	K	D	2.6	0.7	16.7	14.9
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	GFGFITPEDGSKDVFVHFSAIQTNGFK	2945.4	K	T	5.5	0.5	63.7	18.4
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	GGESVNDQGAEDQR	1461.6	-	-	3.7	-0.6	59.7	7.0
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	GPSAANVIAL	912.5	K	-	3.0	0.6	50.3	13.6
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	IADGQQKQENQIK	1499.8	-	-	3.5	0.4	32.7	16.1
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	KLNMMNAEHRK	1371.7	-	-	3.7	0.3	45.6	16.2
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	TLAEGQR	774.4	K	V	1.6	0.0	35.7	18.4
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	TLAEGQRVEFEITNGAK	1863.9	K	G	8.0	0.9	90.7	17.6
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	3.6	0.9	0.0	0.0
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	VEFEITNGAK	1108.6	R	G	3.1	0.7	0.0	0.0
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	VEFEITNGAKGPSAANVIAL	2001.1	R	-	4.3	0.5	17.1	16.1
P0A972	7445.6	S	U	T	C	ETD+CID	LIT	9	78.3	VLENAEGDR	1002.5	-	-	2.9	0.3	25.6	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	DVFVHFSAIQTNGFK	1710.8	K	T	0.0	0.0	76.7	16.7
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	GFGFITPEDGSK	1254.6	K	D	0.0	0.0	26.8	14.6
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	GFGFITPEDGSKDVFVHFSAIQTNGFK	2945.4	K	T	0.0	0.0	70.5	18.3
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	GPSAANVIAL	912.5	K	-	0.0	0.0	50.2	14.1
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	TLAEGQR	774.4	K	V	0.0	0.0	27.2	18.4
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	TLAEGQRVEFEITNGAK	1863.9	K	G	0.0	0.0	67.8	17.1
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	TLAEGQRVEFEITNGAKGPSAANVIAL	2757.4	K	-	0.0	0.0	42.0	17.4
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	VEFEITNGAK	1108.6	R	G	0.0	0.0	40.9	15.3
P0A972	7445.6	S	U	T	B	HCD	FT	7	78.3	VEFEITNGAKGPSAANVIAL	2001.1	R	-	0.0	0.0	24.1	16.9
P0A972	7445.6	S	U	T	A	HCD	FT	4	46.4	DVFVHFSAIQTNGFK	1710.8	K	T	3.5	0.6	82.1	16.9
P0A972	7445.6	S	U	T	A	HCD	FT	4	46.4	TLAEGQR	774.4	K	V	1.8	0.0	32.4	18.4
P0A972	7445.6	S	U	T	A	HCD	FT	4	46.4	TLAEGQRVEFEITNGAK	1863.9	K	G	4.2	0.0	59.2	17.0
P0A972	7445.6	S	U	T	A	HCD	FT	4	46.4	VEFEITNGAK	1108.6	R	G	1.0	0.0	28.0	15.2
P0A972	7445.6	S	U	T	B	HCD	FT	5	60.9	DVFVHFSAIQTNGFK	1710.8	K	T	2.7	0.7	61.6	16.7
P0A972	7445.6	S	U	T	B	HCD	FT	5	60.9	GPSAANVIAL	912.5	K	-	2.0	0.5	31.0	13.6
P0A972	7445.6	S	U	T	B	HCD	FT	5	60.9	TLAEGQR	774.4	K	V	2.1	0.0	36.0	18.4
P0A972	7445.6	S	U	T	B	HCD	FT	5	60.9	TLAEGQRVEFEITNGAK	1863.9	K	G	4.8	0.0	51.0	17.2
P0A972	7445.6	S	U	T	B	HCD	FT	5	60.9	VEFEITNGAK	1108.6	R	G	1.3	0.0	33.8	15.3
P0A972	7445.6	S	U	T	C	HCD	FT	3	68.1	GFGFITPEDGSKDVFVHFSAIQTNGFK	2945.4	K	T	5.3	0.0	38.9	18.4
P0A972	7445.6	S	U	T	C	HCD	FT	3	68.1	GPSAANVIAL	912.5	K	-	2.7	0.4	43.3	13.6
P0A972	7445.6	S	U	T	C	HCD	FT	3	68.1	VEFEITNGAK	1108.6	R	G	1.8	0.8	33.3	15.2
P0ADW8	7580.6	G	U	A	B	CID	LIT	2	39.4	DIVECVKCGHQMREA	1831.8	I	D	3.1	0.0	17.9	10.8
P0ADW8	7580.6	G	U	A	B	CID	LIT	2	39.4	DSMAMWRENNI	1366.6	Q	D	3.0	0.0	20.8	9.0
P36995	7698.9	G	U	T	A	CID	LIT	2	26.8	MTGLVK	648.4	K	W	1.7	0.4	4.0	16.9
P36995	7698.9	G	U	T	A	CID	LIT	2	26.8	TLFEGQK	822.4	R	V	2.4	0.6	24.6	14.1
P36995	7698.9	G	U	T	A	CID	LIT	2	26.8	WFNADK	780.4	K	G	1.8	0.7	14.6	11.5
P0C0L9	7714.0	G	U	T	A	CID	LIT	2	60.6	EIGEALYDAYPDLDPK	1808.9	R	T	3.1	0.0	61.3	11.1
P0C0L9	7714.0	G	U	T	A	CID	LIT	2	60.6	FTDMHQWICDLEDFDDDPQASNEK	2956.2	R	I	3.5	0.0	73.4	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C0L9	7714.0	G	U	A	A	CID	LIT	3	36.4	DAYPDLDPKTVRFT	1637.8	Y	D	1.9	0.6	30.6	14.1
P0C0L9	7714.0	G	U	A	A	CID	LIT	3	36.4	DLDPKTVRFT	1191.6	P	D	2.1	0.7	30.2	15.9
P0C0L9	7714.0	G	U	A	A	CID	LIT	3	36.4	DSREIGEALY	1152.6	T	D	2.6	0.7	25.0	13.6
P0C0L9	7714.0	G	U	T	B	CID	LIT	2	60.6	EIGEALYDAYPDLDPK	1808.9	R	T	3.4	0.0	82.4	10.8
P0C0L9	7714.0	G	U	T	B	CID	LIT	2	60.6	FTDMHQWICDLEDFDDDPQASNEK	2956.2	R	I	5.6	0.0	50.8	0.0
P0C0L9	7714.0	G	U	A	B	CID	LIT	4	47.0	DDPQASNEKIL	1229.6	D	E	2.0	0.5	6.2	12.0
P0C0L9	7714.0	G	U	A	B	CID	LIT	4	47.0	DLDPKTVRFT	1191.6	P	D	1.5	0.3	18.3	15.6
P0C0L9	7714.0	G	U	A	B	CID	LIT	4	47.0	DPKTVRFT	963.5	L	D	2.1	0.3	22.4	15.2
P0C0L9	7714.0	G	U	A	B	CID	LIT	4	47.0	DSREIGEALY	1152.6	T	D	2.3	0.8	26.9	13.6
P0C0L9	7714.0	S	U	T	B	ETD+CID	LIT	2	31.8	EIGEALYDAYPDLDPK	1808.9	R	T	3.6	0.5	30.6	16.5
P0C0L9	7714.0	S	U	T	B	ETD+CID	LIT	2	31.8	WTDSR	664.3	K	E	1.6	0.6	16.1	8.5
P0A7M9	7853.1	G	U	T	A	CID	LIT	3	51.4	FNIPGSK	762.4	R	-	2.2	0.3	28.5	15.6
P0A7M9	7853.1	G	U	T	A	CID	LIT	3	51.4	STVGHDLNLDVCSK	1544.7	R	C	5.2	0.9	66.2	11.8
P0A7M9	7853.1	G	U	T	A	CID	LIT	3	51.4	YEEITASCSCGNVMK	1748.7	K	I	4.4	0.0	101.0	6.0
P0A7M9	7853.1	G	T	T	A	CID	LIT	6	78.6	CHPFFTGK	993.5	K	Q	3.0	0.6	20.9	9.5
P0A7M9	7853.1	G	T	T	A	CID	LIT	6	78.6	DVATGGRVDR	1045.5	R	F	2.4	0.2	36.6	13.4
P0A7M9	7853.1	G	T	T	A	CID	LIT	6	78.6	FNIPGSK	762.4	R	-	1.9	0.3	31.0	15.6
P0A7M9	7853.1	G	T	T	A	CID	LIT	6	78.6	RFNIPGSK	918.5	K	-	2.2	0.3	6.8	13.4
P0A7M9	7853.1	G	T	T	A	CID	LIT	6	78.6	STVGHDLNLDVCSK	1544.7	R	C	4.8	0.7	80.2	11.8
P0A7M9	7853.1	G	T	T	A	CID	LIT	6	78.6	YEEITASCSCGNVMK	1764.7	K	I	4.7	0.0	105.0	0.0
P0A7M9	7853.1	G	U	A	A	CID	LIT	3	71.4	DIHPKYEEITASCSCGNVMKIRSTVGH	3089.5	K	D	4.8	0.5	22.5	8.5
P0A7M9	7853.1	G	U	A	A	CID	LIT	3	71.4	DVATGGRV	774.4	R	D	2.2	0.5	21.6	17.5
P0A7M9	7853.1	G	U	A	A	CID	LIT	3	71.4	DVCSKCHPFFTGKQR	1866.9	L	D	5.1	0.7	57.4	11.1
P0A7M9	7853.1	G	T	A	A	CID	LIT	3	71.4	DIHPKYEEITASCSCGNVMKIRSTVGH	3089.5	K	D	3.8	0.4	7.3	9.5
P0A7M9	7853.1	G	T	A	A	CID	LIT	3	71.4	DVATGGRV	774.4	R	D	2.3	0.6	24.8	17.5
P0A7M9	7853.1	G	T	A	A	CID	LIT	3	71.4	DVCSKCHPFFTGKQR	1866.9	L	D	4.3	0.7	61.3	11.5
P0A7M9	7853.1	G	T	T	B	CID	LIT	2	35.7	DVATGGRVDR	1045.5	R	F	2.5	0.1	29.4	13.2
P0A7M9	7853.1	G	T	T	B	CID	LIT	2	35.7	YEEITASCSCGNVMK	1748.7	K	I	4.5	0.0	66.0	6.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7M9	7853.1	G	U	T	B	CID	LIT	4	61.4	DVATGGR	675.3	R	V	2.4	0.4	28.5	16.0
P0A7M9	7853.1	G	U	T	B	CID	LIT	4	61.4	FNIPGSK	762.4	R	-	2.1	0.2	35.8	15.6
P0A7M9	7853.1	G	U	T	B	CID	LIT	4	61.4	STVGHDLNLDVCSK	1544.7	R	C	4.4	0.8	57.7	11.8
P0A7M9	7853.1	G	U	T	B	CID	LIT	4	61.4	YEEITASCSCGNVMK	1748.7	K	I	4.7	0.0	87.6	6.0
P0A7M9	7853.1	G	T	A	B	CID	LIT	2	60.0	DIHPKYEEITASCSCGNVMKIRSTVGH	3089.5	K	D	3.5	0.0	10.8	9.0
P0A7M9	7853.1	G	T	A	B	CID	LIT	2	60.0	DVCSKCHPFFTGKQR	1866.9	L	D	3.9	0.0	71.1	11.1
P0A7M9	7853.1	G	U	A	B	CID	LIT	4	90.0	DIHPKYEEITASCSCGNVMKIRSTVGH	3089.5	K	D	3.6	0.0	38.6	9.0
P0A7M9	7853.1	G	U	A	B	CID	LIT	4	90.0	DRFNKRFNIPGSK	1578.9	V	-	2.3	0.8	13.7	13.6
P0A7M9	7853.1	G	U	A	B	CID	LIT	4	90.0	DVATGGRV	774.4	R	D	2.2	0.4	20.8	17.5
P0A7M9	7853.1	G	U	A	B	CID	LIT	4	90.0	DVCSKCHPFFTGKQR	1866.9	L	D	3.6	0.8	56.6	12.0
P0A7M9	7853.1	S	U	T	C	CID	LIT	3	51.4	FNIPGSK	762.4	R	-	1.8	0.0	28.9	16.9
P0A7M9	7853.1	S	U	T	C	CID	LIT	3	51.4	STVGHDLNLDVCSK	1544.7	R	C	4.3	0.5	53.6	14.3
P0A7M9	7853.1	S	U	T	C	CID	LIT	3	51.4	YEEITASCSCGNVMK	1748.7	K	I	3.3	0.8	46.2	9.5
P0A7M9	7853.1	S	U	T	A	ETD	LIT	2	41.4	STVGHDLNLDVCSK	1544.7	R	C	2.5	0.8	25.0	14.9
P0A7M9	7853.1	S	U	T	A	ETD	LIT	2	41.4	YEEITASCSCGNVMK	1748.7	K	I	0.7	0.0	22.8	9.0
P0A7M9	7853.1	S	U	T	B	ETD	LIT	2	41.4	STVGHDLNLDVCSK	1544.7	R	C	5.0	0.5	43.7	14.9
P0A7M9	7853.1	S	U	T	B	ETD	LIT	2	41.4	YEEITASCSCGNVMK	1748.7	K	I	1.0	0.0	34.7	9.0
P0A7M9	7853.1	S	U	T	C	ETD	LIT	3	52.9	CHPFFTGK	993.5	K	Q	1.8	0.5	15.5	12.6
P0A7M9	7853.1	S	U	T	C	ETD	LIT	3	52.9	STVGHDLNLDVCSK	1544.7	R	C	3.5	0.5	0.0	0.0
P0A7M9	7853.1	S	U	T	C	ETD	LIT	3	52.9	YEEITASCSCGNVMK	1748.7	K	I	0.0	0.0	44.0	9.5
P0A7M9	7853.1	S	U	T	C	ETD+CID	LIT	2	31.4	FNIPGSK	762.4	R	-	2.0	0.4	26.2	16.1
P0A7M9	7853.1	S	U	T	C	ETD+CID	LIT	2	31.4	YEEITASCSCGNVMK	1748.7	K	I	0.0	0.0	69.2	9.5
P65294	7859.0	G	T	A	A	CID	LIT	2	25.0	DGRMILT	805.4	K	D	1.7	0.1	26.9	13.4
P65294	7859.0	G	T	A	A	CID	LIT	2	25.0	DQQGNAMQINR	1290.6	H	D	3.6	0.0	62.7	11.1
P26649	7873.9	G	U	T	B	CID	LIT	2	27.3	ELELEH	769.4	R	-	1.7	0.0	28.9	8.5
P26649	7873.9	G	U	T	B	CID	LIT	2	27.3	YAWYCQQMMQAR	1635.7	R	E	3.1	0.0	56.5	0.0
P0ACX5	7889.3	G	U	T	A	CID	LIT	3	33.3	HIVIAGVLR	977.6	K	T	2.6	0.0	28.8	0.0
P0ACX5	7889.3	G	U	T	A	CID	LIT	3	33.3	TKEDELYR	1053.5	R	E	2.4	0.3	11.4	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACX5	7889.3	G	U	T	A	CID	LIT	3	33.3	VVLEMR	746.4	K	D	1.4	0.6	12.3	14.1
P0ACX5	7889.3	G	U	T	B	CID	LIT	3	36.2	QAMETVINALVK	1316.7	K	-	3.1	0.4	64.3	11.8
P0ACX5	7889.3	G	U	T	B	CID	LIT	3	36.2	TALANKR	773.5	R	I	1.7	0.0	18.8	14.9
P0ACX5	7889.3	G	U	T	B	CID	LIT	3	36.2	VVLEMR	746.4	K	D	1.5	0.6	10.4	14.1
P0A968	7950.6	G	U	T	A	CID	LIT	5	91.9	AGQSVQFDVHQGPK	1497.7	K	G	4.9	0.8	86.6	9.5
P0A968	7950.6	G	U	T	A	CID	LIT	5	91.9	GFGFICPEGGGEDIFAHYSTIQMDGYR	3040.3	K	T	3.6	0.0	21.6	7.0
P0A968	7950.6	G	U	T	A	CID	LIT	5	91.9	GNHASVIVPVEVEAAVA	1661.9	K	-	2.2	0.4	9.6	13.4
P0A968	7950.6	G	U	T	A	CID	LIT	5	91.9	MEKGTVK	792.4	-	W	1.9	0.5	9.5	13.8
P0A968	7950.6	G	U	T	A	CID	LIT	5	91.9	TLKAGQSVQFDVHQGPK	1840.0	R	G	3.5	0.8	11.8	12.0
P0A968	7950.6	G	T	T	A	CID	LIT	2	23.0	AGQSVQFDVHQGPK	1497.7	K	G	4.6	0.8	83.3	10.0
P0A968	7950.6	G	T	T	A	CID	LIT	2	23.0	TLKAGQSVQFDVHQGPK	1840.0	R	G	4.5	0.0	55.4	12.0
P0A968	7950.6	G	U	A	A	CID	LIT	2	51.4	DGYRTLKAGQSVQF	1569.8	M	D	3.0	0.5	22.9	13.6
P0A968	7950.6	G	U	A	A	CID	LIT	2	51.4	DVHQGPKGNHASVIVPVEVEAAVA	2423.3	F	-	4.4	0.7	35.9	14.6
P0A968	7950.6	G	T	A	A	CID	LIT	2	51.4	DGYRTLKAGQSVQF	1569.8	M	D	2.6	0.8	27.4	13.6
P0A968	7950.6	G	T	A	A	CID	LIT	2	51.4	DVHQGPKGNHASVIVPVEVEAAVA	2423.3	F	-	3.3	0.0	34.6	14.6
P0A968	7950.6	G	T	T	B	CID	LIT	2	41.9	AGQSVQFDVHQGPK	1497.7	K	G	2.4	0.7	23.3	10.0
P0A968	7950.6	G	T	T	B	CID	LIT	2	41.9	GNHASVIVPVEVEAAVA	1661.9	K	-	2.2	0.4	0.0	0.0
P0A968	7950.6	G	U	T	B	CID	LIT	2	41.9	AGQSVQFDVHQGPK	1497.7	K	G	4.0	0.0	59.2	9.5
P0A968	7950.6	G	U	T	B	CID	LIT	2	41.9	GNHASVIVPVEVEAAVA	1661.9	K	-	2.7	0.5	19.6	13.4
P0A968	7950.6	G	U	A	B	CID	LIT	2	33.8	DGYRTLKAGQSVQF	1569.8	M	D	3.5	0.5	34.0	14.9
P0A968	7950.6	G	U	A	B	CID	LIT	2	33.8	DIFAHYSTIQM	1325.6	E	D	2.7	0.0	29.3	15.2
P0A968	7950.6	S	U	T	A	CID	LIT	2	59.5	GFGFICPEGGGEDIFAHYSTIQMDGYR	3024.3	K	T	4.6	0.0	36.2	12.3
P0A968	7950.6	S	U	T	A	CID	LIT	2	59.5	GNHASVIVPVEVEAAVA	1661.9	K	-	1.8	0.5	0.0	0.0
P0A968	7950.6	S	U	T	C	CID	LIT	3	78.4	AGQSVQFDVHQGPK	1497.7	K	G	1.9	0.5	0.0	0.0
P0A968	7950.6	S	U	T	C	CID	LIT	3	78.4	GFGFICPEGGGEDIFAHYSTIQMDGYR	3024.3	K	T	4.4	0.0	33.7	12.3
P0A968	7950.6	S	U	T	C	CID	LIT	3	78.4	GNHASVIVPVEVEAAVA	1661.9	K	-	2.9	0.6	24.7	16.8
P0A968	7950.6	S	U	T	B	ETD	LIT	2	55.4	AGQSVQFDVHQGPK	1497.7	K	G	2.7	0.5	48.7	15.3
P0A968	7950.6	S	U	T	B	ETD	LIT	2	55.4	GFGFICPEGGGEDIFAHYSTIQMDGYR	3024.3	K	T	3.9	0.0	32.3	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A968	7950.6	S	U	T	C	ETD	LIT	3	78.4	AGQSVQFDVHQGPK	1497.7	K	G	2.4	0.5	48.8	15.9
P0A968	7950.6	S	U	T	C	ETD	LIT	3	78.4	GFGFICPEGGGEDIFAHYSTIQMDGYR	3024.3	K	T	0.0	0.0	57.5	12.3
P0A968	7950.6	S	U	T	C	ETD	LIT	3	78.4	GNHASVIVPVEVEAAVA	1661.9	K	-	3.2	0.4	0.0	0.0
P0A968	7950.6	S	U	T	C	ETD+CID	LIT	2	41.9	AGQSVQFDVHQGPK	1497.7	K	G	2.0	0.4	3.0	16.1
P0A968	7950.6	S	U	T	C	ETD+CID	LIT	2	41.9	GNHASVIVPVEVEAAVA	1661.9	K	-	2.1	0.6	14.6	17.6
P76575	7975.8	G	U	T	A	CID	LIT	3	57.7	ACGAVDYFCQHGHGLISK	2019.9	K	K	5.3	0.0	64.9	8.5
P76575	7975.8	G	U	T	A	CID	LIT	3	57.7	ALCPDCHQPLQVLK	1678.8	K	A	3.5	0.6	32.7	12.3
P76575	7975.8	G	U	T	A	CID	LIT	3	57.7	SCGEFIEMK	1116.5	R	A	2.4	0.0	42.6	0.0
P76575	7975.8	G	U	T	B	CID	LIT	4	67.6	ACGAVDYFCQHGHGLISK	2019.9	K	K	4.3	0.0	56.0	9.0
P76575	7975.8	G	U	T	B	CID	LIT	4	67.6	ALCPDCHQPLQVLK	1678.8	K	A	2.3	0.3	13.4	12.3
P76575	7975.8	G	U	T	B	CID	LIT	4	67.6	RVEFVLA	833.5	K	-	1.2	0.2	16.6	11.5
P76575	7975.8	G	U	T	B	CID	LIT	4	67.6	SCGEFIEMK	1100.5	R	A	2.9	0.0	32.1	0.0
P76575	7975.8	G	U	A	B	CID	LIT	2	38.0	DCHQPLQVLKACGAV	1695.8	P	D	3.7	0.7	21.5	15.4
P76575	7975.8	G	U	A	B	CID	LIT	2	38.0	MELHCPQCQHVL	1551.7	-	D	3.1	0.7	24.3	13.8
P76575	7975.8	S	U	T	A	CID	LIT	2	45.1	ACGAVDYFCQHGHGLISK	2019.9	K	K	2.8	0.8	2.4	14.5
P76575	7975.8	S	U	T	A	CID	LIT	2	45.1	ALCPDCHQPLQVLK	1678.8	K	A	3.6	0.4	27.4	16.8
P76575	7975.8	S	U	T	B	CID	LIT	3	46.5	ACGAVDYFCQHGHGLISK	2019.9	K	K	3.2	0.5	0.5	14.5
P76575	7975.8	S	U	T	B	CID	LIT	3	46.5	ACGAVDYFCQHGHGLISKK	2148.0	K	R	2.4	0.3	11.6	17.5
P76575	7975.8	S	U	T	B	CID	LIT	3	46.5	ALCPDCHQPLQVLK	1678.8	K	A	4.3	0.5	57.2	17.3
P76575	7975.8	S	U	T	C	CID	LIT	4	74.6	ACGAVDYFCQHGHGLISK	2019.9	K	K	6.1	0.7	61.5	14.8
P76575	7975.8	S	U	T	C	CID	LIT	4	74.6	ACGAVDYFCQHGHGLISKK	2148.0	K	R	4.8	0.6	56.5	17.6
P76575	7975.8	S	U	T	C	CID	LIT	4	74.6	ALCPDCHQPLQVLK	1678.8	K	A	3.6	0.5	26.5	16.9
P76575	7975.8	S	U	T	C	CID	LIT	4	74.6	MELHCPQCQHVLDQDNGHAR	2445.1	-	C	3.1	0.7	22.3	10.0
P76575	7975.8	S	U	T	A	ETD	LIT	3	73.2	ACGAVDYFCQHGHGLISK	2019.9	K	K	5.9	0.0	55.3	14.5
P76575	7975.8	S	U	T	A	ETD	LIT	3	73.2	ALCPDCHQPLQVLK	1678.8	K	A	3.0	0.4	0.0	0.0
P76575	7975.8	S	U	T	A	ETD	LIT	3	73.2	MELHCPQCQHVLDQDNGHAR	2446.0	-	C	5.0	0.0	16.5	7.8
P76575	7975.8	S	U	T	B	ETD	LIT	3	73.2	ACGAVDYFCQHGHGLISK	2019.9	K	K	0.0	0.0	67.5	15.2
P76575	7975.8	S	U	T	B	ETD	LIT	3	73.2	ALCPDCHQPLQVLK	1678.8	K	A	3.9	0.4	18.0	17.6

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		digestion	lysis	protease	replicate												
P76575	7975.8	S	U	T	B	ETD	LIT	3	73.2	MELHCPQCQHVLDQDNGHAR	2446.0	-	C	3.9	0.0	25.0	7.8
P76575	7975.8	S	U	T	C	ETD	LIT	3	59.2	ALCPDCHQPLQVLK	1678.8	K	A	2.6	0.3	3.1	17.5
P76575	7975.8	S	U	T	C	ETD	LIT	3	59.2	KRVEFVLA	961.6	K	-	1.5	0.3	11.4	12.3
P76575	7975.8	S	U	T	C	ETD	LIT	3	59.2	MELHCPQCQHVLDQDNGHAR	2446.0	-	C	5.4	0.0	29.3	7.8
P76575	7975.8	S	U	T	B	ETD+CID	LIT	2	26.8	ACGAVDYFCQHGHGLISK	2019.9	K	K	0.0	0.0	73.0	14.6
P76575	7975.8	S	U	T	B	ETD+CID	LIT	2	26.8	ACGAVDYFCQHGHGLISKK	2148.0	K	R	0.0	0.0	42.8	17.2
P76575	7975.8	S	U	T	B	ETD+CID	LIT	3	46.5	ACGAVDYFCQHGHGLISK	2019.9	K	K	0.0	0.0	73.0	14.6
P76575	7975.8	S	U	T	B	ETD+CID	LIT	3	46.5	ACGAVDYFCQHGHGLISKK	2148.0	K	R	0.0	0.0	42.8	17.2
P76575	7975.8	S	U	T	B	ETD+CID	LIT	3	46.5	ALCPDCHQPLQVLK	1678.8	K	A	0.0	0.0	17.2	17.3
P76575	7975.8	S	U	T	B	ETD+CID	LIT	2	26.8	ACGAVDYFCQHGHGLISK	2019.9	K	K	7.6	0.0	73.0	14.6
P76575	7975.8	S	U	T	B	ETD+CID	LIT	2	26.8	ACGAVDYFCQHGHGLISKK	2148.0	K	R	0.4	-0.9	42.8	17.2
P76575	7975.8	S	U	T	B	ETD+CID	LIT	2	26.8	YDTYSGR	861.4	-	-	1.9	0.3	20.3	7.0
P76575	7975.8	S	U	T	C	ETD+CID	LIT	3	54.9	ACGAVDYFCQHGHGLISK	2019.9	K	K	0.0	0.0	62.8	13.2
P76575	7975.8	S	U	T	C	ETD+CID	LIT	3	54.9	ACGAVDYFCQHGHGLISKK	2148.0	K	R	5.6	0.7	58.0	17.7
P76575	7975.8	S	U	T	C	ETD+CID	LIT	3	54.9	MELHCPQCQHVLDQDNGHAR	2446.0	-	C	5.0	0.0	48.7	7.8
P76575	7975.8	S	U	T	B	HCD	FT	2	26.8	ACGAVDYFCQHGHGLISK	2019.9	K	K	0.0	0.0	76.8	15.1
P76575	7975.8	S	U	T	B	HCD	FT	2	26.8	ACGAVDYFCQHGHGLISKK	2148.0	K	R	0.0	0.0	26.0	17.2
Q2M7R5	7977.8	G	U	T	A	CID	LIT	5	69.6	AVDFMASSQAFR	1329.6	K	E	3.7	0.8	70.5	10.0
Q2M7R5	7977.8	G	U	T	A	CID	LIT	5	69.6	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	42.5	7.0
Q2M7R5	7977.8	G	U	T	A	CID	LIT	5	69.6	LGENVPLLIDK	1210.7	K	A	3.3	0.6	34.6	7.0
Q2M7R5	7977.8	G	U	T	A	CID	LIT	5	69.6	LYRPK	676.4	R	Q	1.5	0.7	10.1	11.1
Q2M7R5	7977.8	G	U	T	A	CID	LIT	5	69.6	NAIPSGIPDESVPLYLQR	1969.0	R	L	4.1	0.6	42.7	11.8
Q2M7R5	7977.8	G	T	T	A	CID	LIT	5	69.6	AVDFMASSQAFR	1345.6	K	E	3.4	0.8	59.3	8.5
Q2M7R5	7977.8	G	T	T	A	CID	LIT	5	69.6	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	59.9	7.0
Q2M7R5	7977.8	G	T	T	A	CID	LIT	5	69.6	LEYYR	743.4	R	R	1.5	0.5	16.6	12.3
Q2M7R5	7977.8	G	T	T	A	CID	LIT	5	69.6	LGENVPLLIDK	1210.7	K	A	3.4	0.8	23.4	7.0
Q2M7R5	7977.8	G	T	T	A	CID	LIT	5	69.6	NAIPSGIPDESVPLYLQR	1969.0	R	L	3.9	0.5	40.8	12.8
Q2M7R5	7977.8	G	T	A	A	CID	LIT	5	76.8	DESVPLYLQRL	1332.7	P	E	2.1	0.0	18.6	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
Q2M7R5	7977.8	G	T	A	A	CID	LIT	5	76.8	DFMASSQAFR	1159.5	V	E	2.5	0.0	37.3	12.6
Q2M7R5	7977.8	G	T	A	A	CID	LIT	5	76.8	DKAVDFMASSQAFR	1588.7	I	E	4.3	0.6	63.7	12.8
Q2M7R5	7977.8	G	T	A	A	CID	LIT	5	76.8	EYLKKLPPRNAIPSGIP	1893.1	R	D	2.1	0.0	21.1	8.5
Q2M7R5	7977.8	G	T	A	A	CID	LIT	5	76.8	GKLGENVPLLI	1152.7	M	D	0.0	0.0	25.6	3.0
Q2M7R5	7977.8	G	T	T	B	CID	LIT	3	36.2	AVDFMASSQAFR	1329.6	K	E	3.5	0.4	58.8	9.0
Q2M7R5	7977.8	G	T	T	B	CID	LIT	3	36.2	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	48.0	7.0
Q2M7R5	7977.8	G	T	T	B	CID	LIT	3	36.2	LGENVPLLIDK	1210.7	K	A	2.7	0.3	30.2	7.0
Q2M7R5	7977.8	G	U	T	B	CID	LIT	3	62.3	AVDFMASSQAFR	1329.6	K	E	3.7	0.9	70.8	10.0
Q2M7R5	7977.8	G	U	T	B	CID	LIT	3	62.3	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	33.2	7.8
Q2M7R5	7977.8	G	U	T	B	CID	LIT	3	62.3	NAIPSGIPDESVPLYLQR	1969.0	R	L	3.6	0.5	39.3	11.5
Q2M7R5	7977.8	G	T	A	B	CID	LIT	3	36.2	DFMASSQAFR	1159.5	V	E	3.1	0.8	35.9	10.4
Q2M7R5	7977.8	G	T	A	B	CID	LIT	3	36.2	DKAVDFMASSQAFR	1572.7	I	E	2.8	0.7	18.1	14.3
Q2M7R5	7977.8	G	T	A	B	CID	LIT	3	36.2	GKLGENVPLLI	1152.7	M	D	0.0	0.0	29.1	3.0
Q2M7R5	7977.8	S	U	T	A	CID	LIT	3	59.4	AVDFMASSQAFR	1329.6	K	E	1.9	0.4	11.2	13.4
Q2M7R5	7977.8	S	U	T	A	CID	LIT	3	59.4	LGENVPLLIDK	1210.7	K	A	2.6	0.4	32.9	10.4
Q2M7R5	7977.8	S	U	T	A	CID	LIT	3	59.4	NAIPSGIPDESVPLYLQR	1970.0	R	L	4.7	0.7	27.6	16.8
Q2M7R5	7977.8	S	U	T	B	CID	LIT	2	43.5	AVDFMASSQAFR	1329.6	K	E	2.2	0.7	2.0	13.6
Q2M7R5	7977.8	S	U	T	B	CID	LIT	2	43.5	NAIPSGIPDESVPLYLQR	1970.0	R	L	4.7	0.6	27.9	16.8
Q2M7R5	7977.8	S	U	T	C	CID	LIT	4	62.3	AVDFMASSQAFR	1329.6	K	E	4.0	0.6	38.9	13.6
Q2M7R5	7977.8	S	U	T	C	CID	LIT	4	62.3	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	47.8	9.5
Q2M7R5	7977.8	S	U	T	C	CID	LIT	4	62.3	LGENVPLLIDK	1210.7	K	A	3.5	0.8	46.2	10.4
Q2M7R5	7977.8	S	U	T	C	CID	LIT	4	62.3	NAIPSGIPDESVPLYLQR	1969.0	R	L	4.1	0.5	24.1	16.8
Q2M7R5	7977.8	S	U	T	A	ETD	LIT	2	42.0	LGENVPLLIDK	1210.7	K	A	3.1	0.4	27.5	10.4
Q2M7R5	7977.8	S	U	T	A	ETD	LIT	2	42.0	NAIPSGIPDESVPLYLQR	1969.0	R	L	0.0	0.0	46.6	17.2
Q2M7R5	7977.8	S	U	T	B	ETD	LIT	2	42.0	LGENVPLLIDK	1210.7	K	A	2.6	0.3	32.2	10.4
Q2M7R5	7977.8	S	U	T	B	ETD	LIT	2	42.0	NAIPSGIPDESVPLYLQR	1969.0	R	L	2.3	0.6	0.0	0.0
Q2M7R5	7977.8	S	U	T	C	ETD	LIT	3	44.9	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	33.2	9.5
Q2M7R5	7977.8	S	U	T	C	ETD	LIT	3	44.9	LGENVPLLIDK	1210.7	K	A	2.4	0.2	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
Q2M7R5	7977.8	S	U	T	C	ETD	LIT	3	44.9	NAIPSGIPDESVPLYLQR	1969.0	R	L	2.3	0.0	44.7	17.0
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	2	44.9	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	40.6	9.5
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	2	44.9	NAIPSGIPDESVPLYLQR	1969.0	R	L	0.0	0.0	63.4	16.9
Q2M7R5	7977.8	S	U	T	A	ETD+CID	LIT	4	62.3	AVDFMASSQAFR	1329.6	K	E	2.7	0.5	19.0	12.8
Q2M7R5	7977.8	S	U	T	A	ETD+CID	LIT	4	62.3	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	41.2	9.5
Q2M7R5	7977.8	S	U	T	A	ETD+CID	LIT	4	62.3	LGENVPLLIDK	1210.7	K	A	3.7	0.0	43.3	10.4
Q2M7R5	7977.8	S	U	T	A	ETD+CID	LIT	4	62.3	NAIPSGIPDESVPLYLQR	1969.0	R	L	4.8	0.6	64.0	16.9
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	2	43.5	AVDFMASSQAFR	1329.6	K	E	2.5	0.8	0.0	0.0
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	2	43.5	NAIPSGIPDESVPLYLQR	1970.0	R	L	3.3	0.7	0.0	0.0
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	4	62.3	AVDFMASSQAFR	1329.6	K	E	2.5	0.8	1.5	13.6
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	4	62.3	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	40.6	9.5
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	4	62.3	LGENVPLLIDK	1210.7	K	A	2.0	0.7	17.5	10.4
Q2M7R5	7977.8	S	U	T	B	ETD+CID	LIT	4	62.3	NAIPSGIPDESVPLYLQR	1969.0	R	L	4.6	0.6	0.0	0.0
Q2M7R5	7977.8	S	U	T	C	ETD+CID	LIT	4	62.3	AVDFMASSQAFR	1329.6	K	E	3.9	0.6	42.4	12.8
Q2M7R5	7977.8	S	U	T	C	ETD+CID	LIT	4	62.3	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	51.8	12.6
Q2M7R5	7977.8	S	U	T	C	ETD+CID	LIT	4	62.3	LGENVPLLIDK	1210.7	K	A	3.6	0.8	45.6	10.4
Q2M7R5	7977.8	S	U	T	C	ETD+CID	LIT	4	62.3	NAIPSGIPDESVPLYLQR	1969.0	R	L	3.7	0.5	21.7	17.1
Q2M7R5	7977.8	S	U	T	B	HCD	FT	2	44.9	GKLGENVPLLIDK	1395.8	M	A	0.0	0.0	40.6	9.5
Q2M7R5	7977.8	S	U	T	B	HCD	FT	2	44.9	NAIPSGIPDESVPLYLQR	1969.0	R	L	0.0	0.0	63.4	16.9
P0A8R4	8196.6	G	U	T	A	CID	LIT	5	59.7	ASQPSNIASQAEETPPPHY	2023.9	K	-	4.2	0.0	86.3	7.8
P0A8R4	8196.6	G	U	T	A	CID	LIT	5	59.7	LAELESR	817.4	R	L	2.5	0.6	36.2	15.9
P0A8R4	8196.6	G	U	T	A	CID	LIT	5	59.7	LKASQPSNIASQAEETPPPHY	2265.1	K	-	5.4	0.7	69.1	13.2
P0A8R4	8196.6	G	U	T	A	CID	LIT	5	59.7	LRDHLR	809.5	K	L	2.1	0.4	16.8	12.0
P0A8R4	8196.6	G	U	T	A	CID	LIT	5	59.7	MQDLSLEAR	1062.5	-	L	2.2	0.3	28.8	13.2
P0A8R4	8196.6	G	T	T	A	CID	LIT	2	18.1	LAELESR	817.4	R	L	2.1	0.6	11.6	15.3
P0A8R4	8196.6	G	T	T	A	CID	LIT	2	18.1	LRDHLR	809.5	K	L	1.9	0.0	18.7	12.0
P0A8R4	8196.6	G	U	T	B	CID	LIT	3	48.6	ASQPSNIASQAEETPPPHY	2023.9	K	-	3.8	0.0	87.5	8.5
P0A8R4	8196.6	G	U	T	B	CID	LIT	3	48.6	LAELESR	817.4	R	L	2.2	0.0	24.4	15.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8R4	8196.6	G	U	T	B	CID	LIT	3	48.6	MQDLSLEAR	1062.5	-	L	2.9	0.0	66.7	13.2
P0A8R4	8196.6	S	U	T	C	ETD+CID	LIT	2	36.1	ASQPSNIASQAEETPPPHY	2023.9	K	-	5.3	0.9	77.7	16.1
P0A8R4	8196.6	S	U	T	C	ETD+CID	LIT	2	36.1	LAELESR	817.4	R	L	1.8	0.5	1.3	18.5
P0AD07	8220.6	G	U	T	B	CID	LIT	2	51.4	QLALIEDETQAAVFSK	1762.9	K	T	4.4	0.0	63.0	12.6
P0AD07	8220.6	G	U	T	B	CID	LIT	2	51.4	STPDFSTAENNQELANEVSCLK	2454.1	M	A	0.0	0.0	99.1	9.5
P0AD07	8220.6	S	U	T	C	CID	LIT	2	51.4	QLALIEDETQAAVFSK	1762.9	K	T	4.1	0.6	42.0	17.6
P0AD07	8220.6	S	U	T	C	CID	LIT	2	51.4	STPDFSTAENNQELANEVSCLK	2454.1	M	A	0.0	0.0	120.0	14.3
P0AD07	8220.6	S	U	T	B	ETD+CID	LIT	2	51.4	QLALIEDETQAAVFSK	1762.9	K	T	0.0	0.0	34.8	17.9
P0AD07	8220.6	S	U	T	B	ETD+CID	LIT	2	51.4	STPDFSTAENNQELANEVSCLK	2454.1	M	A	0.0	0.0	96.6	14.1
P0AD07	8220.6	S	U	T	B	ETD+CID	LIT	2	51.4	QLALIEDETQAAVFSK	1762.9	K	T	3.0	0.4	34.8	17.9
P0AD07	8220.6	S	U	T	B	ETD+CID	LIT	2	51.4	STPDFSTAENNQELANEVSCLK	2454.1	M	A	0.0	0.0	96.6	14.1
P0AD07	8220.6	S	U	T	C	ETD+CID	LIT	2	51.4	QLALIEDETQAAVFSK	1762.9	K	T	3.9	0.5	39.4	17.8
P0AD07	8220.6	S	U	T	C	ETD+CID	LIT	2	51.4	STPDFSTAENNQELANEVSCLK	2454.1	M	A	0.0	0.0	87.0	14.1
P0AD07	8220.6	S	U	T	B	HCD	FT	2	51.4	QLALIEDETQAAVFSK	1762.9	K	T	0.0	0.0	34.8	17.9
P0AD07	8220.6	S	U	T	B	HCD	FT	2	51.4	STPDFSTAENNQELANEVSCLK	2454.1	M	A	0.0	0.0	96.6	14.1
P69222	8231.7	G	U	T	A	CID	LIT	6	86.1	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	114.0	12.6
P69222	8231.7	G	U	T	A	CID	LIT	6	86.1	EDNIEMQGTVLETLPNTMFR	2338.1	K	V	4.4	0.0	59.0	10.0
P69222	8231.7	G	U	T	A	CID	LIT	6	86.1	GRIVFR	747.5	K	S	1.9	0.3	24.1	4.8
P69222	8231.7	G	U	T	A	CID	LIT	6	86.1	ILTGDKVTVELTPYDLSK	1992.1	R	G	5.6	0.7	74.9	11.5
P69222	8231.7	G	U	T	A	CID	LIT	6	86.1	VELENGHVVTAHISGK	1689.9	R	M	5.2	0.8	89.1	12.3
P69222	8231.7	G	U	T	A	CID	LIT	6	86.1	VTVELTPYDLSK	1364.7	K	G	4.2	0.7	53.0	8.5
P69222	8231.7	G	T	T	A	CID	LIT	2	47.2	ILTGDKVTVELTPYDLSK	1992.1	R	G	5.4	0.0	49.3	11.5
P69222	8231.7	G	T	T	A	CID	LIT	2	47.2	VELENGHVVTAHISGK	1689.9	R	M	5.1	0.0	65.7	11.5
P69222	8231.7	G	U	T	B	CID	LIT	4	77.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	102.0	12.6
P69222	8231.7	G	U	T	B	CID	LIT	4	77.8	ILTGDKVTVELTPYDLSK	1992.1	R	G	5.4	0.8	62.8	10.0
P69222	8231.7	G	U	T	B	CID	LIT	4	77.8	VELENGHVVTAHISGK	1689.9	R	M	5.2	0.7	68.4	12.3
P69222	8231.7	G	U	T	B	CID	LIT	4	77.8	VTVELTPYDLSK	1364.7	K	G	4.0	0.8	52.4	9.5
P69222	8231.7	G	U	A	B	CID	LIT	2	27.8	DKVTVELTPY	1164.6	G	D	2.7	0.7	41.7	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69222	8231.7	G	U	A	B	CID	LIT	2	27.8	DNIEMQGTVL	1119.5	E	E	2.5	0.0	40.4	12.3
P69222	8231.7	S	U	T	A	CID	LIT	3	77.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	56.4	18.5
P69222	8231.7	S	U	T	A	CID	LIT	3	77.8	ILTGDKVTVELTPYDLSK	1992.1	R	G	6.1	0.7	82.1	15.8
P69222	8231.7	S	U	T	A	CID	LIT	3	77.8	VELENGHVVTAHISGK	1690.9	R	M	5.4	0.6	90.1	17.0
P69222	8231.7	S	U	T	B	CID	LIT	4	77.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	101.0	18.8
P69222	8231.7	S	U	T	B	CID	LIT	4	77.8	ILTGDKVTVELTPYDLSK	1992.1	R	G	6.1	0.7	63.0	15.6
P69222	8231.7	S	U	T	B	CID	LIT	4	77.8	VELENGHVVTAHISGK	1690.9	R	M	5.1	0.6	65.2	16.6
P69222	8231.7	S	U	T	B	CID	LIT	4	77.8	VTVELTPYDLSK	1364.7	K	G	3.3	0.0	44.9	13.0
P69222	8231.7	S	U	T	C	CID	LIT	5	84.7	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	82.4	18.6
P69222	8231.7	S	U	T	C	CID	LIT	5	84.7	ILTGDKVTVELTPYDLSK	1992.1	R	G	6.3	0.7	66.7	15.7
P69222	8231.7	S	U	T	C	CID	LIT	5	84.7	KNYIR	693.4	R	I	1.5	0.3	19.2	14.8
P69222	8231.7	S	U	T	C	CID	LIT	5	84.7	VELENGHVVTAHISGK	1689.9	R	M	5.9	0.7	90.3	16.2
P69222	8231.7	S	U	T	C	CID	LIT	5	84.7	VTVELTPYDLSK	1364.7	K	G	3.6	0.8	48.7	13.8
P69222	8231.7	S	U	T	C	CID	FT	2	52.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	49.6	18.8
P69222	8231.7	S	U	T	C	CID	FT	2	52.8	VELENGHVVTAHISGK	1690.9	R	M	4.3	0.0	93.2	16.3
P69222	8231.7	S	U	T	A	ETD	LIT	3	54.2	ILTGDKVTVELTPYDLSK	1992.1	R	G	4.1	0.5	0.0	0.0
P69222	8231.7	S	U	T	A	ETD	LIT	3	54.2	KNYIR	693.4	R	I	1.4	0.7	17.9	14.8
P69222	8231.7	S	U	T	A	ETD	LIT	3	54.2	VELENGHVVTAHISGK	1690.9	R	M	6.0	0.6	59.6	16.4
P69222	8231.7	S	U	T	B	ETD	LIT	3	77.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	30.9	18.6
P69222	8231.7	S	U	T	B	ETD	LIT	3	77.8	ILTGDKVTVELTPYDLSK	1992.1	R	G	4.3	0.6	57.0	16.4
P69222	8231.7	S	U	T	B	ETD	LIT	3	77.8	VELENGHVVTAHISGK	1690.9	R	M	6.7	0.5	79.2	17.2
P69222	8231.7	S	U	T	C	ETD	LIT	5	84.7	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	61.7	18.6
P69222	8231.7	S	U	T	C	ETD	LIT	5	84.7	ILTGDKVTVELTPYDLSK	1992.1	R	G	8.6	0.7	74.4	15.8
P69222	8231.7	S	U	T	C	ETD	LIT	5	84.7	KNYIR	693.4	R	I	1.6	0.6	24.3	14.8
P69222	8231.7	S	U	T	C	ETD	LIT	5	84.7	VELENGHVVTAHISGK	1690.9	R	M	4.1	0.6	63.3	16.1
P69222	8231.7	S	U	T	C	ETD	LIT	5	84.7	VTVELTPYDLSK	1364.7	K	G	2.5	0.5	37.5	13.0
P69222	8231.7	S	U	T	B	ETD+CID	LIT	2	55.6	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	79.1	18.7
P69222	8231.7	S	U	T	B	ETD+CID	LIT	2	55.6	ILTGDKVTVELTPYDLSK	1992.1	R	G	0.0	0.0	69.5	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69222	8231.7	S	U	T	A	ETD+CID	LIT	3	77.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	40.0	18.6
P69222	8231.7	S	U	T	A	ETD+CID	LIT	3	77.8	ILTGDKVTVELTPYDLSK	1992.1	R	G	4.6	0.6	37.7	15.7
P69222	8231.7	S	U	T	A	ETD+CID	LIT	3	77.8	VELENGHVVTAHISGK	1690.9	R	M	5.5	0.7	81.5	16.1
P69222	8231.7	S	U	T	B	ETD+CID	LIT	3	77.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	79.1	18.7
P69222	8231.7	S	U	T	B	ETD+CID	LIT	3	77.8	ILTGDKVTVELTPYDLSK	1992.1	R	G	6.2	0.7	69.5	15.8
P69222	8231.7	S	U	T	B	ETD+CID	LIT	3	77.8	VELENGHVVTAHISGK	1690.9	R	M	2.3	0.7	9.7	17.2
P69222	8231.7	S	U	T	C	ETD+CID	LIT	4	77.8	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	88.6	18.8
P69222	8231.7	S	U	T	C	ETD+CID	LIT	4	77.8	ILTGDKVTVELTPYDLSK	1992.1	R	G	6.0	0.7	71.2	15.8
P69222	8231.7	S	U	T	C	ETD+CID	LIT	4	77.8	VELENGHVVTAHISGK	1689.9	R	M	5.7	0.7	83.5	17.0
P69222	8231.7	S	U	T	C	ETD+CID	LIT	4	77.8	VTVELTPYDLSK	1364.7	K	G	3.2	0.8	38.3	13.8
P69222	8231.7	S	U	T	B	HCD	FT	2	55.6	AKEDNIEMQGTVLETLPNTMFR	2537.2	M	V	0.0	0.0	79.1	18.7
P69222	8231.7	S	U	T	B	HCD	FT	2	55.6	ILTGDKVTVELTPYDLSK	1992.1	R	G	0.0	0.0	69.5	15.8
P69222	8231.7	S	U	T	B	HCD	FT	3	45.8	KNYIR	693.4	R	I	1.2	0.0	21.1	14.8
P69222	8231.7	S	U	T	B	HCD	FT	3	45.8	VELENGHVVTAHISGK	1690.9	R	M	1.8	0.7	29.6	16.1
P69222	8231.7	S	U	T	B	HCD	FT	3	45.8	VTVELTPYDLSK	1364.7	K	G	2.6	0.0	49.3	13.0
P0AD24	8270.7	G	T	T	A	CID	LIT	2	28.0	ALQSSINEDKAH	1312.6	R	-	4.0	0.8	75.0	12.0
P0AD24	8270.7	G	T	T	A	CID	LIT	2	28.0	QAIANSFAR	977.5	R	A	2.2	0.0	37.0	12.3
P69776	8305.7	G	U	T	A	CID	LIT	2	33.3	IDQLSSDVQTLNAK	1531.8	K	V	3.0	0.7	47.6	14.3
P69776	8305.7	G	U	T	A	CID	LIT	2	33.3	SDVQAAKDDAAR	1246.6	R	A	3.5	0.8	50.5	10.4
P69776	8305.7	G	U	A	A	CID	LIT	3	32.1	DDAARANQRL	1129.6	K	D	1.5	0.6	11.6	14.3
P69776	8305.7	G	U	A	A	CID	LIT	3	32.1	DNMATKYRK	1126.6	L	-	2.9	0.5	35.1	13.4
P69776	8305.7	G	U	A	A	CID	LIT	3	32.1	DVQAAKDDAARANQRL	1741.9	S	D	2.1	0.5	14.0	14.6
P69776	8305.7	G	U	T	B	CID	LIT	3	48.7	IDQLSSDVQTLNAK	1531.8	K	V	3.5	0.5	56.3	14.3
P69776	8305.7	G	U	T	B	CID	LIT	3	48.7	SDVQAAKDDAAR	1246.6	R	A	3.3	0.8	51.3	10.4
P69776	8305.7	G	U	T	B	CID	LIT	3	48.7	VDQLSNDVNAMR	1377.6	K	S	3.4	0.5	41.8	9.5
P69776	8305.7	G	T	A	B	CID	LIT	2	24.4	DDAARANQRL	1129.6	K	D	2.5	0.0	20.0	14.3
P69776	8305.7	G	T	A	B	CID	LIT	2	24.4	DVQTLNAKV	987.5	S	D	1.6	0.5	10.3	16.9
P69776	8305.7	G	U	A	B	CID	LIT	3	35.9	DDAARANQRL	1129.6	K	D	1.8	0.5	26.5	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69776	8305.7	G	U	A	B	CID	LIT	3	35.9	DNMATKYRK	1126.6	L	-	2.3	0.4	0.0	0.0
P69776	8305.7	G	U	A	B	CID	LIT	3	35.9	DVQTLNAKV	987.5	S	D	3.0	0.6	31.3	16.9
P69776	8305.7	S	U	T	C	ETD+CID	LIT	2	30.8	SDVQAAKDDAAR	1246.6	R	A	2.8	0.8	4.7	15.2
P69776	8305.7	S	U	T	C	ETD+CID	LIT	2	30.8	VDQLSNDVNAMR	1361.6	K	S	1.8	0.5	0.0	0.0
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	DQAEKEVVDWETR	1604.8	K	N	4.5	0.8	58.5	7.8
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	EVVDWETR	1033.5	K	N	2.2	0.8	23.8	10.8
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	LTDDDMTIIEGK	1366.6	K	R	3.4	0.6	67.1	13.2
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	LTDDDMTIIEGKR	1506.7	K	D	4.0	0.8	119.0	12.0
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	MNKDEAGGNWK	1249.6	-	Q	3.9	0.8	49.6	10.4
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	RDQLVGK	815.5	K	I	2.2	0.5	26.1	17.3
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	VKEQWGK	874.5	K	L	2.4	0.4	21.5	16.0
P68206	8307.3	G	U	T	A	CID	LIT	8	79.7	YGYQKDQAEK	1229.6	R	E	4.0	0.8	60.7	7.8
P68206	8307.3	G	T	T	A	CID	LIT	7	71.0	DQAEKEVVDWETR	1604.8	K	N	4.1	0.8	75.7	8.5
P68206	8307.3	G	T	T	A	CID	LIT	7	71.0	EVVDWETR	1033.5	K	N	2.1	0.0	32.1	11.1
P68206	8307.3	G	T	T	A	CID	LIT	7	71.0	LTDDDMTIIEGK	1350.6	K	R	3.1	0.6	62.8	12.8
P68206	8307.3	G	T	T	A	CID	LIT	7	71.0	LTDDDMTIIEGKR	1506.7	K	D	4.0	0.0	79.4	12.3
P68206	8307.3	G	T	T	A	CID	LIT	7	71.0	MNKDEAGGNWK	1249.6	-	Q	2.5	0.4	10.6	10.0
P68206	8307.3	G	T	T	A	CID	LIT	7	71.0	VKEQWGK	874.5	K	L	2.1	0.4	30.8	16.0
P68206	8307.3	G	T	T	A	CID	LIT	7	71.0	YGYQKDQAEK	1229.6	R	E	3.6	0.9	48.2	7.8
P68206	8307.3	G	U	A	A	CID	LIT	7	94.2	DDMTIIEGKR	1177.6	D	D	2.8	0.4	15.9	17.2
P68206	8307.3	G	U	A	A	CID	LIT	7	94.2	DEAGGNWKQFKGKVKEQWGKLT	2534.3	K	D	2.8	0.7	0.0	0.0
P68206	8307.3	G	U	A	A	CID	LIT	7	94.2	DMTIIEGKR	1078.6	D	D	2.0	0.6	14.7	17.2
P68206	8307.3	G	U	A	A	CID	LIT	7	94.2	DQAEKEVV	917.5	K	D	2.2	0.5	27.6	16.1
P68206	8307.3	G	U	A	A	CID	LIT	7	94.2	DQLVGKIQ	900.5	R	E	2.1	0.1	17.2	15.8
P68206	8307.3	G	U	A	A	CID	LIT	7	94.2	DQLVGKIQERYGYQK	1825.0	R	D	4.8	0.6	63.7	15.6
P68206	8307.3	G	U	A	A	CID	LIT	7	94.2	DWETRNEYRW	1454.6	V	-	2.4	0.3	7.9	11.5
P68206	8307.3	G	T	A	A	CID	LIT	3	65.2	DEAGGNWKQFKGKVKEQWGKLT	2534.3	K	D	3.1	0.7	0.0	0.0
P68206	8307.3	G	T	A	A	CID	LIT	3	65.2	DQAEKEVV	917.5	K	D	1.7	0.5	14.7	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68206	8307.3	G	T	A	A	CID	LIT	3	65.2	DQLVGKIQERYGYQK	1825.0	R	D	2.8	0.6	12.8	14.9
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	DQAEKEVVDWETR	1604.8	K	N	3.9	0.7	48.2	7.8
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	DQLVGKIQER	1185.7	R	Y	2.6	0.1	23.4	12.8
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	EQWGKLTDDDMTIIEGK	1978.9	K	R	6.2	0.6	69.9	11.5
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	EVVDWETR	1033.5	K	N	2.2	0.8	16.6	11.8
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	LTDDDMTIIEGK	1350.6	K	R	4.1	0.7	70.8	13.2
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	LTDDDMTIIEGKR	1506.7	K	D	3.2	0.6	46.9	13.2
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	MNKDEAGGNWK	1249.6	-	Q	4.2	0.5	42.3	10.0
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	RDQLVGK	815.5	K	I	1.8	0.4	11.0	17.5
P68206	8307.3	G	T	T	B	CID	LIT	9	82.6	YGYQKDQAEK	1229.6	R	E	3.8	0.8	69.0	7.8
P68206	8307.3	G	U	T	B	CID	LIT	6	60.9	DQAEKEVVDWETR	1604.8	K	N	4.7	0.0	75.7	7.8
P68206	8307.3	G	U	T	B	CID	LIT	6	60.9	EVVDWETR	1033.5	K	N	2.3	0.6	13.1	11.8
P68206	8307.3	G	U	T	B	CID	LIT	6	60.9	LTDDDMTIIEGK	1350.6	K	R	3.3	0.8	44.7	12.6
P68206	8307.3	G	U	T	B	CID	LIT	6	60.9	LTDDDMTIIEGKR	1506.7	K	D	3.8	0.0	90.4	12.3
P68206	8307.3	G	U	T	B	CID	LIT	6	60.9	MNKDEAGGNWK	1249.6	-	Q	3.1	0.0	53.9	10.0
P68206	8307.3	G	U	T	B	CID	LIT	6	60.9	YGYQKDQAEK	1229.6	R	E	3.8	0.0	53.0	7.8
P68206	8307.3	G	T	A	B	CID	LIT	5	94.2	DDMTIIEGKR	1177.6	D	D	2.9	0.4	43.6	16.6
P68206	8307.3	G	T	A	B	CID	LIT	5	94.2	DEAGGNWKQFKGKVKEQWGKLT	2534.3	K	D	2.6	0.6	0.0	0.0
P68206	8307.3	G	T	A	B	CID	LIT	5	94.2	DQAEKEVV	917.5	K	D	2.0	0.7	23.9	16.1
P68206	8307.3	G	T	A	B	CID	LIT	5	94.2	DQLVGKIQERYGYQK	1825.0	R	D	4.5	0.7	53.1	14.9
P68206	8307.3	G	T	A	B	CID	LIT	5	94.2	DWETRNEYRW	1454.6	V	-	1.7	0.6	10.6	11.5
P68206	8307.3	G	U	A	B	CID	LIT	6	94.2	DDMTIIEGKR	1177.6	D	D	2.8	0.4	23.1	17.2
P68206	8307.3	G	U	A	B	CID	LIT	6	94.2	DEAGGNWKQFKGKVKEQWGKLT	2534.3	K	D	3.6	0.5	19.4	15.7
P68206	8307.3	G	U	A	B	CID	LIT	6	94.2	DQAEKEVV	917.5	K	D	2.4	0.5	24.0	16.1
P68206	8307.3	G	U	A	B	CID	LIT	6	94.2	DQLVGKIQ	900.5	R	E	2.5	0.1	38.0	15.8
P68206	8307.3	G	U	A	B	CID	LIT	6	94.2	DQLVGKIQERYGYQK	1825.0	R	D	4.1	0.6	60.0	15.9
P68206	8307.3	G	U	A	B	CID	LIT	6	94.2	DWETRNEYRW	1454.6	V	-	2.0	0.7	8.7	11.5
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	DQAEKEVVDWETR	1604.8	K	N	4.6	0.6	88.9	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	EQWGKLTDDDMTIIEGK	1978.9	K	R	4.1	0.7	42.6	17.2
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	EVVDWETR	1033.5	K	N	2.5	0.0	33.4	13.2
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	GKVKEQWGK	1059.6	K	L	2.2	0.3	12.2	16.7
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	LTDDDMTIIEGK	1350.6	K	R	2.3	0.6	27.5	14.6
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	LTDDDMTIIEGKR	1506.7	K	D	2.9	0.4	77.5	16.8
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	MNKDEAGGNWK	1249.6	-	Q	2.8	0.5	22.5	12.0
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	RDQLVGK	815.5	K	I	2.3	0.3	15.4	18.3
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	VKEQWGK	874.5	K	L	1.7	0.5	9.6	18.4
P68206	8307.3	S	U	T	A	CID	LIT	10	82.6	YGYQKDQAEK	1229.6	R	E	2.7	0.7	28.2	12.8
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	DQAEKEVVDWETR	1604.8	K	N	4.2	0.6	66.6	14.1
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	EQWGKLTDDDMTIIEGK	1978.9	K	R	4.7	0.7	51.9	17.2
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	EVVDWETR	1033.5	K	N	2.5	0.6	32.3	15.4
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	GKVKEQWGK	1059.6	K	L	2.0	0.4	6.5	16.6
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	LTDDDMTIIEGK	1350.6	K	R	2.9	0.5	28.7	14.6
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	LTDDDMTIIEGKR	1506.7	K	D	3.8	0.5	74.4	16.5
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	MNKDEAGGNWK	1249.6	-	Q	3.7	0.3	48.6	13.2
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	VKEQWGK	874.5	K	L	1.8	0.3	17.4	18.4
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	5.1	0.6	39.0	18.8
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	YGYQKDQAEK	1229.6	R	E	3.2	0.7	49.6	13.0
P68206	8307.3	S	U	T	B	CID	LIT	11	73.9	YGYQKDQAEKEVVDWETR	2244.1	R	N	6.0	0.7	75.7	17.3
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	DQAEKEVVDWETR	1604.8	K	N	3.5	0.3	11.7	14.8
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	EQWGKLTDDDMTIIEGK	1978.9	K	R	5.5	0.7	66.0	17.4
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	LTDDDMTIIEGK	1350.6	K	R	3.8	0.5	64.5	15.3
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	LTDDDMTIIEGKR	1506.7	K	D	3.3	0.6	31.9	16.7
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	MNKDEAGGNWK	1249.6	-	Q	4.2	0.4	41.9	12.0
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	RDQLVGK	815.5	K	I	2.4	0.4	15.3	18.7
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	5.2	0.6	56.2	18.7
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	YGYQKDQAEK	1229.6	R	E	3.4	0.8	27.7	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68206	8307.3	S	U	T	C	CID	LIT	9	79.7	YGYQKDQAEKEVVDWETR	2244.1	R	N	6.3	0.7	86.9	17.4
P68206	8307.3	S	U	T	C	CID	FT	2	37.7	DQAEKEVVDWETR	1604.8	K	N	4.0	0.0	78.4	14.6
P68206	8307.3	S	U	T	C	CID	FT	2	37.7	LTDDDMTIIEGKR	1506.7	K	D	3.0	0.0	105.0	16.5
P68206	8307.3	S	U	T	A	ETD	LIT	7	76.8	DQAEKEVVDWETR	1604.8	K	N	5.0	0.4	56.0	14.8
P68206	8307.3	S	U	T	A	ETD	LIT	7	76.8	EQWGKLTDDDMTIIEGK	1978.9	K	R	2.1	0.5	28.9	17.2
P68206	8307.3	S	U	T	A	ETD	LIT	7	76.8	LTDDDMTIIEGK	1350.6	K	R	2.1	0.2	36.8	16.1
P68206	8307.3	S	U	T	A	ETD	LIT	7	76.8	MNKDEAGGNWK	1249.6	-	Q	5.0	0.4	59.5	13.2
P68206	8307.3	S	U	T	A	ETD	LIT	7	76.8	RDQLVGK	815.5	K	I	2.5	0.3	60.9	18.3
P68206	8307.3	S	U	T	A	ETD	LIT	7	76.8	YGYQKDQAEK	1229.6	R	E	3.7	0.7	36.3	12.8
P68206	8307.3	S	U	T	A	ETD	LIT	7	76.8	YGYQKDQAEKEVVDWETR	2244.1	R	N	0.0	0.0	64.8	17.4
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	DQAEKEVVDWETR	1604.8	K	N	3.1	0.5	0.0	0.0
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	EVVDWETR	1033.5	K	N	2.5	0.0	17.9	15.4
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	LTDDDMTIIEGK	1350.6	K	R	2.1	0.1	34.5	16.1
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	LTDDDMTIIEGKR	1506.7	K	D	2.5	0.5	55.8	16.8
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	MNKDEAGGNWK	1249.6	-	Q	5.6	0.5	55.5	12.0
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	RDQLVGK	815.5	K	I	2.0	0.2	46.0	18.3
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	VKEQWGK	874.5	K	L	1.5	0.2	21.1	18.4
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	YGYQKDQAEK	1229.6	R	E	3.2	0.6	31.6	12.8
P68206	8307.3	S	U	T	B	ETD	LIT	9	79.7	YGYQKDQAEKEVVDWETR	2244.1	R	N	5.3	0.0	45.3	17.3
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	DQAEKEVVDWETR	1604.8	K	N	6.1	0.5	84.6	14.8
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	EQWGKLTDDDMTIIEGK	1978.9	K	R	4.1	0.5	15.2	17.8
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	EVVDWETR	1033.5	K	N	2.5	0.2	23.2	15.7
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	LTDDDMTIIEGK	1350.6	K	R	2.2	0.2	44.0	15.9
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	LTDDDMTIIEGKR	1506.7	K	D	3.2	0.5	61.9	17.4
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	MNKDEAGGNWK	1249.6	-	Q	5.8	0.4	63.6	13.4
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	RDQLVGK	815.5	K	I	2.5	0.2	60.8	18.5
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	VKEQWGK	874.5	K	L	1.6	0.1	16.7	18.4
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	6.4	0.5	57.9	18.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	YGYQKDQAEK	1229.6	R	E	3.4	0.0	41.7	12.8
P68206	8307.3	S	U	T	C	ETD	LIT	11	79.7	YGYQKDQAEKEVVDWETR	2244.1	R	N	6.7	0.5	63.9	17.4
P68206	8307.3	S	U	T	A	ETD	FT	2	29.0	DQAEKEVVDWETR	1604.8	K	N	0.0	0.0	47.3	14.1
P68206	8307.3	S	U	T	A	ETD	FT	2	29.0	VKEQWGK	874.5	K	L	0.0	0.0	19.8	18.4
P68206	8307.3	S	U	T	B	ETD	FT	3	42.0	DQAEKEVVDWETR	1604.8	K	N	1.4	0.0	50.8	14.8
P68206	8307.3	S	U	T	B	ETD	FT	3	42.0	MNKDEAGGNWK	1249.6	-	Q	3.5	0.3	67.9	12.0
P68206	8307.3	S	U	T	B	ETD	FT	3	42.0	YGYQKDQAEKEVVDWETR	2244.1	R	N	2.5	0.0	25.5	17.4
P68206	8307.3	S	U	T	C	ETD	FT	2	37.7	DQAEKEVVDWETR	1604.8	K	N	0.9	0.0	37.5	14.6
P68206	8307.3	S	U	T	C	ETD	FT	2	37.7	LTDDDMTIIEGKR	1506.7	K	D	2.7	0.0	43.4	16.7
P68206	8307.3	S	U	T	B	ETD+CID	LIT	2	29.0	LTDDDMTIIEGKR	1506.7	K	D	0.0	0.0	38.5	17.4
P68206	8307.3	S	U	T	B	ETD+CID	LIT	2	29.0	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	0.0	0.0	54.7	18.6
P68206	8307.3	S	U	T	B	ETD+CID	LIT	7	71.0	DQAEKEVVDWETR	1604.8	K	N	0.0	0.0	88.8	14.6
P68206	8307.3	S	U	T	B	ETD+CID	LIT	7	71.0	EQWGKLTDDDMTIIEGK	1978.9	K	R	0.0	0.0	73.0	17.2
P68206	8307.3	S	U	T	B	ETD+CID	LIT	7	71.0	LTDDDMTIIEGK	1350.6	K	R	0.0	0.0	49.7	16.1
P68206	8307.3	S	U	T	B	ETD+CID	LIT	7	71.0	LTDDDMTIIEGKR	1506.7	K	D	0.0	0.0	58.7	16.5
P68206	8307.3	S	U	T	B	ETD+CID	LIT	7	71.0	MNKDEAGGNWK	1249.6	-	Q	0.0	0.0	50.4	14.8
P68206	8307.3	S	U	T	B	ETD+CID	LIT	7	71.0	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	0.0	0.0	54.7	18.6
P68206	8307.3	S	U	T	B	ETD+CID	LIT	7	71.0	YGYQKDQAEK	1229.6	R	E	0.0	0.0	31.3	13.0
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	DQAEKEVVDWETR	1604.8	K	N	4.3	0.6	69.6	14.6
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	DVFVHFSAIQTNGFK	1710.8	-	-	6.4	0.6	59.9	16.9
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	EQWGKLTDDDMTIIEGK	1978.9	K	R	4.8	0.0	68.1	17.4
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	LTDDDMTIIEGK	1350.6	K	R	2.8	0.7	25.1	16.1
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	LTDDDMTIIEGKR	1506.7	K	D	3.4	0.5	78.4	16.7
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	MNKDEAGGNWK	1249.6	-	Q	3.2	0.3	41.6	14.8
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	QLQRDENEAQSLR	1586.8	-	-	2.4	0.6	0.0	0.0
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	RDQLVGK	815.5	K	I	2.6	0.4	25.9	18.3
P68206	8307.3	S	U	T	A	ETD+CID	LIT	8	76.8	YGYQKDQAEK	1229.6	R	E	2.4	0.5	27.6	13.4
P68206	8307.3	S	U	T	B	ETD+CID	LIT	2	24.6	EQWGKLTDDDMTIIEGK	1978.9	K	R	5.3	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68206	8307.3	S	U	T	B	ETD+CID	LIT	2	24.6	LTDDDMTIIEGK	1350.6	K	R	3.4	0.6	0.0	0.0
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	DQAEKEVVDWETR	1604.8	K	N	4.8	0.0	88.8	14.6
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	EQWGKLTDDDMTIIEGK	1978.9	K	R	5.3	0.6	73.0	17.2
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	LTDDDMTIIEGK	1350.6	K	R	3.4	0.6	49.7	16.1
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	LTDDDMTIIEGKR	1506.7	K	D	3.7	0.4	58.7	16.5
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	MNKDEAGGNWK	1249.6	-	Q	3.7	0.3	50.4	14.8
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	RDQLVGK	815.5	K	I	2.2	0.3	13.7	18.3
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	7.3	0.7	54.7	18.6
P68206	8307.3	S	U	T	B	ETD+CID	LIT	8	79.7	YGYQKDQAEK	1229.6	R	E	2.0	0.4	11.3	13.8
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	DQAEKEVVDWETR	1604.8	K	N	4.3	0.6	38.3	14.1
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	EQWGKLTDDDMTIIEGK	1978.9	K	R	5.5	0.7	66.2	17.8
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	EVVDWETR	1033.5	K	N	2.3	0.3	18.0	15.4
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	GKVKEQWGK	1059.6	K	L	2.1	0.5	0.0	0.0
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	LTDDDMTIIEGK	1350.6	K	R	4.1	0.5	72.9	16.1
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	LTDDDMTIIEGKR	1506.7	K	D	3.9	0.6	95.0	16.5
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	MNKDEAGGNWK	1249.6	-	Q	3.9	0.4	45.3	13.2
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	RDQLVGK	815.5	K	I	2.4	0.2	26.7	18.3
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	6.1	0.6	60.3	18.6
P68206	8307.3	S	U	T	C	ETD+CID	LIT	9	82.6	YGYQKDQAEK	1229.6	R	E	1.7	0.4	13.8	13.0
P68206	8307.3	S	U	T	B	HCD	FT	7	71.0	DQAEKEVVDWETR	1604.8	K	N	0.0	0.0	88.8	14.6
P68206	8307.3	S	U	T	B	HCD	FT	7	71.0	EQWGKLTDDDMTIIEGK	1978.9	K	R	0.0	0.0	73.0	17.2
P68206	8307.3	S	U	T	B	HCD	FT	7	71.0	LTDDDMTIIEGK	1350.6	K	R	0.0	0.0	49.7	16.1
P68206	8307.3	S	U	T	B	HCD	FT	7	71.0	LTDDDMTIIEGKR	1506.7	K	D	0.0	0.0	58.7	16.5
P68206	8307.3	S	U	T	B	HCD	FT	7	71.0	MNKDEAGGNWK	1249.6	-	Q	0.0	0.0	50.4	14.8
P68206	8307.3	S	U	T	B	HCD	FT	7	71.0	VKEQWGKLTDDDMTIIEGK	2206.1	K	R	0.0	0.0	46.4	18.8
P68206	8307.3	S	U	T	B	HCD	FT	7	71.0	YGYQKDQAEK	1229.6	R	E	0.0	0.0	31.3	13.0
P68206	8307.3	S	U	T	B	HCD	FT	2	37.7	DQAEKEVVDWETR	1604.8	K	N	3.6	0.0	70.1	14.6
P68206	8307.3	S	U	T	B	HCD	FT	2	37.7	LTDDDMTIIEGKR	1506.7	K	D	3.5	0.0	84.8	17.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68206	8307.3	S	U	T	C	HCD	FT	2	26.1	DQAEKEVVDWETR	1604.8	K	N	3.6	0.0	66.9	14.6
P68206	8307.3	S	U	T	C	HCD	FT	2	26.1	YGYQKDQAEKEVVDWETR	2244.1	R	N	4.7	0.0	84.8	17.4
P21418	8333.0	G	U	T	A	CID	LIT	4	72.2	AAALSIAR	772.5	K	M	2.7	0.4	29.6	18.3
P21418	8333.0	G	U	T	A	CID	LIT	4	72.2	AKQAENLSALEQDITNLEK	2115.1	R	A	5.0	0.8	45.0	12.3
P21418	8333.0	G	U	T	A	CID	LIT	4	72.2	EPVIIAPDYTDDELYEWMR	2355.1	R	Q	4.3	0.0	47.4	6.0
P21418	8333.0	G	U	T	A	CID	LIT	4	72.2	MITYPR	780.4	R	-	1.6	0.6	19.7	10.0
P21418	8333.0	G	U	A	A	CID	LIT	2	23.6	EWMRQKINAAQ	1374.7	Y	D	3.4	0.5	26.5	14.9
P21418	8333.0	G	U	A	A	CID	LIT	2	23.6	EWMRQKINAAQDLKWAN	2102.1	Y	E	1.9	0.4	0.0	0.0
P64467	8398.9	G	U	T	A	CID	LIT	6	80.3	ISSLESLEK	1005.5	K	L	2.5	0.7	38.4	13.2
P64467	8398.9	G	U	T	A	CID	LIT	6	80.3	KISSLESLEK	1133.6	R	L	3.0	0.0	42.5	12.3
P64467	8398.9	G	U	T	A	CID	LIT	6	80.3	LFDLGQVPK	1016.6	R	S	2.5	0.4	17.3	15.2
P64467	8398.9	G	U	T	A	CID	LIT	6	80.3	LYDHLNYTLTDDQELINMYR	2530.2	K	A	5.7	0.6	90.7	10.0
P64467	8398.9	G	U	T	A	CID	LIT	6	80.3	MTVQDYLLK	1110.6	-	F	2.5	0.4	14.1	12.0
P64467	8398.9	G	U	T	A	CID	LIT	6	80.3	RAELVSGGR	944.5	R	L	3.5	0.4	38.5	14.0
P64467	8398.9	G	T	T	A	CID	LIT	2	25.4	LFDLGQVPK	1016.6	R	S	2.6	0.2	18.4	15.2
P64467	8398.9	G	T	T	A	CID	LIT	2	25.4	RAELVSGGR	944.5	R	L	2.9	0.4	14.2	15.8
P64467	8398.9	G	U	A	A	CID	LIT	2	36.6	DDQELINMYRAA	1454.7	T	D	2.4	0.7	29.5	13.4
P64467	8398.9	G	U	A	A	CID	LIT	2	36.6	DLGQVPKSVWHYVQ	1655.9	F	-	3.3	0.7	35.0	15.8
P64467	8398.9	G	U	T	B	CID	LIT	6	62.0	ISSLESLEK	1005.5	K	L	2.5	0.6	38.0	14.0
P64467	8398.9	G	U	T	B	CID	LIT	6	62.0	KISSLESLEK	1133.6	R	L	3.7	0.8	39.5	12.3
P64467	8398.9	G	U	T	B	CID	LIT	6	62.0	LFDLGQVPK	1016.6	R	S	2.4	0.5	39.6	15.2
P64467	8398.9	G	U	T	B	CID	LIT	6	62.0	MTVQDYLLK	1110.6	-	F	2.1	0.4	15.9	12.0
P64467	8398.9	G	U	T	B	CID	LIT	6	62.0	RAELVSGGR	944.5	R	L	3.3	0.4	33.1	15.8
P64467	8398.9	G	U	T	B	CID	LIT	6	62.0	SVWHYVQ	918.4	K	-	2.0	0.2	9.6	12.3
P64467	8398.9	G	U	A	B	CID	LIT	2	28.2	DDQELINMYRAA	1438.7	T	D	2.9	0.8	46.0	12.8
P64467	8398.9	G	U	A	B	CID	LIT	2	28.2	DHLNYTLT	976.5	Y	D	1.5	0.3	21.8	17.3
P64467	8398.9	S	U	T	C	CID	LIT	2	40.8	LFDLGQVPK	1016.6	R	S	3.1	0.5	34.8	18.9
P64467	8398.9	S	U	T	C	CID	LIT	2	40.8	LYDHLNYTLTDDQELINMYR	2530.2	K	A	5.8	0.7	78.8	17.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64467	8398.9	S	U	T	B	ETD+CID	LIT	2	40.8	LFDLGQVPK	1016.6	R	S	0.0	0.0	36.5	18.9
P64467	8398.9	S	U	T	B	ETD+CID	LIT	2	40.8	LYDHLNYTLTDDQELINMYR	2530.2	K	A	0.0	0.0	24.9	17.9
P64467	8398.9	S	U	T	B	ETD+CID	LIT	3	53.5	LFDLGQVPK	1016.6	R	S	2.9	0.5	36.5	18.9
P64467	8398.9	S	U	T	B	ETD+CID	LIT	3	53.5	LYDHLNYTLTDDQELINMYR	2530.2	K	A	4.5	0.0	24.9	17.9
P64467	8398.9	S	U	T	B	ETD+CID	LIT	3	53.5	MTVQDYLLK	1110.6	-	F	2.0	0.6	14.1	14.1
P64467	8398.9	S	U	T	C	ETD+CID	LIT	2	25.4	LFDLGQVPK	1016.6	R	S	3.1	0.5	38.1	18.9
P64467	8398.9	S	U	T	C	ETD+CID	LIT	2	25.4	MTVQDYLLK	1110.6	-	F	1.9	0.5	22.0	14.1
P64467	8398.9	S	U	T	B	HCD	FT	2	40.8	LFDLGQVPK	1016.6	R	S	0.0	0.0	36.5	18.9
P64467	8398.9	S	U	T	B	HCD	FT	2	40.8	LYDHLNYTLTDDQELINMYR	2530.2	K	A	0.0	0.0	24.9	17.9
P67624	8451.4	G	U	T	B	CID	LIT	2	22.2	EGTDYGEHER	1192.5	R	T	2.3	0.0	19.6	0.0
P67624	8451.4	G	U	T	B	CID	LIT	2	22.2	VADVKR	687.4	K	Q	1.7	0.3	35.4	18.6
P67624	8451.4	G	U	A	B	CID	LIT	3	33.3	DVKRQLQCG	1103.6	A	E	2.0	0.7	20.4	14.8
P67624	8451.4	G	U	A	B	CID	LIT	3	33.3	ESFVLREGT	1037.5	I	D	2.6	0.5	35.1	16.0
P67624	8451.4	G	U	A	B	CID	LIT	3	33.3	MLIPWQ	787.4	-	D	2.1	0.1	21.7	18.2
P68679	8482.1	G	U	T	A	CID	LIT	7	53.5	AGVLAEVR	814.5	K	R	2.9	0.4	40.1	15.3
P68679	8482.1	G	U	T	A	CID	LIT	7	53.5	AGVLAEVRR	970.6	K	R	1.6	0.6	13.8	12.3
P68679	8482.1	G	U	T	A	CID	LIT	7	53.5	ASAVKR	631.4	K	H	1.3	0.4	24.4	16.1
P68679	8482.1	G	U	T	A	CID	LIT	7	53.5	EFYEKPTTER	1299.6	R	K	2.6	0.0	37.2	11.1
P68679	8482.1	G	U	T	A	CID	LIT	7	53.5	ENEPFDVALR	1189.6	R	R	2.8	0.6	32.2	14.3
P68679	8482.1	G	U	T	A	CID	LIT	7	53.5	REFYEKPTTER	1455.7	R	K	3.1	0.6	36.2	13.0
P68679	8482.1	G	U	T	A	CID	LIT	7	53.5	VRENEPFDVALR	1444.8	K	R	3.5	0.0	35.9	12.0
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	AGVLAEVR	814.5	K	R	2.8	0.3	34.3	15.4
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	ASAVKR	631.4	K	H	1.5	0.0	30.2	16.1
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	EFYEKPTTER	1299.6	R	K	2.3	0.6	20.6	11.8
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	EFYEKPTTERK	1427.7	R	R	3.4	0.5	0.0	0.0
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	ENEPFDVALR	1189.6	R	R	2.5	0.7	34.5	13.4
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	ENEPFDVALRR	1345.7	R	F	1.6	0.7	10.6	14.0
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	REFYEKPTTER	1455.7	R	K	2.5	0.0	30.8	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68679	8482.1	G	T	T	A	CID	LIT	8	54.9	VRENEPFDVALR	1444.8	K	R	3.8	0.5	36.3	12.0
P68679	8482.1	G	T	T	B	CID	LIT	2	16.9	ENEPFDVALR	1189.6	R	R	1.9	0.2	0.0	0.0
P68679	8482.1	G	T	T	B	CID	LIT	2	16.9	VRENEPFDVALR	1444.8	K	R	3.8	0.6	32.3	11.1
P68679	8482.1	G	U	T	B	CID	LIT	3	26.8	AGVLAEVR	814.5	K	R	3.1	0.3	53.2	15.3
P68679	8482.1	G	U	T	B	CID	LIT	3	26.8	EFYEKPTTER	1299.6	R	K	2.3	0.8	36.2	11.5
P68679	8482.1	G	U	T	B	CID	LIT	3	26.8	EFYEKPTTERK	1427.7	R	R	2.1	0.6	10.5	12.8
P68679	8482.1	S	U	T	A	CID	LIT	4	35.2	EFYEKPTTER	1299.6	R	K	2.7	0.6	30.2	16.2
P68679	8482.1	S	U	T	A	CID	LIT	4	35.2	ENEPFDVALR	1189.6	R	R	2.1	0.3	26.2	18.0
P68679	8482.1	S	U	T	A	CID	LIT	4	35.2	RREFYEKPTTER	1611.8	R	K	2.7	0.4	16.5	16.4
P68679	8482.1	S	U	T	A	CID	LIT	4	35.2	VRENEPFDVALRR	1600.9	K	F	3.4	0.5	23.2	16.9
P68679	8482.1	S	U	T	B	CID	LIT	6	36.6	EFYEKPTTER	1299.6	R	K	2.5	0.6	18.0	16.1
P68679	8482.1	S	U	T	B	CID	LIT	6	36.6	EFYEKPTTERK	1427.7	R	R	3.4	0.5	28.5	16.3
P68679	8482.1	S	U	T	B	CID	LIT	6	36.6	ENEPFDVALR	1189.6	R	R	2.3	0.3	32.0	18.0
P68679	8482.1	S	U	T	B	CID	LIT	6	36.6	REFYEKPTTER	1455.7	R	K	2.4	0.4	24.1	15.4
P68679	8482.1	S	U	T	B	CID	LIT	6	36.6	RREFYEKPTTER	1611.8	R	K	3.7	0.6	28.5	17.4
P68679	8482.1	S	U	T	B	CID	LIT	6	36.6	VRENEPFDVALRR	1600.9	K	F	2.1	0.3	0.0	0.0
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	EFYEKPTTER	1299.6	R	K	2.8	0.4	20.4	16.2
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	EFYEKPTTERK	1427.7	R	R	3.2	0.5	26.0	17.2
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	ENEPFDVALR	1189.6	R	R	2.6	0.6	35.0	17.0
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	ENEPFDVALRR	1345.7	R	F	1.1	0.5	21.0	16.9
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	REFYEKPTTER	1455.7	R	K	3.9	0.5	32.4	15.3
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	RREFYEKPTTER	1611.8	R	K	3.6	0.6	34.0	16.3
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	VRENEPFDVALR	1444.8	K	R	3.8	0.5	36.8	16.7
P68679	8482.1	S	U	T	C	CID	LIT	8	36.6	VRENEPFDVALRR	1600.9	K	F	3.8	0.6	31.9	16.5
P68679	8482.1	S	U	T	C	CID	FT	2	18.3	ENEPFDVALR	1189.6	R	R	3.0	0.0	42.2	18.0
P68679	8482.1	S	U	T	C	CID	FT	2	18.3	VRENEPFDVALRR	1600.9	K	F	3.1	0.0	46.2	16.7
P68679	8482.1	S	U	T	A	ETD	LIT	4	36.6	EFYEKPTTERK	1427.7	R	R	3.4	0.3	12.1	17.2
P68679	8482.1	S	U	T	A	ETD	LIT	4	36.6	RREFYEKPTTER	1611.8	R	K	6.8	0.5	57.7	16.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68679	8482.1	S	U	T	A	ETD	LIT	4	36.6	VRENEPFDVALR	1444.8	K	R	3.3	0.5	52.6	18.5
P68679	8482.1	S	U	T	A	ETD	LIT	4	36.6	VRENEPFDVALRR	1600.9	K	F	4.1	0.5	0.0	0.0
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	AGVLAEVR	814.5	K	R	2.6	0.2	43.0	16.6
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	EFYEKPTTER	1299.6	R	K	2.7	0.7	0.0	0.0
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	EFYEKPTTERK	1427.7	R	R	4.4	0.6	32.5	16.8
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	ENEPFDVALR	1189.6	R	R	1.5	0.4	15.9	17.0
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	ENEPFDVALRR	1345.7	R	F	3.6	0.4	0.0	0.0
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	REFYEKPTTER	1455.7	R	K	5.2	0.7	49.7	14.3
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	RREFYEKPTTER	1611.8	R	K	6.0	0.5	79.6	17.4
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	VRENEPFDVALR	1444.8	K	R	4.7	0.4	0.0	0.0
P68679	8482.1	S	U	T	C	ETD	LIT	8	47.9	VRENEPFDVALRR	1600.9	K	F	3.1	0.3	16.7	17.2
P68679	8482.1	S	U	T	A	ETD	FT	2	16.9	EFYEKPTTER	1299.6	R	K	0.0	0.0	26.2	16.2
P68679	8482.1	S	U	T	A	ETD	FT	2	16.9	RREFYEKPTTER	1611.8	R	K	3.7	0.0	48.8	16.4
P68679	8482.1	S	U	T	C	ETD	FT	4	46.5	AGVLAEVR	814.5	K	R	1.6	0.0	39.8	16.6
P68679	8482.1	S	U	T	C	ETD	FT	4	46.5	REFYEKPTTER	1455.7	R	K	3.3	0.0	33.8	15.6
P68679	8482.1	S	U	T	C	ETD	FT	4	46.5	RREFYEKPTTER	1611.8	R	K	6.0	0.5	54.8	16.8
P68679	8482.1	S	U	T	C	ETD	FT	4	46.5	VRENEPFDVALRR	1600.9	K	F	1.5	0.0	27.8	15.9
P68679	8482.1	S	U	T	B	ETD+CID	LIT	3	32.4	EFYEKPTTERK	1427.7	R	R	0.0	0.0	28.6	17.1
P68679	8482.1	S	U	T	B	ETD+CID	LIT	3	32.4	ENEPFDVALR	1189.6	R	R	0.0	0.0	24.4	18.0
P68679	8482.1	S	U	T	B	ETD+CID	LIT	3	32.4	RREFYEKPTTER	1611.8	R	K	0.0	0.0	32.2	15.8
P68679	8482.1	S	U	T	A	ETD+CID	LIT	2	18.3	EFYEKPTTERK	1427.7	R	R	1.7	0.5	18.0	17.1
P68679	8482.1	S	U	T	A	ETD+CID	LIT	2	18.3	RREFYEKPTTER	1611.8	R	K	6.0	0.7	45.4	16.6
P68679	8482.1	S	U	T	B	ETD+CID	LIT	2	29.6	EFYEKPTTERK	1427.7	R	R	3.0	0.5	0.0	0.0
P68679	8482.1	S	U	T	B	ETD+CID	LIT	2	29.6	ENEPFDVALR	1189.6	R	R	2.0	0.4	0.0	0.0
P68679	8482.1	S	U	T	B	ETD+CID	LIT	3	32.4	EFYEKPTTERK	1427.7	R	R	3.0	0.5	28.6	17.1
P68679	8482.1	S	U	T	B	ETD+CID	LIT	3	32.4	ENEPFDVALR	1189.6	R	R	2.0	0.4	24.4	18.0
P68679	8482.1	S	U	T	B	ETD+CID	LIT	3	32.4	RREFYEKPTTER	1611.8	R	K	3.0	0.5	17.5	16.1
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	AGVLAEVR	814.5	K	R	2.8	0.4	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	EFYEKPTTERK	1427.7	R	R	4.3	0.4	42.5	17.1
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	EFYEKPTTERKR	1583.8	R	A	2.7	0.2	0.0	0.0
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	ENEPFDVALR	1189.6	R	R	2.8	0.5	44.2	17.0
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	ENEPFDVALRR	1345.7	R	F	0.9	0.0	21.4	18.5
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	REFYEKPTTER	1455.7	R	K	2.9	0.7	25.0	16.2
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	RREFYEKPTTER	1611.8	R	K	3.1	0.4	29.8	15.8
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	VRENEPFDVALR	1444.8	K	R	3.3	0.5	31.7	16.8
P68679	8482.1	S	U	T	C	ETD+CID	LIT	9	49.3	VRENEPFDVALRR	1600.9	K	F	4.2	0.5	38.0	16.3
P68679	8482.1	S	U	T	B	HCD	FT	3	32.4	EFYEKPTTERK	1427.7	R	R	0.0	0.0	28.6	17.1
P68679	8482.1	S	U	T	B	HCD	FT	3	32.4	ENEPFDVALR	1189.6	R	R	0.0	0.0	24.4	18.0
P68679	8482.1	S	U	T	B	HCD	FT	3	32.4	RREFYEKPTTER	1611.8	R	K	0.0	0.0	32.2	15.8
P0AB14	8506.4	G	U	T	A	CID	LIT	4	76.0	AHHVGEWASLR	1262.6	K	N	4.2	0.5	39.8	14.0
P0AB14	8506.4	G	U	T	A	CID	LIT	4	76.0	IWEEGSDEVLVK	1403.7	K	A	3.4	0.5	30.3	11.8
P0AB14	8506.4	G	U	T	A	CID	LIT	4	76.0	NTSPEIAEAIFEVAGYDEK	2083.0	R	M	5.3	0.8	88.8	11.5
P0AB14	8506.4	G	U	T	A	CID	LIT	4	76.0	TDKDSLFWGEQTIER	1824.9	K	K	4.7	0.7	67.8	10.4
P0AB14	8506.4	G	T	T	A	CID	LIT	4	76.0	AHHVGEWASLR	1262.6	K	N	3.1	0.4	28.9	14.3
P0AB14	8506.4	G	T	T	A	CID	LIT	4	76.0	IWEEGSDEVLVK	1403.7	K	A	3.6	0.0	56.9	10.8
P0AB14	8506.4	G	T	T	A	CID	LIT	4	76.0	NTSPEIAEAIFEVAGYDEK	2083.0	R	M	4.9	0.0	69.3	11.1
P0AB14	8506.4	G	T	T	A	CID	LIT	4	76.0	TDKDSLFWGEQTIER	1824.9	K	K	3.5	0.6	45.2	11.8
P0AB14	8506.4	G	U	A	A	CID	LIT	3	37.3	DEVLVKAFAKTDK	1463.8	S	D	4.3	0.6	39.4	12.6
P0AB14	8506.4	G	U	A	A	CID	LIT	3	37.3	DSLFWGEQTIERKNV	1821.9	K	-	3.1	0.0	37.9	14.8
P0AB14	8506.4	G	U	A	A	CID	LIT	3	37.3	EQTIERKNV	1116.6	G	-	2.1	0.3	21.8	14.9
P0AB14	8506.4	G	U	T	B	CID	LIT	4	76.0	AHHVGEWASLR	1262.6	K	N	3.5	0.6	42.1	13.0
P0AB14	8506.4	G	U	T	B	CID	LIT	4	76.0	IWEEGSDEVLVK	1403.7	K	A	3.2	0.6	57.0	11.1
P0AB14	8506.4	G	U	T	B	CID	LIT	4	76.0	NTSPEIAEAIFEVAGYDEK	2083.0	R	M	4.1	0.0	100.0	11.1
P0AB14	8506.4	G	U	T	B	CID	LIT	4	76.0	TDKDSLFWGEQTIER	1824.9	K	K	4.4	0.0	46.8	10.8
P0AB14	8506.4	G	U	A	B	CID	LIT	6	60.0	DEVLVKAFAKT	1220.7	S	D	2.4	0.8	27.5	11.5
P0AB14	8506.4	G	U	A	B	CID	LIT	6	60.0	DEVLVKAFAKTDK	1463.8	S	D	2.9	0.7	23.1	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB14	8506.4	G	U	A	B	CID	LIT	6	60.0	DSLFWGEQTIERKNV	1821.9	K	-	1.2	0.5	12.8	14.6
P0AB14	8506.4	G	U	A	B	CID	LIT	6	60.0	EAIFEVAGY	998.5	A	D	2.6	0.8	32.5	14.3
P0AB14	8506.4	G	U	A	B	CID	LIT	6	60.0	EKIWEEGS	977.5	A	D	2.1	0.6	18.9	17.2
P0AB14	8506.4	G	U	A	B	CID	LIT	6	60.0	EQTIERKNV	1116.6	G	-	2.4	0.4	21.8	14.9
P0AB14	8506.4	S	U	T	A	CID	LIT	3	62.7	IWEEGSDEVLVK	1403.7	K	A	2.6	0.7	14.4	17.0
P0AB14	8506.4	S	U	T	A	CID	LIT	3	62.7	NTSPEIAEAIFEVAGYDEK	2083.0	R	M	6.4	0.6	115.0	16.5
P0AB14	8506.4	S	U	T	A	CID	LIT	3	62.7	TDKDSLFWGEQTIERK	1953.0	K	N	4.2	0.6	62.2	18.1
P0AB14	8506.4	S	U	T	B	CID	LIT	4	62.7	IWEEGSDEVLVK	1403.7	K	A	3.2	0.6	29.7	17.2
P0AB14	8506.4	S	U	T	B	CID	LIT	4	62.7	NTSPEIAEAIFEVAGYDEK	2083.0	R	M	2.8	0.4	10.1	16.7
P0AB14	8506.4	S	U	T	B	CID	LIT	4	62.7	TDKDSLFWGEQTIER	1824.9	K	K	3.0	0.5	12.1	16.9
P0AB14	8506.4	S	U	T	B	CID	LIT	4	62.7	TDKDSLFWGEQTIERK	1953.0	K	N	3.7	0.5	52.0	18.1
P0AB14	8506.4	S	U	T	C	CID	LIT	4	52.0	AHHVGEWASLR	1262.6	K	N	4.1	0.3	35.8	18.0
P0AB14	8506.4	S	U	T	C	CID	LIT	4	52.0	IWEEGSDEVLVK	1403.7	K	A	2.9	0.6	30.0	17.6
P0AB14	8506.4	S	U	T	C	CID	LIT	4	52.0	TDKDSLFWGEQTIER	1824.9	K	K	4.2	0.5	33.7	16.7
P0AB14	8506.4	S	U	T	C	CID	LIT	4	52.0	TDKDSLFWGEQTIERK	1953.0	K	N	3.6	0.4	66.8	18.3
P0AB14	8506.4	S	U	T	A	ETD	LIT	4	61.3	AHHVGEWASLR	1262.6	K	N	4.6	0.5	0.0	0.0
P0AB14	8506.4	S	U	T	A	ETD	LIT	4	61.3	NTSPEIAEAIFEVAGYDEK	2083.0	R	M	2.9	0.6	21.0	16.9
P0AB14	8506.4	S	U	T	A	ETD	LIT	4	61.3	TDKDSLFWGEQTIER	1824.9	K	K	5.4	0.0	64.8	16.9
P0AB14	8506.4	S	U	T	A	ETD	LIT	4	61.3	TDKDSLFWGEQTIERK	1953.0	K	N	5.6	0.6	78.2	18.1
P0AB14	8506.4	S	U	T	B	ETD	LIT	3	36.0	AHHVGEWASLR	1262.6	K	N	2.7	0.4	28.8	18.0
P0AB14	8506.4	S	U	T	B	ETD	LIT	3	36.0	TDKDSLFWGEQTIER	1824.9	K	K	7.3	0.0	65.3	16.6
P0AB14	8506.4	S	U	T	B	ETD	LIT	3	36.0	TDKDSLFWGEQTIERK	1953.0	K	N	5.9	0.5	65.0	18.2
P0AB14	8506.4	S	U	T	C	ETD	LIT	4	61.3	AHHVGEWASLR	1262.6	K	N	2.7	0.4	0.0	0.0
P0AB14	8506.4	S	U	T	C	ETD	LIT	4	61.3	NTSPEIAEAIFEVAGYDEK	2083.0	R	M	0.0	0.0	27.7	16.7
P0AB14	8506.4	S	U	T	C	ETD	LIT	4	61.3	TDKDSLFWGEQTIER	1824.9	K	K	3.3	0.5	27.5	16.9
P0AB14	8506.4	S	U	T	C	ETD	LIT	4	61.3	TDKDSLFWGEQTIERK	1953.0	K	N	5.2	0.6	51.9	17.5
P0AB14	8506.4	S	U	T	A	ETD+CID	LIT	3	37.3	IWEEGSDEVLVK	1403.7	K	A	2.9	0.7	23.0	17.6
P0AB14	8506.4	S	U	T	A	ETD+CID	LIT	3	37.3	TDKDSLFWGEQTIER	1824.9	K	K	3.7	0.6	26.4	17.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB14	8506.4	S	U	T	A	ETD+CID	LIT	3	37.3	TDKDSLFWGEQTIERK	1953.0	K	N	4.3	0.4	51.7	18.0
P0AB14	8506.4	S	U	T	B	ETD+CID	LIT	2	37.3	IWEEGSDEVLVK	1403.7	K	A	2.9	0.0	18.7	17.1
P0AB14	8506.4	S	U	T	B	ETD+CID	LIT	2	37.3	TDKDSLFWGEQTIERK	1953.0	K	N	4.2	0.5	51.8	17.9
P0AB14	8506.4	S	U	T	C	ETD+CID	LIT	4	52.0	AHHVGEWASLR	1262.6	K	N	3.9	0.5	28.6	17.6
P0AB14	8506.4	S	U	T	C	ETD+CID	LIT	4	52.0	IWEEGSDEVLVK	1403.7	K	A	2.9	0.6	32.8	16.9
P0AB14	8506.4	S	U	T	C	ETD+CID	LIT	4	52.0	TDKDSLFWGEQTIER	1824.9	K	K	4.1	0.5	34.5	16.8
P0AB14	8506.4	S	U	T	C	ETD+CID	LIT	4	52.0	TDKDSLFWGEQTIERK	1953.0	K	N	4.3	0.5	78.3	18.0
P0AF59	8531.9	G	U	A	A	CID	LIT	2	32.9	DGGYRCYTGEKI	1418.6	L	D	3.1	0.8	9.3	12.8
P0AF59	8531.9	G	U	A	A	CID	LIT	2	32.9	DTCPSGALKYRHK	1532.8	I	-	3.7	0.7	52.6	15.8
P0AF59	8531.9	G	T	A	B	CID	LIT	3	44.7	DGGYRCYTGEKI	1418.6	L	D	2.7	0.3	0.0	0.0
P0AF59	8531.9	G	T	A	B	CID	LIT	3	44.7	DTCPSGALKYRHK	1532.8	I	-	1.2	0.6	10.3	16.2
P0AF59	8531.9	G	T	A	B	CID	LIT	3	44.7	DVATVVKVI	943.6	V	D	2.9	0.7	41.7	12.6
P0AF59	8531.9	G	U	A	B	CID	LIT	2	32.9	DGGYRCYTGEKI	1418.6	L	D	2.4	0.1	16.3	13.0
P0AF59	8531.9	G	U	A	B	CID	LIT	2	32.9	DTCPSGALKYRHK	1532.8	I	-	3.0	0.7	31.2	15.8
P64519	8561.0	G	U	T	A	CID	LIT	2	25.3	EYHTWR	891.4	R	E	1.6	0.4	13.9	10.0
P64519	8561.0	G	U	T	A	CID	LIT	2	25.3	SQNDSEHVSVDGR	1429.6	R	E	4.0	0.0	91.5	8.5
P64519	8561.0	G	U	A	A	CID	LIT	3	26.7	DFSVSEVNR	1052.5	H	-	2.5	0.7	29.3	14.1
P64519	8561.0	G	U	A	A	CID	LIT	3	26.7	DIHDFSVSEVNR	1417.7	L	-	3.1	0.9	48.0	13.4
P64519	8561.0	G	U	A	A	CID	LIT	3	26.7	MKTAKEYS	957.5	-	D	2.0	0.7	16.0	13.8
P64519	8561.0	G	T	A	B	CID	LIT	3	42.7	DFSVSEVNR	1052.5	H	-	1.9	0.0	15.4	14.5
P64519	8561.0	G	T	A	B	CID	LIT	3	42.7	DGREYHTWRELA	1532.7	V	D	1.7	0.7	10.0	14.0
P64519	8561.0	G	T	A	B	CID	LIT	3	42.7	DTAKREVSVDV	1218.6	S	D	2.3	0.6	11.1	15.8
P64519	8561.0	G	U	A	B	CID	LIT	2	24.0	DSEHVSV	772.3	N	D	2.3	0.5	22.1	12.3
P64519	8561.0	G	U	A	B	CID	LIT	2	24.0	DTAKREVSVDV	1218.6	S	D	2.6	0.4	34.8	15.2
P0ACE3	8610.6	G	U	T	A	CID	LIT	3	54.2	LAELTMNK	919.5	R	L	2.6	0.0	36.7	15.7
P0ACE3	8610.6	G	U	T	A	CID	LIT	3	54.2	LYDKIPSSVWK	1335.7	K	F	3.8	0.5	48.3	14.0
P0ACE3	8610.6	G	U	T	A	CID	LIT	3	54.2	NKYELSDNELAVFYSAADHR	2342.1	K	L	5.6	0.7	47.7	12.0
P0ACE3	8610.6	G	U	A	A	CID	LIT	2	34.7	DHRLAELTMNKLY	1619.8	A	D	2.2	0.7	11.6	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACE3	8610.6	G	U	A	A	CID	LIT	2	34.7	DKIPSSVWKFIR	1475.8	Y	-	2.8	0.0	31.5	10.4
P0AA31	8621.2	G	T	T	A	CID	LIT	6	100.0	KGEILEVVSDCPQSINNIPLDAR	2567.3	K	N	4.8	0.7	62.3	11.1
P0AA31	8621.2	G	T	T	A	CID	LIT	6	100.0	LDMVGEPCPYPAVATLEAMPQLK	2530.2	R	K	3.5	0.8	29.3	10.4
P0AA31	8621.2	G	T	T	A	CID	LIT	6	100.0	MKNIVPDYR	1135.6	-	L	3.3	0.7	40.3	11.5
P0AA31	8621.2	G	T	T	A	CID	LIT	6	100.0	NHGYTVLDIQQDGPTIR	1927.0	R	Y	5.9	0.7	77.5	12.8
P0AA31	8621.2	G	T	T	A	CID	LIT	6	100.0	NIVPDYRLDMVGEPCPYPAVATLEAMPQLK	3387.7	K	K	5.2	0.0	23.9	9.0
P0AA31	8621.2	G	T	T	A	CID	LIT	6	100.0	YLIQK	664.4	R	-	1.7	0.3	19.0	12.8
P0AA31	8621.2	G	T	A	A	CID	LIT	2	32.5	DARNHGYTVL	1145.6	L	D	2.1	0.7	28.2	16.0
P0AA31	8621.2	G	T	A	A	CID	LIT	2	32.5	DIQQDGPTIRYLIQK	1788.0	L	-	4.0	0.5	30.0	13.8
P0AA31	8621.2	G	T	T	B	CID	LIT	2	51.9	KGEILEVVSDCPQSINNIPLDAR	2567.3	K	N	5.5	0.6	50.8	11.8
P0AA31	8621.2	G	T	T	B	CID	LIT	2	51.9	NHGYTVLDIQQDGPTIR	1927.0	R	Y	2.8	0.3	17.0	12.0
P0A6A8	8621.4	G	U	T	A	CID	LIT	3	33.3	IIGEQLGVK	956.6	K	Q	1.9	0.7	4.0	10.4
P0A6A8	8621.4	G	U	T	A	CID	LIT	3	33.3	ITTVQAAIDYINGHQA	1714.9	K	-	5.3	0.7	99.2	13.6
P0A6A8	8621.4	G	U	T	A	CID	LIT	3	33.3	KIIGEQLGVK	1084.7	K	Q	2.4	0.7	18.3	12.8
P0A6A8	8621.4	G	T	T	A	CID	LIT	2	12.8	IIGEQLGVK	956.6	K	Q	2.0	0.7	37.3	10.4
P0A6A8	8621.4	G	T	T	A	CID	LIT	2	12.8	KIIGEQLGVK	1084.7	K	Q	3.5	0.5	32.6	12.8
P0A6A8	8621.4	G	T	T	B	CID	LIT	6	44.9	IIGEQLGVK	956.6	K	Q	1.9	0.6	9.8	10.4
P0A6A8	8621.4	G	T	T	B	CID	LIT	6	44.9	ITTVQAAIDYINGHQA	1714.9	K	-	5.2	0.7	64.3	13.4
P0A6A8	8621.4	G	T	T	B	CID	LIT	6	44.9	KIIGEQLGVK	1084.7	K	Q	2.3	0.3	18.5	12.8
P0A6A8	8621.4	G	T	T	B	CID	LIT	6	44.9	MSTIEER	865.4	-	V	2.1	0.5	27.0	12.3
P0A6A8	8621.4	G	T	T	B	CID	LIT	6	44.9	MSTIEERVK	1092.6	-	K	2.3	0.5	24.4	14.3
P0A6A8	8621.4	G	T	T	B	CID	LIT	6	44.9	STIEERVK	961.5	M	K	0.0	0.0	38.6	14.1
P0A6A8	8621.4	G	T	A	B	CID	LIT	4	41.0	DYINGHQA	917.4	I	-	2.2	0.0	15.8	10.4
P0A6A8	8621.4	G	T	A	B	CID	LIT	4	41.0	EAEKITTVQAAI	1273.7	E	D	2.4	0.2	9.1	14.1
P0A6A8	8621.4	G	T	A	B	CID	LIT	4	41.0	EKITTVQAAI	1073.6	A	D	3.7	0.8	41.5	11.5
P0A6A8	8621.4	G	T	A	B	CID	LIT	4	41.0	STIEERVKKIIG	1372.8	M	E	0.0	0.0	22.3	8.5
P0A6A8	8621.4	G	U	A	B	CID	LIT	2	23.1	DYINGHQA	917.4	I	-	2.2	0.0	15.3	8.5
P0A6A8	8621.4	G	U	A	B	CID	LIT	2	23.1	EKITTVQAAI	1073.6	A	D	3.8	0.0	50.1	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6A8	8621.4	S	U	T	C	CID	LIT	2	33.3	ITTVQAAIDYINGHQA	1714.9	K	-	4.3	0.6	37.4	18.6
P0A6A8	8621.4	S	U	T	C	CID	LIT	2	33.3	KIIGEQLGVK	1084.7	K	Q	3.5	0.5	34.0	14.0
P0A6A8	8621.4	S	U	T	A	ETD	LIT	2	20.5	KIIGEQLGVK	1084.7	K	Q	2.8	0.3	23.0	14.0
P0A6A8	8621.4	S	U	T	A	ETD	LIT	2	20.5	STIEER	734.4	M	V	0.0	0.0	40.9	14.8
P0A6A8	8621.4	S	U	T	B	ETD	LIT	2	33.3	ITTVQAAIDYINGHQA	1715.9	K	-	0.0	0.0	36.7	18.1
P0A6A8	8621.4	S	U	T	B	ETD	LIT	2	33.3	KIIGEQLGVK	1084.7	K	Q	5.1	0.5	70.8	14.0
P0A6A8	8621.4	S	U	T	C	ETD	LIT	2	33.3	ITTVQAAIDYINGHQA	1715.9	K	-	0.0	0.0	26.8	18.0
P0A6A8	8621.4	S	U	T	C	ETD	LIT	2	33.3	KIIGEQLGVK	1084.7	K	Q	4.7	0.5	64.7	14.0
P0A6A8	8621.4	S	U	T	B	ETD+CID	LIT	2	28.2	ITTVQAAIDYINGHQA	1715.9	K	-	0.0	0.0	75.6	18.1
P0A6A8	8621.4	S	U	T	B	ETD+CID	LIT	2	28.2	STIEER	734.4	M	V	0.0	0.0	23.4	15.6
P0A6A8	8621.4	S	U	T	A	ETD+CID	LIT	2	28.2	ITTVQAAIDYINGHQA	1715.9	K	-	5.2	0.6	43.2	17.4
P0A6A8	8621.4	S	U	T	A	ETD+CID	LIT	2	28.2	STIEER	734.4	M	V	0.0	0.0	25.8	14.8
P0A6A8	8621.4	S	U	T	B	ETD+CID	LIT	2	28.2	ITTVQAAIDYINGHQA	1715.9	K	-	4.4	0.6	75.6	18.1
P0A6A8	8621.4	S	U	T	B	ETD+CID	LIT	2	28.2	STIEER	734.4	M	V	0.0	0.0	23.4	15.6
P0A6A8	8621.4	S	U	T	C	ETD+CID	LIT	2	33.3	ITTVQAAIDYINGHQA	1714.9	K	-	4.6	0.6	44.8	19.0
P0A6A8	8621.4	S	U	T	C	ETD+CID	LIT	2	33.3	KIIGEQLGVK	1084.7	K	Q	2.3	0.2	22.0	14.0
P0A6A8	8621.4	S	U	T	B	HCD	FT	2	28.2	ITTVQAAIDYINGHQA	1715.9	K	-	0.0	0.0	75.6	18.1
P0A6A8	8621.4	S	U	T	B	HCD	FT	2	28.2	STIEER	734.4	M	V	0.0	0.0	23.4	15.6
P31992	8655.4	G	U	A	A	CID	LIT	2	26.0	DEQQKAALAA	1044.5	L	D	2.1	0.5	17.6	16.2
P31992	8655.4	G	U	A	A	CID	LIT	2	26.0	DVIIRHLNSK	1194.7	T	D	3.2	0.0	30.4	4.8
P31992	8655.4	G	T	A	A	CID	LIT	2	26.0	DEQQKAALAA	1044.5	L	D	1.9	0.6	42.4	16.2
P31992	8655.4	G	T	A	A	CID	LIT	2	26.0	DVIIRHLNSK	1194.7	T	D	2.7	0.7	14.7	4.8
P31992	8655.4	G	T	A	B	CID	LIT	3	37.7	DEQQKAALAA	1044.5	L	D	3.1	0.4	25.6	15.4
P31992	8655.4	G	T	A	B	CID	LIT	3	37.7	DIKCFPREL	1177.6	I	D	2.0	0.2	5.1	14.1
P31992	8655.4	G	T	A	B	CID	LIT	3	37.7	DVIIRHLNSK	1194.7	T	D	3.9	0.0	20.5	4.8
P64503	8735.1	G	U	T	A	CID	LIT	3	41.0	IGAFEIDDGELHGESPGDR	2013.9	R	T	4.9	0.0	85.3	4.8
P64503	8735.1	G	U	T	A	CID	LIT	3	41.0	TRYDQQSDAWIMR	1669.8	R	L	4.4	0.8	54.3	11.5
P64503	8735.1	G	U	T	A	CID	LIT	3	41.0	YDQQSDAWIMR	1412.6	R	L	2.4	0.0	28.4	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64503	8735.1	G	T	T	A	CID	LIT	5	57.7	IGAFEIDDGELHGESPGDR	2013.9	R	T	3.7	0.8	34.5	7.0
P64503	8735.1	G	T	T	A	CID	LIT	5	57.7	MKTSVR	721.4	-	I	1.6	0.6	13.9	15.2
P64503	8735.1	G	T	T	A	CID	LIT	5	57.7	TLTIPCK	832.5	R	S	1.8	0.6	17.8	13.2
P64503	8735.1	G	T	T	A	CID	LIT	5	57.7	TRYDQQSDAWIMR	1669.8	R	L	4.4	0.8	50.2	11.1
P64503	8735.1	G	T	T	A	CID	LIT	5	57.7	YDQQSDAWIMR	1412.6	R	L	3.7	0.0	53.6	9.5
P64503	8735.1	G	T	A	A	CID	LIT	3	33.3	DAWIMRLA	975.5	S	-	2.1	0.7	23.9	15.7
P64503	8735.1	G	T	A	A	CID	LIT	3	33.3	DRTLTIPCKSDP	1402.7	G	D	2.0	0.0	65.6	13.0
P64503	8735.1	G	T	A	A	CID	LIT	3	33.3	DRTLTIPCKSDPDLCMQL	2179.0	G	D	3.2	0.0	25.0	11.1
P64503	8735.1	G	U	T	B	CID	LIT	3	50.0	IGAFEIDDGELHGESPGDR	2013.9	R	T	4.4	0.0	66.3	7.0
P64503	8735.1	G	U	T	B	CID	LIT	3	50.0	TLTIPCK	832.5	R	S	1.8	0.2	5.7	14.5
P64503	8735.1	G	U	T	B	CID	LIT	3	50.0	TRYDQQSDAWIMR	1669.8	R	L	2.6	0.0	15.5	10.8
P64503	8735.1	G	T	A	B	CID	LIT	2	43.6	DAETSIPALLNGEHSVLYRTRY	2505.3	W	D	0.7	0.3	28.6	15.6
P64503	8735.1	G	T	A	B	CID	LIT	2	43.6	DRTLTIPCKSDP	1402.7	G	D	2.8	0.8	41.3	13.2
P64503	8735.1	G	U	A	B	CID	LIT	4	66.7	DAETSIPALLNGEHSVLYRTRY	2505.3	W	D	1.3	0.0	40.2	14.8
P64503	8735.1	G	U	A	B	CID	LIT	4	66.7	DAWIMRLA	975.5	S	-	2.3	0.5	23.1	15.9
P64503	8735.1	G	U	A	B	CID	LIT	4	66.7	DGELHGESPG	997.4	D	D	2.0	0.0	29.1	9.0
P64503	8735.1	G	U	A	B	CID	LIT	4	66.7	DRTLTIPCKSDP	1402.7	G	D	3.0	0.4	23.6	13.2
P64503	8735.1	S	U	T	A	CID	LIT	2	41.0	IGAFEIDDGELHGESPGDR	2013.9	R	T	5.3	0.6	67.8	15.1
P64503	8735.1	S	U	T	A	CID	LIT	2	41.0	TRYDQQSDAWIMR	1669.8	R	L	4.5	0.7	46.8	15.1
P64503	8735.1	S	U	T	C	CID	LIT	2	41.0	IGAFEIDDGELHGESPGDR	2013.9	R	T	5.7	0.6	85.6	15.1
P64503	8735.1	S	U	T	C	CID	LIT	2	41.0	TRYDQQSDAWIMR	1669.8	R	L	4.8	0.7	45.6	15.1
P64503	8735.1	S	U	T	A	ETD	LIT	2	41.0	IGAFEIDDGELHGESPGDR	2013.9	R	T	6.1	0.3	60.8	14.6
P64503	8735.1	S	U	T	A	ETD	LIT	2	41.0	TRYDQQSDAWIMR	1669.8	R	L	0.0	0.0	21.8	14.8
P64503	8735.1	S	U	T	A	ETD+CID	LIT	2	41.0	IGAFEIDDGELHGESPGDR	2013.9	R	T	5.2	0.6	66.5	15.2
P64503	8735.1	S	U	T	A	ETD+CID	LIT	2	41.0	TRYDQQSDAWIMR	1669.8	R	L	4.3	0.6	50.0	15.1
P64503	8735.1	S	U	T	C	ETD+CID	LIT	2	41.0	IGAFEIDDGELHGESPGDR	2013.9	R	T	5.3	0.6	80.6	15.2
P64503	8735.1	S	U	T	C	ETD+CID	LIT	2	41.0	TRYDQQSDAWIMR	1669.8	R	L	4.6	0.6	49.2	15.1
P30748	8739.8	G	U	T	A	CID	LIT	2	35.8	ELVGTDATEVAADFPTVEALR	2204.1	R	Q	4.0	0.0	83.3	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P30748	8739.8	G	U	T	A	CID	LIT	2	35.8	VLFFAQVR	979.6	K	E	2.1	0.7	30.2	7.8
P30748	8739.8	G	T	T	A	CID	LIT	2	35.8	ELVGTDATEVAADFPTVEALR	2204.1	R	Q	5.0	0.8	93.7	12.0
P30748	8739.8	G	T	T	A	CID	LIT	2	35.8	VLFFAQVR	979.6	K	E	2.6	0.0	22.3	7.8
P30748	8739.8	G	U	A	B	CID	LIT	2	24.7	DEVAFFPPVTGG	1235.6	G	-	2.2	0.5	0.0	16.3
P30748	8739.8	G	U	A	B	CID	LIT	2	24.7	DRWALALE	973.5	S	D	2.0	0.2	10.6	14.9
P30748	8739.8	S	U	T	C	CID	LIT	2	35.8	ELVGTDATEVAADFPTVEALR	2204.1	R	Q	4.9	0.6	82.1	19.3
P30748	8739.8	S	U	T	C	CID	LIT	2	35.8	VLFFAQVR	979.6	K	E	2.5	0.0	33.2	8.5
P30748	8739.8	S	U	T	A	ETD	LIT	2	35.8	ELVGTDATEVAADFPTVEALR	2204.1	R	Q	3.7	0.0	23.3	19.6
P30748	8739.8	S	U	T	A	ETD	LIT	2	35.8	VLFFAQVR	979.6	K	E	1.1	0.0	24.9	8.5
P30748	8739.8	S	U	T	B	ETD+CID	LIT	2	35.8	ELVGTDATEVAADFPTVEALR	2204.1	R	Q	0.0	0.0	79.6	19.3
P30748	8739.8	S	U	T	B	ETD+CID	LIT	2	35.8	VLFFAQVR	979.6	K	E	0.0	0.0	29.3	8.5
P30748	8739.8	S	U	T	B	ETD+CID	LIT	2	35.8	ELVGTDATEVAADFPTVEALR	2204.1	R	Q	5.3	0.6	79.6	19.3
P30748	8739.8	S	U	T	B	ETD+CID	LIT	2	35.8	VLFFAQVR	979.6	K	E	2.8	0.0	29.3	8.5
P30748	8739.8	S	U	T	B	HCD	FT	2	35.8	ELVGTDATEVAADFPTVEALR	2204.1	R	Q	0.0	0.0	79.6	19.3
P30748	8739.8	S	U	T	B	HCD	FT	2	35.8	VLFFAQVR	979.6	K	E	0.0	0.0	29.3	8.5
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	HEQLTK	755.4	R	G	2.5	0.7	41.5	6.0
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	HKEDMEAR	1015.5	K	H	2.2	0.0	25.9	7.0
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	LRTAIAHHGR	1131.7	R	K	3.5	0.7	40.4	11.5
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	MSHLDEVIAR	1170.6	-	V	2.7	0.7	29.0	11.5
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	SHLDEVIAR	1039.6	M	V	0.0	0.0	37.6	10.8
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	TAIAHHGR	862.5	R	K	1.9	0.7	39.5	14.0
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	TAIAHHGRK	990.6	R	H	2.0	0.7	3.9	13.0
P64455	8782.0	G	U	T	A	CID	LIT	8	53.2	YTQQQR	823.4	R	L	1.7	0.5	12.3	11.5
P64455	8782.0	G	U	A	A	CID	LIT	5	33.8	DEVIARV	801.4	L	D	1.9	0.4	15.7	17.9
P64455	8782.0	G	U	A	A	CID	LIT	5	33.8	DMEARHEQLTKGGTIL	1798.9	E	-	3.2	0.5	36.8	15.6
P64455	8782.0	G	U	A	A	CID	LIT	5	33.8	EARHEQLTKGGTIL	1552.8	M	-	2.9	0.8	31.2	13.4
P64455	8782.0	G	U	A	A	CID	LIT	5	33.8	EQLTKGGTIL	1059.6	H	-	2.4	0.6	16.3	12.0
P64455	8782.0	G	U	A	A	CID	LIT	5	33.8	SHLDEVIARV	1138.6	M	D	0.0	0.0	25.4	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64455	8782.0	G	T	T	B	CID	LIT	3	32.5	EDRYTQQQR	1223.6	R	L	2.8	0.4	14.7	10.8
P64455	8782.0	G	T	T	B	CID	LIT	3	32.5	HKEDMEAR	1015.5	K	H	1.2	0.4	11.7	6.0
P64455	8782.0	G	T	T	B	CID	LIT	3	32.5	TAIAHHGR	862.5	R	K	2.0	0.6	19.6	14.0
P64455	8782.0	G	U	T	B	CID	LIT	6	53.2	EDRYTQQQR	1223.6	R	L	1.8	0.4	4.8	10.4
P64455	8782.0	G	U	T	B	CID	LIT	6	53.2	HEQLTK	755.4	R	G	2.1	0.2	26.8	6.0
P64455	8782.0	G	U	T	B	CID	LIT	6	53.2	HKEDMEAR	1015.5	K	H	2.2	0.0	22.0	7.0
P64455	8782.0	G	U	T	B	CID	LIT	6	53.2	MSHLDEVIAR	1170.6	-	V	2.9	0.8	25.6	10.8
P64455	8782.0	G	U	T	B	CID	LIT	6	53.2	SHLDEVIAR	1039.6	M	V	0.0	0.0	25.5	11.5
P64455	8782.0	G	U	T	B	CID	LIT	6	53.2	TAIAHHGR	862.5	R	K	2.8	0.8	38.1	14.0
P64455	8782.0	G	T	A	B	CID	LIT	2	29.9	DEVIARV	801.4	L	D	2.3	0.2	22.8	17.9
P64455	8782.0	G	T	A	B	CID	LIT	2	29.9	DMEARHEQLTKGGTIL	1798.9	E	-	3.7	0.4	2.6	15.2
P64455	8782.0	G	U	A	B	CID	LIT	4	46.8	DAAIEESVIAHMN	1399.7	V	E	3.6	0.7	55.8	12.8
P64455	8782.0	G	U	A	B	CID	LIT	4	46.8	DEVIARV	801.4	L	D	2.4	0.3	29.5	17.9
P64455	8782.0	G	U	A	B	CID	LIT	4	46.8	DMEARHEQLTKGGTIL	1798.9	E	-	3.3	0.6	28.9	15.9
P64455	8782.0	G	U	A	B	CID	LIT	4	46.8	EQLTKGGTIL	1059.6	H	-	2.2	0.2	14.9	12.0
P64455	8782.0	S	U	T	B	CID	LIT	2	48.1	KHKEDMEAR	1143.6	R	H	2.4	0.7	15.6	11.5
P64455	8782.0	S	U	T	B	CID	LIT	2	48.1	VDAAIEESVIAHMNELLIALSDDAELSR	3024.5	R	E	4.4	0.4	52.4	19.2
P64455	8782.0	S	U	T	C	CID	LIT	2	49.4	MSHLDEVIAR	1170.6	-	V	3.5	0.6	33.3	13.4
P64455	8782.0	S	U	T	C	CID	LIT	2	49.4	VDAAIEESVIAHMNELLIALSDDAELSR	3024.5	R	E	4.2	0.5	33.6	19.2
P64455	8782.0	S	U	T	B	ETD	LIT	2	59.7	SHLDEVIAR	1039.6	M	V	0.0	0.0	48.6	15.2
P64455	8782.0	S	U	T	B	ETD	LIT	2	59.7	VDAAIEESVIAHMNELLIALSDDAELSREDRYTQQQR	4229.1	R	L	0.0	0.0	16.5	18.6
P64455	8782.0	S	U	T	C	ETD	LIT	2	61.0	MSHLDEVIAR	1170.6	-	V	2.6	0.3	15.4	13.4
P64455	8782.0	S	U	T	C	ETD	LIT	2	61.0	VDAAIEESVIAHMNELLIALSDDAELSREDRYTQQQR	4229.1	R	L	0.0	0.0	45.7	18.5
P64455	8782.0	S	U	T	A	ETD+CID	LIT	2	48.1	EIQDVEKK	988.5	-	-	0.7	-0.6	24.6	15.6
P64455	8782.0	S	U	T	A	ETD+CID	LIT	2	48.1	VDAAIEESVIAHMNELLIALSDDAELSR	3024.5	R	E	3.4	0.7	20.7	19.2
P64455	8782.0	S	U	T	A	ETD+CID	LIT	2	48.1	VDAAIEESVIAHMNELLIALSDDAELSREDRYTQQQR	4229.1	R	L	0.0	0.0	19.1	18.5
P64455	8782.0	S	U	T	C	ETD+CID	LIT	2	49.4	MSHLDEVIAR	1170.6	-	V	3.4	0.5	39.8	13.6
P64455	8782.0	S	U	T	C	ETD+CID	LIT	2	49.4	VDAAIEESVIAHMNELLIALSDDAELSR	3024.5	R	E	4.1	0.4	19.4	19.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABS8	8828.5	G	U	T	A	CID	LIT	2	26.3	LASVNLSR	859.5	R	L	2.3	0.3	40.6	15.2
P0ABS8	8828.5	G	U	T	A	CID	LIT	2	26.3	YNMPVIAEAVER	1391.7	R	E	2.4	0.7	12.2	12.0
P0ABS8	8828.5	G	U	T	B	CID	LIT	2	38.2	LASVNLSR	859.5	R	L	2.1	0.2	18.5	15.4
P0ABS8	8828.5	G	U	T	B	CID	LIT	2	38.2	LDQTEMDKVNVDLAAAGVAFK	2235.1	K	E	5.3	0.5	35.7	13.8
P0ACW6	8860.7	G	U	T	A	CID	LIT	5	37.8	GYNAEVVR	907.5	R	M	2.7	0.6	35.8	14.8
P0ACW6	8860.7	G	U	T	A	CID	LIT	5	37.8	HNKLDHEIAR	1232.7	K	K	3.0	0.0	41.6	12.3
P0ACW6	8860.7	G	U	T	A	CID	LIT	5	37.8	ILQQESVK	944.5	K	E	2.1	0.6	35.0	15.6
P0ACW6	8860.7	G	U	T	A	CID	LIT	5	37.8	ILQQESVKEV	1172.7	K	-	3.2	0.0	40.8	13.6
P0ACW6	8860.7	G	U	T	A	CID	LIT	5	37.8	LDHEIAR	853.5	K	K	2.0	0.2	19.4	12.6
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	DLISR	603.3	R	L	1.6	0.3	16.8	20.0
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	GYNAEVVR	907.5	R	M	3.1	0.5	37.0	14.8
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	HNKLDHEIAR	1232.7	K	K	3.4	0.6	43.3	12.3
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	ILQQESVK	944.5	K	E	2.1	0.0	32.5	15.9
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	ILQQESVKEV	1172.7	K	-	3.3	0.7	40.9	13.0
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	LDHEIAR	853.5	K	K	2.5	0.7	41.8	11.8
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	LKNENPR	870.5	R	F	2.1	0.7	21.1	12.0
P0ACW6	8860.7	G	T	T	A	CID	LIT	8	66.2	LQLKDEMLK	1117.6	K	I	2.9	0.6	45.0	11.5
P0ACW6	8860.7	G	T	T	B	CID	LIT	2	20.3	DLISR	603.3	R	L	1.7	0.1	21.2	20.0
P0ACW6	8860.7	G	T	T	B	CID	LIT	2	20.3	ILQQESVKEV	1172.7	K	-	2.5	0.4	20.6	13.0
P0ACW6	8860.7	S	U	T	C	CID	LIT	2	25.7	HNKLDHEIAR	1232.7	K	K	2.4	0.5	22.1	16.6
P0ACW6	8860.7	S	U	T	C	CID	LIT	2	25.7	LQLKDEMLK	1117.6	K	I	2.6	0.2	24.6	14.9
P0ABR1	8931.2	G	U	T	A	CID	LIT	3	59.3	RIQYAFPDNEGHVSVR	1887.9	R	Y	4.7	0.7	53.2	12.8
P0ABR1	8931.2	G	U	T	A	CID	LIT	3	59.3	TSPLPAGAIDALAGELSR	1738.9	K	R	4.2	0.6	54.2	8.5
P0ABR1	8931.2	G	U	T	A	CID	LIT	3	59.3	YAAANNLSVIGATK	1392.7	R	E	2.9	0.8	39.6	13.4
P0A8G9	8934.1	G	U	T	A	CID	LIT	2	35.0	ALSELEQIVTR	1258.7	K	L	3.1	0.6	19.3	11.8
P0A8G9	8934.1	G	U	T	A	CID	LIT	2	35.0	LESGDLPLEEALNEFER	1961.0	R	G	5.4	0.7	82.5	13.8
P0A8G9	8934.1	G	T	T	A	CID	LIT	3	42.5	ALSELEQIVTR	1258.7	K	L	2.2	0.0	17.8	10.0
P0A8G9	8934.1	G	T	T	A	CID	LIT	3	42.5	GVQLAR	643.4	R	Q	1.5	0.6	20.9	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8G9	8934.1	G	T	T	A	CID	LIT	3	42.5	LESGDLPLEEALNEFER	1961.0	R	G	4.4	0.0	36.3	13.8
P0A8G9	8934.1	S	U	T	B	ETD+CID	LIT	2	35.0	ALSELEQIVTR	1258.7	K	L	0.0	0.0	27.4	15.8
P0A8G9	8934.1	S	U	T	B	ETD+CID	LIT	2	35.0	ALSELEQIVTRLESGDLPLEEALNEFER	3200.6	K	G	0.0	0.0	22.3	18.2
P0A8G9	8934.1	S	U	T	B	ETD+CID	LIT	2	35.0	ALSELEQIVTR	1258.7	K	L	3.1	0.5	0.0	0.0
P0A8G9	8934.1	S	U	T	B	ETD+CID	LIT	2	35.0	ALSELEQIVTRLESGDLPLEEALNEFER	3200.6	K	G	3.6	0.3	0.0	0.0
P0A8G9	8934.1	S	U	T	B	ETD+CID	LIT	2	35.0	ALSELEQIVTR	1258.7	K	L	3.1	0.5	27.4	15.8
P0A8G9	8934.1	S	U	T	B	ETD+CID	LIT	2	35.0	ALSELEQIVTRLESGDLPLEEALNEFER	3200.6	K	G	3.6	0.3	22.3	18.2
P0A8G9	8934.1	S	U	T	B	HCD	FT	2	35.0	ALSELEQIVTR	1258.7	K	L	0.0	0.0	27.4	15.8
P0A8G9	8934.1	S	U	T	B	HCD	FT	2	35.0	ALSELEQIVTRLESGDLPLEEALNEFER	3200.6	K	G	0.0	0.0	22.3	18.2
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	AKYQR	665.4	R	Q	1.9	0.5	24.6	13.0
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	DIATLK	660.4	K	N	1.7	0.5	19.3	13.8
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	DIATLKNYITESGK	1552.8	K	I	1.7	0.4	0.0	11.8
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	FTAEGVQEIDYK	1399.7	R	D	4.5	0.6	63.7	13.6
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	FTAEGVQEIDYKDIATLK	2041.0	R	N	4.6	0.7	76.4	11.8
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	NYITESGK	911.4	K	I	2.0	0.0	40.8	9.0
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	NYITESGKIVPSR	1463.8	K	I	4.3	0.6	66.2	10.8
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	YLSLLPYTDR	1240.7	R	H	2.8	0.8	21.1	11.8
P0A7T7	8969.0	G	U	T	A	CID	LIT	9	64.0	YLSLLPYTDRHQ	1505.8	R	-	3.7	0.7	37.6	13.8
P0A7T7	8969.0	G	T	T	A	CID	LIT	6	57.3	FTAEGVQEIDYK	1399.7	R	D	3.7	0.8	51.7	12.0
P0A7T7	8969.0	G	T	T	A	CID	LIT	6	57.3	FTAEGVQEIDYKDIATLK	2041.0	R	N	4.9	0.0	82.8	12.3
P0A7T7	8969.0	G	T	T	A	CID	LIT	6	57.3	NYITESGK	911.4	K	I	2.2	0.0	33.3	10.0
P0A7T7	8969.0	G	T	T	A	CID	LIT	6	57.3	NYITESGKIVPSR	1463.8	K	I	3.4	0.0	41.4	11.5
P0A7T7	8969.0	G	T	T	A	CID	LIT	6	57.3	YLSLLPYTDR	1240.7	R	H	2.0	0.8	26.2	12.6
P0A7T7	8969.0	G	T	T	A	CID	LIT	6	57.3	YLSLLPYTDRHQ	1505.8	R	-	3.3	0.6	30.5	13.8
P0A7T7	8969.0	G	U	T	B	CID	LIT	7	57.3	AKYQR	665.4	R	Q	1.6	0.2	13.0	13.0
P0A7T7	8969.0	G	U	T	B	CID	LIT	7	57.3	DIATLK	660.4	K	N	2.2	0.2	20.1	13.8
P0A7T7	8969.0	G	U	T	B	CID	LIT	7	57.3	FTAEGVQEIDYK	1399.7	R	D	4.4	0.7	71.8	12.0
P0A7T7	8969.0	G	U	T	B	CID	LIT	7	57.3	FTAEGVQEIDYKDIATLK	2041.0	R	N	5.1	0.0	88.9	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7T7	8969.0	G	U	T	B	CID	LIT	7	57.3	NYITESGK	911.4	K	I	2.4	0.0	42.5	9.0
P0A7T7	8969.0	G	U	T	B	CID	LIT	7	57.3	YLSLLPYTDR	1240.7	R	H	2.6	0.0	23.0	11.8
P0A7T7	8969.0	G	U	T	B	CID	LIT	7	57.3	YLSLLPYTDRHQ	1505.8	R	-	3.5	0.4	27.6	13.8
P0A7T7	8969.0	S	U	T	A	CID	LIT	6	50.7	FTAEGVQEIDYK	1399.7	R	D	3.6	0.8	60.8	15.7
P0A7T7	8969.0	S	U	T	A	CID	LIT	6	50.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	4.9	0.6	81.6	16.6
P0A7T7	8969.0	S	U	T	A	CID	LIT	6	50.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	4.9	0.4	34.5	18.7
P0A7T7	8969.0	S	U	T	A	CID	LIT	6	50.7	NYITESGK	911.4	K	I	2.2	0.0	26.3	11.1
P0A7T7	8969.0	S	U	T	A	CID	LIT	6	50.7	YLSLLPYTDR	1240.7	R	H	2.6	0.7	23.7	15.9
P0A7T7	8969.0	S	U	T	A	CID	LIT	6	50.7	YLSLLPYTDRHQ	1505.8	R	-	2.4	0.3	10.9	17.3
P0A7T7	8969.0	S	U	T	B	CID	LIT	5	50.7	FTAEGVQEIDYK	1399.7	R	D	3.0	0.8	51.3	16.1
P0A7T7	8969.0	S	U	T	B	CID	LIT	5	50.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	4.9	0.5	95.5	17.2
P0A7T7	8969.0	S	U	T	B	CID	LIT	5	50.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	4.5	0.6	29.9	18.4
P0A7T7	8969.0	S	U	T	B	CID	LIT	5	50.7	YLSLLPYTDR	1240.7	R	H	2.6	0.7	17.8	15.9
P0A7T7	8969.0	S	U	T	B	CID	LIT	5	50.7	YLSLLPYTDRHQ	1505.8	R	-	4.0	0.5	45.0	17.3
P0A7T7	8969.0	S	U	T	C	CID	LIT	4	40.0	FTAEGVQEIDYK	1399.7	R	D	3.6	0.7	51.0	15.6
P0A7T7	8969.0	S	U	T	C	CID	LIT	4	40.0	FTAEGVQEIDYKDIATLK	2041.0	R	N	5.4	0.6	79.1	17.0
P0A7T7	8969.0	S	U	T	C	CID	LIT	4	40.0	YLSLLPYTDR	1240.7	R	H	2.6	0.8	20.9	15.9
P0A7T7	8969.0	S	U	T	C	CID	LIT	4	40.0	YLSLLPYTDRHQ	1505.8	R	-	3.9	0.5	36.6	17.2
P0A7T7	8969.0	S	U	T	A	CID	FT	2	24.0	FTAEGVQEIDYK	1399.7	R	D	2.0	0.0	43.5	15.6
P0A7T7	8969.0	S	U	T	A	CID	FT	2	24.0	FTAEGVQEIDYKDIATLK	2041.0	R	N	3.5	0.0	39.8	17.1
P0A7T7	8969.0	S	U	T	B	CID	FT	3	37.3	FTAEGVQEIDYK	1399.7	R	D	3.6	0.0	36.0	15.6
P0A7T7	8969.0	S	U	T	B	CID	FT	3	37.3	FTAEGVQEIDYKDIATLK	2041.0	R	N	4.6	0.0	62.2	16.8
P0A7T7	8969.0	S	U	T	B	CID	FT	3	37.3	YLSLLPYTDR	1240.7	R	H	2.2	0.0	22.5	15.9
P0A7T7	8969.0	S	U	T	A	ETD	LIT	5	50.7	FTAEGVQEIDYK	1399.7	R	D	2.1	0.7	0.0	0.0
P0A7T7	8969.0	S	U	T	A	ETD	LIT	5	50.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	0.0	0.0	87.5	16.6
P0A7T7	8969.0	S	U	T	A	ETD	LIT	5	50.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	4.1	0.0	30.1	18.3
P0A7T7	8969.0	S	U	T	A	ETD	LIT	5	50.7	YLSLLPYTDR	1240.7	R	H	2.6	0.7	0.0	0.0
P0A7T7	8969.0	S	U	T	A	ETD	LIT	5	50.7	YLSLLPYTDRHQ	1505.8	R	-	5.2	0.6	67.2	17.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7T7	8969.0	S	U	T	B	ETD	LIT	6	57.3	FTAEGVQEIDYK	1399.7	R	D	1.8	0.8	0.0	0.0
P0A7T7	8969.0	S	U	T	B	ETD	LIT	6	57.3	FTAEGVQEIDYKDIATLK	2041.0	R	N	6.9	0.6	90.9	16.8
P0A7T7	8969.0	S	U	T	B	ETD	LIT	6	57.3	NYITESGK	911.4	K	I	2.7	0.5	29.1	11.5
P0A7T7	8969.0	S	U	T	B	ETD	LIT	6	57.3	NYITESGKIVPSR	1463.8	K	I	3.8	0.5	43.2	17.6
P0A7T7	8969.0	S	U	T	B	ETD	LIT	6	57.3	YLSLLPYTDR	1240.7	R	H	0.0	0.0	32.4	15.4
P0A7T7	8969.0	S	U	T	B	ETD	LIT	6	57.3	YLSLLPYTDRHQ	1505.8	R	-	5.4	0.6	49.3	17.3
P0A7T7	8969.0	S	U	T	C	ETD	LIT	6	57.3	FTAEGVQEIDYK	1399.7	R	D	2.4	0.7	0.0	0.0
P0A7T7	8969.0	S	U	T	C	ETD	LIT	6	57.3	FTAEGVQEIDYKDIATLK	2041.0	R	N	7.9	0.6	82.9	16.8
P0A7T7	8969.0	S	U	T	C	ETD	LIT	6	57.3	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	5.0	0.0	25.7	18.7
P0A7T7	8969.0	S	U	T	C	ETD	LIT	6	57.3	NYITESGKIVPSR	1463.8	K	I	2.5	0.0	40.8	15.7
P0A7T7	8969.0	S	U	T	C	ETD	LIT	6	57.3	YLSLLPYTDR	1240.7	R	H	2.0	0.7	0.0	0.0
P0A7T7	8969.0	S	U	T	C	ETD	LIT	6	57.3	YLSLLPYTDRHQ	1505.8	R	-	5.4	0.6	50.3	17.9
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	4	50.7	FTAEGVQEIDYK	1399.7	R	D	0.0	0.0	67.6	15.8
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	4	50.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	0.0	0.0	67.9	17.0
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	4	50.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	0.0	0.0	34.2	18.6
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	4	50.7	YLSLLPYTDRHQ	1505.8	R	-	0.0	0.0	54.8	17.9
P0A7T7	8969.0	S	U	T	A	ETD+CID	LIT	5	50.7	FTAEGVQEIDYK	1399.7	R	D	3.3	0.8	0.0	0.0
P0A7T7	8969.0	S	U	T	A	ETD+CID	LIT	5	50.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	5.4	0.5	74.2	17.1
P0A7T7	8969.0	S	U	T	A	ETD+CID	LIT	5	50.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	6.2	0.6	51.1	18.7
P0A7T7	8969.0	S	U	T	A	ETD+CID	LIT	5	50.7	YLSLLPYTDR	1240.7	R	H	2.5	0.8	22.0	15.9
P0A7T7	8969.0	S	U	T	A	ETD+CID	LIT	5	50.7	YLSLLPYTDRHQ	1505.8	R	-	3.7	0.5	36.0	17.3
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	3	34.7	FTAEGVQEIDYK	1399.7	R	D	4.0	0.8	0.0	0.0
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	3	34.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	3.4	0.9	0.0	0.0
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	3	34.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	4.7	0.6	0.0	0.0
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	5	50.7	FTAEGVQEIDYK	1399.7	R	D	4.0	0.8	67.6	15.8
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	5	50.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	5.7	0.5	67.9	17.0
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	5	50.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	4.7	0.6	34.2	18.6
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	5	50.7	YLSLLPYTDR	1240.7	R	H	2.3	0.7	17.8	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7T7	8969.0	S	U	T	B	ETD+CID	LIT	5	50.7	YLSLLPYTDRHQ	1505.8	R	-	1.6	0.6	23.9	17.3
P0A7T7	8969.0	S	U	T	C	ETD+CID	LIT	6	57.3	FTAEGVQEIDYK	1399.7	R	D	4.1	0.8	60.7	15.7
P0A7T7	8969.0	S	U	T	C	ETD+CID	LIT	6	57.3	FTAEGVQEIDYKDIATLK	2041.0	R	N	5.5	0.6	81.8	16.8
P0A7T7	8969.0	S	U	T	C	ETD+CID	LIT	6	57.3	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	4.8	0.0	38.6	18.6
P0A7T7	8969.0	S	U	T	C	ETD+CID	LIT	6	57.3	NYITESGKIVPSR	1463.8	K	I	3.5	0.5	52.7	17.1
P0A7T7	8969.0	S	U	T	C	ETD+CID	LIT	6	57.3	YLSLLPYTDR	1240.7	R	H	2.5	0.8	18.8	15.1
P0A7T7	8969.0	S	U	T	C	ETD+CID	LIT	6	57.3	YLSLLPYTDRHQ	1505.8	R	-	3.6	0.0	31.5	16.8
P0A7T7	8969.0	S	U	T	B	HCD	FT	4	50.7	FTAEGVQEIDYK	1399.7	R	D	0.0	0.0	67.6	15.8
P0A7T7	8969.0	S	U	T	B	HCD	FT	4	50.7	FTAEGVQEIDYKDIATLK	2041.0	R	N	0.0	0.0	67.9	17.0
P0A7T7	8969.0	S	U	T	B	HCD	FT	4	50.7	FTAEGVQEIDYKDIATLKNYITESGK	2933.5	R	I	0.0	0.0	34.2	18.6
P0A7T7	8969.0	S	U	T	B	HCD	FT	4	50.7	YLSLLPYTDRHQ	1505.8	R	-	0.0	0.0	23.9	17.3
P0A7T7	8969.0	S	U	T	A	HCD	FT	2	24.0	FTAEGVQEIDYK	1399.7	R	D	1.4	0.0	34.8	15.6
P0A7T7	8969.0	S	U	T	A	HCD	FT	2	24.0	FTAEGVQEIDYKDIATLK	2041.0	R	N	4.7	0.0	57.2	16.8
P0A7T7	8969.0	S	U	T	B	HCD	FT	2	24.0	FTAEGVQEIDYK	1399.7	R	D	1.3	0.0	38.0	15.7
P0A7T7	8969.0	S	U	T	B	HCD	FT	2	24.0	FTAEGVQEIDYKDIATLK	2041.0	R	N	3.6	0.0	63.7	16.8
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	FLPNLHSHR	1120.6	R	F	2.9	0.7	52.8	15.1
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	FWVESEKR	1080.5	R	F	2.7	0.4	22.1	13.8
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	GIDTVLAELR	1086.6	K	A	3.6	0.5	76.1	13.6
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	RFLPNLHSHR	1276.7	R	F	3.6	0.6	22.3	11.8
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	RFVTLR	791.5	K	V	2.3	0.3	15.1	10.4
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	RPVTGNNR	913.5	K	S	3.2	0.0	27.7	9.0
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	RPVTGNNRSHALNATK	1735.9	K	R	3.4	0.8	27.9	11.1
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	SHALNATK	841.5	R	R	2.3	0.0	28.3	12.6
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	SHALNATKR	997.6	R	R	2.6	0.8	23.1	9.5
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	SRVCQVTGK	1034.5	M	R	0.0	0.0	43.5	13.2
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	VCQVTGKRPVTGNNR	1685.9	R	S	3.8	0.7	25.7	13.6
P0A7M2	8988.5	G	U	T	A	CID	LIT	12	82.1	VIDKK	602.4	R	G	1.7	0.6	12.6	15.2
P0A7M2	8988.5	G	T	T	A	CID	LIT	7	57.7	FLPNLHSHR	1120.6	R	F	2.4	0.0	39.9	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7M2	8988.5	G	T	T	A	CID	LIT	7	57.7	GIDTVLAELR	1086.6	K	A	4.1	0.4	72.5	13.6
P0A7M2	8988.5	G	T	T	A	CID	LIT	7	57.7	RPVTGNNR	913.5	K	S	3.4	0.0	30.2	9.0
P0A7M2	8988.5	G	T	T	A	CID	LIT	7	57.7	SHALNATK	841.5	R	R	2.0	0.7	27.7	12.6
P0A7M2	8988.5	G	T	T	A	CID	LIT	7	57.7	SHALNATKR	997.6	R	R	2.8	0.0	29.4	9.5
P0A7M2	8988.5	G	T	T	A	CID	LIT	7	57.7	SRVCQVTGK	1034.5	M	R	0.0	0.0	31.1	14.5
P0A7M2	8988.5	G	T	T	A	CID	LIT	7	57.7	VCQVTGKRPVTGNNR	1685.9	R	S	4.1	0.6	30.8	14.8
P0A7M2	8988.5	G	T	T	B	CID	LIT	2	21.8	RPVTGNNR	913.5	K	S	3.2	0.0	19.6	9.0
P0A7M2	8988.5	G	T	T	B	CID	LIT	2	21.8	SHALNATKR	997.6	R	R	2.5	0.8	17.9	7.8
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	FLPNLHSHR	1120.6	R	F	2.3	0.4	14.2	15.3
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	FVTLR	635.4	R	V	1.6	0.0	18.1	15.4
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	FWVESEK	924.4	R	R	2.0	0.0	24.8	9.5
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	FWVESEKR	1080.5	R	F	2.6	0.8	35.5	13.8
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	GIDTVLAELR	1086.6	K	A	4.3	0.6	78.3	13.6
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	KGIDTVLAELR	1214.7	K	A	3.7	0.5	48.1	11.8
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	RFLPNLHSHR	1276.7	R	F	3.7	0.7	25.0	11.8
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	RPVTGNNR	913.5	K	S	2.5	0.7	19.4	9.0
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	RPVTGNNRSHALNATK	1735.9	K	R	2.2	0.7	21.1	11.8
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	SHALNATK	841.5	R	R	2.4	0.0	25.1	11.8
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	SHALNATKR	997.6	R	R	2.9	0.0	30.1	9.5
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	SRVCQVTGK	1034.5	M	R	0.0	0.0	37.3	14.5
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	VCQVTGK	791.4	R	R	2.8	0.4	40.6	17.2
P0A7M2	8988.5	G	U	T	B	CID	LIT	14	82.1	VIDKK	602.4	R	G	1.5	0.1	22.9	15.2
P0A7M2	8988.5	S	U	T	A	CID	LIT	3	25.6	GIDTVLAELR	1086.6	K	A	3.9	0.3	54.1	16.9
P0A7M2	8988.5	S	U	T	A	CID	LIT	3	25.6	KGIDTVLAELR	1214.7	K	A	1.8	0.5	0.0	0.0
P0A7M2	8988.5	S	U	T	A	CID	LIT	3	25.6	SRVCQVTGK	1034.5	M	R	0.0	0.0	30.0	17.2
P0A7M2	8988.5	S	U	T	B	CID	LIT	6	47.4	GIDTVLAELR	1086.6	K	A	3.7	0.4	62.7	16.9
P0A7M2	8988.5	S	U	T	B	CID	LIT	6	47.4	KGIDTVLAELR	1214.7	K	A	2.7	0.3	21.5	14.9
P0A7M2	8988.5	S	U	T	B	CID	LIT	6	47.4	RPVTGNNRSHALNATK	1736.9	K	R	2.5	0.7	25.2	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7M2	8988.5	S	U	T	B	CID	LIT	6	47.4	RPVTGNNRSHALNATKR	1893.0	K	R	3.0	0.6	9.8	17.1
P0A7M2	8988.5	S	U	T	B	CID	LIT	6	47.4	SRVCQVTGK	1034.5	M	R	0.0	0.0	27.6	17.2
P0A7M2	8988.5	S	U	T	B	CID	LIT	6	47.4	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	28.1	17.2
P0A7M2	8988.5	S	U	T	C	CID	LIT	6	66.7	FWVESEK	924.4	R	R	2.0	0.2	7.9	15.1
P0A7M2	8988.5	S	U	T	C	CID	LIT	6	66.7	GIDTVLAELR	1086.6	K	A	4.0	0.4	70.2	16.9
P0A7M2	8988.5	S	U	T	C	CID	LIT	6	66.7	RFLPNLHSHR	1276.7	R	F	3.1	0.5	32.0	15.8
P0A7M2	8988.5	S	U	T	C	CID	LIT	6	66.7	RPVTGNNRSHALNATK	1736.9	K	R	3.3	0.6	15.6	17.8
P0A7M2	8988.5	S	U	T	C	CID	LIT	6	66.7	SRVCQVTGK	1034.5	M	R	0.0	0.0	30.9	17.2
P0A7M2	8988.5	S	U	T	C	CID	LIT	6	66.7	VCQVTGKRPVTGNNR	1685.9	R	S	3.5	0.4	19.9	17.9
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	FWVESEKR	1080.5	R	F	3.1	0.2	14.3	15.9
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	GIDTVLAELR	1086.6	K	A	3.1	0.5	33.7	16.9
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	KGIDTVLAELR	1214.7	K	A	2.5	0.2	47.9	14.9
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	RFLPNLHSHR	1276.7	R	F	2.3	0.7	7.4	15.8
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	SHALNATKR	997.6	R	R	3.3	0.0	52.7	10.8
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	SRVCQVTGK	1034.5	M	R	0.0	0.0	35.1	17.2
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	34.5	16.7
P0A7M2	8988.5	S	U	T	A	ETD	LIT	8	70.5	VCQVTGKRPVTGNNR	1685.9	R	S	3.5	0.5	48.0	18.1
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	FLPNLHSHR	1120.6	R	F	3.8	0.3	18.3	15.6
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	FWVESEKR	1080.5	R	F	2.3	0.1	29.2	16.0
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	GIDTVLAELR	1086.6	K	A	2.7	0.3	0.0	0.0
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	RFLPNLHSHR	1276.7	R	F	4.0	0.4	42.8	15.8
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	RPVTGNNRSHALNATK	1736.9	K	R	2.4	0.0	18.7	17.9
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	SRVCQVTGK	1034.5	M	R	0.0	0.0	24.4	17.2
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	62.1	17.2
P0A7M2	8988.5	S	U	T	B	ETD	LIT	8	67.9	VCQVTGKRPVTGNNR	1685.9	R	S	4.2	0.4	30.2	18.1
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	FLPNLHSHR	1120.6	R	F	4.1	0.4	25.7	17.1
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	GIDTVLAELR	1086.6	K	A	2.6	0.0	42.9	16.9
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	KGIDTVLAELR	1214.7	K	A	3.1	0.5	26.4	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	RFLPNLHSHR	1276.7	R	F	3.7	0.7	46.2	15.2
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	RPVTGNNRSHALNATK	1736.9	K	R	3.8	0.0	20.4	17.9
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	SHALNATKR	997.6	R	R	2.7	0.0	30.7	9.0
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	SRVCQVTGK	1034.5	M	R	0.0	0.0	39.9	17.2
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	43.4	17.2
P0A7M2	8988.5	S	U	T	C	ETD	LIT	9	60.3	VCQVTGKRPVTGNNR	1685.9	R	S	4.3	0.6	49.1	18.1
P0A7M2	8988.5	S	U	T	C	ETD	FT	2	16.7	FVTLR	635.4	R	V	1.1	0.0	20.6	15.8
P0A7M2	8988.5	S	U	T	C	ETD	FT	2	16.7	FWVESEKR	1080.5	R	F	2.6	0.4	34.0	14.3
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	3	33.3	SHALNATKR	998.5	R	R	0.0	0.0	31.6	12.3
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	3	33.3	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	38.7	17.3
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	3	33.3	VCQVTGKRPVTGNNR	1685.9	R	S	0.0	0.0	28.6	18.1
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	GIDTVLAELR	1086.6	K	A	0.0	0.0	21.6	16.9
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	KGIDTVLAELR	1214.7	K	A	0.0	0.0	25.6	14.9
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	RPVTGNNRSHALNATK	1736.9	K	R	0.0	0.0	17.4	17.9
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	SHALNATKR	998.5	R	R	0.0	0.0	31.6	12.3
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	SRVCQVTGK	1034.5	M	R	0.0	0.0	24.9	17.2
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	38.7	17.3
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	VCQVTGK	791.4	R	R	0.0	0.0	25.0	18.5
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	8	47.4	VCQVTGKRPVTGNNR	1685.9	R	S	0.0	0.0	28.6	18.1
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	FWVESEK	924.4	R	R	1.6	0.6	12.6	12.0
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	GIDTVLAELR	1086.6	K	A	4.1	0.4	73.4	16.9
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	KGIDTVLAELR	1214.7	K	A	2.2	0.3	15.5	15.8
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	LIDQATAEIVETAKR	1657.9	-	-	2.3	0.3	37.4	16.6
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	RPVTGNNRSHALNATK	1736.9	K	R	5.9	0.0	85.3	17.9
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	RPVTGNNRSHALNATKR	1893.0	K	R	2.3	0.3	0.0	0.0
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	SHALNATKR	998.5	R	R	2.5	0.8	43.8	12.3
P0A7M2	8988.5	S	U	T	A	ETD+CID	LIT	7	56.4	SRVCQVTGK	1034.5	M	R	0.0	0.0	27.4	17.2
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	GIDTVLAELR	1086.6	K	A	1.9	0.2	21.6	16.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	KGIDTVLAELR	1214.7	K	A	2.7	0.4	25.6	14.9
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	-	-	1.3	-0.5	61.3	16.2
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	RPVTGNNRSHALNATK	1736.9	K	R	2.2	0.5	17.4	17.9
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	SHALNATKR	998.5	R	R	2.6	0.8	19.0	11.8
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	SRVCQVTGK	1034.5	M	R	0.0	0.0	24.9	17.2
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	38.7	17.3
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	VCQVTGK	791.4	R	R	2.4	0.3	25.0	18.5
P0A7M2	8988.5	S	U	T	B	ETD+CID	LIT	9	47.4	VCQVTGKRPVTGNNR	1685.9	R	S	2.8	0.4	28.6	18.1
P0A7M2	8988.5	S	U	T	C	ETD+CID	LIT	6	60.3	GIDTVLAELR	1086.6	K	A	4.0	0.4	75.8	16.9
P0A7M2	8988.5	S	U	T	C	ETD+CID	LIT	6	60.3	KGIDTVLAELR	1214.7	K	A	2.0	0.1	23.1	14.9
P0A7M2	8988.5	S	U	T	C	ETD+CID	LIT	6	60.3	RFLPNLHSHR	1276.7	R	F	3.5	0.5	0.0	0.0
P0A7M2	8988.5	S	U	T	C	ETD+CID	LIT	6	60.3	SHALNATKR	997.6	R	R	1.9	0.8	16.1	10.8
P0A7M2	8988.5	S	U	T	C	ETD+CID	LIT	6	60.3	SRVCQVTGK	1034.5	M	R	0.0	0.0	30.7	17.2
P0A7M2	8988.5	S	U	T	C	ETD+CID	LIT	6	60.3	VCQVTGKRPVTGNNR	1685.9	R	S	1.1	0.3	18.3	18.1
P0A7M2	8988.5	S	U	T	B	HCD	FT	7	46.2	GIDTVLAELR	1086.6	K	A	0.0	0.0	21.6	16.9
P0A7M2	8988.5	S	U	T	B	HCD	FT	7	46.2	KGIDTVLAELR	1214.7	K	A	0.0	0.0	25.6	14.9
P0A7M2	8988.5	S	U	T	B	HCD	FT	7	46.2	RPVTGNNRSHALNATK	1736.9	K	R	0.0	0.0	17.4	17.9
P0A7M2	8988.5	S	U	T	B	HCD	FT	7	46.2	SRVCQVTGK	1034.5	M	R	0.0	0.0	24.9	17.2
P0A7M2	8988.5	S	U	T	B	HCD	FT	7	46.2	SRVCQVTGKRPVTGNNR	1929.0	M	S	0.0	0.0	17.3	17.3
P0A7M2	8988.5	S	U	T	B	HCD	FT	7	46.2	VCQVTGK	791.4	R	R	0.0	0.0	25.0	18.5
P0A7M2	8988.5	S	U	T	B	HCD	FT	7	46.2	VCQVTGKRPVTGNNR	1685.9	R	S	0.0	0.0	29.2	17.9
P0A7M2	8988.5	S	U	T	C	HCD	FT	2	17.9	FVTLR	635.4	R	V	1.5	0.0	23.6	15.8
P0A7M2	8988.5	S	U	T	C	HCD	FT	2	17.9	SHALNATKR	997.6	R	R	2.9	0.0	31.4	9.0
P0C079	9054.0	G	U	T	A	CID	LIT	3	41.8	LMLEYIADNERLPFK	1852.0	R	Q	3.5	0.5	13.2	12.6
P0C079	9054.0	G	U	T	A	CID	LIT	3	41.8	LRNPKPVR	979.6	R	V	2.5	0.0	22.8	0.0
P0C079	9054.0	G	U	T	A	CID	LIT	3	41.8	MGVTPSEALR	1060.5	K	L	3.1	0.8	48.9	13.8
P0C079	9054.0	S	U	T	C	CID	LIT	2	31.6	LMLEYIADNERLPFK	1852.0	R	Q	2.7	0.4	25.9	16.8
P0C079	9054.0	S	U	T	C	CID	LIT	2	31.6	MGVTPSEALR	1060.5	K	L	2.5	0.4	40.3	16.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C079	9054.0	S	U	T	C	ETD	LIT	2	41.8	LMLEYIADNERLPFK	1852.0	R	Q	2.9	0.2	58.9	16.9
P0C079	9054.0	S	U	T	C	ETD	LIT	2	41.8	QTLLSDEDAELVEIVKER	2087.1	K	L	3.9	0.2	32.7	18.3
P0C079	9054.0	S	U	T	B	ETD+CID	LIT	2	31.6	LMLEYIADNERLPFK	1852.0	R	Q	0.0	0.0	30.8	17.5
P0C079	9054.0	S	U	T	B	ETD+CID	LIT	2	31.6	MGVTPSEALR	1060.5	K	L	0.0	0.0	27.9	16.4
P0C079	9054.0	S	U	T	C	ETD+CID	LIT	2	31.6	LMLEYIADNERLPFK	1852.0	R	Q	4.3	0.4	46.3	17.3
P0C079	9054.0	S	U	T	C	ETD+CID	LIT	2	31.6	MGVTPSEALR	1060.5	K	L	2.7	0.3	50.3	16.5
P0C079	9054.0	S	U	T	B	HCD	FT	2	31.6	LMLEYIADNERLPFK	1852.0	R	Q	0.0	0.0	30.8	17.5
P0C079	9054.0	S	U	T	B	HCD	FT	2	31.6	MGVTPSEALR	1060.5	K	L	0.0	0.0	27.9	16.4
P0A890	9076.9	G	U	T	A	CID	LIT	2	30.9	ETDGLPYR	950.5	K	Y	2.1	0.4	18.6	14.6
P0A890	9076.9	G	U	T	A	CID	LIT	2	30.9	TDLFSSPDHTLDALGLR	1857.9	M	C	0.0	0.0	37.1	13.6
P0A890	9076.9	S	U	T	B	CID	LIT	2	43.2	DIPGFCTFMEHELVAK	1893.9	R	E	3.0	0.6	18.4	16.5
P0A890	9076.9	S	U	T	B	CID	LIT	2	43.2	NMQPGETLLIIADDPATTR	2056.0	R	D	5.5	0.7	77.5	18.5
P0A890	9076.9	S	U	T	C	CID	LIT	3	64.2	DIPGFCTFMEHELVAK	1893.9	R	E	3.7	0.6	33.1	17.0
P0A890	9076.9	S	U	T	C	CID	LIT	3	64.2	NMQPGETLLIIADDPATTR	2056.0	R	D	5.1	0.6	53.3	18.5
P0A890	9076.9	S	U	T	C	CID	LIT	3	64.2	TDLFSSPDHTLDALGLR	1857.9	M	C	0.0	0.0	35.4	17.6
P0A890	9076.9	S	U	T	C	ETD+CID	LIT	2	43.2	DIPGFCTFMEHELVAK	1893.9	R	E	3.6	0.5	27.3	16.6
P0A890	9076.9	S	U	T	C	ETD+CID	LIT	2	43.2	NMQPGETLLIIADDPATTR	2056.0	R	D	5.3	0.5	66.6	19.1
P0AA04	9101.2	G	U	T	A	CID	LIT	7	88.2	AVEHLVK	795.5	K	L	2.6	0.8	50.2	4.8
P0AA04	9101.2	G	U	T	A	CID	LIT	7	88.2	EAKGFTSEITVTSNGK	1668.8	K	S	4.0	0.7	66.1	12.0
P0AA04	9101.2	G	U	T	A	CID	LIT	7	88.2	GFTSEITVTSNGK	1340.7	K	S	5.1	0.9	81.9	11.8
P0AA04	9101.2	G	U	T	A	CID	LIT	7	88.2	GFTSEITVTSNGKSASAK	1784.9	K	S	4.9	0.6	78.2	12.8
P0AA04	9101.2	G	U	T	A	CID	LIT	7	88.2	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	6.2	0.7	47.7	9.0
P0AA04	9101.2	G	U	T	A	CID	LIT	7	88.2	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	4.3	0.0	63.8	8.5
P0AA04	9101.2	G	U	T	A	CID	LIT	7	88.2	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	4.1	0.0	39.6	8.5
P0AA04	9101.2	G	T	T	A	CID	LIT	5	82.4	AVEHLVK	795.5	K	L	2.6	0.7	34.1	4.8
P0AA04	9101.2	G	T	T	A	CID	LIT	5	82.4	EAKGFTSEITVTSNGK	1668.8	K	S	3.6	0.6	31.8	12.0
P0AA04	9101.2	G	T	T	A	CID	LIT	5	82.4	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	5.3	0.0	105.0	10.0
P0AA04	9101.2	G	T	T	A	CID	LIT	5	82.4	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	4.9	0.0	69.7	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA04	9101.2	G	T	T	A	CID	LIT	5	82.4	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	4.2	0.0	39.3	8.5
P0AA04	9101.2	G	T	T	B	CID	LIT	5	78.8	AVEHLVK	795.5	K	L	2.5	0.8	43.5	7.0
P0AA04	9101.2	G	T	T	B	CID	LIT	5	78.8	GFTSEITVTSNGK	1340.7	K	S	4.3	0.0	44.8	11.8
P0AA04	9101.2	G	T	T	B	CID	LIT	5	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	5.1	0.0	116.0	11.5
P0AA04	9101.2	G	T	T	B	CID	LIT	5	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	3.6	0.0	66.1	7.8
P0AA04	9101.2	G	T	T	B	CID	LIT	5	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	3.2	0.0	25.8	9.5
P0AA04	9101.2	G	U	T	B	CID	LIT	4	78.8	GFTSEITVTSNGK	1340.7	K	S	5.2	0.0	56.1	12.0
P0AA04	9101.2	G	U	T	B	CID	LIT	4	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	4.8	0.0	99.2	9.5
P0AA04	9101.2	G	U	T	B	CID	LIT	4	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	5.4	0.0	65.2	9.5
P0AA04	9101.2	G	U	T	B	CID	LIT	4	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	3.8	0.0	32.1	8.5
P0AA04	9101.2	S	U	T	A	CID	LIT	7	84.7	AVEHLVK	795.5	K	L	2.5	0.8	47.8	7.0
P0AA04	9101.2	S	U	T	A	CID	LIT	7	84.7	FQQEVTITAPNGLHTRPAAQFVK	2554.3	M	E	0.0	0.0	30.0	17.7
P0AA04	9101.2	S	U	T	A	CID	LIT	7	84.7	GFTSEITVTSNGK	1341.7	K	S	4.5	0.7	78.7	13.6
P0AA04	9101.2	S	U	T	A	CID	LIT	7	84.7	GFTSEITVTSNGKSASAK	1785.9	K	S	4.6	0.5	58.3	16.0
P0AA04	9101.2	S	U	T	A	CID	LIT	7	84.7	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	5.2	0.6	116.0	17.7
P0AA04	9101.2	S	U	T	A	CID	LIT	7	84.7	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	4.3	0.6	57.3	16.1
P0AA04	9101.2	S	U	T	A	CID	LIT	7	84.7	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	4.4	0.6	38.8	17.8
P0AA04	9101.2	S	U	T	B	CID	LIT	4	78.8	GFTSEITVTSNGK	1341.7	K	S	3.9	0.9	62.7	12.8
P0AA04	9101.2	S	U	T	B	CID	LIT	4	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	5.1	0.6	99.2	17.5
P0AA04	9101.2	S	U	T	B	CID	LIT	4	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	3.9	0.0	64.7	16.1
P0AA04	9101.2	S	U	T	B	CID	LIT	4	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	3.6	0.6	8.5	17.6
P0AA04	9101.2	S	U	T	C	CID	LIT	6	84.7	AVEHLVK	795.5	K	L	1.9	0.7	10.3	7.0
P0AA04	9101.2	S	U	T	C	CID	LIT	6	84.7	GFTSEITVTSNGK	1341.7	K	S	4.6	0.7	84.9	14.1
P0AA04	9101.2	S	U	T	C	CID	LIT	6	84.7	GFTSEITVTSNGKSASAK	1785.9	K	S	4.8	0.6	39.2	16.3
P0AA04	9101.2	S	U	T	C	CID	LIT	6	84.7	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	4.8	0.6	103.0	18.0
P0AA04	9101.2	S	U	T	C	CID	LIT	6	84.7	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	4.3	0.6	55.0	16.2
P0AA04	9101.2	S	U	T	C	CID	LIT	6	84.7	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	4.1	0.6	26.1	17.4
P0AA04	9101.2	S	U	T	A	CID	FT	3	43.5	FQQEVTITAPNGLHTRPAAQFVK	2554.3	M	E	0.0	0.0	24.5	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA04	9101.2	S	U	T	A	CID	FT	3	43.5	GFTSEITVTSNGK	1341.7	K	S	4.2	0.0	74.7	12.6
P0AA04	9101.2	S	U	T	A	CID	FT	3	43.5	MFQQEVTITAPNGLHTRPAAQFVK	2701.4	-	E	0.0	0.0	43.4	19.0
P0AA04	9101.2	S	U	T	B	CID	FT	2	43.5	GFTSEITVTSNGK	1341.7	K	S	2.7	0.0	58.2	12.8
P0AA04	9101.2	S	U	T	B	CID	FT	2	43.5	MFQQEVTITAPNGLHTRPAAQFVK	2685.4	-	E	1.7	0.0	23.6	17.9
P0AA04	9101.2	S	U	T	C	CID	FT	2	50.6	GFTSEITVTSNGK	1341.7	K	S	3.5	0.0	54.8	12.8
P0AA04	9101.2	S	U	T	C	CID	FT	2	50.6	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	6.0	0.0	39.9	16.2
P0AA04	9101.2	S	U	T	A	ETD	LIT	6	84.7	FQQEVTITAPNGLHTRPAAQFVK	2554.3	M	E	0.0	0.0	49.3	17.9
P0AA04	9101.2	S	U	T	A	ETD	LIT	6	84.7	GFTSEITVTSNGK	1341.7	K	S	3.1	0.5	50.9	14.6
P0AA04	9101.2	S	U	T	A	ETD	LIT	6	84.7	GFTSEITVTSNGKSASAK	1785.9	K	S	3.1	0.0	36.9	16.2
P0AA04	9101.2	S	U	T	A	ETD	LIT	6	84.7	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	1.9	0.7	16.4	17.6
P0AA04	9101.2	S	U	T	A	ETD	LIT	6	84.7	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	0.0	0.0	65.2	16.0
P0AA04	9101.2	S	U	T	A	ETD	LIT	6	84.7	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	5.8	0.0	62.8	17.6
P0AA04	9101.2	S	U	T	B	ETD	LIT	5	78.8	AVEHLVK	795.5	K	L	1.7	0.6	13.8	7.0
P0AA04	9101.2	S	U	T	B	ETD	LIT	5	78.8	GFTSEITVTSNGK	1341.7	K	S	2.9	0.7	42.6	12.8
P0AA04	9101.2	S	U	T	B	ETD	LIT	5	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	1.9	0.8	14.0	17.3
P0AA04	9101.2	S	U	T	B	ETD	LIT	5	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	3.2	0.3	35.7	16.0
P0AA04	9101.2	S	U	T	B	ETD	LIT	5	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2685.4	-	E	7.2	0.0	80.1	18.1
P0AA04	9101.2	S	U	T	C	ETD	LIT	6	84.7	FQQEVTITAPNGLHTRPAAQFVK	2554.3	M	E	0.0	0.0	28.2	17.9
P0AA04	9101.2	S	U	T	C	ETD	LIT	6	84.7	GFTSEITVTSNGK	1340.7	K	S	2.6	0.4	39.4	14.5
P0AA04	9101.2	S	U	T	C	ETD	LIT	6	84.7	GFTSEITVTSNGKSASAK	1785.9	K	S	3.2	0.0	26.2	16.1
P0AA04	9101.2	S	U	T	C	ETD	LIT	6	84.7	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	4.5	0.0	39.8	17.6
P0AA04	9101.2	S	U	T	C	ETD	LIT	6	84.7	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	3.9	0.3	31.0	16.2
P0AA04	9101.2	S	U	T	C	ETD	LIT	6	84.7	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	5.9	0.7	68.8	17.2
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	GFTSEITVTSNGK	1341.7	K	S	0.0	0.0	92.6	12.8
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	0.0	0.0	121.0	17.9
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	0.0	0.0	61.3	16.2
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2685.4	-	E	0.0	0.0	66.0	18.3
P0AA04	9101.2	S	U	T	A	ETD+CID	LIT	4	84.7	FQQEVTITAPNGLHTRPAAQFVK	2554.3	M	E	0.0	0.0	55.9	17.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA04	9101.2	S	U	T	A	ETD+CID	LIT	4	84.7	GFTSEITVTSNGK	1341.7	K	S	5.0	0.7	74.9	12.8
P0AA04	9101.2	S	U	T	A	ETD+CID	LIT	4	84.7	GFTSEITVTSNGKSASAK	1785.9	K	S	4.4	0.5	77.2	16.1
P0AA04	9101.2	S	U	T	A	ETD+CID	LIT	4	84.7	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	5.6	0.7	116.0	17.2
P0AA04	9101.2	S	U	T	A	ETD+CID	LIT	4	84.7	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	0.0	0.0	64.8	16.1
P0AA04	9101.2	S	U	T	A	ETD+CID	LIT	4	84.7	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	3.8	0.7	20.2	16.9
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	GFTSEITVTSNGK	1341.7	K	S	4.5	0.7	0.0	0.0
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	2.0	0.7	0.0	0.0
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	3.1	0.5	0.0	0.0
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2685.4	-	E	4.4	0.3	0.0	0.0
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	GFTSEITVTSNGK	1341.7	K	S	4.7	0.6	71.3	12.8
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	5.2	0.6	116.0	17.5
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	6.2	0.3	51.8	16.2
P0AA04	9101.2	S	U	T	B	ETD+CID	LIT	2	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2685.4	-	E	7.1	0.0	66.0	18.3
P0AA04	9101.2	S	U	T	C	ETD+CID	LIT	5	84.7	AVEHLVK	795.5	K	L	1.9	0.2	4.7	9.0
P0AA04	9101.2	S	U	T	C	ETD+CID	LIT	5	84.7	GFTSEITVTSNGK	1341.7	K	S	4.9	0.7	85.8	13.2
P0AA04	9101.2	S	U	T	C	ETD+CID	LIT	5	84.7	GFTSEITVTSNGKSASAK	1785.9	K	S	4.5	0.5	57.3	15.9
P0AA04	9101.2	S	U	T	C	ETD+CID	LIT	5	84.7	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	4.9	0.7	134.0	17.8
P0AA04	9101.2	S	U	T	C	ETD+CID	LIT	5	84.7	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	6.7	0.3	46.0	16.2
P0AA04	9101.2	S	U	T	C	ETD+CID	LIT	5	84.7	LTNGFEVTSYIGGEGHNLQEHSVILIR	2983.5	-	-	1.9	-0.7	47.6	17.3
P0AA04	9101.2	S	U	T	C	ETD+CID	LIT	5	84.7	MFQQEVTITAPNGLHTRPAAQFVK	2685.4	-	E	0.0	0.0	78.6	18.4
P0AA04	9101.2	S	U	T	B	HCD	FT	2	78.8	GFTSEITVTSNGK	1341.7	K	S	0.0	0.0	92.6	12.8
P0AA04	9101.2	S	U	T	B	HCD	FT	2	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	0.0	0.0	121.0	17.9
P0AA04	9101.2	S	U	T	B	HCD	FT	2	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	0.0	0.0	59.8	16.1
P0AA04	9101.2	S	U	T	B	HCD	FT	2	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2701.4	-	E	0.0	0.0	58.7	19.0
P0AA04	9101.2	S	U	T	A	HCD	FT	4	78.8	GFTSEITVTSNGK	1341.7	K	S	3.0	0.0	72.9	13.4
P0AA04	9101.2	S	U	T	A	HCD	FT	4	78.8	LQTLGLTQGTVVTISAEGEDEQK	2417.2	K	A	3.6	0.0	58.6	17.3
P0AA04	9101.2	S	U	T	A	HCD	FT	4	78.8	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	5.7	0.0	40.0	16.0
P0AA04	9101.2	S	U	T	A	HCD	FT	4	78.8	MFQQEVTITAPNGLHTRPAAQFVK	2684.4	-	E	3.9	0.0	19.8	17.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA04	9101.2	S	U	T	B	HCD	FT	2	50.6	GFTSEITVTSNGK	1341.7	K	S	2.1	0.7	38.9	13.2
P0AA04	9101.2	S	U	T	B	HCD	FT	2	50.6	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	5.4	0.0	41.7	16.0
P0AA04	9101.2	S	U	T	C	HCD	FT	2	50.6	GFTSEITVTSNGK	1341.7	K	S	2.7	0.0	77.9	14.1
P0AA04	9101.2	S	U	T	C	HCD	FT	2	50.6	LQTLGLTQGTVVTISAEGEDEQKAVEHLVK	3193.7	K	L	7.2	0.0	39.2	16.1
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	DHTLFAK	831.4	R	A	2.4	0.6	12.5	17.0
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	FEVKGPK	804.5	K	N	1.9	0.4	15.1	13.0
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	FGGESVLAGSIIVR	1404.8	R	Q	4.6	0.8	68.0	11.5
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	FHAGANVGCGR	1145.5	K	D	3.3	0.9	41.1	7.8
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	FHAGANVGCGRDHTLFAK	1957.9	K	A	4.9	0.7	58.5	11.1
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	GTKFHAGANVGCGR	1431.7	R	D	5.3	0.0	87.0	12.0
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	KFISIEAE	936.5	R	-	2.7	0.8	45.3	10.4
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	RFGGESVLAGSIIVR	1560.9	K	Q	4.2	0.6	40.5	10.4
P0A7L8	9106.6	G	U	T	A	CID	LIT	9	62.4	VKFEVK	749.5	K	G	1.6	0.5	17.7	12.0
P0A7L8	9106.6	G	T	T	A	CID	LIT	5	48.2	DHTLFAK	831.4	R	A	2.1	0.7	18.7	12.8
P0A7L8	9106.6	G	T	T	A	CID	LIT	5	48.2	FGGESVLAGSIIVR	1404.8	R	Q	4.4	0.0	70.9	11.5
P0A7L8	9106.6	G	T	T	A	CID	LIT	5	48.2	FHAGANVGCGR	1145.5	K	D	3.4	0.0	36.2	8.5
P0A7L8	9106.6	G	T	T	A	CID	LIT	5	48.2	KFISIEAE	936.5	R	-	2.2	0.7	19.6	12.3
P0A7L8	9106.6	G	T	T	A	CID	LIT	5	48.2	RFGGESVLAGSIIVR	1560.9	K	Q	5.2	0.6	54.6	10.0
P0A7L8	9106.6	G	U	T	B	CID	LIT	5	54.1	DHTLFAK	831.4	R	A	2.1	0.7	20.2	15.1
P0A7L8	9106.6	G	U	T	B	CID	LIT	5	54.1	FGGESVLAGSIIVR	1404.8	R	Q	4.5	0.7	63.0	11.5
P0A7L8	9106.6	G	U	T	B	CID	LIT	5	54.1	FHAGANVGCGR	1145.5	K	D	3.0	0.0	48.0	8.5
P0A7L8	9106.6	G	U	T	B	CID	LIT	5	54.1	KFISIEAE	936.5	R	-	2.4	0.6	22.9	10.8
P0A7L8	9106.6	G	U	T	B	CID	LIT	5	54.1	VKFEVK	749.5	K	G	1.8	0.0	18.2	12.0
P0A7L8	9106.6	G	U	A	B	CID	LIT	2	28.2	DHTLFAKA	902.5	R	D	2.4	0.7	24.9	16.4
P0A7L8	9106.6	G	U	A	B	CID	LIT	2	28.2	EVKGPKNRKFISIEAE	1845.0	F	-	2.5	0.0	33.2	13.2
P0A7L8	9106.6	S	U	T	A	CID	LIT	5	43.5	FGGESVLAGSIIVR	1404.8	R	Q	3.6	0.7	68.6	16.2
P0A7L8	9106.6	S	U	T	A	CID	LIT	5	43.5	FHAGANVGCGR	1145.5	K	D	2.7	0.0	33.6	11.5
P0A7L8	9106.6	S	U	T	A	CID	LIT	5	43.5	GTKFHAGANVGCGR	1431.7	R	D	3.2	0.0	39.3	16.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7L8	9106.6	S	U	T	A	CID	LIT	5	43.5	KFISIEAE	936.5	R	-	2.4	0.8	31.0	15.2
P0A7L8	9106.6	S	U	T	A	CID	LIT	5	43.5	RFGGESVLAGSIIVR	1560.9	K	Q	2.2	0.6	0.0	0.0
P0A7L8	9106.6	S	U	T	B	CID	LIT	3	30.6	FGGESVLAGSIIVR	1404.8	R	Q	4.5	0.7	72.3	16.2
P0A7L8	9106.6	S	U	T	B	CID	LIT	3	30.6	FHAGANVGCGR	1145.5	K	D	3.1	0.8	24.3	11.5
P0A7L8	9106.6	S	U	T	B	CID	LIT	3	30.6	RFGGESVLAGSIIVR	1560.9	K	Q	3.9	0.6	29.9	14.0
P0A7L8	9106.6	S	U	T	C	CID	LIT	5	48.2	FGGESVLAGSIIVR	1404.8	R	Q	4.2	0.5	72.3	17.4
P0A7L8	9106.6	S	U	T	C	CID	LIT	5	48.2	FHAGANVGCGR	1145.5	K	D	2.9	0.8	36.1	12.3
P0A7L8	9106.6	S	U	T	C	CID	LIT	5	48.2	FHAGANVGCGRDHTLFAK	1957.9	K	A	2.1	0.6	2.0	17.4
P0A7L8	9106.6	S	U	T	C	CID	LIT	5	48.2	KFISIEAE	936.5	R	-	2.7	0.6	39.7	15.3
P0A7L8	9106.6	S	U	T	C	CID	LIT	5	48.2	RFGGESVLAGSIIVR	1560.9	K	Q	3.3	0.6	45.0	13.8
P0A7L8	9106.6	S	U	T	A	CID	FT	3	38.8	FGGESVLAGSIIVR	1404.8	R	Q	2.6	0.0	41.1	16.2
P0A7L8	9106.6	S	U	T	A	CID	FT	3	38.8	FHAGANVGCGR	1145.5	K	D	3.2	0.0	45.5	11.5
P0A7L8	9106.6	S	U	T	A	CID	FT	3	38.8	KFISIEAE	936.5	R	-	2.5	0.0	17.0	15.3
P0A7L8	9106.6	S	U	T	C	CID	FT	3	38.8	FGGESVLAGSIIVR	1404.8	R	Q	3.7	0.8	55.6	17.2
P0A7L8	9106.6	S	U	T	C	CID	FT	3	38.8	FHAGANVGCGR	1145.5	K	D	3.7	0.0	42.5	11.5
P0A7L8	9106.6	S	U	T	C	CID	FT	3	38.8	KFISIEAE	936.5	R	-	2.8	0.0	27.9	15.2
P0A7L8	9106.6	S	U	T	A	ETD	LIT	4	38.8	FGGESVLAGSIIVR	1404.8	R	Q	2.2	0.6	55.8	16.2
P0A7L8	9106.6	S	U	T	A	ETD	LIT	4	38.8	FHAGANVGCGR	1145.5	K	D	4.9	0.0	59.0	9.5
P0A7L8	9106.6	S	U	T	A	ETD	LIT	4	38.8	FHAGANVGCGRDHTLFAK	1957.9	K	A	5.4	0.6	51.7	17.4
P0A7L8	9106.6	S	U	T	A	ETD	LIT	4	38.8	RFGGESVLAGSIIVR	1560.9	K	Q	3.8	0.5	66.0	13.8
P0A7L8	9106.6	S	U	T	B	ETD	LIT	4	40.0	FGGESVLAGSIIVR	1404.8	R	Q	2.2	0.6	71.7	16.0
P0A7L8	9106.6	S	U	T	B	ETD	LIT	4	40.0	FHAGANVGCGR	1145.5	K	D	5.0	0.9	66.7	11.1
P0A7L8	9106.6	S	U	T	B	ETD	LIT	4	40.0	KFISIEAE	936.5	R	-	2.3	0.7	12.9	15.2
P0A7L8	9106.6	S	U	T	B	ETD	LIT	4	40.0	RFGGESVLAGSIIVR	1560.9	K	Q	3.8	0.6	43.5	13.8
P0A7L8	9106.6	S	U	T	C	ETD	LIT	4	38.8	FGGESVLAGSIIVR	1404.8	R	Q	2.8	0.6	91.2	16.2
P0A7L8	9106.6	S	U	T	C	ETD	LIT	4	38.8	FHAGANVGCGR	1145.5	K	D	3.2	0.9	0.0	0.0
P0A7L8	9106.6	S	U	T	C	ETD	LIT	4	38.8	FHAGANVGCGRDHTLFAK	1957.9	K	A	5.2	0.5	52.7	17.2
P0A7L8	9106.6	S	U	T	C	ETD	LIT	4	38.8	RFGGESVLAGSIIVR	1560.9	K	Q	4.2	0.6	65.2	14.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7L8	9106.6	S	U	T	C	ETD	FT	2	37.6	FGGESVLAGSIIVR	1404.8	R	Q	0.0	0.0	30.0	16.2
P0A7L8	9106.6	S	U	T	C	ETD	FT	2	37.6	FHAGANVGCGRDHTLFAK	1957.9	K	A	0.0	0.0	26.8	17.2
P0A7L8	9106.6	S	U	T	C	ETD+CID	LIT	3	48.2	FGGESVLAGSIIVR	1404.8	R	Q	4.9	0.7	72.5	16.2
P0A7L8	9106.6	S	U	T	C	ETD+CID	LIT	3	48.2	FHAGANVGCGR	1145.5	K	D	1.8	-0.1	53.3	11.5
P0A7L8	9106.6	S	U	T	C	ETD+CID	LIT	3	48.2	FHAGANVGCGRDHTLFAK	1957.9	K	A	1.4	-0.8	68.2	17.4
P0A7L8	9106.6	S	U	T	C	ETD+CID	LIT	3	48.2	KFISIEAE	936.5	R	-	2.6	0.5	21.2	15.3
P0A7L8	9106.6	S	U	T	C	ETD+CID	LIT	3	48.2	RFGGESVLAGSIIVR	1560.9	K	Q	3.0	0.6	39.1	14.0
P0A7L8	9106.6	S	U	T	C	HCD	FT	2	22.4	FHAGANVGCGR	1145.5	K	D	3.1	0.0	51.0	11.5
P0A7L8	9106.6	S	U	T	C	HCD	FT	2	22.4	KFISIEAE	936.5	R	-	2.7	0.0	38.6	15.3
P0AC62	9119.9	G	U	T	A	CID	LIT	2	27.7	GGLDPLLK	812.5	R	-	2.2	0.2	33.4	7.8
P0AC62	9119.9	G	U	T	A	CID	LIT	2	27.7	GVSFQELPIDGNAAK	1545.8	K	R	4.0	0.6	28.0	13.8
P0AC62	9119.9	G	T	T	A	CID	LIT	4	67.5	ANVEIYTK	937.5	M	E	0.0	0.0	32.5	12.3
P0AC62	9119.9	G	T	T	A	CID	LIT	4	67.5	GGLDPLLK	812.5	R	-	2.8	0.3	30.2	7.8
P0AC62	9119.9	G	T	T	A	CID	LIT	4	67.5	GVSFQELPIDGNAAK	1545.8	K	R	4.2	0.5	34.1	13.8
P0AC62	9119.9	G	T	T	A	CID	LIT	4	67.5	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	4.1	0.0	35.4	12.6
P0AC62	9119.9	G	T	A	A	CID	LIT	2	24.1	DAQHIGGCD	972.4	I	D	3.0	0.0	35.8	4.8
P0AC62	9119.9	G	T	A	A	CID	LIT	2	24.1	DARGGLDPLLK	1154.7	L	-	2.2	0.8	0.0	0.0
P0AC62	9119.9	G	T	T	B	CID	LIT	6	78.3	ANVEIYTK	937.5	M	E	0.0	0.0	37.7	12.3
P0AC62	9119.9	G	T	T	B	CID	LIT	6	78.3	ETCPYCHR	1122.4	K	A	2.8	0.0	43.7	0.0
P0AC62	9119.9	G	T	T	B	CID	LIT	6	78.3	GGLDPLLK	812.5	R	-	1.9	0.6	5.0	8.5
P0AC62	9119.9	G	T	T	B	CID	LIT	6	78.3	GVSFQELPIDGNAAK	1545.8	K	R	3.1	0.4	19.3	14.0
P0AC62	9119.9	G	T	T	B	CID	LIT	6	78.3	MANVEIYTK	1068.5	-	E	2.8	0.3	13.6	11.8
P0AC62	9119.9	G	T	T	B	CID	LIT	6	78.3	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	5.1	0.8	43.3	13.0
P0AC62	9119.9	G	U	T	B	CID	LIT	2	27.7	GGLDPLLK	812.5	R	-	2.7	0.3	31.8	8.5
P0AC62	9119.9	G	U	T	B	CID	LIT	2	27.7	GVSFQELPIDGNAAK	1545.8	K	R	3.1	0.0	41.1	14.3
P0AC62	9119.9	G	T	A	B	CID	LIT	5	73.5	ANVEIYTK	937.5	M	E	0.0	0.0	51.9	12.6
P0AC62	9119.9	G	T	A	B	CID	LIT	5	73.5	DAQHIGGCD	972.4	I	D	2.5	0.0	27.4	3.0
P0AC62	9119.9	G	T	A	B	CID	LIT	5	73.5	DARGGLDPLLK	1154.7	L	-	3.5	0.0	31.3	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AC62	9119.9	G	T	A	B	CID	LIT	5	73.5	ETCPYCHRAKALLSSKGVSFQELPIDGNAAKR	3603.8	K	E	3.9	0.0	27.3	11.1
P0AC62	9119.9	G	T	A	B	CID	LIT	5	73.5	MANVEIYTK	1068.5	-	E	2.3	0.7	22.3	14.8
P0AC62	9119.9	S	U	T	A	CID	LIT	2	48.2	GVSFQELPIDGNAAK	1545.8	K	R	2.1	0.5	6.7	18.3
P0AC62	9119.9	S	U	T	A	CID	LIT	2	48.2	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	3.0	0.0	29.5	19.1
P0AC62	9119.9	S	U	T	B	CID	LIT	2	48.2	GVSFQELPIDGNAAK	1545.8	K	R	3.2	0.5	23.5	18.1
P0AC62	9119.9	S	U	T	B	CID	LIT	2	48.2	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	3.3	0.0	18.9	19.0
P0AC62	9119.9	S	U	T	C	CID	LIT	3	57.8	ETCPYCHR	1122.4	K	A	2.0	0.7	15.3	4.8
P0AC62	9119.9	S	U	T	C	CID	LIT	3	57.8	GVSFQELPIDGNAAK	1545.8	K	R	4.0	0.6	41.9	18.0
P0AC62	9119.9	S	U	T	C	CID	LIT	3	57.8	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	2.9	0.0	32.2	19.1
P0AC62	9119.9	S	U	T	C	ETD	LIT	2	48.2	GVSFQELPIDGNAAK	1545.8	K	R	3.7	0.5	36.8	18.3
P0AC62	9119.9	S	U	T	C	ETD	LIT	2	48.2	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	4.9	0.0	62.3	19.1
P0AC62	9119.9	S	U	T	B	ETD+CID	LIT	2	48.2	GVSFQELPIDGNAAK	1545.8	K	R	2.6	0.5	7.1	18.4
P0AC62	9119.9	S	U	T	B	ETD+CID	LIT	2	48.2	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	2.9	0.0	24.0	19.2
P0AC62	9119.9	S	U	T	C	ETD+CID	LIT	2	48.2	GVSFQELPIDGNAAK	1545.8	K	R	4.6	0.6	54.8	18.1
P0AC62	9119.9	S	U	T	C	ETD+CID	LIT	2	48.2	TTVPQIFIDAQHIGGCDDLYALDAR	2789.4	R	G	3.6	0.8	42.0	19.2
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	EEGTRLDLDR	1203.6	K	I	2.5	0.7	26.1	12.8
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	IAHWVGQGATISDR	1510.8	R	V	4.3	0.8	54.5	10.4
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	IAHWVGQGATISDRVAALIK	2106.2	R	E	5.6	0.0	66.5	4.8
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	KRPFYQVVVADSR	1564.9	K	N	4.4	0.8	54.4	12.3
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	LDLDR	631.3	R	I	1.9	0.1	24.6	18.0
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	MVTIR	619.4	-	L	1.5	0.7	16.9	13.6
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	NGRFIER	891.5	R	V	2.3	0.0	29.2	14.1
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	RPFYQVVVADSR	1436.8	K	N	4.0	0.6	48.9	8.5
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	VAALIK	614.4	R	E	1.8	0.5	11.1	10.4
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	VAALIKEVNK	1084.7	R	A	3.1	0.0	43.5	12.8
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	VGFFNPIASEK	1208.6	R	E	3.1	0.7	60.5	10.8
P0A7T3	9172.6	G	U	T	A	CID	LIT	12	85.4	VGFFNPIASEKEEGTR	1780.9	R	L	4.8	0.7	106.0	12.6
P0A7T3	9172.6	G	T	T	A	CID	LIT	4	59.8	IAHWVGQGATISDR	1510.8	R	V	4.2	0.7	58.4	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7T3	9172.6	G	T	T	A	CID	LIT	4	59.8	KRPFYQVVVADSR	1564.9	K	N	3.4	0.5	29.6	12.0
P0A7T3	9172.6	G	T	T	A	CID	LIT	4	59.8	VAALIK	614.4	R	E	1.4	0.5	14.0	10.4
P0A7T3	9172.6	G	T	T	A	CID	LIT	4	59.8	VGFFNPIASEKEEGTR	1780.9	R	L	3.3	0.5	25.4	12.0
P0A7T3	9172.6	G	U	A	A	CID	LIT	3	36.6	DLDRIAHWVGQGATIS	1738.9	L	D	2.7	0.6	28.9	14.3
P0A7T3	9172.6	G	U	A	A	CID	LIT	3	36.6	DRIAHWVGQGATIS	1510.8	L	D	3.3	0.5	51.3	11.5
P0A7T3	9172.6	G	U	A	A	CID	LIT	3	36.6	DRVAALIKEVNKAA	1497.9	S	-	3.1	0.8	30.1	10.4
P0A7T3	9172.6	G	U	T	B	CID	LIT	7	65.9	IAHWVGQGATISDR	1510.8	R	V	4.7	0.0	60.8	10.4
P0A7T3	9172.6	G	U	T	B	CID	LIT	7	65.9	KRPFYQVVVADSR	1564.9	K	N	3.2	0.5	34.0	12.0
P0A7T3	9172.6	G	U	T	B	CID	LIT	7	65.9	LDLDR	631.3	R	I	1.8	0.4	27.4	18.0
P0A7T3	9172.6	G	U	T	B	CID	LIT	7	65.9	RPFYQVVVADSR	1436.8	K	N	3.6	0.9	31.9	8.5
P0A7T3	9172.6	G	U	T	B	CID	LIT	7	65.9	VAALIK	614.4	R	E	2.2	0.1	33.9	10.4
P0A7T3	9172.6	G	U	T	B	CID	LIT	7	65.9	VGFFNPIASEK	1208.6	R	E	3.3	0.8	64.6	10.8
P0A7T3	9172.6	G	U	T	B	CID	LIT	7	65.9	VGFFNPIASEKEEGTR	1780.9	R	L	4.1	0.6	73.8	13.4
P0A7T3	9172.6	G	T	A	B	CID	LIT	2	34.1	DRIAHWVGQGATIS	1510.8	L	D	2.0	0.4	28.8	11.5
P0A7T3	9172.6	G	T	A	B	CID	LIT	2	34.1	DRVAALIKEVNKAA	1497.9	S	-	2.9	0.8	30.2	10.4
P0A7T3	9172.6	G	U	A	B	CID	LIT	4	36.6	DLDRIAHWVGQGATIS	1738.9	L	D	2.9	0.0	52.4	14.0
P0A7T3	9172.6	G	U	A	B	CID	LIT	4	36.6	DRIAHWVGQGATIS	1510.8	L	D	4.1	0.6	61.7	11.5
P0A7T3	9172.6	G	U	A	B	CID	LIT	4	36.6	DRVAALIK	885.6	S	E	2.2	0.1	18.8	13.8
P0A7T3	9172.6	G	U	A	B	CID	LIT	4	36.6	DRVAALIKEVNKAA	1497.9	S	-	3.3	0.9	23.4	10.4
P0A7T3	9172.6	S	U	T	A	CID	LIT	7	65.9	IAHWVGQGATISDR	1510.8	R	V	2.4	0.7	15.7	15.1
P0A7T3	9172.6	S	U	T	A	CID	LIT	7	65.9	IAHWVGQGATISDRVAALIK	2106.2	R	E	4.8	0.0	53.7	13.0
P0A7T3	9172.6	S	U	T	A	CID	LIT	7	65.9	KRPFYQVVVADSR	1564.9	K	N	5.3	0.7	49.6	14.5
P0A7T3	9172.6	S	U	T	A	CID	LIT	7	65.9	RPFYQVVVADSR	1436.8	K	N	3.8	0.7	36.3	15.2
P0A7T3	9172.6	S	U	T	A	CID	LIT	7	65.9	VGFFNPIASEK	1208.6	R	E	3.3	0.7	58.6	16.3
P0A7T3	9172.6	S	U	T	A	CID	LIT	7	65.9	VGFFNPIASEKEEGTR	1780.9	R	L	4.5	0.5	59.8	17.6
P0A7T3	9172.6	S	U	T	A	CID	LIT	7	65.9	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	3.4	0.4	12.2	18.8
P0A7T3	9172.6	S	U	T	B	CID	LIT	7	65.9	IAHWVGQGATISDR	1510.8	R	V	4.1	0.8	65.0	16.0
P0A7T3	9172.6	S	U	T	B	CID	LIT	7	65.9	IAHWVGQGATISDRVAALIK	2106.2	R	E	1.9	0.0	18.4	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7T3	9172.6	S	U	T	B	CID	LIT	7	65.9	KRPFYQVVVADSR	1564.9	K	N	5.1	0.7	47.6	14.3
P0A7T3	9172.6	S	U	T	B	CID	LIT	7	65.9	RPFYQVVVADSR	1436.8	K	N	3.1	0.6	27.5	14.6
P0A7T3	9172.6	S	U	T	B	CID	LIT	7	65.9	VGFFNPIASEK	1208.6	R	E	3.2	0.6	59.3	15.4
P0A7T3	9172.6	S	U	T	B	CID	LIT	7	65.9	VGFFNPIASEKEEGTR	1780.9	R	L	4.3	0.6	73.1	17.2
P0A7T3	9172.6	S	U	T	B	CID	LIT	7	65.9	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	2.8	0.4	6.2	19.1
P0A7T3	9172.6	S	U	T	C	CID	LIT	6	58.5	IAHWVGQGATISDR	1510.8	R	V	4.5	0.8	45.5	14.9
P0A7T3	9172.6	S	U	T	C	CID	LIT	6	58.5	KRPFYQVVVADSR	1564.9	K	N	3.5	0.6	25.6	14.3
P0A7T3	9172.6	S	U	T	C	CID	LIT	6	58.5	RPFYQVVVADSR	1436.8	K	N	3.2	0.0	16.8	14.5
P0A7T3	9172.6	S	U	T	C	CID	LIT	6	58.5	VGFFNPIASEK	1208.6	R	E	3.1	0.7	43.5	16.3
P0A7T3	9172.6	S	U	T	C	CID	LIT	6	58.5	VGFFNPIASEKEEGTR	1780.9	R	L	4.7	0.6	60.7	17.2
P0A7T3	9172.6	S	U	T	C	CID	LIT	6	58.5	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	3.4	0.3	9.3	19.0
P0A7T3	9172.6	S	U	T	A	CID	FT	2	25.6	VGFFNPIASEK	1208.6	R	E	2.3	0.0	69.4	15.6
P0A7T3	9172.6	S	U	T	A	CID	FT	2	25.6	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	4.5	0.0	22.6	18.9
P0A7T3	9172.6	S	U	T	C	CID	FT	2	32.9	IAHWVGQGATISDR	1510.8	R	V	2.6	0.0	35.7	15.8
P0A7T3	9172.6	S	U	T	C	CID	FT	2	32.9	KRPFYQVVVADSR	1564.9	K	N	2.6	0.0	15.9	14.6
P0A7T3	9172.6	S	U	T	A	ETD	LIT	7	65.9	IAHWVGQGATISDR	1510.8	R	V	7.2	0.7	64.1	15.1
P0A7T3	9172.6	S	U	T	A	ETD	LIT	7	65.9	IAHWVGQGATISDRVAALIK	2106.2	R	E	8.4	0.0	90.7	12.8
P0A7T3	9172.6	S	U	T	A	ETD	LIT	7	65.9	KRPFYQVVVADSR	1564.9	K	N	5.7	0.8	0.0	0.0
P0A7T3	9172.6	S	U	T	A	ETD	LIT	7	65.9	RPFYQVVVADSR	1436.8	K	N	1.7	0.0	31.3	14.3
P0A7T3	9172.6	S	U	T	A	ETD	LIT	7	65.9	VGFFNPIASEK	1208.6	R	E	2.6	0.6	21.0	16.3
P0A7T3	9172.6	S	U	T	A	ETD	LIT	7	65.9	VGFFNPIASEKEEGTR	1780.9	R	L	4.4	0.5	69.3	17.4
P0A7T3	9172.6	S	U	T	A	ETD	LIT	7	65.9	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	6.7	0.6	86.2	18.3
P0A7T3	9172.6	S	U	T	B	ETD	LIT	7	65.9	IAHWVGQGATISDR	1510.8	R	V	7.4	0.7	51.0	16.4
P0A7T3	9172.6	S	U	T	B	ETD	LIT	7	65.9	IAHWVGQGATISDRVAALIK	2106.2	R	E	7.4	0.0	78.4	13.4
P0A7T3	9172.6	S	U	T	B	ETD	LIT	7	65.9	KRPFYQVVVADSR	1564.9	K	N	0.0	0.0	73.7	14.5
P0A7T3	9172.6	S	U	T	B	ETD	LIT	7	65.9	RPFYQVVVADSR	1436.8	K	N	4.4	0.8	87.1	15.2
P0A7T3	9172.6	S	U	T	B	ETD	LIT	7	65.9	VGFFNPIASEK	1208.6	R	E	2.7	0.0	16.8	16.3
P0A7T3	9172.6	S	U	T	B	ETD	LIT	7	65.9	VGFFNPIASEKEEGTR	1780.9	R	L	6.3	0.7	53.5	17.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7T3	9172.6	S	U	T	B	ETD	LIT	7	65.9	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	7.8	0.7	84.6	19.1
P0A7T3	9172.6	S	U	T	C	ETD	LIT	6	58.5	IAHWVGQGATISDR	1510.8	R	V	5.7	0.6	0.0	0.0
P0A7T3	9172.6	S	U	T	C	ETD	LIT	6	58.5	KRPFYQVVVADSR	1564.9	K	N	5.0	0.6	69.9	14.3
P0A7T3	9172.6	S	U	T	C	ETD	LIT	6	58.5	RPFYQVVVADSR	1436.8	K	N	2.8	0.8	32.9	14.6
P0A7T3	9172.6	S	U	T	C	ETD	LIT	6	58.5	VGFFNPIASEK	1208.6	R	E	2.5	0.0	25.0	16.3
P0A7T3	9172.6	S	U	T	C	ETD	LIT	6	58.5	VGFFNPIASEKEEGTR	1780.9	R	L	3.9	0.5	66.9	17.4
P0A7T3	9172.6	S	U	T	C	ETD	LIT	6	58.5	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	8.2	0.7	0.0	0.0
P0A7T3	9172.6	S	U	T	B	ETD	FT	2	32.9	IAHWVGQGATISDR	1510.8	R	V	5.5	0.7	68.1	16.8
P0A7T3	9172.6	S	U	T	B	ETD	FT	2	32.9	KRPFYQVVVADSR	1564.9	K	N	3.2	0.0	22.4	13.6
P0A7T3	9172.6	S	U	T	C	ETD	FT	2	32.9	IAHWVGQGATISDR	1510.8	R	V	4.6	0.0	67.7	15.4
P0A7T3	9172.6	S	U	T	C	ETD	FT	2	32.9	KRPFYQVVVADSR	1564.9	K	N	5.8	0.0	65.6	14.1
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	4	58.5	IAHWVGQGATISDR	1510.8	R	V	0.0	0.0	60.7	16.8
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	4	58.5	KRPFYQVVVADSR	1564.9	K	N	0.0	0.0	20.4	14.3
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	4	58.5	VGFFNPIASEK	1208.6	R	E	0.0	0.0	47.9	16.3
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	4	58.5	VGFFNPIASEKEEGTR	1780.9	R	L	0.0	0.0	82.6	17.4
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	4	58.5	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	0.0	0.0	66.4	19.1
P0A7T3	9172.6	S	U	T	A	ETD+CID	LIT	5	65.9	IAHWVGQGATISDR	1510.8	R	V	7.3	0.8	66.4	15.1
P0A7T3	9172.6	S	U	T	A	ETD+CID	LIT	5	65.9	IAHWVGQGATISDRVAALIK	2106.2	R	E	8.0	0.0	86.5	12.8
P0A7T3	9172.6	S	U	T	A	ETD+CID	LIT	5	65.9	KRPFYQVVVADSR	1564.9	K	N	2.5	0.4	11.5	14.3
P0A7T3	9172.6	S	U	T	A	ETD+CID	LIT	5	65.9	VGFFNPIASEK	1208.6	R	E	3.5	0.8	47.5	15.2
P0A7T3	9172.6	S	U	T	A	ETD+CID	LIT	5	65.9	VGFFNPIASEKEEGTR	1780.9	R	L	6.9	0.6	62.6	17.1
P0A7T3	9172.6	S	U	T	A	ETD+CID	LIT	5	65.9	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	7.5	0.9	63.3	19.1
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	2	42.7	IAHWVGQGATISDR	1510.8	R	V	3.3	0.6	0.0	0.0
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	2	42.7	VGFFNPIASEK	1208.6	R	E	3.5	0.6	0.0	0.0
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	2	42.7	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	7.6	0.7	0.0	0.0
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	5	65.9	IAHWVGQGATISDR	1510.8	R	V	4.9	0.6	65.6	16.8
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	5	65.9	IAHWVGQGATISDRVAALIK	2106.2	R	E	1.7	0.6	10.4	13.4
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	5	65.9	KRPFYQVVVADSR	1564.9	K	N	2.3	0.7	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	5	65.9	VGFFNPIASEK	1208.6	R	E	3.5	0.6	47.9	16.3
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	5	65.9	VGFFNPIASEKEEGTR	1780.9	R	L	4.7	0.5	82.6	17.4
P0A7T3	9172.6	S	U	T	B	ETD+CID	LIT	5	65.9	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	6.5	0.6	66.4	19.1
P0A7T3	9172.6	S	U	T	C	ETD+CID	LIT	4	58.5	GEREPVTEAER	1272.6	-	-	2.7	0.4	26.4	15.4
P0A7T3	9172.6	S	U	T	C	ETD+CID	LIT	4	58.5	IAHWVGQGATISDR	1510.8	R	V	3.4	0.6	33.4	14.9
P0A7T3	9172.6	S	U	T	C	ETD+CID	LIT	4	58.5	KRPFYQVVVADSR	1564.9	K	N	5.0	0.8	70.3	14.5
P0A7T3	9172.6	S	U	T	C	ETD+CID	LIT	4	58.5	VGFFNPIASEK	1208.6	R	E	3.1	0.6	29.8	14.3
P0A7T3	9172.6	S	U	T	C	ETD+CID	LIT	4	58.5	VGFFNPIASEKEEGTR	1780.9	R	L	4.8	0.0	78.8	17.2
P0A7T3	9172.6	S	U	T	C	ETD+CID	LIT	4	58.5	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	6.2	0.8	54.5	19.0
P0A7T3	9172.6	S	U	T	B	HCD	FT	3	52.4	IAHWVGQGATISDR	1510.8	R	V	0.0	0.0	65.6	16.8
P0A7T3	9172.6	S	U	T	B	HCD	FT	3	52.4	KRPFYQVVVADSR	1564.9	K	N	0.0	0.0	20.4	14.3
P0A7T3	9172.6	S	U	T	B	HCD	FT	3	52.4	VGFFNPIASEK	1208.6	R	E	0.0	0.0	47.9	16.3
P0A7T3	9172.6	S	U	T	B	HCD	FT	3	52.4	VGFFNPIASEKEEGTR	1780.9	R	L	0.0	0.0	82.6	17.4
P0A7T3	9172.6	S	U	T	B	HCD	FT	2	25.6	VGFFNPIASEK	1208.6	R	E	2.3	0.0	55.1	15.1
P0A7T3	9172.6	S	U	T	B	HCD	FT	2	25.6	VGFFNPIASEKEEGTRLDLDR	2393.2	R	I	4.6	0.0	51.0	18.9
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	ALDAIIASVTESLK	1430.8	R	E	5.0	0.8	72.7	7.8
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	3.9	0.0	32.9	10.0
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	ALKDAVN	730.4	K	-	1.9	0.4	0.0	0.0
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	EGDDVALVGFGTFAVK	1624.8	K	E	4.8	0.7	58.2	13.0
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	EITIAAAK	816.5	K	V	2.1	0.6	24.7	15.8
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	IAAGADISK	845.5	K	A	2.7	0.7	50.2	16.7
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	MNKSQLIDK	1076.6	-	I	2.5	0.5	24.2	14.5
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	NPQTGKEITIAAAK	1441.8	R	V	4.8	0.6	69.7	8.5
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	SQLIDKIAAGADISK	1529.9	K	A	5.7	0.6	94.2	12.8
P0ACF4	9208.0	G	U	T	A	CID	LIT	10	80.0	TGRNPQTGK	958.5	R	E	2.6	0.4	14.0	12.8
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	ALDAIIASVTESLK	1430.8	R	E	4.5	0.0	58.6	8.5
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	EGDDVALVGFGTFAVK	1624.8	K	E	4.0	0.6	57.3	12.6
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	EITIAAAK	816.5	K	V	2.2	0.8	21.7	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	IAAGADISK	845.5	K	A	2.2	0.6	36.3	15.9
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	MNKSQLIDK	1076.6	-	I	2.8	0.5	45.1	14.5
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	NPQTGKEITIAAAK	1441.8	R	V	4.7	0.6	59.6	9.0
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	SQLIDKIAAGADISK	1529.9	K	A	5.2	0.6	84.9	12.8
P0ACF4	9208.0	G	T	T	A	CID	LIT	8	72.2	TGRNPQTGK	958.5	R	E	2.9	0.4	27.6	15.2
P0ACF4	9208.0	G	U	A	A	CID	LIT	5	43.3	DAIIASVTESLKEG	1432.8	L	D	3.1	0.6	41.9	16.6
P0ACF4	9208.0	G	U	A	A	CID	LIT	5	43.3	DISKAAAGRAL	1072.6	A	D	2.8	0.7	28.5	14.0
P0ACF4	9208.0	G	U	A	A	CID	LIT	5	43.3	DKIAAGADISKAAAGRAL	1699.0	I	D	5.0	0.8	74.1	13.6
P0ACF4	9208.0	G	U	A	A	CID	LIT	5	43.3	MNKSQLI	833.5	-	D	2.4	0.3	44.7	12.8
P0ACF4	9208.0	G	U	A	A	CID	LIT	5	43.3	MNKSQLIDKIAAGA	1459.8	-	D	3.7	0.4	30.0	15.6
P0ACF4	9208.0	G	T	A	A	CID	LIT	4	43.3	DAIIASVTESLKEG	1432.8	L	D	2.3	0.5	39.2	16.6
P0ACF4	9208.0	G	T	A	A	CID	LIT	4	43.3	DISKAAAGRAL	1072.6	A	D	2.2	0.3	31.4	14.6
P0ACF4	9208.0	G	T	A	A	CID	LIT	4	43.3	DKIAAGADISKAAAGRAL	1699.0	I	D	2.5	0.0	40.1	13.6
P0ACF4	9208.0	G	T	A	A	CID	LIT	4	43.3	MNKSQLI	833.5	-	D	2.3	0.3	39.1	12.8
P0ACF4	9208.0	G	U	T	B	CID	LIT	6	74.4	ALDAIIASVTESLK	1430.8	R	E	4.9	0.0	80.6	7.8
P0ACF4	9208.0	G	U	T	B	CID	LIT	6	74.4	EGDDVALVGFGTFAVK	1624.8	K	E	4.3	0.0	57.1	13.2
P0ACF4	9208.0	G	U	T	B	CID	LIT	6	74.4	EITIAAAK	816.5	K	V	2.0	0.0	28.0	15.8
P0ACF4	9208.0	G	U	T	B	CID	LIT	6	74.4	IAAGADISK	845.5	K	A	2.6	0.4	46.8	15.9
P0ACF4	9208.0	G	U	T	B	CID	LIT	6	74.4	SQLIDKIAAGADISK	1529.9	K	A	5.1	0.6	87.6	12.8
P0ACF4	9208.0	G	U	T	B	CID	LIT	6	74.4	TGRNPQTGK	958.5	R	E	2.8	0.4	32.3	15.2
P0ACF4	9208.0	G	U	T	B	CID	LIT	6	74.4	VPSFR	605.3	K	A	1.4	0.7	32.1	15.2
P0ACF4	9208.0	G	T	A	B	CID	LIT	3	35.6	DAIIASVTESLKEG	1432.8	L	D	3.2	0.5	46.0	16.6
P0ACF4	9208.0	G	T	A	B	CID	LIT	3	35.6	DISKAAAGRAL	1072.6	A	D	2.4	0.7	24.9	14.6
P0ACF4	9208.0	G	T	A	B	CID	LIT	3	35.6	MNKSQLI	833.5	-	D	1.7	0.3	25.0	14.1
P0ACF4	9208.0	G	U	A	B	CID	LIT	5	58.9	DAIIASVTESLKEG	1432.8	L	D	3.2	0.6	75.0	16.6
P0ACF4	9208.0	G	U	A	B	CID	LIT	5	58.9	DDVALVGFGTFAVK	1438.8	G	E	3.2	0.0	28.6	14.0
P0ACF4	9208.0	G	U	A	B	CID	LIT	5	58.9	DISKAAAGRAL	1072.6	A	D	3.0	0.7	37.5	14.6
P0ACF4	9208.0	G	U	A	B	CID	LIT	5	58.9	DKIAAGA	645.4	I	D	2.2	0.3	22.8	20.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF4	9208.0	G	U	A	B	CID	LIT	5	58.9	MNKSQLI	833.5	-	D	2.0	0.2	29.3	12.8
P0ACF4	9208.0	S	U	T	A	CID	LIT	5	57.8	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	5.2	0.7	41.2	15.9
P0ACF4	9208.0	S	U	T	A	CID	LIT	5	57.8	ALKDAVN	730.4	K	-	2.5	0.5	28.3	20.3
P0ACF4	9208.0	S	U	T	A	CID	LIT	5	57.8	IAAGADISK	845.5	K	A	2.0	0.4	27.5	19.3
P0ACF4	9208.0	S	U	T	A	CID	LIT	5	57.8	SQLIDK	703.4	K	I	1.6	0.4	22.4	18.6
P0ACF4	9208.0	S	U	T	A	CID	LIT	5	57.8	SQLIDKIAAGADISK	1529.9	K	A	5.3	0.6	86.8	15.8
P0ACF4	9208.0	S	U	T	B	CID	LIT	4	53.3	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	4.7	0.7	45.3	16.1
P0ACF4	9208.0	S	U	T	B	CID	LIT	4	53.3	IAAGADISK	845.5	K	A	2.5	0.4	28.1	19.3
P0ACF4	9208.0	S	U	T	B	CID	LIT	4	53.3	MNKSQLIDKIAAGADISK	1903.0	-	A	2.4	0.4	0.0	0.0
P0ACF4	9208.0	S	U	T	B	CID	LIT	4	53.3	SQLIDKIAAGADISK	1529.9	K	A	5.2	0.5	68.9	16.0
P0ACF4	9208.0	S	U	T	C	CID	LIT	4	53.3	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	4.5	0.7	29.6	16.1
P0ACF4	9208.0	S	U	T	C	CID	LIT	4	53.3	IAAGADISK	845.5	K	A	2.3	0.0	37.5	19.7
P0ACF4	9208.0	S	U	T	C	CID	LIT	4	53.3	MNKSQLIDKIAAGADISK	1903.0	-	A	4.4	0.5	33.6	15.9
P0ACF4	9208.0	S	U	T	C	CID	LIT	4	53.3	SQLIDKIAAGADISK	1529.9	K	A	5.4	0.6	86.0	16.0
P0ACF4	9208.0	S	U	T	A	ETD	LIT	2	50.0	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	5.0	0.0	33.0	16.0
P0ACF4	9208.0	S	U	T	A	ETD	LIT	2	50.0	SQLIDKIAAGADISK	1529.9	K	A	2.8	0.3	48.4	15.8
P0ACF4	9208.0	S	U	T	B	ETD	LIT	4	35.6	EITIAAAK	816.5	K	V	2.7	0.4	41.5	18.4
P0ACF4	9208.0	S	U	T	B	ETD	LIT	4	35.6	IAAGADISK	845.5	K	A	3.0	0.3	36.8	19.3
P0ACF4	9208.0	S	U	T	B	ETD	LIT	4	35.6	SQLIDKIAAGADISK	1529.9	K	A	3.7	0.4	45.9	16.0
P0ACF4	9208.0	S	U	T	B	ETD	LIT	4	35.6	TGRNPQTGKEITIAAAK	1756.0	R	V	7.0	0.4	57.1	14.9
P0ACF4	9208.0	S	U	T	C	ETD	LIT	4	38.9	IAAGADISK	845.5	K	A	2.8	0.3	36.5	19.3
P0ACF4	9208.0	S	U	T	C	ETD	LIT	4	38.9	MNKSQLIDKIAAGADISK	1903.0	-	A	4.8	0.4	52.7	16.1
P0ACF4	9208.0	S	U	T	C	ETD	LIT	4	38.9	SQLIDKIAAGADISK	1529.9	K	A	5.2	0.5	68.4	15.9
P0ACF4	9208.0	S	U	T	C	ETD	LIT	4	38.9	TGRNPQTGKEITIAAAK	1756.0	R	V	6.1	0.3	81.5	14.9
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	2	50.0	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	0.0	0.0	44.0	16.0
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	2	50.0	IAAGADISK	845.5	K	A	0.0	0.0	36.1	19.7
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	2	50.0	SQLIDKIAAGADISK	1529.9	K	A	0.0	0.0	78.6	16.2
P0ACF4	9208.0	S	U	T	A	ETD+CID	LIT	2	50.0	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	5.0	0.0	43.0	16.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF4	9208.0	S	U	T	A	ETD+CID	LIT	2	50.0	IAAGADISK	845.5	K	A	2.4	0.4	0.0	0.0
P0ACF4	9208.0	S	U	T	A	ETD+CID	LIT	2	50.0	SQLIDKIAAGADISK	1529.9	K	A	4.7	0.5	62.8	16.0
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	3	53.3	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	4.8	0.0	43.7	16.0
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	3	53.3	IAAGADISK	845.5	K	A	2.6	0.7	36.1	19.7
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	3	53.3	LATQQSHIPAK	1193.7	-	-	1.1	-0.3	71.1	14.9
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	3	53.3	MNKSQLIDKIAAGADISK	1903.0	-	A	3.3	0.3	7.5	16.3
P0ACF4	9208.0	S	U	T	B	ETD+CID	LIT	3	53.3	SQLIDKIAAGADISK	1529.9	K	A	5.1	0.5	0.0	0.0
P0ACF4	9208.0	S	U	T	C	ETD+CID	LIT	4	62.2	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	5.3	0.7	41.6	15.8
P0ACF4	9208.0	S	U	T	C	ETD+CID	LIT	4	62.2	EITIAAAK	816.5	K	V	2.0	0.5	25.8	18.4
P0ACF4	9208.0	S	U	T	C	ETD+CID	LIT	4	62.2	IAAGADISK	845.5	K	A	0.0	0.0	34.8	19.8
P0ACF4	9208.0	S	U	T	C	ETD+CID	LIT	4	62.2	IAHWVGQGATISDR	1510.8	-	-	2.0	0.1	76.0	15.1
P0ACF4	9208.0	S	U	T	C	ETD+CID	LIT	4	62.2	MNKSQLIDKIAAGADISK	1903.0	-	A	4.6	0.6	50.2	16.1
P0ACF4	9208.0	S	U	T	C	ETD+CID	LIT	4	62.2	SQLIDKIAAGADISK	1529.9	K	A	2.0	0.5	0.0	0.0
P0ACF4	9208.0	S	U	T	B	HCD	FT	2	50.0	ALDAIIASVTESLKEGDDVALVGFGTFAVK	3036.6	R	E	0.0	0.0	44.0	16.0
P0ACF4	9208.0	S	U	T	B	HCD	FT	2	50.0	IAAGADISK	845.5	K	A	0.0	0.0	36.1	19.7
P0ACF4	9208.0	S	U	T	B	HCD	FT	2	50.0	SQLIDKIAAGADISK	1529.9	K	A	0.0	0.0	78.6	16.2
P0AE60	9358.8	G	U	T	A	CID	LIT	2	25.0	QIISYVPR	975.6	R	T	1.7	0.3	18.9	13.4
P0AE60	9358.8	G	U	T	A	CID	LIT	2	25.0	SPAFTVPESAQR	1289.6	R	W	3.2	0.5	36.6	12.6
P0AE60	9358.8	G	U	T	B	CID	LIT	2	25.0	QIISYVPR	975.6	R	T	2.1	0.7	49.3	14.1
P0AE60	9358.8	G	U	T	B	CID	LIT	2	25.0	SPAFTVPESAQR	1289.6	R	W	3.5	0.9	40.8	13.2
P0AE60	9358.8	S	U	T	C	CID	LIT	2	25.0	QIISYVPR	975.6	R	T	2.5	0.4	53.0	15.6
P0AE60	9358.8	S	U	T	C	CID	LIT	2	25.0	SPAFTVPESAQR	1289.6	R	W	2.6	0.4	8.9	17.1
P0AE60	9358.8	S	U	T	C	ETD+CID	LIT	2	25.0	QIISYVPR	975.6	R	T	2.4	0.6	53.5	15.4
P0AE60	9358.8	S	U	T	C	ETD+CID	LIT	2	25.0	SPAFTVPESAQR	1289.6	R	W	2.8	0.4	13.2	17.5
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	EHEDTLAGIEATGVTQR	1826.9	R	N	6.1	0.7	101.0	12.0
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	ETLLKEANK	1045.6	R	I	2.5	0.2	20.0	12.6
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	ETQPIDRETLLK	1442.8	K	E	3.2	0.4	16.5	12.3
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	HLAHVLSEK	1033.6	K	Y	3.5	0.7	43.7	13.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	IIREHEDTLAGIEATGVTQR	2209.2	K	N	4.6	0.9	77.6	12.0
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	MNKETQPIDR	1231.6	-	E	4.0	0.5	59.0	12.8
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	5.1	0.8	83.8	12.0
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	STAVFNMFK	1060.5	K	H	3.0	0.6	29.7	11.5
P0AB61	9367.8	G	U	T	A	CID	LIT	9	100.0	YHLVD	646.3	K	-	1.5	0.6	12.8	15.1
P0AB61	9367.8	G	T	T	A	CID	LIT	7	89.2	EHEDTLAGIEATGVTQR	1826.9	R	N	6.0	0.7	111.0	12.6
P0AB61	9367.8	G	T	T	A	CID	LIT	7	89.2	ETQPIDRETLLK	1442.8	K	E	2.4	0.4	5.6	11.5
P0AB61	9367.8	G	T	T	A	CID	LIT	7	89.2	HLAHVLSEK	1033.6	K	Y	4.0	0.9	29.7	13.4
P0AB61	9367.8	G	T	T	A	CID	LIT	7	89.2	IIREHEDTLAGIEATGVTQR	2209.2	K	N	5.3	0.5	63.6	11.8
P0AB61	9367.8	G	T	T	A	CID	LIT	7	89.2	MNKETQPIDR	1231.6	-	E	3.6	0.5	58.8	11.8
P0AB61	9367.8	G	T	T	A	CID	LIT	7	89.2	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	4.4	0.0	95.7	11.5
P0AB61	9367.8	G	T	T	A	CID	LIT	7	89.2	STAVFNMFK	1044.5	K	H	2.6	0.0	37.1	11.5
P0AB61	9367.8	G	T	T	B	CID	LIT	6	78.3	EHEDTLAGIEATGVTQR	1826.9	R	N	6.0	0.8	102.0	13.2
P0AB61	9367.8	G	T	T	B	CID	LIT	6	78.3	ETQPIDR	858.4	K	E	1.9	0.2	3.2	6.0
P0AB61	9367.8	G	T	T	B	CID	LIT	6	78.3	HLAHVLSEKYHLVD	1660.9	K	-	2.8	0.6	20.8	11.1
P0AB61	9367.8	G	T	T	B	CID	LIT	6	78.3	IIREHEDTLAGIEATGVTQR	2209.2	K	N	3.1	0.5	1.2	12.0
P0AB61	9367.8	G	T	T	B	CID	LIT	6	78.3	MNKETQPIDR	1231.6	-	E	3.1	0.4	57.1	11.8
P0AB61	9367.8	G	T	T	B	CID	LIT	6	78.3	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	4.7	0.0	51.1	12.6
P0AB61	9367.8	G	U	T	B	CID	LIT	7	89.2	EHEDTLAGIEATGVTQR	1826.9	R	N	6.5	0.7	97.6	12.0
P0AB61	9367.8	G	U	T	B	CID	LIT	7	89.2	ETQPIDRETLLK	1442.8	K	E	3.1	0.5	29.2	11.5
P0AB61	9367.8	G	U	T	B	CID	LIT	7	89.2	HLAHVLSEK	1033.6	K	Y	3.4	0.6	25.3	13.2
P0AB61	9367.8	G	U	T	B	CID	LIT	7	89.2	IIREHEDTLAGIEATGVTQR	2209.2	K	N	4.3	0.6	78.1	11.8
P0AB61	9367.8	G	U	T	B	CID	LIT	7	89.2	MNKETQPIDR	1231.6	-	E	3.5	0.5	61.4	12.0
P0AB61	9367.8	G	U	T	B	CID	LIT	7	89.2	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	4.4	0.6	72.7	11.8
P0AB61	9367.8	G	U	T	B	CID	LIT	7	89.2	STAVFNMFK	1044.5	K	H	2.6	0.0	47.5	11.5
P0AB61	9367.8	S	U	T	A	CID	LIT	6	77.1	EHEDTLAGIEATGVTQR	1826.9	R	N	6.6	0.8	108.0	17.1
P0AB61	9367.8	S	U	T	A	CID	LIT	6	77.1	HLAHVLSEK	1033.6	K	Y	2.6	0.6	35.0	16.1
P0AB61	9367.8	S	U	T	A	CID	LIT	6	77.1	HLAHVLSEKYHLVD	1660.9	K	-	4.0	0.7	33.5	16.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB61	9367.8	S	U	T	A	CID	LIT	6	77.1	IIREHEDTLAGIEATGVTQR	2209.2	K	N	5.0	0.6	84.2	17.6
P0AB61	9367.8	S	U	T	A	CID	LIT	6	77.1	NGVLVFTGDYFLDEQGLPTAK	2285.1	R	S	3.9	0.0	60.9	18.7
P0AB61	9367.8	S	U	T	A	CID	LIT	6	77.1	STAVFNMFK	1044.5	K	H	2.6	0.0	19.8	14.1
P0AB61	9367.8	S	U	T	B	CID	LIT	5	81.9	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	5.4	0.7	42.6	17.6
P0AB61	9367.8	S	U	T	B	CID	LIT	5	81.9	HLAHVLSEK	1033.6	K	Y	3.1	0.7	25.8	16.1
P0AB61	9367.8	S	U	T	B	CID	LIT	5	81.9	HLAHVLSEKYHLVD	1660.9	K	-	3.9	0.6	34.2	16.6
P0AB61	9367.8	S	U	T	B	CID	LIT	5	81.9	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	2.4	0.6	0.0	0.0
P0AB61	9367.8	S	U	T	B	CID	LIT	5	81.9	STAVFNMFK	1044.5	K	H	2.2	0.3	6.4	14.1
P0AB61	9367.8	S	U	T	C	CID	LIT	7	89.2	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	6.0	0.7	81.5	17.6
P0AB61	9367.8	S	U	T	C	CID	LIT	7	89.2	EHEDTLAGIEATGVTQR	1826.9	R	N	6.4	0.7	109.0	17.2
P0AB61	9367.8	S	U	T	C	CID	LIT	7	89.2	ETQPIDRETLLK	1442.8	K	E	2.5	0.2	11.9	16.1
P0AB61	9367.8	S	U	T	C	CID	LIT	7	89.2	HLAHVLSEK	1033.6	K	Y	3.2	0.8	35.8	16.1
P0AB61	9367.8	S	U	T	C	CID	LIT	7	89.2	HLAHVLSEKYHLVD	1660.9	K	-	3.7	0.5	28.1	17.3
P0AB61	9367.8	S	U	T	C	CID	LIT	7	89.2	MNKETQPIDRETLLK	1816.0	-	E	4.9	0.3	57.2	17.4
P0AB61	9367.8	S	U	T	C	CID	LIT	7	89.2	NGVLVFTGDYFLDEQGLPTAK	2285.1	R	S	3.3	0.6	34.2	18.5
P0AB61	9367.8	S	U	T	A	CID	FT	2	24.1	EHEDTLAGIEATGVTQR	1826.9	R	N	4.4	0.0	105.0	17.8
P0AB61	9367.8	S	U	T	A	CID	FT	2	24.1	IIREHEDTLAGIEATGVTQR	2209.2	K	N	3.8	0.9	66.8	18.1
P0AB61	9367.8	S	U	T	A	ETD	LIT	4	55.4	EHEDTLAGIEATGVTQR	1826.9	R	N	7.3	0.0	99.2	17.3
P0AB61	9367.8	S	U	T	A	ETD	LIT	4	55.4	HLAHVLSEK	1033.6	K	Y	3.3	0.3	0.0	0.0
P0AB61	9367.8	S	U	T	A	ETD	LIT	4	55.4	HLAHVLSEKYHLVD	1660.9	K	-	4.0	0.4	23.3	17.3
P0AB61	9367.8	S	U	T	A	ETD	LIT	4	55.4	MNKETQPIDRETLLK	1816.0	-	E	4.4	0.6	12.8	17.2
P0AB61	9367.8	S	U	T	B	ETD	LIT	5	53.0	EHEDTLAGIEATGVTQR	1826.9	R	N	2.3	0.8	90.6	16.8
P0AB61	9367.8	S	U	T	B	ETD	LIT	5	53.0	ETQPIDRETLLK	1442.8	K	E	2.1	0.5	11.6	16.1
P0AB61	9367.8	S	U	T	B	ETD	LIT	5	53.0	HLAHVLSEK	1033.6	K	Y	3.0	0.5	37.8	16.1
P0AB61	9367.8	S	U	T	B	ETD	LIT	5	53.0	IIREHEDTLAGIEATGVTQR	2209.2	K	N	4.7	0.0	17.1	17.8
P0AB61	9367.8	S	U	T	B	ETD	LIT	5	53.0	MNKETQPIDRETLLK	1816.0	-	E	5.3	0.6	30.6	17.9
P0AB61	9367.8	S	U	T	C	ETD	LIT	5	55.4	EHEDTLAGIEATGVTQR	1826.9	R	N	2.9	0.7	107.0	17.9
P0AB61	9367.8	S	U	T	C	ETD	LIT	5	55.4	ETQPIDRETLLK	1442.8	K	E	4.4	0.4	28.5	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB61	9367.8	S	U	T	C	ETD	LIT	5	55.4	HLAHVLSEK	1033.6	K	Y	2.7	0.3	17.1	16.0
P0AB61	9367.8	S	U	T	C	ETD	LIT	5	55.4	HLAHVLSEKYHLVD	1660.9	K	-	3.9	0.4	23.3	17.3
P0AB61	9367.8	S	U	T	C	ETD	LIT	5	55.4	MNKETQPIDRETLLK	1816.0	-	E	6.3	0.6	37.8	17.6
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	3	65.1	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	0.0	0.0	57.9	17.5
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	3	65.1	HLAHVLSEK	1033.6	K	Y	0.0	0.0	44.4	16.1
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	3	65.1	NGVLVFTGDYFLDEQGLPTAK	2285.1	R	S	0.0	0.0	40.2	18.6
P0AB61	9367.8	S	U	T	A	ETD+CID	LIT	5	75.9	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	4.0	0.7	69.6	17.3
P0AB61	9367.8	S	U	T	A	ETD+CID	LIT	5	75.9	EHEDTLAGIEATGVTQR	1826.9	R	N	2.3	0.2	4.8	17.1
P0AB61	9367.8	S	U	T	A	ETD+CID	LIT	5	75.9	HLAHVLSEK	1033.6	K	Y	3.4	0.5	33.3	16.1
P0AB61	9367.8	S	U	T	A	ETD+CID	LIT	5	75.9	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	4.0	0.7	49.7	18.2
P0AB61	9367.8	S	U	T	A	ETD+CID	LIT	5	75.9	STAVFNMFK	1044.5	K	H	2.7	0.4	25.3	14.1
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	2	54.2	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	3.2	0.5	0.0	0.0
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	2	54.2	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	3.7	0.7	0.0	0.0
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	4	75.9	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	3.2	0.5	57.9	17.5
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	4	75.9	HLAHVLSEK	1033.6	K	Y	3.4	0.8	0.0	0.0
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	4	75.9	NGVLVFTGDYFLDEQGLPTAK	2285.1	R	S	4.5	0.6	40.2	18.6
P0AB61	9367.8	S	U	T	B	ETD+CID	LIT	4	75.9	STAVFNMFK	1044.5	K	H	2.1	0.2	4.1	14.1
P0AB61	9367.8	S	U	T	C	ETD+CID	LIT	7	100.0	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	5.6	0.0	80.4	17.7
P0AB61	9367.8	S	U	T	C	ETD+CID	LIT	7	100.0	EHEDTLAGIEATGVTQR	1826.9	R	N	0.0	0.0	111.0	16.9
P0AB61	9367.8	S	U	T	C	ETD+CID	LIT	7	100.0	HLAHVLSEK	1033.6	K	Y	3.1	0.7	0.0	0.0
P0AB61	9367.8	S	U	T	C	ETD+CID	LIT	7	100.0	HLAHVLSEKYHLVD	1660.9	K	-	3.9	0.8	68.1	17.3
P0AB61	9367.8	S	U	T	C	ETD+CID	LIT	7	100.0	MNKETQPIDRETLLK	1816.0	-	E	4.5	0.3	33.6	17.1
P0AB61	9367.8	S	U	T	C	ETD+CID	LIT	7	100.0	NGVLVFTGDYFLDEQGLPTAK	2284.2	R	S	4.3	0.7	53.8	18.6
P0AB61	9367.8	S	U	T	C	ETD+CID	LIT	7	100.0	STAVFNMFK	1044.5	K	H	2.4	0.4	29.6	14.1
P0AB61	9367.8	S	U	T	B	HCD	FT	3	65.1	EANKIIREHEDTLAGIEATGVTQR	2651.4	K	N	0.0	0.0	57.9	17.5
P0AB61	9367.8	S	U	T	B	HCD	FT	3	65.1	HLAHVLSEK	1033.6	K	Y	0.0	0.0	44.4	16.1
P0AB61	9367.8	S	U	T	B	HCD	FT	3	65.1	NGVLVFTGDYFLDEQGLPTAK	2285.1	R	S	0.0	0.0	40.2	18.6
Q47150	9388.4	G	U	T	A	CID	LIT	3	32.6	AANAFVR	748.4	M	A	0.0	0.0	32.5	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
Q47150	9388.4	G	U	T	A	CID	LIT	3	32.6	DADDLFDKLGI	1221.6	K	-	2.5	0.7	11.0	11.8
Q47150	9388.4	G	U	T	A	CID	LIT	3	32.6	NSEAGIDVHK	1069.5	K	A	2.7	0.7	42.5	9.5
Q47150	9388.4	G	T	T	A	CID	LIT	3	36.0	AKDADDLFDK	1137.5	K	L	2.6	0.7	8.6	13.8
Q47150	9388.4	G	T	T	A	CID	LIT	3	36.0	EPNQLTIQSIK	1270.7	R	N	2.4	0.6	22.5	12.0
Q47150	9388.4	G	T	T	A	CID	LIT	3	36.0	NSEAGIDVHK	1069.5	K	A	3.1	0.0	45.0	9.5
P0A9W6	9433.6	G	U	T	A	CID	LIT	4	39.3	AYTPAEWAR	1064.5	K	D	2.4	0.3	25.0	12.6
P0A9W6	9433.6	G	U	T	A	CID	LIT	4	39.3	IHAVSIK	767.5	R	A	2.2	0.0	25.1	3.0
P0A9W6	9433.6	G	U	T	A	CID	LIT	4	39.3	KQQTVYGPLMEYIADNR	2026.0	K	I	4.7	0.7	43.7	12.6
P0A9W6	9433.6	G	U	T	A	CID	LIT	4	39.3	QQTVYGPLMEYIADNR	1897.9	K	I	4.3	0.0	58.2	11.5
P0A9W6	9433.6	G	U	A	A	CID	LIT	2	39.3	DGSHFQVIAVGELF	1518.8	G	D	2.1	0.6	14.8	16.9
P0A9W6	9433.6	G	U	A	A	CID	LIT	2	39.3	DNRIHAVSIKAYTPAEWAR	2198.1	A	D	4.9	0.6	55.9	16.2
P0A9W6	9433.6	G	U	T	B	CID	LIT	3	31.0	AYTPAEWAR	1064.5	K	D	2.4	0.8	28.6	12.8
P0A9W6	9433.6	G	U	T	B	CID	LIT	3	31.0	KQQTVYGPLMEYIADNR	2026.0	K	I	4.3	0.0	28.8	12.3
P0A9W6	9433.6	G	U	T	B	CID	LIT	3	31.0	QQTVYGPLMEYIADNR	1897.9	K	I	4.5	0.0	56.7	11.5
P0A9W6	9433.6	G	T	A	B	CID	LIT	2	50.0	DNRIHAVSIKAYTPAEWAR	2198.1	A	D	4.4	0.8	41.5	16.3
P0A9W6	9433.6	G	T	A	B	CID	LIT	2	50.0	MENNEIQSVLMNALSLQEVHVSG	2542.2	-	D	0.0	0.0	50.2	12.3
P0A9W6	9433.6	G	U	A	B	CID	LIT	6	91.7	DGMSRVKKQQTVYGPLM	1938.0	F	E	3.7	0.6	34.3	15.2
P0A9W6	9433.6	G	U	A	B	CID	LIT	6	91.7	DGMSRVKKQQTVYGPLMEYIA	2414.2	F	D	3.0	0.9	23.5	15.1
P0A9W6	9433.6	G	U	A	B	CID	LIT	6	91.7	DGSHFQVIAVGELF	1518.8	G	D	2.8	0.7	30.9	16.7
P0A9W6	9433.6	G	U	A	B	CID	LIT	6	91.7	DNRIHAVSIKAYTPAEWAR	2198.1	A	D	3.8	0.7	46.2	16.0
P0A9W6	9433.6	G	U	A	B	CID	LIT	6	91.7	MENNEIQSVLMNALSLQ	1933.9	-	E	2.2	0.6	6.4	14.6
P0A9W6	9433.6	G	U	A	B	CID	LIT	6	91.7	MENNEIQSVLMNALSLQEVHVSG	2542.2	-	D	0.0	0.0	66.1	12.0
P0A9W6	9433.6	S	U	T	B	CID	LIT	2	20.2	KQQTVYGPLMEYIADNR	2026.0	K	I	3.0	0.5	5.5	18.3
P0A9W6	9433.6	S	U	T	B	CID	LIT	2	20.2	QQTVYGPLMEYIADNR	1897.9	K	I	4.7	0.5	52.5	16.8
P0A9W6	9433.6	S	U	T	C	CID	LIT	2	20.2	KQQTVYGPLMEYIADNR	2026.0	K	I	3.7	0.0	17.4	18.7
P0A9W6	9433.6	S	U	T	C	CID	LIT	2	20.2	QQTVYGPLMEYIADNR	1897.9	K	I	4.4	0.7	47.4	16.8
P0A9W6	9433.6	S	U	T	A	ETD	LIT	2	29.8	AYTPAEWAR	1064.5	K	D	2.0	0.0	23.4	15.6
P0A9W6	9433.6	S	U	T	A	ETD	LIT	2	29.8	QQTVYGPLMEYIADNR	1897.9	K	I	1.8	0.0	27.7	17.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9W6	9433.6	S	U	T	C	ETD	LIT	2	29.8	AYTPAEWAR	1064.5	K	D	1.7	0.3	10.7	16.1
P0A9W6	9433.6	S	U	T	C	ETD	LIT	2	29.8	QQTVYGPLMEYIADNR	1897.9	K	I	1.8	0.6	14.5	17.2
P0A9W6	9433.6	S	U	T	B	ETD+CID	LIT	2	20.2	KQQTVYGPLMEYIADNR	2026.0	K	I	0.0	0.0	21.9	17.8
P0A9W6	9433.6	S	U	T	B	ETD+CID	LIT	2	20.2	QQTVYGPLMEYIADNR	1897.9	K	I	0.0	0.0	22.4	16.9
P0A9W6	9433.6	S	U	T	B	ETD+CID	LIT	2	20.2	KQQTVYGPLMEYIADNR	2026.0	K	I	3.8	0.5	21.9	17.8
P0A9W6	9433.6	S	U	T	B	ETD+CID	LIT	2	20.2	QQTVYGPLMEYIADNR	1897.9	K	I	3.7	0.4	22.4	16.9
P0A9W6	9433.6	S	U	T	C	ETD+CID	LIT	2	20.2	KQQTVYGPLMEYIADNR	2026.0	K	I	4.0	0.6	24.9	18.6
P0A9W6	9433.6	S	U	T	C	ETD+CID	LIT	2	20.2	QQTVYGPLMEYIADNR	1897.9	K	I	4.8	0.6	46.1	16.8
P0A9W6	9433.6	S	U	T	B	HCD	FT	2	20.2	KQQTVYGPLMEYIADNR	2026.0	K	I	0.0	0.0	21.9	17.8
P0A9W6	9433.6	S	U	T	B	HCD	FT	2	20.2	QQTVYGPLMEYIADNR	1897.9	K	I	0.0	0.0	22.4	16.9
P0AFW8	9461.7	G	U	T	A	CID	LIT	3	38.1	ITSFSHPEIGTVVVSES	1788.9	K	-	3.0	0.8	33.0	12.8
P0AFW8	9461.7	G	U	T	A	CID	LIT	3	38.1	KNVEYLVVEAAGETR	1677.9	R	E	5.1	0.7	94.7	13.0
P0AFW8	9461.7	G	U	T	A	CID	LIT	3	38.1	NVEYLVVEAAGETR	1549.8	K	E	4.0	0.0	75.0	11.1
P0AFW8	9461.7	G	T	T	A	CID	LIT	5	45.2	ELRLDK	773.5	R	I	2.2	0.2	21.5	17.9
P0AFW8	9461.7	G	T	T	A	CID	LIT	5	45.2	ITSFSHPEIGTVVVSES	1788.9	K	-	4.0	0.8	29.0	12.3
P0AFW8	9461.7	G	T	T	A	CID	LIT	5	45.2	KNVEYLVVEAAGETR	1677.9	R	E	5.0	0.8	94.9	13.4
P0AFW8	9461.7	G	T	T	A	CID	LIT	5	45.2	LDKITSFSHPEIGTVVVSES	2145.1	R	-	5.8	0.0	54.4	11.1
P0AFW8	9461.7	G	T	T	A	CID	LIT	5	45.2	NVEYLVVEAAGETR	1549.8	K	E	4.5	0.8	81.5	11.1
P0AFW8	9461.7	G	U	A	A	CID	LIT	2	35.7	DKITSFSHPEIGTVVVSES	2032.0	L	-	5.4	0.7	63.5	14.0
P0AFW8	9461.7	G	U	A	A	CID	LIT	2	35.7	DTYQPINCDDY	1403.5	N	D	2.5	0.0	29.7	7.0
P0AFW8	9461.7	G	T	A	A	CID	LIT	4	69.0	DGEKLQAKAS	1046.5	K	D	2.5	0.0	17.5	14.6
P0AFW8	9461.7	G	T	A	A	CID	LIT	4	69.0	DKITSFSHPEIGTVVVSES	2032.0	L	-	4.8	0.6	41.8	14.3
P0AFW8	9461.7	G	T	A	A	CID	LIT	4	69.0	DNLELACQHHLMLTLELK	2194.1	Y	D	4.0	0.8	46.8	15.4
P0AFW8	9461.7	G	T	A	A	CID	LIT	4	69.0	DTYQPINCDDY	1403.5	N	D	2.8	0.0	33.2	7.0
P0AFW8	9461.7	G	T	T	B	CID	LIT	2	36.9	ITSFSHPEIGTVVVSES	1788.9	K	-	3.5	0.6	12.0	13.4
P0AFW8	9461.7	G	T	T	B	CID	LIT	2	36.9	NVEYLVVEAAGETR	1549.8	K	E	2.4	0.4	0.0	0.0
P0AFW8	9461.7	G	U	A	B	CID	LIT	4	65.5	DGEKLQAKAS	1046.5	K	D	2.6	0.7	13.1	14.8
P0AFW8	9461.7	G	U	A	B	CID	LIT	4	65.5	DKITSFSHPEIGTVVVSES	2032.0	L	-	4.3	0.6	47.4	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFW8	9461.7	G	U	A	B	CID	LIT	4	65.5	DNLELACQHHLMLTLELK	2178.1	Y	D	2.2	0.3	17.5	15.4
P0AFW8	9461.7	G	U	A	B	CID	LIT	4	65.5	DTYQPINC	1010.4	N	D	1.8	0.7	8.8	11.5
P0AFW8	9461.7	S	U	T	A	CID	LIT	3	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	3.8	0.6	23.5	17.3
P0AFW8	9461.7	S	U	T	A	CID	LIT	3	41.7	KNVEYLVVEAAGETR	1677.9	R	E	4.1	0.6	46.8	16.6
P0AFW8	9461.7	S	U	T	A	CID	LIT	3	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	5.9	0.7	61.6	18.9
P0AFW8	9461.7	S	U	T	B	CID	LIT	3	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	4.0	0.6	24.1	17.2
P0AFW8	9461.7	S	U	T	B	CID	LIT	3	41.7	KNVEYLVVEAAGETR	1677.9	R	E	4.7	0.6	65.7	16.6
P0AFW8	9461.7	S	U	T	B	CID	LIT	3	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	4.2	0.6	51.1	18.4
P0AFW8	9461.7	S	U	T	C	CID	LIT	4	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	3.6	0.5	37.6	17.3
P0AFW8	9461.7	S	U	T	C	CID	LIT	4	41.7	KNVEYLVVEAAGETR	1677.9	R	E	4.8	0.6	76.0	16.6
P0AFW8	9461.7	S	U	T	C	CID	LIT	4	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	5.5	0.6	57.0	19.0
P0AFW8	9461.7	S	U	T	C	CID	LIT	4	41.7	NVEYLVVEAAGETR	1549.8	K	E	3.3	0.6	49.1	16.6
P0AFW8	9461.7	S	U	T	B	ETD	LIT	2	23.8	ITSFSHPEIGTVVVSES	1788.9	K	-	3.3	0.7	37.7	17.2
P0AFW8	9461.7	S	U	T	B	ETD	LIT	2	23.8	LDKITSFSHPEIGTVVVSES	2145.1	R	-	2.8	0.3	23.1	18.3
P0AFW8	9461.7	S	U	T	C	ETD	LIT	2	23.8	ITSFSHPEIGTVVVSES	1788.9	K	-	3.8	0.6	40.8	17.8
P0AFW8	9461.7	S	U	T	C	ETD	LIT	2	23.8	LDKITSFSHPEIGTVVVSES	2145.1	R	-	5.5	0.5	52.2	18.3
P0AFW8	9461.7	S	U	T	B	ETD+CID	LIT	3	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	0.0	0.0	26.3	17.2
P0AFW8	9461.7	S	U	T	B	ETD+CID	LIT	3	41.7	KNVEYLVVEAAGETR	1677.9	R	E	0.0	0.0	74.0	16.6
P0AFW8	9461.7	S	U	T	B	ETD+CID	LIT	3	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	0.0	0.0	81.6	18.3
P0AFW8	9461.7	S	U	T	A	ETD+CID	LIT	3	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	0.0	0.0	28.8	17.8
P0AFW8	9461.7	S	U	T	A	ETD+CID	LIT	3	41.7	KNVEYLVVEAAGETR	1677.9	R	E	4.5	0.6	67.2	17.4
P0AFW8	9461.7	S	U	T	A	ETD+CID	LIT	3	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	5.6	0.7	51.2	19.0
P0AFW8	9461.7	S	U	T	B	ETD+CID	LIT	3	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	4.2	0.6	26.3	17.2
P0AFW8	9461.7	S	U	T	B	ETD+CID	LIT	3	41.7	KNVEYLVVEAAGETR	1677.9	R	E	4.8	0.6	74.0	16.6
P0AFW8	9461.7	S	U	T	B	ETD+CID	LIT	3	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	5.3	0.7	81.6	18.3
P0AFW8	9461.7	S	U	T	C	ETD+CID	LIT	4	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	4.2	0.6	27.0	17.1
P0AFW8	9461.7	S	U	T	C	ETD+CID	LIT	4	41.7	KNVEYLVVEAAGETR	1677.9	R	E	4.9	0.6	72.3	17.1
P0AFW8	9461.7	S	U	T	C	ETD+CID	LIT	4	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	5.6	0.7	47.2	19.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFW8	9461.7	S	U	T	C	ETD+CID	LIT	4	41.7	NVEYLVVEAAGETR	1549.8	K	E	2.8	0.5	21.6	17.1
P0AFW8	9461.7	S	U	T	B	HCD	FT	3	41.7	ITSFSHPEIGTVVVSES	1788.9	K	-	0.0	0.0	26.3	17.2
P0AFW8	9461.7	S	U	T	B	HCD	FT	3	41.7	KNVEYLVVEAAGETR	1677.9	R	E	0.0	0.0	74.0	16.6
P0AFW8	9461.7	S	U	T	B	HCD	FT	3	41.7	LDKITSFSHPEIGTVVVSES	2145.1	R	-	0.0	0.0	81.6	18.3
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	AALESTLAAITESLK	1517.8	K	E	4.0	0.7	75.9	9.0
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	4.9	0.0	45.2	10.0
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	EGDAVQLVGFGTFK	1467.7	K	V	4.3	0.5	76.8	12.3
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	IAAANVPAFVSGK	1244.7	K	A	3.8	0.8	45.1	12.6
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	MNKTQLIDVIAEK	1502.8	-	A	5.4	0.7	33.2	10.4
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	TGRNPQTGK	958.5	R	E	2.6	0.4	14.0	12.8
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	TQLIDVIAEK	1129.6	K	A	2.8	0.0	36.9	10.0
P0ACF0	9517.2	G	U	T	A	CID	LIT	7	76.7	TQLIDVIAEKAELSK	1657.9	K	T	4.3	0.7	55.5	11.1
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	AALESTLAAITESLK	1517.8	K	E	4.3	0.0	83.8	9.0
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	4.0	0.0	29.5	10.4
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	EGDAVQLVGFGTFK	1467.7	K	V	4.1	0.6	112.0	12.3
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	IAAANVPAFVSGK	1244.7	K	A	3.0	0.6	23.7	12.6
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	MNKTQLIDVIAEK	1502.8	-	A	4.7	0.7	55.7	10.4
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	TGRNPQTGK	958.5	R	E	2.9	0.4	27.6	15.2
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	TQLIDVIAEK	1129.6	K	A	3.0	0.0	42.7	10.0
P0ACF0	9517.2	G	T	T	A	CID	LIT	7	76.7	TQLIDVIAEKAELSK	1657.9	K	T	3.5	0.0	38.2	10.4
P0ACF0	9517.2	G	U	A	A	CID	LIT	3	34.4	DAVQLVGFGTFKVNHRA	1859.0	G	E	2.1	0.3	11.5	14.0
P0ACF0	9517.2	G	U	A	A	CID	LIT	3	34.4	DVIAEKA	745.4	I	E	2.0	0.5	21.9	20.3
P0ACF0	9517.2	G	U	A	A	CID	LIT	3	34.4	MNKTQLI	847.5	-	D	2.2	0.2	34.5	13.6
P0ACF0	9517.2	G	U	T	B	CID	LIT	7	76.7	AALESTLAAITESLK	1517.8	K	E	4.5	0.8	68.8	11.8
P0ACF0	9517.2	G	U	T	B	CID	LIT	7	76.7	EGDAVQLVGFGTFK	1467.7	K	V	3.9	0.7	70.4	13.0
P0ACF0	9517.2	G	U	T	B	CID	LIT	7	76.7	IAAANVPAFVSGK	1244.7	K	A	4.0	0.8	50.8	12.6
P0ACF0	9517.2	G	U	T	B	CID	LIT	7	76.7	MNKTQLIDVIAEK	1502.8	-	A	4.7	0.5	71.9	11.1
P0ACF0	9517.2	G	U	T	B	CID	LIT	7	76.7	TGRNPQTGK	958.5	R	E	2.8	0.4	32.3	15.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF0	9517.2	G	U	T	B	CID	LIT	7	76.7	TQLIDVIAEK	1129.6	K	A	2.6	0.0	33.7	10.0
P0ACF0	9517.2	G	U	T	B	CID	LIT	7	76.7	TQLIDVIAEKAELSK	1657.9	K	T	4.6	0.7	76.2	11.1
P0ACF0	9517.2	G	T	A	B	CID	LIT	4	67.8	DAVQLVGFGTFKVNHRA	1859.0	G	E	3.1	0.7	25.3	13.2
P0ACF0	9517.2	G	T	A	B	CID	LIT	4	67.8	DVIAEKA	745.4	I	E	2.0	0.5	21.1	20.2
P0ACF0	9517.2	G	T	A	B	CID	LIT	4	67.8	ERTGRNPQTGKEIKIAAANVPAFVSGKALK	3151.8	A	D	2.6	0.0	13.4	9.0
P0ACF0	9517.2	G	T	A	B	CID	LIT	4	67.8	MNKTQLI	847.5	-	D	1.6	0.4	23.3	13.6
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	DAVQLVGFGTFKVNHRA	1859.0	G	E	4.3	0.8	51.7	14.1
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	DVIAEKA	745.4	I	E	2.1	0.7	25.0	20.3
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	DVIAEKAELSKTQAKAAL	1886.1	I	E	4.5	0.6	30.7	12.0
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	ELSKTQAKAAL	1159.7	A	E	2.7	0.0	29.6	12.3
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	ELSKTQAKAALESTLAAIT	1946.1	A	E	2.8	0.0	19.1	11.8
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	ERTGRNPQTGKEIKIAAANVPAFVSGKALK	3151.8	A	D	5.1	0.0	70.3	10.4
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	ESTLAAITESLKEG	1448.7	L	D	2.9	0.6	6.9	15.3
P0ACF0	9517.2	G	U	A	B	CID	LIT	8	95.6	MNKTQLI	847.5	-	D	2.3	0.2	46.6	13.6
P0ACF0	9517.2	S	U	T	A	CID	LIT	7	74.4	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	4.1	0.5	15.6	14.8
P0ACF0	9517.2	S	U	T	A	CID	LIT	7	74.4	ALKDAVK	744.5	K	-	2.6	0.3	33.1	18.0
P0ACF0	9517.2	S	U	T	A	CID	LIT	7	74.4	EGDAVQLVGFGTFK	1467.7	K	V	4.0	0.6	75.4	17.2
P0ACF0	9517.2	S	U	T	A	CID	LIT	7	74.4	IAAANVPAFVSGK	1244.7	K	A	3.7	0.8	43.7	16.1
P0ACF0	9517.2	S	U	T	A	CID	LIT	7	74.4	MNKTQLIDVIAEK	1502.8	-	A	4.1	0.5	52.0	16.9
P0ACF0	9517.2	S	U	T	A	CID	LIT	7	74.4	MNKTQLIDVIAEKAELSK	2031.1	-	T	4.9	0.7	81.0	14.9
P0ACF0	9517.2	S	U	T	A	CID	LIT	7	74.4	TQLIDVIAEKAELSK	1657.9	K	T	4.6	0.5	59.1	14.8
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	AALESTLAAITESLK	1517.8	K	E	5.2	0.7	70.1	14.8
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	5.2	0.6	60.9	15.4
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	ALKDAVK	744.5	K	-	2.5	0.3	30.6	18.0
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	EGDAVQLVGFGTFK	1467.7	K	V	1.8	0.4	0.0	0.0
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	IAAANVPAFVSGK	1244.7	K	A	3.7	0.8	37.0	16.1
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	MNKTQLIDVIAEK	1502.8	-	A	4.7	0.6	69.6	16.9
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	MNKTQLIDVIAEKAELSK	2031.1	-	T	5.9	0.7	100.0	15.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	TQLIDVIAEK	1129.6	K	A	3.1	0.6	41.0	13.6
P0ACF0	9517.2	S	U	T	B	CID	LIT	9	74.4	TQLIDVIAEKAELSK	1657.9	K	T	4.6	0.5	65.2	15.3
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	4.2	0.6	60.1	14.9
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	ALKDAVK	744.5	K	-	2.6	0.3	31.0	18.0
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	EGDAVQLVGFGTFK	1467.7	K	V	3.5	0.5	28.4	17.2
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	IAAANVPAFVSGK	1244.7	K	A	4.0	0.8	47.3	16.1
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	MNKTQLIDVIAEK	1502.8	-	A	5.3	0.5	89.3	17.0
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	MNKTQLIDVIAEKAELSK	2031.1	-	T	5.5	0.7	88.1	15.6
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	TGRNPQTGKEIK	1328.7	R	I	2.9	0.7	27.0	16.4
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	TQLIDVIAEK	1129.6	K	A	2.6	0.6	35.7	14.5
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	TQLIDVIAEKAELSK	1657.9	K	T	4.6	0.5	54.4	14.8
P0ACF0	9517.2	S	U	T	C	CID	LIT	10	92.2	TQLIDVIAEKAELSKTQAK	2086.2	K	A	2.8	0.2	0.0	0.0
P0ACF0	9517.2	S	U	T	B	CID	FT	2	30.0	EGDAVQLVGFGTFK	1467.7	K	V	3.5	0.0	68.4	17.2
P0ACF0	9517.2	S	U	T	B	CID	FT	2	30.0	IAAANVPAFVSGK	1244.7	K	A	3.3	0.0	36.9	16.1
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	AALESTLAAITESLK	1517.8	K	E	2.2	0.4	24.9	14.9
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	0.0	0.0	28.2	15.4
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	ALKDAVK	744.5	K	-	1.5	0.4	25.1	18.0
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	EGDAVQLVGFGTFK	1467.7	K	V	3.3	0.5	21.4	17.8
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	IAAANVPAFVSGK	1244.7	K	A	3.5	0.4	43.7	16.2
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	MNKTQLIDVIAEK	1502.8	-	A	7.2	0.6	71.2	16.7
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	MNKTQLIDVIAEKAELSK	2031.1	-	T	7.5	0.7	86.3	15.1
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	TGRNPQTGKEIK	1328.7	R	I	1.2	0.7	11.5	16.1
P0ACF0	9517.2	S	U	T	A	ETD	LIT	9	87.8	TQLIDVIAEKAELSK	1657.9	K	T	5.6	0.5	81.6	15.1
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	AALESTLAAITESLK	1517.8	K	E	3.7	0.5	61.4	14.9
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	3.9	0.0	29.1	15.2
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	EGDAVQLVGFGTFK	1467.7	K	V	2.6	0.5	23.5	17.2
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	IAAANVPAFVSGK	1244.7	K	A	3.7	0.4	43.2	16.3
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	MNKTQLIDVIAEK	1502.8	-	A	7.5	0.6	87.6	16.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	MNKTQLIDVIAEKAELSK	2031.1	-	T	10.3	0.0	92.8	15.3
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	TQLIDVIAEK	1129.6	K	A	2.5	0.4	39.4	13.8
P0ACF0	9517.2	S	U	T	B	ETD	LIT	8	66.7	TQLIDVIAEKAELSK	1657.9	K	T	6.8	0.5	85.5	15.1
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	7.8	0.0	62.8	14.8
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	ALKDAVK	744.5	K	-	1.8	0.1	29.7	18.0
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	EGDAVQLVGFGTFK	1467.7	K	V	3.8	0.8	45.6	17.2
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	IAAANVPAFVSGK	1244.7	K	A	1.3	0.3	38.8	16.1
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	MNKTQLIDVIAEK	1502.8	-	A	3.4	0.5	40.6	17.0
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	MNKTQLIDVIAEKAELSK	2031.1	-	T	0.0	0.0	94.0	15.3
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	TGRNPQTGKEIK	1328.7	R	I	3.1	0.1	22.4	16.5
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	TQLIDVIAEK	1129.6	K	A	2.5	0.4	22.9	14.5
P0ACF0	9517.2	S	U	T	C	ETD	LIT	9	87.8	TQLIDVIAEKAELSK	1657.9	K	T	4.0	0.4	42.5	14.9
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	6	74.4	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	0.0	0.0	55.0	14.8
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	6	74.4	ALKDAVK	744.5	K	-	0.0	0.0	22.6	18.0
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	6	74.4	IAAANVPAFVSGK	1244.7	K	A	0.0	0.0	40.1	16.1
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	6	74.4	MNKTQLIDVIAEK	1502.8	-	A	0.0	0.0	18.5	16.7
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	6	74.4	MNKTQLIDVIAEKAELSK	2031.1	-	T	0.0	0.0	114.0	15.2
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	6	74.4	TQLIDVIAEKAELSK	1657.9	K	T	0.0	0.0	63.5	15.1
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	5.6	0.0	45.1	15.2
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	ALKDAVK	744.5	K	-	2.6	0.1	25.3	18.0
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	EGDAVQLVGFGTFK	1467.7	K	V	2.9	0.5	31.2	17.0
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	IAAANVPAFVSGK	1244.7	K	A	3.7	0.7	44.5	16.2
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	MNKTQLIDVIAEK	1502.8	-	A	5.1	0.5	76.0	16.9
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	MNKTQLIDVIAEKAELSK	2031.1	-	T	0.7	-0.3	89.9	15.4
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	TGRNPQTGKEIK	1328.7	R	I	0.8	-0.3	30.4	16.4
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	TQLIDVIAEK	1129.6	K	A	2.6	0.7	18.1	13.6
P0ACF0	9517.2	S	U	T	A	ETD+CID	LIT	9	87.8	TQLIDVIAEKAELSK	1657.9	K	T	7.2	0.6	68.3	14.5
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	2	35.6	EGDAVQLVGFGTFK	1467.7	K	V	2.5	0.4	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	2	35.6	MNKTQLIDVIAEKAELSK	2032.1	-	T	2.9	0.7	0.0	0.0
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	5.4	0.0	55.0	14.8
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	ALKDAVK	744.5	K	-	2.5	0.5	22.6	18.0
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	EGDAVQLVGFGTFK	1467.7	K	V	2.5	0.4	0.0	0.0
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	IAAANVPAFVSGK	1244.7	K	A	3.9	0.8	40.1	16.1
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	LATQQSHIPAK	1193.7	-	-	1.1	-0.3	71.1	14.9
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	MNKTQLIDVIAEK	1502.8	-	A	1.9	0.4	18.5	16.7
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	MNKTQLIDVIAEKAELSK	2031.1	-	T	6.3	0.7	114.0	15.2
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	TGRNPQTGKEIK	1328.7	R	I	1.4	0.4	18.6	16.4
P0ACF0	9517.2	S	U	T	B	ETD+CID	LIT	9	87.8	TQLIDVIAEKAELSK	1657.9	K	T	4.8	0.5	63.5	15.1
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	4.7	0.6	70.7	15.1
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	ALKDAVK	744.5	K	-	2.9	0.3	27.0	18.0
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	EGDAVQLVGFGTFK	1467.7	K	V	3.7	0.5	88.0	17.4
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	IAAANVPAFVSGK	1244.7	K	A	3.9	0.8	47.3	16.1
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	MNKTQLIDVIAEK	1502.8	-	A	4.2	0.6	50.7	16.9
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	MNKTQLIDVIAEKAELSK	2031.1	-	T	6.5	0.7	93.9	14.5
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	TGRNPQTGKEIK	1328.7	R	I	1.6	0.1	44.4	16.1
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	TQLIDVIAEK	1129.6	K	A	3.1	0.8	0.0	0.0
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	TQLIDVIAEKAELSK	1657.9	K	T	4.4	0.5	38.6	15.4
P0ACF0	9517.2	S	U	T	C	ETD+CID	LIT	9	87.8	VRPDMAQNNADR	1386.7	-	-	3.8	-0.4	41.7	12.8
P0ACF0	9517.2	S	U	T	B	HCD	FT	6	74.4	AALESTLAAITESLKEGDAVQLVGFGTFK	2966.6	K	V	0.0	0.0	55.0	14.8
P0ACF0	9517.2	S	U	T	B	HCD	FT	6	74.4	ALKDAVK	744.5	K	-	0.0	0.0	22.6	18.0
P0ACF0	9517.2	S	U	T	B	HCD	FT	6	74.4	IAAANVPAFVSGK	1244.7	K	A	0.0	0.0	40.1	16.1
P0ACF0	9517.2	S	U	T	B	HCD	FT	6	74.4	MNKTQLIDVIAEK	1502.8	-	A	0.0	0.0	18.5	16.7
P0ACF0	9517.2	S	U	T	B	HCD	FT	6	74.4	MNKTQLIDVIAEKAELSK	2031.1	-	T	0.0	0.0	114.0	15.2
P0ACF0	9517.2	S	U	T	B	HCD	FT	6	74.4	TQLIDVIAEKAELSK	1657.9	K	T	0.0	0.0	63.5	15.1
P0AF36	9616.6	G	U	T	A	CID	LIT	5	66.7	EELERENNHLK	1410.7	R	E	3.3	0.7	31.8	14.3
P0AF36	9616.6	G	U	T	A	CID	LIT	5	66.7	LQALLGR	770.5	R	M	2.2	0.1	45.1	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AF36	9616.6	G	U	T	A	CID	LIT	5	66.7	NNSLSQEVQNAQHQR	1752.8	K	E	4.4	0.8	84.1	12.0
P0AF36	9616.6	G	U	T	A	CID	LIT	5	66.7	NNSLSQEVQNAQHQREELER	2409.2	K	E	2.9	0.0	40.9	12.6
P0AF36	9616.6	G	U	T	A	CID	LIT	5	66.7	VQQAIDTITLLQMEIEELKEK	2472.3	K	N	6.0	0.6	101.0	12.0
P0AF36	9616.6	G	T	T	A	CID	LIT	4	59.3	LQALLGR	770.5	R	M	2.4	0.2	36.4	12.3
P0AF36	9616.6	G	T	T	A	CID	LIT	4	59.3	NNSLSQEVQNAQHQR	1752.8	K	E	2.0	0.7	0.0	0.0
P0AF36	9616.6	G	T	T	A	CID	LIT	4	59.3	NNSLSQEVQNAQHQREELER	2409.2	K	E	2.7	0.0	38.4	12.3
P0AF36	9616.6	G	T	T	A	CID	LIT	4	59.3	VQQAIDTITLLQMEIEELKEK	2472.3	K	N	5.2	0.6	84.2	12.6
P0AF36	9616.6	G	U	T	B	CID	LIT	5	66.7	EELERENNHLK	1410.7	R	E	3.1	0.8	39.0	14.1
P0AF36	9616.6	G	U	T	B	CID	LIT	5	66.7	LQALLGR	770.5	R	M	2.2	0.1	31.2	12.3
P0AF36	9616.6	G	U	T	B	CID	LIT	5	66.7	NNSLSQEVQNAQHQR	1752.8	K	E	3.7	0.7	49.8	12.8
P0AF36	9616.6	G	U	T	B	CID	LIT	5	66.7	NNSLSQEVQNAQHQREELER	2409.2	K	E	2.4	0.0	43.4	11.1
P0AF36	9616.6	G	U	T	B	CID	LIT	5	66.7	VQQAIDTITLLQMEIEELKEK	2472.3	K	N	3.3	0.0	24.7	12.0
P0AF36	9616.6	G	U	A	B	CID	LIT	2	34.6	EKLEAKVQQAI	1256.7	F	D	3.5	0.6	25.2	13.4
P0AF36	9616.6	G	U	A	B	CID	LIT	2	34.6	EKNNSLSQEVQNAQHQR	2010.0	K	E	4.7	0.9	27.7	15.6
P0AF36	9616.6	S	U	T	A	CID	LIT	2	33.3	LQALLGR	770.5	R	M	1.9	0.0	31.8	13.4
P0AF36	9616.6	S	U	T	A	CID	LIT	2	33.3	NNSLSQEVQNAQHQREELER	2409.2	K	E	2.7	0.6	4.4	18.1
P0AF36	9616.6	S	U	T	B	CID	LIT	2	34.6	LQALLGR	770.5	R	M	1.9	0.6	28.7	13.4
P0AF36	9616.6	S	U	T	B	CID	LIT	2	34.6	VQQAIDTITLLQMEIEELKEK	2472.3	K	N	2.7	0.0	29.1	15.3
P0AF36	9616.6	S	U	T	C	CID	LIT	2	33.3	LQALLGR	770.5	R	M	1.6	0.4	23.6	13.4
P0AF36	9616.6	S	U	T	C	CID	LIT	2	33.3	NNSLSQEVQNAQHQREELER	2409.2	K	E	3.2	0.0	43.7	17.8
P0AF36	9616.6	S	U	T	B	ETD	LIT	3	33.3	LQALLGR	770.5	R	M	2.2	0.1	33.9	13.4
P0AF36	9616.6	S	U	T	B	ETD	LIT	3	33.3	NNSLSQEVQNAQHQR	1752.8	K	E	2.5	0.2	56.1	17.7
P0AF36	9616.6	S	U	T	B	ETD	LIT	3	33.3	NNSLSQEVQNAQHQREELER	2409.2	K	E	2.4	0.0	50.7	18.0
P68688	9666.8	G	U	T	A	CID	LIT	3	42.4	AEGITKEDLQQK	1359.7	R	A	4.2	0.7	44.7	13.2
P68688	9666.8	G	U	T	A	CID	LIT	3	42.4	LSNERDDFQYQYVDIR	2061.0	K	A	3.9	0.6	42.7	9.0
P68688	9666.8	G	U	T	A	CID	LIT	3	42.4	MQTVIFGR	951.5	-	S	2.2	0.0	28.9	12.6
P68688	9666.8	G	T	T	A	CID	LIT	2	32.9	AEGITKEDLQQK	1359.7	R	A	3.9	0.5	52.8	13.2
P68688	9666.8	G	T	T	A	CID	LIT	2	32.9	LSNERDDFQYQYVDIR	2061.0	K	A	3.6	0.0	25.5	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68688	9666.8	G	U	T	B	CID	LIT	4	51.8	AEGITKEDLQQK	1359.7	R	A	4.4	0.6	55.5	13.0
P68688	9666.8	G	U	T	B	CID	LIT	4	51.8	LSNERDDFQYQYVDIR	2061.0	K	A	3.1	0.7	27.7	9.0
P68688	9666.8	G	U	T	B	CID	LIT	4	51.8	MQTVIFGR	951.5	-	S	2.5	0.0	47.8	12.6
P68688	9666.8	G	U	T	B	CID	LIT	4	51.8	SGCPYCVR	998.4	R	A	1.9	0.0	36.1	6.0
P68688	9666.8	G	T	A	B	CID	LIT	3	43.5	DIRAEGITKE	1131.6	V	D	3.0	0.2	21.2	15.8
P68688	9666.8	G	T	A	B	CID	LIT	3	43.5	DQQHIGGYT	1018.5	V	D	2.0	0.0	23.8	9.5
P68688	9666.8	G	T	A	B	CID	LIT	3	43.5	MQTVIFGRSGCPYCVRAK	2130.0	-	D	3.1	0.9	23.9	15.8
P68688	9666.8	G	U	A	B	CID	LIT	6	85.9	DDFQYQYV	1077.5	R	D	2.3	0.0	32.3	9.0
P68688	9666.8	G	U	A	B	CID	LIT	6	85.9	DIRAEGITKE	1131.6	V	D	2.1	0.0	15.9	15.2
P68688	9666.8	G	U	A	B	CID	LIT	6	85.9	DLAEKLSNER	1174.6	K	D	3.0	0.4	40.5	16.9
P68688	9666.8	G	U	A	B	CID	LIT	6	85.9	DLQQKAGKPVETVPQIFV	1997.1	E	D	3.5	0.6	24.2	12.0
P68688	9666.8	G	U	A	B	CID	LIT	6	85.9	DQQHIGGYT	1018.5	V	D	2.3	0.0	21.6	10.4
P68688	9666.8	G	U	A	B	CID	LIT	6	85.9	MQTVIFGRSGCPYCVRAK	2130.0	-	D	2.6	0.6	23.0	15.8
P68688	9666.8	S	U	T	C	CID	LIT	2	32.9	AEGITKEDLQQK	1359.7	R	A	3.8	0.5	45.7	18.1
P68688	9666.8	S	U	T	C	CID	LIT	2	32.9	LSNERDDFQYQYVDIR	2061.0	K	A	3.9	0.4	29.6	17.3
P0A7U7	9666.9	G	U	T	A	CID	LIT	2	25.3	AFNEMQPIVDR	1319.6	K	Q	4.2	0.0	62.3	13.4
P0A7U7	9666.9	G	U	T	A	CID	LIT	2	25.3	HKANLTAQINK	1237.7	R	L	3.8	0.7	53.5	9.0
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	AFNEMQPIVDR	1319.6	K	Q	2.8	0.6	52.2	13.4
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	AIQSEK	675.4	R	A	1.2	0.5	16.4	13.6
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	ANLTAQINK	972.5	K	L	3.1	0.7	43.3	15.6
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	ANLTAQINKLA	1156.7	K	-	2.6	0.4	16.1	11.5
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	HKANLTAQINK	1237.7	R	L	4.2	0.7	47.2	9.0
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	KVYAAIEAGDK	1164.6	K	A	4.0	0.7	64.1	13.0
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	VYAAIEAGDK	1036.5	K	A	3.2	0.5	33.9	14.5
P0A7U7	9666.9	G	T	T	A	CID	LIT	8	52.9	VYAAIEAGDKAAAQK	1505.8	K	A	5.5	0.7	69.2	14.1
P0A7U7	9666.9	S	U	T	A	CID	LIT	2	25.3	AFNEMQPIVDR	1319.6	K	Q	2.3	0.3	7.9	15.8
P0A7U7	9666.9	S	U	T	A	CID	LIT	2	25.3	HKANLTAQINK	1237.7	R	L	3.1	0.3	28.1	12.3
P0A7U7	9666.9	S	U	T	B	CID	LIT	2	25.3	AFNEMQPIVDR	1319.6	K	Q	2.0	0.2	1.4	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7U7	9666.9	S	U	T	B	CID	LIT	2	25.3	HKANLTAQINK	1237.7	R	L	3.4	0.5	35.3	13.0
P0A7U7	9666.9	S	U	T	C	CID	LIT	2	25.3	AFNEMQPIVDR	1319.6	K	Q	1.8	0.4	0.0	0.0
P0A7U7	9666.9	S	U	T	C	CID	LIT	2	25.3	HKANLTAQINK	1237.7	R	L	3.8	0.0	38.5	11.1
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	FVKHPIYGK	1088.6	R	F	2.5	0.8	37.7	14.1
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	LHVHDENNECGIGDVVEIR	2205.0	K	E	5.4	0.8	96.3	10.0
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	LHVHDENNECGIGDVVEIRECRPLSK	3075.5	K	T	2.3	0.0	33.0	10.4
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	SIVVAIER	886.5	K	F	2.9	0.3	34.8	14.9
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	SWTLVR	761.4	K	V	1.5	0.4	17.4	14.3
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	TDKIR	632.4	M	T	0.0	0.0	32.6	18.8
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	TKSWTLVR	990.6	K	V	2.9	0.3	24.3	14.1
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	TTKLHVHDENNECGIGDVVEIR	2535.2	R	E	8.2	0.7	82.5	12.3
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	VVEKAVL	757.5	R	-	2.2	0.7	25.5	11.5
P0AG63	9686.3	G	U	T	A	CID	LIT	10	88.1	VVSDKMEK	935.5	R	S	2.3	0.7	43.5	13.6
P0AG63	9686.3	G	T	T	B	CID	LIT	2	19.0	SIVVAIER	886.5	K	F	2.0	0.3	0.0	0.0
P0AG63	9686.3	G	T	T	B	CID	LIT	2	19.0	VVSDKMEK	935.5	R	S	2.5	0.8	34.3	13.8
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	ECRPLSK	889.5	R	T	2.5	0.0	24.3	14.8
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	FVKHPIYGK	1088.6	R	F	2.6	0.7	24.6	14.1
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	HPIYGK	714.4	K	F	2.0	0.0	15.9	7.0
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	LHVHDENNECGIGDVVEIR	2205.0	K	E	5.8	0.0	58.0	9.5
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	SIVVAIER	886.5	K	F	2.7	0.3	53.8	14.9
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	SWTLVR	761.4	K	V	1.2	0.3	15.5	14.8
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	TDKIR	632.4	M	T	0.0	0.0	36.0	18.8
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	TKSWTLVR	990.6	K	V	2.3	0.6	27.6	14.1
P0AG63	9686.3	G	U	T	B	CID	LIT	9	76.2	VVSDKMEK	935.5	R	S	2.6	0.0	31.8	13.4
P0AG63	9686.3	G	U	A	B	CID	LIT	3	33.3	DENNECGIG	1007.4	H	D	2.7	0.0	23.7	7.8
P0AG63	9686.3	G	U	A	B	CID	LIT	3	33.3	DVVEIR	730.4	G	E	1.8	0.3	13.6	19.5
P0AG63	9686.3	G	U	A	B	CID	LIT	3	33.3	TDKIRTLQGRVVS	1472.9	M	D	0.0	0.0	24.1	10.4
P0AG63	9686.3	S	U	T	A	CID	LIT	7	63.1	FVKHPIYGK	1088.6	R	F	2.4	0.7	19.4	16.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG63	9686.3	S	U	T	A	CID	LIT	7	63.1	HPIYGK	714.4	K	F	2.3	0.8	13.1	9.5
P0AG63	9686.3	S	U	T	A	CID	LIT	7	63.1	LHVHDENNECGIGDVVEIR	2205.0	K	E	7.3	0.7	95.6	16.9
P0AG63	9686.3	S	U	T	A	CID	LIT	7	63.1	SIVVAIER	886.5	K	F	2.9	0.2	31.5	17.4
P0AG63	9686.3	S	U	T	A	CID	LIT	7	63.1	SWTLVR	761.4	K	V	1.3	0.0	24.8	15.7
P0AG63	9686.3	S	U	T	A	CID	LIT	7	63.1	TTKLHVHDENNECGIGDVVEIR	2535.2	R	E	6.9	0.5	69.8	19.2
P0AG63	9686.3	S	U	T	A	CID	LIT	7	63.1	VVSDKMEK	935.5	R	S	2.3	0.7	22.2	16.1
P0AG63	9686.3	S	U	T	B	CID	LIT	6	59.5	HPIYGK	714.4	K	F	2.0	0.7	13.1	9.0
P0AG63	9686.3	S	U	T	B	CID	LIT	6	59.5	LHVHDENNECGIGDVVEIR	2205.0	K	E	7.3	0.7	97.9	16.9
P0AG63	9686.3	S	U	T	B	CID	LIT	6	59.5	SIVVAIER	886.5	K	F	2.4	0.3	33.4	17.5
P0AG63	9686.3	S	U	T	B	CID	LIT	6	59.5	SWTLVR	761.4	K	V	1.2	0.6	28.1	15.7
P0AG63	9686.3	S	U	T	B	CID	LIT	6	59.5	TTKLHVHDENNECGIGDVVEIR	2535.2	R	E	4.6	0.5	66.3	18.9
P0AG63	9686.3	S	U	T	B	CID	LIT	6	59.5	VVSDKMEK	935.5	R	S	2.2	0.7	48.7	16.1
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	ECRPLSK	889.5	R	T	2.2	0.2	18.2	17.2
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	FVKHPIYGK	1088.6	R	F	2.4	0.6	28.2	16.8
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	LHVHDENNECGIGDVVEIR	2205.0	K	E	7.2	0.7	98.0	16.9
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	LHVHDENNECGIGDVVEIRECRPLSK	3075.5	K	T	2.6	0.2	4.6	19.0
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	SIVVAIER	886.5	K	F	2.8	0.3	36.1	17.5
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	SWTLVR	761.4	K	V	1.2	0.6	30.9	15.7
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	TTKLHVHDENNECGIGDVVEIR	2535.2	R	E	5.6	0.6	47.2	19.1
P0AG63	9686.3	S	U	T	C	CID	LIT	8	71.4	VVSDKMEK	935.5	R	S	2.0	0.6	33.5	16.2
P0AG63	9686.3	S	U	T	A	CID	FT	2	26.2	LHVHDENNECGIGDVVEIR	2205.0	K	E	3.6	0.0	40.6	17.0
P0AG63	9686.3	S	U	T	A	CID	FT	2	26.2	TTKLHVHDENNECGIGDVVEIR	2535.2	R	E	2.7	0.0	22.8	19.0
P0AG63	9686.3	S	U	T	B	CID	FT	2	32.1	LHVHDENNECGIGDVVEIR	2205.0	K	E	6.6	0.0	94.2	16.7
P0AG63	9686.3	S	U	T	B	CID	FT	2	32.1	SIVVAIER	886.5	K	F	2.2	0.3	30.5	17.4
P0AG63	9686.3	S	U	T	C	CID	FT	3	41.7	LHVHDENNECGIGDVVEIR	2205.0	K	E	5.2	0.0	106.0	16.8
P0AG63	9686.3	S	U	T	C	CID	FT	3	41.7	SIVVAIER	886.5	K	F	2.6	0.3	32.2	17.2
P0AG63	9686.3	S	U	T	C	CID	FT	3	41.7	VVSDKMEK	935.5	R	S	1.3	0.0	25.4	16.2
P0AG63	9686.3	S	U	T	A	ETD	LIT	6	63.1	FVKHPIYGK	1088.6	R	F	4.1	0.6	30.6	16.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG63	9686.3	S	U	T	A	ETD	LIT	6	63.1	HPIYGK	714.4	K	F	2.0	0.0	31.3	7.8
P0AG63	9686.3	S	U	T	A	ETD	LIT	6	63.1	LHVHDENNECGIGDVVEIR	2205.0	K	E	5.8	0.0	30.4	16.8
P0AG63	9686.3	S	U	T	A	ETD	LIT	6	63.1	SIVVAIER	886.5	K	F	2.5	0.3	0.0	0.0
P0AG63	9686.3	S	U	T	A	ETD	LIT	6	63.1	SWTLVR	761.4	K	V	0.0	0.0	35.6	15.7
P0AG63	9686.3	S	U	T	A	ETD	LIT	6	63.1	TTKLHVHDENNECGIGDVVEIR	2535.2	R	E	4.7	0.0	58.2	18.8
P0AG63	9686.3	S	U	T	A	ETD	LIT	6	63.1	VVSDKMEK	935.5	R	S	2.2	0.6	31.9	16.2
P0AG63	9686.3	S	U	T	B	ETD	LIT	6	61.9	FVKHPIYGK	1088.6	R	F	4.0	0.6	36.5	16.2
P0AG63	9686.3	S	U	T	B	ETD	LIT	6	61.9	HPIYGK	714.4	K	F	1.8	0.0	31.0	7.8
P0AG63	9686.3	S	U	T	B	ETD	LIT	6	61.9	LHVHDENNECGIGDVVEIR	2205.0	K	E	5.9	0.6	0.0	0.0
P0AG63	9686.3	S	U	T	B	ETD	LIT	6	61.9	SIVVAIER	886.5	K	F	2.7	0.3	0.0	0.0
P0AG63	9686.3	S	U	T	B	ETD	LIT	6	61.9	SWTLVR	761.4	K	V	1.8	0.6	37.8	16.0
P0AG63	9686.3	S	U	T	B	ETD	LIT	6	61.9	TKSWTLVR	990.6	K	V	2.0	0.2	10.5	15.4
P0AG63	9686.3	S	U	T	B	ETD	LIT	6	61.9	VVSDKMEK	935.5	R	S	3.1	0.4	36.9	16.2
P0AG63	9686.3	S	U	T	C	ETD	LIT	6	59.5	FVKHPIYGK	1088.6	R	F	4.0	0.6	41.2	15.9
P0AG63	9686.3	S	U	T	C	ETD	LIT	6	59.5	HPIYGK	714.4	K	F	1.7	0.0	31.8	7.0
P0AG63	9686.3	S	U	T	C	ETD	LIT	6	59.5	LHVHDENNECGIGDVVEIR	2205.0	K	E	8.1	0.0	56.7	16.8
P0AG63	9686.3	S	U	T	C	ETD	LIT	6	59.5	SIVVAIER	886.5	K	F	2.5	0.3	53.7	17.5
P0AG63	9686.3	S	U	T	C	ETD	LIT	6	59.5	SWTLVR	761.4	K	V	1.5	0.0	30.7	15.7
P0AG63	9686.3	S	U	T	C	ETD	LIT	6	59.5	VVSDKMEK	935.5	R	S	3.4	0.4	41.9	16.2
P0AG63	9686.3	S	U	T	B	ETD	FT	3	29.8	FVKHPIYGK	1088.6	R	F	2.3	0.0	41.8	16.2
P0AG63	9686.3	S	U	T	B	ETD	FT	3	29.8	SIVVAIER	886.5	K	F	0.0	0.0	26.9	17.5
P0AG63	9686.3	S	U	T	B	ETD	FT	3	29.8	VVSDKMEK	935.5	R	S	1.0	0.0	23.9	16.2
P0AG63	9686.3	S	U	T	C	ETD	FT	4	28.6	SIVVAIER	886.5	K	F	1.2	0.0	53.3	17.5
P0AG63	9686.3	S	U	T	C	ETD	FT	4	28.6	SWTLVR	761.4	K	V	0.7	0.0	48.6	15.7
P0AG63	9686.3	S	U	T	C	ETD	FT	4	28.6	TKSWTLVR	990.6	K	V	2.3	0.0	42.0	15.4
P0AG63	9686.3	S	U	T	C	ETD	FT	4	28.6	VVSDKMEK	935.5	R	S	2.6	0.0	37.5	16.2
P0AG63	9686.3	S	U	T	A	ETD+CID	LIT	2	42.9	FVKHPIYGK	1088.6	R	F	2.8	0.0	28.8	15.2
P0AG63	9686.3	S	U	T	A	ETD+CID	LIT	2	42.9	HPIYGK	714.4	K	F	1.9	0.6	13.3	7.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG63	9686.3	S	U	T	A	ETD+CID	LIT	2	42.9	LHVHDENNECGIGDVVEIR	2205.0	K	E	7.1	0.7	96.4	17.2
P0AG63	9686.3	S	U	T	A	ETD+CID	LIT	2	42.9	VVSDKMEK	935.5	R	S	0.6	0.0	23.6	16.2
P0AG63	9686.3	S	U	T	C	ETD+CID	LIT	3	52.4	FVKHPIYGK	1088.6	R	F	2.8	0.4	0.0	0.0
P0AG63	9686.3	S	U	T	C	ETD+CID	LIT	3	52.4	HPIYGK	714.4	K	F	2.2	0.8	13.2	7.0
P0AG63	9686.3	S	U	T	C	ETD+CID	LIT	3	52.4	LHVHDENNECGIGDVVEIR	2205.0	K	E	0.0	0.0	96.1	16.9
P0AG63	9686.3	S	U	T	C	ETD+CID	LIT	3	52.4	SIVVAIER	886.5	K	F	2.5	0.3	0.0	0.0
P0AG63	9686.3	S	U	T	C	ETD+CID	LIT	3	52.4	VVSDKMEK	935.5	R	S	1.6	0.0	41.8	16.1
P52102	9773.1	G	T	A	B	CID	LIT	2	41.9	DKCTECVGHYETPTCQKVCPIPNTIVK	3234.5	S	D	4.9	0.0	33.6	8.5
P52102	9773.1	G	T	A	B	CID	LIT	2	41.9	DKFVLMHHA	1097.6	W	D	2.5	0.5	11.6	14.3
P0A8J4	9809.2	G	U	T	A	CID	LIT	5	63.2	HAPGDYTPTVKPSSK	1584.8	R	G	3.5	0.8	15.4	11.1
P0A8J4	9809.2	G	U	T	A	CID	LIT	5	63.2	IDIVR	615.4	K	M	1.6	0.1	29.9	17.8
P0A8J4	9809.2	G	U	T	A	CID	LIT	5	63.2	LNELLEFPTPFTYK	1711.9	K	V	4.2	0.6	52.0	13.0
P0A8J4	9809.2	G	U	T	A	CID	LIT	5	63.2	TKLNELLEFPTPFTYK	1941.0	K	V	5.9	0.8	62.1	10.0
P0A8J4	9809.2	G	U	T	A	CID	LIT	5	63.2	VMGQALPELVDQVVEVVQR	2109.1	K	H	6.2	0.8	102.0	11.8
P0A8J4	9809.2	G	U	T	B	CID	LIT	4	60.9	HAPGDYTPTVKPSSK	1584.8	R	G	3.5	0.0	52.2	11.1
P0A8J4	9809.2	G	U	T	B	CID	LIT	4	60.9	IDIVR	615.4	K	M	1.9	0.1	18.9	17.8
P0A8J4	9809.2	G	U	T	B	CID	LIT	4	60.9	LNELLEFPTPFTYK	1711.9	K	V	5.1	0.6	42.8	12.6
P0A8J4	9809.2	G	U	T	B	CID	LIT	4	60.9	VMGQALPELVDQVVEVVQR	2109.1	K	H	5.5	0.8	89.3	11.8
P0A8J4	9809.2	G	T	A	B	CID	LIT	2	14.9	DIVRMVL	845.5	I	-	1.8	0.7	20.5	11.8
P0A8J4	9809.2	G	T	A	B	CID	LIT	2	14.9	EELGKI	688.4	Y	D	1.8	0.1	8.9	19.8
P0A8J4	9809.2	G	U	A	B	CID	LIT	4	55.2	DIVRMVL	845.5	I	-	2.0	0.5	21.3	11.8
P0A8J4	9809.2	G	U	A	B	CID	LIT	4	55.2	DQVVEVVQRHAPG	1433.8	V	D	3.6	0.6	55.8	16.0
P0A8J4	9809.2	G	U	A	B	CID	LIT	4	55.2	EFPTPFTYKVMGQALPELV	2167.1	L	D	2.7	0.4	22.8	13.6
P0A8J4	9809.2	G	U	A	B	CID	LIT	4	55.2	MKTKLNELL	1089.6	-	E	2.3	0.8	22.7	10.0
P0A8J4	9809.2	S	U	T	A	CID	LIT	4	57.5	HAPGDYTPTVKPSSK	1584.8	R	G	3.3	0.7	35.0	15.8
P0A8J4	9809.2	S	U	T	A	CID	LIT	4	57.5	LNELLEFPTPFTYK	1711.9	K	V	5.0	0.6	53.5	16.9
P0A8J4	9809.2	S	U	T	A	CID	LIT	4	57.5	TKLNELLEFPTPFTYK	1941.0	K	V	5.6	0.6	62.1	17.0
P0A8J4	9809.2	S	U	T	A	CID	LIT	4	57.5	VMGQALPELVDQVVEVVQR	2109.1	K	H	6.1	0.7	115.0	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8J4	9809.2	S	U	T	B	CID	LIT	4	57.5	HAPGDYTPTVKPSSK	1584.8	R	G	4.4	0.8	32.9	15.6
P0A8J4	9809.2	S	U	T	B	CID	LIT	4	57.5	LNELLEFPTPFTYK	1711.9	K	V	5.0	0.7	61.9	16.6
P0A8J4	9809.2	S	U	T	B	CID	LIT	4	57.5	TKLNELLEFPTPFTYK	1941.0	K	V	4.6	0.5	33.5	17.1
P0A8J4	9809.2	S	U	T	B	CID	LIT	4	57.5	VMGQALPELVDQVVEVVQR	2109.1	K	H	6.9	0.6	97.6	15.3
P0A8J4	9809.2	S	U	T	C	CID	LIT	3	55.2	HAPGDYTPTVKPSSK	1584.8	R	G	3.8	0.0	55.2	15.3
P0A8J4	9809.2	S	U	T	C	CID	LIT	3	55.2	LNELLEFPTPFTYK	1711.9	K	V	4.6	0.6	59.7	17.2
P0A8J4	9809.2	S	U	T	C	CID	LIT	3	55.2	VMGQALPELVDQVVEVVQR	2109.1	K	H	5.5	0.8	106.0	16.0
P0A8J4	9809.2	S	U	T	A	ETD	LIT	4	57.5	HAPGDYTPTVKPSSK	1584.8	R	G	5.2	0.7	54.0	15.6
P0A8J4	9809.2	S	U	T	A	ETD	LIT	4	57.5	LNELLEFPTPFTYK	1711.9	K	V	2.5	0.6	26.9	16.7
P0A8J4	9809.2	S	U	T	A	ETD	LIT	4	57.5	TKLNELLEFPTPFTYK	1941.0	K	V	5.3	0.6	70.3	17.0
P0A8J4	9809.2	S	U	T	A	ETD	LIT	4	57.5	VMGQALPELVDQVVEVVQR	2109.1	K	H	3.3	0.0	48.5	16.0
P0A8J4	9809.2	S	U	T	B	ETD	LIT	3	55.2	HAPGDYTPTVKPSSK	1584.8	R	G	0.0	0.0	50.8	15.6
P0A8J4	9809.2	S	U	T	B	ETD	LIT	3	55.2	LNELLEFPTPFTYK	1711.9	K	V	3.0	0.0	21.4	16.7
P0A8J4	9809.2	S	U	T	B	ETD	LIT	3	55.2	VMGQALPELVDQVVEVVQR	2109.1	K	H	5.5	0.7	51.3	16.0
P0A8J4	9809.2	S	U	T	C	ETD	LIT	2	39.1	HAPGDYTPTVKPSSK	1584.8	R	G	4.7	0.7	46.2	15.2
P0A8J4	9809.2	S	U	T	C	ETD	LIT	2	39.1	VMGQALPELVDQVVEVVQR	2109.1	K	H	3.6	0.9	62.3	15.2
P0A8J4	9809.2	S	U	T	C	ETD	FT	2	33.3	HAPGDYTPTVKPSSK	1584.8	R	G	2.9	0.0	26.5	15.6
P0A8J4	9809.2	S	U	T	C	ETD	FT	2	33.3	LNELLEFPTPFTYK	1711.9	K	V	2.9	0.0	40.1	17.1
P0A8J4	9809.2	S	U	T	B	ETD+CID	LIT	2	37.9	LNELLEFPTPFTYK	1711.9	K	V	0.0	0.0	36.8	16.6
P0A8J4	9809.2	S	U	T	B	ETD+CID	LIT	2	37.9	VMGQALPELVDQVVEVVQR	2109.1	K	H	0.0	0.0	94.2	15.2
P0A8J4	9809.2	S	U	T	A	ETD+CID	LIT	4	57.5	HAPGDYTPTVKPSSK	1584.8	R	G	0.0	0.0	56.9	15.8
P0A8J4	9809.2	S	U	T	A	ETD+CID	LIT	4	57.5	LNELLEFPTPFTYK	1711.9	K	V	4.6	0.6	50.0	16.5
P0A8J4	9809.2	S	U	T	A	ETD+CID	LIT	4	57.5	TKLNELLEFPTPFTYK	1941.0	K	V	5.5	0.6	55.2	17.3
P0A8J4	9809.2	S	U	T	A	ETD+CID	LIT	4	57.5	VMGQALPELVDQVVEVVQR	2109.1	K	H	5.0	0.7	90.0	16.0
P0A8J4	9809.2	S	U	T	B	ETD+CID	LIT	3	40.2	LNELLEFPTPFTYK	1711.9	K	V	3.9	0.6	36.8	16.6
P0A8J4	9809.2	S	U	T	B	ETD+CID	LIT	3	40.2	TKLNELLEFPTPFTYK	1941.0	K	V	2.9	0.4	15.4	17.0
P0A8J4	9809.2	S	U	T	B	ETD+CID	LIT	3	40.2	VMGQALPELVDQVVEVVQR	2109.1	K	H	6.5	0.6	94.2	15.2
P0A8J4	9809.2	S	U	T	C	ETD+CID	LIT	2	39.1	HAPGDYTPTVKPSSK	1584.8	R	G	1.9	0.6	10.5	15.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8J4	9809.2	S	U	T	C	ETD+CID	LIT	2	39.1	VMGQALPELVDQVVEVVQR	2109.1	K	H	4.9	0.6	38.8	15.2
P0A8J4	9809.2	S	U	T	B	HCD	FT	2	37.9	LNELLEFPTPFTYK	1711.9	K	V	0.0	0.0	36.8	16.6
P0A8J4	9809.2	S	U	T	B	HCD	FT	2	37.9	VMGQALPELVDQVVEVVQR	2109.1	K	H	0.0	0.0	94.2	15.2
P0ABF4	9847.4	G	T	T	A	CID	LIT	2	26.8	AATDAGAAAAQR	1073.5	K	I	4.2	0.5	82.6	10.4
P0ABF4	9847.4	G	T	T	A	CID	LIT	2	26.8	GLVALIEASDAMVK	1416.8	R	A	3.0	0.0	44.6	10.4
P0ABF4	9847.4	G	T	T	B	CID	LIT	2	22.7	AATDAGAAAAQR	1073.5	K	I	4.2	0.6	86.7	10.4
P0ABF4	9847.4	G	T	T	B	CID	LIT	2	22.7	MEALGMIETR	1150.6	-	G	3.1	0.7	43.2	12.3
P0ABF4	9847.4	G	T	A	B	CID	LIT	3	37.1	DAGAAAAQRIGELVSVHVIPRPHG	2421.3	T	D	2.5	0.7	25.5	14.0
P0ABF4	9847.4	G	T	A	B	CID	LIT	3	37.1	DLEEVFPIGLKG	1316.7	G	D	3.6	0.5	42.6	16.4
P0ABF4	9847.4	G	T	A	B	CID	LIT	3	37.1	EVFPIGLKG	959.6	E	D	1.5	0.6	25.1	10.0
P0ABF4	9847.4	G	U	A	B	CID	LIT	2	12.4	DLEEVFPIGLKG	1316.7	G	D	3.5	0.5	27.7	15.8
P0ABF4	9847.4	G	U	A	B	CID	LIT	2	12.4	EVFPIGLKG	959.6	E	D	1.3	0.4	20.9	14.0
P37590	9852.4	G	U	T	A	CID	LIT	3	43.2	MEWLVKK	933.5	-	S	1.7	0.4	29.4	14.8
P37590	9852.4	G	U	T	A	CID	LIT	3	43.2	VGDLLSPLQNALYCINR	1946.0	K	E	4.8	0.0	52.8	11.5
P37590	9852.4	G	U	T	A	CID	LIT	3	43.2	VLSASSYSPDEWER	1625.7	K	Q	4.1	0.8	53.9	7.8
P37590	9852.4	G	U	T	B	CID	LIT	5	64.8	EKLHTVK	854.5	R	V	1.9	0.0	25.6	9.5
P37590	9852.4	G	U	T	B	CID	LIT	5	64.8	HVLMLCDAGGAIK	1384.7	R	M	3.8	0.0	60.7	11.5
P37590	9852.4	G	U	T	B	CID	LIT	5	64.8	MEWLVK	805.4	-	K	2.1	0.6	29.8	15.6
P37590	9852.4	G	U	T	B	CID	LIT	5	64.8	VGDLLSPLQNALYCINR	1946.0	K	E	4.8	0.0	67.5	11.5
P37590	9852.4	G	U	T	B	CID	LIT	5	64.8	VLSASSYSPDEWER	1625.7	K	Q	3.2	0.0	34.0	7.8
P37590	9852.4	G	U	A	B	CID	LIT	5	54.5	DAGGAIKMIAEVKS	1389.7	C	D	2.5	0.5	15.7	14.0
P37590	9852.4	G	U	A	B	CID	LIT	5	54.5	DEWERQCKVAGKTQ	1734.8	P	-	3.1	0.6	22.5	14.1
P37590	9852.4	G	U	A	B	CID	LIT	5	54.5	DFAVKVG	735.4	S	D	2.3	0.3	29.2	12.6
P37590	9852.4	G	U	A	B	CID	LIT	5	54.5	ERQCKVAGKTQ	1304.7	W	-	3.4	0.6	27.4	13.2
P37590	9852.4	G	U	A	B	CID	LIT	5	54.5	MEWLVKKSCCNKQ	1710.8	-	D	3.6	0.7	33.6	15.4
P37590	9852.4	S	U	T	B	CID	LIT	2	35.2	VGDLLSPLQNALYCINR	1947.0	K	E	3.5	0.4	37.3	17.9
P37590	9852.4	S	U	T	B	CID	LIT	2	35.2	VLSASSYSPDEWER	1625.7	K	Q	4.4	0.7	54.6	13.0
P37590	9852.4	S	U	T	C	CID	LIT	3	50.0	HVLMLCDAGGAIK	1384.7	R	M	3.7	0.8	44.2	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P37590	9852.4	S	U	T	C	CID	LIT	3	50.0	VGDLLSPLQNALYCINR	1947.0	K	E	4.2	0.6	50.8	18.2
P37590	9852.4	S	U	T	C	CID	LIT	3	50.0	VLSASSYSPDEWER	1625.7	K	Q	4.0	0.7	59.0	12.6
P75694	9877.8	G	U	T	A	CID	LIT	3	62.6	AEFEKVESQYEK	1486.7	K	I	4.2	0.5	48.8	11.8
P75694	9877.8	G	U	T	A	CID	LIT	3	62.6	GADVLVLTSGQTDNKIHGTANIYK	2515.3	K	K	4.4	0.0	35.7	12.3
P75694	9877.8	G	U	T	A	CID	LIT	3	62.6	IGDISTSNEMSTADAKEDLIK	2238.1	K	K	3.8	0.0	28.0	12.3
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	ADEKGADVLVLTSGQTDNK	1961.0	K	I	5.3	0.0	54.0	13.0
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	AEFEKVESQYEK	1486.7	K	I	4.1	0.6	59.3	11.8
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	GADVLVLTSGQTDNK	1517.8	K	I	5.0	0.9	88.2	12.3
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	GADVLVLTSGQTDNKIHGTANIYK	2515.3	K	K	4.3	0.7	36.5	11.8
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	IGDISTSNEMSTADAK	1639.7	K	E	4.4	0.9	69.0	10.8
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	IGDISTSNEMSTADAKEDLIK	2238.1	K	K	4.9	0.6	84.3	12.3
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	IHGTANIYK	1016.6	K	K	2.7	0.8	26.3	14.3
P75694	9877.8	G	T	T	A	CID	LIT	8	68.1	IHGTANIYKK	1144.6	K	-	3.1	0.8	36.6	13.8
P75694	9877.8	G	U	A	A	CID	LIT	4	49.5	DAKEDLIKKA	1130.6	A	D	3.5	0.6	28.5	13.0
P75694	9877.8	G	U	A	A	CID	LIT	4	49.5	DISTSNEMSTA	1171.5	G	D	2.4	0.7	10.9	9.0
P75694	9877.8	G	U	A	A	CID	LIT	4	49.5	DNKIHGTANIYKKK	1629.9	T	-	3.6	0.8	24.7	11.1
P75694	9877.8	G	U	A	A	CID	LIT	4	49.5	DVLVLTSGQTDNKIHGTANIYKKK	2643.4	A	-	4.4	0.6	32.0	12.3
P75694	9877.8	G	T	A	A	CID	LIT	5	49.5	DAKEDLIKKA	1130.6	A	D	3.3	0.7	35.0	13.6
P75694	9877.8	G	T	A	A	CID	LIT	5	49.5	DISTSNEMSTA	1155.5	G	D	2.9	0.8	43.9	10.4
P75694	9877.8	G	T	A	A	CID	LIT	5	49.5	DNKIHGTANIYKKK	1629.9	T	-	3.9	0.8	13.9	11.5
P75694	9877.8	G	T	A	A	CID	LIT	5	49.5	DVLVLTSGQT	1032.6	A	D	2.1	0.7	35.2	15.1
P75694	9877.8	G	T	A	A	CID	LIT	5	49.5	DVLVLTSGQTDNKIHGTANIYKKK	2643.4	A	-	2.4	0.7	0.0	0.0
P75694	9877.8	G	T	T	B	CID	LIT	4	39.6	AEFEKVESQYEK	1486.7	K	I	4.2	0.6	66.3	11.1
P75694	9877.8	G	T	T	B	CID	LIT	4	39.6	GADVLVLTSGQTDNK	1517.8	K	I	4.1	0.7	81.2	13.6
P75694	9877.8	G	T	T	B	CID	LIT	4	39.6	GADVLVLTSGQTDNKIHGTANIYK	2515.3	K	K	3.3	0.8	11.2	11.1
P75694	9877.8	G	T	T	B	CID	LIT	4	39.6	IHGTANIYK	1016.6	K	K	2.6	0.7	22.2	12.0
P75694	9877.8	G	U	T	B	CID	LIT	2	36.3	AEFEKVESQYEK	1486.7	K	I	3.6	0.6	53.1	11.5
P75694	9877.8	G	U	T	B	CID	LIT	2	36.3	IGDISTSNEMSTADAKEDLIK	2238.1	K	K	3.8	0.0	40.0	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P75694	9877.8	G	T	A	B	CID	LIT	4	38.5	DISTSNEMSTA	1155.5	G	D	2.9	0.4	12.0	10.8
P75694	9877.8	G	T	A	B	CID	LIT	4	38.5	DNKIHGTANIYKKK	1629.9	T	-	2.8	0.3	0.0	0.0
P75694	9877.8	G	T	A	B	CID	LIT	4	38.5	DVLVLTSGQT	1032.6	A	D	2.7	0.8	38.6	15.1
P75694	9877.8	G	T	A	B	CID	LIT	4	38.5	DVLVLTSGQTDNKIHGTANIYKKK	2643.4	A	-	3.9	0.0	23.9	12.3
P75694	9877.8	G	U	A	B	CID	LIT	3	38.5	DISTSNEMSTA	1155.5	G	D	3.3	0.0	48.1	10.4
P75694	9877.8	G	U	A	B	CID	LIT	3	38.5	DNKIHGTANIYKKK	1629.9	T	-	3.9	0.0	31.3	11.1
P75694	9877.8	G	U	A	B	CID	LIT	3	38.5	DVLVLTSGQT	1032.6	A	D	2.5	0.7	45.7	15.1
P75694	9877.8	S	U	T	C	ETD	LIT	2	24.2	IGDISTSNEMSTADAKEDLIK	2238.1	K	K	5.1	0.7	70.6	18.1
P75694	9877.8	S	U	T	C	ETD	LIT	2	24.2	IGDISTSNEMSTADAKEDLIKK	2366.2	K	A	6.4	0.0	66.6	18.2
P0AAN9	9919.9	G	U	T	A	CID	LIT	3	48.8	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	5.1	0.6	55.5	11.1
P0AAN9	9919.9	G	U	T	A	CID	LIT	3	48.8	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	5.8	0.0	66.2	11.1
P0AAN9	9919.9	G	U	T	A	CID	LIT	3	48.8	MKNLIAELLFK	1319.8	-	L	3.6	0.0	45.8	3.0
P0AAN9	9919.9	G	U	A	A	CID	LIT	2	30.2	DQQRLIDQVEGALY	1647.8	N	E	3.7	0.8	68.7	15.3
P0AAN9	9919.9	G	U	A	A	CID	LIT	2	30.2	DYVKKLLKHPRQ	1524.9	R	-	3.4	0.0	54.7	9.0
P0AAN9	9919.9	G	U	T	B	CID	LIT	5	64.0	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	3.8	0.0	58.9	10.8
P0AAN9	9919.9	G	U	T	B	CID	LIT	5	64.0	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	3.6	0.0	13.1	11.5
P0AAN9	9919.9	G	U	T	B	CID	LIT	5	64.0	LLKHPR	763.5	K	-	1.8	0.0	25.8	3.0
P0AAN9	9919.9	G	U	T	B	CID	LIT	5	64.0	NLIAELLFK	1060.6	K	L	2.2	0.0	15.8	7.0
P0AAN9	9919.9	G	U	T	B	CID	LIT	5	64.0	NMAQNDQQR	1104.5	R	L	2.5	0.0	31.4	7.8
P0AAN9	9919.9	G	U	A	B	CID	LIT	4	46.5	DQQRLI	772.4	N	D	1.7	0.0	20.1	16.6
P0AAN9	9919.9	G	U	A	B	CID	LIT	4	46.5	DQVEGALY	894.4	I	E	1.9	0.6	24.5	17.7
P0AAN9	9919.9	G	U	A	B	CID	LIT	4	46.5	DYVKKLLKHPRQ	1524.9	R	-	3.2	0.0	36.8	9.0
P0AAN9	9919.9	G	U	A	B	CID	LIT	4	46.5	EIIVTAMLRNMAQN	1603.8	L	D	4.2	0.7	24.9	14.8
P0AAN9	9919.9	S	U	T	A	CID	LIT	2	36.0	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	4.0	0.3	36.4	19.4
P0AAN9	9919.9	S	U	T	A	CID	LIT	2	36.0	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	3.8	0.0	26.6	18.6
P0AAN9	9919.9	S	U	T	B	CID	LIT	4	77.9	LAQKEEESKELCAQVEALEIIVTAMLR	3101.6	K	N	3.7	0.0	29.8	16.5
P0AAN9	9919.9	S	U	T	B	CID	LIT	4	77.9	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	5.1	0.5	43.1	19.3
P0AAN9	9919.9	S	U	T	B	CID	LIT	4	77.9	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	5.3	0.0	73.7	18.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAN9	9919.9	S	U	T	B	CID	LIT	4	77.9	NLIAELLFK	1060.6	K	L	2.0	0.7	37.1	9.5
P0AAN9	9919.9	S	U	T	C	CID	LIT	3	37.2	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	5.1	0.6	31.6	18.7
P0AAN9	9919.9	S	U	T	C	CID	LIT	3	37.2	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	3.6	0.0	18.1	18.5
P0AAN9	9919.9	S	U	T	C	CID	LIT	3	37.2	LIDQVEGALYEVKPDASIPDDDTELLRDYVKK	3647.9	R	L	3.6	0.8	0.0	0.0
P0AAN9	9919.9	S	U	T	B	ETD	LIT	2	36.0	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	4.6	0.0	53.4	19.3
P0AAN9	9919.9	S	U	T	B	ETD	LIT	2	36.0	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	0.0	0.0	26.0	18.6
P0AAN9	9919.9	S	U	T	C	ETD	LIT	2	36.0	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	2.5	0.0	23.9	19.4
P0AAN9	9919.9	S	U	T	C	ETD	LIT	2	36.0	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	0.0	0.0	23.7	19.2
P0AAN9	9919.9	S	U	T	C	ETD+CID	LIT	2	37.2	LIDQVEGALYEVKPDASIPDDDTELLR	3014.5	R	D	4.7	0.5	40.5	18.8
P0AAN9	9919.9	S	U	T	C	ETD+CID	LIT	2	37.2	LIDQVEGALYEVKPDASIPDDDTELLRDYVK	3519.8	R	K	4.9	0.0	58.9	19.1
P0AAN9	9919.9	S	U	T	C	ETD+CID	LIT	2	37.2	LIDQVEGALYEVKPDASIPDDDTELLRDYVKK	3647.9	R	L	3.0	0.2	9.6	18.1
P76227	9929.1	G	T	T	A	CID	LIT	2	22.2	AEGILLQCQR	1187.6	K	D	3.1	0.5	40.0	15.2
P76227	9929.1	G	T	T	A	CID	LIT	2	22.2	TLSTNPLVWR	1186.7	K	R	2.5	0.8	14.0	14.0
P64540	9982.2	G	U	T	A	CID	LIT	3	53.3	AIGAGELSPR	970.5	K	D	3.3	0.7	37.5	13.0
P64540	9982.2	G	U	T	A	CID	LIT	3	53.3	GHLTLAIAELESGDDHSAQAVHTTVSQSLEK	3244.6	R	A	3.6	0.0	38.1	11.1
P64540	9982.2	G	U	T	A	CID	LIT	3	53.3	MIAEFESR	982.5	-	I	2.5	0.0	22.7	12.0
P64540	9982.2	G	U	T	B	CID	LIT	2	19.6	AIGAGELSPR	970.5	K	D	2.7	0.7	29.3	13.0
P64540	9982.2	G	U	T	B	CID	LIT	2	19.6	MIAEFESR	982.5	-	I	2.9	0.9	44.3	12.3
P64540	9982.2	G	U	A	B	CID	LIT	2	23.9	DGMVDHASD	946.4	I	D	2.8	0.7	23.4	9.0
P64540	9982.2	G	U	A	B	CID	LIT	2	23.9	DMWENLFQQASQQ	1624.7	T	-	2.5	0.0	50.4	9.0
P37188	10204.2	G	U	T	A	CID	LIT	2	46.8	SFGDIPLVHGMPFISGIGIEALQNK	2656.4	R	I	5.6	0.7	51.0	10.8
P37188	10204.2	G	U	T	A	CID	LIT	2	46.8	VNEIETYMDGVHLICTTAK	2194.1	R	V	5.2	0.8	73.2	11.8
P37188	10204.2	G	U	A	A	CID	LIT	2	18.1	DGVHLICTTAKV	1313.7	M	D	4.0	0.7	22.8	14.0
P37188	10204.2	G	U	A	A	CID	LIT	2	18.1	DGVHLICTTAKVDRSFG	1875.9	M	D	4.0	0.8	60.6	16.4
P37188	10204.2	G	U	T	B	CID	LIT	3	63.8	ELCQNHNIPVELIQCR	2023.0	K	V	4.7	0.0	43.5	8.5
P37188	10204.2	G	U	T	B	CID	LIT	3	63.8	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	5.9	0.0	29.9	10.0
P37188	10204.2	G	U	T	B	CID	LIT	3	63.8	VNEIETYMDGVHLICTTAK	2210.0	R	V	2.6	0.7	44.2	11.8
P37188	10204.2	G	U	A	B	CID	LIT	3	43.6	DGVHLICTTAKV	1313.7	M	D	2.8	0.7	35.1	13.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P37188	10204.2	G	U	A	B	CID	LIT	3	43.6	DGVHLICTTAKVDRSFG	1875.9	M	D	4.0	0.6	43.6	16.4
P37188	10204.2	G	U	A	B	CID	LIT	3	43.6	MKRKIIVACGGAVATSTMAAEEIK	2535.3	-	E	5.5	0.7	61.6	13.2
P37188	10204.2	S	U	T	A	CID	LIT	3	63.8	ELCQNHNIPVELIQCR	2023.0	K	V	5.2	0.6	69.4	16.9
P37188	10204.2	S	U	T	A	CID	LIT	3	63.8	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	5.6	0.7	47.1	16.5
P37188	10204.2	S	U	T	A	CID	LIT	3	63.8	VNEIETYMDGVHLICTTAK	2194.1	R	V	4.9	0.6	55.0	17.6
P37188	10204.2	S	U	T	B	CID	LIT	4	67.0	ELCQNHNIPVELIQCR	2023.0	K	V	5.3	0.6	49.1	16.9
P37188	10204.2	S	U	T	B	CID	LIT	4	67.0	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	6.3	0.7	47.8	16.7
P37188	10204.2	S	U	T	B	CID	LIT	4	67.0	VNEIETYMDGVHLICTTAK	2210.0	R	V	2.3	0.6	3.2	17.2
P37188	10204.2	S	U	T	B	CID	LIT	4	67.0	VNEIETYMDGVHLICTTAKVDR	2564.2	R	S	2.4	0.1	17.6	18.9
P37188	10204.2	S	U	T	C	CID	LIT	4	86.2	ELCQNHNIPVELIQCR	2023.0	K	V	5.1	0.6	69.6	16.9
P37188	10204.2	S	U	T	C	CID	LIT	4	86.2	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	2.9	0.5	0.0	0.0
P37188	10204.2	S	U	T	C	CID	LIT	4	86.2	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	6.8	0.7	46.9	16.7
P37188	10204.2	S	U	T	C	CID	LIT	4	86.2	VNEIETYMDGVHLICTTAK	2194.1	R	V	4.2	0.5	46.4	17.6
P37188	10204.2	S	U	T	A	ETD	LIT	4	57.4	ILTILQG	757.5	K	-	1.7	0.4	0.0	0.0
P37188	10204.2	S	U	T	A	ETD	LIT	4	57.4	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	6.4	0.9	57.2	17.4
P37188	10204.2	S	U	T	A	ETD	LIT	4	57.4	VNEIETYMDGVHLICTTAK	2194.1	R	V	4.6	0.5	43.6	17.4
P37188	10204.2	S	U	T	A	ETD	LIT	4	57.4	VNEIETYMDGVHLICTTAKVDR	2564.2	R	S	4.4	0.0	23.0	18.8
P37188	10204.2	S	U	T	B	ETD	LIT	5	89.4	ELCQNHNIPVELIQCR	2023.0	K	V	4.6	0.5	31.9	17.0
P37188	10204.2	S	U	T	B	ETD	LIT	5	89.4	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	0.0	0.0	37.2	18.3
P37188	10204.2	S	U	T	B	ETD	LIT	5	89.4	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	8.1	0.7	61.0	16.4
P37188	10204.2	S	U	T	B	ETD	LIT	5	89.4	VNEIETYMDGVHLICTTAK	2194.1	R	V	4.1	0.0	43.6	17.1
P37188	10204.2	S	U	T	B	ETD	LIT	5	89.4	VNEIETYMDGVHLICTTAKVDR	2564.2	R	S	3.7	0.4	34.9	18.8
P37188	10204.2	S	U	T	C	ETD	LIT	4	86.2	ELCQNHNIPVELIQCR	2023.0	K	V	4.8	0.5	50.7	16.9
P37188	10204.2	S	U	T	C	ETD	LIT	4	86.2	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	0.0	0.0	44.5	18.3
P37188	10204.2	S	U	T	C	ETD	LIT	4	86.2	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	0.0	0.0	53.3	16.9
P37188	10204.2	S	U	T	C	ETD	LIT	4	86.2	VNEIETYMDGVHLICTTAK	2194.1	R	V	7.4	0.8	72.6	17.2
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	ELCQNHNIPVELIQCR	2023.0	K	V	0.0	0.0	43.6	17.3
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	0.0	0.0	63.4	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	0.0	0.0	49.8	16.3
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	VNEIETYMDGVHLICTTAK	2194.1	R	V	0.0	0.0	59.8	17.7
P37188	10204.2	S	U	T	A	ETD+CID	LIT	5	89.4	ELCQNHNIPVELIQCR	2023.0	K	V	5.2	0.6	43.4	17.2
P37188	10204.2	S	U	T	A	ETD+CID	LIT	5	89.4	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	5.3	0.0	33.0	18.3
P37188	10204.2	S	U	T	A	ETD+CID	LIT	5	89.4	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	6.4	0.6	51.8	16.6
P37188	10204.2	S	U	T	A	ETD+CID	LIT	5	89.4	VNEIETYMDGVHLICTTAK	2194.1	R	V	0.0	0.0	60.1	17.9
P37188	10204.2	S	U	T	A	ETD+CID	LIT	5	89.4	VNEIETYMDGVHLICTTAKVDR	2564.2	R	S	4.4	0.0	24.7	18.8
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	ELCQNHNIPVELIQCR	2023.0	K	V	5.0	0.5	43.6	17.3
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	4.7	0.0	63.4	18.3
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	6.4	0.6	49.8	16.3
P37188	10204.2	S	U	T	B	ETD+CID	LIT	4	86.2	VNEIETYMDGVHLICTTAK	2194.1	R	V	4.3	0.6	59.8	17.7
P37188	10204.2	S	U	T	C	ETD+CID	LIT	4	86.2	ELCQNHNIPVELIQCR	2023.0	K	V	5.1	0.5	49.5	17.0
P37188	10204.2	S	U	T	C	ETD+CID	LIT	4	86.2	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	5.2	0.0	68.5	18.3
P37188	10204.2	S	U	T	C	ETD+CID	LIT	4	86.2	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	7.0	0.8	42.4	17.1
P37188	10204.2	S	U	T	C	ETD+CID	LIT	4	86.2	VNEIETYMDGVHLICTTAK	2194.1	R	V	6.3	0.7	71.7	17.5
P37188	10204.2	S	U	T	B	HCD	FT	4	86.2	ELCQNHNIPVELIQCR	2023.0	K	V	0.0	0.0	43.6	17.3
P37188	10204.2	S	U	T	B	HCD	FT	4	86.2	KIIVACGGAVATSTMAAEEIKELCQNHNIPVELIQCR	4124.1	R	V	0.0	0.0	63.4	18.3
P37188	10204.2	S	U	T	B	HCD	FT	4	86.2	SFGDIPLVHGMPFISGIGIEALQNK	2640.4	R	I	0.0	0.0	49.8	16.3
P37188	10204.2	S	U	T	B	HCD	FT	4	86.2	VNEIETYMDGVHLICTTAK	2194.1	R	V	0.0	0.0	59.8	17.7
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	AKTAAALHILVK	1235.8	M	E	0.0	0.0	55.1	0.0
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	GGDLGEFR	850.4	R	Q	2.6	0.8	42.0	12.3
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	KHSICPSGK	1013.5	K	R	2.4	0.4	16.6	11.5
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	LALDLLEQIK	1155.7	K	N	3.9	0.8	53.7	8.5
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	LALDLLEQIKNGADFGK	1845.0	K	L	4.7	0.0	38.7	12.6
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	RGGDLGEFR	1006.5	K	Q	2.1	0.6	18.6	12.3
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	TAAALHILVK	1036.7	K	E	3.6	0.0	53.6	4.8
P0A9L5	10214.4	G	U	T	A	CID	LIT	8	53.8	TAAALHILVKEEK	1422.8	K	L	4.8	0.0	76.4	6.0
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	AKTAAALHILVK	1235.8	M	E	0.0	0.0	26.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	GGDLGEFR	850.4	R	Q	2.7	0.8	35.3	12.3
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	HSICPSGKR	1041.5	K	G	2.2	0.8	15.2	11.5
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	KHSICPSGK	1013.5	K	R	2.0	0.4	30.5	11.5
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	LALDLLEQIK	1155.7	K	N	4.0	0.0	52.1	8.5
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	QGQMVPAFDK	1120.5	R	V	2.8	0.6	15.8	12.0
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	RGGDLGEFR	1006.5	K	Q	3.1	0.3	23.1	11.8
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	TAAALHILVK	1036.7	K	E	3.0	0.0	55.9	4.8
P0A9L5	10214.4	G	U	T	B	CID	LIT	9	57.0	TAAALHILVKEEK	1422.8	K	L	4.7	0.0	76.0	6.0
P0A9L5	10214.4	G	U	A	B	CID	LIT	4	65.6	AKTAAALHILVKEEKLAL	1919.2	M	D	0.0	0.0	37.3	0.0
P0A9L5	10214.4	G	U	A	B	CID	LIT	4	65.6	DFGKLAKKHSICPSGKRGG	2043.1	A	D	4.3	0.0	19.0	13.4
P0A9L5	10214.4	G	U	A	B	CID	LIT	4	65.6	DLGEFRQGQMVPAF	1594.8	G	D	1.9	0.6	26.1	15.2
P0A9L5	10214.4	G	U	A	B	CID	LIT	4	65.6	DLLEQIKNGA	1100.6	L	D	3.4	0.5	48.3	13.0
P0A9L5	10214.4	S	U	T	A	CID	LIT	2	44.1	LALDLLEQIKNGADFGK	1846.0	K	L	5.2	0.6	43.8	16.8
P0A9L5	10214.4	S	U	T	A	CID	LIT	2	44.1	VVFSCPVLEPTGPLHTQFGYHIIK	2739.4	K	V	2.8	0.8	0.5	18.2
P0A9L5	10214.4	S	U	T	B	CID	LIT	2	54.8	LALDLLEQIKNGADFGK	1846.0	K	L	4.6	0.6	27.2	17.6
P0A9L5	10214.4	S	U	T	B	CID	LIT	2	54.8	QGQMVPAFDKVVFSCPVLEPTGPLHTQFGYHIIK	3841.0	R	V	2.7	0.4	1.7	18.6
P0A9L5	10214.4	S	U	T	C	CID	LIT	3	44.1	LALDLLEQIK	1155.7	K	N	2.1	0.7	7.4	12.0
P0A9L5	10214.4	S	U	T	C	CID	LIT	3	44.1	LALDLLEQIKNGADFGK	1846.0	K	L	4.6	0.7	40.4	17.1
P0A9L5	10214.4	S	U	T	C	CID	LIT	3	44.1	VVFSCPVLEPTGPLHTQFGYHIIK	2739.4	K	V	2.6	0.5	8.3	17.3
P0A9L5	10214.4	S	U	T	A	ETD	LIT	3	44.1	LALDLLEQIK	1155.7	K	N	1.8	0.1	35.4	12.0
P0A9L5	10214.4	S	U	T	A	ETD	LIT	3	44.1	LALDLLEQIKNGADFGK	1846.0	K	L	6.1	0.2	73.4	17.6
P0A9L5	10214.4	S	U	T	A	ETD	LIT	3	44.1	VVFSCPVLEPTGPLHTQFGYHIIK	2739.4	K	V	0.0	0.0	17.6	17.0
P0A9L5	10214.4	S	U	T	B	ETD	LIT	4	37.6	KHSICPSGK	1013.5	K	R	2.4	0.8	4.4	13.2
P0A9L5	10214.4	S	U	T	B	ETD	LIT	4	37.6	LALDLLEQIK	1155.7	K	N	1.7	0.4	41.4	12.0
P0A9L5	10214.4	S	U	T	B	ETD	LIT	4	37.6	LALDLLEQIKNGADFGK	1846.0	K	L	5.2	0.2	54.7	17.6
P0A9L5	10214.4	S	U	T	B	ETD	LIT	4	37.6	RGGDLGEFR	1006.5	K	Q	2.4	0.3	18.9	15.7
P0A9L5	10214.4	S	U	T	C	ETD	LIT	6	74.2	KHSICPSGK	1013.5	K	R	1.8	0.6	11.9	13.2
P0A9L5	10214.4	S	U	T	C	ETD	LIT	6	74.2	LALDLLEQIK	1155.7	K	N	2.1	0.2	25.5	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9L5	10214.4	S	U	T	C	ETD	LIT	6	74.2	LALDLLEQIKNGADFGK	1846.0	K	L	5.2	0.1	63.5	17.6
P0A9L5	10214.4	S	U	T	C	ETD	LIT	6	74.2	QGQMVPAFDKVVFSCPVLEPTGPLHTQFGYHIIK	3841.0	R	V	0.0	0.0	23.2	17.9
P0A9L5	10214.4	S	U	T	C	ETD	LIT	6	74.2	RGGDLGEFR	1006.5	K	Q	2.8	0.4	27.8	15.7
P0A9L5	10214.4	S	U	T	C	ETD	LIT	6	74.2	VVFSCPVLEPTGPLHTQFGYHIIK	2739.4	K	V	4.1	0.0	37.1	17.0
P0A9L5	10214.4	S	U	T	C	ETD+CID	LIT	2	54.8	LALDLLEQIKNGADFGK	1845.0	K	L	2.2	0.6	16.1	16.3
P0A9L5	10214.4	S	U	T	C	ETD+CID	LIT	2	54.8	QGQMVPAFDKVVFSCPVLEPTGPLHTQFGYHIIK	3841.0	R	V	2.1	0.0	22.2	18.6
P0C037	10216.1	G	U	T	A	CID	LIT	3	25.5	MLQSNEYFSGK	1303.6	-	V	3.2	0.5	29.2	8.5
P0C037	10216.1	G	U	T	A	CID	LIT	3	25.5	SIGFSSSSTGR	1085.5	K	A	3.0	0.0	50.4	9.0
P0C037	10216.1	G	U	T	A	CID	LIT	3	25.5	VKSIGFSSSSTGR	1312.7	K	A	3.5	0.0	48.6	11.1
P0C037	10216.1	G	T	T	A	CID	LIT	2	23.4	MLQSNEYFSGK	1303.6	-	V	2.4	0.7	23.1	9.5
P0C037	10216.1	G	T	T	A	CID	LIT	2	23.4	SIGFSSSSTGR	1085.5	K	A	3.2	0.0	52.0	9.5
P0C037	10216.1	G	T	T	B	CID	LIT	2	13.8	MLQSNEYFSGK	1303.6	-	V	2.9	0.0	37.1	9.0
P0C037	10216.1	G	T	T	B	CID	LIT	2	13.8	MLQSNEYFSGKVK	1530.8	-	S	3.7	0.4	28.2	14.3
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	ALLDFFLSR	1081.6	M	K	0.0	0.0	40.2	9.0
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	DGDISILELNVTLPEAEELK	2198.1	K	-	4.3	0.7	77.0	10.0
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	DILEVICK	989.5	K	Y	2.8	0.8	27.7	13.6
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	KDILEVICK	1117.6	R	Y	2.7	0.6	5.7	11.5
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	LQIIVAERR	1097.7	R	R	2.6	0.2	30.8	7.8
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	RSDAEPHYLPQLR	1581.8	R	K	2.8	0.5	28.9	13.8
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	SDAEPHYLPQLR	1425.7	R	K	3.2	0.5	26.6	14.0
P0A734	10217.4	G	U	T	A	CID	LIT	8	86.4	YVQIDPEMVTVQLEQK	1920.0	K	D	4.4	0.6	59.8	14.0
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	ALLDFFLSR	1081.6	M	K	0.0	0.0	37.1	9.0
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	DGDISILELNVTLPEAEELK	2198.1	K	-	4.5	0.0	66.6	10.4
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	DILEVICK	989.5	K	Y	2.8	0.0	46.0	13.6
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	KDILEVICK	1117.6	R	Y	3.6	0.7	74.2	11.5
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	LQIIVAER	941.6	R	R	2.2	0.3	28.3	10.4
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	NTANIAK	731.4	K	E	1.4	0.0	26.0	19.4
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	RSDAEPHYLPQLR	1581.8	R	K	3.3	0.8	26.1	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	SDAEPHYLPQLR	1425.7	R	K	3.3	0.8	22.0	14.0
P0A734	10217.4	G	U	T	B	CID	LIT	9	93.2	YVQIDPEMVTVQLEQK	1920.0	K	D	4.0	0.5	56.9	13.6
P0A734	10217.4	S	U	T	A	CID	LIT	4	43.2	KDILEVICK	1117.6	R	Y	3.2	0.0	34.8	15.2
P0A734	10217.4	S	U	T	A	CID	LIT	4	43.2	RSDAEPHYLPQLR	1581.8	R	K	3.4	0.6	41.6	17.4
P0A734	10217.4	S	U	T	A	CID	LIT	4	43.2	SDAEPHYLPQLR	1425.7	R	K	2.6	0.6	23.8	16.5
P0A734	10217.4	S	U	T	A	CID	LIT	4	43.2	YVQIDPEMVTVQLEQK	1920.0	K	D	4.0	0.5	42.4	18.3
P0A734	10217.4	S	U	T	B	CID	LIT	5	52.3	KDILEVICK	1117.6	R	Y	3.3	0.6	49.9	15.2
P0A734	10217.4	S	U	T	B	CID	LIT	5	52.3	LQIIVAER	941.6	R	R	1.6	0.6	11.0	11.5
P0A734	10217.4	S	U	T	B	CID	LIT	5	52.3	RSDAEPHYLPQLR	1581.8	R	K	3.4	0.5	21.9	17.7
P0A734	10217.4	S	U	T	B	CID	LIT	5	52.3	SDAEPHYLPQLR	1425.7	R	K	3.1	0.6	27.8	16.4
P0A734	10217.4	S	U	T	B	CID	LIT	5	52.3	YVQIDPEMVTVQLEQK	1920.0	K	D	3.3	0.3	24.0	18.6
P0A734	10217.4	S	U	T	C	CID	LIT	4	43.2	KDILEVICK	1117.6	R	Y	3.4	0.8	43.8	15.2
P0A734	10217.4	S	U	T	C	CID	LIT	4	43.2	RSDAEPHYLPQLR	1581.8	R	K	2.6	0.7	16.1	17.8
P0A734	10217.4	S	U	T	C	CID	LIT	4	43.2	SDAEPHYLPQLR	1425.7	R	K	3.2	0.4	33.8	16.5
P0A734	10217.4	S	U	T	C	CID	LIT	4	43.2	YVQIDPEMVTVQLEQK	1920.0	K	D	3.6	0.3	13.2	18.5
P0A734	10217.4	S	U	T	C	CID	FT	2	23.9	KDILEVICK	1117.6	R	Y	2.5	0.8	53.0	15.2
P0A734	10217.4	S	U	T	C	CID	FT	2	23.9	SDAEPHYLPQLR	1425.7	R	K	2.9	0.0	28.9	16.5
P0A734	10217.4	S	U	T	A	ETD	LIT	3	25.0	DILEVICK	989.5	K	Y	1.6	0.5	19.1	14.1
P0A734	10217.4	S	U	T	A	ETD	LIT	3	25.0	KDILEVICK	1117.6	R	Y	1.0	0.4	19.1	14.9
P0A734	10217.4	S	U	T	A	ETD	LIT	3	25.0	RSDAEPHYLPQLR	1581.8	R	K	4.1	0.0	39.4	17.9
P0A734	10217.4	S	U	T	B	ETD	LIT	7	62.5	ALLDFFLSR	1081.6	M	K	0.0	0.0	53.8	11.1
P0A734	10217.4	S	U	T	B	ETD	LIT	7	62.5	DILEVICK	989.5	K	Y	1.7	0.5	18.4	16.4
P0A734	10217.4	S	U	T	B	ETD	LIT	7	62.5	KDILEVICK	1117.6	R	Y	2.3	0.2	24.3	15.3
P0A734	10217.4	S	U	T	B	ETD	LIT	7	62.5	LQIIVAER	941.6	R	R	2.5	0.0	36.6	11.5
P0A734	10217.4	S	U	T	B	ETD	LIT	7	62.5	RSDAEPHYLPQLR	1581.8	R	K	4.0	0.4	41.0	18.3
P0A734	10217.4	S	U	T	B	ETD	LIT	7	62.5	SDAEPHYLPQLR	1425.7	R	K	2.3	0.7	0.0	0.0
P0A734	10217.4	S	U	T	B	ETD	LIT	7	62.5	YVQIDPEMVTVQLEQK	1920.0	K	D	2.1	0.2	18.1	18.5
P0A734	10217.4	S	U	T	C	ETD	LIT	3	25.0	KDILEVICK	1117.6	R	Y	1.9	0.4	31.7	15.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A734	10217.4	S	U	T	C	ETD	LIT	3	25.0	RSDAEPHYLPQLR	1581.8	R	K	4.3	0.5	41.9	17.6
P0A734	10217.4	S	U	T	C	ETD	LIT	3	25.0	SDAEPHYLPQLR	1425.7	R	K	4.1	0.6	27.3	15.4
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	DILEVICK	989.5	K	Y	0.0	0.0	42.0	16.7
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	KDILEVICK	1117.6	R	Y	0.0	0.0	54.3	15.2
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	SDAEPHYLPQLR	1425.7	R	K	0.0	0.0	24.5	16.5
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	YVQIDPEMVTVQLEQK	1920.0	K	D	0.0	0.0	36.6	18.5
P0A734	10217.4	S	U	T	A	ETD+CID	LIT	4	43.2	KDILEVICK	1117.6	R	Y	3.0	0.8	36.3	15.2
P0A734	10217.4	S	U	T	A	ETD+CID	LIT	4	43.2	RSDAEPHYLPQLR	1581.8	R	K	2.6	0.3	7.1	17.2
P0A734	10217.4	S	U	T	A	ETD+CID	LIT	4	43.2	SDAEPHYLPQLR	1425.7	R	K	2.6	0.7	17.9	15.4
P0A734	10217.4	S	U	T	A	ETD+CID	LIT	4	43.2	YVQIDPEMVTVQLEQK	1920.0	K	D	4.0	0.4	42.0	18.5
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	DILEVICK	989.5	K	Y	2.8	0.7	42.0	16.7
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	KDILEVICK	1117.6	R	Y	3.4	0.0	54.3	15.2
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	SDAEPHYLPQLR	1425.7	R	K	3.0	0.5	24.5	16.5
P0A734	10217.4	S	U	T	B	ETD+CID	LIT	4	42.0	YVQIDPEMVTVQLEQK	1920.0	K	D	3.9	0.5	36.6	18.5
P0A734	10217.4	S	U	T	C	ETD+CID	LIT	5	52.3	KDILEVICK	1117.6	R	Y	3.4	0.0	43.8	15.2
P0A734	10217.4	S	U	T	C	ETD+CID	LIT	5	52.3	LQIIVAER	941.6	R	R	1.8	0.4	19.9	11.5
P0A734	10217.4	S	U	T	C	ETD+CID	LIT	5	52.3	RSDAEPHYLPQLR	1581.8	R	K	2.9	0.7	15.5	17.2
P0A734	10217.4	S	U	T	C	ETD+CID	LIT	5	52.3	SDAEPHYLPQLR	1425.7	R	K	4.5	0.9	0.0	0.0
P0A734	10217.4	S	U	T	C	ETD+CID	LIT	5	52.3	YVQIDPEMVTVQLEQK	1936.0	K	D	3.4	0.4	39.9	17.6
P0A734	10217.4	S	U	T	B	HCD	FT	4	42.0	DILEVICK	989.5	K	Y	0.0	0.0	42.0	16.7
P0A734	10217.4	S	U	T	B	HCD	FT	4	42.0	KDILEVICK	1117.6	R	Y	0.0	0.0	54.3	15.2
P0A734	10217.4	S	U	T	B	HCD	FT	4	42.0	SDAEPHYLPQLR	1425.7	R	K	0.0	0.0	24.5	16.5
P0A734	10217.4	S	U	T	B	HCD	FT	4	42.0	YVQIDPEMVTVQLEQK	1920.0	K	D	0.0	0.0	36.6	18.5
P0A800	10218.3	G	U	T	A	CID	LIT	7	69.2	ARVTVQDAVEK	1215.7	M	I	0.0	0.0	51.7	14.0
P0A800	10218.3	G	U	T	A	CID	LIT	7	69.2	EIEEGLINNQILDVR	1754.9	R	E	4.5	0.6	66.9	11.8
P0A800	10218.3	G	U	T	A	CID	LIT	7	69.2	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	6.0	0.8	59.5	11.8
P0A800	10218.3	G	U	T	A	CID	LIT	7	69.2	IGNRFDLVLVAAR	1443.8	K	R	2.2	0.5	4.8	7.0
P0A800	10218.3	G	U	T	A	CID	LIT	7	69.2	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	5.4	0.0	91.1	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A800	10218.3	G	U	T	A	CID	LIT	7	69.2	QEQQEQEAAELQAVTAIAEGRR	2455.2	R	-	3.4	0.4	74.8	13.2
P0A800	10218.3	G	U	T	A	CID	LIT	7	69.2	VTVQDAVEK	988.5	R	I	2.8	0.7	42.5	14.0
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	ARVTVQDAVEK	1215.7	M	I	0.0	0.0	51.8	13.4
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	EIEEGLINNQILDVR	1754.9	R	E	5.2	0.6	67.0	12.0
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	5.5	0.7	83.2	12.6
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	FDLVLVAAR	1003.6	R	R	3.3	0.7	39.3	13.4
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	IGNRFDLVLVAAR	1443.8	K	R	4.0	0.0	51.2	7.0
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	QEQQEQEAAELQAVTAIAEGRR	2455.2	R	-	2.4	0.3	60.2	13.2
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	TTVIALR	773.5	K	E	1.7	0.6	19.4	13.2
P0A800	10218.3	G	T	T	A	CID	LIT	8	76.9	VTVQDAVEK	988.5	R	I	2.9	0.7	47.8	13.6
P0A800	10218.3	G	U	A	A	CID	LIT	2	17.6	ARVTVQDAVEKIGNRF	1803.0	M	D	0.0	0.0	27.1	12.8
P0A800	10218.3	G	U	A	A	CID	LIT	2	17.6	DAVEKIGNRF	1148.6	Q	D	3.0	0.8	37.2	13.6
P0A800	10218.3	G	T	T	B	CID	LIT	4	53.8	ARVTVQDAVEK	1215.7	M	I	0.0	0.0	37.3	14.0
P0A800	10218.3	G	T	T	B	CID	LIT	4	53.8	EIEEGLINNQILDVR	1754.9	R	E	4.6	0.5	70.9	12.0
P0A800	10218.3	G	T	T	B	CID	LIT	4	53.8	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	6.5	0.6	105.0	12.0
P0A800	10218.3	G	T	T	B	CID	LIT	4	53.8	VTVQDAVEK	988.5	R	I	2.8	0.4	51.6	13.6
P0A800	10218.3	G	U	T	B	CID	LIT	3	28.6	ARVTVQDAVEK	1215.7	M	I	0.0	0.0	52.1	13.4
P0A800	10218.3	G	U	T	B	CID	LIT	3	28.6	EIEEGLINNQILDVR	1754.9	R	E	3.9	0.6	49.7	11.8
P0A800	10218.3	G	U	T	B	CID	LIT	3	28.6	VTVQDAVEK	988.5	R	I	2.9	0.5	56.7	13.6
P0A800	10218.3	G	T	A	B	CID	LIT	3	38.5	DAVEKIGNRF	1148.6	Q	D	2.9	0.4	32.7	13.2
P0A800	10218.3	G	T	A	B	CID	LIT	3	38.5	DKTTVIALREIE	1387.8	N	E	3.8	0.0	41.8	12.6
P0A800	10218.3	G	T	A	B	CID	LIT	3	38.5	ELQAVTAIAEGRR	1413.8	A	-	2.9	0.8	23.2	12.3
P0A800	10218.3	G	U	A	B	CID	LIT	3	38.5	DAVEKIGNRF	1148.6	Q	D	2.8	0.8	31.7	13.2
P0A800	10218.3	G	U	A	B	CID	LIT	3	38.5	DKTTVIALREIE	1387.8	N	E	3.0	0.0	35.5	12.6
P0A800	10218.3	G	U	A	B	CID	LIT	3	38.5	ELQAVTAIAEGRR	1413.8	A	-	2.9	0.5	20.6	12.6
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	EIEEGLINNQILDVR	1754.9	R	E	4.5	0.4	35.5	17.3
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	5.9	0.6	81.9	18.5
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	ERQEQQEQEAAELQAVTAIAEGRR	2740.4	R	-	3.0	0.5	38.7	19.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	FDLVLVAAR	1003.6	R	R	3.2	0.7	68.4	14.9
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	IGNRFDLVLVAAR	1443.8	K	R	2.6	0.7	21.0	11.8
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	6.0	0.7	94.5	17.6
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	4.6	0.5	61.0	16.7
P0A800	10218.3	S	U	T	A	CID	LIT	8	93.4	VTVQDAVEK	988.5	R	I	2.7	0.7	41.5	15.9
P0A800	10218.3	S	U	T	B	CID	LIT	7	83.5	EIEEGLINNQILDVR	1754.9	R	E	4.4	0.4	51.3	16.9
P0A800	10218.3	S	U	T	B	CID	LIT	7	83.5	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	6.7	0.6	88.0	18.5
P0A800	10218.3	S	U	T	B	CID	LIT	7	83.5	FDLVLVAAR	1003.6	R	R	2.7	0.5	25.5	14.9
P0A800	10218.3	S	U	T	B	CID	LIT	7	83.5	IGNRFDLVLVAAR	1443.8	K	R	3.0	0.6	32.7	11.8
P0A800	10218.3	S	U	T	B	CID	LIT	7	83.5	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	6.5	0.7	92.5	17.6
P0A800	10218.3	S	U	T	B	CID	LIT	7	83.5	QEQQEQEAAELQAVTAIAEGRR	2455.2	R	-	2.3	0.1	42.1	19.4
P0A800	10218.3	S	U	T	B	CID	LIT	7	83.5	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	4.0	0.5	71.8	15.9
P0A800	10218.3	S	U	T	C	CID	LIT	5	82.4	EIEEGLINNQILDVR	1755.9	R	E	4.7	0.3	55.0	17.8
P0A800	10218.3	S	U	T	C	CID	LIT	5	82.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	6.4	0.6	77.0	18.7
P0A800	10218.3	S	U	T	C	CID	LIT	5	82.4	IGNRFDLVLVAAR	1443.8	K	R	2.9	0.8	29.4	10.4
P0A800	10218.3	S	U	T	C	CID	LIT	5	82.4	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	5.6	0.0	80.0	17.7
P0A800	10218.3	S	U	T	C	CID	LIT	5	82.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	4.6	0.6	62.6	16.0
P0A800	10218.3	S	U	T	A	ETD	LIT	5	82.4	EIEEGLINNQILDVR	1754.9	R	E	2.7	0.3	75.0	17.2
P0A800	10218.3	S	U	T	A	ETD	LIT	5	82.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	0.0	0.0	22.1	18.3
P0A800	10218.3	S	U	T	A	ETD	LIT	5	82.4	FDLVLVAAR	1003.6	R	R	1.8	0.4	25.8	14.9
P0A800	10218.3	S	U	T	A	ETD	LIT	5	82.4	IGNRFDLVLVAAR	1443.8	K	R	2.4	0.6	20.0	10.4
P0A800	10218.3	S	U	T	A	ETD	LIT	5	82.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	7.1	0.0	83.7	15.7
P0A800	10218.3	S	U	T	B	ETD	LIT	5	82.4	EIEEGLINNQILDVR	1754.9	R	E	2.0	0.2	53.0	17.4
P0A800	10218.3	S	U	T	B	ETD	LIT	5	82.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	4.6	0.0	37.6	18.5
P0A800	10218.3	S	U	T	B	ETD	LIT	5	82.4	FDLVLVAAR	1003.6	R	R	2.3	0.0	41.1	14.9
P0A800	10218.3	S	U	T	B	ETD	LIT	5	82.4	IGNRFDLVLVAAR	1443.8	K	R	2.9	0.6	0.0	0.0
P0A800	10218.3	S	U	T	B	ETD	LIT	5	82.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	8.4	0.8	83.7	15.9
P0A800	10218.3	S	U	T	C	ETD	LIT	6	92.3	EIEEGLINNQILDVR	1754.9	R	E	0.0	0.0	78.9	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A800	10218.3	S	U	T	C	ETD	LIT	6	92.3	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	3.2	0.3	15.2	18.3
P0A800	10218.3	S	U	T	C	ETD	LIT	6	92.3	FDLVLVAAR	1003.6	R	R	1.3	0.0	24.2	14.9
P0A800	10218.3	S	U	T	C	ETD	LIT	6	92.3	IGNRFDLVLVAAR	1443.8	K	R	3.9	0.0	42.5	10.4
P0A800	10218.3	S	U	T	C	ETD	LIT	6	92.3	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	6.9	0.0	81.0	17.7
P0A800	10218.3	S	U	T	C	ETD	LIT	6	92.3	VTVQDAVEK	988.5	R	I	0.0	0.0	31.2	14.6
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	EIEEGLINNQILDVR	1754.9	R	E	0.0	0.0	46.5	17.2
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	0.0	0.0	66.9	18.3
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	FDLVLVAAR	1003.6	R	R	0.0	0.0	69.0	14.9
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	IGNRFDLVLVAAR	1443.8	K	R	0.0	0.0	26.2	10.4
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	0.0	0.0	112.0	17.6
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	0.0	0.0	55.0	16.2
P0A800	10218.3	S	U	T	A	ETD+CID	LIT	5	83.5	EIEEGLINNQILDVR	1754.9	R	E	5.0	0.5	0.0	0.0
P0A800	10218.3	S	U	T	A	ETD+CID	LIT	5	83.5	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	5.8	0.7	59.5	18.3
P0A800	10218.3	S	U	T	A	ETD+CID	LIT	5	83.5	ERQEQQEQEAAELQAVTAIAEGRR	2740.4	R	-	4.9	0.5	32.8	19.3
P0A800	10218.3	S	U	T	A	ETD+CID	LIT	5	83.5	IGNRFDLVLVAAR	1443.8	K	R	3.0	0.7	0.0	0.0
P0A800	10218.3	S	U	T	A	ETD+CID	LIT	5	83.5	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	5.8	0.7	81.7	18.0
P0A800	10218.3	S	U	T	A	ETD+CID	LIT	5	83.5	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	3.1	0.5	59.9	15.7
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	3	53.8	EIEEGLINNQILDVR	1755.9	R	E	4.7	0.4	0.0	0.0
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	3	53.8	FDLVLVAAR	1003.6	R	R	3.7	0.6	0.0	0.0
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	3	53.8	IGNRFDLVLVAAR	1443.8	K	R	2.5	0.8	0.0	0.0
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	3	53.8	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	6.0	0.8	0.0	0.0
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	EIEEGLINNQILDVR	1754.9	R	E	5.1	0.5	46.5	17.2
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	6.3	0.6	66.9	18.3
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	FDLVLVAAR	1003.6	R	R	3.7	0.6	69.0	14.9
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	IGNRFDLVLVAAR	1443.8	K	R	2.5	0.8	0.0	0.0
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	6.0	0.8	112.0	17.6
P0A800	10218.3	S	U	T	B	ETD+CID	LIT	5	82.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	4.8	0.5	55.0	16.2
P0A800	10218.3	S	U	T	C	ETD+CID	LIT	6	93.4	EIEEGLINNQILDVR	1754.9	R	E	4.8	0.5	49.5	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A800	10218.3	S	U	T	C	ETD+CID	LIT	6	93.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	5.7	0.6	57.2	18.4
P0A800	10218.3	S	U	T	C	ETD+CID	LIT	6	93.4	ERQEQQEQEAAELQAVTAIAEGRR	2740.4	R	-	5.2	0.5	11.1	19.4
P0A800	10218.3	S	U	T	C	ETD+CID	LIT	6	93.4	IGNRFDLVLVAAR	1443.8	K	R	2.9	0.8	0.0	0.0
P0A800	10218.3	S	U	T	C	ETD+CID	LIT	6	93.4	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	5.2	0.8	86.0	17.8
P0A800	10218.3	S	U	T	C	ETD+CID	LIT	6	93.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	5.5	0.6	52.4	15.8
P0A800	10218.3	S	U	T	C	ETD+CID	LIT	6	93.4	VTVQDAVEK	988.5	R	I	3.0	0.5	45.1	15.9
P0A800	10218.3	S	U	T	B	HCD	FT	5	82.4	EIEEGLINNQILDVR	1754.9	R	E	0.0	0.0	46.5	17.2
P0A800	10218.3	S	U	T	B	HCD	FT	5	82.4	ERQEQQEQEAAELQAVTAIAEGR	2584.3	R	-	0.0	0.0	66.9	18.3
P0A800	10218.3	S	U	T	B	HCD	FT	5	82.4	FDLVLVAAR	1003.6	R	R	0.0	0.0	69.0	14.9
P0A800	10218.3	S	U	T	B	HCD	FT	5	82.4	IGNRFDLVLVAAR	1443.8	K	R	0.0	0.0	24.4	10.8
P0A800	10218.3	S	U	T	B	HCD	FT	5	82.4	QEQQEQEAAELQAVTAIAEGR	2299.1	R	-	0.0	0.0	112.0	17.6
P0A800	10218.3	S	U	T	B	HCD	FT	5	82.4	QMQVGGKDPLVPEENDKTTVIALR	2638.4	R	E	0.0	0.0	55.0	16.2
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	3.4	0.0	56.2	11.1
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	3.5	0.0	17.2	9.5
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	DVARYTQLIER	1363.7	K	L	3.1	0.5	26.1	12.0
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	IVSEFGR	807.4	K	D	2.2	0.8	20.4	14.8
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	KLLDYLK	892.6	R	R	2.8	0.4	38.3	3.0
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	LLDYLK	764.5	K	R	1.4	0.6	11.0	8.5
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	LLDYLKR	920.6	K	K	2.4	0.0	24.3	7.0
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	SLSTEATAK	907.5	M	I	0.0	0.0	35.5	11.8
P0ADZ4	10251.0	G	U	T	A	CID	LIT	9	74.2	YTQLIER	922.5	R	L	2.9	0.6	33.2	13.8
P0ADZ4	10251.0	G	T	T	A	CID	LIT	3	22.5	IVSEFGR	807.4	K	D	1.6	0.6	23.7	15.2
P0ADZ4	10251.0	G	T	T	A	CID	LIT	3	22.5	LLDYLK	764.5	K	R	1.7	0.4	15.8	8.5
P0ADZ4	10251.0	G	T	T	A	CID	LIT	3	22.5	YTQLIER	922.5	R	L	2.8	0.6	32.9	13.8
P0ADZ4	10251.0	G	U	T	B	CID	LIT	7	75.3	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	4.8	0.0	51.5	7.8
P0ADZ4	10251.0	G	U	T	B	CID	LIT	7	75.3	IVSEFGR	807.4	K	D	1.6	0.7	11.4	15.2
P0ADZ4	10251.0	G	U	T	B	CID	LIT	7	75.3	KDHHSR	779.4	K	R	2.0	0.5	8.3	12.8
P0ADZ4	10251.0	G	U	T	B	CID	LIT	7	75.3	KLLDYLK	892.6	R	R	2.8	0.0	37.8	3.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADZ4	10251.0	G	U	T	B	CID	LIT	7	75.3	LLDYLKR	920.6	K	K	2.2	0.0	31.7	7.0
P0ADZ4	10251.0	G	U	T	B	CID	LIT	7	75.3	SLSTEATAK	907.5	M	I	0.0	0.0	44.3	12.3
P0ADZ4	10251.0	G	U	T	B	CID	LIT	7	75.3	YTQLIER	922.5	R	L	3.0	0.5	32.0	14.0
P0ADZ4	10251.0	G	U	A	B	CID	LIT	3	49.4	DTGSTEVQVALLTAQINHLQGHFA	2550.3	N	E	4.6	0.0	74.2	13.2
P0ADZ4	10251.0	G	U	A	B	CID	LIT	3	49.4	DTGSTEVQVALLTAQINHLQGHFAEHKK	3072.6	N	D	4.3	0.6	49.6	15.1
P0ADZ4	10251.0	G	U	A	B	CID	LIT	3	49.4	SLSTEATAKIVSEFGR	1695.9	M	D	0.0	0.0	122.0	14.0
P0ADZ4	10251.0	S	U	T	A	CID	LIT	5	59.6	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	2.6	0.6	0.0	0.0
P0ADZ4	10251.0	S	U	T	A	CID	LIT	5	59.6	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	4.5	0.6	60.9	18.9
P0ADZ4	10251.0	S	U	T	A	CID	LIT	5	59.6	KDHHSRR	935.5	K	G	1.4	0.4	15.5	17.9
P0ADZ4	10251.0	S	U	T	A	CID	LIT	5	59.6	KLLDYLK	892.6	R	R	2.4	0.3	30.8	3.0
P0ADZ4	10251.0	S	U	T	A	CID	LIT	5	59.6	SLSTEATAK	907.5	M	I	0.0	0.0	30.1	13.6
P0ADZ4	10251.0	S	U	T	B	CID	LIT	7	59.6	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	3.8	0.6	0.0	0.0
P0ADZ4	10251.0	S	U	T	B	CID	LIT	7	59.6	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	5.8	0.7	51.6	18.8
P0ADZ4	10251.0	S	U	T	B	CID	LIT	7	59.6	KDHHSR	779.4	K	R	2.1	0.4	29.2	14.9
P0ADZ4	10251.0	S	U	T	B	CID	LIT	7	59.6	KLLDYLK	892.6	R	R	2.6	0.4	31.9	3.0
P0ADZ4	10251.0	S	U	T	B	CID	LIT	7	59.6	KLLDYLKR	1048.7	R	K	2.1	0.8	34.3	7.8
P0ADZ4	10251.0	S	U	T	B	CID	LIT	7	59.6	LLDYLK	764.5	K	R	2.2	0.3	30.4	11.5
P0ADZ4	10251.0	S	U	T	B	CID	LIT	7	59.6	SLSTEATAK	907.5	M	I	0.0	0.0	27.0	13.6
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	2.4	0.6	0.0	0.0
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	2.2	0.6	28.3	18.8
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	IVSEFGR	807.4	K	D	2.0	0.0	37.7	17.1
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	KDHHSR	779.4	K	R	1.9	0.5	17.7	14.9
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	KDHHSRR	935.5	K	G	1.4	0.7	10.2	14.8
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	KLLDYLKR	1048.7	R	K	2.0	0.6	46.1	7.8
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	LLDYLKR	920.6	K	K	2.4	0.6	35.9	8.5
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	SLSTEATAK	907.5	M	I	0.0	0.0	38.6	13.6
P0ADZ4	10251.0	S	U	T	C	CID	LIT	9	76.4	YTQLIER	922.5	R	L	2.1	0.0	30.7	16.8
P0ADZ4	10251.0	S	U	T	A	CID	FT	2	9.0	KLLDYLK	892.6	R	R	2.9	0.0	34.2	3.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADZ4	10251.0	S	U	T	A	CID	FT	2	9.0	KLLDYLKR	1048.7	R	K	2.9	0.3	24.6	7.8
P0ADZ4	10251.0	S	U	T	C	CID	FT	5	49.4	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	6.5	0.0	48.5	18.8
P0ADZ4	10251.0	S	U	T	C	CID	FT	5	49.4	KDHHSR	779.4	K	R	2.0	0.0	24.6	14.9
P0ADZ4	10251.0	S	U	T	C	CID	FT	5	49.4	KLLDYLK	892.6	R	R	2.9	0.0	37.7	3.0
P0ADZ4	10251.0	S	U	T	C	CID	FT	5	49.4	KLLDYLKR	1048.7	R	K	2.8	0.3	28.1	7.8
P0ADZ4	10251.0	S	U	T	C	CID	FT	5	49.4	LLDYLKR	920.6	K	K	2.1	0.7	21.8	8.5
P0ADZ4	10251.0	S	U	T	A	ETD	LIT	6	55.1	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3245.6	R	K	5.9	0.0	48.7	19.7
P0ADZ4	10251.0	S	U	T	A	ETD	LIT	6	55.1	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	2.1	0.0	37.8	18.9
P0ADZ4	10251.0	S	U	T	A	ETD	LIT	6	55.1	KDHHSRR	935.5	K	G	2.4	0.7	29.3	17.9
P0ADZ4	10251.0	S	U	T	A	ETD	LIT	6	55.1	KLLDYLKR	1048.7	R	K	3.8	0.4	41.4	7.8
P0ADZ4	10251.0	S	U	T	A	ETD	LIT	6	55.1	LLDYLKR	920.6	K	K	2.0	0.5	0.0	0.0
P0ADZ4	10251.0	S	U	T	A	ETD	LIT	6	55.1	RGLLR	614.4	R	M	1.5	0.0	23.9	16.7
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	0.0	0.0	41.7	19.2
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	0.0	0.0	22.7	18.9
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	KDHHSRR	935.5	K	G	2.4	0.3	23.3	17.9
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	KLLDYLKR	1048.7	R	K	3.4	0.3	0.0	0.0
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	LLDYLK	764.5	K	R	1.2	0.0	30.5	11.5
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	LLDYLKR	920.6	K	K	3.5	0.6	40.3	8.5
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	SLSTEATAK	907.5	M	I	0.0	0.0	41.9	13.6
P0ADZ4	10251.0	S	U	T	B	ETD	LIT	8	68.5	YTQLIER	922.5	R	L	2.1	0.4	0.0	0.0
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	0.0	0.0	37.1	18.8
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	0.0	0.0	31.0	18.8
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	IVSEFGR	807.4	K	D	2.2	0.3	27.3	17.1
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	KDHHSR	779.4	K	R	2.3	0.1	16.6	14.6
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	KDHHSRR	935.5	K	G	2.5	0.6	27.3	17.9
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	KLLDYLK	892.6	R	R	2.4	0.0	19.8	3.0
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	KLLDYLKR	1048.7	R	K	3.7	0.3	38.6	7.8
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	LLDYLK	764.5	K	R	0.0	0.0	30.0	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	LLDYLKR	920.6	K	K	3.4	0.6	0.0	0.0
P0ADZ4	10251.0	S	U	T	C	ETD	LIT	10	68.5	SLSTEATAK	907.5	M	I	0.0	0.0	39.4	13.6
P0ADZ4	10251.0	S	U	T	A	ETD	FT	3	19.1	KLLDYLK	892.6	R	R	1.4	0.0	24.3	3.0
P0ADZ4	10251.0	S	U	T	A	ETD	FT	3	19.1	KLLDYLKR	1048.7	R	K	3.0	0.3	42.0	7.8
P0ADZ4	10251.0	S	U	T	A	ETD	FT	3	19.1	SLSTEATAK	907.5	M	I	0.0	0.0	37.7	13.4
P0ADZ4	10251.0	S	U	T	B	ETD	FT	2	19.1	KLLDYLKR	1048.7	R	K	3.0	0.4	43.2	7.8
P0ADZ4	10251.0	S	U	T	B	ETD	FT	2	19.1	SLSTEATAK	907.5	M	I	0.0	0.0	30.3	13.4
P0ADZ4	10251.0	S	U	T	C	ETD	FT	4	18.0	KLLDYLKR	1048.7	R	K	2.8	0.3	42.7	7.8
P0ADZ4	10251.0	S	U	T	C	ETD	FT	4	18.0	LLDYLKR	920.6	K	K	1.7	0.0	30.6	8.5
P0ADZ4	10251.0	S	U	T	C	ETD	FT	4	18.0	RKLLDYLK	1048.7	R	R	2.8	0.1	26.1	7.8
P0ADZ4	10251.0	S	U	T	C	ETD	FT	4	18.0	YTQLIER	922.5	R	L	0.6	0.0	49.0	16.8
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3245.6	R	K	0.0	0.0	94.0	19.2
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	0.0	0.0	69.0	18.8
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	IVSEFGR	807.4	K	D	0.0	0.0	35.5	17.1
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	KDHHSR	779.4	K	R	0.0	0.0	28.4	14.9
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	KLLDYLK	892.6	R	R	0.0	0.0	32.7	3.0
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	KLLDYLKR	1048.7	R	K	0.0	0.0	31.6	7.8
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	SLSTEATAK	907.5	M	I	0.0	0.0	36.4	13.4
P0ADZ4	10251.0	S	U	T	A	ETD+CID	LIT	8	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	6.0	0.7	72.4	19.1
P0ADZ4	10251.0	S	U	T	A	ETD+CID	LIT	8	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	5.9	0.8	0.0	0.0
P0ADZ4	10251.0	S	U	T	A	ETD+CID	LIT	8	67.4	IVSEFGR	807.4	K	D	2.0	0.0	37.3	17.1
P0ADZ4	10251.0	S	U	T	A	ETD+CID	LIT	8	67.4	KDHHSR	779.4	K	R	2.2	0.5	18.8	14.9
P0ADZ4	10251.0	S	U	T	A	ETD+CID	LIT	8	67.4	KDHHSRR	935.5	K	G	2.0	0.4	0.0	0.0
P0ADZ4	10251.0	S	U	T	A	ETD+CID	LIT	8	67.4	KLLDYLK	892.6	R	R	2.5	0.3	34.1	3.0
P0ADZ4	10251.0	S	U	T	A	ETD+CID	LIT	8	67.4	SLSTEATAK	907.5	M	I	0.0	0.0	31.5	13.6
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	3	42.7	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3245.6	R	K	5.7	0.6	0.0	0.0
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	3	42.7	KLLDYLK	892.6	R	R	2.5	0.3	0.0	0.0
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	3	42.7	KLLDYLKR	1048.7	R	K	2.0	0.7	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3245.6	R	K	5.7	0.6	94.0	19.2
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	6.6	0.0	69.0	18.8
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	IVSEFGR	807.4	K	D	1.9	0.7	35.5	17.1
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	KDHHSR	779.4	K	R	2.2	0.0	28.4	14.9
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	KLLDYLK	892.6	R	R	2.5	0.3	32.7	3.0
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	KLLDYLKR	1048.7	R	K	2.0	0.7	0.0	0.0
P0ADZ4	10251.0	S	U	T	B	ETD+CID	LIT	7	67.4	SLSTEATAK	907.5	M	I	0.0	0.0	36.4	13.4
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	3.2	0.5	0.0	0.0
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	3.4	0.4	75.1	18.9
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	IVSEFGR	807.4	K	D	2.0	0.0	37.8	17.1
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	KDHHSR	779.4	K	R	2.5	0.0	18.8	14.9
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	KDHHSRR	935.5	K	G	2.0	0.7	26.6	14.5
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	KLLDYLKR	1048.7	R	K	2.6	0.8	0.0	0.0
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	LLDYLKR	920.6	K	K	3.6	0.6	35.2	7.8
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	SLSTEATAK	907.5	M	I	0.0	0.0	33.7	13.6
P0ADZ4	10251.0	S	U	T	C	ETD+CID	LIT	9	76.4	YTQLIER	922.5	R	L	2.7	0.5	36.2	16.8
P0ADZ4	10251.0	S	U	T	B	HCD	FT	7	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3245.6	R	K	0.0	0.0	94.0	19.2
P0ADZ4	10251.0	S	U	T	B	HCD	FT	7	67.4	DANDTGSTEVQVALLTAQINHLQGHFAEHKK	3372.7	R	D	0.0	0.0	69.0	18.8
P0ADZ4	10251.0	S	U	T	B	HCD	FT	7	67.4	IVSEFGR	807.4	K	D	0.0	0.0	35.5	17.1
P0ADZ4	10251.0	S	U	T	B	HCD	FT	7	67.4	KDHHSR	779.4	K	R	0.0	0.0	28.4	14.9
P0ADZ4	10251.0	S	U	T	B	HCD	FT	7	67.4	KLLDYLK	892.6	R	R	0.0	0.0	32.7	3.0
P0ADZ4	10251.0	S	U	T	B	HCD	FT	7	67.4	KLLDYLKR	1048.7	R	K	0.0	0.0	31.6	7.8
P0ADZ4	10251.0	S	U	T	B	HCD	FT	7	67.4	SLSTEATAK	907.5	M	I	0.0	0.0	36.4	13.4
P0ADZ4	10251.0	S	U	T	A	HCD	FT	2	42.7	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	3.1	0.0	21.8	18.6
P0ADZ4	10251.0	S	U	T	A	HCD	FT	2	42.7	KLLDYLKR	1048.7	R	K	2.6	0.3	24.7	7.8
P0ADZ4	10251.0	S	U	T	C	HCD	FT	4	50.6	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3244.6	R	K	7.9	0.0	57.2	18.9
P0ADZ4	10251.0	S	U	T	C	HCD	FT	4	50.6	IVSEFGR	807.4	K	D	2.2	0.0	38.5	17.1
P0ADZ4	10251.0	S	U	T	C	HCD	FT	4	50.6	KLLDYLKR	1048.7	R	K	3.2	0.3	23.6	7.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADZ4	10251.0	S	U	T	C	HCD	FT	4	50.6	LLDYLK	764.5	K	R	1.7	0.0	25.0	11.5
P0ADP9	10255.7	G	U	T	A	CID	LIT	6	76.4	DAVIPGLQK	940.5	K	D	2.0	0.6	9.4	10.8
P0ADP9	10255.7	G	U	T	A	CID	LIT	6	76.4	DAVIPGLQKDYEEDFK	1866.9	K	T	3.0	0.0	34.9	11.1
P0ADP9	10255.7	G	U	T	A	CID	LIT	6	76.4	DYEEDFKTALLR	1499.7	K	A	3.5	0.5	52.8	10.8
P0ADP9	10255.7	G	U	T	A	CID	LIT	6	76.4	EPDLNLLQFLQK	1457.8	K	L	2.7	0.0	33.4	12.0
P0ADP9	10255.7	G	U	T	A	CID	LIT	6	76.4	ESGFDGELADLTDDILIYHLK	2364.2	K	M	2.2	0.2	10.9	13.0
P0ADP9	10255.7	G	U	T	A	CID	LIT	6	76.4	LNEVIELLQPAWQK	1680.9	R	E	3.7	0.6	50.1	8.5
P0ADP9	10255.7	G	U	T	B	CID	LIT	5	52.8	DAVIPGLQKDYEEDFK	1866.9	K	T	2.3	0.0	29.4	11.8
P0ADP9	10255.7	G	U	T	B	CID	LIT	5	52.8	DYEEDFK	945.4	K	T	2.4	0.0	23.2	3.0
P0ADP9	10255.7	G	U	T	B	CID	LIT	5	52.8	DYEEDFKTALLR	1499.7	K	A	3.8	0.6	54.3	11.5
P0ADP9	10255.7	G	U	T	B	CID	LIT	5	52.8	EPDLNLLQFLQK	1457.8	K	L	3.1	0.0	33.9	11.5
P0ADP9	10255.7	G	U	T	B	CID	LIT	5	52.8	LNEVIELLQPAWQK	1680.9	R	E	4.7	0.6	61.8	9.5
P0ADP9	10255.7	G	T	A	B	CID	LIT	2	22.5	DAVIPGLQK	940.5	K	D	2.2	0.8	17.0	7.8
P0ADP9	10255.7	G	T	A	B	CID	LIT	2	22.5	DDILIYHLKMR	1416.8	T	D	2.8	0.7	27.3	15.4
P0ADP9	10255.7	G	U	A	B	CID	LIT	2	22.5	DAVIPGLQK	940.5	K	D	2.0	0.0	38.4	7.8
P0ADP9	10255.7	G	U	A	B	CID	LIT	2	22.5	DDILIYHLKMR	1416.8	T	D	2.8	0.7	22.2	15.8
P0ADP9	10255.7	S	U	T	A	CID	LIT	5	82.0	DSAKDAVIPGLQKDYEEDFK	2268.1	R	T	2.9	0.5	2.4	17.2
P0ADP9	10255.7	S	U	T	A	CID	LIT	5	82.0	DYEEDFKTALLR	1499.7	K	A	2.0	0.4	25.1	16.3
P0ADP9	10255.7	S	U	T	A	CID	LIT	5	82.0	ESGFDGELADLTDDILIYHLK	2364.2	K	M	4.2	0.8	59.9	19.6
P0ADP9	10255.7	S	U	T	A	CID	LIT	5	82.0	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	5.9	0.8	45.0	12.6
P0ADP9	10255.7	S	U	T	A	CID	LIT	5	82.0	RLNEVIELLQPAWQKEPDLNLLQFLQK	3275.8	K	L	3.8	0.0	24.9	9.5
P0ADP9	10255.7	S	U	T	B	CID	LIT	4	66.3	DYEEDFKTALLR	1499.7	K	A	2.7	0.7	31.6	16.4
P0ADP9	10255.7	S	U	T	B	CID	LIT	4	66.3	ESGFDGELADLTDDILIYHLK	2364.2	K	M	4.2	0.6	41.2	19.7
P0ADP9	10255.7	S	U	T	B	CID	LIT	4	66.3	LNEVIELLQPAWQK	1680.9	R	E	3.7	0.3	15.6	14.3
P0ADP9	10255.7	S	U	T	B	CID	LIT	4	66.3	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	6.9	0.7	54.7	12.8
P0ADP9	10255.7	S	U	T	C	CID	LIT	3	57.3	DSAKDAVIPGLQKDYEEDFK	2268.1	R	T	2.6	0.4	0.0	0.0
P0ADP9	10255.7	S	U	T	C	CID	LIT	3	57.3	DYEEDFKTALLR	1499.7	K	A	2.5	0.4	29.5	16.3
P0ADP9	10255.7	S	U	T	C	CID	LIT	3	57.3	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	6.5	0.0	47.8	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADP9	10255.7	S	U	T	B	ETD	LIT	4	69.7	DYEEDFKTALLR	1499.7	K	A	2.1	0.6	12.6	16.8
P0ADP9	10255.7	S	U	T	B	ETD	LIT	4	69.7	ESGFDGELADLTDDILIYHLK	2364.2	K	M	5.5	0.0	47.8	19.8
P0ADP9	10255.7	S	U	T	B	ETD	LIT	4	69.7	LAKESGFDGELADLTDDILIYHLK	2676.4	K	M	5.2	0.0	32.6	18.5
P0ADP9	10255.7	S	U	T	B	ETD	LIT	4	69.7	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	3.5	0.0	36.1	12.6
P0ADP9	10255.7	S	U	T	C	ETD	LIT	2	30.3	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	3.4	0.0	32.7	13.0
P0ADP9	10255.7	S	U	T	C	ETD	LIT	2	30.3	RLNEVIELLQPAWQKEPDLNLLQFLQK	3275.8	K	L	2.7	0.2	24.7	9.5
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	67.4	DYEEDFKTALLR	1499.7	K	A	0.0	0.0	30.5	16.3
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	67.4	ESGFDGELADLTDDILIYHLK	2364.2	K	M	0.0	0.0	36.6	19.5
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	67.4	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	0.0	0.0	49.5	12.6
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	67.4	RLNEVIELLQPAWQKEPDLNLLQFLQK	3275.8	K	L	0.0	0.0	19.8	10.4
P0ADP9	10255.7	S	U	T	A	ETD+CID	LIT	4	76.4	DAVIPGLQKDYEEDFKTALLR	2421.3	K	A	3.6	0.0	14.2	16.1
P0ADP9	10255.7	S	U	T	A	ETD+CID	LIT	4	76.4	DYEEDFKTALLR	1499.7	K	A	2.1	0.5	1.5	16.4
P0ADP9	10255.7	S	U	T	A	ETD+CID	LIT	4	76.4	ESGFDGELADLTDDILIYHLK	2364.2	K	M	3.0	0.8	0.0	0.0
P0ADP9	10255.7	S	U	T	A	ETD+CID	LIT	4	76.4	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	5.9	0.0	47.6	13.0
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	66.3	DYEEDFKTALLR	1499.7	K	A	2.3	0.6	0.0	0.0
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	66.3	ESGFDGELADLTDDILIYHLK	2364.2	K	M	3.5	0.6	0.0	0.0
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	66.3	LNEVIELLQPAWQK	1680.9	R	E	2.5	0.3	0.0	0.0
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	4	66.3	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	5.5	0.7	0.0	0.0
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	5	67.4	DYEEDFKTALLR	1499.7	K	A	2.3	0.6	30.5	16.3
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	5	67.4	ESGFDGELADLTDDILIYHLK	2364.2	K	M	3.5	0.7	36.6	19.5
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	5	67.4	LNEVIELLQPAWQK	1680.9	R	E	2.5	0.3	0.0	0.0
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	5	67.4	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	5.5	0.7	49.5	12.6
P0ADP9	10255.7	S	U	T	B	ETD+CID	LIT	5	67.4	RLNEVIELLQPAWQKEPDLNLLQFLQK	3275.8	K	L	5.1	0.0	19.8	10.4
P0ADP9	10255.7	S	U	T	C	ETD+CID	LIT	2	42.7	DYEEDFKTALLR	1499.7	K	A	2.4	0.7	11.0	16.9
P0ADP9	10255.7	S	U	T	C	ETD+CID	LIT	2	42.7	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	6.2	0.0	47.9	12.6
P0ADP9	10255.7	S	U	T	B	HCD	FT	4	67.4	DYEEDFKTALLR	1499.7	K	A	0.0	0.0	30.5	16.3
P0ADP9	10255.7	S	U	T	B	HCD	FT	4	67.4	ESGFDGELADLTDDILIYHLK	2364.2	K	M	0.0	0.0	36.6	19.5
P0ADP9	10255.7	S	U	T	B	HCD	FT	4	67.4	LNEVIELLQPAWQKEPDLNLLQFLQK	3119.7	R	L	0.0	0.0	49.5	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADP9	10255.7	S	U	T	B	HCD	FT	4	67.4	RLNEVIELLQPAWQKEPDLNLLQFLQK	3275.8	K	L	0.0	0.0	19.8	10.4
P0AB65	10281.5	G	U	T	A	CID	LIT	2	23.9	LMQWLK	818.5	K	S	2.2	0.1	14.4	16.1
P0AB65	10281.5	G	U	T	A	CID	LIT	2	23.9	VLSEPHHPSGELTDFR	1820.9	R	I	3.3	0.8	40.4	12.6
P0AB65	10281.5	G	T	T	A	CID	LIT	2	26.1	LGLTGYAK	822.5	R	N	2.2	0.7	16.8	13.2
P0AB65	10281.5	G	T	T	A	CID	LIT	2	26.1	VLSEPHHPSGELTDFR	1820.9	R	I	2.5	0.7	25.3	13.0
P0AB65	10281.5	G	U	T	B	CID	LIT	5	42.4	LGLTGYAK	822.5	R	N	2.2	0.0	51.0	13.2
P0AB65	10281.5	G	U	T	B	CID	LIT	5	42.4	LMQWLK	818.5	K	S	2.1	0.2	14.9	16.3
P0AB65	10281.5	G	U	T	B	CID	LIT	5	42.4	VLSEPHHPSGELTDFR	1820.9	R	I	3.6	0.0	22.8	12.6
P0AB65	10281.5	G	U	T	B	CID	LIT	5	42.4	YTTQYEAK	1003.5	R	R	2.0	0.0	21.1	8.5
P0AB65	10281.5	G	U	T	B	CID	LIT	5	42.4	YTTQYEAKR	1159.6	R	L	2.4	0.8	35.2	12.8
P0AB65	10281.5	S	U	T	B	ETD	LIT	2	26.1	VLSEPHHPSGELTDFR	1820.9	R	I	2.8	0.5	39.2	16.4
P0AB65	10281.5	S	U	T	B	ETD	LIT	2	26.1	YTTQYEAK	1003.5	R	R	1.5	0.4	15.4	13.8
P0AD33	10299.6	G	U	T	A	CID	LIT	4	41.5	AEAEQTLAALTEK	1374.7	R	A	4.8	0.8	85.2	11.8
P0AD33	10299.6	G	U	T	A	CID	LIT	4	41.5	ITPTFTEESDGVR	1451.7	K	L	3.1	0.8	49.4	12.0
P0AD33	10299.6	G	U	T	A	CID	LIT	4	41.5	SVESEPCKITPTFTEESDGVR	2368.1	R	L	5.3	0.7	59.1	10.4
P0AD33	10299.6	G	U	T	A	CID	LIT	4	41.5	VFANRAEAEQTLAALTEK	1962.0	R	A	6.1	0.7	73.3	13.4
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	AEAEQTLAALTEK	1374.7	R	A	5.1	0.8	86.9	13.0
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	ARSVESEPCK	1162.6	K	I	3.2	0.0	39.5	11.1
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	ITPTFTEESDGVR	1451.7	K	L	3.4	0.9	73.0	11.1
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	ITPTFTEESDGVRLDIDFTFACEAEMLIFQLGLR	3934.9	K	-	5.4	0.6	61.3	10.0
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	87.0	0.0
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	SVESEPCK	935.4	R	I	2.7	0.0	38.1	7.0
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	SVESEPCKITPTFTEESDGVR	2368.1	R	L	4.1	0.6	54.0	10.4
P0AD33	10299.6	G	T	T	A	CID	LIT	8	98.9	VFANRAEAEQTLAALTEK	1962.0	R	A	5.4	0.7	65.5	13.0
P0AD33	10299.6	G	T	A	A	CID	LIT	5	41.5	DCTASYSRVFANRAEA	1817.8	S	E	2.6	0.0	33.7	10.4
P0AD33	10299.6	G	T	A	A	CID	LIT	5	41.5	DETPVCCCM	1171.4	A	D	2.8	0.0	41.4	3.0
P0AD33	10299.6	G	T	A	A	CID	LIT	5	41.5	DETPVCCCMDVGTIM	1819.7	A	D	0.0	0.0	27.1	3.0
P0AD33	10299.6	G	T	A	A	CID	LIT	5	41.5	DNSDCTASYSRVFANRAEA	2133.9	M	E	3.6	0.0	36.5	3.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AD33	10299.6	G	T	A	A	CID	LIT	5	41.5	SKCSADETPVCCCM	1720.6	M	D	0.0	0.0	53.3	0.0
P0AD33	10299.6	G	U	T	B	CID	LIT	2	27.7	AEAEQTLAALTEK	1374.7	R	A	3.8	0.6	66.6	11.8
P0AD33	10299.6	G	U	T	B	CID	LIT	2	27.7	ITPTFTEESDGVR	1451.7	K	L	2.4	0.0	56.2	12.6
P0AD33	10299.6	G	T	A	B	CID	LIT	2	26.6	DCTASYSRVFANRAEA	1817.8	S	E	2.6	0.0	42.2	10.4
P0AD33	10299.6	G	T	A	B	CID	LIT	2	26.6	DETPVCCCM	1171.4	A	D	2.2	0.0	36.7	3.0
P0AD33	10299.6	G	U	A	B	CID	LIT	3	34.0	DCTASYSRVFANRA	1617.7	S	E	2.6	0.4	17.2	11.8
P0AD33	10299.6	G	U	A	B	CID	LIT	3	34.0	DCTASYSRVFANRAEA	1817.8	S	E	3.5	0.0	20.2	10.8
P0AD33	10299.6	G	U	A	B	CID	LIT	3	34.0	EQTLAALTEKARSVES	1732.9	A	E	3.5	0.0	25.3	15.9
P0AD33	10299.6	S	U	T	A	CID	LIT	3	41.5	AEAEQTLAALTEK	1374.7	R	A	4.1	0.5	63.0	16.5
P0AD33	10299.6	S	U	T	A	CID	LIT	3	41.5	SVESEPCKITPTFTEESDGVR	2368.1	R	L	4.8	0.5	68.8	16.8
P0AD33	10299.6	S	U	T	A	CID	LIT	3	41.5	VFANRAEAEQTLAALTEK	1962.0	R	A	6.2	0.6	70.1	16.9
P0AD33	10299.6	S	U	T	B	CID	LIT	4	74.5	AEAEQTLAALTEK	1374.7	R	A	3.5	0.5	51.6	16.4
P0AD33	10299.6	S	U	T	B	CID	LIT	4	74.5	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	77.6	0.0
P0AD33	10299.6	S	U	T	B	CID	LIT	4	74.5	SVESEPCKITPTFTEESDGVR	2368.1	R	L	4.1	0.5	57.4	16.8
P0AD33	10299.6	S	U	T	B	CID	LIT	4	74.5	VFANRAEAEQTLAALTEK	1962.0	R	A	5.0	0.6	63.0	17.6
P0AD33	10299.6	S	U	T	C	CID	LIT	4	74.5	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	76.8	0.0
P0AD33	10299.6	S	U	T	C	CID	LIT	4	74.5	SVESEPCK	935.4	R	I	2.0	0.7	23.7	11.5
P0AD33	10299.6	S	U	T	C	CID	LIT	4	74.5	SVESEPCKITPTFTEESDGVR	2368.1	R	L	4.3	0.4	46.3	16.7
P0AD33	10299.6	S	U	T	C	CID	LIT	4	74.5	VFANRAEAEQTLAALTEK	1962.0	R	A	5.7	0.6	85.6	16.9
P0AD33	10299.6	S	U	T	A	ETD	LIT	4	33.0	AEAEQTLAALTEK	1374.7	R	A	3.9	0.4	49.5	17.6
P0AD33	10299.6	S	U	T	A	ETD	LIT	4	33.0	ITPTFTEESDGVR	1451.7	K	L	2.4	0.0	53.2	16.8
P0AD33	10299.6	S	U	T	A	ETD	LIT	4	33.0	VFANR	606.3	R	A	1.0	0.1	22.8	14.0
P0AD33	10299.6	S	U	T	A	ETD	LIT	4	33.0	VFANRAEAEQTLAALTEK	1962.0	R	A	7.0	0.6	73.8	17.9
P0AD33	10299.6	S	U	T	B	ETD	LIT	4	60.6	AEAEQTLAALTEK	1374.7	R	A	2.7	0.3	26.4	16.4
P0AD33	10299.6	S	U	T	B	ETD	LIT	4	60.6	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	27.6	0.0
P0AD33	10299.6	S	U	T	B	ETD	LIT	4	60.6	SVESEPCK	935.4	R	I	1.5	0.6	13.8	11.5
P0AD33	10299.6	S	U	T	B	ETD	LIT	4	60.6	VFANRAEAEQTLAALTEK	1962.0	R	A	5.2	0.6	60.0	17.9
P0AD33	10299.6	S	U	T	C	ETD	LIT	4	41.5	AEAEQTLAALTEK	1374.7	R	A	3.3	0.3	27.5	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AD33	10299.6	S	U	T	C	ETD	LIT	4	41.5	SVESEPCK	935.4	R	I	1.1	0.5	17.6	11.5
P0AD33	10299.6	S	U	T	C	ETD	LIT	4	41.5	SVESEPCKITPTFTEESDGVR	2368.1	R	L	4.1	0.0	28.7	16.3
P0AD33	10299.6	S	U	T	C	ETD	LIT	4	41.5	VFANRAEAEQTLAALTEK	1962.0	R	A	3.0	0.7	46.7	17.3
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	AEAEQTLAALTEK	1374.7	R	A	0.0	0.0	63.4	16.4
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	90.8	0.0
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	SVESEPCK	935.4	R	I	0.0	0.0	23.4	11.5
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	VFANRAEAEQTLAALTEK	1962.0	R	A	0.0	0.0	70.5	18.1
P0AD33	10299.6	S	U	T	A	ETD+CID	LIT	3	27.7	AEAEQTLAALTEK	1374.7	R	A	3.7	0.5	64.3	17.6
P0AD33	10299.6	S	U	T	A	ETD+CID	LIT	3	27.7	SVESEPCK	935.4	R	I	2.0	0.7	28.2	11.5
P0AD33	10299.6	S	U	T	A	ETD+CID	LIT	3	27.7	VFANRAEAEQTLAALTEK	1962.0	R	A	6.2	0.6	71.8	17.3
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	AEAEQTLAALTEK	1374.7	R	A	4.2	0.5	63.4	16.4
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	90.8	0.0
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	SVESEPCK	935.4	R	I	1.7	0.5	23.4	11.5
P0AD33	10299.6	S	U	T	B	ETD+CID	LIT	4	60.6	VFANRAEAEQTLAALTEK	1962.0	R	A	5.8	0.6	70.5	18.1
P0AD33	10299.6	S	U	T	C	ETD+CID	LIT	2	52.1	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	70.5	0.0
P0AD33	10299.6	S	U	T	C	ETD+CID	LIT	2	52.1	VFANRAEAEQTLAALTEK	1962.0	R	A	5.9	0.6	55.7	17.0
P0AD33	10299.6	S	U	T	B	HCD	FT	4	60.6	AEAEQTLAALTEK	1374.7	R	A	0.0	0.0	63.4	16.4
P0AD33	10299.6	S	U	T	B	HCD	FT	4	60.6	SKCSADETPVCCCMDVGTIMDNSDCTASYSR	3577.4	M	V	0.0	0.0	90.8	0.0
P0AD33	10299.6	S	U	T	B	HCD	FT	4	60.6	SVESEPCK	935.4	R	I	0.0	0.0	23.4	11.5
P0AD33	10299.6	S	U	T	B	HCD	FT	4	60.6	VFANRAEAEQTLAALTEK	1962.0	R	A	0.0	0.0	70.5	18.1
P0AAP3	10299.8	G	U	T	A	CID	LIT	4	36.3	EVSQSVDDTIELVR	1589.8	R	A	3.8	0.8	63.6	12.8
P0AAP3	10299.8	G	U	T	A	CID	LIT	4	36.3	GQIDALER	901.5	R	S	2.5	0.4	24.5	13.6
P0AAP3	10299.8	G	U	T	A	CID	LIT	4	36.3	IRGQIDALER	1170.7	R	S	2.6	0.0	28.8	11.5
P0AAP3	10299.8	G	U	T	A	CID	LIT	4	36.3	SLEGDAECR	1036.4	R	A	2.7	0.0	46.4	6.0
P0AAP3	10299.8	G	U	T	B	CID	LIT	5	57.1	AILQQIAAVR	1082.7	R	G	3.0	0.3	34.1	7.8
P0AAP3	10299.8	G	U	T	B	CID	LIT	5	57.1	ETFDRNDCYSR	1462.6	R	E	2.8	0.0	18.2	3.0
P0AAP3	10299.8	G	U	T	B	CID	LIT	5	57.1	EVSQSVDDTIELVR	1589.8	R	A	4.2	0.5	60.3	12.8
P0AAP3	10299.8	G	U	T	B	CID	LIT	5	57.1	GQIDALER	901.5	R	S	2.3	0.0	37.6	13.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAP3	10299.8	G	U	T	B	CID	LIT	5	57.1	SLEGDAECR	1036.4	R	A	2.3	0.0	22.2	6.0
P0AAP3	10299.8	G	U	A	B	CID	LIT	2	22.0	DALERSLEG	989.5	I	D	2.8	0.4	29.5	16.3
P0AAP3	10299.8	G	U	A	B	CID	LIT	2	22.0	DTIELVRAYLK	1320.8	D	-	3.2	0.0	37.4	10.0
P0AEM4	10322.9	G	T	T	A	CID	LIT	3	42.3	ETTDAPVTNSR	1190.6	R	A	2.5	0.8	28.5	12.0
P0AEM4	10322.9	G	T	T	A	CID	LIT	3	42.3	LMQPGSSDINLER	1459.7	K	V	3.6	0.0	56.4	12.3
P0AEM4	10322.9	G	T	T	A	CID	LIT	3	42.3	TTASTSTSVTLSDAQAK	1668.8	K	L	4.2	0.0	70.4	13.4
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	GEVLAVGNGR	971.5	R	I	3.6	0.7	50.9	12.0
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	ILENGEVKPLDVK	1453.8	R	V	3.9	0.8	59.4	10.4
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	MNIRPLHDR	1151.6	-	V	3.3	0.5	38.2	13.6
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	SAGGIVLTGSAAAK	1202.7	K	S	4.6	0.8	78.8	11.5
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	3.4	0.5	32.7	13.6
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	STRGEVLAVGNGR	1315.7	K	I	4.6	0.6	48.0	13.6
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	VGDIVIFNDGYGVK	1495.8	K	S	3.9	0.6	52.0	12.8
P0A6F9	10369.0	G	U	T	A	CID	LIT	8	88.7	VGDIVIFNDGYGVKSEK	1839.9	K	I	4.8	0.0	53.9	12.8
P0A6F9	10369.0	G	T	T	A	CID	LIT	3	38.1	MNIRPLHDR	1151.6	-	V	2.3	0.2	0.0	0.0
P0A6F9	10369.0	G	T	T	A	CID	LIT	3	38.1	SAGGIVLTGSAAAK	1202.7	K	S	4.1	0.5	35.0	12.6
P0A6F9	10369.0	G	T	T	A	CID	LIT	3	38.1	VGDIVIFNDGYGVK	1495.8	K	S	4.0	0.8	50.0	13.4
P0A6F9	10369.0	G	U	A	A	CID	LIT	5	30.9	DGYGVKSEKI	1095.6	N	D	2.0	0.6	8.1	13.2
P0A6F9	10369.0	G	U	A	A	CID	LIT	5	30.9	DGYGVKSEKIDN	1324.6	N	E	3.3	0.5	25.1	12.8
P0A6F9	10369.0	G	U	A	A	CID	LIT	5	30.9	DVKVGDIVIFN	1218.7	L	D	3.1	0.8	34.8	13.4
P0A6F9	10369.0	G	U	A	A	CID	LIT	5	30.9	MNIRPLH	880.5	-	D	2.4	0.8	15.2	12.0
P0A6F9	10369.0	G	U	A	A	CID	LIT	5	30.9	NIRPLH	749.4	M	D	0.0	0.0	26.3	0.0
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	GEVLAVGNGR	971.5	R	I	3.2	0.4	18.3	12.0
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	ILENGEVKPLDVK	1453.8	R	V	3.7	0.6	29.1	7.0
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	MNIRPLHDR	1151.6	-	V	2.1	0.5	12.8	12.3
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	MNIRPLHDRVIVK	1590.9	-	R	2.4	0.2	7.5	4.8
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	SAGGIVLTGSAAAK	1202.7	K	S	4.9	0.7	59.1	11.5
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	STRGEVLAVGNGR	1315.7	K	I	4.0	0.6	34.8	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	VGDIVIFNDGYGVK	1495.8	K	S	4.0	0.9	45.0	13.2
P0A6F9	10369.0	G	T	T	B	CID	LIT	8	72.2	VGDIVIFNDGYGVKSEK	1839.9	K	I	3.3	0.0	22.8	12.8
P0A6F9	10369.0	G	U	T	B	CID	LIT	5	51.5	MNIRPLHDR	1151.6	-	V	2.7	0.8	23.3	11.8
P0A6F9	10369.0	G	U	T	B	CID	LIT	5	51.5	NIRPLHDR	1020.6	M	V	0.0	0.0	28.5	10.8
P0A6F9	10369.0	G	U	T	B	CID	LIT	5	51.5	SAGGIVLTGSAAAK	1202.7	K	S	3.9	0.8	22.1	12.6
P0A6F9	10369.0	G	U	T	B	CID	LIT	5	51.5	STRGEVLAVGNGR	1315.7	K	I	4.2	0.6	47.2	13.0
P0A6F9	10369.0	G	U	T	B	CID	LIT	5	51.5	VGDIVIFNDGYGVK	1495.8	K	S	4.1	0.6	31.7	12.8
P0A6F9	10369.0	G	T	A	B	CID	LIT	2	17.5	DGYGVKSEKI	1095.6	N	D	2.8	0.7	25.0	14.0
P0A6F9	10369.0	G	T	A	B	CID	LIT	2	17.5	MNIRPLH	880.5	-	D	2.7	0.8	33.6	12.0
P0A6F9	10369.0	G	U	A	B	CID	LIT	2	17.5	DGYGVKSEKI	1095.6	N	D	2.6	0.7	21.4	13.2
P0A6F9	10369.0	G	U	A	B	CID	LIT	2	17.5	MNIRPLH	880.5	-	D	2.4	0.0	30.0	0.0
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	IDNEEVLIMSESDILAIVEA	2203.1	K	-	3.1	0.7	55.2	18.3
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	ILENGEVKPLDVK	1454.8	R	V	4.6	0.6	59.7	12.8
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	MNIRPLHDR	1151.6	-	V	2.0	0.6	24.7	14.3
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	SAGGIVLTGSAAAK	1202.7	K	S	4.8	0.7	74.2	15.9
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	4.5	0.4	61.6	19.0
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	STRGEVLAVGNGR	1316.7	K	I	2.3	0.7	11.8	17.8
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	VGDIVIFNDGYGVK	1495.8	K	S	4.6	0.7	63.2	17.2
P0A6F9	10369.0	S	U	T	A	CID	LIT	8	88.7	VGDIVIFNDGYGVKSEK	1839.9	K	I	5.0	0.7	52.8	17.1
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	GEVLAVGNGR	972.5	R	I	3.5	0.7	56.8	15.7
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	IDNEEVLIMSESDILAIVEA	2203.1	K	-	3.3	0.6	52.1	17.9
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	ILENGEVKPLDVK	1454.8	R	V	4.0	0.6	53.5	13.4
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	MNIRPLHDR	1151.6	-	V	3.0	0.5	39.4	15.9
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	SAGGIVLTGSAAAK	1202.7	K	S	4.7	0.7	67.4	15.9
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	4.5	0.3	66.0	18.9
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	VGDIVIFNDGYGVK	1495.8	K	S	4.1	0.7	54.3	17.3
P0A6F9	10369.0	S	U	T	B	CID	LIT	8	85.6	VGDIVIFNDGYGVKSEK	1839.9	K	I	4.9	0.6	65.7	17.9
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	GEVLAVGNGR	972.5	R	I	3.5	0.0	54.1	16.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	IDNEEVLIMSESDILAIVEA	2203.1	K	-	3.5	0.6	52.3	18.3
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	ILENGEVKPLDVK	1454.8	R	V	4.2	0.5	58.2	12.6
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	MNIRPLHDR	1151.6	-	V	3.2	0.4	32.1	14.3
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	SAGGIVLTGSAAAK	1202.7	K	S	4.2	0.6	64.5	15.9
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	4.1	0.3	59.2	19.0
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	STRGEVLAVGNGR	1316.7	K	I	3.1	0.2	0.0	0.0
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	VGDIVIFNDGYGVK	1495.8	K	S	4.1	0.7	50.2	17.2
P0A6F9	10369.0	S	U	T	C	CID	LIT	9	88.7	VGDIVIFNDGYGVKSEK	1839.9	K	I	4.8	0.6	76.2	17.9
P0A6F9	10369.0	S	U	T	A	CID	FT	3	45.4	ILENGEVKPLDVK	1454.8	R	V	3.0	0.0	39.8	12.6
P0A6F9	10369.0	S	U	T	A	CID	FT	3	45.4	SAGGIVLTGSAAAK	1202.7	K	S	3.4	0.0	72.1	16.2
P0A6F9	10369.0	S	U	T	A	CID	FT	3	45.4	VGDIVIFNDGYGVKSEK	1839.9	K	I	2.9	0.0	73.5	17.1
P0A6F9	10369.0	S	U	T	B	CID	FT	5	55.7	GEVLAVGNGR	972.5	R	I	3.2	0.0	51.2	16.5
P0A6F9	10369.0	S	U	T	B	CID	FT	5	55.7	ILENGEVKPLDVK	1454.8	R	V	2.3	0.0	46.8	12.6
P0A6F9	10369.0	S	U	T	B	CID	FT	5	55.7	SAGGIVLTGSAAAK	1202.7	K	S	2.9	0.0	45.1	16.2
P0A6F9	10369.0	S	U	T	B	CID	FT	5	55.7	STRGEVLAVGNGR	1316.7	K	I	1.9	0.7	0.0	0.0
P0A6F9	10369.0	S	U	T	B	CID	FT	5	55.7	VGDIVIFNDGYGVK	1495.8	K	S	4.3	0.8	63.4	16.4
P0A6F9	10369.0	S	U	T	C	CID	FT	2	27.8	ILENGEVKPLDVK	1454.8	R	V	3.4	0.0	38.8	12.3
P0A6F9	10369.0	S	U	T	C	CID	FT	2	27.8	SAGGIVLTGSAAAK	1202.7	K	S	2.8	0.0	69.7	15.8
P0A6F9	10369.0	S	U	T	A	ETD	LIT	7	70.1	GEVLAVGNGR	972.5	R	I	3.4	0.4	43.9	15.9
P0A6F9	10369.0	S	U	T	A	ETD	LIT	7	70.1	ILENGEVKPLDVK	1453.8	R	V	4.6	0.7	50.4	10.4
P0A6F9	10369.0	S	U	T	A	ETD	LIT	7	70.1	MNIRPLHDR	1151.6	-	V	3.7	0.4	34.4	15.9
P0A6F9	10369.0	S	U	T	A	ETD	LIT	7	70.1	SAGGIVLTGSAAAK	1202.7	K	S	3.8	0.6	43.7	15.8
P0A6F9	10369.0	S	U	T	A	ETD	LIT	7	70.1	VGDIVIFNDGYGVK	1495.8	K	S	3.7	0.7	66.5	17.4
P0A6F9	10369.0	S	U	T	A	ETD	LIT	7	70.1	VGDIVIFNDGYGVKSEK	1839.9	K	I	3.8	0.5	69.5	17.8
P0A6F9	10369.0	S	U	T	A	ETD	LIT	7	70.1	VIVKR	614.4	R	K	1.6	0.7	21.6	9.0
P0A6F9	10369.0	S	U	T	B	ETD	LIT	7	68.0	GEVLAVGNGR	972.5	R	I	3.2	0.4	0.0	0.0
P0A6F9	10369.0	S	U	T	B	ETD	LIT	7	68.0	ILENGEVKPLDVK	1453.8	R	V	5.3	0.7	49.1	10.4
P0A6F9	10369.0	S	U	T	B	ETD	LIT	7	68.0	MNIRPLHDR	1151.6	-	V	3.6	0.4	39.9	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6F9	10369.0	S	U	T	B	ETD	LIT	7	68.0	SAGGIVLTGSAAAK	1202.7	K	S	3.9	0.5	51.4	16.7
P0A6F9	10369.0	S	U	T	B	ETD	LIT	7	68.0	STRGEVLAVGNGR	1315.7	K	I	3.5	0.5	38.8	17.2
P0A6F9	10369.0	S	U	T	B	ETD	LIT	7	68.0	VGDIVIFNDGYGVK	1495.8	K	S	4.0	0.7	60.4	17.3
P0A6F9	10369.0	S	U	T	B	ETD	LIT	7	68.0	VGDIVIFNDGYGVKSEK	1839.9	K	I	6.8	0.5	78.2	17.9
P0A6F9	10369.0	S	U	T	C	ETD	LIT	6	68.0	ILENGEVKPLDVK	1454.8	R	V	5.9	0.5	54.6	11.8
P0A6F9	10369.0	S	U	T	C	ETD	LIT	6	68.0	MNIRPLHDR	1151.6	-	V	3.7	0.5	33.4	15.9
P0A6F9	10369.0	S	U	T	C	ETD	LIT	6	68.0	SAGGIVLTGSAAAK	1202.7	K	S	3.7	0.5	55.5	15.9
P0A6F9	10369.0	S	U	T	C	ETD	LIT	6	68.0	STRGEVLAVGNGR	1315.7	K	I	3.5	0.5	0.0	0.0
P0A6F9	10369.0	S	U	T	C	ETD	LIT	6	68.0	VGDIVIFNDGYGVK	1495.8	K	S	3.7	0.6	55.8	17.4
P0A6F9	10369.0	S	U	T	C	ETD	LIT	6	68.0	VGDIVIFNDGYGVKSEK	1839.9	K	I	7.3	0.6	0.0	0.0
P0A6F9	10369.0	S	U	T	A	ETD	FT	2	22.7	ILENGEVKPLDVK	1453.8	R	V	2.0	0.0	20.6	12.6
P0A6F9	10369.0	S	U	T	A	ETD	FT	2	22.7	MNIRPLHDR	1151.6	-	V	0.0	0.0	23.0	14.1
P0A6F9	10369.0	S	U	T	B	ETD	FT	2	27.8	ILENGEVKPLDVK	1453.8	R	V	4.0	0.0	51.0	12.6
P0A6F9	10369.0	S	U	T	B	ETD	FT	2	27.8	SAGGIVLTGSAAAK	1202.7	K	S	2.2	0.0	57.3	16.7
P0A6F9	10369.0	S	U	T	C	ETD	FT	5	50.5	GEVLAVGNGR	972.5	R	I	0.7	0.0	35.7	16.0
P0A6F9	10369.0	S	U	T	C	ETD	FT	5	50.5	ILENGEVKPLDVK	1454.8	R	V	3.4	0.0	48.2	12.6
P0A6F9	10369.0	S	U	T	C	ETD	FT	5	50.5	MNIRPLHDR	1151.6	-	V	2.6	0.7	0.0	0.0
P0A6F9	10369.0	S	U	T	C	ETD	FT	5	50.5	SAGGIVLTGSAAAK	1202.7	K	S	1.7	0.3	55.7	15.8
P0A6F9	10369.0	S	U	T	C	ETD	FT	5	50.5	STRGEVLAVGNGR	1316.7	K	I	2.2	0.0	30.9	17.9
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	GEVLAVGNGR	972.5	R	I	0.0	0.0	54.4	15.7
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	IDNEEVLIMSESDILAIVEA	2203.1	K	-	0.0	0.0	53.4	18.0
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	ILENGEVKPLDVK	1454.8	R	V	0.0	0.0	60.2	12.6
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	MNIRPLHDR	1151.6	-	V	0.0	0.0	19.3	14.1
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	SAGGIVLTGSAAAK	1202.7	K	S	0.0	0.0	67.7	15.9
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	0.0	0.0	59.5	18.9
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	VGDIVIFNDGYGVK	1495.8	K	S	0.0	0.0	63.1	17.2
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	7	85.6	VGDIVIFNDGYGVKSEK	1839.9	K	I	0.0	0.0	66.7	17.2
P0A6F9	10369.0	S	U	T	A	ETD+CID	LIT	5	66.0	IDNEEVLIMSESDILAIVEA	2219.1	K	-	2.4	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6F9	10369.0	S	U	T	A	ETD+CID	LIT	5	66.0	ILENGEVKPLDVK	1454.8	R	V	5.3	0.8	50.4	12.6
P0A6F9	10369.0	S	U	T	A	ETD+CID	LIT	5	66.0	SAGGIVLTGSAAAK	1202.7	K	S	4.9	0.7	56.5	15.8
P0A6F9	10369.0	S	U	T	A	ETD+CID	LIT	5	66.0	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	4.6	0.4	73.3	18.9
P0A6F9	10369.0	S	U	T	A	ETD+CID	LIT	5	66.0	VGDIVIFNDGYGVK	1495.8	K	S	4.4	0.6	65.4	17.3
P0A6F9	10369.0	S	U	T	A	ETD+CID	LIT	5	66.0	VGDIVIFNDGYGVKSEK	1839.9	K	I	5.0	0.7	75.7	17.9
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	3	61.9	IDNEEVLIMSESDILAIVEA	2203.1	K	-	2.9	0.6	0.0	0.0
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	3	61.9	ILENGEVKPLDVK	1454.8	R	V	5.5	0.5	0.0	0.0
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	3	61.9	STRGEVLAVGNGR	1316.7	K	I	1.8	0.4	0.0	0.0
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	3	61.9	VGDIVIFNDGYGVK	1496.8	K	S	3.9	0.6	0.0	0.0
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	GEVLAVGNGR	972.5	R	I	3.5	0.0	54.4	15.7
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	IDNEEVLIMSESDILAIVEA	2203.1	K	-	2.9	0.6	53.4	18.0
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	ILENGEVKPLDVK	1454.8	R	V	5.5	0.5	60.2	12.6
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	MNIRPLHDR	1151.6	-	V	2.1	0.7	19.3	14.1
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	SAGGIVLTGSAAAK	1202.7	K	S	4.6	0.6	66.6	16.2
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	4.3	0.3	50.8	18.9
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	STRGEVLAVGNGR	1316.7	K	I	1.8	0.4	0.0	0.0
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	VGDIVIFNDGYGVK	1495.8	K	S	4.2	0.6	57.6	16.4
P0A6F9	10369.0	S	U	T	B	ETD+CID	LIT	8	88.7	VGDIVIFNDGYGVKSEK	1839.9	K	I	4.9	0.6	0.0	0.0
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	GEVLAVGNGR	972.5	R	I	3.4	0.8	58.6	15.9
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	IDNEEVLIMSESDILAIVEA	2203.1	K	-	3.2	0.4	0.0	0.0
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	ILENGEVKPLDVK	1454.8	R	V	4.2	0.7	0.0	0.0
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	MNIRPLHDR	1151.6	-	V	3.7	0.8	35.5	14.1
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	SAGGIVLTGSAAAK	1202.7	K	S	4.5	0.6	62.6	16.2
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	4.6	0.4	66.2	19.1
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	VGDIVIFNDGYGVK	1495.8	K	S	4.2	0.6	57.0	17.2
P0A6F9	10369.0	S	U	T	C	ETD+CID	LIT	7	85.6	VGDIVIFNDGYGVKSEK	1839.9	K	I	4.9	0.6	64.3	17.7
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	GEVLAVGNGR	972.5	R	I	0.0	0.0	54.4	15.7
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	IDNEEVLIMSESDILAIVEA	2203.1	K	-	0.0	0.0	53.4	18.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	ILENGEVKPLDVK	1454.8	R	V	0.0	0.0	57.7	14.3
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	MNIRPLHDR	1151.6	-	V	0.0	0.0	19.3	14.1
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	SAGGIVLTGSAAAK	1202.7	K	S	0.0	0.0	67.7	15.9
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	SEKIDNEEVLIMSESDILAIVEA	2547.3	K	-	0.0	0.0	59.5	18.9
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	VGDIVIFNDGYGVK	1495.8	K	S	0.0	0.0	63.1	17.2
P0A6F9	10369.0	S	U	T	B	HCD	FT	7	85.6	VGDIVIFNDGYGVKSEK	1839.9	K	I	0.0	0.0	66.7	17.2
P0A6F9	10369.0	S	U	T	A	HCD	FT	3	42.3	ILENGEVKPLDVK	1454.8	R	V	3.1	0.0	57.5	11.8
P0A6F9	10369.0	S	U	T	A	HCD	FT	3	42.3	SAGGIVLTGSAAAK	1202.7	K	S	4.1	0.0	64.2	16.2
P0A6F9	10369.0	S	U	T	A	HCD	FT	3	42.3	VGDIVIFNDGYGVK	1495.8	K	S	3.9	0.8	77.0	17.2
P0A6F9	10369.0	S	U	T	B	HCD	FT	4	47.4	ILENGEVKPLDVK	1454.8	R	V	3.4	0.8	61.7	13.4
P0A6F9	10369.0	S	U	T	B	HCD	FT	4	47.4	SAGGIVLTGSAAAK	1202.7	K	S	2.6	0.0	68.0	15.9
P0A6F9	10369.0	S	U	T	B	HCD	FT	4	47.4	VGDIVIFNDGYGVK	1496.8	K	S	2.8	0.0	27.8	16.9
P0A6F9	10369.0	S	U	T	B	HCD	FT	4	47.4	VIVKR	614.4	R	K	1.1	0.0	27.5	9.0
P0A6F9	10369.0	S	U	T	C	HCD	FT	2	27.8	ILENGEVKPLDVK	1454.8	R	V	2.6	0.0	51.3	12.6
P0A6F9	10369.0	S	U	T	C	HCD	FT	2	27.8	SAGGIVLTGSAAAK	1202.7	K	S	2.1	0.0	60.0	15.8
P0A7U3	10412.6	G	U	T	A	CID	LIT	6	58.7	AVESGDKKPLR	1199.7	K	T	3.6	0.5	54.8	11.8
P0A7U3	10412.6	G	U	T	A	CID	LIT	6	58.7	GPFIDLHLLK	1152.7	K	K	2.7	0.7	25.3	7.8
P0A7U3	10412.6	G	U	T	A	CID	LIT	6	58.7	KGPFIDLHLLK	1280.8	K	K	4.4	0.6	46.3	7.8
P0A7U3	10412.6	G	U	T	A	CID	LIT	6	58.7	LGEFAPTR	890.5	K	T	2.5	0.5	34.5	17.0
P0A7U3	10412.6	G	U	T	A	CID	LIT	6	58.7	QHVPVFVTDEMVGHK	1722.9	R	L	3.2	0.8	33.9	13.8
P0A7U3	10412.6	G	U	T	A	CID	LIT	6	58.7	TYRGHAADK	1018.5	R	K	2.2	0.7	18.4	12.3
P0A7U3	10412.6	G	T	T	A	CID	LIT	6	58.7	AVESGDKKPLR	1199.7	K	T	3.4	0.5	96.5	11.8
P0A7U3	10412.6	G	T	T	A	CID	LIT	6	58.7	GPFIDLHLLK	1152.7	K	K	2.6	0.7	24.4	7.8
P0A7U3	10412.6	G	T	T	A	CID	LIT	6	58.7	KGPFIDLHLLK	1280.8	K	K	4.3	0.6	43.7	7.8
P0A7U3	10412.6	G	T	T	A	CID	LIT	6	58.7	LGEFAPTR	890.5	K	T	2.5	0.8	35.0	12.8
P0A7U3	10412.6	G	T	T	A	CID	LIT	6	58.7	QHVPVFVTDEMVGHK	1722.9	R	L	2.9	0.8	28.9	13.0
P0A7U3	10412.6	G	T	T	A	CID	LIT	6	58.7	TYRGHAADK	1018.5	R	K	2.0	0.6	17.3	12.3
P0A7U3	10412.6	G	T	A	A	CID	LIT	2	40.2	DEMVGHKLGEFAPTRTYRGHAA	2443.2	T	D	3.0	0.8	6.2	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7U3	10412.6	G	T	A	A	CID	LIT	2	40.2	DLHLLKKVEKAVESG	1666.0	I	D	3.5	0.0	27.1	10.0
P0A7U3	10412.6	G	T	T	B	CID	LIT	2	25.0	LGEFAPTR	890.5	K	T	2.4	0.2	17.2	17.0
P0A7U3	10412.6	G	T	T	B	CID	LIT	2	25.0	QHVPVFVTDEMVGHK	1722.9	R	L	2.1	0.3	4.2	13.8
P0A7U3	10412.6	G	U	T	B	CID	LIT	2	20.7	AVESGDKKPLR	1199.7	K	T	3.5	0.5	60.9	12.3
P0A7U3	10412.6	G	U	T	B	CID	LIT	2	20.7	LGEFAPTR	890.5	K	T	2.7	0.4	23.2	17.0
P0A7U3	10412.6	G	T	A	B	CID	LIT	2	40.2	DEMVGHKLGEFAPTRTYRGHAA	2443.2	T	D	2.9	0.0	28.3	14.1
P0A7U3	10412.6	G	T	A	B	CID	LIT	2	40.2	DLHLLKKVEKAVESG	1666.0	I	D	3.1	0.7	36.2	10.0
P0A7U3	10412.6	G	U	A	B	CID	LIT	2	40.2	DEMVGHKLGEFAPTRTYRGHAA	2443.2	T	D	3.9	0.0	27.5	14.0
P0A7U3	10412.6	G	U	A	B	CID	LIT	2	40.2	DLHLLKKVEKAVESG	1666.0	I	D	2.4	0.7	21.0	9.5
P0A7U3	10412.6	S	U	T	A	CID	LIT	4	40.2	AVESGDKKPLR	1199.7	K	T	3.0	0.5	54.2	15.6
P0A7U3	10412.6	S	U	T	A	CID	LIT	4	40.2	GPFIDLHLLK	1152.7	K	K	2.8	0.6	44.4	9.5
P0A7U3	10412.6	S	U	T	A	CID	LIT	4	40.2	KGPFIDLHLLK	1280.8	K	K	3.6	0.6	41.8	7.0
P0A7U3	10412.6	S	U	T	A	CID	LIT	4	40.2	QHVPVFVTDEMVGHK	1722.9	R	L	3.3	0.5	29.9	18.0
P0A7U3	10412.6	S	U	T	B	CID	LIT	2	12.0	GPFIDLHLLK	1152.7	K	K	2.6	0.6	34.6	9.5
P0A7U3	10412.6	S	U	T	B	CID	LIT	2	12.0	KGPFIDLHLLK	1280.8	K	K	3.0	0.5	48.2	9.0
P0A7U3	10412.6	S	U	T	C	CID	LIT	5	48.9	AVESGDKKPLR	1199.7	K	T	3.1	0.5	67.2	15.9
P0A7U3	10412.6	S	U	T	C	CID	LIT	5	48.9	GPFIDLHLLK	1152.7	K	K	3.0	0.7	49.7	9.5
P0A7U3	10412.6	S	U	T	C	CID	LIT	5	48.9	KGPFIDLHLLK	1280.8	K	K	3.3	0.4	56.5	9.0
P0A7U3	10412.6	S	U	T	C	CID	LIT	5	48.9	LGEFAPTR	890.5	K	T	2.7	0.6	37.5	18.1
P0A7U3	10412.6	S	U	T	C	CID	LIT	5	48.9	QHVPVFVTDEMVGHK	1722.9	R	L	4.1	0.8	50.9	18.5
P0A7U3	10412.6	S	U	T	A	ETD	LIT	5	48.9	AVESGDKKPLR	1199.7	K	T	3.0	0.4	41.0	15.8
P0A7U3	10412.6	S	U	T	A	ETD	LIT	5	48.9	GPFIDLHLLK	1152.7	K	K	2.0	0.0	27.1	9.5
P0A7U3	10412.6	S	U	T	A	ETD	LIT	5	48.9	KGPFIDLHLLK	1280.8	K	K	5.4	0.6	60.7	10.0
P0A7U3	10412.6	S	U	T	A	ETD	LIT	5	48.9	LGEFAPTR	890.5	K	T	2.2	0.2	25.7	18.8
P0A7U3	10412.6	S	U	T	A	ETD	LIT	5	48.9	QHVPVFVTDEMVGHK	1722.9	R	L	3.4	0.9	45.6	18.4
P0A7U3	10412.6	S	U	T	B	ETD	LIT	4	32.6	AVESGDKKPLR	1199.7	K	T	3.3	0.4	43.5	15.8
P0A7U3	10412.6	S	U	T	B	ETD	LIT	4	32.6	GPFIDLHLLK	1152.7	K	K	2.7	0.0	37.8	9.5
P0A7U3	10412.6	S	U	T	B	ETD	LIT	4	32.6	KGPFIDLHLLK	1280.8	K	K	5.0	0.6	65.0	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7U3	10412.6	S	U	T	B	ETD	LIT	4	32.6	LGEFAPTR	890.5	K	T	2.1	0.5	0.0	0.0
P0A7U3	10412.6	S	U	T	C	ETD	LIT	5	48.9	AVESGDKKPLR	1199.7	K	T	3.3	0.5	39.8	15.8
P0A7U3	10412.6	S	U	T	C	ETD	LIT	5	48.9	GPFIDLHLLK	1152.7	K	K	3.9	0.6	50.3	9.5
P0A7U3	10412.6	S	U	T	C	ETD	LIT	5	48.9	KGPFIDLHLLK	1280.8	K	K	2.3	0.7	19.7	7.0
P0A7U3	10412.6	S	U	T	C	ETD	LIT	5	48.9	LGEFAPTR	890.5	K	T	2.0	0.5	30.3	14.9
P0A7U3	10412.6	S	U	T	C	ETD	LIT	5	48.9	QHVPVFVTDEMVGHK	1722.9	R	L	2.3	0.7	41.3	18.0
P0A7U3	10412.6	S	U	T	B	ETD+CID	LIT	3	23.9	AVESGDKKPLR	1199.7	K	T	0.0	0.0	55.4	15.6
P0A7U3	10412.6	S	U	T	B	ETD+CID	LIT	3	23.9	GPFIDLHLLK	1152.7	K	K	0.0	0.0	24.2	9.5
P0A7U3	10412.6	S	U	T	B	ETD+CID	LIT	3	23.9	KGPFIDLHLLK	1280.8	K	K	0.0	0.0	42.8	9.0
P0A7U3	10412.6	S	U	T	A	ETD+CID	LIT	3	23.9	AVESGDKKPLR	1199.7	K	T	3.2	0.6	66.1	15.6
P0A7U3	10412.6	S	U	T	A	ETD+CID	LIT	3	23.9	GPFIDLHLLK	1152.7	K	K	2.8	0.6	46.2	9.5
P0A7U3	10412.6	S	U	T	A	ETD+CID	LIT	3	23.9	KGPFIDLHLLK	1280.8	K	K	3.1	0.5	0.0	0.0
P0A7U3	10412.6	S	U	T	B	ETD+CID	LIT	3	23.9	AVESGDKKPLR	1199.7	K	T	2.5	0.5	55.4	15.6
P0A7U3	10412.6	S	U	T	B	ETD+CID	LIT	3	23.9	GPFIDLHLLK	1152.7	K	K	2.3	0.6	24.2	9.5
P0A7U3	10412.6	S	U	T	B	ETD+CID	LIT	3	23.9	KGPFIDLHLLK	1280.8	K	K	3.9	0.6	0.0	0.0
P0A7U3	10412.6	S	U	T	C	ETD+CID	LIT	6	68.5	AVESGDKKPLR	1199.7	K	T	3.0	0.5	57.8	15.6
P0A7U3	10412.6	S	U	T	C	ETD+CID	LIT	6	68.5	GPFIDLHLLK	1152.7	K	K	2.8	0.7	44.7	9.5
P0A7U3	10412.6	S	U	T	C	ETD+CID	LIT	6	68.5	KGPFIDLHLLK	1280.8	K	K	4.4	0.8	64.1	9.0
P0A7U3	10412.6	S	U	T	C	ETD+CID	LIT	6	68.5	LGEFAPTR	890.5	K	T	2.7	0.6	34.2	14.9
P0A7U3	10412.6	S	U	T	C	ETD+CID	LIT	6	68.5	QHVPVFVTDEMVGHK	1722.9	R	L	3.7	0.6	0.0	0.0
P0A7U3	10412.6	S	U	T	C	ETD+CID	LIT	6	68.5	STIFPNMIGLTIAVHNGR	1942.0	R	Q	3.4	0.4	0.0	0.0
P0A7U3	10412.6	S	U	T	B	HCD	FT	3	23.9	AVESGDKKPLR	1199.7	K	T	0.0	0.0	55.4	15.6
P0A7U3	10412.6	S	U	T	B	HCD	FT	3	23.9	GPFIDLHLLK	1152.7	K	K	0.0	0.0	24.2	9.5
P0A7U3	10412.6	S	U	T	B	HCD	FT	3	23.9	KGPFIDLHLLK	1280.8	K	K	0.0	0.0	42.8	9.0
P64476	10436.5	G	U	T	A	CID	LIT	2	14.6	DQSNLSPAQYLK	1363.7	R	R	3.9	0.6	49.0	14.5
P64476	10436.5	G	U	T	A	CID	LIT	2	14.6	DQSNLSPAQYLKR	1519.8	R	L	3.0	0.7	36.0	13.8
P52060	10438.2	G	U	T	A	CID	LIT	3	35.4	DSIVGLHGDEVK	1268.6	R	V	3.1	0.8	20.4	10.8
P52060	10438.2	G	U	T	A	CID	LIT	3	35.4	IINPQQIPPEIAALIN	1744.0	K	-	2.9	0.0	33.6	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P52060	10438.2	G	U	T	A	CID	LIT	3	35.4	LYIQPK	761.5	R	A	1.3	0.6	13.4	11.5
P52060	10438.2	S	U	T	B	CID	LIT	2	31.2	DSIVGLHGDEVK	1268.6	R	V	3.2	0.3	39.7	14.6
P52060	10438.2	S	U	T	B	CID	LIT	2	31.2	VAITAPPVDGQANSHLVK	1817.0	K	F	4.4	0.8	36.8	15.6
P52060	10438.2	S	U	T	C	CID	LIT	2	31.2	DSIVGLHGDEVK	1268.6	R	V	3.3	0.3	40.8	15.1
P52060	10438.2	S	U	T	C	CID	LIT	2	31.2	VAITAPPVDGQANSHLVK	1817.0	K	F	3.2	0.0	35.9	15.6
P52060	10438.2	S	U	T	C	ETD+CID	LIT	2	31.2	DSIVGLHGDEVK	1268.6	R	V	3.3	0.4	38.3	15.1
P52060	10438.2	S	U	T	C	ETD+CID	LIT	2	31.2	VAITAPPVDGQANSHLVK	1817.0	K	F	2.0	0.8	12.7	15.2
P39274	10450.4	G	U	A	B	CID	LIT	2	33.3	EIVFVPTGENLAIIEHT	1882.0	A	D	3.6	0.0	30.1	13.8
P39274	10450.4	G	U	A	B	CID	LIT	2	33.3	MEIREGHNKFYIN	1650.8	-	D	2.2	0.0	16.4	15.4
P39274	10450.4	S	U	T	A	CID	LIT	2	47.8	KIIPLCPFAK	1186.7	R	H	2.4	0.5	13.6	13.0
P39274	10450.4	S	U	T	A	CID	LIT	2	47.8	QIAEIVFVPTGENLAIIEHTDVDESLKGQGIGK	3520.9	K	Q	2.3	0.3	11.9	16.6
P76172	10458.5	G	T	T	A	CID	LIT	3	34.7	ILYTR	665.4	K	T	1.8	0.6	20.4	13.2
P76172	10458.5	G	T	T	A	CID	LIT	3	34.7	IQSDISQR	946.5	R	I	2.9	0.1	41.9	14.9
P76172	10458.5	G	T	T	A	CID	LIT	3	34.7	TTSGNVSAPAQSSQDGAPAEPQ	2099.9	R	-	4.5	0.0	81.7	3.0
P76172	10458.5	G	T	A	A	CID	LIT	5	69.3	DISQRIINNGVPESSFTLSIVPNDQV	2842.5	S	D	2.5	0.2	9.6	13.8
P76172	10458.5	G	T	A	A	CID	LIT	5	69.3	DQPDSQVVGHCAN	1426.6	V	D	3.5	0.7	54.1	12.6
P76172	10458.5	G	T	A	A	CID	LIT	5	69.3	DQVDQPDSQVVGHCAN	1768.8	N	D	2.8	0.7	38.5	11.5
P76172	10458.5	G	T	A	A	CID	LIT	5	69.3	DTHKILYTRTTSGNVSAPAQSSQ	2462.2	N	D	5.8	0.5	58.4	15.3
P76172	10458.5	G	T	A	A	CID	LIT	5	69.3	DTHKILYTRTTSGNVSAPAQSSQDGAPAEPQ	3227.6	N	-	4.9	0.0	66.5	13.4
P76172	10458.5	G	T	T	B	CID	LIT	3	34.7	ILYTR	665.4	K	T	1.4	0.6	11.9	13.2
P76172	10458.5	G	T	T	B	CID	LIT	3	34.7	IQSDISQR	946.5	R	I	2.9	0.1	32.2	15.8
P76172	10458.5	G	T	T	B	CID	LIT	3	34.7	TTSGNVSAPAQSSQDGAPAEPQ	2099.9	R	-	3.8	0.0	64.7	3.0
P76172	10458.5	G	T	A	B	CID	LIT	6	69.3	DGAPAEPQ	784.3	Q	-	1.8	0.0	16.8	10.4
P76172	10458.5	G	T	A	B	CID	LIT	6	69.3	DISQRIINNGVPESSFTLSIVPN	2500.3	S	D	2.1	0.7	0.0	0.0
P76172	10458.5	G	T	A	B	CID	LIT	6	69.3	DISQRIINNGVPESSFTLSIVPNDQV	2842.5	S	D	3.0	0.5	13.6	14.0
P76172	10458.5	G	T	A	B	CID	LIT	6	69.3	DQPDSQVVGHCAN	1426.6	V	D	3.4	0.7	41.7	11.8
P76172	10458.5	G	T	A	B	CID	LIT	6	69.3	DQVDQPDSQVVGHCAN	1768.8	N	D	3.4	0.7	63.7	11.1
P76172	10458.5	G	T	A	B	CID	LIT	6	69.3	DTHKILYTRTTSGNVSAPAQSSQ	2462.2	N	D	4.1	0.7	72.2	15.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB55	10584.1	G	U	T	A	CID	LIT	6	36.7	ADSLEKR	818.4	K	L	2.2	0.5	42.6	16.5
P0AB55	10584.1	G	U	T	A	CID	LIT	6	36.7	LQLLHDEGR	1080.6	R	L	3.5	0.8	63.2	12.3
P0AB55	10584.1	G	U	T	A	CID	LIT	6	36.7	LSVRPAHLAR	1119.7	R	L	3.2	0.8	28.4	7.0
P0AB55	10584.1	G	U	T	A	CID	LIT	6	36.7	MLYVIYAQDK	1243.6	-	A	3.4	0.9	28.0	11.5
P0AB55	10584.1	G	U	T	A	CID	LIT	6	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	4.2	0.6	56.1	13.4
P0AB55	10584.1	G	U	T	A	CID	LIT	6	36.7	RLSVRPAHLAR	1275.8	K	L	2.7	0.0	31.7	3.0
P0AB55	10584.1	G	T	T	A	CID	LIT	6	36.7	ADSLEKR	818.4	K	L	2.1	0.5	43.1	17.0
P0AB55	10584.1	G	T	T	A	CID	LIT	6	36.7	LQLLHDEGR	1080.6	R	L	3.2	0.7	59.3	12.3
P0AB55	10584.1	G	T	T	A	CID	LIT	6	36.7	LSVRPAHLAR	1119.7	R	L	3.0	0.0	27.8	7.0
P0AB55	10584.1	G	T	T	A	CID	LIT	6	36.7	MLYVIYAQDK	1243.6	-	A	3.2	0.6	13.4	10.4
P0AB55	10584.1	G	T	T	A	CID	LIT	6	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	4.2	0.6	60.0	13.0
P0AB55	10584.1	G	T	T	A	CID	LIT	6	36.7	RLSVRPAHLAR	1275.8	K	L	2.7	0.7	25.0	4.8
P0AB55	10584.1	G	U	A	A	CID	LIT	5	52.0	DADPYVAAGVYEHVSVKPFKKVF	2566.3	A	-	4.5	0.7	13.9	13.6
P0AB55	10584.1	G	U	A	A	CID	LIT	5	52.0	DEGRLLTAGPMPAV	1426.7	H	D	3.2	0.7	45.5	15.4
P0AB55	10584.1	G	U	A	A	CID	LIT	5	52.0	DEGRLLTAGPMPAVDSN	1758.8	H	D	4.1	0.7	61.1	14.1
P0AB55	10584.1	G	U	A	A	CID	LIT	5	52.0	DPYVAAGVYEHVSVKPFKKVF	2380.3	A	-	2.2	0.7	35.9	13.4
P0AB55	10584.1	G	U	A	A	CID	LIT	5	52.0	MLYVIYAQDKA	1314.7	-	D	4.1	0.6	57.8	14.9
P0AB55	10584.1	G	T	A	A	CID	LIT	5	52.0	DADPYVAAGVYEHVSVKPFKKVF	2566.3	A	-	2.9	0.8	11.7	13.6
P0AB55	10584.1	G	T	A	A	CID	LIT	5	52.0	DEGRLLTAGPMPAV	1426.7	H	D	2.9	0.8	52.8	14.3
P0AB55	10584.1	G	T	A	A	CID	LIT	5	52.0	DEGRLLTAGPMPAVDSN	1758.8	H	D	3.8	0.6	41.7	14.6
P0AB55	10584.1	G	T	A	A	CID	LIT	5	52.0	DPYVAAGVYEHVSVKPFKKVF	2380.3	A	-	2.5	0.6	47.2	13.4
P0AB55	10584.1	G	T	A	A	CID	LIT	5	52.0	MLYVIYAQDKA	1314.7	-	D	2.5	0.7	25.8	14.9
P0AB55	10584.1	G	T	T	B	CID	LIT	3	26.5	ADSLEKR	818.4	K	L	2.2	0.5	35.3	16.5
P0AB55	10584.1	G	T	T	B	CID	LIT	3	26.5	LQLLHDEGR	1080.6	R	L	3.2	0.7	51.3	12.3
P0AB55	10584.1	G	T	T	B	CID	LIT	3	26.5	MLYVIYAQDKADSLEK	1887.0	-	R	2.1	0.8	0.9	13.0
P0AB55	10584.1	G	U	T	B	CID	LIT	5	36.7	ADSLEKR	818.4	K	L	2.0	0.5	35.4	16.5
P0AB55	10584.1	G	U	T	B	CID	LIT	5	36.7	LQLLHDEGR	1080.6	R	L	3.0	0.8	62.5	12.3
P0AB55	10584.1	G	U	T	B	CID	LIT	5	36.7	LSVRPAHLAR	1119.7	R	L	2.9	0.8	23.6	7.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB55	10584.1	G	U	T	B	CID	LIT	5	36.7	MLYVIYAQDK	1243.6	-	A	2.8	0.0	23.2	11.1
P0AB55	10584.1	G	U	T	B	CID	LIT	5	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	4.1	0.0	66.0	13.0
P0AB55	10584.1	G	T	A	B	CID	LIT	5	66.3	DEGRLLTAGPMPAV	1426.7	H	D	3.3	0.7	67.9	15.4
P0AB55	10584.1	G	T	A	B	CID	LIT	5	66.3	DEGRLLTAGPMPAVDSN	1742.8	H	D	4.0	0.6	43.9	14.1
P0AB55	10584.1	G	T	A	B	CID	LIT	5	66.3	DPGAAGFTGSTVIAEFESL	1868.9	N	E	3.0	0.7	30.5	14.0
P0AB55	10584.1	G	T	A	B	CID	LIT	5	66.3	DPYVAAGVYEHVSVKPFKKVF	2380.3	A	-	5.8	0.7	41.2	13.2
P0AB55	10584.1	G	T	A	B	CID	LIT	5	66.3	MLYVIYAQ	1000.5	-	D	2.0	0.8	31.0	13.4
P0AB55	10584.1	G	U	A	B	CID	LIT	6	66.3	DEGRLLTAGPMPAV	1426.7	H	D	3.8	0.6	58.7	15.4
P0AB55	10584.1	G	U	A	B	CID	LIT	6	66.3	DEGRLLTAGPMPAVDSN	1742.8	H	D	4.4	0.6	53.7	14.1
P0AB55	10584.1	G	U	A	B	CID	LIT	6	66.3	DPGAAGFTGSTVIAEFESL	1868.9	N	E	3.1	0.6	21.9	14.0
P0AB55	10584.1	G	U	A	B	CID	LIT	6	66.3	DPYVAAGVYEHVSVKPFKKVF	2380.3	A	-	3.5	0.5	27.9	13.0
P0AB55	10584.1	G	U	A	B	CID	LIT	6	66.3	EHVSVKPFKKVF	1444.8	Y	-	3.2	0.0	25.0	7.0
P0AB55	10584.1	G	U	A	B	CID	LIT	6	66.3	MLYVIYAQ	1000.5	-	D	2.6	0.0	28.0	11.8
P0AB55	10584.1	S	U	T	A	CID	LIT	4	27.6	LSVRPAHLAR	1119.7	R	L	2.7	0.7	17.1	10.0
P0AB55	10584.1	S	U	T	A	CID	LIT	4	27.6	MLYVIYAQDKADSLEK	1887.0	-	R	5.0	0.7	64.0	18.1
P0AB55	10584.1	S	U	T	A	CID	LIT	4	27.6	MLYVIYAQDKADSLEKR	2043.1	-	L	5.3	0.7	82.1	17.7
P0AB55	10584.1	S	U	T	A	CID	LIT	4	27.6	RLSVRPAHLAR	1275.8	K	L	1.6	0.6	34.9	7.0
P0AB55	10584.1	S	U	T	B	CID	LIT	4	27.6	LSVRPAHLAR	1119.7	R	L	2.4	0.7	11.7	10.0
P0AB55	10584.1	S	U	T	B	CID	LIT	4	27.6	MLYVIYAQDKADSLEK	1887.0	-	R	5.1	0.7	70.8	18.1
P0AB55	10584.1	S	U	T	B	CID	LIT	4	27.6	MLYVIYAQDKADSLEKR	2043.1	-	L	5.5	0.6	95.2	18.1
P0AB55	10584.1	S	U	T	B	CID	LIT	4	27.6	RLSVRPAHLAR	1275.8	K	L	2.0	0.8	0.0	0.0
P0AB55	10584.1	S	U	T	C	CID	LIT	5	36.7	LQLLHDEGR	1080.6	R	L	1.9	0.7	17.2	14.3
P0AB55	10584.1	S	U	T	C	CID	LIT	5	36.7	LSVRPAHLAR	1119.7	R	L	1.9	0.8	14.2	10.0
P0AB55	10584.1	S	U	T	C	CID	LIT	5	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	5.4	0.7	79.0	17.9
P0AB55	10584.1	S	U	T	C	CID	LIT	5	36.7	MLYVIYAQDKADSLEKR	2043.1	-	L	5.3	0.7	73.9	17.7
P0AB55	10584.1	S	U	T	C	CID	LIT	5	36.7	RLSVRPAHLAR	1275.8	K	L	1.9	0.7	30.0	7.8
P0AB55	10584.1	S	U	T	A	ETD	LIT	5	36.7	LQLLHDEGR	1080.6	R	L	3.0	0.5	0.0	0.0
P0AB55	10584.1	S	U	T	A	ETD	LIT	5	36.7	LSVRPAHLAR	1119.7	R	L	3.0	0.7	32.3	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB55	10584.1	S	U	T	A	ETD	LIT	5	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	6.1	0.5	55.7	18.0
P0AB55	10584.1	S	U	T	A	ETD	LIT	5	36.7	MLYVIYAQDKADSLEKR	2043.1	-	L	4.4	0.0	59.2	17.5
P0AB55	10584.1	S	U	T	A	ETD	LIT	5	36.7	RLSVRPAHLAR	1275.8	K	L	3.7	0.6	26.7	7.0
P0AB55	10584.1	S	U	T	B	ETD	LIT	4	36.7	LQLLHDEGR	1080.6	R	L	4.2	0.5	35.7	13.8
P0AB55	10584.1	S	U	T	B	ETD	LIT	4	36.7	LSVRPAHLAR	1119.7	R	L	2.7	0.6	18.6	9.5
P0AB55	10584.1	S	U	T	B	ETD	LIT	4	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	7.0	0.6	62.3	18.1
P0AB55	10584.1	S	U	T	B	ETD	LIT	4	36.7	MLYVIYAQDKADSLEKR	2043.1	-	L	0.0	0.0	47.5	18.8
P0AB55	10584.1	S	U	T	C	ETD	LIT	5	36.7	LQLLHDEGR	1080.6	R	L	3.1	0.7	23.2	13.6
P0AB55	10584.1	S	U	T	C	ETD	LIT	5	36.7	LSVRPAHLAR	1119.7	R	L	2.6	0.7	21.1	9.5
P0AB55	10584.1	S	U	T	C	ETD	LIT	5	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	4.7	0.6	49.6	17.7
P0AB55	10584.1	S	U	T	C	ETD	LIT	5	36.7	MLYVIYAQDKADSLEKR	2043.1	-	L	8.8	0.6	77.4	17.8
P0AB55	10584.1	S	U	T	C	ETD	LIT	5	36.7	RLSVRPAHLAR	1275.8	K	L	2.6	0.0	44.5	7.0
P0AB55	10584.1	S	U	T	A	ETD	FT	2	11.2	LSVRPAHLAR	1119.7	R	L	0.0	0.0	38.5	10.0
P0AB55	10584.1	S	U	T	A	ETD	FT	2	11.2	RLSVRPAHLAR	1275.8	K	L	4.2	0.6	55.1	7.0
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	2	27.6	LSVRPAHLAR	1119.7	R	L	0.0	0.0	19.9	9.5
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	2	27.6	MLYVIYAQDKADSLEKR	2043.1	-	L	0.0	0.0	79.1	18.1
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	LSVRPAHLAR	1119.7	R	L	0.0	0.0	19.9	9.5
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	MLYVIYAQDKADSLEK	1887.0	-	R	0.0	0.0	70.5	18.3
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	MLYVIYAQDKADSLEKR	2043.1	-	L	0.0	0.0	79.1	18.1
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	RLSVRPAHLAR	1275.8	K	L	0.0	0.0	33.3	7.0
P0AB55	10584.1	S	U	T	A	ETD+CID	LIT	3	27.6	MLYVIYAQDKADSLEK	1887.0	-	R	5.5	0.6	66.7	18.1
P0AB55	10584.1	S	U	T	A	ETD+CID	LIT	3	27.6	MLYVIYAQDKADSLEKR	2043.1	-	L	5.4	0.7	89.8	18.1
P0AB55	10584.1	S	U	T	A	ETD+CID	LIT	3	27.6	RLSVRPAHLAR	1275.8	K	L	1.6	0.2	27.8	7.0
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	LSVRPAHLAR	1119.7	R	L	2.1	0.7	17.2	10.0
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	MLYVIYAQDKADSLEK	1887.0	-	R	4.8	0.7	70.5	18.3
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	MLYVIYAQDKADSLEKR	2043.1	-	L	0.9	0.0	79.1	18.1
P0AB55	10584.1	S	U	T	B	ETD+CID	LIT	4	27.6	RLSVRPAHLAR	1275.8	K	L	1.8	0.0	33.3	7.0
P0AB55	10584.1	S	U	T	C	ETD+CID	LIT	5	36.7	DATKAEIK	875.5	-	-	2.3	0.1	17.1	15.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB55	10584.1	S	U	T	C	ETD+CID	LIT	5	36.7	LQLLHDEGR	1080.6	R	L	3.2	0.0	43.8	13.6
P0AB55	10584.1	S	U	T	C	ETD+CID	LIT	5	36.7	LSVRPAHLAR	1119.7	R	L	3.7	0.6	19.1	10.0
P0AB55	10584.1	S	U	T	C	ETD+CID	LIT	5	36.7	MLYVIYAQDKADSLEK	1887.0	-	R	5.0	0.7	64.2	17.9
P0AB55	10584.1	S	U	T	C	ETD+CID	LIT	5	36.7	MLYVIYAQDKADSLEKR	2043.1	-	L	5.4	0.7	85.2	18.2
P0AB55	10584.1	S	U	T	C	ETD+CID	LIT	5	36.7	RLSVRPAHLAR	1275.8	K	L	3.5	0.7	27.4	7.0
P0AB55	10584.1	S	U	T	B	HCD	FT	4	27.6	LSVRPAHLAR	1119.7	R	L	0.0	0.0	17.2	10.0
P0AB55	10584.1	S	U	T	B	HCD	FT	4	27.6	MLYVIYAQDKADSLEK	1887.0	-	R	0.0	0.0	70.5	18.3
P0AB55	10584.1	S	U	T	B	HCD	FT	4	27.6	MLYVIYAQDKADSLEKR	2043.1	-	L	0.0	0.0	77.6	18.1
P0AB55	10584.1	S	U	T	B	HCD	FT	4	27.6	RLSVRPAHLAR	1275.8	K	L	0.0	0.0	33.3	7.0
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	EMLEHMASTLAQGER	1702.8	K	I	4.6	0.0	72.7	8.5
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	GFGSFSLHYR	1170.6	R	A	2.8	0.8	57.9	12.3
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	LATQQSHIPAK	1193.7	R	T	3.8	0.7	51.9	11.5
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	LATQQSHIPAKTVEDAVK	1936.1	R	E	3.3	0.5	35.7	11.1
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	MTKSELIER	1106.6	-	L	3.2	0.5	54.8	14.0
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	SELIER	746.4	K	L	1.6	0.5	18.8	16.6
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	TGDKVELEGK	1075.6	K	Y	3.3	0.9	60.3	13.2
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	3.8	0.0	59.9	8.5
P0A6Y1	10633.4	G	U	T	A	CID	LIT	9	78.7	YVPHFKPGKELR	1470.8	K	D	2.7	0.0	20.2	11.1
P0A6Y1	10633.4	G	T	T	A	CID	LIT	3	33.0	GFGSFSLHYR	1170.6	R	A	2.9	0.8	46.4	12.3
P0A6Y1	10633.4	G	T	T	A	CID	LIT	3	33.0	LATQQSHIPAK	1193.7	R	T	3.2	0.8	46.8	11.5
P0A6Y1	10633.4	G	T	T	A	CID	LIT	3	33.0	TGDKVELEGK	1075.6	K	Y	3.4	0.8	51.6	13.4
P0A6Y1	10633.4	G	T	T	B	CID	LIT	2	22.3	LATQQSHIPAK	1193.7	R	T	3.6	0.0	52.5	11.5
P0A6Y1	10633.4	G	T	T	B	CID	LIT	2	22.3	TGDKVELEGK	1075.6	K	Y	2.7	0.4	28.0	13.4
P0A6Y1	10633.4	G	U	T	B	CID	LIT	5	55.3	EMLEHMASTLAQGER	1702.8	K	I	4.2	0.0	56.9	8.5
P0A6Y1	10633.4	G	U	T	B	CID	LIT	5	55.3	GFGSFSLHYR	1170.6	R	A	3.0	0.0	59.4	12.3
P0A6Y1	10633.4	G	U	T	B	CID	LIT	5	55.3	LATQQSHIPAK	1193.7	R	T	3.3	0.8	43.4	11.5
P0A6Y1	10633.4	G	U	T	B	CID	LIT	5	55.3	SELIER	746.4	K	L	2.0	0.6	25.1	16.7
P0A6Y1	10633.4	G	U	T	B	CID	LIT	5	55.3	TGDKVELEGK	1075.6	K	Y	3.3	0.0	23.6	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6Y1	10633.4	S	U	T	A	CID	LIT	5	56.4	EMLEHMASTLAQGER	1702.8	K	I	4.9	0.5	68.5	14.3
P0A6Y1	10633.4	S	U	T	A	CID	LIT	5	56.4	GFGSFSLHYR	1170.6	R	A	3.0	0.0	63.7	13.0
P0A6Y1	10633.4	S	U	T	A	CID	LIT	5	56.4	LATQQSHIPAK	1193.7	R	T	2.9	0.0	44.0	15.4
P0A6Y1	10633.4	S	U	T	A	CID	LIT	5	56.4	TGDKVELEGK	1075.6	K	Y	2.9	0.5	21.2	16.5
P0A6Y1	10633.4	S	U	T	A	CID	LIT	5	56.4	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	5.7	0.6	78.0	18.3
P0A6Y1	10633.4	S	U	T	B	CID	LIT	4	45.7	EMLEHMASTLAQGER	1702.8	K	I	3.7	0.5	54.0	14.5
P0A6Y1	10633.4	S	U	T	B	CID	LIT	4	45.7	GFGSFSLHYR	1170.6	R	A	2.8	0.8	49.0	13.8
P0A6Y1	10633.4	S	U	T	B	CID	LIT	4	45.7	LATQQSHIPAK	1193.7	R	T	3.6	0.6	54.5	14.5
P0A6Y1	10633.4	S	U	T	B	CID	LIT	4	45.7	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	2.9	0.6	0.0	0.0
P0A6Y1	10633.4	S	U	T	C	CID	LIT	6	55.3	EMLEHMASTLAQGER	1702.8	K	I	4.4	0.6	67.4	14.5
P0A6Y1	10633.4	S	U	T	C	CID	LIT	6	55.3	GFGSFSLHYR	1170.6	R	A	3.0	0.0	59.5	13.0
P0A6Y1	10633.4	S	U	T	C	CID	LIT	6	55.3	LATQQSHIPAK	1193.7	R	T	4.0	0.7	55.7	14.5
P0A6Y1	10633.4	S	U	T	C	CID	LIT	6	55.3	LATQQSHIPAKTVEDAVK	1936.1	R	E	3.3	0.7	31.7	15.4
P0A6Y1	10633.4	S	U	T	C	CID	LIT	6	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	5.6	0.7	70.7	18.0
P0A6Y1	10633.4	S	U	T	C	CID	LIT	6	55.3	YVPHFKPGK	1072.6	K	E	1.9	0.6	14.6	17.5
P0A6Y1	10633.4	S	U	T	A	CID	FT	2	22.3	GFGSFSLHYR	1170.6	R	A	2.3	0.0	65.4	13.8
P0A6Y1	10633.4	S	U	T	A	CID	FT	2	22.3	LATQQSHIPAK	1193.7	R	T	3.0	0.0	61.2	14.5
P0A6Y1	10633.4	S	U	T	A	ETD	LIT	4	55.3	GFGSFSLHYR	1170.6	R	A	2.6	0.0	21.4	13.8
P0A6Y1	10633.4	S	U	T	A	ETD	LIT	4	55.3	LATQQSHIPAK	1193.7	R	T	4.1	0.5	60.7	14.6
P0A6Y1	10633.4	S	U	T	A	ETD	LIT	4	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	4.7	0.6	26.7	18.0
P0A6Y1	10633.4	S	U	T	A	ETD	LIT	4	55.3	YVPHFKPGK	1072.6	K	E	2.3	0.7	26.7	17.5
P0A6Y1	10633.4	S	U	T	B	ETD	LIT	5	55.3	EMLEHMASTLAQGER	1702.8	K	I	2.8	0.4	57.3	12.3
P0A6Y1	10633.4	S	U	T	B	ETD	LIT	5	55.3	GFGSFSLHYR	1170.6	R	A	2.5	0.8	40.7	13.6
P0A6Y1	10633.4	S	U	T	B	ETD	LIT	5	55.3	LATQQSHIPAK	1193.7	R	T	1.7	0.6	35.1	14.5
P0A6Y1	10633.4	S	U	T	B	ETD	LIT	5	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	6.6	0.6	73.1	18.3
P0A6Y1	10633.4	S	U	T	B	ETD	LIT	5	55.3	YVPHFKPGK	1072.6	K	E	2.3	0.5	13.1	14.8
P0A6Y1	10633.4	S	U	T	C	ETD	LIT	5	55.3	EMLEHMASTLAQGER	1702.8	K	I	2.3	0.2	28.6	12.0
P0A6Y1	10633.4	S	U	T	C	ETD	LIT	5	55.3	GFGSFSLHYR	1170.6	R	A	3.9	0.0	49.2	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6Y1	10633.4	S	U	T	C	ETD	LIT	5	55.3	LATQQSHIPAK	1193.7	R	T	4.3	0.4	50.8	14.5
P0A6Y1	10633.4	S	U	T	C	ETD	LIT	5	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	6.1	0.6	47.5	18.2
P0A6Y1	10633.4	S	U	T	C	ETD	LIT	5	55.3	YVPHFKPGK	1072.6	K	E	2.2	0.7	19.9	14.8
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	2	44.7	LATQQSHIPAK	1193.7	R	T	0.0	0.0	71.1	14.9
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	2	44.7	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	0.0	0.0	66.3	18.4
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	2	44.7	YVPHFKPGK	1072.6	K	E	0.0	0.0	22.8	17.5
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	EMLEHMASTLAQGER	1702.8	K	I	0.0	0.0	48.7	14.3
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	GFGSFSLHYR	1170.6	R	A	0.0	0.0	63.0	13.8
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	LATQQSHIPAK	1193.7	R	T	0.0	0.0	71.1	14.9
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	0.0	0.0	66.3	18.4
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	YVPHFKPGK	1072.6	K	E	0.0	0.0	22.8	17.5
P0A6Y1	10633.4	S	U	T	A	ETD+CID	LIT	4	55.3	EMLEHMASTLAQGER	1702.8	K	I	4.2	0.5	54.8	14.5
P0A6Y1	10633.4	S	U	T	A	ETD+CID	LIT	4	55.3	GFGSFSLHYR	1170.6	R	A	2.7	0.7	38.6	13.6
P0A6Y1	10633.4	S	U	T	A	ETD+CID	LIT	4	55.3	LATQQSHIPAK	1194.6	R	T	3.4	0.8	37.1	13.0
P0A6Y1	10633.4	S	U	T	A	ETD+CID	LIT	4	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	2.9	0.2	0.0	0.0
P0A6Y1	10633.4	S	U	T	A	ETD+CID	LIT	4	55.3	YVPHFKPGK	1072.6	K	E	3.5	0.9	20.9	17.5
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	EMLEHMASTLAQGER	1702.8	K	I	4.7	0.5	48.7	14.3
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	GFGSFSLHYR	1170.6	R	A	2.9	0.7	63.0	13.8
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	LATQQSHIPAK	1194.6	R	T	3.7	0.8	51.4	13.0
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	7.1	0.6	66.3	18.4
P0A6Y1	10633.4	S	U	T	B	ETD+CID	LIT	4	55.3	YVPHFKPGK	1072.6	K	E	3.4	0.5	22.8	17.5
P0A6Y1	10633.4	S	U	T	C	ETD+CID	LIT	4	55.3	EMLEHMASTLAQGER	1702.8	K	I	4.0	0.5	49.2	14.0
P0A6Y1	10633.4	S	U	T	C	ETD+CID	LIT	4	55.3	GFGSFSLHYR	1170.6	R	A	3.1	0.8	24.6	13.8
P0A6Y1	10633.4	S	U	T	C	ETD+CID	LIT	4	55.3	LATQQSHIPAK	1193.7	R	T	4.0	0.5	63.7	14.5
P0A6Y1	10633.4	S	U	T	C	ETD+CID	LIT	4	55.3	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	6.5	0.5	56.9	18.4
P0A6Y1	10633.4	S	U	T	C	ETD+CID	LIT	4	55.3	YVPHFKPGK	1072.6	K	E	1.9	0.6	15.6	17.2
P0A6Y1	10633.4	S	U	T	B	HCD	FT	3	45.7	EMLEHMASTLAQGER	1702.8	K	I	0.0	0.0	48.7	14.3
P0A6Y1	10633.4	S	U	T	B	HCD	FT	3	45.7	GFGSFSLHYR	1170.6	R	A	0.0	0.0	63.0	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6Y1	10633.4	S	U	T	B	HCD	FT	3	45.7	LATQQSHIPAK	1193.7	R	T	0.0	0.0	62.3	14.9
P0A6Y1	10633.4	S	U	T	B	HCD	FT	3	45.7	TVEDAVKEMLEHMASTLAQGER	2445.2	K	I	0.0	0.0	63.3	18.2
P64602	10662.7	G	U	T	B	CID	LIT	2	20.6	GITCIDLSR	1034.5	K	V	2.2	0.2	22.0	15.3
P64602	10662.7	G	U	T	B	CID	LIT	2	20.6	LYNLPADVLPR	1270.7	K	-	3.3	0.0	47.8	10.8
P64602	10662.7	G	U	A	B	CID	LIT	3	41.2	DKVYTLAKLYNLPA	1608.9	N	D	4.6	0.6	50.1	9.5
P64602	10662.7	G	U	A	B	CID	LIT	3	41.2	DLAKKQGNNVTLQGVN	1698.9	I	D	2.6	0.0	18.6	14.9
P64602	10662.7	G	U	A	B	CID	LIT	3	41.2	EEAVKGITCI	1119.6	R	D	2.1	0.0	25.4	15.4
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	AANKFPAIIYGGK	1349.8	R	E	3.3	0.8	31.9	10.8
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	AEFYSEVLTIVVDGK	1669.9	K	E	3.1	0.7	56.8	12.0
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	AQDVQR	716.4	K	H	1.9	0.0	28.9	13.2
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	AQDVQRHPYKPK	1466.8	K	L	3.4	0.7	28.2	8.5
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	EAPLAIELDHDK	1350.7	K	V	3.8	0.9	53.3	12.0
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	EAPLAIELDHDKVMNMQAK	2153.1	K	A	4.9	0.7	69.7	13.0
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	FPAIIYGGK	965.5	K	E	2.4	0.7	30.2	11.1
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	HPYKPK	769.4	R	L	2.1	0.2	13.0	12.8
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	LQHIDFVR	1027.6	K	-	2.8	0.7	31.2	11.5
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	LQHIDFVRA	1098.6	K	-	2.0	0.8	32.5	10.4
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	MFTINAEVR	1080.6	-	K	2.4	0.6	27.2	12.8
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	MFTINAEVRK	1208.6	-	E	2.6	0.6	34.2	12.6
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	VKAQDVQR	943.5	K	H	3.1	0.5	46.1	13.6
P68919	10675.6	G	U	T	A	CID	LIT	14	85.1	VMNMQAK	821.4	K	A	2.2	0.2	34.3	13.0
P68919	10675.6	G	T	T	A	CID	LIT	3	38.3	AEFYSEVLTIVVDGK	1669.9	K	E	3.8	0.9	56.7	11.5
P68919	10675.6	G	T	T	A	CID	LIT	3	38.3	AQDVQRHPYKPK	1466.8	K	L	2.1	0.6	0.0	0.0
P68919	10675.6	G	T	T	A	CID	LIT	3	38.3	LQHIDFVRA	1098.6	K	-	2.4	0.0	23.9	10.4
P68919	10675.6	G	U	A	A	CID	LIT	4	30.9	DFVRA	607.3	I	-	1.4	0.3	21.4	14.1
P68919	10675.6	G	U	A	A	CID	LIT	4	30.9	DGKEIKVKAQ	1115.6	V	D	2.8	0.5	35.6	13.4
P68919	10675.6	G	U	A	A	CID	LIT	4	30.9	DVQRHPYKPKLQHI	1759.0	Q	D	3.9	0.6	35.4	11.8
P68919	10675.6	G	U	A	A	CID	LIT	4	30.9	DVQRHPYKPKLQHIDFVRA	2347.3	Q	-	3.8	0.8	45.5	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68919	10675.6	G	T	T	B	CID	LIT	2	14.9	AQDVQRHPYKPK	1466.8	K	L	2.6	0.0	16.8	10.8
P68919	10675.6	G	T	T	B	CID	LIT	2	14.9	VKAQDVQR	943.5	K	H	2.5	0.3	20.7	13.6
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	AANKFPAIIYGGK	1349.8	R	E	2.9	0.7	17.9	10.8
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	AEFYSEVLTIVVDGK	1669.9	K	E	4.3	0.5	44.7	12.0
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	EAPLAIELDHDK	1350.7	K	V	3.4	0.0	49.0	10.4
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	EAPLAIELDHDKVMNMQAK	2169.1	K	A	3.9	0.9	60.3	11.1
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	FPAIIYGGK	965.5	K	E	2.5	0.6	36.6	11.1
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	LQHIDFVR	1027.6	K	-	2.1	0.6	18.0	11.5
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	LQHIDFVRA	1098.6	K	-	2.0	0.5	25.8	12.3
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	MFTINAEVR	1080.6	-	K	2.8	0.8	51.2	12.8
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	MFTINAEVRK	1208.6	-	E	2.7	0.0	29.4	12.3
P68919	10675.6	G	U	T	B	CID	LIT	10	78.7	VKAQDVQR	943.5	K	H	2.8	0.6	45.0	13.6
P68919	10675.6	G	T	A	B	CID	LIT	2	25.5	DKVMNMQAKA	1135.6	H	E	2.5	0.6	11.3	16.0
P68919	10675.6	G	T	A	B	CID	LIT	2	25.5	DVQRHPYKPKLQHI	1759.0	Q	D	2.9	0.5	10.2	11.8
P68919	10675.6	G	U	A	B	CID	LIT	7	54.3	DFVRA	607.3	I	-	1.4	0.5	21.4	14.1
P68919	10675.6	G	U	A	B	CID	LIT	7	54.3	DGKEIKVKAQ	1115.6	V	D	3.3	0.5	42.8	13.0
P68919	10675.6	G	U	A	B	CID	LIT	7	54.3	DHDKVMNMQAKA	1387.6	L	E	2.7	0.6	7.1	13.8
P68919	10675.6	G	U	A	B	CID	LIT	7	54.3	DKVMNMQAKA	1135.6	H	E	2.9	0.8	38.5	16.0
P68919	10675.6	G	U	A	B	CID	LIT	7	54.3	DVQRHPYKPKLQHI	1759.0	Q	D	3.9	0.5	53.4	11.5
P68919	10675.6	G	U	A	B	CID	LIT	7	54.3	DVQRHPYKPKLQHIDFVRA	2347.3	Q	-	3.9	0.0	39.5	12.8
P68919	10675.6	G	U	A	B	CID	LIT	7	54.3	MFTINAEVRK	1208.6	-	E	2.1	0.4	27.0	11.5
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	AANKFPAIIYGGK	1349.8	R	E	3.0	0.6	24.5	13.8
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	AEFYSEVLTIVVDGK	1669.9	K	E	5.1	0.6	73.1	17.5
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	EAPLAIELDHDKVMNMQAK	2153.1	K	A	5.9	0.6	64.7	18.9
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	FPAIIYGGK	965.5	K	E	2.4	0.4	29.3	14.8
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	LQHIDFVR	1027.6	K	-	2.4	0.6	24.9	10.4
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	LQHIDFVRA	1098.6	K	-	2.1	0.8	39.7	13.4
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	MFTINAEVR	1080.6	-	K	2.4	0.7	54.7	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	VKAQDVQR	943.5	K	H	2.3	0.6	25.1	16.0
P68919	10675.6	S	U	T	A	CID	LIT	9	84.0	VKAQDVQRHPYKPK	1694.0	K	L	1.8	0.6	8.1	11.8
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	AEFYSEVLTIVVDGK	1669.9	K	E	4.0	0.7	76.1	17.5
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	EAPLAIELDHDK	1350.7	K	V	2.9	0.4	40.3	15.9
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	EAPLAIELDHDKVMNMQAK	2153.1	K	A	6.0	0.6	79.9	19.0
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	FPAIIYGGK	965.5	K	E	2.4	0.4	37.7	14.8
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	LQHIDFVR	1027.6	K	-	2.6	0.7	33.1	12.8
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	LQHIDFVRA	1098.6	K	-	2.0	0.7	32.3	12.6
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	MFTINAEVR	1080.6	-	K	2.7	0.7	42.9	14.3
P68919	10675.6	S	U	T	B	CID	LIT	8	79.8	VKAQDVQRHPYKPK	1694.0	K	L	2.4	0.6	19.7	12.6
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	AANKFPAIIYGGK	1349.8	R	E	5.0	0.8	41.6	12.3
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	AEFYSEVLTIVVDGK	1669.9	K	E	3.9	0.6	72.8	17.5
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	EAPLAIELDHDKVMNMQAK	2153.1	K	A	5.7	0.6	59.0	19.0
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	FPAIIYGGK	965.5	K	E	2.5	0.4	32.0	14.8
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	LQHIDFVR	1027.6	K	-	2.6	0.7	29.2	12.8
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	LQHIDFVRA	1098.6	K	-	2.4	0.8	37.1	12.6
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	MFTINAEVR	1080.6	-	K	2.4	0.7	43.5	14.3
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	VKAQDVQR	943.5	K	H	3.0	0.6	42.2	15.3
P68919	10675.6	S	U	T	C	CID	LIT	9	84.0	VKAQDVQRHPYKPK	1694.0	K	L	2.7	0.7	21.9	11.5
P68919	10675.6	S	U	T	A	CID	FT	2	23.4	AANKFPAIIYGGK	1349.8	R	E	2.9	0.0	15.5	13.0
P68919	10675.6	S	U	T	A	CID	FT	2	23.4	MFTINAEVR	1080.6	-	K	2.5	0.0	52.2	14.3
P68919	10675.6	S	U	T	B	CID	FT	2	23.4	AANKFPAIIYGGK	1349.8	R	E	5.0	0.0	40.5	13.8
P68919	10675.6	S	U	T	B	CID	FT	2	23.4	MFTINAEVR	1080.6	-	K	1.8	0.0	22.9	14.3
P68919	10675.6	S	U	T	C	CID	FT	2	25.5	AEFYSEVLTIVVDGK	1669.9	K	E	3.0	0.7	74.6	16.8
P68919	10675.6	S	U	T	C	CID	FT	2	25.5	LQHIDFVRA	1098.6	K	-	2.6	0.0	14.3	12.6
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	AANKFPAIIYGGK	1349.8	R	E	5.4	0.7	41.9	12.3
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	AEFYSEVLTIVVDGK	1669.9	K	E	3.4	0.5	0.0	0.0
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	AQDVQRHPYKPK	1466.8	K	L	2.5	0.3	34.8	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	EAPLAIELDHDKVMNMQAK	2153.1	K	A	5.8	0.5	68.3	19.0
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	FPAIIYGGK	965.5	K	E	2.6	0.4	25.1	14.8
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	LQHIDFVR	1027.6	K	-	2.0	0.6	0.0	0.0
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	LQHIDFVRA	1098.6	K	-	4.3	0.5	0.0	0.0
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	MFTINAEVR	1080.6	-	K	1.9	0.6	14.7	14.3
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	VKAQDVQR	943.5	K	H	4.0	0.3	30.6	15.3
P68919	10675.6	S	U	T	A	ETD	LIT	10	84.0	VKAQDVQRHPYKPK	1694.0	K	L	3.5	0.0	40.0	11.1
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	AANKFPAIIYGGK	1349.8	R	E	5.2	0.6	48.8	13.8
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	AEFYSEVLTIVVDGK	1669.9	K	E	4.3	0.3	39.1	17.2
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	AQDVQRHPYKPK	1466.8	K	L	2.0	0.3	0.0	0.0
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	EAPLAIELDHDK	1350.7	K	V	2.4	0.7	41.0	16.2
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	EAPLAIELDHDKVMNMQAK	2153.1	K	A	0.0	0.0	75.8	19.1
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	LQHIDFVRA	1098.6	K	-	4.2	0.6	40.2	13.4
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	MFTINAEVR	1080.6	-	K	2.2	0.4	42.0	15.6
P68919	10675.6	S	U	T	B	ETD	LIT	8	84.0	VKAQDVQR	943.5	K	H	3.3	0.2	34.0	15.3
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	AANKFPAIIYGGK	1349.8	R	E	5.3	0.8	38.0	12.3
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	AEFYSEVLTIVVDGK	1669.9	K	E	3.3	0.8	0.0	0.0
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	EAPLAIELDHDK	1350.7	K	V	1.3	0.5	26.7	15.7
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	EAPLAIELDHDKVMNMQAK	2153.1	K	A	6.9	0.7	0.0	0.0
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	FPAIIYGGK	965.5	K	E	2.0	0.0	16.9	11.8
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	LQHIDFVR	1027.6	K	-	3.6	0.7	39.3	12.8
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	LQHIDFVRA	1098.6	K	-	3.9	0.5	0.0	0.0
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	MFTINAEVR	1080.6	-	K	2.5	0.8	0.0	0.0
P68919	10675.6	S	U	T	C	ETD	LIT	9	77.7	VKAQDVQR	943.5	K	H	3.8	0.3	29.0	16.0
P68919	10675.6	S	U	T	A	ETD	FT	2	24.5	LQHIDFVRA	1098.6	K	-	2.3	0.0	44.4	12.8
P68919	10675.6	S	U	T	A	ETD	FT	2	24.5	VKAQDVQRHPYKPK	1694.0	K	L	1.3	0.0	28.3	12.6
P68919	10675.6	S	U	T	B	ETD	FT	2	9.6	LQHIDFVR	1027.6	K	-	2.8	0.0	40.7	10.4
P68919	10675.6	S	U	T	B	ETD	FT	2	9.6	LQHIDFVRA	1098.6	K	-	2.5	0.0	19.2	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68919	10675.6	S	U	T	C	ETD	FT	3	22.3	EAPLAIELDHDK	1350.7	K	V	2.2	0.0	17.9	16.9
P68919	10675.6	S	U	T	C	ETD	FT	3	22.3	LQHIDFVR	1027.6	K	-	3.0	0.0	40.7	12.8
P68919	10675.6	S	U	T	C	ETD	FT	3	22.3	LQHIDFVRA	1098.6	K	-	1.7	0.7	42.9	12.6
P68919	10675.6	S	U	T	B	ETD+CID	LIT	3	44.7	AEFYSEVLTIVVDGK	1669.9	K	E	0.0	0.0	28.9	17.2
P68919	10675.6	S	U	T	B	ETD+CID	LIT	3	44.7	EAPLAIELDHDKVMNMQAK	2153.1	K	A	0.0	0.0	34.8	18.9
P68919	10675.6	S	U	T	B	ETD+CID	LIT	3	44.7	LQHIDFVR	1027.6	K	-	0.0	0.0	44.5	10.4
P68919	10675.6	S	U	T	B	ETD+CID	LIT	7	72.3	AEFYSEVLTIVVDGK	1669.9	K	E	0.0	0.0	75.2	17.5
P68919	10675.6	S	U	T	B	ETD+CID	LIT	7	72.3	EAPLAIELDHDK	1350.7	K	V	0.0	0.0	43.7	15.9
P68919	10675.6	S	U	T	B	ETD+CID	LIT	7	72.3	EAPLAIELDHDKVMNMQAK	2153.1	K	A	0.0	0.0	51.5	18.9
P68919	10675.6	S	U	T	B	ETD+CID	LIT	7	72.3	FPAIIYGGK	965.5	K	E	0.0	0.0	34.7	14.8
P68919	10675.6	S	U	T	B	ETD+CID	LIT	7	72.3	LQHIDFVR	1027.6	K	-	0.0	0.0	44.5	10.4
P68919	10675.6	S	U	T	B	ETD+CID	LIT	7	72.3	MFTINAEVR	1080.6	-	K	0.0	0.0	63.3	14.3
P68919	10675.6	S	U	T	B	ETD+CID	LIT	7	72.3	VKAQDVQR	943.5	K	H	0.0	0.0	27.4	16.0
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	AANKFPAIIYGGK	1350.7	R	E	2.5	0.3	7.0	15.7
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	AEFYSEVLTIVVDGK	1669.9	K	E	4.2	0.6	60.0	17.3
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	AQDVQRHPYKPK	1466.8	K	L	2.2	0.5	2.2	15.6
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	EAPLAIELDHDK	1350.7	K	V	3.6	0.5	43.1	16.9
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	EAPLAIELDHDKVMNMQAK	2153.1	K	A	5.3	0.7	62.5	19.0
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	FPAIIYGGK	965.5	K	E	2.4	0.5	38.3	14.8
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	LQHIDFVR	1027.6	K	-	2.3	0.4	17.0	12.8
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	LQHIDFVRA	1099.6	K	-	2.4	0.8	32.6	13.0
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	MFTINAEVR	1080.6	-	K	1.9	0.6	0.0	0.0
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	VKAQDVQR	943.5	K	H	3.2	0.5	27.0	16.0
P68919	10675.6	S	U	T	A	ETD+CID	LIT	10	84.0	VKAQDVQRHPYKPK	1694.0	K	L	2.5	0.6	20.7	10.0
P68919	10675.6	S	U	T	B	ETD+CID	LIT	2	38.3	AANKFPAIIYGGK	1349.8	R	E	1.9	0.6	0.0	0.0
P68919	10675.6	S	U	T	B	ETD+CID	LIT	2	38.3	AEFYSEVLTIVVDGK	1669.9	K	E	3.8	0.6	0.0	0.0
P68919	10675.6	S	U	T	B	ETD+CID	LIT	2	38.3	LQHIDFVR	1027.6	K	-	2.6	0.7	0.0	0.0
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	AANKFPAIIYGGK	1349.8	R	E	1.9	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	AEFYSEVLTIVVDGK	1669.9	K	E	4.3	0.6	75.2	17.5
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	EAPLAIELDHDK	1350.7	K	V	3.2	0.5	43.7	15.9
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	EAPLAIELDHDKVMNMQAK	2153.1	K	A	5.2	0.6	51.5	18.9
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	FPAIIYGGK	965.5	K	E	2.6	0.0	34.7	14.8
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	LQHIDFVR	1027.6	K	-	2.6	0.7	29.1	12.8
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	MFTINAEVR	1080.6	-	K	3.3	0.7	49.8	15.1
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	VKAQDVQR	943.5	K	H	2.1	0.5	23.8	16.0
P68919	10675.6	S	U	T	B	ETD+CID	LIT	8	83.0	VKAQDVQRHPYKPK	1694.0	K	L	2.1	0.6	11.6	11.1
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	AANKFPAIIYGGK	1349.8	R	E	4.6	0.7	38.0	13.8
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	AEFYSEVLTIVVDGK	1669.9	K	E	3.9	0.7	78.5	16.6
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	EAPLAIELDHDKVMNMQAK	2153.1	K	A	5.6	0.6	60.1	19.0
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	LQHIDFVR	1027.6	K	-	2.6	0.7	0.0	0.0
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	LQHIDFVRA	1098.6	K	-	2.1	0.7	0.0	0.0
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	MFTINAEVR	1080.6	-	K	2.5	0.7	42.1	15.8
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	SGFQYHGR	951.4	-	-	1.7	0.3	12.1	15.2
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	VKAQDVQR	943.5	K	H	0.9	-0.6	33.5	15.3
P68919	10675.6	S	U	T	C	ETD+CID	LIT	7	84.0	VKAQDVQRHPYKPK	1694.0	K	L	2.7	0.4	10.4	11.8
P68919	10675.6	S	U	T	B	HCD	FT	7	72.3	AEFYSEVLTIVVDGK	1669.9	K	E	0.0	0.0	75.2	17.5
P68919	10675.6	S	U	T	B	HCD	FT	7	72.3	EAPLAIELDHDK	1350.7	K	V	0.0	0.0	43.7	15.9
P68919	10675.6	S	U	T	B	HCD	FT	7	72.3	EAPLAIELDHDKVMNMQAK	2153.1	K	A	0.0	0.0	51.5	18.9
P68919	10675.6	S	U	T	B	HCD	FT	7	72.3	FPAIIYGGK	965.5	K	E	0.0	0.0	34.7	14.8
P68919	10675.6	S	U	T	B	HCD	FT	7	72.3	LQHIDFVR	1027.6	K	-	0.0	0.0	29.1	12.8
P68919	10675.6	S	U	T	B	HCD	FT	7	72.3	MFTINAEVR	1080.6	-	K	0.0	0.0	63.3	14.3
P68919	10675.6	S	U	T	B	HCD	FT	7	72.3	VKAQDVQR	943.5	K	H	0.0	0.0	27.4	16.0
P68919	10675.6	S	U	T	A	HCD	FT	2	23.4	AANKFPAIIYGGK	1349.8	R	E	3.7	0.0	67.6	13.8
P68919	10675.6	S	U	T	A	HCD	FT	2	23.4	MFTINAEVR	1080.6	-	K	2.3	0.8	35.8	14.3
P68919	10675.6	S	U	T	B	HCD	FT	5	61.7	AANKFPAIIYGGK	1349.8	R	E	3.0	0.0	44.9	14.0
P68919	10675.6	S	U	T	B	HCD	FT	5	61.7	AEFYSEVLTIVVDGK	1669.9	K	E	2.1	0.8	60.8	17.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68919	10675.6	S	U	T	B	HCD	FT	5	61.7	EAPLAIELDHDK	1350.7	K	V	2.2	0.0	25.8	17.8
P68919	10675.6	S	U	T	B	HCD	FT	5	61.7	LQHIDFVRA	1099.6	K	-	2.5	0.0	15.5	13.4
P68919	10675.6	S	U	T	B	HCD	FT	5	61.7	MFTINAEVR	1080.6	-	K	2.2	0.0	62.3	14.3
P0AFX0	10732.3	G	T	T	A	CID	LIT	2	24.2	EFVTAK	694.4	R	F	1.7	0.5	16.7	14.5
P0AFX0	10732.3	G	T	T	A	CID	LIT	2	24.2	MQLNITGNNVEITEALR	1932.0	-	E	0.0	0.0	47.0	13.2
P0AFX0	10732.3	G	U	A	A	CID	LIT	3	36.8	DATLHVNGGEIHASAEGQ	1805.8	S	D	5.8	0.7	60.1	14.0
P0AFX0	10732.3	G	U	A	A	CID	LIT	3	36.8	DKLARQLTKHK	1337.8	I	D	1.7	0.6	14.7	6.0
P0AFX0	10732.3	G	U	A	A	CID	LIT	3	36.8	DKLKQH	768.4	K	-	1.7	0.5	14.8	8.5
P0AFX0	10732.3	G	U	T	B	CID	LIT	3	64.2	INQVYVVLK	1075.7	R	V	3.4	0.4	39.8	9.0
P0AFX0	10732.3	G	U	T	B	CID	LIT	3	64.2	MQLNITGNNVEITEALR	1916.0	-	E	5.6	0.7	103.0	13.6
P0AFX0	10732.3	G	U	T	B	CID	LIT	3	64.2	VTHTSDATLHVNGGEIHASAEGQDMYAAIDGLIDK	3636.7	K	L	3.6	0.0	14.3	8.5
P0AFX0	10732.3	G	T	A	B	CID	LIT	5	67.4	DATLHVNGGEIHASAEGQ	1805.8	S	D	5.5	0.8	50.9	14.1
P0AFX0	10732.3	G	T	A	B	CID	LIT	5	67.4	DKLARQLTKHK	1337.8	I	D	2.4	0.0	25.6	6.0
P0AFX0	10732.3	G	T	A	B	CID	LIT	5	67.4	DKLKQH	768.4	K	-	1.8	0.6	17.4	9.0
P0AFX0	10732.3	G	T	A	B	CID	LIT	5	67.4	DMYAAIDGLI	1081.5	Q	D	1.4	0.5	36.4	13.2
P0AFX0	10732.3	G	T	A	B	CID	LIT	5	67.4	DRINQVYVVLKVEKVTHTS	2228.2	F	D	3.5	0.8	21.4	12.0
P0AFX0	10732.3	G	U	A	B	CID	LIT	3	36.8	DATLHVNGGEIHASAEGQ	1805.8	S	D	3.5	0.8	30.4	14.1
P0AFX0	10732.3	G	U	A	B	CID	LIT	3	36.8	DKLARQLTKHK	1337.8	I	D	2.5	0.0	28.7	6.0
P0AFX0	10732.3	G	U	A	B	CID	LIT	3	36.8	DKLKQH	768.4	K	-	1.6	0.6	12.1	9.0
P0AFX0	10732.3	S	U	T	A	ETD	LIT	2	23.2	FAKLEQYFDR	1316.7	K	I	1.9	0.0	24.5	17.2
P0AFX0	10732.3	S	U	T	A	ETD	LIT	2	23.2	LEQYFDRINQVYVVLKVEK	2383.3	K	V	5.1	0.0	28.4	14.6
P0AFX0	10732.3	S	U	T	B	ETD	LIT	4	37.9	INQVYVVLK	1075.7	R	V	0.8	0.4	20.4	11.1
P0AFX0	10732.3	S	U	T	B	ETD	LIT	4	37.9	LEQYFDRINQVYVVLK	2027.1	K	V	3.4	0.5	22.0	16.4
P0AFX0	10732.3	S	U	T	B	ETD	LIT	4	37.9	LEQYFDRINQVYVVLKVEK	2383.3	K	V	3.1	0.0	21.9	14.1
P0AFX0	10732.3	S	U	T	B	ETD	LIT	4	37.9	MQLNITGNNVEITEALR	1916.0	-	E	1.3	0.3	69.1	19.0
P0AFX0	10732.3	S	U	T	C	ETD	LIT	2	37.9	LEQYFDRINQVYVVLKVEK	2383.3	K	V	3.1	0.0	24.4	14.1
P0AFX0	10732.3	S	U	T	C	ETD	LIT	2	37.9	MQLNITGNNVEITEALR	1916.0	-	E	1.2	0.4	27.9	18.9
P0AFX0	10732.3	S	U	T	B	ETD+CID	LIT	2	25.3	LEQYFDR	970.5	K	I	0.0	0.0	38.1	12.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFX0	10732.3	S	U	T	B	ETD+CID	LIT	2	25.3	MQLNITGNNVEITEALR	1916.0	-	E	0.0	0.0	52.9	18.8
P0AFX0	10732.3	S	U	T	B	ETD+CID	LIT	2	25.3	LEQYFDR	970.5	K	I	2.5	0.7	38.1	12.8
P0AFX0	10732.3	S	U	T	B	ETD+CID	LIT	2	25.3	MQLNITGNNVEITEALR	1916.0	-	E	3.7	0.5	52.9	18.8
P0AFX0	10732.3	S	U	T	B	HCD	FT	2	25.3	LEQYFDR	970.5	K	I	0.0	0.0	38.1	12.8
P0AFX0	10732.3	S	U	T	B	HCD	FT	2	25.3	MQLNITGNNVEITEALR	1916.0	-	E	0.0	0.0	52.9	18.8
P32162	10758.6	G	U	T	A	CID	LIT	2	34.3	FFATREEAESFMTK	1693.8	R	L	4.6	0.0	53.2	9.5
P32162	10758.6	G	U	T	A	CID	LIT	2	34.3	LKELAAATSSADEGASVAYK	1982.0	K	I	5.1	0.7	51.9	14.3
P32162	10758.6	G	T	T	A	CID	LIT	5	52.5	ELAAATSSADEGASVAYK	1740.8	K	I	5.1	0.0	88.7	11.8
P32162	10758.6	G	T	T	A	CID	LIT	5	52.5	FFATR	641.3	R	E	1.1	0.5	18.2	8.5
P32162	10758.6	G	T	T	A	CID	LIT	5	52.5	FFATREEAESFMTK	1709.8	R	L	2.8	0.0	35.9	8.5
P32162	10758.6	G	T	T	A	CID	LIT	5	52.5	GCAIDIGTVIDNDNCTSK	1952.9	K	F	4.8	0.7	66.1	9.0
P32162	10758.6	G	T	T	A	CID	LIT	5	52.5	LKELAAATSSADEGASVAYK	1982.0	K	I	4.9	0.7	47.3	13.0
P32162	10758.6	G	U	A	A	CID	LIT	2	21.2	DEGASVAYKIK	1180.6	A	D	2.7	0.8	37.7	13.0
P32162	10758.6	G	U	A	A	CID	LIT	2	21.2	DKCSTKGCAI	1139.5	V	D	2.2	0.4	19.9	13.2
P32162	10758.6	G	U	T	B	CID	LIT	4	52.5	EEAESFMTK	1071.5	R	L	1.8	0.0	24.1	7.0
P32162	10758.6	G	U	T	B	CID	LIT	4	52.5	FFATR	641.3	R	E	1.2	0.5	14.8	8.5
P32162	10758.6	G	U	T	B	CID	LIT	4	52.5	GCAIDIGTVIDNDNCTSK	1952.9	K	F	4.0	0.0	53.4	7.8
P32162	10758.6	G	U	T	B	CID	LIT	4	52.5	LKELAAATSSADEGASVAYK	1982.0	K	I	5.8	0.0	115.0	13.8
P32162	10758.6	G	T	A	B	CID	LIT	2	27.3	DEGASVAYKIK	1180.6	A	D	3.2	0.9	39.5	13.0
P32162	10758.6	G	T	A	B	CID	LIT	2	27.3	DKCSTKGCAIDIGTVI	1737.9	V	D	1.8	0.5	9.0	15.3
P32162	10758.6	G	U	A	B	CID	LIT	4	46.5	DEGASVAYKIK	1180.6	A	D	3.5	0.8	45.2	13.0
P32162	10758.6	G	U	A	B	CID	LIT	4	46.5	DKCSTKGCAIDIGTVI	1737.9	V	D	3.3	0.0	33.4	15.3
P32162	10758.6	G	U	A	B	CID	LIT	4	46.5	DKCSTKGCAIDIGTVIDN	1966.9	V	D	2.8	0.7	14.7	14.9
P32162	10758.6	G	U	A	B	CID	LIT	4	46.5	ESFMTKLKELAAATSSA	1784.9	A	D	1.8	0.6	0.0	0.0
P32162	10758.6	S	U	T	B	CID	LIT	3	35.4	FFATREEAESFMTK	1693.8	R	L	3.8	0.5	33.3	14.8
P32162	10758.6	S	U	T	B	CID	LIT	3	35.4	GCAIDIGTVIDNDNCTSK	1952.9	K	F	5.8	0.7	70.1	13.8
P32162	10758.6	S	U	T	B	CID	LIT	3	35.4	GCAIDIGTVIDNDNCTSKFSR	2343.1	K	F	3.7	0.5	18.3	14.9
P32162	10758.6	S	U	T	B	ETD+CID	LIT	2	32.3	FFATREEAESFMTK	1693.8	R	L	0.0	0.0	32.9	14.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P32162	10758.6	S	U	T	B	ETD+CID	LIT	2	32.3	GCAIDIGTVIDNDNCTSK	1952.9	K	F	0.0	0.0	78.1	14.3
P32162	10758.6	S	U	T	B	ETD+CID	LIT	3	52.5	FFATREEAESFMTK	1693.8	R	L	3.7	0.5	32.9	14.6
P32162	10758.6	S	U	T	B	ETD+CID	LIT	3	52.5	GCAIDIGTVIDNDNCTSK	1952.9	K	F	5.6	0.7	78.1	14.3
P32162	10758.6	S	U	T	B	ETD+CID	LIT	3	52.5	LKELAAATSSADEGASVAYK	1982.0	K	I	2.1	0.3	5.4	18.3
P32162	10758.6	S	U	T	B	HCD	FT	2	32.3	FFATREEAESFMTK	1693.8	R	L	0.0	0.0	32.9	14.6
P32162	10758.6	S	U	T	B	HCD	FT	2	32.3	GCAIDIGTVIDNDNCTSK	1952.9	K	F	0.0	0.0	78.1	14.3
P0AGK4	10765.8	G	U	T	A	CID	LIT	6	48.5	ETGACNVQVIGK	1275.6	R	T	3.1	0.7	34.7	12.8
P0AGK4	10765.8	G	U	T	A	CID	LIT	6	48.5	IATEDRETK	1062.5	K	T	1.8	0.6	8.9	10.4
P0AGK4	10765.8	G	U	T	A	CID	LIT	6	48.5	KISLPR	713.5	R	-	1.9	0.7	25.0	12.3
P0AGK4	10765.8	G	U	T	A	CID	LIT	6	48.5	TLIVEAIVR	1013.6	K	E	2.7	0.6	47.8	9.5
P0AGK4	10765.8	G	U	T	A	CID	LIT	6	48.5	TLVLYRPTK	1090.7	K	E	2.4	0.0	26.0	6.0
P0AGK4	10765.8	G	U	T	A	CID	LIT	6	48.5	TLVLYRPTKER	1375.8	K	K	2.9	0.4	16.0	9.0
P0AGK4	10765.8	G	U	T	B	CID	LIT	6	46.4	ETGACNVQVIGK	1275.6	R	T	3.0	0.8	40.7	14.1
P0AGK4	10765.8	G	U	T	B	CID	LIT	6	46.4	IATEDR	704.4	K	E	1.8	0.6	33.3	14.3
P0AGK4	10765.8	G	U	T	B	CID	LIT	6	46.4	IATEDRETK	1062.5	K	T	3.2	0.0	20.3	10.4
P0AGK4	10765.8	G	U	T	B	CID	LIT	6	46.4	KISLPR	713.5	R	-	1.7	0.0	22.9	12.3
P0AGK4	10765.8	G	U	T	B	CID	LIT	6	46.4	TLIVEAIVR	1013.6	K	E	2.9	0.7	35.4	9.5
P0AGK4	10765.8	G	U	T	B	CID	LIT	6	46.4	TLVLYRPTK	1090.7	K	E	2.3	0.0	26.9	6.0
P0AGK4	10765.8	S	U	T	B	CID	LIT	3	57.7	GLAHPLKPVVLLGSNGLTEGVLAEIEQALEHHELIK	3826.1	K	V	3.3	0.0	26.5	10.4
P0AGK4	10765.8	S	U	T	B	CID	LIT	3	57.7	TLIVEAIVR	1013.6	K	E	2.7	0.7	23.2	10.8
P0AGK4	10765.8	S	U	T	B	CID	LIT	3	57.7	VKIATEDRETK	1289.7	K	T	3.1	0.6	25.1	16.1
P0AGK4	10765.8	S	U	T	C	CID	LIT	4	67.0	GLAHPLKPVVLLGSNGLTEGVLAEIEQALEHHELIK	3826.1	K	V	3.7	0.0	14.0	10.0
P0AGK4	10765.8	S	U	T	C	CID	LIT	4	67.0	TLIVEAIVR	1013.6	K	E	2.7	0.0	31.3	10.8
P0AGK4	10765.8	S	U	T	C	CID	LIT	4	67.0	TLVLYRPTK	1090.7	K	E	2.8	0.7	19.1	9.0
P0AGK4	10765.8	S	U	T	C	CID	LIT	4	67.0	VKIATEDRETK	1289.7	K	T	3.0	0.4	26.1	16.1
P0AGK4	10765.8	S	U	T	A	ETD	LIT	4	64.9	GLAHPLKPVVLLGSNGLTEGVLAEIEQALEHHELIK	3825.1	K	V	0.0	0.0	31.4	9.0
P0AGK4	10765.8	S	U	T	A	ETD	LIT	4	64.9	IATEDRETK	1062.5	K	T	2.5	0.3	34.9	15.4
P0AGK4	10765.8	S	U	T	A	ETD	LIT	4	64.9	TLIVEAIVR	1013.6	K	E	2.4	0.3	17.2	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AGK4	10765.8	S	U	T	A	ETD	LIT	4	64.9	TLVLYRPTK	1090.7	K	E	1.8	0.2	33.1	9.0
P0AGK4	10765.8	S	U	T	B	ETD	LIT	3	30.9	ETGACNVQVIGK	1275.6	R	T	2.6	0.6	37.4	17.2
P0AGK4	10765.8	S	U	T	B	ETD	LIT	3	30.9	TLIVEAIVR	1013.6	K	E	1.9	0.0	25.1	11.5
P0AGK4	10765.8	S	U	T	B	ETD	LIT	3	30.9	TLVLYRPTK	1090.7	K	E	1.9	0.3	33.2	9.0
P0AGK4	10765.8	S	U	T	B	ETD+CID	LIT	2	48.5	GLAHPLKPVVLLGSNGLTEGVLAEIEQALEHHELIK	3826.1	K	V	0.0	0.0	48.7	10.0
P0AGK4	10765.8	S	U	T	B	ETD+CID	LIT	2	48.5	IATEDRETK	1062.5	K	T	0.0	0.0	28.6	15.4
P0AGK4	10765.8	S	U	T	B	ETD+CID	LIT	2	48.5	VKIATEDRETK	1289.7	K	T	0.0	0.0	25.6	16.0
P0AGK4	10765.8	S	U	T	A	ETD+CID	LIT	2	18.6	IATEDRETK	1062.5	K	T	1.6	0.2	31.5	15.4
P0AGK4	10765.8	S	U	T	A	ETD+CID	LIT	2	18.6	TLIVEAIVR	1013.6	K	E	0.0	0.0	58.9	10.8
P0AGK4	10765.8	S	U	T	B	ETD+CID	LIT	2	48.5	GLAHPLKPVVLLGSNGLTEGVLAEIEQALEHHELIK	3826.1	K	V	0.0	0.0	48.7	10.0
P0AGK4	10765.8	S	U	T	B	ETD+CID	LIT	2	48.5	IATEDRETK	1062.5	K	T	2.8	0.5	28.6	15.4
P0AGK4	10765.8	S	U	T	B	ETD+CID	LIT	2	48.5	IGNRFDLVLVAAR	1443.8	-	-	2.4	0.7	4.5	10.4
P0AGK4	10765.8	S	U	T	B	ETD+CID	LIT	2	48.5	VKIATEDRETK	1289.7	K	T	2.9	0.3	25.6	16.0
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	ASGLLELR	858.5	R	T	3.0	0.4	40.6	16.8
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	IAVEVAYALPEK	1302.7	K	Q	3.7	0.6	49.8	13.0
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	LSDSVHDGDR	1100.5	K	V	3.5	0.5	70.1	8.5
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	NKVGIYSRPAK	1232.7	K	L	3.0	0.5	49.6	12.0
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	QYLQR	707.4	K	V	1.9	0.2	20.5	16.5
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	TDIDLTK	805.4	R	N	2.1	0.7	13.3	10.0
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	TDIDLTKNK	1047.6	R	V	2.3	0.7	17.3	14.6
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	VGIYSRPAK	990.6	K	L	2.9	0.4	46.6	13.6
P52119	10771.7	G	T	T	A	CID	LIT	9	69.8	VTLQEGATVEEAIR	1515.8	R	A	4.4	0.8	83.9	12.0
P52119	10771.7	G	T	T	B	CID	LIT	2	16.7	IAVEVAYALPEK	1302.7	K	Q	3.4	0.3	47.6	12.8
P52119	10771.7	G	T	T	B	CID	LIT	2	16.7	MPGKIAVEVAYALPEK	1715.9	-	Q	2.1	0.2	0.0	0.0
P52119	10771.7	G	T	A	B	CID	LIT	4	33.3	DGDRVEIYRPLIA	1516.8	H	D	2.5	0.6	29.4	16.0
P52119	10771.7	G	T	A	B	CID	LIT	4	33.3	DIDLTKNKVGIYSRPAKLS	2118.2	T	D	3.7	0.0	28.8	11.1
P52119	10771.7	G	T	A	B	CID	LIT	4	33.3	DLTKNKVGIYSRPAKLS	1890.1	I	D	2.4	0.3	11.0	10.4
P52119	10771.7	G	T	A	B	CID	LIT	4	33.3	DRVEIYRPLIA	1344.8	G	D	2.6	0.0	15.0	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69822	10877.5	G	U	T	A	CID	LIT	2	24.8	LLEVIKEHFPQDVK	1694.9	K	-	3.8	0.5	17.0	8.5
P69822	10877.5	G	U	T	A	CID	LIT	2	24.8	NMLSPADFGPK	1176.6	R	L	2.0	0.7	16.9	10.8
P69822	10877.5	G	T	T	A	CID	LIT	2	24.8	LLEVIKEHFPQDVK	1694.9	K	-	2.9	0.4	21.9	7.8
P69822	10877.5	G	T	T	A	CID	LIT	2	24.8	NMLSPADFGPK	1192.6	R	L	2.5	0.0	32.8	12.0
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	EAEGQDFQLYPGELGK	1780.8	R	R	3.4	0.0	45.9	11.1
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	EAEGQDFQLYPGELGKR	1936.9	R	I	3.1	0.0	52.8	10.0
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	EAWAQWQHK	1183.6	K	Q	2.5	0.8	16.0	10.0
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	EVHIEGYTPEDK	1416.7	K	-	3.1	0.7	21.4	10.0
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	EVHIEGYTPEDKK	1544.8	K	-	3.7	0.7	40.4	13.6
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	IYNEISK	866.5	R	E	2.0	0.7	38.1	13.8
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	IYNEISKEAWAQWQHK	2031.0	R	Q	5.2	0.7	53.9	12.3
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	KLLEQEMVNFLFEGK	1841.0	R	E	4.4	0.6	30.5	11.8
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	KLNMMNAEHR	1243.6	K	K	3.1	0.6	38.2	12.0
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	LLEQEMVNFLFEGK	1696.9	K	E	2.9	0.7	57.8	11.8
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	LNMMNAEHR	1115.5	K	K	2.8	0.7	55.1	4.8
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	LNMMNAEHRK	1243.6	K	L	2.2	0.4	15.9	12.3
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	QTMLINEK	976.5	K	K	2.1	0.7	23.0	15.6
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	QTMLINEKK	1104.6	K	L	2.7	0.6	29.5	13.2
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	RIYNEISK	1022.6	K	E	3.0	0.5	30.0	8.5
P0A8P3	10934.8	G	U	T	A	CID	LIT	16	96.7	TIFCTFLQR	1185.6	R	E	2.8	0.7	46.2	13.2
P0A8P3	10934.8	G	T	T	A	CID	LIT	6	75.8	EAEGQDFQLYPGELGK	1780.8	R	R	2.6	0.0	41.8	10.8
P0A8P3	10934.8	G	T	T	A	CID	LIT	6	75.8	EAWAQWQHK	1183.6	K	Q	2.7	0.0	28.8	10.0
P0A8P3	10934.8	G	T	T	A	CID	LIT	6	75.8	EVHIEGYTPEDKK	1544.8	K	-	4.3	0.7	54.8	13.6
P0A8P3	10934.8	G	T	T	A	CID	LIT	6	75.8	LLEQEMVNFLFEGK	1696.9	K	E	2.8	0.5	51.4	12.6
P0A8P3	10934.8	G	T	T	A	CID	LIT	6	75.8	RIYNEISK	1022.6	K	E	2.8	0.4	22.9	8.5
P0A8P3	10934.8	G	T	T	A	CID	LIT	6	75.8	TIFCTFLQR	1185.6	R	E	2.6	0.7	39.1	13.2
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	EAEGQDFQLYPGELGK	1780.8	R	R	4.8	0.0	41.4	10.4
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	EAEGQDFQLYPGELGKR	1936.9	R	I	4.1	0.8	57.0	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	EAWAQWQHK	1183.6	K	Q	2.4	0.7	22.4	10.0
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	EVHIEGYTPEDKK	1544.8	K	-	4.5	0.7	54.2	12.8
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	KLLEQEMVNFLFEGK	1825.0	R	E	4.4	0.6	28.0	11.5
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	KLNMMNAEHR	1243.6	K	K	3.2	0.3	46.8	12.6
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	LLEQEMVNFLFEGK	1696.9	K	E	4.3	0.0	67.7	11.1
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	LNMMNAEHR	1115.5	K	K	2.9	0.5	49.8	7.8
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	QTMLINEK	976.5	K	K	2.3	0.2	25.5	15.6
P0A8P3	10934.8	G	T	T	B	CID	LIT	10	79.1	QTMLINEKK	1104.6	K	L	2.6	0.2	11.1	13.4
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	EAEGQDFQLYPGELGK	1780.8	R	R	3.1	0.0	24.9	10.4
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	EAWAQWQHK	1183.6	K	Q	2.6	0.7	16.0	10.0
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	EVHIEGYTPEDKK	1544.8	K	-	2.5	0.8	34.2	12.8
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	IYNEISK	866.5	R	E	2.0	0.0	32.7	13.8
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	KLNMMNAEHR	1243.6	K	K	3.5	0.7	58.8	12.0
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	LLEQEMVNFLFEGK	1696.9	K	E	3.9	0.7	63.0	13.2
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	LNMMNAEHR	1115.5	K	K	3.1	0.0	57.6	7.0
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	LNMMNAEHRK	1243.6	K	L	3.1	0.5	40.8	12.3
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	QTMLINEK	976.5	K	K	2.0	0.0	23.0	15.3
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	RIYNEISK	1022.6	K	E	3.2	0.8	33.0	8.5
P0A8P3	10934.8	G	U	T	B	CID	LIT	11	96.7	TIFCTFLQR	1185.6	R	E	2.8	0.7	38.2	13.2
P0A8P3	10934.8	G	U	A	B	CID	LIT	2	34.1	DFQLYPGELGKRIYN	1812.9	Q	E	3.2	0.7	14.6	14.9
P0A8P3	10934.8	G	U	A	B	CID	LIT	2	34.1	SRTIFCTFLQREAEGQ	1942.9	M	D	0.0	0.0	31.1	16.2
P0A8P3	10934.8	S	U	T	A	CID	LIT	7	73.6	EAEGQDFQLYPGELGK	1780.8	R	R	4.0	0.6	40.2	16.3
P0A8P3	10934.8	S	U	T	A	CID	LIT	7	73.6	EAEGQDFQLYPGELGKR	1936.9	R	I	4.1	0.5	52.3	17.3
P0A8P3	10934.8	S	U	T	A	CID	LIT	7	73.6	IYNEISKEAWAQWQHK	2031.0	R	Q	5.2	0.5	45.0	18.8
P0A8P3	10934.8	S	U	T	A	CID	LIT	7	73.6	KLLEQEMVNFLFEGK	1825.0	R	E	5.7	0.6	101.0	16.8
P0A8P3	10934.8	S	U	T	A	CID	LIT	7	73.6	KLNMMNAEHR	1243.6	K	K	3.0	0.4	10.1	15.6
P0A8P3	10934.8	S	U	T	A	CID	LIT	7	73.6	RIYNEISK	1022.6	K	E	2.5	0.5	28.5	12.8
P0A8P3	10934.8	S	U	T	A	CID	LIT	7	73.6	TIFCTFLQR	1185.6	R	E	2.8	0.9	35.6	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	EAEGQDFQLYPGELGK	1780.8	R	R	3.8	0.6	31.2	16.2
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	EAEGQDFQLYPGELGKR	1936.9	R	I	4.0	0.0	51.5	18.3
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	IYNEISKEAWAQWQHK	2031.0	R	Q	5.8	0.5	46.4	18.6
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	KLLEQEMVNFLFEGK	1825.0	R	E	5.6	0.7	91.0	16.8
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	KLNMMNAEHR	1243.6	K	K	3.6	0.5	41.2	14.6
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	KLNMMNAEHRK	1371.7	K	L	3.1	0.4	31.3	16.4
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	LLEQEMVNFLFEGK	1696.9	K	E	4.5	0.8	73.8	17.7
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	LLEQEMVNFLFEGKEVHIEGYTPEDKK	3222.6	K	-	2.3	0.7	1.7	19.2
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	LNMMNAEHR	1115.5	K	K	3.2	0.6	29.3	11.8
P0A8P3	10934.8	S	U	T	B	CID	LIT	10	78.0	RIYNEISK	1022.6	K	E	2.3	0.5	18.2	12.8
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	EAEGQDFQLYPGELGK	1780.8	R	R	2.4	0.2	5.8	15.6
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	EAEGQDFQLYPGELGKR	1936.9	R	I	3.9	0.5	57.2	17.2
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	IYNEISKEAWAQWQHK	2031.0	R	Q	6.0	0.5	47.5	18.8
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	KLLEQEMVNFLFEGK	1825.0	R	E	5.9	0.6	104.0	16.3
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	KLNMMNAEHR	1243.6	K	K	4.5	0.6	46.8	14.8
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	KLNMMNAEHRK	1371.7	K	L	3.5	0.5	40.2	16.4
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	LLEQEMVNFLFEGKEVHIEGYTPEDKK	3222.6	K	-	3.5	0.8	0.0	0.0
P0A8P3	10934.8	S	U	T	C	CID	LIT	8	78.0	RIYNEISK	1022.6	K	E	2.8	0.5	20.0	12.8
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	EAEGQDFQLYPGELGK	1780.8	R	R	4.0	0.0	43.2	15.8
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	EAEGQDFQLYPGELGKR	1936.9	R	I	6.8	0.7	76.7	18.3
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	IYNEISK	866.5	R	E	1.9	0.0	21.1	15.3
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	IYNEISKEAWAQWQHK	2031.0	R	Q	5.4	0.4	79.1	18.3
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	KLLEQEMVNFLFEGK	1825.0	R	E	2.8	0.0	38.7	16.8
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	KLNMMNAEHR	1243.6	K	K	4.0	0.5	48.1	15.9
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	RIYNEISK	1022.6	K	E	2.3	0.5	0.0	0.0
P0A8P3	10934.8	S	U	T	A	ETD	LIT	8	63.7	RIYNEISKEAWAQWQHK	2187.1	K	Q	4.1	0.5	23.6	17.8
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	EAEGQDFQLYPGELGK	1780.8	R	R	3.4	0.8	47.5	16.0
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	EAEGQDFQLYPGELGKR	1936.9	R	I	5.5	0.4	75.0	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	EVHIEGYTPEDKK	1544.8	K	-	5.8	0.5	62.7	17.2
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	IYNEISKEAWAQWQHK	2031.0	R	Q	5.0	0.4	53.3	17.9
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	KLLEQEMVNFLFEGK	1825.9	R	E	4.0	0.5	53.2	17.6
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	KLNMMNAEHR	1243.6	K	K	2.1	0.4	21.5	15.4
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	RIYNEISK	1022.6	K	E	2.5	0.2	33.6	12.8
P0A8P3	10934.8	S	U	T	B	ETD	LIT	8	87.9	TIFCTFLQR	1185.6	R	E	1.7	0.3	0.0	0.0
P0A8P3	10934.8	S	U	T	C	ETD	LIT	7	63.7	EAEGQDFQLYPGELGK	1780.8	R	R	2.8	0.7	51.2	16.0
P0A8P3	10934.8	S	U	T	C	ETD	LIT	7	63.7	EAEGQDFQLYPGELGKR	1936.9	R	I	5.8	0.6	75.4	17.9
P0A8P3	10934.8	S	U	T	C	ETD	LIT	7	63.7	EAWAQWQHK	1183.6	K	Q	2.5	0.4	0.0	0.0
P0A8P3	10934.8	S	U	T	C	ETD	LIT	7	63.7	IYNEISKEAWAQWQHK	2031.0	R	Q	6.7	0.6	50.1	18.3
P0A8P3	10934.8	S	U	T	C	ETD	LIT	7	63.7	KLLEQEMVNFLFEGK	1825.0	R	E	5.7	0.6	79.3	16.1
P0A8P3	10934.8	S	U	T	C	ETD	LIT	7	63.7	KLNMMNAEHR	1243.6	K	K	4.7	0.6	67.9	14.8
P0A8P3	10934.8	S	U	T	C	ETD	LIT	7	63.7	RIYNEISK	1022.6	K	E	2.4	0.7	49.2	12.8
P0A8P3	10934.8	S	U	T	B	ETD	FT	2	20.9	KLNMMNAEHRK	1371.7	K	L	4.0	0.1	62.5	15.9
P0A8P3	10934.8	S	U	T	B	ETD	FT	2	20.9	RIYNEISK	1022.6	K	E	1.8	0.0	37.1	13.8
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	2	34.1	IYNEISKEAWAQWQHK	2031.0	R	Q	0.0	0.0	63.2	17.3
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	2	34.1	KLLEQEMVNFLFEGK	1825.0	R	E	0.0	0.0	70.9	16.9
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	7	73.6	EAEGQDFQLYPGELGK	1780.8	R	R	0.0	0.0	37.9	16.1
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	7	73.6	EAEGQDFQLYPGELGKR	1936.9	R	I	0.0	0.0	75.2	17.6
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	7	73.6	IYNEISKEAWAQWQHK	2031.0	R	Q	0.0	0.0	63.2	17.3
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	7	73.6	KLLEQEMVNFLFEGK	1825.0	R	E	0.0	0.0	104.0	16.3
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	7	73.6	KLNMMNAEHR	1243.6	K	K	0.0	0.0	52.6	14.8
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	7	73.6	KLNMMNAEHRK	1371.7	K	L	0.0	0.0	49.3	16.4
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	7	73.6	TIFCTFLQR	1185.6	R	E	0.0	0.0	40.7	15.9
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	EAEGQDFQLYPGELGK	1780.8	R	R	3.9	0.0	36.8	15.9
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	EAEGQDFQLYPGELGKR	1936.9	R	I	3.6	0.5	61.2	17.6
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	EVHIEGYTPEDKK	1544.8	K	-	4.4	0.8	52.2	16.9
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	IYNEISKEAWAQWQHK	2031.0	R	Q	6.2	0.7	48.6	17.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	KLLEQEMVNFLFEGK	1825.0	R	E	4.7	0.6	45.3	16.3
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	RIYNEISK	1022.6	K	E	2.7	0.4	41.3	13.8
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	RIYNEISKEAWAQWQHK	2187.1	K	Q	4.7	0.6	30.3	17.9
P0A8P3	10934.8	S	U	T	A	ETD+CID	LIT	8	76.9	TIFCTFLQR	1185.6	R	E	0.0	0.0	32.3	15.4
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	3	52.7	EAEGQDFQLYPGELGKR	1936.9	R	I	4.6	0.5	0.0	0.0
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	3	52.7	IYNEISKEAWAQWQHK	2031.0	R	Q	4.7	0.5	0.0	0.0
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	3	52.7	KLLEQEMVNFLFEGK	1825.0	R	E	6.0	0.6	0.0	0.0
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	EAEGQDFQLYPGELGK	1780.8	R	R	4.0	0.0	37.9	16.1
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	EAEGQDFQLYPGELGKR	1936.9	R	I	4.6	0.5	75.2	17.6
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	IYNEISKEAWAQWQHK	2031.0	R	Q	4.7	0.5	43.1	18.2
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	KLLEQEMVNFLFEGK	1825.0	R	E	6.0	0.6	104.0	16.3
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	KLNMMNAEHR	1243.6	K	K	4.8	0.7	52.6	14.8
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	KLNMMNAEHRK	1371.7	K	L	0.7	-0.2	49.3	16.4
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	RIYNEISK	1022.6	K	E	1.8	0.5	9.9	12.8
P0A8P3	10934.8	S	U	T	B	ETD+CID	LIT	8	73.6	TIFCTFLQR	1185.6	R	E	2.5	0.8	40.7	15.9
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	EAEGQDFQLYPGELGK	1780.8	R	R	4.4	0.6	41.0	16.1
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	EAEGQDFQLYPGELGKR	1936.9	R	I	4.5	0.5	105.0	17.9
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	EAWAQWQHK	1183.6	K	Q	3.2	0.4	24.4	13.2
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	IYNEISKEAWAQWQHK	2031.0	R	Q	5.8	0.5	46.2	18.8
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	KLLEQEMVNFLFEGK	1825.9	R	E	3.5	0.7	56.9	16.9
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	KLNMMNAEHR	1243.6	K	K	3.8	0.5	48.5	15.9
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	KLNMMNAEHRK	1371.7	K	L	3.7	0.3	45.6	16.2
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	RIYNEISK	1022.6	K	E	2.9	0.7	31.3	12.8
P0A8P3	10934.8	S	U	T	C	ETD+CID	LIT	9	73.6	TIFCTFLQR	1185.6	R	E	0.0	0.0	47.4	15.3
P0A8P3	10934.8	S	U	T	B	HCD	FT	7	73.6	EAEGQDFQLYPGELGK	1780.8	R	R	0.0	0.0	37.9	16.1
P0A8P3	10934.8	S	U	T	B	HCD	FT	7	73.6	EAEGQDFQLYPGELGKR	1936.9	R	I	0.0	0.0	75.2	17.6
P0A8P3	10934.8	S	U	T	B	HCD	FT	7	73.6	IYNEISKEAWAQWQHK	2031.0	R	Q	0.0	0.0	43.1	18.2
P0A8P3	10934.8	S	U	T	B	HCD	FT	7	73.6	KLLEQEMVNFLFEGK	1825.0	R	E	0.0	0.0	104.0	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8P3	10934.8	S	U	T	B	HCD	FT	7	73.6	KLNMMNAEHR	1243.6	K	K	0.0	0.0	52.6	14.8
P0A8P3	10934.8	S	U	T	B	HCD	FT	7	73.6	KLNMMNAEHRK	1371.7	K	L	0.0	0.0	49.3	16.4
P0A8P3	10934.8	S	U	T	B	HCD	FT	7	73.6	TIFCTFLQR	1185.6	R	E	0.0	0.0	40.7	15.9
P0A8P3	10934.8	S	U	T	C	HCD	FT	2	31.9	EVHIEGYTPEDKK	1544.8	K	-	3.8	0.7	30.7	17.2
P0A8P3	10934.8	S	U	T	C	HCD	FT	2	31.9	IYNEISKEAWAQWQHK	2031.0	R	Q	3.8	0.0	51.6	17.9
P64581	11033.7	G	U	T	A	CID	LIT	3	27.7	LGETGDAIAK	974.5	R	Q	2.3	0.6	63.3	14.8
P64581	11033.7	G	U	T	A	CID	LIT	3	27.7	SLSDTLEEVLSSSGEK	1680.8	K	S	4.4	0.7	79.7	12.0
P64581	11033.7	G	U	T	A	CID	LIT	3	27.7	YRLGETGDAIAK	1293.7	R	Q	3.2	0.5	22.7	12.8
P64581	11033.7	G	T	T	B	CID	LIT	2	19.8	LGETGDAIAK	974.5	R	Q	2.1	0.6	0.0	0.0
P64581	11033.7	G	T	T	B	CID	LIT	2	19.8	SKEHTTEHLR	1237.6	M	A	0.0	0.0	33.8	13.0
P64581	11033.7	G	U	T	B	CID	LIT	2	25.7	LGETGDAIAK	974.5	R	Q	2.9	0.5	26.9	14.8
P64581	11033.7	G	U	T	B	CID	LIT	2	25.7	SLSDTLEEVLSSSGEK	1680.8	K	S	3.6	0.0	63.9	12.3
Q2M7X4	11052.1	G	T	T	A	CID	LIT	4	24.7	ICTPQASLSDEAWEK	1734.8	K	L	3.5	0.0	29.4	10.4
Q2M7X4	11052.1	G	T	T	A	CID	LIT	4	24.7	KICTPQASLSDEAWEK	1862.9	R	L	4.5	0.7	56.2	13.0
Q2M7X4	11052.1	G	T	T	A	CID	LIT	4	24.7	TTVLQDLR	945.5	K	K	2.8	0.5	48.1	16.6
Q2M7X4	11052.1	G	T	T	A	CID	LIT	4	24.7	TTVLQDLRK	1073.6	K	I	1.9	0.6	29.6	10.8
Q2M7X4	11052.1	G	T	A	A	CID	LIT	2	32.0	DLRKICTPQASLS	1488.8	Q	D	2.8	0.7	19.1	15.6
Q2M7X4	11052.1	G	T	A	A	CID	LIT	2	32.0	ESPFSSLQSAKEKTTVLQ	1980.0	A	D	3.4	0.0	31.5	15.2
P0ADF8	11087.6	S	U	T	B	CID	LIT	2	32.3	LEQMISQIDKLEDVVK	1888.0	R	V	2.3	0.6	18.9	17.5
P0ADF8	11087.6	S	U	T	B	CID	LIT	2	32.3	NHPGVMTHVCGLFAR	1695.8	R	R	2.9	0.0	16.5	16.3
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	AEIKAAVQK	957.6	K	L	2.5	0.3	31.9	15.4
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	APHVSEK	767.4	R	A	1.8	0.5	17.2	13.0
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	APHVSEKASTAMEK	1501.7	R	S	2.2	0.7	15.0	10.4
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	ASTAMEKSNTIVLK	1492.8	K	V	3.7	0.0	75.2	11.8
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	AYVTLK	694.4	K	E	1.9	0.8	26.8	10.8
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	AYVTLKEGQNLDFVGGAE	1911.0	K	-	5.1	0.5	64.9	14.0
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	EGQNLDFVGGAE	1235.6	K	-	3.0	0.0	49.6	9.0
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	KAYVTLK	822.5	K	E	2.6	0.8	35.9	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	LLKVLR	741.5	R	A	1.2	0.4	12.5	6.0
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	MIREER	833.4	-	L	2.0	0.3	10.3	14.8
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	SNTIVLK	774.5	K	V	2.9	0.3	39.6	13.0
P0ADZ0	11180.9	G	U	T	A	CID	LIT	12	61.0	VLRAPHVSEK	1135.7	K	A	3.3	0.0	39.1	4.8
P0ADZ0	11180.9	G	U	T	B	CID	LIT	6	42.0	APHVSEK	767.4	R	A	1.9	0.0	27.7	12.3
P0ADZ0	11180.9	G	U	T	B	CID	LIT	6	42.0	ASTAMEK	737.4	K	S	1.8	0.8	30.4	13.0
P0ADZ0	11180.9	G	U	T	B	CID	LIT	6	42.0	EGQNLDFVGGAE	1235.6	K	-	2.0	0.0	17.7	9.0
P0ADZ0	11180.9	G	U	T	B	CID	LIT	6	42.0	MIREER	833.4	-	L	1.8	0.0	21.7	15.3
P0ADZ0	11180.9	G	U	T	B	CID	LIT	6	42.0	SNTIVLK	774.5	K	V	2.4	0.3	19.4	13.0
P0ADZ0	11180.9	G	U	T	B	CID	LIT	6	42.0	VLRAPHVSEK	1135.7	K	A	2.7	0.0	30.6	4.8
P0ADZ0	11180.9	G	U	A	B	CID	LIT	3	34.0	DWKKAYVTLKEGQNL	1793.0	S	D	4.5	0.6	45.0	14.1
P0ADZ0	11180.9	G	U	A	B	CID	LIT	3	34.0	EKASTAMEKSNTIVLKVAK	2048.1	S	D	2.3	0.6	18.9	13.4
P0ADZ0	11180.9	G	U	A	B	CID	LIT	3	34.0	EKSNTIVLKVAK	1329.8	M	D	2.9	0.0	47.6	6.0
P0ADZ0	11180.9	S	U	T	A	CID	LIT	5	48.0	DATKAEIK	875.5	K	A	2.4	0.1	28.2	17.9
P0ADZ0	11180.9	S	U	T	A	CID	LIT	5	48.0	EGQNLDFVGGAE	1235.6	K	-	2.0	0.5	0.0	0.0
P0ADZ0	11180.9	S	U	T	A	CID	LIT	5	48.0	LFEVEVEVVNTLVVK	1717.0	K	G	4.2	0.7	62.5	14.3
P0ADZ0	11180.9	S	U	T	A	CID	LIT	5	48.0	VAKDATKAEIK	1173.7	K	A	1.9	0.3	21.6	12.6
P0ADZ0	11180.9	S	U	T	A	CID	LIT	5	48.0	VLRAPHVSEK	1135.7	K	A	2.5	0.0	20.9	7.8
P0ADZ0	11180.9	S	U	T	B	CID	LIT	4	48.0	EGQNLDFVGGAE	1235.6	K	-	3.4	0.8	56.9	14.5
P0ADZ0	11180.9	S	U	T	B	CID	LIT	4	48.0	LFEVEVEVVNTLVVK	1717.0	K	G	4.5	0.7	67.2	14.1
P0ADZ0	11180.9	S	U	T	B	CID	LIT	4	48.0	VAKDATKAEIK	1173.7	K	A	1.9	0.6	12.6	12.6
P0ADZ0	11180.9	S	U	T	B	CID	LIT	4	48.0	VLRAPHVSEK	1135.7	K	A	2.7	0.7	23.7	7.8
P0ADZ0	11180.9	S	U	T	C	CID	LIT	4	45.0	DATKAEIK	875.5	K	A	2.2	0.0	24.1	15.4
P0ADZ0	11180.9	S	U	T	C	CID	LIT	4	45.0	EGQNLDFVGGAE	1235.6	K	-	3.6	0.8	68.7	14.5
P0ADZ0	11180.9	S	U	T	C	CID	LIT	4	45.0	LFEVEVEVVNTLVVK	1717.0	K	G	4.0	0.7	59.2	14.3
P0ADZ0	11180.9	S	U	T	C	CID	LIT	4	45.0	VLRAPHVSEK	1135.7	K	A	2.9	0.0	32.4	7.8
P0ADZ0	11180.9	S	U	T	A	ETD	LIT	2	25.0	LFEVEVEVVNTLVVK	1717.0	K	G	3.0	0.5	58.8	14.1
P0ADZ0	11180.9	S	U	T	A	ETD	LIT	2	25.0	VLRAPHVSEK	1135.7	K	A	3.9	0.7	33.3	7.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADZ0	11180.9	S	U	T	C	ETD	LIT	2	25.0	LFEVEVEVVNTLVVK	1717.0	K	G	3.3	0.7	0.0	0.0
P0ADZ0	11180.9	S	U	T	C	ETD	LIT	2	25.0	VLRAPHVSEK	1135.7	K	A	3.6	0.6	25.9	7.8
P0ADZ0	11180.9	S	U	T	B	ETD+CID	LIT	2	27.0	EGQNLDFVGGAE	1235.6	K	-	0.0	0.0	46.1	13.8
P0ADZ0	11180.9	S	U	T	B	ETD+CID	LIT	2	27.0	LFEVEVEVVNTLVVK	1717.0	K	G	0.0	0.0	49.3	12.6
P0ADZ0	11180.9	S	U	T	A	ETD+CID	LIT	5	48.0	DATKAEIK	875.5	K	A	2.1	0.2	20.7	15.4
P0ADZ0	11180.9	S	U	T	A	ETD+CID	LIT	5	48.0	EGQNLDFVGGAE	1235.6	K	-	2.4	0.6	0.0	0.0
P0ADZ0	11180.9	S	U	T	A	ETD+CID	LIT	5	48.0	LFEVEVEVVNTLVVK	1717.0	K	G	4.9	0.6	64.7	14.1
P0ADZ0	11180.9	S	U	T	A	ETD+CID	LIT	5	48.0	VAKDATKAEIK	1173.7	K	A	2.1	0.3	13.1	12.6
P0ADZ0	11180.9	S	U	T	A	ETD+CID	LIT	5	48.0	VLRAPHVSEK	1135.7	K	A	2.9	0.6	30.0	7.8
P0ADZ0	11180.9	S	U	T	B	ETD+CID	LIT	3	37.0	EGQNLDFVGGAE	1235.6	K	-	2.9	0.6	0.0	0.0
P0ADZ0	11180.9	S	U	T	B	ETD+CID	LIT	3	37.0	LFEVEVEVVNTLVVK	1717.0	K	G	4.8	0.6	48.2	14.1
P0ADZ0	11180.9	S	U	T	B	ETD+CID	LIT	3	37.0	VLRAPHVSEK	1135.7	K	A	2.1	0.7	16.2	7.8
P0ADZ0	11180.9	S	U	T	C	ETD+CID	LIT	4	45.0	DATKAEIK	875.5	K	A	2.3	0.1	17.1	15.4
P0ADZ0	11180.9	S	U	T	C	ETD+CID	LIT	4	45.0	EGQNLDFVGGAE	1235.6	K	-	0.0	0.0	25.9	14.5
P0ADZ0	11180.9	S	U	T	C	ETD+CID	LIT	4	45.0	LFEVEVEVVNTLVVK	1717.0	K	G	5.1	0.8	54.1	14.0
P0ADZ0	11180.9	S	U	T	C	ETD+CID	LIT	4	45.0	LQLLHDEGR	1080.6	-	-	2.3	0.1	39.8	14.5
P0ADZ0	11180.9	S	U	T	C	ETD+CID	LIT	4	45.0	VLRAPHVSEK	1135.7	K	A	2.9	0.6	30.0	7.8
P0ADZ0	11180.9	S	U	T	B	HCD	FT	2	27.0	EGQNLDFVGGAE	1235.6	K	-	0.0	0.0	46.1	13.8
P0ADZ0	11180.9	S	U	T	B	HCD	FT	2	27.0	LFEVEVEVVNTLVVK	1717.0	K	G	0.0	0.0	49.3	12.6
P0A6R3	11221.9	G	U	A	A	CID	LIT	3	27.6	DQVTQKPLR	1084.6	Q	D	2.8	0.4	33.1	11.8
P0A6R3	11221.9	G	U	A	A	CID	LIT	3	27.6	DVLTVSTVNSQ	1162.6	S	D	1.8	0.7	0.0	0.0
P0A6R3	11221.9	G	U	A	A	CID	LIT	3	27.6	FEQRVNS	879.4	M	D	0.0	0.0	26.3	15.7
P64461	11236.6	G	U	T	A	CID	LIT	2	27.1	FDVLQDPEVNSR	1418.7	R	F	3.3	0.0	50.9	11.8
P64461	11236.6	G	U	T	A	CID	LIT	2	27.1	QNHLGSVQEEGNLR	1580.8	R	F	3.7	0.5	25.9	13.4
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	EEFDVQTQVLLR	1476.8	R	T	2.6	0.6	25.0	14.3
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	EFGEDVEKK	1080.5	R	I	2.1	0.3	14.8	12.3
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	EKLALLEQR	1099.6	R	I	2.9	0.4	28.6	13.8
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	GIREFGEDVEK	1278.6	K	K	3.3	0.5	26.8	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	IRQTLQAQLTR	1327.8	K	L	4.4	0.0	48.2	8.5
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	ISELENR	860.4	R	S	2.1	0.0	34.2	15.1
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	KIEQIAR	857.5	K	Q	1.8	0.1	20.2	15.8
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	KQPDPETLPPTL	1335.7	K	-	2.6	0.7	16.2	13.0
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	LALLEQR	842.5	K	I	1.9	0.8	39.4	13.8
Q46868	11258.3	G	U	T	A	CID	LIT	10	72.9	QTLQAQLTR	1058.6	R	L	2.1	0.3	52.3	15.2
Q46868	11258.3	G	U	T	B	CID	LIT	3	16.7	EFGEDVEK	952.4	R	K	1.7	0.0	23.2	7.8
Q46868	11258.3	G	U	T	B	CID	LIT	3	16.7	EFGEDVEKK	1080.5	R	I	2.5	0.5	23.8	12.6
Q46868	11258.3	G	U	T	B	CID	LIT	3	16.7	ISELENR	860.4	R	S	2.4	0.2	31.0	15.1
Q46868	11258.3	S	U	T	A	CID	LIT	4	35.4	EKLALLEQR	1099.6	R	I	2.1	0.2	16.9	16.3
Q46868	11258.3	S	U	T	A	CID	LIT	4	35.4	KIEQIAR	857.5	K	Q	2.1	0.2	16.7	17.6
Q46868	11258.3	S	U	T	A	CID	LIT	4	35.4	LALLEQR	842.5	K	I	2.2	0.6	44.8	15.4
Q46868	11258.3	S	U	T	A	CID	LIT	4	35.4	LDLVSREEFDVQTQVLLR	2160.2	R	T	4.3	0.6	28.3	15.9
Q46868	11258.3	S	U	T	B	CID	LIT	5	50.0	EFGEDVEKK	1080.5	R	I	2.0	0.2	25.6	15.7
Q46868	11258.3	S	U	T	B	CID	LIT	5	50.0	EKLALLEQR	1099.6	R	I	1.8	0.0	27.3	16.0
Q46868	11258.3	S	U	T	B	CID	LIT	5	50.0	KQPDPETLPPTL	1335.7	K	-	2.1	0.3	0.0	0.0
Q46868	11258.3	S	U	T	B	CID	LIT	5	50.0	LALLEQR	842.5	K	I	2.2	0.6	37.4	15.4
Q46868	11258.3	S	U	T	B	CID	LIT	5	50.0	LDLVSREEFDVQTQVLLR	2160.2	R	T	2.2	0.2	4.3	16.6
Q46868	11258.3	S	U	T	C	CID	LIT	2	28.1	EFGEDVEKK	1080.5	R	I	2.3	0.3	4.4	15.8
Q46868	11258.3	S	U	T	C	CID	LIT	2	28.1	LDLVSREEFDVQTQVLLR	2160.2	R	T	4.1	0.6	7.4	15.9
Q46868	11258.3	S	U	T	B	ETD	LIT	3	18.8	EFGEDVEKK	1080.5	R	I	2.4	0.4	31.1	15.6
Q46868	11258.3	S	U	T	B	ETD	LIT	3	18.8	EKLALLEQR	1099.6	R	I	1.9	0.1	24.8	16.3
Q46868	11258.3	S	U	T	B	ETD	LIT	3	18.8	LALLEQR	842.5	K	I	2.4	0.3	0.0	0.0
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	3	37.5	EFGEDVEKK	1080.5	R	I	0.0	0.0	25.9	14.6
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	3	37.5	EKLALLEQR	1099.6	R	I	0.0	0.0	25.1	15.9
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	3	37.5	LDLVSREEFDVQTQVLLR	2160.2	R	T	0.0	0.0	17.2	15.9
Q46868	11258.3	S	U	T	A	ETD+CID	LIT	3	37.5	EFGEDVEKK	1080.5	R	I	2.3	0.6	25.5	14.5
Q46868	11258.3	S	U	T	A	ETD+CID	LIT	3	37.5	EKLALLEQR	1099.6	R	I	2.3	0.3	28.5	16.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
Q46868	11258.3	S	U	T	A	ETD+CID	LIT	3	37.5	LDLVSREEFDVQTQVLLR	2160.2	R	T	4.1	0.5	18.4	15.9
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	2	18.8	EFGEDVEKK	1080.5	R	I	2.1	0.5	0.0	0.0
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	2	18.8	EKLALLEQR	1099.6	R	I	1.8	0.5	0.0	0.0
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	4	50.0	EFGEDVEKK	1080.5	R	I	2.1	0.5	25.9	14.6
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	4	50.0	EKLALLEQR	1099.6	R	I	1.8	0.5	25.1	15.9
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	4	50.0	KQPDPETLPPTL	1335.7	K	-	2.3	0.2	0.0	0.0
Q46868	11258.3	S	U	T	B	ETD+CID	LIT	4	50.0	LDLVSREEFDVQTQVLLR	2160.2	R	T	3.8	0.6	17.2	15.9
Q46868	11258.3	S	U	T	C	ETD+CID	LIT	4	40.6	EKLALLEQR	1099.6	R	I	2.0	0.4	15.3	16.2
Q46868	11258.3	S	U	T	C	ETD+CID	LIT	4	40.6	KQPDPETLPPTL	1335.7	K	-	2.6	0.3	0.0	0.0
Q46868	11258.3	S	U	T	C	ETD+CID	LIT	4	40.6	LALLEQR	842.5	K	I	1.6	0.5	48.6	15.4
Q46868	11258.3	S	U	T	C	ETD+CID	LIT	4	40.6	LDLVSREEFDVQTQVLLR	2160.2	R	T	4.3	0.4	0.0	0.0
Q46868	11258.3	S	U	T	B	HCD	FT	3	37.5	EFGEDVEKK	1080.5	R	I	0.0	0.0	25.9	14.6
Q46868	11258.3	S	U	T	B	HCD	FT	3	37.5	EKLALLEQR	1099.6	R	I	0.0	0.0	25.1	15.9
Q46868	11258.3	S	U	T	B	HCD	FT	3	37.5	LDLVSREEFDVQTQVLLR	2160.2	R	T	0.0	0.0	17.2	15.9
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	LKNLGVEEVVAK	1298.8	R	V	3.7	0.7	32.8	7.0
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	NHEAGGIYLFTDEK	1593.8	K	S	4.8	0.0	39.3	7.0
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	NLGVEEVVAK	1057.6	K	V	2.8	0.8	35.1	14.5
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	SALAYLEK	894.5	K	H	1.9	0.7	6.8	9.0
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	SALAYLEKHTAR	1359.7	K	L	2.5	0.6	25.0	10.8
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	VFDVNEPLSQINQAK	1701.9	K	L	5.3	0.7	65.7	13.6
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	VWTESEK	878.4	K	N	2.0	0.4	4.7	12.3
P0ACX3	11270.1	G	U	T	A	CID	LIT	8	59.4	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	5.3	0.0	60.3	12.0
P0ACX3	11270.1	G	T	T	A	CID	LIT	3	26.7	LKNLGVEEVVAK	1298.8	R	V	3.0	0.4	20.0	7.8
P0ACX3	11270.1	G	T	T	A	CID	LIT	3	26.7	NLGVEEVVAK	1057.6	K	V	2.3	0.7	13.3	13.8
P0ACX3	11270.1	G	T	T	A	CID	LIT	3	26.7	VFDVNEPLSQINQAK	1701.9	K	L	4.9	0.8	60.8	13.6
P0ACX3	11270.1	G	U	A	A	CID	LIT	3	25.7	DAMAEQLKPLA	1186.6	G	E	1.9	0.6	17.8	14.1
P0ACX3	11270.1	G	U	A	A	CID	LIT	3	25.7	DVNEPLSQINQAKLA	1639.9	F	-	4.3	0.6	64.0	14.9
P0ACX3	11270.1	G	U	A	A	CID	LIT	3	25.7	EPLSQINQAKLA	1311.7	N	-	2.5	0.4	13.8	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACX3	11270.1	G	U	T	B	CID	LIT	6	55.4	LKNLGVEEVVAK	1298.8	R	V	3.6	0.0	66.8	7.0
P0ACX3	11270.1	G	U	T	B	CID	LIT	6	55.4	NHEAGGIYLFTDEK	1593.8	K	S	4.5	0.0	59.9	9.0
P0ACX3	11270.1	G	U	T	B	CID	LIT	6	55.4	NLGVEEVVAK	1057.6	K	V	2.4	0.0	22.5	13.8
P0ACX3	11270.1	G	U	T	B	CID	LIT	6	55.4	SALAYLEK	894.5	K	H	2.4	0.8	18.2	10.4
P0ACX3	11270.1	G	U	T	B	CID	LIT	6	55.4	VFDVNEPLSQINQAK	1701.9	K	L	5.3	0.7	54.1	13.6
P0ACX3	11270.1	G	U	T	B	CID	LIT	6	55.4	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	2.3	0.0	16.2	11.1
P0ACX3	11270.1	G	U	A	B	CID	LIT	3	25.7	DAMAEQLKPLA	1186.6	G	E	2.6	0.0	45.2	14.1
P0ACX3	11270.1	G	U	A	B	CID	LIT	3	25.7	DVNEPLSQINQAKLA	1639.9	F	-	3.8	0.8	46.9	14.5
P0ACX3	11270.1	G	U	A	B	CID	LIT	3	25.7	EPLSQINQAKLA	1311.7	N	-	3.0	0.4	31.2	11.1
P0ACX3	11270.1	S	U	T	A	CID	LIT	6	59.4	LKNLGVEEVVAK	1298.8	R	V	3.4	0.5	62.6	13.0
P0ACX3	11270.1	S	U	T	A	CID	LIT	6	59.4	NLGVEEVVAK	1057.6	K	V	1.8	0.3	8.5	16.3
P0ACX3	11270.1	S	U	T	A	CID	LIT	6	59.4	SALAYLEKHTAR	1359.7	K	L	2.8	0.5	24.6	15.9
P0ACX3	11270.1	S	U	T	A	CID	LIT	6	59.4	VFDVNEPLSQINQAK	1701.9	K	L	4.7	0.4	55.0	18.1
P0ACX3	11270.1	S	U	T	A	CID	LIT	6	59.4	VWTESEKNHEAGGIYLFTDEK	2454.1	K	S	4.7	0.6	53.5	17.5
P0ACX3	11270.1	S	U	T	A	CID	LIT	6	59.4	VWTESEKNHEAGGIYLFTDEKSALAYLEK	3328.6	K	H	4.3	0.0	29.9	19.0
P0ACX3	11270.1	S	U	T	B	CID	LIT	4	55.4	LKNLGVEEVVAK	1298.8	R	V	3.7	0.6	61.4	13.0
P0ACX3	11270.1	S	U	T	B	CID	LIT	4	55.4	VFDVNEPLSQINQAK	1701.9	K	L	5.2	0.5	67.6	18.5
P0ACX3	11270.1	S	U	T	B	CID	LIT	4	55.4	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	5.7	0.7	76.9	17.9
P0ACX3	11270.1	S	U	T	B	CID	LIT	4	55.4	VWTESEKNHEAGGIYLFTDEKSALAYLEK	3328.6	K	H	2.7	0.0	27.0	18.8
P0ACX3	11270.1	S	U	T	C	CID	LIT	3	26.7	LKNLGVEEVVAK	1298.8	R	V	3.6	0.5	56.6	12.8
P0ACX3	11270.1	S	U	T	C	CID	LIT	3	26.7	NLGVEEVVAK	1057.6	K	V	2.4	0.4	28.6	16.4
P0ACX3	11270.1	S	U	T	C	CID	LIT	3	26.7	VFDVNEPLSQINQAK	1701.9	K	L	4.3	0.5	68.2	18.4
P0ACX3	11270.1	S	U	T	A	ETD	LIT	6	55.4	LKNLGVEEVVAK	1298.8	R	V	6.2	0.5	79.2	13.0
P0ACX3	11270.1	S	U	T	A	ETD	LIT	6	55.4	NLGVEEVVAK	1057.6	K	V	2.3	0.5	10.8	16.3
P0ACX3	11270.1	S	U	T	A	ETD	LIT	6	55.4	SALAYLEK	894.5	K	H	1.9	0.5	28.2	11.5
P0ACX3	11270.1	S	U	T	A	ETD	LIT	6	55.4	VFDVNEPLSQINQAK	1701.9	K	L	3.3	0.5	0.0	0.0
P0ACX3	11270.1	S	U	T	A	ETD	LIT	6	55.4	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	5.6	0.0	39.4	17.9
P0ACX3	11270.1	S	U	T	A	ETD	LIT	6	55.4	VWTESEKNHEAGGIYLFTDEKSALAYLEK	3328.6	K	H	0.0	0.0	18.7	19.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACX3	11270.1	S	U	T	B	ETD	LIT	2	26.7	LKNLGVEEVVAK	1298.8	R	V	6.0	0.5	83.9	14.1
P0ACX3	11270.1	S	U	T	B	ETD	LIT	2	26.7	VFDVNEPLSQINQAK	1701.9	K	L	3.2	0.4	44.6	18.4
P0ACX3	11270.1	S	U	T	C	ETD	LIT	3	34.7	LKNLGVEEVVAK	1298.8	R	V	3.6	0.5	42.2	12.8
P0ACX3	11270.1	S	U	T	C	ETD	LIT	3	34.7	SALAYLEK	894.5	K	H	2.3	0.3	26.5	12.3
P0ACX3	11270.1	S	U	T	C	ETD	LIT	3	34.7	VFDVNEPLSQINQAK	1701.9	K	L	3.7	0.3	16.9	17.9
P0ACX3	11270.1	S	U	T	B	ETD+CID	LIT	2	35.6	VFDVNEPLSQINQAK	1701.9	K	L	0.0	0.0	67.3	18.5
P0ACX3	11270.1	S	U	T	B	ETD+CID	LIT	2	35.6	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	0.0	0.0	41.3	18.2
P0ACX3	11270.1	S	U	T	A	ETD+CID	LIT	3	43.6	SHQTGVNGENNSVR	1500.7	-	-	3.8	-0.4	57.8	14.3
P0ACX3	11270.1	S	U	T	A	ETD+CID	LIT	3	43.6	VFDVNEPLSQINQAK	1701.9	K	L	5.2	0.4	0.0	0.0
P0ACX3	11270.1	S	U	T	A	ETD+CID	LIT	3	43.6	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	5.1	0.6	0.0	0.0
P0ACX3	11270.1	S	U	T	A	ETD+CID	LIT	3	43.6	VWTESEKNHEAGGIYLFTDEKSALAYLEK	3328.6	K	H	3.1	-0.5	47.5	18.8
P0ACX3	11270.1	S	U	T	B	ETD+CID	LIT	3	43.6	VFDVNEPLSQINQAK	1701.9	K	L	5.3	0.4	67.3	18.5
P0ACX3	11270.1	S	U	T	B	ETD+CID	LIT	3	43.6	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	2.8	0.4	8.1	17.9
P0ACX3	11270.1	S	U	T	B	ETD+CID	LIT	3	43.6	VWTESEKNHEAGGIYLFTDEKSALAYLEK	3328.6	K	H	4.8	0.0	14.9	18.8
P0ACX3	11270.1	S	U	T	C	ETD+CID	LIT	3	47.5	LKNLGVEEVVAK	1298.8	R	V	3.7	0.7	57.8	12.3
P0ACX3	11270.1	S	U	T	C	ETD+CID	LIT	3	47.5	VFDVNEPLSQINQAK	1701.9	K	L	5.1	0.5	70.7	18.4
P0ACX3	11270.1	S	U	T	C	ETD+CID	LIT	3	47.5	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	3.8	0.6	30.9	17.9
P0ACX3	11270.1	S	U	T	B	HCD	FT	3	43.6	VFDVNEPLSQINQAK	1701.9	K	L	0.0	0.0	67.3	18.5
P0ACX3	11270.1	S	U	T	B	HCD	FT	3	43.6	VWTESEKNHEAGGIYLFTDEK	2453.2	K	S	0.0	0.0	41.3	18.2
P0ACX3	11270.1	S	U	T	B	HCD	FT	3	43.6	VWTESEKNHEAGGIYLFTDEKSALAYLEK	3328.6	K	H	0.0	0.0	14.9	18.8
P0AEH5	11288.0	G	U	T	A	CID	LIT	3	41.6	IDDDLTLLSETLEEVLR	1974.0	R	S	4.8	0.8	70.1	11.5
P0AEH5	11288.0	G	U	T	A	CID	LIT	3	41.6	SSGDPADQKYVELK	1536.8	R	A	3.8	0.8	49.8	13.4
P0AEH5	11288.0	G	U	T	A	CID	LIT	3	41.6	VSQASDSYYYR	1338.6	R	A	3.0	0.8	60.3	9.0
P0AEH5	11288.0	G	U	A	A	CID	LIT	2	21.8	DDVKKRVSQAS	1232.7	L	D	2.4	0.6	22.1	14.0
P0AEH5	11288.0	G	U	A	A	CID	LIT	2	21.8	DQKYVELKARA	1320.7	A	E	2.3	0.8	19.6	13.6
P0AEH5	11288.0	G	T	A	B	CID	LIT	3	35.6	DDVKKRVSQAS	1232.7	L	D	2.3	0.0	22.2	14.0
P0AEH5	11288.0	G	T	A	B	CID	LIT	3	35.6	DQKYVELKARA	1320.7	A	E	1.6	0.5	10.1	13.2
P0AEH5	11288.0	G	T	A	B	CID	LIT	3	35.6	DSYYYRAKQAVYRA	1753.9	S	D	2.1	0.1	16.7	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AEH5	11288.0	G	U	A	B	CID	LIT	4	46.5	DDVKKRVSQAS	1232.7	L	D	2.4	0.8	17.2	14.0
P0AEH5	11288.0	G	U	A	B	CID	LIT	4	46.5	DQKYVELKARA	1320.7	A	E	2.6	0.8	35.7	13.6
P0AEH5	11288.0	G	U	A	B	CID	LIT	4	46.5	DSYYYRAKQAVYRA	1753.9	S	D	2.8	0.7	17.5	14.5
P0AEH5	11288.0	G	U	A	B	CID	LIT	4	46.5	EEVLRSSGDPA	1159.6	L	D	2.8	0.3	30.6	15.3
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	ADRVGFR	820.4	K	F	1.9	0.2	11.0	13.8
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	DDEVIVLTGK	1088.6	R	D	3.7	0.8	66.8	14.6
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	DDEVIVLTGKDK	1331.7	R	G	3.5	0.0	51.2	14.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	EAAIQVSNVAIFNAATGK	1804.0	K	A	5.5	0.7	78.2	11.1
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	EAAIQVSNVAIFNAATGKADR	2146.1	K	V	4.9	0.7	103.0	13.6
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	FEDGKK	723.4	R	V	1.9	0.7	17.5	11.1
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	FFKSNSETIK	1200.6	R	-	2.8	0.7	22.9	12.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	HQKPVPALNQPGGIVEK	1812.0	K	E	4.4	0.8	47.7	9.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	KHQKPVPALNQPGGIVEK	1940.1	K	E	4.7	0.0	57.4	6.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	NVLSSGKVIVEGINLVK	1769.1	K	K	5.1	0.6	50.8	6.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	RDDEVIVLTGK	1244.7	R	D	3.9	0.6	63.0	14.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	VGFRFEDGK	1054.5	R	K	2.1	0.7	23.6	12.8
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	VIVEGINLVK	1083.7	K	K	3.2	0.0	54.6	6.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	VIVEGINLVKK	1211.8	K	H	2.8	0.0	34.2	3.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	VKNVLSSGK	931.6	K	V	2.6	0.7	35.0	10.0
P60624	11298.3	G	U	T	A	CID	LIT	16	89.4	VRFFK	696.4	K	S	1.8	0.2	12.7	10.8
P60624	11298.3	G	T	T	A	CID	LIT	5	62.5	EAAIQVSNVAIFNAATGK	1804.0	K	A	5.6	0.6	72.9	12.0
P60624	11298.3	G	T	T	A	CID	LIT	5	62.5	HQKPVPALNQPGGIVEK	1812.0	K	E	3.3	0.0	19.9	9.0
P60624	11298.3	G	T	T	A	CID	LIT	5	62.5	RDDEVIVLTGK	1244.7	R	D	3.0	0.0	25.2	12.3
P60624	11298.3	G	T	T	A	CID	LIT	5	62.5	VIVEGINLVK	1083.7	K	K	1.7	0.7	0.0	0.0
P60624	11298.3	G	T	T	A	CID	LIT	5	62.5	VKNVLSSGK	931.6	K	V	2.6	0.7	20.1	10.0
P60624	11298.3	G	U	A	A	CID	LIT	3	32.7	DDEVIVLTGK	1088.6	R	D	2.3	0.5	19.5	16.1
P60624	11298.3	G	U	A	A	CID	LIT	3	32.7	DGKKVRFFKSNSETIK	1884.0	E	-	3.8	0.6	23.5	12.6
P60624	11298.3	G	U	A	A	CID	LIT	3	32.7	DRVGFRFE	1025.5	A	D	2.9	0.6	34.4	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60624	11298.3	G	T	A	A	CID	LIT	2	26.0	DRVGFRFE	1025.5	A	D	3.1	0.9	30.5	12.0
P60624	11298.3	G	T	A	A	CID	LIT	2	26.0	EAAIQVSNVAIFNAATGKA	1875.0	K	D	5.1	0.8	43.7	14.5
P60624	11298.3	G	T	T	B	CID	LIT	6	52.9	EAAIQVSNVAIFNAATGK	1804.0	K	A	2.6	0.3	1.9	12.6
P60624	11298.3	G	T	T	B	CID	LIT	6	52.9	HQKPVPALNQPGGIVEK	1812.0	K	E	2.7	0.4	0.0	0.0
P60624	11298.3	G	T	T	B	CID	LIT	6	52.9	KHQKPVPALNQPGGIVEK	1940.1	K	E	4.6	0.0	23.1	7.0
P60624	11298.3	G	T	T	B	CID	LIT	6	52.9	NVLSSGK	704.4	K	V	1.8	0.5	3.4	13.2
P60624	11298.3	G	T	T	B	CID	LIT	6	52.9	VIVEGINLVK	1083.7	K	K	3.5	0.0	59.0	6.0
P60624	11298.3	G	T	T	B	CID	LIT	6	52.9	VKNVLSSGK	931.6	K	V	3.0	0.4	27.9	9.5
P60624	11298.3	G	U	T	B	CID	LIT	2	16.3	SNSETIK	778.4	K	-	2.4	0.0	26.6	10.8
P60624	11298.3	G	U	T	B	CID	LIT	2	16.3	VIVEGINLVK	1083.7	K	K	3.1	0.0	31.1	6.0
P60624	11298.3	G	T	A	B	CID	LIT	2	17.3	DDEVIVLTGK	1088.6	R	D	4.0	0.6	57.7	16.6
P60624	11298.3	G	T	A	B	CID	LIT	2	17.3	DRVGFRFE	1025.5	A	D	2.8	0.8	37.6	12.0
P60624	11298.3	G	U	A	B	CID	LIT	4	32.7	DDEVIVLTGK	1088.6	R	D	3.3	0.7	56.1	16.1
P60624	11298.3	G	U	A	B	CID	LIT	4	32.7	DEVIVLTGK	973.6	D	D	2.2	0.0	33.3	13.2
P60624	11298.3	G	U	A	B	CID	LIT	4	32.7	DGKKVRFFKSNSETIK	1884.0	E	-	3.8	0.6	24.5	12.3
P60624	11298.3	G	U	A	B	CID	LIT	4	32.7	DRVGFRFE	1025.5	A	D	2.6	0.5	49.7	12.0
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	DDEVIVLTGK	1088.6	R	D	3.9	0.6	66.2	17.6
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	EAAIQVSNVAIFNAATGK	1804.0	K	A	6.1	0.7	83.3	16.8
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	EAAIQVSNVAIFNAATGKADR	2146.1	K	V	2.6	0.5	7.6	17.9
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGKADR	3939.1	K	V	3.7	0.0	25.0	12.8
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	IRRDDEVIVLTGK	1513.9	K	D	3.1	0.7	48.6	15.2
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	NVLSSGK	704.4	K	V	1.6	0.4	16.0	16.2
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	RDDEVIVLTGK	1244.7	R	D	4.1	0.6	62.3	18.4
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	VIVEGINLVK	1083.7	K	K	3.7	0.8	54.8	10.4
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	VIVEGINLVKK	1211.8	K	H	3.6	0.8	33.7	8.5
P60624	11298.3	S	U	T	A	CID	LIT	10	68.3	VKNVLSSGK	931.6	K	V	2.6	0.6	28.1	12.6
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	DDEVIVLTGK	1088.6	R	D	3.6	0.5	44.7	17.1
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	EAAIQVSNVAIFNAATGK	1804.0	K	A	4.9	0.7	90.4	17.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	EAAIQVSNVAIFNAATGKADR	2146.1	K	V	2.3	0.3	0.0	0.0
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	HQKPVPALNQPGGIVEK	1813.0	K	E	2.6	0.5	0.0	0.0
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	4.2	0.0	19.4	12.8
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	IRRDDEVIVLTGK	1513.9	K	D	3.9	0.5	37.1	14.0
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	KHQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3725.1	K	A	5.2	0.0	27.0	12.3
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	NVLSSGK	704.4	K	V	1.7	0.0	27.1	16.2
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	RDDEVIVLTGK	1244.7	R	D	3.6	0.5	53.5	18.4
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	RDDEVIVLTGKDK	1487.8	R	G	4.4	0.7	56.2	16.4
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	VIVEGINLVK	1083.7	K	K	2.9	0.0	34.3	10.4
P60624	11298.3	S	U	T	B	CID	LIT	12	68.3	VIVEGINLVKK	1211.8	K	H	3.3	0.0	33.7	8.5
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	DDEVIVLTGK	1088.6	R	D	2.9	0.5	37.2	17.6
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	DDEVIVLTGKDK	1331.7	R	G	2.8	0.3	16.8	16.9
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	DDEVIVLTGKDKGK	1516.8	R	R	3.2	0.4	21.4	16.9
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	EAAIQVSNVAIFNAATGK	1804.0	K	A	5.4	0.7	90.6	16.8
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	EAAIQVSNVAIFNAATGKADR	2146.1	K	V	1.9	0.5	11.2	17.9
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	HQKPVPALNQPGGIVEK	1812.0	K	E	3.7	0.7	27.3	14.5
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	4.4	0.0	28.1	11.5
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	IRRDDEVIVLTGK	1513.9	K	D	3.8	0.5	45.6	13.8
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	KHQKPVPALNQPGGIVEK	1940.1	K	E	4.0	0.9	41.0	11.5
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	NVLSSGK	704.4	K	V	1.9	0.6	14.3	16.2
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	RDDEVIVLTGK	1244.7	R	D	3.8	0.6	61.6	18.3
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	RDDEVIVLTGKDK	1487.8	R	G	4.2	0.6	44.2	16.4
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	VGFRFEDGK	1054.5	R	K	2.8	0.0	30.0	15.7
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	VIVEGINLVK	1084.7	K	K	3.0	0.6	15.0	10.4
P60624	11298.3	S	U	T	C	CID	LIT	15	78.8	VIVEGINLVKK	1211.8	K	H	3.7	0.8	35.8	8.5
P60624	11298.3	S	U	T	A	CID	FT	2	27.9	EAAIQVSNVAIFNAATGK	1804.0	K	A	3.8	0.0	67.1	16.8
P60624	11298.3	S	U	T	A	CID	FT	2	27.9	VIVEGINLVKK	1211.8	K	H	2.0	0.0	20.2	7.8
P60624	11298.3	S	U	T	B	CID	FT	3	37.5	DDEVIVLTGK	1088.6	R	D	1.8	0.0	28.9	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60624	11298.3	S	U	T	B	CID	FT	3	37.5	EAAIQVSNVAIFNAATGK	1804.0	K	A	4.4	0.0	75.3	17.6
P60624	11298.3	S	U	T	B	CID	FT	3	37.5	VIVEGINLVKK	1211.8	K	H	2.7	0.0	35.4	8.5
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	DDEVIVLTGKDK	1331.7	R	G	3.4	0.5	38.8	16.9
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	DDEVIVLTGKDKGK	1516.8	R	R	3.5	0.5	37.2	17.0
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	EAAIQVSNVAIFNAATGK	1804.0	K	A	3.4	0.6	48.0	17.2
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	HQKPVPALNQPGGIVEK	1812.0	K	E	7.1	0.7	0.0	0.0
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	5.2	0.0	43.2	11.8
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	IRRDDEVIVLTGK	1513.9	K	D	5.5	0.5	88.7	15.2
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	KHQKPVPALNQPGGIVEK	1940.1	K	E	7.6	0.6	0.0	0.0
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	KHQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3725.1	K	A	0.0	0.0	18.4	12.3
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	NVLSSGK	704.4	K	V	1.5	0.3	28.2	16.2
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	RDDEVIVLTGK	1244.7	R	D	3.0	0.3	58.0	17.2
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	RDDEVIVLTGKDK	1487.8	R	G	5.1	0.5	70.9	17.5
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	VGFRFEDGK	1054.5	R	K	3.0	0.8	24.1	15.7
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	VIVEGINLVK	1083.7	K	K	3.0	0.3	0.0	0.0
P60624	11298.3	S	U	T	A	ETD	LIT	14	76.0	VIVEGINLVKK	1211.8	K	H	4.8	0.6	51.8	8.5
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	DDEVIVLTGK	1088.6	R	D	2.3	0.5	29.6	17.4
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	DDEVIVLTGKDK	1331.7	R	G	3.6	0.4	59.2	18.0
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	EAAIQVSNVAIFNAATGK	1804.0	K	A	2.9	0.4	70.3	16.9
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	HQKPVPALNQPGGIVEK	1812.0	K	E	4.4	0.0	34.2	14.0
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	IRRDDEVIVLTGK	1513.9	K	D	2.8	0.5	0.0	0.0
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	KHQKPVPALNQPGGIVEK	1940.1	K	E	7.4	0.6	55.4	11.5
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	KHQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3725.1	K	A	0.0	0.0	23.3	12.3
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	RDDEVIVLTGK	1244.7	R	D	2.9	0.4	46.4	17.2
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	RDDEVIVLTGKDK	1487.8	R	G	5.6	0.5	52.8	17.7
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	VGFRFEDGK	1054.5	R	K	4.5	0.6	0.0	0.0
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	VIVEGINLVK	1083.7	K	K	2.9	0.2	0.0	0.0
P60624	11298.3	S	U	T	B	ETD	LIT	12	67.3	VIVEGINLVKK	1211.8	K	H	4.1	0.5	52.7	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	DDEVIVLTGK	1088.6	R	D	1.7	0.5	22.6	17.6
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	DDEVIVLTGKDK	1331.7	R	G	3.5	0.5	0.0	0.0
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	EAAIQVSNVAIFNAATGK	1804.0	K	A	3.4	0.6	0.0	0.0
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	HQKPVPALNQPGGIVEK	1812.0	K	E	7.1	0.7	57.4	14.8
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	0.0	0.0	31.6	11.8
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	IRRDDEVIVLTGK	1513.9	K	D	3.3	0.6	48.4	14.5
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	KHQKPVPALNQPGGIVEK	1940.1	K	E	7.9	0.5	51.1	10.8
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	NVLSSGK	704.4	K	V	2.0	0.4	27.8	16.2
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	RDDEVIVLTGK	1244.7	R	D	2.5	0.4	43.9	17.2
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	RDDEVIVLTGKDK	1487.8	R	G	5.8	0.6	60.5	17.5
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	VGFRFEDGK	1054.5	R	K	4.2	0.6	31.3	15.7
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	VGFRFEDGKK	1182.6	R	V	4.7	0.6	0.0	0.0
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	VIVEGINLVK	1083.7	K	K	2.7	0.2	0.0	0.0
P60624	11298.3	S	U	T	C	ETD	LIT	14	75.0	VIVEGINLVKK	1211.8	K	H	4.7	0.5	62.0	8.5
P60624	11298.3	S	U	T	C	ETD	FT	6	48.1	IRRDDEVIVLTGK	1513.9	K	D	3.8	0.4	79.3	14.5
P60624	11298.3	S	U	T	C	ETD	FT	6	48.1	KHQKPVPALNQPGGIVEK	1940.1	K	E	6.4	0.0	46.8	11.8
P60624	11298.3	S	U	T	C	ETD	FT	6	48.1	NVLSSGK	704.4	K	V	1.1	0.0	28.6	16.2
P60624	11298.3	S	U	T	C	ETD	FT	6	48.1	RDDEVIVLTGKDK	1487.8	R	G	3.4	0.4	59.2	17.5
P60624	11298.3	S	U	T	C	ETD	FT	6	48.1	VGFRFEDGK	1054.5	R	K	2.2	0.0	41.5	15.7
P60624	11298.3	S	U	T	C	ETD	FT	6	48.1	VGFRFEDGKK	1182.6	R	V	3.8	0.0	47.3	12.3
P60624	11298.3	S	U	T	B	ETD+CID	LIT	2	21.2	IRRDDEVIVLTGK	1513.9	K	D	0.0	0.0	52.1	15.8
P60624	11298.3	S	U	T	B	ETD+CID	LIT	2	21.2	VGFRFEDGK	1054.5	R	K	0.0	0.0	43.2	15.7
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	DDEVIVLTGK	1088.6	R	D	0.0	0.0	46.0	17.6
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	EAAIQVSNVAIFNAATGK	1804.0	K	A	0.0	0.0	86.0	16.7
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	HQKPVPALNQPGGIVEK	1812.0	K	E	0.0	0.0	29.9	14.8
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	0.0	0.0	15.9	11.8
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	IRRDDEVIVLTGK	1513.9	K	D	0.0	0.0	52.1	15.8
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	RDDEVIVLTGKDK	1487.8	R	G	0.0	0.0	19.8	17.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	VGFRFEDGK	1054.5	R	K	0.0	0.0	43.2	15.7
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	VIVEGINLVK	1083.7	K	K	0.0	0.0	28.2	10.4
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	67.3	VIVEGINLVKK	1211.8	K	H	0.0	0.0	32.1	7.8
P60624	11298.3	S	U	T	A	ETD+CID	LIT	7	56.7	DDEVIVLTGK	1088.6	R	D	3.1	0.6	37.2	17.6
P60624	11298.3	S	U	T	A	ETD+CID	LIT	7	56.7	EAAIQVSNVAIFNAATGK	1804.0	K	A	5.9	0.7	91.6	16.9
P60624	11298.3	S	U	T	A	ETD+CID	LIT	7	56.7	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	4.8	0.0	25.3	11.8
P60624	11298.3	S	U	T	A	ETD+CID	LIT	7	56.7	IRRDDEVIVLTGK	1513.9	K	D	5.2	0.4	69.7	15.8
P60624	11298.3	S	U	T	A	ETD+CID	LIT	7	56.7	KHQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3725.1	K	A	0.0	0.0	27.8	12.3
P60624	11298.3	S	U	T	A	ETD+CID	LIT	7	56.7	VIVEGINLVK	1084.7	K	K	3.1	0.7	12.8	10.4
P60624	11298.3	S	U	T	A	ETD+CID	LIT	7	56.7	VIVEGINLVKK	1211.8	K	H	4.2	0.9	42.7	8.5
P60624	11298.3	S	U	T	B	ETD+CID	LIT	3	36.5	EAAIQVSNVAIFNAATGK	1804.0	K	A	5.5	0.7	0.0	0.0
P60624	11298.3	S	U	T	B	ETD+CID	LIT	3	36.5	EAAIQVSNVAIFNAATGKADR	2146.1	K	V	2.2	0.5	0.0	0.0
P60624	11298.3	S	U	T	B	ETD+CID	LIT	3	36.5	HQKPVPALNQPGGIVEK	1812.0	K	E	4.2	0.5	0.0	0.0
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	DDEVIVLTGK	1088.6	R	D	3.8	0.6	46.0	17.6
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	EAAIQVSNVAIFNAATGK	1804.0	K	A	5.9	0.7	86.0	16.7
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	EAAIQVSNVAIFNAATGKADR	2146.1	K	V	2.2	0.5	2.4	17.9
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	HQKPVPALNQPGGIVEK	1812.0	K	E	4.2	0.5	0.0	0.0
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	IRRDDEVIVLTGK	1513.9	K	D	0.4	-0.5	52.1	15.8
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	RDDEVIVLTGKDK	1487.8	R	G	3.5	0.4	19.8	17.5
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	VGFRFEDGK	1054.5	R	K	3.9	0.8	43.2	15.7
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	VIVEGINLVK	1083.7	K	K	2.6	0.8	0.0	0.0
P60624	11298.3	S	U	T	B	ETD+CID	LIT	9	70.2	VIVEGINLVKK	1211.8	K	H	3.7	0.0	34.4	8.5
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	DDEVIVLTGK	1088.6	R	D	4.0	0.7	50.3	17.6
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	EAAIQVSNVAIFNAATGK	1804.0	K	A	5.7	0.7	91.4	16.9
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	EAAIQVSNVAIFNAATGKADR	2146.1	K	V	2.4	0.5	7.0	17.9
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	HQKPVPALNQPGGIVEK	1812.0	K	E	7.0	0.7	0.0	0.0
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	5.4	0.0	21.2	11.8
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	IRRDDEVIVLTGK	1513.9	K	D	5.3	0.4	88.5	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	KHQKPVPALNQPGGIVEK	1940.1	K	E	3.3	0.8	33.5	12.3
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	RDDEVIVLTGK	1244.7	R	D	3.7	0.5	61.8	17.2
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	RDDEVIVLTGKDK	1487.8	R	G	3.9	0.6	0.0	0.0
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	VGFRFEDGK	1054.5	R	K	2.3	0.6	24.3	15.6
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	VIVEGINLVK	1084.7	K	K	2.4	0.5	4.6	10.4
P60624	11298.3	S	U	T	C	ETD+CID	LIT	12	70.2	VIVEGINLVKK	1211.8	K	H	2.9	0.0	34.4	8.5
P60624	11298.3	S	U	T	B	HCD	FT	7	56.7	DDEVIVLTGK	1088.6	R	D	0.0	0.0	46.0	17.6
P60624	11298.3	S	U	T	B	HCD	FT	7	56.7	EAAIQVSNVAIFNAATGK	1804.0	K	A	0.0	0.0	86.0	16.7
P60624	11298.3	S	U	T	B	HCD	FT	7	56.7	HQKPVPALNQPGGIVEK	1812.0	K	E	0.0	0.0	29.9	14.8
P60624	11298.3	S	U	T	B	HCD	FT	7	56.7	HQKPVPALNQPGGIVEKEAAIQVSNVAIFNAATGK	3597.0	K	A	0.0	0.0	15.9	11.8
P60624	11298.3	S	U	T	B	HCD	FT	7	56.7	RDDEVIVLTGKDK	1487.8	R	G	0.0	0.0	19.8	17.5
P60624	11298.3	S	U	T	B	HCD	FT	7	56.7	VIVEGINLVK	1083.7	K	K	0.0	0.0	28.2	10.4
P60624	11298.3	S	U	T	B	HCD	FT	7	56.7	VIVEGINLVKK	1211.8	K	H	0.0	0.0	32.1	7.8
P60624	11298.3	S	U	T	A	HCD	FT	2	26.0	EAAIQVSNVAIFNAATGK	1804.0	K	A	3.5	0.0	68.7	16.5
P60624	11298.3	S	U	T	A	HCD	FT	2	26.0	VGFRFEDGK	1054.5	R	K	2.5	0.0	23.6	14.1
P60624	11298.3	S	U	T	B	HCD	FT	2	27.9	EAAIQVSNVAIFNAATGK	1804.0	K	A	4.9	0.0	83.4	16.9
P60624	11298.3	S	U	T	B	HCD	FT	2	27.9	VIVEGINLVKK	1211.8	K	H	2.9	0.0	57.0	8.5
P60624	11298.3	S	U	T	C	HCD	FT	2	26.9	KHQKPVPALNQPGGIVEK	1940.1	K	E	8.1	0.8	56.0	12.0
P60624	11298.3	S	U	T	C	HCD	FT	2	26.9	VIVEGINLVKK	1211.8	K	H	2.8	0.0	59.4	8.5
P0A6X7	11336.5	G	U	T	A	CID	LIT	3	20.2	RVVTFRPGQK	1187.7	R	L	3.0	0.0	25.5	9.0
P0A6X7	11336.5	G	U	T	A	CID	LIT	3	20.2	TGEDIPITAR	1072.6	K	R	3.1	0.4	59.3	10.4
P0A6X7	11336.5	G	U	T	A	CID	LIT	3	20.2	VVTFRPGQK	1031.6	R	L	1.9	0.5	14.1	10.8
P0A6X7	11336.5	G	T	T	A	CID	LIT	4	29.3	ALENGEQVK	987.5	R	L	2.5	0.0	21.0	12.6
P0A6X7	11336.5	G	T	T	A	CID	LIT	4	29.3	RVVTFRPGQK	1187.7	R	L	2.9	0.0	21.7	9.0
P0A6X7	11336.5	G	T	T	A	CID	LIT	4	29.3	TGEDIPITAR	1072.6	K	R	2.9	0.4	41.2	10.8
P0A6X7	11336.5	G	T	T	A	CID	LIT	4	29.3	VVTFRPGQK	1031.6	R	L	2.4	0.7	22.4	10.8
P0A6X7	11336.5	G	T	A	A	CID	LIT	2	20.2	ALTKAEMSEYLF	1402.7	M	D	0.0	0.0	32.0	14.1
P0A6X7	11336.5	G	T	A	A	CID	LIT	2	20.2	DKLGLSKR	916.6	F	D	2.4	0.0	21.6	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6X7	11336.5	S	U	T	C	CID	LIT	3	31.3	LSGFGNFDLR	1125.6	K	D	2.8	0.3	58.0	15.3
P0A6X7	11336.5	S	U	T	C	CID	LIT	3	31.3	SRVENASPKDE	1231.6	K	-	2.2	0.6	24.1	14.3
P0A6X7	11336.5	S	U	T	C	CID	LIT	3	31.3	TGEDIPITAR	1072.6	K	R	2.8	0.5	41.9	14.6
P0A6X7	11336.5	S	U	T	A	ETD	LIT	2	25.3	AEMSEYLFDKLGLSK	1730.9	K	R	2.4	0.2	14.9	17.9
P0A6X7	11336.5	S	U	T	A	ETD	LIT	2	25.3	LSGFGNFDLR	1125.6	K	D	2.4	0.7	28.1	13.8
P0A6X7	11336.5	S	U	T	B	ETD	LIT	3	36.4	AEMSEYLFDKLGLSKR	1887.0	K	D	3.2	0.0	21.5	17.6
P0A6X7	11336.5	S	U	T	B	ETD	LIT	3	36.4	LSGFGNFDLR	1125.6	K	D	2.0	0.3	26.4	14.6
P0A6X7	11336.5	S	U	T	B	ETD	LIT	3	36.4	TGEDIPITAR	1072.6	K	R	1.2	0.6	31.6	14.6
P0A6X7	11336.5	S	U	T	C	ETD	LIT	3	36.4	AEMSEYLFDKLGLSKR	1887.0	K	D	5.8	0.7	48.9	17.6
P0A6X7	11336.5	S	U	T	C	ETD	LIT	3	36.4	LSGFGNFDLR	1125.6	K	D	3.0	0.3	36.6	15.3
P0A6X7	11336.5	S	U	T	C	ETD	LIT	3	36.4	TGEDIPITAR	1072.6	K	R	1.1	0.3	32.2	14.3
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	2	35.4	AEMSEYLFDKLGLSK	1730.9	K	R	0.0	0.0	39.6	18.0
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	2	35.4	LSGFGNFDLR	1125.6	K	D	0.0	0.0	51.4	15.3
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	2	35.4	RVVTFRPGQK	1187.7	R	L	0.0	0.0	39.7	12.3
P0A6X7	11336.5	S	U	T	A	ETD+CID	LIT	2	21.2	LSGFGNFDLR	1125.6	K	D	2.8	0.4	35.1	13.8
P0A6X7	11336.5	S	U	T	A	ETD+CID	LIT	2	21.2	SRVENASPKDE	1231.6	K	-	1.9	0.4	5.5	14.9
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	3	46.5	AEMSEYLFDKLGLSK	1730.9	K	R	0.0	0.0	39.6	18.0
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	3	46.5	LSGFGNFDLR	1125.6	K	D	3.2	0.4	51.4	15.3
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	3	46.5	RVVTFRPGQK	1187.7	R	L	1.8	0.0	39.7	12.3
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	3	46.5	SRVENASPKDE	1231.6	K	-	1.7	0.7	11.1	14.8
P0A6X7	11336.5	S	U	T	B	ETD+CID	LIT	3	46.5	SSDNQFR	853.4	-	-	1.8	0.3	26.5	12.0
P0A6X7	11336.5	S	U	T	C	ETD+CID	LIT	4	56.6	AEMSEYLFDKLGLSK	1730.9	K	R	0.0	0.0	34.6	17.7
P0A6X7	11336.5	S	U	T	C	ETD+CID	LIT	4	56.6	LSGFGNFDLR	1125.6	K	D	3.4	0.5	41.0	15.3
P0A6X7	11336.5	S	U	T	C	ETD+CID	LIT	4	56.6	RVVTFRPGQK	1187.7	R	L	2.1	0.3	20.2	12.3
P0A6X7	11336.5	S	U	T	C	ETD+CID	LIT	4	56.6	SRVENASPKDE	1231.6	K	-	1.5	0.6	12.1	14.8
P0A6X7	11336.5	S	U	T	C	ETD+CID	LIT	4	56.6	TGEDIPITAR	1072.6	K	R	2.4	0.6	50.9	14.6
P0A6X7	11336.5	S	U	T	B	HCD	FT	2	25.3	AEMSEYLFDKLGLSK	1730.9	K	R	0.0	0.0	39.6	18.0
P0A6X7	11336.5	S	U	T	B	HCD	FT	2	25.3	LSGFGNFDLR	1125.6	K	D	0.0	0.0	51.4	15.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P08245	11378.6	G	T	T	A	CID	LIT	3	35.2	GVCLITGVDLDDAELTK	1818.9	K	L	4.2	0.7	52.0	12.8
P08245	11378.6	G	T	T	A	CID	LIT	3	35.2	LAAELKK	772.5	K	K	2.5	0.2	22.2	13.8
P08245	11378.6	G	T	T	A	CID	LIT	3	35.2	LVYSTETGRIDEPK	1607.8	R	A	2.7	0.3	13.4	13.0
P0AF61	11450.8	G	U	T	A	CID	LIT	2	42.9	NKFNTYVVSFDYPSSYSSVFLR	2620.3	K	L	4.0	0.8	25.7	12.3
P0AF61	11450.8	G	U	T	A	CID	LIT	2	42.9	SLMYDMNFSSIVADEYGIPR	2308.1	R	Q	3.3	0.0	96.4	10.4
P23857	11457.2	G	U	T	A	CID	LIT	2	33.7	IATAVPDKNDTVK	1371.7	R	V	3.8	0.7	38.6	12.0
P23857	11457.2	G	U	T	A	CID	LIT	2	33.7	VPEQYQQEHVQGAINIPLKEVK	2547.4	R	E	4.9	0.6	24.4	10.4
P23857	11457.2	G	T	T	A	CID	LIT	6	56.7	EILSEMGYTHVENAGGLK	1947.9	K	D	5.2	0.9	83.8	10.8
P23857	11457.2	G	T	T	A	CID	LIT	6	56.7	EILSEMGYTHVENAGGLKDIAMPK	2603.3	K	V	5.6	0.8	62.8	13.4
P23857	11457.2	G	T	T	A	CID	LIT	6	56.7	IATAVPDK	814.5	R	N	1.9	0.5	9.2	13.4
P23857	11457.2	G	T	T	A	CID	LIT	6	56.7	IATAVPDKNDTVK	1371.7	R	V	3.9	0.6	51.0	11.8
P23857	11457.2	G	T	T	A	CID	LIT	6	56.7	VPEQYQQEHVQGAINIPLK	2191.2	R	E	6.0	0.7	58.3	12.6
P23857	11457.2	G	T	T	A	CID	LIT	6	56.7	VPEQYQQEHVQGAINIPLKEVK	2547.4	R	E	3.7	0.9	0.0	0.0
P23857	11457.2	G	T	A	A	CID	LIT	5	57.7	DIAMPKVKG	974.5	K	-	2.2	0.8	23.8	13.6
P23857	11457.2	G	T	A	A	CID	LIT	5	57.7	DVRVPEQYQQ	1261.6	I	E	2.7	0.7	13.7	15.1
P23857	11457.2	G	T	A	A	CID	LIT	5	57.7	DVRVPEQYQQEHVQGAINIPLK	2561.3	I	E	4.2	0.0	42.2	15.1
P23857	11457.2	G	T	A	A	CID	LIT	5	57.7	EILSEMGYTHVENAGGLK	1947.9	K	D	2.3	0.8	17.5	15.3
P23857	11457.2	G	T	A	A	CID	LIT	5	57.7	ERIATAVPDKN	1213.7	K	D	1.9	0.2	7.9	15.2
P23857	11457.2	G	T	T	B	CID	LIT	4	56.7	EILSEMGYTHVENAGGLK	1947.9	K	D	4.2	0.6	83.5	9.0
P23857	11457.2	G	T	T	B	CID	LIT	4	56.7	EILSEMGYTHVENAGGLKDIAMPK	2603.3	K	V	3.3	0.0	38.9	13.0
P23857	11457.2	G	T	T	B	CID	LIT	4	56.7	IATAVPDKNDTVK	1371.7	R	V	3.2	0.4	39.4	12.0
P23857	11457.2	G	T	T	B	CID	LIT	4	56.7	VPEQYQQEHVQGAINIPLKEVK	2547.4	R	E	5.3	0.5	32.2	10.4
P23857	11457.2	G	T	A	B	CID	LIT	3	47.1	DIAMPKVKG	974.5	K	-	2.1	0.7	19.1	15.1
P23857	11457.2	G	T	A	B	CID	LIT	3	47.1	DVRVPEQYQQEHVQGAINIPLK	2561.3	I	E	5.0	0.7	42.8	14.0
P23857	11457.2	G	T	A	B	CID	LIT	3	47.1	EILSEMGYTHVENAGGLK	1947.9	K	D	2.1	0.8	34.6	14.8
P0ADU2	11514.1	G	U	T	A	CID	LIT	5	40.4	AYSEAVKGDVLEMNIR	1794.9	K	I	5.0	0.8	59.1	13.6
P0ADU2	11514.1	G	U	T	A	CID	LIT	5	40.4	GDVLEMNIR	1046.5	K	I	2.8	0.8	44.6	14.9
P0ADU2	11514.1	G	U	T	A	CID	LIT	5	40.4	MLTVIAEIR	1045.6	-	T	3.5	0.0	53.7	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADU2	11514.1	G	U	T	A	CID	LIT	5	40.4	QAVLDQFAK	1019.6	R	I	2.7	0.6	37.4	15.7
P0ADU2	11514.1	G	U	T	A	CID	LIT	5	40.4	TRPGQHHR	988.5	R	Q	2.5	0.5	24.0	12.8
P0ADU2	11514.1	G	T	T	A	CID	LIT	5	40.4	AYSEAVKGDVLEMNIR	1794.9	K	I	5.3	0.7	61.2	13.8
P0ADU2	11514.1	G	T	T	A	CID	LIT	5	40.4	GDVLEMNIR	1062.5	K	I	2.8	0.6	48.0	13.2
P0ADU2	11514.1	G	T	T	A	CID	LIT	5	40.4	MLTVIAEIR	1045.6	-	T	3.1	0.8	68.0	11.5
P0ADU2	11514.1	G	T	T	A	CID	LIT	5	40.4	QAVLDQFAK	1019.6	R	I	2.4	0.7	26.5	15.7
P0ADU2	11514.1	G	T	T	A	CID	LIT	5	40.4	TRPGQHHR	988.5	R	Q	2.9	0.7	14.7	14.0
P0ADU2	11514.1	G	U	A	A	CID	LIT	2	35.6	DQFAKIVPTVLKEEGCHGYAPMV	2589.3	L	D	4.1	0.5	11.6	15.1
P0ADU2	11514.1	G	U	A	A	CID	LIT	2	35.6	DVLEMNIRILQPGI	1626.9	G	-	2.1	0.5	16.9	13.2
P0ADU2	11514.1	G	T	A	A	CID	LIT	2	36.5	DQFAKIVPTVLKEEGCHGYAPMV	2589.3	L	D	3.9	0.0	30.6	15.1
P0ADU2	11514.1	G	T	A	A	CID	LIT	2	36.5	EIRTRPGQHHRQAVL	1798.0	A	D	2.2	0.6	1.4	14.5
P0ADU2	11514.1	G	T	T	B	CID	LIT	5	40.4	AYSEAVKGDVLEMNIR	1794.9	K	I	4.7	0.6	69.7	13.2
P0ADU2	11514.1	G	T	T	B	CID	LIT	5	40.4	GDVLEMNIR	1046.5	K	I	2.8	0.5	41.2	15.1
P0ADU2	11514.1	G	T	T	B	CID	LIT	5	40.4	MLTVIAEIR	1045.6	-	T	3.0	0.0	58.9	11.5
P0ADU2	11514.1	G	T	T	B	CID	LIT	5	40.4	QAVLDQFAK	1019.6	R	I	2.5	0.5	30.4	15.7
P0ADU2	11514.1	G	T	T	B	CID	LIT	5	40.4	TRPGQHHR	988.5	R	Q	3.7	0.7	27.1	14.0
P0ADU2	11514.1	G	U	T	B	CID	LIT	5	40.4	AYSEAVKGDVLEMNIR	1794.9	K	I	3.8	0.7	57.7	13.8
P0ADU2	11514.1	G	U	T	B	CID	LIT	5	40.4	GDVLEMNIR	1046.5	K	I	2.5	0.4	20.4	14.6
P0ADU2	11514.1	G	U	T	B	CID	LIT	5	40.4	MLTVIAEIR	1045.6	-	T	3.0	0.8	45.5	11.5
P0ADU2	11514.1	G	U	T	B	CID	LIT	5	40.4	QAVLDQFAK	1019.6	R	I	2.6	0.8	31.5	15.7
P0ADU2	11514.1	G	U	T	B	CID	LIT	5	40.4	TRPGQHHR	988.5	R	Q	2.7	0.4	15.0	14.0
P0ADU2	11514.1	G	T	A	B	CID	LIT	7	79.8	DCAAGVSFQSMAP	1340.6	V	D	2.0	0.6	22.9	9.0
P0ADU2	11514.1	G	T	A	B	CID	LIT	7	79.8	DQFAKIVPTVLK	1358.8	L	E	3.5	0.6	31.6	10.0
P0ADU2	11514.1	G	T	A	B	CID	LIT	7	79.8	DQFAKIVPTVLKEEGCHGYAPMV	2605.3	L	D	3.3	0.7	26.1	14.3
P0ADU2	11514.1	G	T	A	B	CID	LIT	7	79.8	DVLEMNIRILQPGI	1610.9	G	-	3.4	0.6	24.5	12.3
P0ADU2	11514.1	G	T	A	B	CID	LIT	7	79.8	EAHLQTPHMKAYSEAVKG	1997.0	L	D	2.5	0.8	0.0	0.0
P0ADU2	11514.1	G	T	A	B	CID	LIT	7	79.8	EIRTRPGQHHRQAVL	1798.0	A	D	1.8	0.7	0.0	0.0
P0ADU2	11514.1	G	T	A	B	CID	LIT	7	79.8	EMNIRILQPGI	1283.7	L	-	2.2	0.7	24.4	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	DCAAGVSFQSMAP	1340.6	V	D	2.0	0.6	17.2	9.0
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	DQFAKIVPTVLK	1358.8	L	E	3.9	0.6	39.7	10.0
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	DQFAKIVPTVLKEEGCHGYAPMV	2605.3	L	D	2.3	0.3	9.3	13.4
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	DVLEMNIRILQPGI	1610.9	G	-	1.9	0.6	0.0	0.0
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	EAHLQTPHMKAYSEAVKG	1997.0	L	D	3.8	0.9	19.4	14.9
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	EEGCHGYAPMV	1249.5	K	D	2.3	0.0	14.9	3.0
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	EIRTRPGQHHRQAVL	1798.0	A	D	1.8	0.6	4.5	14.8
P0ADU2	11514.1	G	U	A	B	CID	LIT	8	79.8	EMNIRILQPGI	1283.7	L	-	2.2	0.6	14.9	11.5
P0ADU2	11514.1	S	U	T	A	CID	LIT	3	24.0	AYSEAVKGDVLEMNIR	1794.9	K	I	5.1	0.7	65.8	17.9
P0ADU2	11514.1	S	U	T	A	CID	LIT	3	24.0	GDVLEMNIR	1046.5	K	I	2.5	0.4	33.8	16.4
P0ADU2	11514.1	S	U	T	A	CID	LIT	3	24.0	MLTVIAEIR	1045.6	-	T	3.2	0.5	53.2	13.6
P0ADU2	11514.1	S	U	T	B	CID	LIT	4	31.7	AYSEAVKGDVLEMNIR	1794.9	K	I	4.3	0.8	73.4	18.1
P0ADU2	11514.1	S	U	T	B	CID	LIT	4	31.7	GDVLEMNIR	1046.5	K	I	3.1	0.4	44.6	16.4
P0ADU2	11514.1	S	U	T	B	CID	LIT	4	31.7	QAVLDQFAK	1019.6	R	I	2.2	0.6	29.7	18.0
P0ADU2	11514.1	S	U	T	B	CID	LIT	4	31.7	TRPGQHHR	988.5	R	Q	2.4	0.4	8.0	17.4
P0ADU2	11514.1	S	U	T	C	CID	LIT	2	24.0	AYSEAVKGDVLEMNIR	1794.9	K	I	5.0	0.7	55.1	18.5
P0ADU2	11514.1	S	U	T	C	CID	LIT	2	24.0	QAVLDQFAK	1019.6	R	I	2.1	0.5	23.6	17.9
P0ADU2	11514.1	S	U	T	A	ETD	LIT	2	23.1	AYSEAVKGDVLEMNIR	1794.9	K	I	3.7	0.5	78.4	17.9
P0ADU2	11514.1	S	U	T	A	ETD	LIT	2	23.1	TRPGQHHR	988.5	R	Q	3.4	0.2	24.9	17.4
P0ADU2	11514.1	S	U	T	B	ETD	LIT	4	40.4	AYSEAVKGDVLEMNIR	1794.9	K	I	3.3	0.6	74.0	17.9
P0ADU2	11514.1	S	U	T	B	ETD	LIT	4	40.4	MLTVIAEIR	1045.6	-	T	1.7	0.7	33.5	13.6
P0ADU2	11514.1	S	U	T	B	ETD	LIT	4	40.4	QAVLDQFAK	1019.6	R	I	2.2	0.5	29.7	17.9
P0ADU2	11514.1	S	U	T	B	ETD	LIT	4	40.4	TRPGQHHR	988.5	R	Q	3.2	0.2	23.5	17.4
P0ADU2	11514.1	S	U	T	C	ETD	LIT	2	23.1	AYSEAVKGDVLEMNIR	1794.9	K	I	3.0	0.5	95.7	18.5
P0ADU2	11514.1	S	U	T	C	ETD	LIT	2	23.1	TRPGQHHR	988.5	R	Q	2.6	0.2	10.2	16.6
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	AYSEAVKGDVLEMNIR	1794.9	K	I	0.0	0.0	66.8	18.0
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	GDVLEMNIR	1046.5	K	I	0.0	0.0	25.8	16.4
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	MLTVIAEIR	1045.6	-	T	0.0	0.0	52.8	13.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	TRPGQHHR	988.5	R	Q	0.0	0.0	17.2	17.4
P0ADU2	11514.1	S	U	T	A	ETD+CID	LIT	4	31.7	AYSEAVKGDVLEMNIR	1794.9	K	I	4.9	0.7	62.3	17.4
P0ADU2	11514.1	S	U	T	A	ETD+CID	LIT	4	31.7	GDVLEMNIR	1046.5	K	I	2.8	0.3	46.4	16.4
P0ADU2	11514.1	S	U	T	A	ETD+CID	LIT	4	31.7	MLTVIAEIR	1045.6	-	T	3.2	0.5	44.4	13.6
P0ADU2	11514.1	S	U	T	A	ETD+CID	LIT	4	31.7	TRPGQHHR	988.5	R	Q	1.8	0.2	6.6	16.6
P0ADU2	11514.1	S	U	T	A	ETD+CID	LIT	4	31.7	VEGGQHLNVNVLR	1434.8	-	-	1.8	0.0	22.0	16.2
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	AYSEAVKGDVLEMNIR	1794.9	K	I	4.3	0.8	66.8	18.0
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	GDVLEMNIR	1046.5	K	I	2.9	0.3	25.8	16.4
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	MLTVIAEIR	1045.6	-	T	3.0	0.6	52.8	13.6
P0ADU2	11514.1	S	U	T	B	ETD+CID	LIT	4	31.7	TRPGQHHR	988.5	R	Q	2.2	0.3	1.3	16.6
P0ADU2	11514.1	S	U	T	B	HCD	FT	3	24.0	AYSEAVKGDVLEMNIR	1794.9	K	I	0.0	0.0	66.8	18.0
P0ADU2	11514.1	S	U	T	B	HCD	FT	3	24.0	GDVLEMNIR	1046.5	K	I	0.0	0.0	25.8	16.4
P0ADU2	11514.1	S	U	T	B	HCD	FT	3	24.0	MLTVIAEIR	1045.6	-	T	0.0	0.0	52.8	13.6
P0AAC8	11537.9	G	U	T	A	CID	LIT	4	47.7	FTNPNVKDECGCGESFHV	2096.9	K	-	3.1	0.0	30.6	6.0
P0AAC8	11537.9	G	U	T	A	CID	LIT	4	47.7	SITLSDSAAAR	1091.6	M	V	0.0	0.0	46.5	13.2
P0AAC8	11537.9	G	U	T	A	CID	LIT	4	47.7	SLQFLDGTQLDFVK	1610.8	K	E	4.9	0.7	68.0	12.8
P0AAC8	11537.9	G	U	T	A	CID	LIT	4	47.7	VNTFLANR	934.5	R	G	2.6	0.7	53.8	13.2
P0AAC8	11537.9	G	U	A	A	CID	LIT	2	28.0	DECGCGESFHV	1296.5	K	-	2.6	0.0	40.7	0.0
P0AAC8	11537.9	G	U	A	A	CID	LIT	2	28.0	DFVKEGLNEGFKFTNPNVK	2183.1	L	D	4.3	0.3	20.4	14.3
P0AAC8	11537.9	G	T	A	B	CID	LIT	5	43.0	DECGCGESFHV	1296.5	K	-	2.3	0.0	29.4	0.0
P0AAC8	11537.9	G	T	A	B	CID	LIT	5	43.0	DFVKEGLNEGFKFTNPNVK	2183.1	L	D	4.5	0.6	48.0	14.3
P0AAC8	11537.9	G	T	A	B	CID	LIT	5	43.0	DGKSLQFL	907.5	V	D	2.1	0.5	11.1	13.0
P0AAC8	11537.9	G	T	A	B	CID	LIT	5	43.0	DKGVKVVV	843.5	E	D	1.7	0.6	22.6	11.5
P0AAC8	11537.9	G	T	A	B	CID	LIT	5	43.0	DKGVKVVVDGKSLQFL	1732.0	E	D	2.7	0.4	13.9	10.0
P0AAC8	11537.9	G	U	A	B	CID	LIT	2	28.0	DECGCGESFHV	1296.5	K	-	3.0	0.0	29.0	0.0
P0AAC8	11537.9	G	U	A	B	CID	LIT	2	28.0	DFVKEGLNEGFKFTNPNVK	2183.1	L	D	4.8	0.5	24.7	14.5
P0AAC8	11537.9	S	U	T	B	ETD	LIT	2	27.1	FTNPNVKDECGCGESFHV	2096.9	K	-	0.0	0.0	33.1	7.0
P0AAC8	11537.9	S	U	T	B	ETD	LIT	2	27.1	SITLSDSAAAR	1091.6	M	V	0.0	0.0	33.7	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAC8	11537.9	S	U	T	C	ETD+CID	LIT	2	24.3	FTNPNVKDECGCGESFHV	2096.9	K	-	3.6	0.0	23.2	7.8
P0AAC8	11537.9	S	U	T	C	ETD+CID	LIT	2	24.3	VNTFLANR	934.5	R	G	2.1	0.5	21.4	15.1
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	AEVVAHGR	838.5	K	G	2.2	0.8	22.7	11.8
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	AEVVAHGRGEK	1152.6	K	V	3.5	0.8	50.6	12.8
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	IGVPFVDGGVIK	1200.7	K	A	2.3	0.8	34.5	13.4
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	IGVPFVDGGVIKAEVVAHGR	2020.1	K	G	1.6	0.7	17.1	9.0
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	MYAVFQSGGK	1087.5	-	Q	3.1	0.5	47.9	10.8
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	MYAVFQSGGKQHR	1508.7	-	V	4.3	0.8	63.9	13.2
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	QHRVSEGQTVR	1296.7	K	L	2.6	0.6	22.6	14.0
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	QWFTDVK	923.5	R	I	1.7	0.6	11.4	12.0
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	VSEGQTVR	875.5	R	L	2.8	0.4	51.1	13.6
P0AG48	11545.9	G	U	T	A	CID	LIT	10	52.4	VSEGQTVRLEK	1245.7	R	L	3.0	0.4	34.6	12.8
P0AG48	11545.9	G	T	T	B	CID	LIT	2	10.7	AEVVAHGR	838.5	K	G	2.2	0.6	21.3	11.1
P0AG48	11545.9	G	T	T	B	CID	LIT	2	10.7	AEVVAHGRGEK	1152.6	K	V	3.7	0.7	38.4	13.0
P0AG48	11545.9	G	U	T	B	CID	LIT	5	39.8	AEVVAHGR	838.5	K	G	2.0	0.0	43.3	11.1
P0AG48	11545.9	G	U	T	B	CID	LIT	5	39.8	AEVVAHGRGEK	1152.6	K	V	3.1	0.8	47.7	12.8
P0AG48	11545.9	G	U	T	B	CID	LIT	5	39.8	IGVPFVDGGVIK	1200.7	K	A	1.9	0.7	16.4	13.4
P0AG48	11545.9	G	U	T	B	CID	LIT	5	39.8	MYAVFQSGGK	1087.5	-	Q	2.3	0.8	15.7	12.0
P0AG48	11545.9	G	U	T	B	CID	LIT	5	39.8	VSEGQTVR	875.5	R	L	2.6	0.7	46.0	15.4
P0AG48	11545.9	G	U	A	B	CID	LIT	3	43.7	DIATGETVEFA	1152.5	L	E	1.8	0.7	16.0	14.0
P0AG48	11545.9	G	U	A	B	CID	LIT	3	43.7	DVKITGISA	903.5	T	-	2.5	0.6	28.7	12.6
P0AG48	11545.9	G	U	A	B	CID	LIT	3	43.7	MYAVFQSGGKQHRVSEGQTVRLEKL	2864.5	-	D	0.0	0.0	24.1	15.1
P0AG48	11545.9	S	U	T	A	CID	LIT	4	29.1	IGVPFVDGGVIK	1200.7	K	A	2.5	0.6	31.8	13.2
P0AG48	11545.9	S	U	T	A	CID	LIT	4	29.1	QWFTDVK	923.5	R	I	1.9	0.3	15.9	14.0
P0AG48	11545.9	S	U	T	A	CID	LIT	4	29.1	VSEGQTVR	875.5	R	L	2.2	0.2	27.8	17.8
P0AG48	11545.9	S	U	T	A	CID	LIT	4	29.1	VSEGQTVRLEK	1245.7	R	L	3.5	0.5	55.3	16.7
P0AG48	11545.9	S	U	T	B	CID	LIT	3	32.0	IGVPFVDGGVIK	1200.7	K	A	1.9	0.4	19.1	13.2
P0AG48	11545.9	S	U	T	B	CID	LIT	3	32.0	MYAVFQSGGK	1087.5	-	Q	3.2	0.9	40.0	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG48	11545.9	S	U	T	B	CID	LIT	3	32.0	VSEGQTVRLEK	1245.7	R	L	3.2	0.5	45.2	16.6
P0AG48	11545.9	S	U	T	C	CID	LIT	5	38.8	IGVPFVDGGVIK	1200.7	K	A	2.0	0.5	20.8	17.3
P0AG48	11545.9	S	U	T	C	CID	LIT	5	38.8	MYAVFQSGGK	1087.5	-	Q	2.7	0.3	25.9	13.6
P0AG48	11545.9	S	U	T	C	CID	LIT	5	38.8	QWFTDVK	923.5	R	I	1.9	0.6	16.0	15.9
P0AG48	11545.9	S	U	T	C	CID	LIT	5	38.8	VSEGQTVR	875.5	R	L	2.7	0.4	50.3	17.8
P0AG48	11545.9	S	U	T	C	CID	LIT	5	38.8	VSEGQTVRLEK	1245.7	R	L	3.0	0.4	43.2	16.7
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	AEVVAHGR	838.5	K	G	2.4	0.0	39.0	13.0
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	AEVVAHGRGEK	1152.6	K	V	4.2	0.6	46.7	15.2
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	IGVPFVDGGVIK	1200.7	K	A	3.0	0.5	32.9	13.2
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	IGVPFVDGGVIKAEVVAHGR	2020.1	K	G	0.0	0.0	50.5	12.3
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	IGVPFVDGGVIKAEVVAHGRGEK	2334.3	K	V	4.9	0.0	58.4	12.3
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	MYAVFQSGGK	1087.5	-	Q	2.2	0.3	0.0	0.0
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	QWFTDVK	923.5	R	I	2.1	0.5	0.0	0.0
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	VSEGQTVR	875.5	R	L	2.0	0.2	34.2	17.9
P0AG48	11545.9	S	U	T	A	ETD	LIT	9	49.5	VSEGQTVRLEK	1245.7	R	L	5.0	0.4	51.3	16.6
P0AG48	11545.9	S	U	T	B	ETD	LIT	4	39.8	IGVPFVDGGVIK	1200.7	K	A	3.0	0.4	44.7	16.0
P0AG48	11545.9	S	U	T	B	ETD	LIT	4	39.8	IGVPFVDGGVIKAEVVAHGR	2020.1	K	G	7.8	0.0	56.2	12.3
P0AG48	11545.9	S	U	T	B	ETD	LIT	4	39.8	MYAVFQSGGK	1087.5	-	Q	2.6	0.0	29.4	13.8
P0AG48	11545.9	S	U	T	B	ETD	LIT	4	39.8	VSEGQTVRLEK	1245.7	R	L	4.4	0.2	43.3	17.1
P0AG48	11545.9	S	U	T	C	ETD	LIT	7	49.5	AEVVAHGRGEK	1152.6	K	V	3.7	0.9	48.9	15.1
P0AG48	11545.9	S	U	T	C	ETD	LIT	7	49.5	IGVPFVDGGVIK	1200.7	K	A	3.3	0.4	42.3	16.0
P0AG48	11545.9	S	U	T	C	ETD	LIT	7	49.5	IGVPFVDGGVIKAEVVAHGR	2020.1	K	G	0.0	0.0	25.4	13.0
P0AG48	11545.9	S	U	T	C	ETD	LIT	7	49.5	MYAVFQSGGK	1087.5	-	Q	0.0	0.0	31.5	13.6
P0AG48	11545.9	S	U	T	C	ETD	LIT	7	49.5	QWFTDVK	923.5	R	I	2.7	0.4	34.3	15.9
P0AG48	11545.9	S	U	T	C	ETD	LIT	7	49.5	VSEGQTVR	875.5	R	L	1.5	0.0	24.5	17.9
P0AG48	11545.9	S	U	T	C	ETD	LIT	7	49.5	VSEGQTVRLEK	1245.7	R	L	4.5	0.4	33.3	17.1
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	2	22.3	AEVVAHGRGEK	1152.6	K	V	0.0	0.0	43.6	15.2
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	2	22.3	IGVPFVDGGVIKAEVVAHGRGEK	2334.3	K	V	0.0	0.0	76.9	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	3	30.1	AEVVAHGRGEK	1152.6	K	V	0.0	0.0	43.6	15.2
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	3	30.1	IGVPFVDGGVIKAEVVAHGRGEK	2334.3	K	V	0.0	0.0	76.9	12.6
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	3	30.1	VSEGQTVR	875.5	R	L	0.0	0.0	35.1	17.9
P0AG48	11545.9	S	U	T	A	ETD+CID	LIT	5	30.1	AEVVAHGR	838.5	K	G	0.9	-0.7	29.0	13.0
P0AG48	11545.9	S	U	T	A	ETD+CID	LIT	5	30.1	AEVVAHGRGEK	1152.6	K	V	4.3	0.8	49.5	15.2
P0AG48	11545.9	S	U	T	A	ETD+CID	LIT	5	30.1	IGVPFVDGGVIKAEVVAHGR	2020.1	K	G	0.0	0.0	17.9	12.3
P0AG48	11545.9	S	U	T	A	ETD+CID	LIT	5	30.1	IGVPFVDGGVIKAEVVAHGRGEK	2334.3	K	V	1.0	-0.8	63.2	12.6
P0AG48	11545.9	S	U	T	A	ETD+CID	LIT	5	30.1	VSEGQTVR	875.5	R	L	2.8	0.3	0.0	0.0
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	2	22.3	AEVVAHGRGEK	1152.6	K	V	3.6	0.9	0.0	0.0
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	2	22.3	IGVPFVDGGVIK	1200.7	K	A	2.1	0.6	0.0	0.0
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	4	30.1	AEVVAHGRGEK	1152.6	K	V	3.6	0.9	43.6	15.2
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	4	30.1	IGVPFVDGGVIK	1200.7	K	A	2.1	0.6	14.3	13.2
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	4	30.1	IGVPFVDGGVIKAEVVAHGRGEK	2334.3	K	V	5.9	0.0	76.9	12.6
P0AG48	11545.9	S	U	T	B	ETD+CID	LIT	4	30.1	VSEGQTVR	875.5	R	L	1.3	-0.1	35.1	17.9
P0AG48	11545.9	S	U	T	C	ETD+CID	LIT	6	46.6	AEVVAHGR	838.5	K	G	1.8	0.6	21.2	13.0
P0AG48	11545.9	S	U	T	C	ETD+CID	LIT	6	46.6	AEVVAHGRGEK	1152.6	K	V	3.3	0.8	30.7	15.2
P0AG48	11545.9	S	U	T	C	ETD+CID	LIT	6	46.6	IGVPFVDGGVIK	1200.7	K	A	2.1	0.2	23.2	16.0
P0AG48	11545.9	S	U	T	C	ETD+CID	LIT	6	46.6	MYAVFQSGGK	1087.5	-	Q	0.0	0.0	38.3	12.3
P0AG48	11545.9	S	U	T	C	ETD+CID	LIT	6	46.6	QWFTDVK	923.5	R	I	1.9	0.6	14.2	15.3
P0AG48	11545.9	S	U	T	C	ETD+CID	LIT	6	46.6	VSEGQTVR	875.5	R	L	2.7	0.4	29.5	17.9
P0AG48	11545.9	S	U	T	B	HCD	FT	2	18.4	AEVVAHGRGEK	1152.6	K	V	0.0	0.0	34.3	15.2
P0AG48	11545.9	S	U	T	B	HCD	FT	2	18.4	VSEGQTVR	875.5	R	L	0.0	0.0	35.1	17.9
P0AG48	11545.9	S	U	T	A	HCD	FT	2	10.7	AEVVAHGR	838.5	K	G	2.2	0.0	54.5	13.0
P0AG48	11545.9	S	U	T	A	HCD	FT	2	10.7	AEVVAHGRGEK	1152.6	K	V	2.9	0.0	44.0	15.2
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	AIISDVNASDEDR	1404.7	K	W	3.6	0.8	55.1	11.1
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	AIISDVNASDEDRWNAVLK	2116.1	K	L	6.3	0.6	60.2	11.8
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	EAAMRGEIPGLK	1271.7	R	K	2.2	0.5	16.8	13.8
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	GEIPGLKK	841.5	R	A	1.8	0.7	12.7	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	KFGLSR	707.4	R	I	1.9	0.5	27.3	13.6
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	LQTLPR	727.4	K	D	1.5	0.6	28.5	12.6
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	QTGRPHGFLR	1168.6	R	K	2.4	0.8	18.6	11.8
P0AG59	11563.0	G	U	T	A	CID	LIT	8	63.4	VALADKYFAK	1125.6	R	R	3.2	0.8	56.9	10.4
P0AG59	11563.0	G	T	T	A	CID	LIT	7	62.4	AIISDVNASDEDR	1404.7	K	W	2.9	0.6	29.1	11.5
P0AG59	11563.0	G	T	T	A	CID	LIT	7	62.4	AIISDVNASDEDRWNAVLK	2116.1	K	L	6.6	0.6	54.8	11.8
P0AG59	11563.0	G	T	T	A	CID	LIT	7	62.4	EAAMRGEIPGLK	1271.7	R	K	2.7	0.7	21.6	13.2
P0AG59	11563.0	G	T	T	A	CID	LIT	7	62.4	KFGLSR	707.4	R	I	1.8	0.5	22.6	13.6
P0AG59	11563.0	G	T	T	A	CID	LIT	7	62.4	LQTLPR	727.4	K	D	1.5	0.6	33.5	12.6
P0AG59	11563.0	G	T	T	A	CID	LIT	7	62.4	QTGRPHGFLR	1168.6	R	K	1.7	0.7	17.7	11.1
P0AG59	11563.0	G	T	T	A	CID	LIT	7	62.4	VALADKYFAK	1125.6	R	R	3.4	0.5	48.0	10.4
P0AG59	11563.0	G	U	A	A	CID	LIT	3	30.7	AKQSMKAREVKRVALA	1802.0	M	D	0.0	0.0	32.8	7.0
P0AG59	11563.0	G	U	A	A	CID	LIT	3	30.7	DKYFAKRA	998.5	A	E	2.0	0.8	27.0	10.8
P0AG59	11563.0	G	U	A	A	CID	LIT	3	30.7	DKYFAKRAELKAIIS	1753.0	A	D	2.2	0.6	27.5	7.8
P0AG59	11563.0	G	T	A	A	CID	LIT	2	15.8	DEDRWNAVLKLQTLPR	1954.1	S	D	3.8	0.4	29.0	12.8
P0AG59	11563.0	G	T	A	A	CID	LIT	2	15.8	DRWNAVLKLQTLPR	1710.0	E	D	3.2	0.0	25.5	8.5
P0AG59	11563.0	G	T	T	B	CID	LIT	2	30.7	AIISDVNASDEDRWNAVLK	2116.1	K	L	6.6	0.6	62.3	12.8
P0AG59	11563.0	G	T	T	B	CID	LIT	2	30.7	EAAMRGEIPGLK	1271.7	R	K	2.3	0.5	14.4	12.3
P0AG59	11563.0	G	U	T	B	CID	LIT	3	23.8	GEIPGLKK	841.5	R	A	1.7	0.7	21.6	10.0
P0AG59	11563.0	G	U	T	B	CID	LIT	3	23.8	LQTLPR	727.4	K	D	1.6	0.0	21.3	12.6
P0AG59	11563.0	G	U	T	B	CID	LIT	3	23.8	QTGRPHGFLR	1168.6	R	K	1.4	0.7	21.6	11.1
P0AG59	11563.0	G	T	A	B	CID	LIT	4	46.5	AKQSMKAREVKRVALA	1786.0	M	D	0.0	0.0	23.2	9.0
P0AG59	11563.0	G	T	A	B	CID	LIT	4	46.5	DEDRWNAVLKLQTLPR	1954.1	S	D	3.4	0.4	32.9	12.6
P0AG59	11563.0	G	T	A	B	CID	LIT	4	46.5	DKYFAKRAELKAIIS	1753.0	A	D	3.0	0.8	4.1	9.0
P0AG59	11563.0	G	T	A	B	CID	LIT	4	46.5	DRWNAVLKLQTLPR	1710.0	E	D	3.2	0.4	45.8	8.5
P0AG59	11563.0	G	U	A	B	CID	LIT	6	62.4	AKQSMKAREVKRVALA	1786.0	M	D	0.0	0.0	20.8	9.0
P0AG59	11563.0	G	U	A	B	CID	LIT	6	62.4	DEDRWNAVLKLQTLPR	1954.1	S	D	4.0	0.7	46.4	13.2
P0AG59	11563.0	G	U	A	B	CID	LIT	6	62.4	DKYFAKRA	998.5	A	E	1.9	0.6	11.3	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG59	11563.0	G	U	A	B	CID	LIT	6	62.4	DKYFAKRAELKAIIS	1753.0	A	D	2.3	0.0	16.2	9.0
P0AG59	11563.0	G	U	A	B	CID	LIT	6	62.4	DRWNAVLKLQTLPR	1710.0	E	D	3.5	0.6	39.4	8.5
P0AG59	11563.0	G	U	A	B	CID	LIT	6	62.4	EAAMRGEIPGLKKASW	1743.9	R	-	3.2	0.5	24.0	16.4
P0AG59	11563.0	S	U	T	A	CID	LIT	2	28.7	AIISDVNASDEDRWNAVLK	2116.1	K	L	6.3	0.5	62.0	17.3
P0AG59	11563.0	S	U	T	A	CID	LIT	2	28.7	QTGRPHGFLR	1168.6	R	K	1.8	0.6	0.0	0.0
P0AG59	11563.0	S	U	T	B	CID	LIT	4	39.6	AIISDVNASDEDRWNAVLK	2116.1	K	L	6.7	0.5	61.6	17.7
P0AG59	11563.0	S	U	T	B	CID	LIT	4	39.6	QTGRPHGFLR	1168.6	R	K	1.9	0.3	25.2	12.8
P0AG59	11563.0	S	U	T	B	CID	LIT	4	39.6	RVALADK	772.5	K	Y	2.3	0.3	14.9	19.6
P0AG59	11563.0	S	U	T	B	CID	LIT	4	39.6	VALADKYFAK	1125.6	R	R	2.2	0.3	4.5	11.1
P0AG59	11563.0	S	U	T	C	CID	LIT	5	45.5	AIISDVNASDEDRWNAVLK	2117.1	K	L	5.9	0.6	62.5	17.4
P0AG59	11563.0	S	U	T	C	CID	LIT	5	45.5	LQTLPR	727.4	K	D	1.5	0.6	32.2	13.4
P0AG59	11563.0	S	U	T	C	CID	LIT	5	45.5	QTGRPHGFLR	1168.6	R	K	1.8	0.6	12.6	12.8
P0AG59	11563.0	S	U	T	C	CID	LIT	5	45.5	VALADKYFAK	1125.6	R	R	3.3	0.6	47.3	12.6
P0AG59	11563.0	S	U	T	C	CID	LIT	5	45.5	VALADKYFAKR	1281.7	R	A	2.7	0.5	17.3	12.6
P0AG59	11563.0	S	U	T	A	ETD	LIT	7	54.5	AIISDVNASDEDRWNAVLK	2116.1	K	L	5.2	0.4	35.1	17.7
P0AG59	11563.0	S	U	T	A	ETD	LIT	7	54.5	GEIPGLKK	841.5	R	A	1.8	0.4	11.2	11.5
P0AG59	11563.0	S	U	T	A	ETD	LIT	7	54.5	LQTLPR	727.4	K	D	0.0	0.0	31.1	13.4
P0AG59	11563.0	S	U	T	A	ETD	LIT	7	54.5	QTGRPHGFLR	1168.6	R	K	4.0	0.6	32.2	12.8
P0AG59	11563.0	S	U	T	A	ETD	LIT	7	54.5	RVALADKYFAK	1281.7	K	R	3.1	0.5	14.8	12.6
P0AG59	11563.0	S	U	T	A	ETD	LIT	7	54.5	VALADKYFAK	1125.6	R	R	2.7	0.4	31.2	12.3
P0AG59	11563.0	S	U	T	A	ETD	LIT	7	54.5	VALADKYFAKR	1281.7	R	A	5.2	0.6	48.6	12.0
P0AG59	11563.0	S	U	T	B	ETD	LIT	5	40.6	AIISDVNASDEDRWNAVLK	2116.1	K	L	6.3	0.6	81.6	17.4
P0AG59	11563.0	S	U	T	B	ETD	LIT	5	40.6	QTGRPHGFLR	1168.6	R	K	3.8	0.6	37.9	12.8
P0AG59	11563.0	S	U	T	B	ETD	LIT	5	40.6	RVALADK	772.5	K	Y	1.9	0.1	40.6	19.6
P0AG59	11563.0	S	U	T	B	ETD	LIT	5	40.6	VALADKYFAK	1125.6	R	R	4.6	0.6	54.2	12.6
P0AG59	11563.0	S	U	T	B	ETD	LIT	5	40.6	VALADKYFAKR	1281.7	R	A	4.5	0.5	41.9	12.8
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	AIISDVNASDEDRWNAVLK	2116.1	K	L	4.1	0.4	40.3	17.4
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	EAAMRGEIPGLK	1271.7	R	K	3.0	0.6	23.9	17.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	LQTLPR	727.4	K	D	1.6	0.6	30.1	13.4
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	QTGRPHGFLR	1168.6	R	K	4.0	0.0	45.1	12.8
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	RVALADK	772.5	K	Y	1.7	0.3	34.3	19.6
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	RVALADKYFAK	1281.7	K	R	2.9	0.6	14.3	12.6
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	VALADKYFAK	1125.6	R	R	4.7	0.6	52.3	12.6
P0AG59	11563.0	S	U	T	C	ETD	LIT	8	58.4	VALADKYFAKR	1281.7	R	A	6.0	0.6	59.0	12.6
P0AG59	11563.0	S	U	T	A	ETD	FT	2	10.9	QTGRPHGFLR	1168.6	R	K	2.7	0.0	39.8	12.8
P0AG59	11563.0	S	U	T	A	ETD	FT	2	10.9	QTGRPHGFLRK	1296.7	R	F	3.2	0.0	30.8	12.3
P0AG59	11563.0	S	U	T	C	ETD	FT	2	11.9	RVALADKYFAK	1281.7	K	R	2.0	0.4	19.7	12.0
P0AG59	11563.0	S	U	T	C	ETD	FT	2	11.9	VALADKYFAKR	1281.7	R	A	4.9	0.4	50.0	12.6
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	AIISDVNASDEDR	1404.7	K	W	0.0	0.0	49.4	14.3
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	AIISDVNASDEDRWNAVLK	2117.1	K	L	0.0	0.0	70.0	17.1
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	LQTLPR	727.4	K	D	0.0	0.0	26.9	13.4
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	QTGRPHGFLR	1168.6	R	K	0.0	0.0	47.6	12.8
P0AG59	11563.0	S	U	T	A	ETD+CID	LIT	4	35.6	AIISDVNASDEDRWNAVLK	2117.1	K	L	6.1	0.6	52.4	17.1
P0AG59	11563.0	S	U	T	A	ETD+CID	LIT	4	35.6	LQTLPR	727.4	K	D	1.2	0.5	13.7	13.4
P0AG59	11563.0	S	U	T	A	ETD+CID	LIT	4	35.6	QTGRPHGFLR	1168.6	R	K	3.7	0.6	45.2	12.8
P0AG59	11563.0	S	U	T	A	ETD+CID	LIT	4	35.6	QTGRPHGFLRK	1296.7	R	F	2.1	0.5	0.2	12.0
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	2	18.8	AIISDVNASDEDR	1404.7	K	W	3.8	0.6	0.0	0.0
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	2	18.8	AIISDVNASDEDRWNAVLK	2116.1	K	L	2.6	0.3	0.0	0.0
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	AIISDVNASDEDR	1404.7	K	W	3.8	0.6	0.0	0.0
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	AIISDVNASDEDRWNAVLK	2117.1	K	L	5.8	0.7	70.0	17.1
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	LQTLPR	727.4	K	D	0.0	0.0	26.9	13.4
P0AG59	11563.0	S	U	T	B	ETD+CID	LIT	4	34.7	QTGRPHGFLR	1168.6	R	K	2.8	0.3	9.5	12.8
P0AG59	11563.0	S	U	T	C	ETD+CID	LIT	4	39.6	AIISDVNASDEDRWNAVLK	2116.1	K	L	6.5	0.5	67.2	17.4
P0AG59	11563.0	S	U	T	C	ETD+CID	LIT	4	39.6	QTGRPHGFLR	1168.6	R	K	3.9	0.6	0.0	0.0
P0AG59	11563.0	S	U	T	C	ETD+CID	LIT	4	39.6	VALADKYFAK	1125.6	R	R	3.4	0.7	37.3	12.3
P0AG59	11563.0	S	U	T	C	ETD+CID	LIT	4	39.6	VALADKYFAKR	1281.7	R	A	1.8	0.7	11.6	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG59	11563.0	S	U	T	B	HCD	FT	3	24.8	AIISDVNASDEDR	1404.7	K	W	0.0	0.0	49.4	14.3
P0AG59	11563.0	S	U	T	B	HCD	FT	3	24.8	AIISDVNASDEDRWNAVLK	2117.1	K	L	0.0	0.0	70.0	17.1
P0AG59	11563.0	S	U	T	B	HCD	FT	3	24.8	LQTLPR	727.4	K	D	0.0	0.0	26.9	13.4
P0AAT6	11564.2	G	U	T	A	CID	LIT	3	31.4	GQDIIALDVQGK	1256.7	K	S	4.1	0.5	48.1	12.8
P0AAT6	11564.2	G	U	T	A	CID	LIT	3	31.4	HVMSIADHVVQESR	1623.8	R	A	4.5	0.9	72.8	10.8
P0AAT6	11564.2	G	U	T	A	CID	LIT	3	31.4	RLYELEK	950.5	R	L	2.6	0.3	25.7	12.3
P0AAT6	11564.2	G	U	A	A	CID	LIT	2	17.1	DKIDDLKGQ	1031.5	I	D	3.5	0.5	44.2	16.1
P0AAT6	11564.2	G	U	A	A	CID	LIT	2	17.1	DVQGKSSIT	934.5	L	D	1.9	0.7	6.6	15.2
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	DARDQYEIR	1165.6	K	T	3.4	0.5	20.5	10.0
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	DQYEIR	823.4	R	T	1.8	0.4	17.8	13.0
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	ERFTVLISPHVNK	1539.9	K	D	4.2	0.9	28.6	9.0
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	FTVLISPHVNK	1254.7	R	D	3.4	0.6	50.9	9.5
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	FTVLISPHVNKDAR	1596.9	R	D	4.0	0.6	45.5	10.4
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	GPIPLPTR	850.5	R	K	1.9	0.7	9.8	10.0
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	GPIPLPTRK	978.6	R	E	2.7	0.0	29.3	3.0
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	LIDQATAEIVETAK	1501.8	R	R	5.0	0.7	90.1	10.8
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	LIDQATAEIVETAKR	1657.9	R	T	3.9	0.9	80.1	13.2
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	LKAFDHR	886.5	R	L	2.4	0.5	26.8	13.8
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	LVDIVEPTEK	1142.6	R	T	3.2	0.3	34.7	12.6
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	LVDIVEPTEKTVDALMR	1929.0	R	L	5.0	0.7	71.2	11.5
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	MQNQR	676.3	-	I	1.8	0.7	17.3	10.0
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	RTGAQVR	787.5	K	G	2.8	0.4	21.5	14.8
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	TGAQVR	631.4	R	G	2.6	0.3	49.8	17.0
P0A7R5	11717.8	G	U	T	A	CID	LIT	16	78.6	TVDALMR	805.4	K	L	2.4	0.7	34.9	15.4
P0A7R5	11717.8	G	T	T	A	CID	LIT	3	24.3	LIDQATAEIVETAK	1501.8	R	R	4.6	0.6	79.0	12.0
P0A7R5	11717.8	G	T	T	A	CID	LIT	3	24.3	LIDQATAEIVETAKR	1657.9	R	T	3.6	0.9	59.4	13.8
P0A7R5	11717.8	G	T	T	A	CID	LIT	3	24.3	LVDIVEPTEK	1142.6	R	T	3.0	0.3	32.6	11.5
P0A7R5	11717.8	G	U	A	A	CID	LIT	5	36.9	DALMRL	718.4	V	D	2.0	0.7	22.6	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R5	11717.8	G	U	A	A	CID	LIT	5	36.9	DHRLI	653.4	F	D	1.4	0.5	10.3	12.8
P0A7R5	11717.8	G	U	A	A	CID	LIT	5	36.9	DHRLIDQATA	1139.6	F	E	2.5	0.6	26.7	13.6
P0A7R5	11717.8	G	U	A	A	CID	LIT	5	36.9	DIVEPTEKTV	1130.6	V	D	2.8	0.7	38.0	13.4
P0A7R5	11717.8	G	U	A	A	CID	LIT	5	36.9	DQYEIRTHLRLV	1542.8	R	D	2.2	0.0	15.8	15.4
P0A7R5	11717.8	G	T	T	B	CID	LIT	5	50.5	FTVLISPHVNKDAR	1596.9	R	D	2.6	0.0	14.0	10.4
P0A7R5	11717.8	G	T	T	B	CID	LIT	5	50.5	GPIPLPTR	850.5	R	K	2.3	0.6	9.5	9.5
P0A7R5	11717.8	G	T	T	B	CID	LIT	5	50.5	LIDQATAEIVETAK	1501.8	R	R	1.9	0.5	0.0	0.0
P0A7R5	11717.8	G	T	T	B	CID	LIT	5	50.5	LVDIVEPTEK	1142.6	R	T	2.6	0.2	18.5	11.5
P0A7R5	11717.8	G	T	T	B	CID	LIT	5	50.5	TGAQVR	631.4	R	G	2.0	0.2	8.2	17.1
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	DARDQYEIR	1165.6	K	T	2.3	0.0	24.8	13.2
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	DQYEIR	823.4	R	T	1.7	0.0	19.6	13.0
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	FTVLISPHVNK	1254.7	R	D	2.4	0.0	15.4	9.5
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	LIDQATAEIVETAK	1501.8	R	R	4.3	0.6	44.9	12.0
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	LIDQATAEIVETAKR	1657.9	R	T	4.1	0.9	61.5	13.4
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	LVDIVEPTEK	1142.6	R	T	3.0	0.3	52.8	11.5
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	RTGAQVR	787.5	K	G	2.4	0.2	13.3	14.8
P0A7R5	11717.8	G	U	T	B	CID	LIT	8	49.5	TGAQVR	631.4	R	G	2.4	0.4	45.8	17.0
P0A7R5	11717.8	G	T	A	B	CID	LIT	2	15.5	DALMRL	718.4	V	D	1.9	0.2	11.9	14.5
P0A7R5	11717.8	G	T	A	B	CID	LIT	2	15.5	DIVEPTEKTV	1130.6	V	D	2.9	0.7	41.8	13.4
P0A7R5	11717.8	G	U	A	B	CID	LIT	3	28.2	DALMRL	718.4	V	D	2.0	0.2	7.8	14.5
P0A7R5	11717.8	G	U	A	B	CID	LIT	3	28.2	DIVEPTEKTV	1130.6	V	D	3.2	0.7	50.4	13.4
P0A7R5	11717.8	G	U	A	B	CID	LIT	3	28.2	ERFTVLISPHVNK	1539.9	K	D	3.0	0.8	16.9	14.0
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	DQYEIR	823.4	R	T	1.7	0.2	17.8	15.2
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	ERFTVLISPHVNK	1539.9	K	D	3.5	0.8	15.5	12.6
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	FTVLISPHVNK	1254.7	R	D	3.8	0.5	38.3	13.2
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	FTVLISPHVNKDAR	1597.9	R	D	2.7	0.4	23.6	17.1
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	FTVLISPHVNKDARDQYEIR	2401.3	R	T	2.5	0.4	11.1	17.6
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	LDLAAGVDVQISLG	1370.8	R	-	3.7	0.7	35.0	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	LIDQATAEIVETAK	1501.8	R	R	4.9	0.6	90.0	16.4
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	LIDQATAEIVETAKR	1657.9	R	T	3.7	0.5	74.3	17.1
P0A7R5	11717.8	S	U	T	A	CID	LIT	9	56.3	LKAFDHR	886.5	R	L	2.1	0.6	20.5	15.1
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	DQYEIR	823.4	R	T	1.6	0.2	18.5	16.2
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	ERFTVLISPHVNK	1539.9	K	D	3.5	0.0	29.6	12.6
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	FTVLISPHVNK	1254.7	R	D	4.0	0.6	66.3	13.2
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	FTVLISPHVNKDAR	1596.9	R	D	4.1	0.6	55.2	14.3
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	GPIPLPTR	850.5	R	K	2.0	0.7	21.0	10.0
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	LDLAAGVDVQISLG	1370.8	R	-	3.4	0.5	17.3	15.1
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	LIDQATAEIVETAK	1501.8	R	R	5.0	0.6	83.8	17.4
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	LIDQATAEIVETAKR	1657.9	R	T	3.9	0.6	73.8	17.1
P0A7R5	11717.8	S	U	T	B	CID	LIT	9	73.8	LVDIVEPTEKTVDALMR	1929.0	R	L	2.9	0.6	19.0	15.7
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	ERFTVLISPHVNK	1539.9	K	D	3.8	0.4	17.5	12.0
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	ERFTVLISPHVNKDAR	1882.0	K	D	3.5	0.7	17.5	15.1
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	FTVLISPHVNK	1254.7	R	D	4.0	0.5	49.0	13.2
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	FTVLISPHVNKDAR	1596.9	R	D	3.9	0.5	35.5	14.0
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	GPIPLPTRK	978.6	R	E	2.4	0.0	22.5	7.8
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	LDLAAGVDVQISLG	1370.8	R	-	3.2	0.7	21.7	15.1
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	LIDQATAEIVETAK	1501.8	R	R	5.4	0.7	80.1	16.6
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	LIDQATAEIVETAKR	1657.9	R	T	2.6	0.7	61.8	17.0
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	LVDIVEPTEK	1142.6	R	T	3.1	0.3	48.1	14.3
P0A7R5	11717.8	S	U	T	C	CID	LIT	10	68.9	LVDIVEPTEKTVDALMR	1929.0	R	L	3.7	0.7	12.1	15.6
P0A7R5	11717.8	S	U	T	A	CID	FT	2	27.2	FTVLISPHVNKDAR	1596.9	R	D	3.0	0.5	0.0	0.0
P0A7R5	11717.8	S	U	T	A	CID	FT	2	27.2	LIDQATAEIVETAK	1501.8	R	R	3.9	0.0	105.0	17.4
P0A7R5	11717.8	S	U	T	B	CID	FT	2	24.3	FTVLISPHVNK	1254.7	R	D	3.1	0.0	50.0	13.2
P0A7R5	11717.8	S	U	T	B	CID	FT	2	24.3	LIDQATAEIVETAK	1501.8	R	R	3.5	0.0	49.5	17.4
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	DQYEIR	823.4	R	T	2.5	0.3	30.5	16.3
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	ERFTVLISPHVNK	1539.9	K	D	2.7	0.8	15.8	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	FTVLISPHVNK	1254.7	R	D	5.2	0.7	65.9	12.8
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	FTVLISPHVNKDAR	1596.9	R	D	6.8	0.6	82.0	13.8
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	LDLAAGVDVQISLG	1370.8	R	-	1.7	0.5	31.0	15.1
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	LIDQATAEIVETAK	1501.8	R	R	3.0	0.5	0.0	0.0
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	LIDQATAEIVETAKR	1657.9	R	T	5.6	0.5	76.0	16.8
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	LVDIVEPTEK	1142.6	R	T	0.0	0.0	27.4	14.5
P0A7R5	11717.8	S	U	T	A	ETD	LIT	9	66.0	LVDIVEPTEKTVDALMR	1929.0	R	L	3.5	0.0	16.2	16.2
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	DQYEIR	823.4	R	T	2.8	0.3	36.5	16.2
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	FTVLISPHVNK	1254.7	R	D	3.0	0.6	52.4	13.2
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	FTVLISPHVNKDAR	1596.9	R	D	6.9	0.7	79.7	14.3
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	GPIPLPTR	850.5	R	K	1.9	0.6	11.7	10.0
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	GPIPLPTRK	978.6	R	E	2.2	0.7	0.0	0.0
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	LDLAAGVDVQISLG	1370.8	R	-	2.0	0.4	10.6	15.3
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	LIDQATAEIVETAK	1501.8	R	R	3.1	0.4	38.5	17.4
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	LIDQATAEIVETAKR	1657.9	R	T	5.9	0.5	0.0	0.0
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	LKAFDHR	886.5	R	L	2.5	0.3	23.7	15.1
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	LVDIVEPTEK	1142.6	R	T	0.0	0.0	37.4	14.5
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	LVDIVEPTEKTVDALMR	1929.0	R	L	5.7	0.0	22.4	15.6
P0A7R5	11717.8	S	U	T	B	ETD	LIT	12	79.6	TVDALMR	805.4	K	L	2.9	0.4	33.2	17.9
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	ERFTVLISPHVNK	1539.9	K	D	3.4	0.5	28.3	12.6
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	FTVLISPHVNK	1254.7	R	D	3.3	0.6	0.0	0.0
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	FTVLISPHVNKDAR	1596.9	R	D	4.0	0.7	54.0	13.4
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	GPIPLPTRK	978.6	R	E	2.1	0.7	0.0	0.0
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	LDLAAGVDVQISLG	1370.8	R	-	2.4	0.4	26.7	15.1
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	LIDQATAEIVETAK	1501.8	R	R	3.0	0.6	57.1	17.4
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	LIDQATAEIVETAKR	1657.9	R	T	3.2	0.5	80.9	16.6
P0A7R5	11717.8	S	U	T	C	ETD	LIT	8	68.9	LVDIVEPTEKTVDALMR	1929.0	R	L	4.6	0.0	18.0	16.1
P0A7R5	11717.8	S	U	T	A	ETD	FT	2	19.4	DQYEIR	823.4	R	T	1.4	0.0	32.8	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R5	11717.8	S	U	T	A	ETD	FT	2	19.4	FTVLISPHVNKDAR	1596.9	R	D	5.0	0.0	57.3	14.0
P0A7R5	11717.8	S	U	T	B	ETD	FT	2	23.3	FTVLISPHVNKDAR	1596.9	R	D	3.9	0.0	59.9	13.4
P0A7R5	11717.8	S	U	T	B	ETD	FT	2	23.3	LVDIVEPTEK	1142.6	R	T	1.9	0.0	28.5	14.3
P0A7R5	11717.8	S	U	T	C	ETD	FT	2	22.3	FTVLISPHVNKDAR	1596.9	R	D	4.5	0.4	61.8	13.4
P0A7R5	11717.8	S	U	T	C	ETD	FT	2	22.3	GPIPLPTRK	978.6	R	E	1.4	0.0	25.2	7.8
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	3	28.2	FTVLISPHVNK	1254.7	R	D	0.0	0.0	50.7	14.8
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	3	28.2	FTVLISPHVNKDAR	1597.9	R	D	0.0	0.0	21.5	15.8
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	3	28.2	LIDQATAEIVETAKR	1657.9	R	T	0.0	0.0	63.9	16.8
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	FTVLISPHVNK	1254.7	R	D	0.0	0.0	50.7	14.8
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	FTVLISPHVNKDAR	1597.9	R	D	0.0	0.0	21.5	15.8
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	LDLAAGVDVQISLG	1370.8	R	-	0.0	0.0	25.8	15.1
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	LIDQATAEIVETAK	1501.8	R	R	0.0	0.0	90.7	16.2
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	LIDQATAEIVETAKR	1657.9	R	T	0.0	0.0	79.4	16.6
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	LKAFDHR	886.5	R	L	0.0	0.0	23.8	15.1
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	LVDIVEPTEK	1142.6	R	T	0.0	0.0	53.7	16.1
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	8	65.0	LVDIVEPTEKTVDALMR	1929.0	R	L	0.0	0.0	22.1	15.7
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	ERFTVLISPHVNK	1539.9	K	D	3.0	0.7	16.5	12.3
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	FTVLISPHVNKDAR	1596.9	R	D	2.6	0.8	21.6	13.4
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	FTVLISPHVNKDARDQYEIR	2401.3	R	T	2.2	0.5	0.9	17.6
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	LDLAAGVDVQISLG	1370.8	R	-	3.3	0.0	20.6	15.1
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	LIDQATAEIVETAK	1501.8	R	R	3.8	0.5	51.0	17.4
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	LIDQATAEIVETAKR	1657.9	R	T	3.3	0.4	54.2	16.6
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	LKAFDHR	886.5	R	L	1.9	0.5	25.2	15.1
P0A7R5	11717.8	S	U	T	A	ETD+CID	LIT	8	72.8	LVDIVEPTEKTVDALMR	1929.0	R	L	3.5	0.4	25.0	15.6
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	2	29.1	ERFTVLISPHVNK	1539.9	K	D	2.5	0.4	0.0	0.0
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	2	29.1	LVDIVEPTEKTVDALMR	1929.0	R	L	3.0	0.8	0.0	0.0
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	DQYEIR	823.4	R	T	1.6	0.2	16.4	16.2
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	ERFTVLISPHVNK	1539.9	K	D	2.5	0.4	8.9	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	FTVLISPHVNK	1254.7	R	D	0.8	-0.2	50.7	14.8
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	FTVLISPHVNKDAR	1597.9	R	D	5.1	0.5	0.0	0.0
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	LDLAAGVDVQISLG	1370.8	R	-	3.0	0.8	25.8	15.1
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	LIDQATAEIVETAK	1501.8	R	R	4.8	0.6	90.3	17.4
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	LIDQATAEIVETAKR	1657.9	R	T	3.9	0.5	79.4	16.6
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	LKAFDHR	886.5	R	L	1.7	0.0	23.8	15.1
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	LVDIVEPTEK	1142.6	R	T	3.4	0.3	0.0	0.0
P0A7R5	11717.8	S	U	T	B	ETD+CID	LIT	10	72.8	LVDIVEPTEKTVDALMR	1929.0	R	L	3.0	0.8	22.1	15.7
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	ERFTVLISPHVNK	1539.9	K	D	3.4	0.8	28.3	12.0
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	ERFTVLISPHVNKDAR	1882.0	K	D	2.4	0.3	11.1	15.8
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	FTVLISPHVNK	1254.7	R	D	5.0	0.6	55.0	13.2
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	FTVLISPHVNKDAR	1596.9	R	D	6.7	0.9	0.0	0.0
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	LDLAAGVDVQISLG	1370.8	R	-	3.3	0.7	36.5	15.1
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	LIDQATAEIVETAK	1501.8	R	R	4.1	0.4	47.9	16.6
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	LIDQATAEIVETAKR	1657.9	R	T	4.2	0.6	85.8	17.1
P0A7R5	11717.8	S	U	T	C	ETD+CID	LIT	8	53.4	LVDIVEPTEK	1142.6	R	T	3.2	0.3	48.0	14.5
P0A7R5	11717.8	S	U	T	B	HCD	FT	7	65.0	FTVLISPHVNKDAR	1596.9	R	D	0.0	0.0	14.9	13.4
P0A7R5	11717.8	S	U	T	B	HCD	FT	7	65.0	LDLAAGVDVQISLG	1370.8	R	-	0.0	0.0	25.8	15.1
P0A7R5	11717.8	S	U	T	B	HCD	FT	7	65.0	LIDQATAEIVETAK	1501.8	R	R	0.0	0.0	90.7	16.2
P0A7R5	11717.8	S	U	T	B	HCD	FT	7	65.0	LIDQATAEIVETAKR	1657.9	R	T	0.0	0.0	79.4	16.6
P0A7R5	11717.8	S	U	T	B	HCD	FT	7	65.0	LKAFDHR	886.5	R	L	0.0	0.0	23.8	15.1
P0A7R5	11717.8	S	U	T	B	HCD	FT	7	65.0	LVDIVEPTEK	1142.6	R	T	0.0	0.0	53.7	16.1
P0A7R5	11717.8	S	U	T	B	HCD	FT	7	65.0	LVDIVEPTEKTVDALMR	1929.0	R	L	0.0	0.0	22.1	15.7
P0A7R5	11717.8	S	U	T	A	HCD	FT	2	28.2	FTVLISPHVNKDAR	1597.9	R	D	3.2	0.0	33.6	16.7
P0A7R5	11717.8	S	U	T	A	HCD	FT	2	28.2	LIDQATAEIVETAKR	1657.9	R	T	2.5	0.0	36.3	16.4
P0A7R5	11717.8	S	U	T	C	HCD	FT	2	27.2	FTVLISPHVNKDAR	1596.9	R	D	3.7	0.0	70.9	14.9
P0A7R5	11717.8	S	U	T	C	HCD	FT	2	27.2	LIDQATAEIVETAK	1501.8	R	R	3.8	0.0	71.1	16.4
P0AB20	11761.1	G	T	A	B	CID	LIT	4	41.0	DDNGLPVHTYLA	1314.6	E	E	2.0	0.8	15.8	14.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB20	11761.1	G	T	A	B	CID	LIT	4	41.0	DEHPEQPSM	1085.4	Q	D	0.0	0.0	28.5	7.8
P0AB20	11761.1	G	T	A	B	CID	LIT	4	41.0	DIDPVYSLSEPSP	1418.7	V	D	3.3	0.0	30.0	12.0
P0AB20	11761.1	G	T	A	B	CID	LIT	4	41.0	EAQLSSELQ	1004.5	A	D	2.6	0.6	13.5	14.6
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	GIPTLLLFK	1001.6	R	N	1.8	0.0	44.8	0.0
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	GQLKEFLDANLA	1318.7	K	-	2.7	0.4	25.8	11.5
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	IIHLTDDSFDTDVLK	1731.9	K	A	4.5	0.7	58.3	14.0
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	LNIDQNPGTAPK	1267.7	K	Y	4.4	0.8	72.6	13.2
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	MIAPILDEIADEYQGK	1805.9	K	L	5.1	0.7	86.0	14.1
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	MIAPILDEIADEYQGKLTVAK	2318.2	K	L	4.2	0.0	51.5	10.4
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	NGEVAATKVGALSK	1344.7	K	G	3.5	0.0	47.6	11.1
P0AA25	11789.4	G	U	T	A	CID	LIT	8	78.9	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	66.2	11.8
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	ADGAILVDFWAEWCGPCK	2094.9	K	M	4.4	0.9	84.7	7.0
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	GIPTLLLFK	1001.6	R	N	2.0	0.0	37.5	0.0
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	GQLKEFLDANLA	1318.7	K	-	3.9	0.9	46.8	11.5
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	IIHLTDDSFDTDVLK	1731.9	K	A	4.6	0.6	55.7	14.5
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	LNIDQNPGTAPK	1267.7	K	Y	4.7	0.8	83.0	13.2
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	LTVAKLNIDQNPGTAPK	1780.0	K	Y	5.3	0.8	67.1	10.0
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	MIAPILDEIADEYQGK	1805.9	K	L	5.2	0.7	80.8	14.1
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	MIAPILDEIADEYQGKLTVAK	2318.2	K	L	3.3	0.0	29.9	9.5
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	NGEVAATK	789.4	K	V	2.8	0.0	57.8	14.1
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	NGEVAATKVGALSK	1344.7	K	G	4.1	0.8	51.1	12.3
P0AA25	11789.4	G	T	T	A	CID	LIT	11	95.4	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	70.9	10.8
P0AA25	11789.4	G	U	A	A	CID	LIT	6	30.3	DEYQGKLTVAKLNI	1591.9	A	D	3.9	0.3	35.5	15.3
P0AA25	11789.4	G	U	A	A	CID	LIT	6	30.3	DKIIHLT	839.5	S	D	1.8	0.0	26.4	3.0
P0AA25	11789.4	G	U	A	A	CID	LIT	6	30.3	DSFDTDVLKA	1110.5	D	D	2.6	0.8	13.7	14.1
P0AA25	11789.4	G	U	A	A	CID	LIT	6	30.3	DTDVLKA	761.4	F	D	2.4	0.3	36.9	16.9
P0AA25	11789.4	G	U	A	A	CID	LIT	6	30.3	SDKIIHLT	926.5	M	D	0.0	0.0	29.0	10.0
P0AA25	11789.4	G	U	A	A	CID	LIT	6	30.3	SDKIIHLTD	1041.6	M	D	0.0	0.0	42.8	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA25	11789.4	G	T	A	A	CID	LIT	5	43.1	DEYQGKLTVAKLNI	1591.9	A	D	4.4	0.5	37.3	13.8
P0AA25	11789.4	G	T	A	A	CID	LIT	5	43.1	DFWAEWCGPCKMIAPIL	2110.0	V	D	1.4	0.7	27.4	11.1
P0AA25	11789.4	G	T	A	A	CID	LIT	5	43.1	DTDVLKA	761.4	F	D	2.0	0.0	25.0	16.3
P0AA25	11789.4	G	T	A	A	CID	LIT	5	43.1	SDKIIHLT	926.5	M	D	0.0	0.0	33.2	10.0
P0AA25	11789.4	G	T	A	A	CID	LIT	5	43.1	SDKIIHLTD	1041.6	M	D	0.0	0.0	44.4	11.1
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	GIPTLLLFK	1001.6	R	N	1.7	0.0	21.8	0.0
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	GQLKEFLDANLA	1318.7	K	-	3.6	0.6	44.0	11.8
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	IIHLTDDSFDTDVLK	1731.9	K	A	2.7	0.5	0.0	0.0
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	LNIDQNPGTAPK	1267.7	K	Y	4.4	0.7	72.6	13.2
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	LNIDQNPGTAPKYGIR	1756.9	K	G	4.7	0.0	65.2	14.1
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	MIAPILDEIADEYQGK	1805.9	K	L	5.1	0.7	93.7	13.4
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	MIAPILDEIADEYQGKLTVAK	2318.2	K	L	2.5	0.0	32.2	9.5
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	NGEVAATK	789.4	K	V	3.0	0.6	47.3	14.1
P0AA25	11789.4	G	T	T	B	CID	LIT	9	77.1	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	50.2	11.1
P0AA25	11789.4	G	U	T	B	CID	LIT	6	60.6	GQLKEFLDANLA	1318.7	K	-	3.8	0.0	45.9	11.5
P0AA25	11789.4	G	U	T	B	CID	LIT	6	60.6	IIHLTDDSFDTDVLK	1731.9	K	A	3.9	0.6	22.2	13.8
P0AA25	11789.4	G	U	T	B	CID	LIT	6	60.6	LNIDQNPGTAPK	1267.7	K	Y	4.3	0.8	64.9	12.0
P0AA25	11789.4	G	U	T	B	CID	LIT	6	60.6	MIAPILDEIADEYQGK	1805.9	K	L	4.3	0.9	98.1	13.8
P0AA25	11789.4	G	U	T	B	CID	LIT	6	60.6	NGEVAATK	789.4	K	V	2.2	0.6	31.4	14.1
P0AA25	11789.4	G	U	T	B	CID	LIT	6	60.6	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	54.9	11.8
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	DEYQGKLTVAKLNI	1591.9	A	D	4.7	0.5	54.4	15.3
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	DFWAEWCGPCKMIAPIL	2110.0	V	D	2.3	0.7	10.8	11.1
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	DKIIHLT	839.5	S	D	2.2	0.0	26.1	3.0
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	DTDVLKA	761.4	F	D	2.3	0.3	39.5	16.3
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	DVLKADGAILV	1113.7	T	D	2.3	0.3	18.6	10.8
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	EWCGPCKMIAPIL	1574.8	A	D	2.9	0.8	14.4	11.1
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	SDKIIHLT	926.5	M	D	0.0	0.0	28.8	10.0
P0AA25	11789.4	G	T	A	B	CID	LIT	8	48.6	SDKIIHLTD	1041.6	M	D	0.0	0.0	42.4	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA25	11789.4	G	U	A	B	CID	LIT	2	20.2	DEYQGKLTVAKLNI	1591.9	A	D	4.1	0.5	53.2	15.3
P0AA25	11789.4	G	U	A	B	CID	LIT	2	20.2	SDKIIHLT	926.5	M	D	0.0	0.0	26.8	10.0
P0AA25	11789.4	S	U	T	A	CID	LIT	5	63.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	5.1	0.6	57.2	14.3
P0AA25	11789.4	S	U	T	A	CID	LIT	5	63.3	GIPTLLLFKNGEVAATK	1773.0	R	V	5.2	0.7	32.3	12.6
P0AA25	11789.4	S	U	T	A	CID	LIT	5	63.3	IIHLTDDSFDTDVLK	1731.9	K	A	4.2	0.7	39.1	19.3
P0AA25	11789.4	S	U	T	A	CID	LIT	5	63.3	MIAPILDEIADEYQGK	1805.9	K	L	5.7	0.6	64.6	17.9
P0AA25	11789.4	S	U	T	A	CID	LIT	5	63.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	62.4	18.1
P0AA25	11789.4	S	U	T	B	CID	LIT	5	63.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	4.1	0.8	68.9	14.3
P0AA25	11789.4	S	U	T	B	CID	LIT	5	63.3	GIPTLLLFKNGEVAATK	1773.0	R	V	3.9	0.7	17.4	11.8
P0AA25	11789.4	S	U	T	B	CID	LIT	5	63.3	IIHLTDDSFDTDVLK	1731.9	K	A	4.5	0.6	34.4	19.0
P0AA25	11789.4	S	U	T	B	CID	LIT	5	63.3	MIAPILDEIADEYQGK	1805.9	K	L	5.6	0.6	84.3	17.6
P0AA25	11789.4	S	U	T	B	CID	LIT	5	63.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	67.6	18.1
P0AA25	11789.4	S	U	T	C	CID	LIT	6	74.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	4.0	0.8	68.3	14.3
P0AA25	11789.4	S	U	T	C	CID	LIT	6	74.3	GIPTLLLFKNGEVAATK	1773.0	R	V	3.8	0.5	14.0	13.2
P0AA25	11789.4	S	U	T	C	CID	LIT	6	74.3	IIHLTDDSFDTDVLK	1731.9	K	A	4.6	0.7	50.4	19.3
P0AA25	11789.4	S	U	T	C	CID	LIT	6	74.3	LNIDQNPGTAPK	1267.7	K	Y	3.6	0.5	11.9	15.7
P0AA25	11789.4	S	U	T	C	CID	LIT	6	74.3	MIAPILDEIADEYQGK	1805.9	K	L	5.4	0.0	91.2	17.6
P0AA25	11789.4	S	U	T	C	CID	LIT	6	74.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	68.4	17.9
P0AA25	11789.4	S	U	T	B	CID	FT	2	16.5	IIHLTDDSFDTDVLK	1731.9	K	A	1.6	0.0	23.9	18.9
P0AA25	11789.4	S	U	T	B	CID	FT	2	16.5	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	72.2	17.9
P0AA25	11789.4	S	U	T	A	ETD	LIT	6	57.8	GIPTLLLFK	1001.6	R	N	2.4	0.0	23.7	6.0
P0AA25	11789.4	S	U	T	A	ETD	LIT	6	57.8	GIPTLLLFKNGEVAATK	1773.0	R	V	3.6	0.0	18.4	13.2
P0AA25	11789.4	S	U	T	A	ETD	LIT	6	57.8	GQLKEFLDANLA	1318.7	K	-	2.9	0.3	7.6	16.1
P0AA25	11789.4	S	U	T	A	ETD	LIT	6	57.8	IIHLTDDSFDTDVLK	1731.9	K	A	2.7	0.5	43.5	19.2
P0AA25	11789.4	S	U	T	A	ETD	LIT	6	57.8	MIAPILDEIADEYQGK	1805.9	K	L	3.1	0.4	39.1	17.9
P0AA25	11789.4	S	U	T	A	ETD	LIT	6	57.8	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	47.7	18.3
P0AA25	11789.4	S	U	T	B	ETD	LIT	7	68.8	GIPTLLLFK	1001.6	R	N	2.7	0.0	29.9	0.0
P0AA25	11789.4	S	U	T	B	ETD	LIT	7	68.8	GIPTLLLFKNGEVAATK	1773.0	R	V	4.5	0.0	25.8	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA25	11789.4	S	U	T	B	ETD	LIT	7	68.8	GQLKEFLDANLA	1318.7	K	-	3.0	0.7	25.2	15.6
P0AA25	11789.4	S	U	T	B	ETD	LIT	7	68.8	IIHLTDDSFDTDVLK	1731.9	K	A	2.1	0.7	34.7	18.7
P0AA25	11789.4	S	U	T	B	ETD	LIT	7	68.8	LNIDQNPGTAPK	1267.7	K	Y	2.3	0.0	35.8	15.6
P0AA25	11789.4	S	U	T	B	ETD	LIT	7	68.8	MIAPILDEIADEYQGK	1805.9	K	L	5.0	0.6	69.2	17.4
P0AA25	11789.4	S	U	T	B	ETD	LIT	7	68.8	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	94.8	18.1
P0AA25	11789.4	S	U	T	C	ETD	LIT	6	57.8	GIPTLLLFK	1001.6	R	N	2.2	0.0	16.3	6.0
P0AA25	11789.4	S	U	T	C	ETD	LIT	6	57.8	GIPTLLLFKNGEVAATK	1773.0	R	V	5.2	0.7	36.0	11.8
P0AA25	11789.4	S	U	T	C	ETD	LIT	6	57.8	GQLKEFLDANLA	1318.7	K	-	2.7	0.7	31.9	16.3
P0AA25	11789.4	S	U	T	C	ETD	LIT	6	57.8	IIHLTDDSFDTDVLK	1731.9	K	A	5.0	0.6	62.0	18.8
P0AA25	11789.4	S	U	T	C	ETD	LIT	6	57.8	MIAPILDEIADEYQGK	1805.9	K	L	0.0	0.0	56.2	17.6
P0AA25	11789.4	S	U	T	C	ETD	LIT	6	57.8	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	87.2	17.9
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	5	63.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	0.0	0.0	88.6	14.3
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	5	63.3	GIPTLLLFKNGEVAATK	1773.0	R	V	0.0	0.0	24.3	11.8
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	5	63.3	IIHLTDDSFDTDVLK	1731.9	K	A	0.0	0.0	86.8	19.2
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	5	63.3	MIAPILDEIADEYQGK	1821.9	K	L	0.0	0.0	91.2	17.7
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	5	63.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	52.9	18.1
P0AA25	11789.4	S	U	T	A	ETD+CID	LIT	6	63.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	0.0	0.0	59.3	14.9
P0AA25	11789.4	S	U	T	A	ETD+CID	LIT	6	63.3	GIPTLLLFK	1001.6	R	N	2.0	0.0	44.2	0.0
P0AA25	11789.4	S	U	T	A	ETD+CID	LIT	6	63.3	GIPTLLLFKNGEVAATK	1773.0	R	V	4.7	0.0	27.4	13.2
P0AA25	11789.4	S	U	T	A	ETD+CID	LIT	6	63.3	IIHLTDDSFDTDVLK	1731.9	K	A	3.7	0.5	46.3	18.9
P0AA25	11789.4	S	U	T	A	ETD+CID	LIT	6	63.3	MIAPILDEIADEYQGK	1821.9	K	L	0.0	0.0	50.7	17.6
P0AA25	11789.4	S	U	T	A	ETD+CID	LIT	6	63.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	70.2	17.9
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	2	24.8	IIHLTDDSFDTDVLK	1731.9	K	A	3.7	0.8	0.0	0.0
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	2	24.8	LNIDQNPGTAPK	1267.7	K	Y	2.9	0.5	0.0	0.0
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	6	74.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	0.0	0.0	88.6	14.3
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	6	74.3	GIPTLLLFKNGEVAATK	1773.0	R	V	0.0	0.0	24.3	11.8
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	6	74.3	IIHLTDDSFDTDVLK	1731.9	K	A	3.7	0.8	86.8	19.2
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	6	74.3	LNIDQNPGTAPK	1267.7	K	Y	2.9	0.5	18.0	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	6	74.3	MIAPILDEIADEYQGK	1821.9	K	L	0.0	0.0	91.2	17.7
P0AA25	11789.4	S	U	T	B	ETD+CID	LIT	6	74.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	52.9	18.1
P0AA25	11789.4	S	U	T	C	ETD+CID	LIT	7	74.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	0.0	0.0	78.4	13.8
P0AA25	11789.4	S	U	T	C	ETD+CID	LIT	7	74.3	GIPTLLLFK	1001.6	R	N	2.1	0.0	44.7	6.0
P0AA25	11789.4	S	U	T	C	ETD+CID	LIT	7	74.3	GIPTLLLFKNGEVAATK	1773.0	R	V	4.5	0.7	25.4	13.2
P0AA25	11789.4	S	U	T	C	ETD+CID	LIT	7	74.3	IIHLTDDSFDTDVLK	1731.9	K	A	3.0	0.4	50.1	18.9
P0AA25	11789.4	S	U	T	C	ETD+CID	LIT	7	74.3	LNIDQNPGTAPK	1267.7	K	Y	2.1	0.6	0.9	15.6
P0AA25	11789.4	S	U	T	C	ETD+CID	LIT	7	74.3	MIAPILDEIADEYQGK	1821.9	K	L	0.0	0.0	78.7	17.7
P0AA25	11789.4	S	U	T	C	ETD+CID	LIT	7	74.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	57.1	17.9
P0AA25	11789.4	S	U	T	B	HCD	FT	5	63.3	ADGAILVDFWAEWCGPCK	2094.9	K	M	0.0	0.0	88.6	14.3
P0AA25	11789.4	S	U	T	B	HCD	FT	5	63.3	GIPTLLLFKNGEVAATK	1773.0	R	V	0.0	0.0	24.3	11.8
P0AA25	11789.4	S	U	T	B	HCD	FT	5	63.3	IIHLTDDSFDTDVLK	1731.9	K	A	0.0	0.0	36.0	19.2
P0AA25	11789.4	S	U	T	B	HCD	FT	5	63.3	MIAPILDEIADEYQGK	1821.9	K	L	0.0	0.0	91.2	17.7
P0AA25	11789.4	S	U	T	B	HCD	FT	5	63.3	SDKIIHLTDDSFDTDVLK	2062.0	M	A	0.0	0.0	52.9	18.1
P0AB46	11834.1	G	U	T	A	CID	LIT	2	25.7	DLKIEQSPELSAK	1457.8	R	V	2.7	0.3	18.7	13.6
P0AB46	11834.1	G	U	T	A	CID	LIT	2	25.7	DPQMLLITAIDDTMR	1732.9	K	A	5.0	0.0	53.1	13.2
P0AB46	11834.1	G	T	T	A	CID	LIT	7	72.5	DLKIEQSPELSAK	1457.8	R	V	3.9	0.6	40.5	12.8
P0AB46	11834.1	G	T	T	A	CID	LIT	7	72.5	DPQMLLITAIDDTMR	1732.9	K	A	5.4	0.9	70.7	13.0
P0AB46	11834.1	G	T	T	A	CID	LIT	7	72.5	IEQSPELSAK	1101.6	K	V	2.4	0.7	20.3	13.0
P0AB46	11834.1	G	T	T	A	CID	LIT	7	72.5	LNQVCAKDPQMLLITAIDDTMR	2546.3	K	A	4.8	0.5	28.0	12.6
P0AB46	11834.1	G	T	T	A	CID	LIT	7	72.5	NGLPSETYITCAEANEMAK	2098.9	K	T	3.3	0.6	82.2	9.0
P0AB46	11834.1	G	T	T	A	CID	LIT	7	72.5	TDSAQVAEIVAVMGNASVASR	2076.0	K	D	4.2	0.6	20.2	12.3
P0AB46	11834.1	G	T	T	A	CID	LIT	7	72.5	VVEKLNQVCAK	1287.7	K	D	3.6	0.8	56.7	13.8
P0AB46	11834.1	G	T	A	A	CID	LIT	3	36.7	DDTMRAIGKK	1134.6	I	-	2.5	0.4	15.3	16.4
P0AB46	11834.1	G	T	A	A	CID	LIT	3	36.7	DPQMLLITAIDDTMRAIGKK	2230.2	K	-	2.3	0.3	3.8	14.6
P0AB46	11834.1	G	T	A	A	CID	LIT	3	36.7	DSAQVAEIVAVMGNASVASR	1975.0	T	D	5.1	0.8	32.9	14.6
P0AB46	11834.1	S	U	T	C	CID	LIT	2	29.4	DLKIEQSPELSAK	1457.8	R	V	1.8	0.6	1.4	16.1
P0AB46	11834.1	S	U	T	C	CID	LIT	2	29.4	NGLPSETYITCAEANEMAK	2098.9	K	T	3.5	0.6	52.7	14.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AES9	11839.6	G	T	T	A	CID	LIT	6	69.1	DKPEDAVLDVQGIATVTPAIVQACTQDK	2982.5	K	Q	8.3	0.8	67.4	12.3
P0AES9	11839.6	G	T	T	A	CID	LIT	6	69.1	DKPEDAVLDVQGIATVTPAIVQACTQDKQANFK	3570.8	K	D	7.7	0.0	78.3	10.0
P0AES9	11839.6	G	T	T	A	CID	LIT	6	69.1	GEWDKIK	875.5	K	K	2.0	0.5	25.9	15.4
P0AES9	11839.6	G	T	T	A	CID	LIT	6	69.1	KPVNSWTCEDFLAVDESFQPTAVGFAEALNNK	3584.7	K	D	7.0	0.0	36.2	7.0
P0AES9	11839.6	G	T	T	A	CID	LIT	6	69.1	QANFKDK	850.4	K	V	2.5	0.7	32.5	14.9
P0AES9	11839.6	G	T	T	A	CID	LIT	6	69.1	VKGEWDK	861.4	K	I	2.1	0.5	17.9	13.0
P0AES9	11839.6	G	U	A	A	CID	LIT	7	68.2	DESFQPTAVGFAEALNNK	1937.9	V	D	5.4	0.7	70.2	15.7
P0AES9	11839.6	G	U	A	A	CID	LIT	7	68.2	DKPEDAVL	886.5	K	D	2.3	0.7	39.0	15.1
P0AES9	11839.6	G	U	A	A	CID	LIT	7	68.2	DKQANFK	850.4	Q	D	1.6	0.6	15.0	15.1
P0AES9	11839.6	G	U	A	A	CID	LIT	7	68.2	DKVKGEW	861.4	K	D	2.0	0.6	17.3	15.4
P0AES9	11839.6	G	U	A	A	CID	LIT	7	68.2	DKVKGEWDKIKK	1473.8	K	D	3.3	0.8	5.2	8.5
P0AES9	11839.6	G	U	A	A	CID	LIT	7	68.2	DNKKPVNSWTCE	1477.7	A	D	2.9	0.4	31.5	12.6
P0AES9	11839.6	G	U	A	A	CID	LIT	7	68.2	DVQGIATVTPAIVQACTQ	1872.0	L	D	2.8	0.7	10.2	15.9
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DESFQPTAVGFAEALNNK	1937.9	V	D	4.8	0.6	85.0	14.8
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DFLAVDESFQPTAVGFA	1813.9	E	E	2.4	0.0	26.2	14.0
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DKIKKDM	877.5	W	-	1.9	0.7	25.8	14.3
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DKPEDAVL	886.5	K	D	2.4	0.4	25.7	15.1
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DKQANFK	850.4	Q	D	2.0	0.8	17.2	15.1
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DKQANFKDKVKGEW	1692.9	Q	D	4.6	0.5	41.4	15.2
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DKVKGEW	861.4	K	D	1.6	0.6	14.2	15.4
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DKVKGEWDKIKK	1473.8	K	D	3.1	0.7	5.9	8.5
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DNKKPVNSWTC	1348.6	A	E	3.0	0.7	24.1	15.3
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DNKKPVNSWTCE	1477.7	A	D	3.1	0.5	63.6	12.3
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DNKKPVNSWTCEDFLAV	2023.0	A	D	3.7	0.5	22.6	14.1
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DVQGIATVTPAIVQACTQ	1872.0	L	D	2.8	0.8	89.4	15.6
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	DVQGIATVTPAIVQACTQDKQANFK	2703.4	L	D	2.9	0.5	22.0	16.1
P0AES9	11839.6	G	T	A	A	CID	LIT	14	74.5	ESFQPTAVGFAEALNNK	1822.9	D	D	4.7	0.0	48.4	16.6
P0AES9	11839.6	G	T	A	B	CID	LIT	6	63.6	DESFQPTAVGFAEALNNK	1937.9	V	D	4.6	0.6	87.4	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AES9	11839.6	G	T	A	B	CID	LIT	6	63.6	DKPEDAVL	886.5	K	D	2.1	0.4	34.7	14.8
P0AES9	11839.6	G	T	A	B	CID	LIT	6	63.6	DKQANFK	850.4	Q	D	2.1	0.1	14.9	14.9
P0AES9	11839.6	G	T	A	B	CID	LIT	6	63.6	DKVKGEW	861.4	K	D	1.8	0.3	11.8	15.4
P0AES9	11839.6	G	T	A	B	CID	LIT	6	63.6	DNKKPVNSWTCE	1477.7	A	D	2.9	0.5	63.4	13.0
P0AES9	11839.6	G	T	A	B	CID	LIT	6	63.6	DVQGIATVTPAIVQACTQ	1872.0	L	D	5.0	0.6	46.2	15.1
P0AES9	11839.6	G	U	A	B	CID	LIT	3	37.3	DESFQPTAVGFAEALNNK	1937.9	V	D	5.0	0.7	79.8	15.9
P0AES9	11839.6	G	U	A	B	CID	LIT	3	37.3	DKIKK	631.4	W	D	1.4	0.1	16.0	4.8
P0AES9	11839.6	G	U	A	B	CID	LIT	3	37.3	DVQGIATVTPAIVQACTQ	1872.0	L	D	2.7	0.6	12.9	15.1
P76076	11860.0	G	T	T	A	CID	LIT	3	30.6	KASYQQLAK	1036.6	R	Q	3.2	0.0	39.1	10.0
P76076	11860.0	G	T	T	A	CID	LIT	3	30.6	QNNVSVDDIAK	1202.6	K	L	2.9	0.4	14.4	14.0
P76076	11860.0	G	T	T	A	CID	LIT	3	30.6	VGETFYGYLVALK	1459.8	R	T	3.7	0.6	45.8	13.2
P0ADZ7	11869.6	G	T	A	B	CID	LIT	2	21.8	DFVAAVLPKGTMKAL	1560.9	R	-	4.2	0.0	28.1	9.0
P0ADZ7	11869.6	G	T	A	B	CID	LIT	2	21.8	DTTEVVIKR	1060.6	N	D	2.2	0.4	19.5	12.6
P67603	11887.7	G	U	T	A	CID	LIT	7	64.1	FQDDILAGR	1034.5	R	K	3.0	0.5	55.9	15.2
P67603	11887.7	G	U	T	A	CID	LIT	7	64.1	FQDDILAGRK	1162.6	R	T	2.4	0.5	29.5	13.6
P67603	11887.7	G	U	T	A	CID	LIT	7	64.1	HAEQENMTLTELK	1543.7	K	K	4.1	0.8	37.5	10.4
P67603	11887.7	G	U	T	A	CID	LIT	7	64.1	HAEQENMTLTELKK	1671.8	K	V	6.3	0.9	72.5	11.8
P67603	11887.7	G	U	T	A	CID	LIT	7	64.1	MQPNDITFFQR	1396.7	-	F	2.0	0.3	11.0	11.1
P67603	11887.7	G	U	T	A	CID	LIT	7	64.1	TITIRDESESHFK	1562.8	K	T	1.7	0.7	23.1	14.5
P67603	11887.7	G	U	T	A	CID	LIT	7	64.1	VIADIYPGQTQFYVIEFK	2131.1	K	C	3.4	0.7	26.7	13.4
P67603	11887.7	G	T	T	A	CID	LIT	7	64.1	FQDDILAGR	1034.5	R	K	2.3	0.6	56.4	15.2
P67603	11887.7	G	T	T	A	CID	LIT	7	64.1	FQDDILAGRK	1162.6	R	T	2.8	0.5	35.5	14.1
P67603	11887.7	G	T	T	A	CID	LIT	7	64.1	HAEQENMTLTELK	1543.7	K	K	4.9	0.8	61.9	10.0
P67603	11887.7	G	T	T	A	CID	LIT	7	64.1	HAEQENMTLTELKK	1671.8	K	V	5.8	0.7	79.6	13.8
P67603	11887.7	G	T	T	A	CID	LIT	7	64.1	MQPNDITFFQR	1396.7	-	F	2.8	0.8	31.8	9.5
P67603	11887.7	G	T	T	A	CID	LIT	7	64.1	TITIRDESESHFK	1562.8	K	T	3.6	0.6	30.6	13.8
P67603	11887.7	G	T	T	A	CID	LIT	7	64.1	VIADIYPGQTQFYVIEFK	2131.1	K	C	4.1	0.7	50.5	13.4
P67603	11887.7	G	U	A	A	CID	LIT	5	51.5	DDILAGRKTITIR	1471.9	Q	D	1.6	0.7	16.4	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P67603	11887.7	G	U	A	A	CID	LIT	5	51.5	DESESHFKTG	1136.5	R	D	1.6	0.7	15.9	11.1
P67603	11887.7	G	U	A	A	CID	LIT	5	51.5	DITFFQRFQ	1201.6	N	D	2.4	0.5	15.2	14.6
P67603	11887.7	G	U	A	A	CID	LIT	5	51.5	DIYPGQTQFYVIEFKCL	2121.0	A	-	2.5	0.4	1.0	13.8
P67603	11887.7	G	U	A	A	CID	LIT	5	51.5	MQPNDITFFQRFQ	1671.8	-	D	3.6	0.7	26.4	13.0
P67603	11887.7	G	T	A	A	CID	LIT	4	35.0	DDILAGRKTITIR	1471.9	Q	D	2.8	0.7	6.1	9.0
P67603	11887.7	G	T	A	A	CID	LIT	4	35.0	DESESHFKTG	1136.5	R	D	3.1	0.0	47.4	11.1
P67603	11887.7	G	T	A	A	CID	LIT	4	35.0	DITFFQRFQ	1201.6	N	D	3.2	0.7	25.6	14.6
P67603	11887.7	G	T	A	A	CID	LIT	4	35.0	MQPNDITFFQRFQ	1671.8	-	D	3.7	0.0	49.1	13.4
P67603	11887.7	G	T	T	B	CID	LIT	3	35.0	FQDDILAGR	1034.5	R	K	2.5	0.3	24.3	15.2
P67603	11887.7	G	T	T	B	CID	LIT	3	35.0	HAEQENMTLTELKK	1671.8	K	V	4.3	0.6	27.6	11.8
P67603	11887.7	G	T	T	B	CID	LIT	3	35.0	TITIRDESESHFK	1562.8	K	T	3.4	0.4	20.2	14.5
P67603	11887.7	G	U	T	B	CID	LIT	3	34.0	FQDDILAGRK	1162.6	R	T	3.3	0.3	41.7	13.6
P67603	11887.7	G	U	T	B	CID	LIT	3	34.0	HAEQENMTLTELKK	1671.8	K	V	5.1	0.7	51.5	12.6
P67603	11887.7	G	U	T	B	CID	LIT	3	34.0	MQPNDITFFQR	1396.7	-	F	2.9	0.0	31.5	9.5
P67603	11887.7	G	T	A	B	CID	LIT	6	39.8	DDILAGRKTITIR	1471.9	Q	D	2.8	0.8	17.8	9.5
P67603	11887.7	G	T	A	B	CID	LIT	6	39.8	DESESHFKTG	1136.5	R	D	3.2	0.0	48.9	11.1
P67603	11887.7	G	T	A	B	CID	LIT	6	39.8	DILAGRKTITIR	1356.8	D	D	1.9	0.4	0.0	0.0
P67603	11887.7	G	T	A	B	CID	LIT	6	39.8	DITFFQRFQ	1201.6	N	D	3.3	0.7	31.5	14.6
P67603	11887.7	G	T	A	B	CID	LIT	6	39.8	DITFFQRFQD	1316.6	N	D	3.0	0.4	19.7	12.0
P67603	11887.7	G	T	A	B	CID	LIT	6	39.8	DVLRVGRFE	1090.6	G	D	1.5	0.6	11.4	10.4
P67603	11887.7	G	U	A	B	CID	LIT	6	47.6	DDILAGRKTITIR	1471.9	Q	D	2.9	0.8	25.6	9.0
P67603	11887.7	G	U	A	B	CID	LIT	6	47.6	DESESHFKTG	1136.5	R	D	3.2	0.0	43.8	11.1
P67603	11887.7	G	U	A	B	CID	LIT	6	47.6	DILAGRKTITIR	1356.8	D	D	0.8	0.0	16.5	6.0
P67603	11887.7	G	U	A	B	CID	LIT	6	47.6	DITFFQRFQ	1201.6	N	D	3.1	0.8	30.2	14.6
P67603	11887.7	G	U	A	B	CID	LIT	6	47.6	DITFFQRFQD	1316.6	N	D	3.5	0.5	32.7	12.0
P67603	11887.7	G	U	A	B	CID	LIT	6	47.6	DIYPGQTQFYVIEFKCL	2121.0	A	-	2.8	0.0	28.8	13.4
P67603	11887.7	S	U	T	A	CID	LIT	4	28.2	FQDDILAGR	1034.5	R	K	2.8	0.4	56.4	17.2
P67603	11887.7	S	U	T	A	CID	LIT	4	28.2	FQDDILAGRK	1162.6	R	T	3.0	0.3	36.8	16.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P67603	11887.7	S	U	T	A	CID	LIT	4	28.2	KVIADIYPGQTQFYVIEFK	2259.2	K	C	5.7	0.7	43.8	16.3
P67603	11887.7	S	U	T	A	CID	LIT	4	28.2	VIADIYPGQTQFYVIEFK	2131.1	K	C	2.9	0.0	25.2	17.4
P67603	11887.7	S	U	T	B	CID	LIT	5	67.0	FQDDILAGRK	1162.6	R	T	2.7	0.3	42.0	16.0
P67603	11887.7	S	U	T	B	CID	LIT	5	67.0	KVIADIYPGQTQFYVIEFK	2259.2	K	C	5.0	0.7	25.2	16.2
P67603	11887.7	S	U	T	B	CID	LIT	5	67.0	MQPNDITFFQR	1396.7	-	F	1.7	0.4	13.3	15.9
P67603	11887.7	S	U	T	B	CID	LIT	5	67.0	VGRFEDDGYFCTIEVTATSTVTLDTLTEK	3268.6	R	H	4.1	0.6	20.2	17.7
P67603	11887.7	S	U	T	B	CID	LIT	5	67.0	VIADIYPGQTQFYVIEFK	2131.1	K	C	4.1	0.0	52.5	17.4
P67603	11887.7	S	U	T	C	CID	LIT	4	66.0	FQDDILAGRK	1162.6	R	T	1.9	0.1	19.0	16.8
P67603	11887.7	S	U	T	C	CID	LIT	4	66.0	MQPNDITFFQR	1396.7	-	F	2.1	0.3	13.9	16.2
P67603	11887.7	S	U	T	C	CID	LIT	4	66.0	VGRFEDDGYFCTIEVTATSTVTLDTLTEK	3268.6	R	H	3.6	0.4	19.0	18.7
P67603	11887.7	S	U	T	C	CID	LIT	4	66.0	VIADIYPGQTQFYVIEFK	2131.1	K	C	4.0	0.7	43.8	17.4
P67603	11887.7	S	U	T	A	ETD	LIT	2	27.2	FQDDILAGRK	1162.6	R	T	3.4	0.4	0.0	0.0
P67603	11887.7	S	U	T	A	ETD	LIT	2	27.2	VIADIYPGQTQFYVIEFK	2131.1	K	C	3.0	0.0	18.9	17.3
P67603	11887.7	S	U	T	B	ETD	LIT	3	22.3	FQDDILAGR	1034.5	R	K	0.0	0.0	24.8	17.2
P67603	11887.7	S	U	T	B	ETD	LIT	3	22.3	FQDDILAGRK	1162.6	R	T	2.3	0.3	28.2	16.0
P67603	11887.7	S	U	T	B	ETD	LIT	3	22.3	TITIRDESESHFK	1562.8	K	T	2.6	0.7	27.3	17.6
P67603	11887.7	S	U	T	C	ETD	LIT	5	40.8	FQDDILAGR	1034.5	R	K	0.0	0.0	36.6	17.6
P67603	11887.7	S	U	T	C	ETD	LIT	5	40.8	FQDDILAGRK	1162.6	R	T	3.1	0.4	25.6	16.0
P67603	11887.7	S	U	T	C	ETD	LIT	5	40.8	KVIADIYPGQTQFYVIEFK	2259.2	K	C	4.7	0.0	39.2	16.1
P67603	11887.7	S	U	T	C	ETD	LIT	5	40.8	TITIRDESESHFK	1562.8	K	T	2.1	0.0	32.1	17.5
P67603	11887.7	S	U	T	C	ETD	LIT	5	40.8	VIADIYPGQTQFYVIEFK	2131.1	K	C	1.1	0.6	12.5	18.6
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	FQDDILAGRK	1162.6	R	T	0.0	0.0	39.2	16.5
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	KVIADIYPGQTQFYVIEFK	2259.2	K	C	0.0	0.0	27.8	16.2
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	MQPNDITFFQR	1396.7	-	F	0.0	0.0	30.2	15.6
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	VIADIYPGQTQFYVIEFK	2131.1	K	C	0.0	0.0	50.7	17.6
P67603	11887.7	S	U	T	A	ETD+CID	LIT	4	55.3	FQDDILAGR	1034.5	R	K	2.8	0.4	57.0	17.8
P67603	11887.7	S	U	T	A	ETD+CID	LIT	4	55.3	KVIADIYPGQTQFYVIEFK	2259.2	K	C	3.7	0.7	40.2	16.1
P67603	11887.7	S	U	T	A	ETD+CID	LIT	4	55.3	VGRFEDDGYFCTIEVTATSTVTLDTLTEK	3268.6	R	H	4.4	0.7	40.0	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P67603	11887.7	S	U	T	A	ETD+CID	LIT	4	55.3	VIADIYPGQTQFYVIEFK	2131.1	K	C	2.7	0.8	13.4	17.4
P67603	11887.7	S	U	T	B	ETD+CID	LIT	2	28.2	FQDDILAGRK	1162.6	R	T	2.5	0.2	0.0	0.0
P67603	11887.7	S	U	T	B	ETD+CID	LIT	2	28.2	KVIADIYPGQTQFYVIEFK	2259.2	K	C	4.0	0.7	0.0	0.0
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	FQDDILAGRK	1162.6	R	T	2.5	0.2	39.2	16.5
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	KVIADIYPGQTQFYVIEFK	2259.2	K	C	4.0	0.7	27.8	16.2
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	MQPNDITFFQR	1396.7	-	F	2.7	0.6	30.2	15.6
P67603	11887.7	S	U	T	B	ETD+CID	LIT	4	38.8	VIADIYPGQTQFYVIEFK	2131.1	K	C	3.7	0.0	50.7	17.6
P67603	11887.7	S	U	T	C	ETD+CID	LIT	5	66.0	FQDDILAGR	1034.5	R	K	2.7	0.3	48.8	17.4
P67603	11887.7	S	U	T	C	ETD+CID	LIT	5	66.0	KVIADIYPGQTQFYVIEFK	2259.2	K	C	4.7	0.7	39.5	16.1
P67603	11887.7	S	U	T	C	ETD+CID	LIT	5	66.0	MQPNDITFFQR	1396.7	-	F	2.5	0.4	0.0	0.0
P67603	11887.7	S	U	T	C	ETD+CID	LIT	5	66.0	VGRFEDDGYFCTIEVTATSTVTLDTLTEK	3268.6	R	H	0.0	0.0	29.3	17.8
P67603	11887.7	S	U	T	C	ETD+CID	LIT	5	66.0	VIADIYPGQTQFYVIEFK	2131.1	K	C	2.7	0.7	15.6	17.9
P67603	11887.7	S	U	T	B	HCD	FT	4	38.8	FQDDILAGRK	1162.6	R	T	0.0	0.0	39.2	16.5
P67603	11887.7	S	U	T	B	HCD	FT	4	38.8	KVIADIYPGQTQFYVIEFK	2259.2	K	C	0.0	0.0	27.8	16.2
P67603	11887.7	S	U	T	B	HCD	FT	4	38.8	MQPNDITFFQR	1396.7	-	F	0.0	0.0	30.2	15.6
P67603	11887.7	S	U	T	B	HCD	FT	4	38.8	VIADIYPGQTQFYVIEFK	2131.1	K	C	0.0	0.0	50.7	17.6
P0ABE2	11975.6	G	U	T	A	CID	LIT	2	26.7	AAFQPVFLEVVDESYR	1869.9	R	H	4.6	0.8	87.6	13.8
P0ABE2	11975.6	G	U	T	A	CID	LIT	2	26.7	HNVPAGSESHFK	1309.6	R	V	5.0	0.6	62.5	11.5
P0ABE2	11975.6	G	U	T	B	CID	LIT	2	26.7	AAFQPVFLEVVDESYR	1869.9	R	H	4.3	0.6	47.4	12.6
P0ABE2	11975.6	G	U	T	B	CID	LIT	2	26.7	HNVPAGSESHFK	1309.6	R	V	5.8	0.7	63.6	12.0
P0ABE2	11975.6	S	U	T	A	CID	LIT	3	41.9	AAFQPVFLEVVDESYRHNVPAGSESHFK	3160.5	R	V	2.7	0.4	18.9	18.6
P0ABE2	11975.6	S	U	T	A	CID	LIT	3	41.9	EWEGLQDTVFASPPCR	1891.9	K	G	2.8	0.4	18.3	14.5
P0ABE2	11975.6	S	U	T	A	CID	LIT	3	41.9	HNVPAGSESHFK	1309.6	R	V	2.5	0.6	21.8	14.3
P0ABE2	11975.6	S	U	T	B	CID	LIT	4	41.9	AAFQPVFLEVVDESYR	1869.9	R	H	3.0	0.8	35.5	17.6
P0ABE2	11975.6	S	U	T	B	CID	LIT	4	41.9	AAFQPVFLEVVDESYRHNVPAGSESHFK	3160.5	R	V	3.6	0.5	40.1	18.5
P0ABE2	11975.6	S	U	T	B	CID	LIT	4	41.9	EWEGLQDTVFASPPCR	1891.9	K	G	3.8	0.5	29.6	15.1
P0ABE2	11975.6	S	U	T	B	CID	LIT	4	41.9	HNVPAGSESHFK	1309.6	R	V	3.5	0.5	39.6	14.3
P0ABE2	11975.6	S	U	T	C	CID	LIT	3	41.9	AAFQPVFLEVVDESYRHNVPAGSESHFK	3160.5	R	V	2.9	0.4	1.8	18.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABE2	11975.6	S	U	T	C	CID	LIT	3	41.9	EWEGLQDTVFASPPCR	1891.9	K	G	2.9	0.3	0.6	15.1
P0ABE2	11975.6	S	U	T	C	CID	LIT	3	41.9	HNVPAGSESHFK	1309.6	R	V	3.7	0.6	44.5	14.5
P0ABE2	11975.6	S	U	T	B	ETD	LIT	2	26.7	AAFQPVFLEVVDESYRHNVPAGSESHFK	3160.5	R	V	0.0	0.0	16.7	18.5
P0ABE2	11975.6	S	U	T	B	ETD	LIT	2	26.7	HNVPAGSESHFK	1309.6	R	V	5.1	0.7	35.1	14.5
P0ABE2	11975.6	S	U	T	C	ETD+CID	LIT	2	41.9	AAFQPVFLEVVDESYRHNVPAGSESHFK	3160.5	R	V	3.5	0.7	24.6	18.5
P0ABE2	11975.6	S	U	T	C	ETD+CID	LIT	2	41.9	EWEGLQDTVFASPPCR	1891.9	K	G	3.3	0.7	29.3	15.1
P0ABE2	11975.6	S	U	T	C	ETD+CID	LIT	2	41.9	HNVPAGSESHFK	1309.6	R	V	3.6	0.5	29.4	14.5
P0A8B5	11996.9	G	U	T	A	CID	LIT	5	55.0	GGLGNLMK	789.4	K	Q	2.1	0.5	18.9	16.1
P0A8B5	11996.9	G	U	T	A	CID	LIT	5	55.0	MASVSSGMQLPPGFK	1536.8	K	M	4.8	0.8	90.7	13.2
P0A8B5	11996.9	G	U	T	A	CID	LIT	5	55.0	MQEEIAQLEVTGESGAGLVK	2089.0	K	V	5.3	0.6	117.0	12.0
P0A8B5	11996.9	G	U	T	A	CID	LIT	5	55.0	RIEETQK	903.5	R	E	2.4	0.3	11.7	14.0
P0A8B5	11996.9	G	U	T	A	CID	LIT	5	55.0	VTINGAHNCR	1141.6	K	R	3.0	0.4	66.4	11.1
P0A8B5	11996.9	G	U	T	B	CID	LIT	3	21.1	GGLGNLMK	789.4	K	Q	1.9	0.0	18.0	15.6
P0A8B5	11996.9	G	U	T	B	CID	LIT	3	21.1	QAQQMQEK	990.5	K	M	1.8	0.3	17.9	11.8
P0A8B5	11996.9	G	U	T	B	CID	LIT	3	21.1	RIEETQK	903.5	R	E	2.4	0.2	18.2	13.4
P0A8B5	11996.9	S	U	T	B	CID	LIT	4	67.9	MASVSSGMQLPPGFK	1536.8	K	M	3.9	0.5	20.9	17.3
P0A8B5	11996.9	S	U	T	B	CID	LIT	4	67.9	MQEEIAQLEVTGESGAGLVK	2089.0	K	V	5.9	0.6	99.6	18.0
P0A8B5	11996.9	S	U	T	B	CID	LIT	4	67.9	RVEIDPSLLEDDKEMLEDLVAAAFNDAAR	3245.6	R	R	5.0	0.0	68.4	20.0
P0A8B5	11996.9	S	U	T	B	CID	LIT	4	67.9	VTINGAHNCR	1143.5	K	R	2.6	0.6	15.5	11.8
P0A8B5	11996.9	S	U	T	C	CID	LIT	3	30.3	GGLGNLMK	789.4	K	Q	1.7	0.4	18.7	17.1
P0A8B5	11996.9	S	U	T	C	CID	LIT	3	30.3	MASVSSGMQLPPGFK	1536.8	K	M	3.3	0.4	10.4	16.8
P0A8B5	11996.9	S	U	T	C	CID	LIT	3	30.3	VTINGAHNCR	1142.5	K	R	2.6	0.4	37.3	12.6
P0A8B5	11996.9	S	U	T	B	ETD+CID	LIT	2	49.5	MASVSSGMQLPPGFK	1536.8	K	M	3.3	0.4	7.2	17.2
P0A8B5	11996.9	S	U	T	B	ETD+CID	LIT	2	49.5	RVEIDPSLLEDDKEMLEDLVAAAFNDAAR	3245.6	R	R	5.3	0.0	74.3	19.9
P0A8B5	11996.9	S	U	T	B	ETD+CID	LIT	2	49.5	VTINGAHNCR	1142.5	K	R	2.7	0.4	39.9	12.6
P0ADB1	12002.5	G	T	T	A	CID	LIT	3	35.7	AQVAQIAGKPSSEVSMIHAR	2080.1	R	G	5.8	0.7	61.9	9.0
P0ADB1	12002.5	G	T	T	A	CID	LIT	3	35.7	DQFVQPVVK	1059.6	K	D	1.7	0.6	7.7	14.0
P0ADB1	12002.5	G	T	T	A	CID	LIT	3	35.7	GTCQTYILGQR	1296.6	R	D	3.3	0.0	49.3	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADB1	12002.5	G	T	A	A	CID	LIT	2	25.0	DDTGHVINSGYQTCAEY	1929.8	L	D	3.7	0.0	47.7	6.0
P0ADB1	12002.5	G	T	A	A	CID	LIT	2	25.0	DGKAETYFVAL	1213.6	R	D	1.8	0.5	0.0	0.0
P0ADB1	12002.5	G	T	A	B	CID	LIT	3	32.1	DDTGHVINSGYQTCAEY	1929.8	L	D	3.1	0.0	55.1	4.8
P0ADB1	12002.5	G	T	A	B	CID	LIT	3	32.1	DGKAETYFVAL	1213.6	R	D	2.2	0.3	24.3	13.0
P0ADB1	12002.5	G	T	A	B	CID	LIT	3	32.1	DTDPQAAK	845.4	Y	-	2.1	0.0	18.5	12.6
P0ADB1	12002.5	G	U	A	B	CID	LIT	2	23.2	DDTGHVINSGYQTCAEY	1929.8	L	D	2.5	0.0	51.3	6.0
P0ADB1	12002.5	G	U	A	B	CID	LIT	2	23.2	DQFVQPVVK	1059.6	K	D	2.7	0.4	31.0	16.7
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	AANHQIIGSSQMYATAQSR	2034.0	K	E	6.1	0.8	85.8	11.5
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	AGNGETILTSELYTSK	1683.8	K	T	4.7	0.8	67.7	11.8
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	AGWFELSK	937.5	M	S	0.0	0.0	54.8	11.1
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	ANGTSQTVKDNT	1235.6	K	-	3.4	0.7	26.3	13.0
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	ETGIASVK	804.4	R	A	2.0	0.2	29.7	13.2
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	FYFNLK	831.4	K	A	1.9	0.8	14.0	15.1
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	SNSPQEER	946.4	R	Y	2.1	0.0	35.2	4.8
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	SNSPQEERYEK	1366.6	R	K	2.7	0.0	25.8	10.0
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	TASNGKFYFNLK	1389.7	K	A	2.2	0.6	14.4	14.6
P76402	12006.6	G	U	T	A	CID	LIT	10	88.2	TSAEKGIASVR	1118.6	K	S	3.1	0.8	56.4	12.0
P76402	12006.6	G	T	T	A	CID	LIT	6	70.0	AANHQIIGSSQMYATAQSR	2034.0	K	E	6.1	0.0	71.6	10.8
P76402	12006.6	G	T	T	A	CID	LIT	6	70.0	AGNGETILTSELYTSK	1683.8	K	T	3.2	0.0	29.5	11.8
P76402	12006.6	G	T	T	A	CID	LIT	6	70.0	ANGTSQTVKDNT	1235.6	K	-	4.0	0.0	38.7	12.0
P76402	12006.6	G	T	T	A	CID	LIT	6	70.0	ETGIASVK	804.4	R	A	2.3	0.3	25.6	13.2
P76402	12006.6	G	T	T	A	CID	LIT	6	70.0	SNSPQEERYEK	1366.6	R	K	3.2	0.6	34.9	10.0
P76402	12006.6	G	T	T	A	CID	LIT	6	70.0	TSAEKGIASVR	1118.6	K	S	3.6	0.6	46.3	12.0
P76402	12006.6	G	U	T	B	CID	LIT	3	16.4	SNSPQEER	946.4	R	Y	1.9	0.7	21.4	4.8
P76402	12006.6	G	U	T	B	CID	LIT	3	16.4	SNSPQEERYEK	1366.6	R	K	3.2	0.5	28.7	10.0
P76402	12006.6	G	U	T	B	CID	LIT	3	16.4	SSDNQFR	853.4	K	F	2.0	0.0	38.0	7.8
P76402	12006.6	S	U	T	A	CID	LIT	6	65.5	AANHQIIGSSQMYATAQSR	2034.0	K	E	6.1	0.6	69.9	16.6
P76402	12006.6	S	U	T	A	CID	LIT	6	65.5	AGNGETILTSELYTSK	1684.8	K	T	4.7	0.7	61.6	16.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76402	12006.6	S	U	T	A	CID	LIT	6	65.5	AGWFELSK	937.5	M	S	0.0	0.0	46.4	16.0
P76402	12006.6	S	U	T	A	CID	LIT	6	65.5	GIASVR	602.4	K	S	1.4	0.3	21.3	22.6
P76402	12006.6	S	U	T	A	CID	LIT	6	65.5	SNSPQEERYEK	1366.6	R	K	2.8	0.7	27.2	13.8
P76402	12006.6	S	U	T	A	CID	LIT	6	65.5	TASNGKFYFNLK	1390.7	K	A	2.6	0.0	30.2	17.3
P76402	12006.6	S	U	T	B	CID	LIT	5	55.5	AANHQIIGSSQMYATAQSR	2034.0	K	E	3.2	0.5	10.6	16.9
P76402	12006.6	S	U	T	B	CID	LIT	5	55.5	AGNGETILTSELYTSK	1684.8	K	T	4.7	0.7	67.8	17.1
P76402	12006.6	S	U	T	B	CID	LIT	5	55.5	AGWFELSK	937.5	M	S	0.0	0.0	34.4	16.0
P76402	12006.6	S	U	T	B	CID	LIT	5	55.5	ANGTSQTVKDNT	1236.6	K	-	3.6	0.6	33.0	15.3
P76402	12006.6	S	U	T	B	CID	LIT	5	55.5	FYFNLK	831.4	K	A	1.7	0.5	17.5	15.9
P76402	12006.6	S	U	T	C	CID	LIT	6	61.8	AANHQIIGSSQMYATAQSR	2034.0	K	E	5.8	0.7	65.4	17.2
P76402	12006.6	S	U	T	C	CID	LIT	6	61.8	AGNGETILTSELYTSK	1684.8	K	T	4.2	0.7	61.4	16.1
P76402	12006.6	S	U	T	C	CID	LIT	6	61.8	AGWFELSK	937.5	M	S	0.0	0.0	47.9	16.0
P76402	12006.6	S	U	T	C	CID	LIT	6	61.8	ANGTSQTVKDNT	1236.6	K	-	3.3	0.0	28.4	15.1
P76402	12006.6	S	U	T	C	CID	LIT	6	61.8	FYFNLK	831.4	K	A	1.7	0.3	4.6	16.1
P76402	12006.6	S	U	T	C	CID	LIT	6	61.8	SSDNQFR	853.4	K	F	1.9	0.3	37.6	11.5
P76402	12006.6	S	U	T	A	CID	FT	2	21.8	AGNGETILTSELYTSK	1683.8	K	T	3.9	0.0	74.6	17.6
P76402	12006.6	S	U	T	A	CID	FT	2	21.8	AGWFELSK	937.5	M	S	0.0	0.0	34.4	16.0
P76402	12006.6	S	U	T	A	ETD	LIT	6	53.6	AGNGETILTSELYTSK	1683.8	K	T	2.8	0.8	51.7	17.6
P76402	12006.6	S	U	T	A	ETD	LIT	6	53.6	ANGTSQTVKDNT	1235.6	K	-	1.6	0.3	27.7	15.6
P76402	12006.6	S	U	T	A	ETD	LIT	6	53.6	KTASNGKFYFNLK	1518.8	K	A	3.0	0.4	14.5	17.9
P76402	12006.6	S	U	T	A	ETD	LIT	6	53.6	SNSPQEERYEK	1366.6	R	K	2.2	0.0	25.1	13.2
P76402	12006.6	S	U	T	A	ETD	LIT	6	53.6	SSDNQFR	853.4	K	F	2.0	0.7	33.0	11.8
P76402	12006.6	S	U	T	A	ETD	LIT	6	53.6	TASNGKFYFNLK	1390.7	K	A	2.9	0.6	16.5	16.7
P76402	12006.6	S	U	T	B	ETD	LIT	4	41.8	AGNGETILTSELYTSK	1683.8	K	T	2.2	0.7	47.9	17.6
P76402	12006.6	S	U	T	B	ETD	LIT	4	41.8	ANGTSQTVKDNT	1236.6	K	-	2.0	0.6	30.5	14.0
P76402	12006.6	S	U	T	B	ETD	LIT	4	41.8	GIASVR	602.4	K	S	1.5	0.0	24.0	22.6
P76402	12006.6	S	U	T	B	ETD	LIT	4	41.8	TASNGKFYFNLK	1390.7	K	A	3.5	0.5	29.1	17.2
P76402	12006.6	S	U	T	C	ETD	LIT	5	60.0	AANHQIIGSSQMYATAQSR	2034.0	K	E	5.5	0.0	93.3	17.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76402	12006.6	S	U	T	C	ETD	LIT	5	60.0	AGNGETILTSELYTSK	1683.8	K	T	3.2	0.8	54.6	17.2
P76402	12006.6	S	U	T	C	ETD	LIT	5	60.0	ANGTSQTVKDNT	1236.6	K	-	1.6	0.0	33.2	14.0
P76402	12006.6	S	U	T	C	ETD	LIT	5	60.0	SSDNQFR	853.4	K	F	1.8	0.0	40.2	11.8
P76402	12006.6	S	U	T	C	ETD	LIT	5	60.0	TASNGKFYFNLK	1390.7	K	A	4.4	0.6	50.6	16.6
P76402	12006.6	S	U	T	B	ETD+CID	LIT	4	49.1	AANHQIIGSSQMYATAQSR	2034.0	K	E	0.0	0.0	31.0	17.5
P76402	12006.6	S	U	T	B	ETD+CID	LIT	4	49.1	AGNGETILTSELYTSK	1684.8	K	T	0.0	0.0	72.4	16.1
P76402	12006.6	S	U	T	B	ETD+CID	LIT	4	49.1	ANGTSQTVKDNT	1235.6	K	-	0.0	0.0	21.4	15.6
P76402	12006.6	S	U	T	B	ETD+CID	LIT	4	49.1	SSDNQFR	853.4	K	F	0.0	0.0	39.9	11.8
P76402	12006.6	S	U	T	A	ETD+CID	LIT	5	41.8	AGNGETILTSELYTSK	1684.8	K	T	4.5	0.7	65.1	16.8
P76402	12006.6	S	U	T	A	ETD+CID	LIT	5	41.8	FYFNLK	831.4	K	A	1.3	0.4	14.5	17.8
P76402	12006.6	S	U	T	A	ETD+CID	LIT	5	41.8	SNSPQEERYEK	1366.6	R	K	1.6	0.3	20.4	13.8
P76402	12006.6	S	U	T	A	ETD+CID	LIT	5	41.8	SSDNQFR	853.4	K	F	1.9	0.4	37.8	11.8
P76402	12006.6	S	U	T	A	ETD+CID	LIT	5	41.8	TASNGKFYFNLK	1390.7	K	A	2.3	0.3	11.9	17.4
P76402	12006.6	S	U	T	B	ETD+CID	LIT	3	42.7	AANHQIIGSSQMYATAQSR	2034.0	K	E	4.1	0.7	0.0	0.0
P76402	12006.6	S	U	T	B	ETD+CID	LIT	3	42.7	AGNGETILTSELYTSK	1684.8	K	T	4.3	0.7	0.0	0.0
P76402	12006.6	S	U	T	B	ETD+CID	LIT	3	42.7	ANGTSQTVKDNT	1236.6	K	-	2.0	0.7	0.0	0.0
P76402	12006.6	S	U	T	B	ETD+CID	LIT	5	49.1	AANHQIIGSSQMYATAQSR	2034.0	K	E	4.1	0.7	31.0	17.5
P76402	12006.6	S	U	T	B	ETD+CID	LIT	5	49.1	AGNGETILTSELYTSK	1684.8	K	T	4.5	0.7	72.4	16.1
P76402	12006.6	S	U	T	B	ETD+CID	LIT	5	49.1	ANGTSQTVKDNT	1236.6	K	-	2.0	0.7	10.8	15.3
P76402	12006.6	S	U	T	B	ETD+CID	LIT	5	49.1	RVVTFRPGQK	1187.7	-	-	1.8	0.0	39.7	12.3
P76402	12006.6	S	U	T	B	ETD+CID	LIT	5	49.1	SSDNQFR	853.4	K	F	2.0	0.8	39.9	11.8
P76402	12006.6	S	U	T	C	ETD+CID	LIT	4	48.2	AANHQIIGSSQMYATAQSR	2034.0	K	E	6.1	0.6	69.1	17.1
P76402	12006.6	S	U	T	C	ETD+CID	LIT	4	48.2	AGNGETILTSELYTSK	1683.8	K	T	4.6	0.8	56.6	16.4
P76402	12006.6	S	U	T	C	ETD+CID	LIT	4	48.2	SNSPQEERYEK	1366.6	R	K	1.7	0.4	16.4	13.8
P76402	12006.6	S	U	T	C	ETD+CID	LIT	4	48.2	SSDNQFR	853.4	K	F	0.4	-0.3	37.8	11.8
P76402	12006.6	S	U	T	B	HCD	FT	4	49.1	AANHQIIGSSQMYATAQSR	2034.0	K	E	0.0	0.0	31.0	17.5
P76402	12006.6	S	U	T	B	HCD	FT	4	49.1	AGNGETILTSELYTSK	1684.8	K	T	0.0	0.0	72.4	16.1
P76402	12006.6	S	U	T	B	HCD	FT	4	49.1	ANGTSQTVKDNT	1235.6	K	-	0.0	0.0	21.4	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76402	12006.6	S	U	T	B	HCD	FT	4	49.1	SSDNQFR	853.4	K	F	0.0	0.0	39.9	11.8
P76402	12006.6	S	U	T	A	HCD	FT	2	21.8	AGNGETILTSELYTSK	1683.8	K	T	2.3	0.0	54.8	17.6
P76402	12006.6	S	U	T	A	HCD	FT	2	21.8	AGWFELSK	937.5	M	S	0.0	0.0	41.1	16.0
P0AET2	12025.1	G	U	T	A	CID	LIT	2	27.8	DMTCQEFIDLNPK	1610.7	K	A	2.8	0.0	48.3	4.8
P0AET2	12025.1	G	U	T	A	CID	LIT	2	27.8	GGDTVTLNETDLTQIPK	1801.9	K	V	4.2	0.7	49.7	11.1
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	AMTPVAWWMLHEETVYK	2108.0	K	G	2.8	0.8	37.4	11.8
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	AMTPVAWWMLHEETVYKGGDTVTLNETDLTQIPK	3874.9	K	V	3.7	0.5	13.8	12.3
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	DMTCQEFIDLNPK	1626.7	K	A	3.8	0.0	73.0	3.0
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	GGDTVTLNETDLTQIPK	1801.9	K	V	4.7	0.8	84.6	11.1
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	NLYTFK	785.4	K	N	1.6	0.7	11.5	11.5
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	NLYTFKNQASNDLPN	1738.8	K	-	4.2	0.9	40.5	12.6
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	NPQKNLYTFK	1252.7	K	N	3.2	0.5	32.0	11.8
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	NQASNDLPN	972.4	K	-	2.7	0.0	59.6	7.0
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	VIEYCK	811.4	K	K	1.8	0.7	14.3	10.0
P0AET2	12025.1	G	T	T	A	CID	LIT	10	67.6	VIEYCKK	939.5	K	N	1.8	0.7	23.6	11.1
P0AET2	12025.1	G	T	A	A	CID	LIT	4	56.5	DLNPKAMTPVAWWMLH	1909.9	I	E	4.0	0.6	25.8	14.6
P0AET2	12025.1	G	T	A	A	CID	LIT	4	56.5	DLNPKAMTPVAWWMLHEETVYKGG	2789.3	I	D	4.0	0.6	3.4	13.2
P0AET2	12025.1	G	T	A	A	CID	LIT	4	56.5	DLTQIPKVIEYCKKNPQKNLYTFKNQASN	3482.8	T	D	3.1	0.8	0.0	0.0
P0AET2	12025.1	G	T	A	A	CID	LIT	4	56.5	DMTCQEFI	1043.4	K	D	2.0	0.0	26.4	4.8
P0AET2	12025.1	G	T	T	B	CID	LIT	2	27.8	DMTCQEFIDLNPK	1610.7	K	A	2.6	0.0	42.8	7.0
P0AET2	12025.1	G	T	T	B	CID	LIT	2	27.8	GGDTVTLNETDLTQIPK	1801.9	K	V	3.9	0.6	44.7	10.0
P0AET2	12025.1	G	U	T	B	CID	LIT	2	27.8	DMTCQEFIDLNPK	1610.7	K	A	2.8	0.0	46.2	7.0
P0AET2	12025.1	G	U	T	B	CID	LIT	2	27.8	GGDTVTLNETDLTQIPK	1801.9	K	V	4.1	0.0	51.6	12.0
P0AET2	12025.1	G	T	A	B	CID	LIT	5	63.9	DLNPKAMTPVAWWMLH	1909.9	I	E	4.0	0.6	30.3	14.0
P0AET2	12025.1	G	T	A	B	CID	LIT	5	63.9	DLNPKAMTPVAWWMLHEETVYKGG	2773.3	I	D	4.9	0.7	37.8	14.8
P0AET2	12025.1	G	T	A	B	CID	LIT	5	63.9	DLTQIPKVIEYCKKNPQKNLYTFKNQASN	3482.8	T	D	4.2	0.7	21.3	14.6
P0AET2	12025.1	G	T	A	B	CID	LIT	5	63.9	DMTCQEFI	1043.4	K	D	0.8	0.4	17.1	4.8
P0AET2	12025.1	G	T	A	B	CID	LIT	5	63.9	DTVTLNET	892.4	G	D	2.0	0.5	20.0	14.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AET2	12025.1	S	U	T	B	CID	LIT	3	43.5	AMTPVAWWMLHEETVYK	2092.0	K	G	5.0	0.6	33.2	17.6
P0AET2	12025.1	S	U	T	B	CID	LIT	3	43.5	DMTCQEFIDLNPK	1610.7	K	A	2.4	0.0	40.0	12.3
P0AET2	12025.1	S	U	T	B	CID	LIT	3	43.5	GGDTVTLNETDLTQIPK	1801.9	K	V	4.1	0.6	27.3	17.2
P0AET2	12025.1	S	U	T	C	CID	LIT	3	43.5	AMTPVAWWMLHEETVYK	2092.0	K	G	4.6	0.6	28.8	17.2
P0AET2	12025.1	S	U	T	C	CID	LIT	3	43.5	DMTCQEFIDLNPK	1610.7	K	A	2.6	0.6	30.3	12.3
P0AET2	12025.1	S	U	T	C	CID	LIT	3	43.5	GGDTVTLNETDLTQIPK	1801.9	K	V	4.1	0.7	38.2	18.2
P0AET2	12025.1	S	U	T	B	ETD	LIT	2	27.8	DMTCQEFIDLNPK	1610.7	K	A	1.6	0.6	45.1	13.2
P0AET2	12025.1	S	U	T	B	ETD	LIT	2	27.8	GGDTVTLNETDLTQIPK	1801.9	K	V	3.4	0.5	119.0	18.2
P0AET2	12025.1	S	U	T	C	ETD	LIT	2	27.8	DMTCQEFIDLNPK	1610.7	K	A	1.5	0.5	28.3	11.5
P0AET2	12025.1	S	U	T	C	ETD	LIT	2	27.8	GGDTVTLNETDLTQIPK	1801.9	K	V	3.4	0.5	0.0	0.0
P0AET2	12025.1	S	U	T	B	ETD+CID	LIT	3	43.5	AMTPVAWWMLHEETVYK	2092.0	K	G	0.0	0.0	32.4	17.7
P0AET2	12025.1	S	U	T	B	ETD+CID	LIT	3	43.5	DMTCQEFIDLNPK	1610.7	K	A	0.0	0.0	45.3	12.3
P0AET2	12025.1	S	U	T	B	ETD+CID	LIT	3	43.5	GGDTVTLNETDLTQIPK	1801.9	K	V	0.0	0.0	79.8	18.2
P0AET2	12025.1	S	U	T	A	ETD+CID	LIT	2	29.6	GGDTVTLNETDLTQIPK	1801.9	K	V	4.1	0.7	57.8	17.7
P0AET2	12025.1	S	U	T	A	ETD+CID	LIT	2	29.6	NLYTFKNQASNDLPN	1738.8	K	-	2.8	0.4	10.4	17.0
P0AET2	12025.1	S	U	T	B	ETD+CID	LIT	3	43.5	AMTPVAWWMLHEETVYK	2092.0	K	G	4.3	0.5	0.0	0.0
P0AET2	12025.1	S	U	T	B	ETD+CID	LIT	3	43.5	DMTCQEFIDLNPK	1610.7	K	A	3.1	0.8	45.3	12.3
P0AET2	12025.1	S	U	T	B	ETD+CID	LIT	3	43.5	GGDTVTLNETDLTQIPK	1801.9	K	V	4.9	0.7	79.8	18.2
P0AET2	12025.1	S	U	T	C	ETD+CID	LIT	3	43.5	AMTPVAWWMLHEETVYK	2092.0	K	G	4.7	0.6	41.4	17.4
P0AET2	12025.1	S	U	T	C	ETD+CID	LIT	3	43.5	DMTCQEFIDLNPK	1610.7	K	A	2.7	0.8	40.5	13.2
P0AET2	12025.1	S	U	T	C	ETD+CID	LIT	3	43.5	GGDTVTLNETDLTQIPK	1801.9	K	V	4.5	0.8	78.8	17.1
P0AET2	12025.1	S	U	T	B	HCD	FT	3	43.5	AMTPVAWWMLHEETVYK	2092.0	K	G	0.0	0.0	32.4	17.7
P0AET2	12025.1	S	U	T	B	HCD	FT	3	43.5	DMTCQEFIDLNPK	1610.7	K	A	0.0	0.0	45.3	12.3
P0AET2	12025.1	S	U	T	B	HCD	FT	3	43.5	GGDTVTLNETDLTQIPK	1801.9	K	V	0.0	0.0	79.8	18.2
P0A6V5	12064.2	G	U	A	A	CID	LIT	2	20.4	DAHQKLQEKEAVLV	1607.9	A	D	2.9	0.7	27.2	12.8
P0A6V5	12064.2	G	U	A	A	CID	LIT	2	20.4	DTLGAFMR	910.4	N	D	2.1	0.0	15.9	12.0
P0A6V5	12064.2	G	T	A	B	CID	LIT	4	54.6	DAHQKLQEKEAVLV	1607.9	A	D	2.8	0.0	30.7	13.0
P0A6V5	12064.2	G	T	A	B	CID	LIT	4	54.6	DGGFEAWQRQFPAEVAYGA	2099.0	I	-	3.1	0.0	31.4	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6V5	12064.2	G	T	A	B	CID	LIT	4	54.6	DPQSFAMGHAVQAFHLTN	1970.9	R	D	4.2	0.7	33.9	12.3
P0A6V5	12064.2	G	T	A	B	CID	LIT	4	54.6	DTLGAFMR	910.4	N	D	2.2	0.0	30.4	12.0
P0A6V5	12064.2	G	U	A	B	CID	LIT	2	29.6	DAHQKLQEKEAVLV	1607.9	A	D	3.2	0.5	22.6	11.8
P0A6V5	12064.2	G	U	A	B	CID	LIT	2	29.6	DPQSFAMGHAVQAFHLTN	1970.9	R	D	3.0	0.7	37.5	12.3
P0AE70	12079.9	G	U	T	A	CID	LIT	2	27.0	KGTVAPEELQLIK	1425.8	K	A	4.3	0.6	56.5	7.0
P0AE70	12079.9	G	U	T	A	CID	LIT	2	27.0	YVPDMGDLIWVDFDPTK	2011.0	R	G	2.4	0.6	34.0	12.0
P0ACC3	12082.6	G	U	T	A	CID	LIT	4	35.1	FIVTNPNAK	1003.6	R	S	2.3	0.5	24.3	15.3
P0ACC3	12082.6	G	U	T	A	CID	LIT	4	35.1	SDDVALPLEFTDAAANK	1776.9	M	V	0.0	0.0	43.3	10.8
P0ACC3	12082.6	G	U	T	A	CID	LIT	4	35.1	SDDVALPLEFTDAAANKVK	2004.0	M	S	0.0	0.0	69.6	13.8
P0ACC3	12082.6	G	U	T	A	CID	LIT	4	35.1	SLIADEDNPNLK	1328.7	K	L	3.8	0.8	75.2	11.5
P0ACC3	12082.6	G	T	A	B	CID	LIT	3	28.1	DAAANKVKSLIA	1200.7	T	D	2.9	0.4	33.3	13.2
P0ACC3	12082.6	G	T	A	B	CID	LIT	3	28.1	DDQVNEG	776.3	F	D	2.0	0.0	16.2	9.0
P0ACC3	12082.6	G	T	A	B	CID	LIT	3	28.1	DMTIEKQGVGLVV	1388.7	G	D	3.1	0.3	14.6	16.3
P0ACC3	12082.6	S	U	T	A	CID	LIT	2	16.7	SDDVALPLEFTDAAANK	1776.9	M	V	0.0	0.0	40.3	17.4
P0ACC3	12082.6	S	U	T	A	CID	LIT	2	16.7	SDDVALPLEFTDAAANKVK	2004.0	M	S	0.0	0.0	62.4	18.5
P0ACC3	12082.6	S	U	T	C	ETD	LIT	2	25.4	SDDVALPLEFTDAAANK	1776.9	M	V	0.0	0.0	25.7	17.0
P0ACC3	12082.6	S	U	T	C	ETD	LIT	2	25.4	SLIADEDNPNLK	1328.7	K	L	1.6	0.5	10.2	15.8
P0ACC3	12082.6	S	U	T	B	ETD+CID	LIT	2	16.7	SDDVALPLEFTDAAANK	1776.9	M	V	0.0	0.0	34.7	16.9
P0ACC3	12082.6	S	U	T	B	ETD+CID	LIT	2	16.7	SDDVALPLEFTDAAANKVK	2004.0	M	S	0.0	0.0	48.4	18.5
P0ACC3	12082.6	S	U	T	B	ETD+CID	LIT	2	16.7	SDDVALPLEFTDAAANK	1776.9	M	V	0.0	0.0	34.7	16.9
P0ACC3	12082.6	S	U	T	B	ETD+CID	LIT	2	16.7	SDDVALPLEFTDAAANKVK	2004.0	M	S	0.0	0.0	48.4	18.5
P0ACC3	12082.6	S	U	T	C	ETD+CID	LIT	2	16.7	SDDVALPLEFTDAAANK	1776.9	M	V	0.0	0.0	46.1	17.0
P0ACC3	12082.6	S	U	T	C	ETD+CID	LIT	2	16.7	SDDVALPLEFTDAAANKVK	2004.0	M	S	0.0	0.0	35.0	18.3
P0ACC3	12082.6	S	U	T	B	HCD	FT	2	16.7	SDDVALPLEFTDAAANK	1776.9	M	V	0.0	0.0	34.7	16.9
P0ACC3	12082.6	S	U	T	B	HCD	FT	2	16.7	SDDVALPLEFTDAAANKVK	2004.0	M	S	0.0	0.0	48.4	18.5
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	AEWSGEYISPYAEHGK	1823.8	M	K	0.0	0.0	60.0	10.0
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	AEWSGEYISPYAEHGKK	1951.9	M	S	0.0	0.0	40.3	13.2
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	ERSDEIPEAAK	1244.6	K	E	3.6	0.4	37.6	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	HATNSELLCEAFLHAFTGQPLPDDADLRK	3266.6	R	E	4.1	0.0	21.7	10.4
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	ILTDER	746.4	K	T	1.5	0.4	28.4	16.7
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	ITVSIPLK	870.6	K	V	2.3	0.6	24.2	6.0
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	KITVSIPLK	998.7	K	V	3.4	0.0	24.8	0.0
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	QVNNLR	743.4	R	H	1.9	0.2	10.4	7.8
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	SDEIPEAAK	959.5	R	E	2.4	0.6	9.4	10.4
P0A8U6	12123.1	G	U	T	A	CID	LIT	10	78.1	SDEIPEAAKEIMR	1488.7	R	E	1.6	0.7	12.0	13.6
P0A8U6	12123.1	G	T	T	A	CID	LIT	2	14.3	ILTDER	746.4	K	T	1.7	0.5	14.5	16.6
P0A8U6	12123.1	G	T	T	A	CID	LIT	2	14.3	SDEIPEAAK	959.5	R	E	2.0	0.7	13.9	10.4
P0A8U6	12123.1	S	U	T	A	CID	LIT	3	38.1	HATNSELLCEAFLHAFTGQPLPDDADLRK	3266.6	R	E	5.1	0.0	54.0	19.0
P0A8U6	12123.1	S	U	T	A	CID	LIT	3	38.1	HATNSELLCEAFLHAFTGQPLPDDADLRKER	3551.7	R	S	4.4	0.0	51.5	18.7
P0A8U6	12123.1	S	U	T	A	CID	LIT	3	38.1	KITVSIPLK	998.7	K	V	2.3	0.0	36.9	4.8
P0A8U6	12123.1	S	U	T	B	CID	LIT	3	52.4	AEWSGEYISPYAEHGKK	1951.9	M	S	0.0	0.0	58.8	18.1
P0A8U6	12123.1	S	U	T	B	CID	LIT	3	52.4	HATNSELLCEAFLHAFTGQPLPDDADLRK	3266.6	R	E	5.4	0.0	44.0	19.4
P0A8U6	12123.1	S	U	T	B	CID	LIT	3	52.4	KITVSIPLK	998.7	K	V	2.4	0.0	40.1	4.8
P0A8U6	12123.1	S	U	T	C	CID	LIT	4	61.0	AEWSGEYISPYAEHGKK	1951.9	M	S	0.0	0.0	55.0	18.3
P0A8U6	12123.1	S	U	T	C	CID	LIT	4	61.0	HATNSELLCEAFLHAFTGQPLPDDADLRK	3266.6	R	E	5.6	0.7	29.7	19.0
P0A8U6	12123.1	S	U	T	C	CID	LIT	4	61.0	KITVSIPLK	998.7	K	V	2.1	0.0	27.0	4.8
P0A8U6	12123.1	S	U	T	C	CID	LIT	4	61.0	SDEIPEAAK	959.5	R	E	2.3	0.5	14.8	11.8
P0A8U6	12123.1	S	U	T	A	ETD	LIT	2	36.2	HATNSELLCEAFLHAFTGQPLPDDADLRK	3266.6	R	E	0.0	0.0	20.0	19.0
P0A8U6	12123.1	S	U	T	A	ETD	LIT	2	36.2	KITVSIPLK	998.7	K	V	2.3	0.6	30.0	4.8
P0A8U6	12123.1	S	U	T	B	ETD	LIT	3	52.4	AEWSGEYISPYAEHGKK	1951.9	M	S	0.0	0.0	58.2	17.6
P0A8U6	12123.1	S	U	T	B	ETD	LIT	3	52.4	HATNSELLCEAFLHAFTGQPLPDDADLRK	3266.6	R	E	0.0	0.0	43.7	19.0
P0A8U6	12123.1	S	U	T	B	ETD	LIT	3	52.4	KITVSIPLK	998.7	K	V	2.0	0.0	35.9	6.0
P0A8U6	12123.1	S	U	T	B	ETD+CID	LIT	2	34.3	HATNSELLCEAFLHAFTGQPLPDDADLRK	3266.6	R	E	4.2	0.0	33.6	19.0
P0A8U6	12123.1	S	U	T	B	ETD+CID	LIT	2	34.3	RQVNNLR	899.5	R	H	1.9	0.3	2.0	13.0
P0A8U6	12123.1	S	U	T	C	ETD+CID	LIT	2	24.8	AEWSGEYISPYAEHGKK	1951.9	M	S	0.0	0.0	65.3	17.9
P0A8U6	12123.1	S	U	T	C	ETD+CID	LIT	2	24.8	KITVSIPLK	998.7	K	V	2.8	0.0	34.5	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	IFVDEGPSMK	1122.6	K	R	3.0	0.8	40.1	11.8
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	IFVDEGPSMKR	1278.7	K	I	2.9	0.7	42.0	13.6
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.0	0.7	56.4	11.8
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	LVADLIR	799.5	R	G	2.4	0.7	29.2	11.1
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	RIMPR	672.4	K	A	2.0	0.2	20.6	11.1
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	RTSHITVVVSDR	1369.8	K	-	3.9	0.7	42.2	10.8
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	TSHITVVVSDR	1213.7	R	-	3.8	0.9	67.0	11.8
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	VLESAIANAEHNDGADIDDLK	2210.1	K	V	4.0	0.6	44.0	13.2
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	5.6	0.7	66.0	12.8
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	VRLVADLIR	1054.7	K	G	3.7	0.4	28.8	10.0
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	VSQALDILTYTNK	1465.8	K	K	4.5	0.8	83.7	11.5
P61175	12208.6	G	U	T	A	CID	LIT	12	68.2	VSQALDILTYTNKK	1593.9	K	A	4.3	0.7	87.3	10.4
P61175	12208.6	G	U	A	A	CID	LIT	4	37.3	DIDDLKVTKIFV	1405.8	A	D	3.7	0.5	38.2	13.2
P61175	12208.6	G	U	A	A	CID	LIT	4	37.3	DLIRGKKVSQAL	1327.8	A	D	3.2	0.0	38.1	4.8
P61175	12208.6	G	U	A	A	CID	LIT	4	37.3	DRILKRTSHITVVVS	1724.0	A	D	2.0	0.6	0.0	0.0
P61175	12208.6	G	U	A	A	CID	LIT	4	37.3	DRILKRTSHITVVVSDR	1995.1	A	-	2.6	0.6	12.9	8.5
P61175	12208.6	G	U	T	B	CID	LIT	5	60.0	IFVDEGPSMK	1122.6	K	R	1.9	0.7	22.4	12.0
P61175	12208.6	G	U	T	B	CID	LIT	5	60.0	LVADLIR	799.5	R	G	1.7	0.0	28.6	11.1
P61175	12208.6	G	U	T	B	CID	LIT	5	60.0	TSHITVVVSDR	1213.7	R	-	2.2	0.7	0.3	11.8
P61175	12208.6	G	U	T	B	CID	LIT	5	60.0	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	3.2	0.0	20.6	12.3
P61175	12208.6	G	U	T	B	CID	LIT	5	60.0	VSQALDILTYTNKK	1593.9	K	A	3.9	0.7	46.1	10.4
P61175	12208.6	G	T	A	B	CID	LIT	3	10.9	DDLKVTKIFV	1177.7	I	D	1.9	0.3	6.4	11.1
P61175	12208.6	G	T	A	B	CID	LIT	3	10.9	DIDDLKVTKIFV	1405.8	A	D	2.3	0.4	0.0	0.0
P61175	12208.6	G	T	A	B	CID	LIT	3	10.9	DLKVTKIFV	1062.7	D	D	2.2	0.0	24.6	6.0
P61175	12208.6	G	U	A	B	CID	LIT	7	65.5	DDLKVTKIFV	1177.7	I	D	3.2	0.7	22.4	11.1
P61175	12208.6	G	U	A	B	CID	LIT	7	65.5	DEGPSMKRIMPRAKGRA	1900.0	V	D	2.2	0.5	3.5	15.2
P61175	12208.6	G	U	A	B	CID	LIT	7	65.5	DIDDLKVTKIFV	1405.8	A	D	3.5	0.4	48.8	13.2
P61175	12208.6	G	U	A	B	CID	LIT	7	65.5	DLIRGKKVSQAL	1327.8	A	D	2.0	0.6	15.8	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61175	12208.6	G	U	A	B	CID	LIT	7	65.5	DLKVTKIFV	1062.7	D	D	2.6	0.8	34.8	6.0
P61175	12208.6	G	U	A	B	CID	LIT	7	65.5	ESAIANAEHN	1055.5	L	D	3.0	0.0	54.5	14.0
P61175	12208.6	G	U	A	B	CID	LIT	7	65.5	METIAKHRHARSSAQKVRLVA	2389.3	-	D	3.3	0.5	0.0	0.0
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	IFVDEGPSMKR	1278.7	K	I	2.3	0.6	23.8	16.3
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	KAAVLVK	728.5	K	K	2.1	0.5	17.1	9.5
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.0	0.7	89.4	18.3
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	7.3	0.7	68.4	17.7
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	KVSQALDILTYTNKK	1722.0	K	A	5.4	0.6	86.2	11.5
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	LVADLIR	799.5	R	G	2.0	0.6	21.9	13.0
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	METIAK	692.4	-	H	1.9	0.5	23.9	14.9
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	RTSHITVVVSDR	1369.8	K	-	1.8	0.5	15.6	13.2
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	TSHITVVVSDR	1213.7	R	-	3.7	0.6	54.3	16.5
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	VLESAIANAEHNDGADIDDLK	2210.1	K	V	6.6	0.6	67.9	18.1
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	6.6	0.7	72.7	19.0
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	VSQALDILTYTNK	1465.8	K	K	4.9	0.6	69.1	16.0
P61175	12208.6	S	U	T	A	CID	LIT	13	74.5	VSQALDILTYTNKK	1593.9	K	A	4.7	0.2	47.9	14.3
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	IFVDEGPSMKR	1278.7	K	I	3.0	0.5	38.3	16.6
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.4	0.7	86.5	18.1
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	6.9	0.7	66.4	17.4
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	KVSQALDILTYTNK	1593.9	K	K	4.8	0.2	64.5	15.2
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	KVSQALDILTYTNKK	1722.0	K	A	5.4	0.7	98.9	11.5
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	TSHITVVVSDR	1213.7	R	-	3.4	0.5	34.5	15.6
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	VLESAIANAEHNDGADIDDLK	2210.1	K	V	7.1	0.7	72.9	18.1
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	6.1	0.7	80.2	18.7
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	VSQALDILTYTNK	1465.8	K	K	4.5	0.8	69.3	15.8
P61175	12208.6	S	U	T	B	CID	LIT	10	56.4	VSQALDILTYTNKK	1594.9	K	A	5.7	0.6	64.7	15.7
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	IFVDEGPSMKR	1278.7	K	I	2.8	0.6	42.4	16.3
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.8	0.7	95.8	18.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	KVLESAIANAEHNDGADIDDLKVTK	2667.3	K	I	7.1	0.7	79.9	17.9
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	KVSQALDILTYTNKK	1722.0	K	A	5.5	0.6	93.0	11.1
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	LVADLIR	799.5	R	G	2.1	0.0	25.1	13.0
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	TSHITVVVSDR	1213.7	R	-	3.3	0.6	45.5	15.7
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	VLESAIANAEHNDGADIDDLK	2210.1	K	V	6.9	0.7	91.2	18.2
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	5.9	0.7	66.0	18.9
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	VSQALDILTYTNK	1465.8	K	K	4.3	0.7	41.8	16.0
P61175	12208.6	S	U	T	C	CID	LIT	10	62.7	VSQALDILTYTNKK	1593.9	K	A	4.7	0.6	69.6	15.4
P61175	12208.6	S	U	T	A	CID	FT	4	29.1	KVLESAIANAEHNDGADIDDLKVTK	2667.3	K	I	4.9	0.0	62.3	17.9
P61175	12208.6	S	U	T	A	CID	FT	4	29.1	LVADLIR	799.5	R	G	2.1	0.0	29.4	13.0
P61175	12208.6	S	U	T	A	CID	FT	4	29.1	VLESAIANAEHNDGADIDDLK	2210.1	K	V	5.3	0.9	77.7	18.1
P61175	12208.6	S	U	T	A	CID	FT	4	29.1	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	4.4	0.0	58.0	18.8
P61175	12208.6	S	U	T	B	CID	FT	3	30.0	KVSQALDILTYTNKK	1722.0	K	A	4.0	0.5	26.9	12.6
P61175	12208.6	S	U	T	B	CID	FT	3	30.0	LVADLIR	799.5	R	G	2.2	0.0	24.4	13.0
P61175	12208.6	S	U	T	B	CID	FT	3	30.0	TSHITVVVSDR	1213.7	R	-	2.1	0.0	20.1	15.2
P61175	12208.6	S	U	T	C	CID	FT	4	55.5	IFVDEGPSMK	1122.6	K	R	2.1	0.0	41.7	14.9
P61175	12208.6	S	U	T	C	CID	FT	4	55.5	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	9.1	0.0	46.7	17.4
P61175	12208.6	S	U	T	C	CID	FT	4	55.5	KVSQALDILTYTNKK	1722.0	K	A	5.2	0.7	38.4	11.8
P61175	12208.6	S	U	T	C	CID	FT	4	55.5	TSHITVVVSDR	1213.7	R	-	2.1	0.0	19.6	15.1
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	GKKVSQALDILTYTNK	1779.0	R	K	3.0	0.3	0.0	0.0
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.6	0.7	64.6	17.9
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	KVLESAIANAEHNDGADIDDLKVTK	2667.3	K	I	8.2	0.6	77.0	17.9
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	KVSQALDILTYTNKK	1722.0	K	A	3.3	0.7	44.8	12.0
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	LVADLIR	799.5	R	G	2.2	0.3	56.8	13.2
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	TSHITVVVSDR	1213.7	R	-	3.1	0.5	0.0	0.0
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	9.8	0.7	87.7	18.4
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	VSQALDILTYTNK	1465.8	K	K	3.4	0.3	45.7	15.9
P61175	12208.6	S	U	T	A	ETD	LIT	9	54.5	VSQALDILTYTNKK	1593.9	K	A	3.9	0.6	76.4	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	AAVLVKK	728.5	K	V	1.0	0.0	24.7	9.5
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	IFVDEGPSMK	1122.6	K	R	2.1	0.0	24.4	14.8
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	0.0	0.0	73.8	17.6
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	KVSQALDILTYTNKK	1722.0	K	A	6.2	0.0	79.7	12.0
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	LVADLIR	799.5	R	G	2.8	0.4	53.6	13.0
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	RTSHITVVVSDR	1369.8	K	-	2.3	0.6	15.5	13.2
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	TSHITVVVSDR	1213.7	R	-	3.3	0.5	0.0	0.0
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	VLESAIANAEHNDGADIDDLK	2210.1	K	V	2.2	0.7	5.0	18.3
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	7.4	0.7	74.3	18.7
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	VSQALDILTYTNK	1465.8	K	K	2.5	0.3	34.2	15.9
P61175	12208.6	S	U	T	B	ETD	LIT	11	68.2	VSQALDILTYTNKK	1593.9	K	A	6.0	0.6	0.0	0.0
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	IFVDEGPSMKR	1278.7	K	I	2.7	0.7	43.5	17.2
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	7.4	0.8	54.2	18.3
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	6.7	0.6	52.5	17.6
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	KVSQALDILTYTNKK	1722.0	K	A	7.3	0.7	83.4	11.8
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	LVADLIR	799.5	R	G	2.2	0.0	31.1	13.2
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	TSHITVVVSDR	1213.7	R	-	3.0	0.7	0.0	0.0
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	VLESAIANAEHNDGADIDDLK	2210.1	K	V	6.7	0.7	79.4	18.2
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	9.0	0.0	74.3	18.6
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	VSQALDILTYTNK	1465.8	K	K	3.1	0.5	28.9	15.9
P61175	12208.6	S	U	T	C	ETD	LIT	10	62.7	VSQALDILTYTNKK	1593.9	K	A	4.6	0.6	60.8	15.2
P61175	12208.6	S	U	T	B	ETD	FT	2	30.0	IFVDEGPSMKR	1278.7	K	I	1.4	0.0	39.7	16.3
P61175	12208.6	S	U	T	B	ETD	FT	2	30.0	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	5.3	0.0	49.5	18.3
P61175	12208.6	S	U	T	C	ETD	FT	2	20.0	IFVDEGPSMKR	1278.7	K	I	1.2	0.0	43.9	16.5
P61175	12208.6	S	U	T	C	ETD	FT	2	20.0	TSHITVVVSDR	1213.7	R	-	2.0	0.0	36.9	15.2
P61175	12208.6	S	U	T	B	ETD+CID	LIT	6	56.4	IFVDEGPSMKR	1278.7	K	I	0.0	0.0	29.0	16.6
P61175	12208.6	S	U	T	B	ETD+CID	LIT	6	56.4	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	0.0	0.0	40.8	17.6
P61175	12208.6	S	U	T	B	ETD+CID	LIT	6	56.4	KVSQALDILTYTNKK	1722.0	K	A	0.0	0.0	112.0	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61175	12208.6	S	U	T	B	ETD+CID	LIT	6	56.4	TSHITVVVSDR	1213.7	R	-	0.0	0.0	29.1	14.5
P61175	12208.6	S	U	T	B	ETD+CID	LIT	6	56.4	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	0.0	0.0	34.3	18.8
P61175	12208.6	S	U	T	B	ETD+CID	LIT	6	56.4	VSQALDILTYTNKK	1593.9	K	A	0.0	0.0	60.3	15.2
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	IFVDEGPSMKR	1278.7	K	I	0.0	0.0	29.0	16.6
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	0.0	0.0	66.8	18.6
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	KVLESAIANAEHNDGADIDDLKVTK	2667.3	K	I	0.0	0.0	56.6	17.8
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	KVSQALDILTYTNKK	1722.0	K	A	0.0	0.0	112.0	12.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	LVADLIR	799.5	R	G	0.0	0.0	25.2	12.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	TSHITVVVSDR	1213.7	R	-	0.0	0.0	29.1	14.5
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	VLESAIANAEHNDGADIDDLK	2210.1	K	V	0.0	0.0	73.8	18.2
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	0.0	0.0	59.3	18.5
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	VSQALDILTYTNK	1465.8	K	K	0.0	0.0	54.3	15.9
P61175	12208.6	S	U	T	B	ETD+CID	LIT	9	62.7	VSQALDILTYTNKK	1594.9	K	A	0.0	0.0	90.0	15.9
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	GKKVSQALDILTYTNK	1779.0	R	K	3.0	0.3	0.0	0.0
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.7	0.7	84.8	17.9
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	KVLESAIANAEHNDGADIDDLKVTK	2667.3	K	I	0.0	0.0	60.0	18.1
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	KVSQALDILTYTNKK	1722.0	K	A	5.8	0.6	112.0	11.5
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	LGGKLENK	858.5	-	-	2.7	0.1	32.5	19.1
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	LVADLIR	799.5	R	G	1.9	0.0	27.5	12.0
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	TSHITVVVSDR	1213.7	R	-	3.6	0.5	48.2	15.6
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	VLESAIANAEHNDGADIDDLK	2210.1	K	V	4.1	0.7	0.0	0.0
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	5.3	0.7	65.1	18.6
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	VSQALDILTYTNK	1465.8	K	K	5.0	0.6	59.1	16.0
P61175	12208.6	S	U	T	A	ETD+CID	LIT	9	54.5	VSQALDILTYTNKK	1593.9	K	A	4.7	0.6	88.6	14.3
P61175	12208.6	S	U	T	B	ETD+CID	LIT	4	44.5	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	3.6	0.4	0.0	0.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	4	44.5	KVSQALDILTYTNKK	1722.0	K	A	6.7	0.7	0.0	0.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	4	44.5	RTSHITVVVSDR	1369.8	K	-	2.3	0.6	0.0	0.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	4	44.5	TSHITVVVSDR	1213.7	R	-	2.7	0.8	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	IFVDEGPSMKR	1278.7	K	I	4.0	0.7	29.0	16.6
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.1	0.7	66.8	18.6
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	KVLESAIANAEHNDGADIDDLKVTK	2667.3	K	I	4.4	0.8	56.6	17.8
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	KVSQALDILTYTNKK	1722.0	K	A	6.7	0.7	112.0	12.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	LVADLIR	799.5	R	G	2.0	0.0	25.2	12.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	RTSHITVVVSDR	1369.8	K	-	2.3	0.6	10.7	14.9
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	TSHITVVVSDR	1213.7	R	-	2.7	0.8	0.0	0.0
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	VLESAIANAEHNDGADIDDLK	2210.1	K	V	7.0	0.6	73.8	18.2
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	5.9	0.7	59.3	18.5
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	VSQALDILTYTNK	1465.8	K	K	4.5	0.7	54.3	15.9
P61175	12208.6	S	U	T	B	ETD+CID	LIT	10	63.6	VSQALDILTYTNKK	1593.9	K	A	6.3	0.6	60.3	15.2
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	IFVDEGPSMKR	1278.7	K	I	4.1	0.9	34.3	16.6
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	6.5	0.7	80.6	18.4
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	4.7	0.8	62.0	17.6
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	KVSQALDILTYTNKK	1722.0	K	A	5.6	0.7	80.5	10.4
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	LVADLIR	799.5	R	G	2.1	0.0	25.3	13.2
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	TSHITVVVSDR	1213.7	R	-	3.7	0.4	45.5	15.1
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	VLESAIANAEHNDGADIDDLK	2210.1	K	V	6.8	0.7	74.3	18.1
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	5.4	0.6	62.4	18.6
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	VSQALDILTYTNK	1465.8	K	K	4.3	0.6	0.0	0.0
P61175	12208.6	S	U	T	C	ETD+CID	LIT	9	62.7	VSQALDILTYTNKK	1593.9	K	A	5.6	0.5	80.5	14.3
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	KVLESAIANAEHNDGADIDDLK	2338.2	K	V	0.0	0.0	66.8	18.6
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	KVLESAIANAEHNDGADIDDLKVTK	2667.3	K	I	0.0	0.0	56.6	17.8
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	KVSQALDILTYTNKK	1722.0	K	A	0.0	0.0	78.3	12.0
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	LVADLIR	799.5	R	G	0.0	0.0	25.2	12.0
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	TSHITVVVSDR	1213.7	R	-	0.0	0.0	23.3	15.6
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	VLESAIANAEHNDGADIDDLK	2210.1	K	V	0.0	0.0	73.8	18.2
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	0.0	0.0	59.3	18.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	VSQALDILTYTNK	1465.8	K	K	0.0	0.0	54.3	15.9
P61175	12208.6	S	U	T	B	HCD	FT	8	52.7	VSQALDILTYTNKK	1594.9	K	A	0.0	0.0	90.0	15.9
P61175	12208.6	S	U	T	A	HCD	FT	5	46.4	KVLESAIANAEHNDGADIDDLKVTK	2666.4	K	I	6.0	0.0	86.1	17.4
P61175	12208.6	S	U	T	A	HCD	FT	5	46.4	KVSQALDILTYTNK	1593.9	K	K	4.7	0.7	96.2	14.3
P61175	12208.6	S	U	T	A	HCD	FT	5	46.4	KVSQALDILTYTNKK	1722.0	K	A	3.1	0.0	69.8	12.0
P61175	12208.6	S	U	T	A	HCD	FT	5	46.4	TSHITVVVSDR	1213.7	R	-	1.8	0.0	27.8	15.3
P61175	12208.6	S	U	T	A	HCD	FT	5	46.4	VLESAIANAEHNDGADIDDLKVTK	2539.3	K	I	3.8	0.0	41.7	18.8
P61175	12208.6	S	U	T	C	HCD	FT	2	21.8	VLESAIANAEHNDGADIDDLK	2210.1	K	V	5.1	0.0	93.7	18.1
P61175	12208.6	S	U	T	C	HCD	FT	2	21.8	VLESAIANAEHNDGADIDDLKVTK	2538.3	K	I	4.6	0.0	77.7	18.6
P27838	12213.7	G	U	T	A	CID	LIT	6	73.6	GDEWICDR	1050.4	K	S	2.5	0.0	21.5	3.0
P27838	12213.7	G	U	T	A	CID	LIT	6	73.6	IIINRQEPLHQVWLATK	2059.2	K	Q	4.5	0.0	45.5	6.0
P27838	12213.7	G	U	T	A	CID	LIT	6	73.6	LADQLWLTIEER	1486.8	R	L	3.6	0.8	58.8	13.4
P27838	12213.7	G	U	T	A	CID	LIT	6	73.6	MNDSEFHR	1035.4	-	L	2.7	0.0	64.4	0.0
P27838	12213.7	G	U	T	A	CID	LIT	6	73.6	QGGYHFDLKGDEWICDR	2095.9	K	S	3.1	0.0	18.5	7.0
P27838	12213.7	G	U	T	A	CID	LIT	6	73.6	SGETFWDLLEQAATQQAGETVSFR	2671.3	R	-	5.6	0.0	104.0	10.4
P27838	12213.7	G	U	A	A	CID	LIT	5	26.4	DLLEQAATQQAGETVSFR	1964.0	W	-	5.0	0.0	78.1	13.6
P27838	12213.7	G	U	A	A	CID	LIT	5	26.4	DSEFHRLA	974.5	N	D	1.6	0.5	18.2	14.0
P27838	12213.7	G	U	A	A	CID	LIT	5	26.4	EQAATQQAGETVSFR	1622.8	L	-	4.1	0.8	76.9	14.9
P27838	12213.7	G	U	A	A	CID	LIT	5	26.4	MNDSEFHRLA	1219.6	-	D	3.1	0.9	39.9	12.3
P27838	12213.7	G	U	A	A	CID	LIT	5	26.4	NDSEFHRLA	1088.5	M	D	0.0	0.0	29.3	13.4
P27838	12213.7	G	U	T	B	CID	LIT	5	42.5	GDEWICDR	1050.4	K	S	2.6	0.0	32.2	3.0
P27838	12213.7	G	U	T	B	CID	LIT	5	42.5	IIINR	628.4	K	Q	1.4	0.4	17.4	15.9
P27838	12213.7	G	U	T	B	CID	LIT	5	42.5	LADQLWLTIEER	1486.8	R	L	4.0	0.7	71.7	13.0
P27838	12213.7	G	U	T	B	CID	LIT	5	42.5	MNDSEFHR	1035.4	-	L	3.0	0.0	55.6	0.0
P27838	12213.7	G	U	T	B	CID	LIT	5	42.5	QEPLHQVWLATK	1449.8	R	Q	2.6	0.0	30.0	10.8
P27838	12213.7	G	T	A	B	CID	LIT	5	36.8	DLLEQAATQQAGETVSFR	1964.0	W	-	4.7	0.9	74.3	13.6
P27838	12213.7	G	T	A	B	CID	LIT	5	36.8	DQLWLTIEERL	1415.8	A	D	3.7	0.6	41.1	16.1
P27838	12213.7	G	T	A	B	CID	LIT	5	36.8	DSEFHRLA	974.5	N	D	1.7	0.0	28.2	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P27838	12213.7	G	T	A	B	CID	LIT	5	36.8	EQAATQQAGETVSFR	1622.8	L	-	3.4	0.8	55.0	14.9
P27838	12213.7	G	T	A	B	CID	LIT	5	36.8	MNDSEFHRLA	1219.6	-	D	2.4	0.7	33.6	12.0
P27838	12213.7	G	U	A	B	CID	LIT	6	52.8	DLLEQAATQQAGETVSFR	1964.0	W	-	5.8	0.8	72.9	13.2
P27838	12213.7	G	U	A	B	CID	LIT	6	52.8	DQLWLTIEERL	1415.8	A	D	3.7	0.6	36.7	16.1
P27838	12213.7	G	U	A	B	CID	LIT	6	52.8	DSEFHRLA	974.5	N	D	1.7	0.0	24.0	14.0
P27838	12213.7	G	U	A	B	CID	LIT	6	52.8	EPLHQVWLATKQGGYHF	2011.0	Q	D	3.0	0.0	18.4	14.9
P27838	12213.7	G	U	A	B	CID	LIT	6	52.8	EQAATQQAGETVSFR	1622.8	L	-	3.9	0.0	90.2	14.6
P27838	12213.7	G	U	A	B	CID	LIT	6	52.8	MNDSEFHRLA	1219.6	-	D	2.9	0.0	31.9	12.0
P27838	12213.7	S	U	T	C	CID	LIT	2	38.7	IIINRQEPLHQVWLATK	2059.2	K	Q	3.6	0.9	25.4	11.5
P27838	12213.7	S	U	T	C	CID	LIT	2	38.7	SGETFWDLLEQAATQQAGETVSFR	2671.3	R	-	4.9	0.0	74.0	17.0
P27838	12213.7	S	U	T	B	ETD+CID	LIT	2	38.7	IIINRQEPLHQVWLATK	2059.2	K	Q	0.0	0.0	31.5	11.5
P27838	12213.7	S	U	T	B	ETD+CID	LIT	2	38.7	SGETFWDLLEQAATQQAGETVSFR	2671.3	R	-	0.0	0.0	98.5	18.1
P27838	12213.7	S	U	T	B	ETD+CID	LIT	2	38.7	IIINRQEPLHQVWLATK	2059.2	K	Q	3.4	0.8	0.0	0.0
P27838	12213.7	S	U	T	B	ETD+CID	LIT	2	38.7	SGETFWDLLEQAATQQAGETVSFR	2671.3	R	-	5.6	0.7	0.0	0.0
P27838	12213.7	S	U	T	B	ETD+CID	LIT	2	38.7	IIINRQEPLHQVWLATK	2059.2	K	Q	3.4	0.8	31.5	11.5
P27838	12213.7	S	U	T	B	ETD+CID	LIT	2	38.7	SGETFWDLLEQAATQQAGETVSFR	2671.3	R	-	5.4	0.7	98.5	18.1
P27838	12213.7	S	U	T	C	ETD+CID	LIT	2	38.7	IIINRQEPLHQVWLATK	2059.2	K	Q	3.9	0.9	24.4	11.1
P27838	12213.7	S	U	T	C	ETD+CID	LIT	2	38.7	SGETFWDLLEQAATQQAGETVSFR	2671.3	R	-	3.4	0.5	0.0	0.0
P27838	12213.7	S	U	T	B	HCD	FT	2	38.7	IIINRQEPLHQVWLATK	2059.2	K	Q	0.0	0.0	31.5	11.5
P27838	12213.7	S	U	T	B	HCD	FT	2	38.7	SGETFWDLLEQAATQQAGETVSFR	2671.3	R	-	0.0	0.0	98.5	18.1
P32156	12246.7	G	T	A	A	CID	LIT	2	31.7	DKARNLLFAMVEIES	1735.9	L	E	2.2	0.2	0.0	0.0
P32156	12246.7	G	T	A	A	CID	LIT	2	31.7	ELEAVLKSHGAHNYAIYL	2028.1	P	D	1.9	0.7	0.0	0.0
P0A9I8	12266.1	G	U	T	A	CID	LIT	5	45.4	FRLSDGLCMEDEQFSVK	2060.9	R	H	3.7	0.5	18.1	9.5
P0A9I8	12266.1	G	U	T	A	CID	LIT	5	45.4	GLIAEHQGELWVASPLKK	1976.1	R	Q	5.9	0.7	65.8	9.5
P0A9I8	12266.1	G	U	T	A	CID	LIT	5	45.4	HYEAR	675.3	K	V	1.9	0.0	21.3	9.0
P0A9I8	12266.1	G	U	T	A	CID	LIT	5	45.4	LSDGLCMEDEQFSVK	1757.8	R	H	3.4	0.0	72.1	3.0
P0A9I8	12266.1	G	U	T	A	CID	LIT	5	45.4	VKDGVVQLR	1013.6	R	-	3.0	0.6	54.8	14.0
P0A9I8	12266.1	G	U	A	A	CID	LIT	4	31.5	DEQFSVKHY	1152.5	E	E	2.1	0.5	8.2	13.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9I8	12266.1	G	U	A	A	CID	LIT	4	31.5	DEQFSVKHYEARVK	1735.9	E	D	3.7	0.8	46.2	15.3
P0A9I8	12266.1	G	U	A	A	CID	LIT	4	31.5	DEQVAIFRPYHS	1461.7	G	D	4.2	0.6	37.6	14.1
P0A9I8	12266.1	G	U	A	A	CID	LIT	4	31.5	DGVVQLRG	843.5	K	-	2.5	0.3	12.2	14.8
P0A9I8	12266.1	S	U	T	A	CID	LIT	2	30.6	GLIAEHQGELWVASPLKK	1976.1	R	Q	3.9	0.8	39.0	13.6
P0A9I8	12266.1	S	U	T	A	CID	LIT	2	30.6	LSDGLCMEDEQFSVK	1757.8	R	H	3.6	0.5	74.2	9.5
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	AAGANKVAVIK	1041.6	K	A	3.6	0.8	48.7	9.0
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	ALEEAGAEVEVK	1244.6	K	-	4.1	0.7	56.5	13.8
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	DLVESAPAALK	1113.6	K	E	3.0	0.0	29.8	10.4
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	DLVESAPAALKEGVSK	1613.9	K	D	4.4	0.6	51.5	14.0
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	EAKDLVESAPAALK	1441.8	K	E	4.0	0.5	64.5	11.1
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	FGVSAAAAVAVAAGPVEAAEEK	2015.0	K	T	2.1	0.5	0.0	0.0
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	GATGLGLK	716.4	R	E	2.2	0.2	31.2	16.6
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	GATGLGLKEAK	1044.6	R	D	3.0	0.5	49.2	12.6
P0A7K2	12277.0	G	U	T	A	CID	LIT	9	66.1	TEFDVILK	964.5	K	A	1.9	0.5	10.5	10.8
P0A7K2	12277.0	G	T	T	A	CID	LIT	5	37.2	AAGANKVAVIK	1041.6	K	A	3.6	0.6	41.8	9.0
P0A7K2	12277.0	G	T	T	A	CID	LIT	5	37.2	ALEEAGAEVEVK	1244.6	K	-	3.4	0.6	48.1	13.8
P0A7K2	12277.0	G	T	T	A	CID	LIT	5	37.2	DLVESAPAALK	1113.6	K	E	2.4	0.0	33.9	10.4
P0A7K2	12277.0	G	T	T	A	CID	LIT	5	37.2	GATGLGLK	716.4	R	E	2.0	0.2	26.2	16.5
P0A7K2	12277.0	G	T	T	A	CID	LIT	5	37.2	GATGLGLKEAK	1044.6	R	D	2.6	0.7	20.0	12.6
P0A7K2	12277.0	G	U	A	A	CID	LIT	2	24.0	DLVESAPAALKEGVSK	1613.9	K	D	3.8	0.6	52.8	14.5
P0A7K2	12277.0	G	U	A	A	CID	LIT	2	24.0	DQIIEAVAAMSVM	1377.7	K	D	2.4	0.8	49.9	15.4
P0A7K2	12277.0	G	T	T	B	CID	LIT	5	38.0	AAGANKVAVIK	1041.6	K	A	3.6	0.4	53.6	9.0
P0A7K2	12277.0	G	T	T	B	CID	LIT	5	38.0	ALEEAGAEVEVK	1244.6	K	-	4.3	0.6	66.0	14.1
P0A7K2	12277.0	G	T	T	B	CID	LIT	5	38.0	DLVESAPAALK	1113.6	K	E	1.8	0.0	17.5	10.4
P0A7K2	12277.0	G	T	T	B	CID	LIT	5	38.0	GATGLGLKEAK	1044.6	R	D	2.6	0.4	18.0	12.6
P0A7K2	12277.0	G	T	T	B	CID	LIT	5	38.0	KALEEAGAEVEVK	1372.7	K	-	3.8	0.4	35.6	12.8
P0A7K2	12277.0	G	T	A	B	CID	LIT	6	81.8	DDAEALKKAL	1073.6	K	E	2.2	0.3	14.9	16.2
P0A7K2	12277.0	G	T	A	B	CID	LIT	6	81.8	DLVESAPAALKEGVSK	1613.9	K	D	4.3	0.7	79.5	15.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7K2	12277.0	G	T	A	B	CID	LIT	6	81.8	DQIIEAVAAMSVM	1377.7	K	D	3.4	0.8	69.1	15.4
P0A7K2	12277.0	G	T	A	B	CID	LIT	6	81.8	DVILKAAGANKVAVIKAVRGATGLGLKEAK	2961.8	F	D	3.7	0.0	26.1	0.0
P0A7K2	12277.0	G	T	A	B	CID	LIT	6	81.8	DVVELISAM	976.5	M	E	2.9	0.7	30.5	15.6
P0A7K2	12277.0	G	T	A	B	CID	LIT	6	81.8	EKFGVSAAAAVAVAAGPVEAA	1886.0	E	E	2.3	0.2	0.0	0.0
P0A7K2	12277.0	G	T	A	B	CID	LIT	6	81.8	ESAPAALKEGVSK	1286.7	V	D	2.7	0.7	46.7	15.2
P0A7K2	12277.0	G	U	A	B	CID	LIT	5	57.0	DDAEALKKAL	1073.6	K	E	2.2	0.2	29.1	16.2
P0A7K2	12277.0	G	U	A	B	CID	LIT	5	57.0	DLVESAPAALKEGVSK	1613.9	K	D	4.0	0.7	69.1	14.5
P0A7K2	12277.0	G	U	A	B	CID	LIT	5	57.0	DQIIEAVAAMSVM	1377.7	K	D	3.1	0.0	86.5	15.2
P0A7K2	12277.0	G	U	A	B	CID	LIT	5	57.0	DVILKAAGANKVAVIKAVRGATGLGLKEAK	2961.8	F	D	3.0	0.0	17.1	0.0
P0A7K2	12277.0	G	U	A	B	CID	LIT	5	57.0	ESAPAALKEGVSK	1286.7	V	D	2.7	0.0	36.8	14.3
P0A7K2	12277.0	S	U	T	A	CID	LIT	4	29.8	ALEEAGAEVEVK	1244.6	K	-	3.3	0.5	31.7	16.5
P0A7K2	12277.0	S	U	T	A	CID	LIT	4	29.8	DLVESAPAALKEGVSK	1613.9	K	D	4.9	0.7	51.6	17.4
P0A7K2	12277.0	S	U	T	A	CID	LIT	4	29.8	DLVESAPAALKEGVSKDDAEALK	2356.2	K	K	3.2	0.0	23.1	17.2
P0A7K2	12277.0	S	U	T	A	CID	LIT	4	29.8	EGVSKDDAEALKK	1389.7	K	A	3.9	0.3	41.8	17.1
P0A7K2	12277.0	S	U	T	B	CID	LIT	6	32.2	ALEEAGAEVEVK	1244.6	K	-	3.3	0.4	38.0	16.5
P0A7K2	12277.0	S	U	T	B	CID	LIT	6	32.2	DLVESAPAALK	1113.6	K	E	2.7	0.7	35.3	12.6
P0A7K2	12277.0	S	U	T	B	CID	LIT	6	32.2	DLVESAPAALKEGVSK	1613.9	K	D	4.2	0.5	38.3	17.4
P0A7K2	12277.0	S	U	T	B	CID	LIT	6	32.2	DLVESAPAALKEGVSKDDAEALK	2356.2	K	K	3.4	0.7	15.3	17.1
P0A7K2	12277.0	S	U	T	B	CID	LIT	6	32.2	EAKDLVESAPAALK	1441.8	K	E	2.2	0.3	10.4	15.8
P0A7K2	12277.0	S	U	T	B	CID	LIT	6	32.2	EGVSKDDAEALKK	1389.7	K	A	4.2	0.5	56.5	17.2
P0A7K2	12277.0	S	U	T	C	CID	LIT	7	57.0	ALEEAGAEVEVK	1244.6	K	-	3.5	0.3	26.1	17.2
P0A7K2	12277.0	S	U	T	C	CID	LIT	7	57.0	DLVESAPAALK	1113.6	K	E	2.4	0.6	18.9	13.4
P0A7K2	12277.0	S	U	T	C	CID	LIT	7	57.0	DLVESAPAALKEGVSKDDAEALK	2356.2	K	K	3.0	0.5	13.3	16.9
P0A7K2	12277.0	S	U	T	C	CID	LIT	7	57.0	EAKDLVESAPAALK	1441.8	K	E	2.7	0.3	0.0	0.0
P0A7K2	12277.0	S	U	T	C	CID	LIT	7	57.0	EGVSKDDAEALK	1261.6	K	K	3.4	0.5	53.8	16.0
P0A7K2	12277.0	S	U	T	C	CID	LIT	7	57.0	EGVSKDDAEALKK	1389.7	K	A	4.4	0.4	58.2	17.1
P0A7K2	12277.0	S	U	T	C	CID	LIT	7	57.0	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	5.2	0.6	37.1	17.7
P0A7K2	12277.0	S	U	T	A	ETD	LIT	3	45.5	ALEEAGAEVEVK	1244.6	K	-	2.7	0.2	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7K2	12277.0	S	U	T	A	ETD	LIT	3	45.5	EGVSKDDAEALKK	1389.7	K	A	6.5	0.4	83.0	18.1
P0A7K2	12277.0	S	U	T	A	ETD	LIT	3	45.5	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	4.8	0.0	36.0	17.9
P0A7K2	12277.0	S	U	T	B	ETD	LIT	3	44.6	DLVESAPAALK	1113.6	K	E	2.6	0.2	15.2	12.6
P0A7K2	12277.0	S	U	T	B	ETD	LIT	3	44.6	EGVSKDDAEALKK	1389.7	K	A	6.7	0.6	88.1	18.2
P0A7K2	12277.0	S	U	T	B	ETD	LIT	3	44.6	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	3.9	0.0	27.9	17.8
P0A7K2	12277.0	S	U	T	C	ETD	LIT	5	57.0	ALEEAGAEVEVK	1244.6	K	-	3.6	0.4	38.1	16.8
P0A7K2	12277.0	S	U	T	C	ETD	LIT	5	57.0	DLVESAPAALKEGVSKDDAEALK	2356.2	K	K	4.0	0.6	32.5	17.0
P0A7K2	12277.0	S	U	T	C	ETD	LIT	5	57.0	EAKDLVESAPAALK	1441.8	K	E	4.6	0.4	61.6	14.5
P0A7K2	12277.0	S	U	T	C	ETD	LIT	5	57.0	EGVSKDDAEALKK	1389.7	K	A	7.1	0.5	84.2	18.2
P0A7K2	12277.0	S	U	T	C	ETD	LIT	5	57.0	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	0.0	0.0	25.6	17.7
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	2	35.5	EGVSKDDAEALKK	1389.7	K	A	0.0	0.0	99.0	17.2
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	2	35.5	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	0.0	0.0	23.7	17.9
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	4	54.5	ALEEAGAEVEVK	1244.6	K	-	0.0	0.0	26.2	16.5
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	4	54.5	DLVESAPAALKEGVSK	1613.9	K	D	0.0	0.0	70.7	17.4
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	4	54.5	EGVSKDDAEALKK	1389.7	K	A	0.0	0.0	99.0	17.2
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	4	54.5	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	0.0	0.0	55.5	17.8
P0A7K2	12277.0	S	U	T	A	ETD+CID	LIT	4	54.5	ALEEAGAEVEVK	1244.6	K	-	3.8	0.6	40.2	16.6
P0A7K2	12277.0	S	U	T	A	ETD+CID	LIT	4	54.5	DLVESAPAALKEGVSKDDAEALK	2356.2	K	K	3.9	0.8	22.2	17.2
P0A7K2	12277.0	S	U	T	A	ETD+CID	LIT	4	54.5	EGVSKDDAEALKK	1389.7	K	A	4.4	0.5	55.7	16.9
P0A7K2	12277.0	S	U	T	A	ETD+CID	LIT	4	54.5	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	4.6	0.5	30.0	17.5
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	2	34.7	ALEEAGAEVEVK	1244.6	K	-	3.4	0.4	0.0	0.0
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	2	34.7	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	3.6	0.5	0.0	0.0
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	5	54.5	ALEEAGAEVEVK	1244.6	K	-	3.4	0.4	26.2	16.5
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	5	54.5	DLVESAPAALKEGVSK	1613.9	K	D	4.5	0.0	70.7	17.4
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	5	54.5	DLVESAPAALKEGVSKDDAEALK	2356.2	K	K	3.3	0.0	16.5	16.8
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	5	54.5	EGVSKDDAEALKK	1389.7	K	A	6.7	0.5	99.0	17.2
P0A7K2	12277.0	S	U	T	B	ETD+CID	LIT	5	54.5	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	3.6	0.5	55.5	17.8
P0A7K2	12277.0	S	U	T	C	ETD+CID	LIT	5	54.5	ALEEAGAEVEVK	1244.6	K	-	3.6	0.4	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7K2	12277.0	S	U	T	C	ETD+CID	LIT	5	54.5	DLVESAPAALK	1113.6	K	E	2.5	0.0	22.2	12.3
P0A7K2	12277.0	S	U	T	C	ETD+CID	LIT	5	54.5	DLVESAPAALKEGVSKDDAEALK	2356.2	K	K	3.5	0.5	23.6	17.2
P0A7K2	12277.0	S	U	T	C	ETD+CID	LIT	5	54.5	EGVSKDDAEALKK	1389.7	K	A	4.3	0.4	0.0	0.0
P0A7K2	12277.0	S	U	T	C	ETD+CID	LIT	5	54.5	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	4.0	0.4	41.9	17.5
P0A7K2	12277.0	S	U	T	B	HCD	FT	4	54.5	ALEEAGAEVEVK	1244.6	K	-	0.0	0.0	26.2	16.5
P0A7K2	12277.0	S	U	T	B	HCD	FT	4	54.5	DLVESAPAALKEGVSK	1613.9	K	D	0.0	0.0	70.7	17.4
P0A7K2	12277.0	S	U	T	B	HCD	FT	4	54.5	EGVSKDDAEALKK	1389.7	K	A	0.0	0.0	56.4	17.1
P0A7K2	12277.0	S	U	T	B	HCD	FT	4	54.5	FGVSAAAAVAVAAGPVEAAEEKTEFDVILK	2960.6	K	A	0.0	0.0	55.5	17.8
P0A9R4	12312.7	G	T	T	A	CID	LIT	4	55.0	IVILPHQDLCPDGAVLEANSGETILDAALR	3200.7	K	N	6.4	0.6	54.1	9.5
P0A9R4	12312.7	G	T	T	A	CID	LIT	4	55.0	SCACTTCHCIVR	1524.6	K	E	3.2	0.0	59.5	0.0
P0A9R4	12312.7	G	T	T	A	CID	LIT	4	55.0	VTDEDLVVEIPR	1384.7	R	Y	3.1	0.5	47.1	10.4
P0A9R4	12312.7	G	T	T	A	CID	LIT	4	55.0	YTINHAR	874.5	R	E	2.1	0.8	37.5	14.1
P0A9R4	12312.7	G	T	T	B	CID	LIT	5	45.0	LSCQAR	734.4	R	V	2.0	0.6	0.0	0.0
P0A9R4	12312.7	G	T	T	B	CID	LIT	5	45.0	NGIEIEHACEK	1299.6	R	S	3.1	0.4	44.0	10.4
P0A9R4	12312.7	G	T	T	B	CID	LIT	5	45.0	SCACTTCHCIVR	1524.6	K	E	3.0	0.0	19.7	0.0
P0A9R4	12312.7	G	T	T	B	CID	LIT	5	45.0	VTDEDLVVEIPR	1384.7	R	Y	2.2	0.2	11.0	11.8
P0A9R4	12312.7	G	T	T	B	CID	LIT	5	45.0	YTINHAREH	1140.6	R	-	2.7	0.8	24.5	11.5
P0A9R4	12312.7	G	T	A	B	CID	LIT	4	55.9	DKAWGLEPESRLSCQARVT	2203.1	L	D	2.7	0.3	14.4	14.6
P0A9R4	12312.7	G	T	A	B	CID	LIT	4	55.9	DLVVEIPRYTINHAREH	2062.1	E	-	3.7	0.0	13.4	15.2
P0A9R4	12312.7	G	T	A	B	CID	LIT	4	55.9	EKSCACTTCHCIVREGF	2114.9	C	D	2.7	0.0	28.9	6.0
P0A9R4	12312.7	G	T	A	B	CID	LIT	4	55.9	PKIVILPHQ	1044.7	M	D	0.0	0.0	63.5	0.0
P0A9R4	12312.7	G	U	A	B	CID	LIT	4	55.9	DKAWGLEPESRLSCQARVT	2203.1	L	D	1.6	0.4	18.0	15.2
P0A9R4	12312.7	G	U	A	B	CID	LIT	4	55.9	DLVVEIPRYTINHAREH	2062.1	E	-	3.4	0.0	17.4	15.3
P0A9R4	12312.7	G	U	A	B	CID	LIT	4	55.9	EKSCACTTCHCIVREGF	2114.9	C	D	3.1	0.0	27.4	3.0
P0A9R4	12312.7	G	U	A	B	CID	LIT	4	55.9	PKIVILPHQ	1044.7	M	D	0.0	0.0	60.6	0.0
P0A9R4	12312.7	S	U	T	B	CID	LIT	3	46.8	EGFDSLPESSEQEDDMLDKAWGLEPESR	3196.4	R	L	4.0	0.0	34.8	14.0
P0A9R4	12312.7	S	U	T	B	CID	LIT	3	46.8	SCACTTCHCIVR	1524.6	K	E	3.9	0.0	104.0	4.8
P0A9R4	12312.7	S	U	T	B	CID	LIT	3	46.8	VTDEDLVVEIPR	1384.7	R	Y	3.7	0.8	43.8	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9R4	12312.7	S	U	T	C	CID	LIT	2	36.0	EGFDSLPESSEQEDDMLDKAWGLEPESR	3196.4	R	L	3.6	0.0	47.8	14.0
P0A9R4	12312.7	S	U	T	C	CID	LIT	2	36.0	SCACTTCHCIVR	1524.6	K	E	3.7	0.0	89.8	3.0
P0A9R4	12312.7	S	U	T	B	ETD	LIT	2	17.1	VTDEDLVVEIPR	1384.7	R	Y	1.6	0.0	35.2	14.5
P0A9R4	12312.7	S	U	T	B	ETD	LIT	2	17.1	YTINHAR	874.5	R	E	1.4	0.4	22.1	16.9
P0A9R4	12312.7	S	U	T	C	ETD	LIT	3	46.8	EGFDSLPESSEQEDDMLDKAWGLEPESR	3196.4	R	L	3.9	0.0	19.8	14.0
P0A9R4	12312.7	S	U	T	C	ETD	LIT	3	46.8	SCACTTCHCIVR	1524.6	K	E	3.3	0.0	49.3	3.0
P0A9R4	12312.7	S	U	T	C	ETD	LIT	3	46.8	VTDEDLVVEIPR	1384.7	R	Y	1.6	0.7	31.9	13.6
P0A9R4	12312.7	S	U	T	B	ETD+CID	LIT	2	36.0	EGFDSLPESSEQEDDMLDKAWGLEPESR	3196.4	R	L	0.0	0.0	28.0	14.1
P0A9R4	12312.7	S	U	T	B	ETD+CID	LIT	2	36.0	SCACTTCHCIVR	1524.6	K	E	0.0	0.0	104.0	4.8
P0A9R4	12312.7	S	U	T	B	ETD+CID	LIT	3	46.8	EGFDSLPESSEQEDDMLDKAWGLEPESR	3196.4	R	L	3.3	0.0	28.0	14.1
P0A9R4	12312.7	S	U	T	B	ETD+CID	LIT	3	46.8	SCACTTCHCIVR	1524.6	K	E	3.4	0.7	104.0	4.8
P0A9R4	12312.7	S	U	T	B	ETD+CID	LIT	3	46.8	VTDEDLVVEIPR	1384.7	R	Y	3.3	0.4	11.5	13.6
P0A9R4	12312.7	S	U	T	C	ETD+CID	LIT	3	46.8	EGFDSLPESSEQEDDMLDKAWGLEPESR	3196.4	R	L	3.2	0.0	43.2	14.1
P0A9R4	12312.7	S	U	T	C	ETD+CID	LIT	3	46.8	SCACTTCHCIVR	1524.6	K	E	4.0	0.0	78.8	3.0
P0A9R4	12312.7	S	U	T	C	ETD+CID	LIT	3	46.8	VTDEDLVVEIPR	1384.7	R	Y	3.6	0.0	34.9	13.0
P0A9R4	12312.7	S	U	T	B	HCD	FT	2	36.0	EGFDSLPESSEQEDDMLDKAWGLEPESR	3196.4	R	L	0.0	0.0	28.0	14.1
P0A9R4	12312.7	S	U	T	B	HCD	FT	2	36.0	SCACTTCHCIVR	1524.6	K	E	0.0	0.0	104.0	4.8
P69488	12313.1	G	U	T	A	CID	LIT	2	34.8	SSNTASVVVLCTAPDEATAQDLAAK	2519.2	K	V	5.1	0.7	62.2	11.1
P69488	12313.1	G	U	T	A	CID	LIT	2	34.8	TTVSHQQALLECLK	1627.8	K	S	4.0	0.0	38.9	13.2
P0AFJ1	12327.5	G	U	T	A	CID	LIT	5	38.7	DANGNLLADGDSVTIIK	1715.9	K	D	3.8	0.8	41.2	12.0
P0AFJ1	12327.5	G	U	T	A	CID	LIT	5	38.7	IDGFGPMK	880.4	K	L	1.8	0.6	6.4	10.8
P0AFJ1	12327.5	G	U	T	A	CID	LIT	5	38.7	LKSEFVK	850.5	K	K	2.2	0.6	27.7	10.4
P0AFJ1	12327.5	G	U	T	A	CID	LIT	5	38.7	LVEGDHNIDCK	1299.6	R	I	2.8	0.8	35.2	10.4
P0AFJ1	12327.5	G	U	T	A	CID	LIT	5	38.7	LVEGDHNIDCKIDGFGPMK	2145.0	R	L	4.4	0.0	37.3	9.5
P0AFJ1	12327.5	G	T	T	A	CID	LIT	7	46.8	DANGNLLADGDSVTIIK	1715.9	K	D	3.8	0.7	24.5	12.0
P0AFJ1	12327.5	G	T	T	A	CID	LIT	7	46.8	IDGFGPMK	864.4	K	L	2.3	0.5	13.0	14.1
P0AFJ1	12327.5	G	T	T	A	CID	LIT	7	46.8	IDGFGPMKLK	1121.6	K	S	2.5	0.6	10.7	12.3
P0AFJ1	12327.5	G	T	T	A	CID	LIT	7	46.8	LKSEFVK	850.5	K	K	2.3	0.8	22.5	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFJ1	12327.5	G	T	T	A	CID	LIT	7	46.8	LVEGDHNIDCK	1299.6	R	I	3.6	0.7	49.2	9.5
P0AFJ1	12327.5	G	T	T	A	CID	LIT	7	46.8	LVEGDHNIDCKIDGFGPMK	2161.0	R	L	3.5	0.3	6.9	10.0
P0AFJ1	12327.5	G	T	T	A	CID	LIT	7	46.8	VKGSSSMLK	936.5	K	I	2.3	0.7	18.8	13.8
P0AFJ1	12327.5	G	U	A	A	CID	LIT	5	56.8	DELIVK	716.4	S	D	1.6	0.4	15.0	17.3
P0AFJ1	12327.5	G	U	A	A	CID	LIT	5	56.8	DGDSVTIIK	947.5	A	D	3.2	0.7	35.4	14.3
P0AFJ1	12327.5	G	U	A	A	CID	LIT	5	56.8	DHNIDCKI	1014.5	G	D	2.8	0.0	39.4	13.0
P0AFJ1	12327.5	G	U	A	A	CID	LIT	5	56.8	DLKVKGSSSMLKIGTKVKNIRLVEG	2716.6	K	D	2.5	0.0	27.4	3.0
P0AFJ1	12327.5	G	U	A	A	CID	LIT	5	56.8	SLPHCPKCNSEYTYE	1884.8	M	D	0.0	0.0	29.7	7.0
P0AFJ1	12327.5	G	T	A	A	CID	LIT	3	20.7	DELIVK	716.4	S	D	1.7	0.3	12.0	17.3
P0AFJ1	12327.5	G	T	A	A	CID	LIT	3	20.7	DGDSVTIIK	947.5	A	D	3.4	0.8	32.2	14.3
P0AFJ1	12327.5	G	T	A	A	CID	LIT	3	20.7	DHNIDCKI	1014.5	G	D	3.1	0.5	40.4	13.0
P0AFJ1	12327.5	G	T	T	B	CID	LIT	4	26.1	GSSSMLKIGTK	1108.6	K	V	1.7	0.0	34.2	13.0
P0AFJ1	12327.5	G	T	T	B	CID	LIT	4	26.1	LVEGDHNIDCK	1299.6	R	I	3.3	0.0	23.2	10.4
P0AFJ1	12327.5	G	T	T	B	CID	LIT	4	26.1	VKGSSSMLK	936.5	K	I	2.4	0.7	21.7	13.8
P0AFJ1	12327.5	G	T	T	B	CID	LIT	4	26.1	VKNIR	629.4	K	L	0.0	0.0	24.5	15.1
P0AFJ1	12327.5	G	T	A	B	CID	LIT	5	34.2	DAEPAQES	846.3	N	D	1.7	0.7	30.4	10.8
P0AFJ1	12327.5	G	T	A	B	CID	LIT	5	34.2	DELIVK	716.4	S	D	1.9	0.4	13.9	16.7
P0AFJ1	12327.5	G	T	A	B	CID	LIT	5	34.2	DGDSVTIIK	947.5	A	D	3.3	0.0	34.8	14.3
P0AFJ1	12327.5	G	T	A	B	CID	LIT	5	34.2	DSVTIIK	775.5	G	D	1.9	0.0	18.6	0.0
P0AFJ1	12327.5	G	T	A	B	CID	LIT	5	34.2	SLPHCPKCNSEYTYE	1884.8	M	D	0.0	0.0	28.8	7.0
P0AFJ1	12327.5	G	U	A	B	CID	LIT	3	50.5	DGFGPMKLKSEFVKKN	1825.0	I	-	2.2	0.3	10.8	14.9
P0AFJ1	12327.5	G	U	A	B	CID	LIT	3	50.5	DLKVKGSSSMLKIGTKVKNIRLVEG	2700.6	K	D	2.5	0.0	16.7	0.0
P0AFJ1	12327.5	G	U	A	B	CID	LIT	3	50.5	SLPHCPKCNSEYTYE	1884.8	M	D	0.0	0.0	26.1	7.0
P0AFJ1	12327.5	S	U	T	A	CID	LIT	2	27.9	DANGNLLADGDSVTIIKDLK	2072.1	K	V	4.2	0.5	33.9	17.7
P0AFJ1	12327.5	S	U	T	A	CID	LIT	2	27.9	LVEGDHNIDCK	1299.6	R	I	3.1	0.4	28.3	12.6
P0AFJ1	12327.5	S	U	T	B	CID	LIT	2	27.9	DANGNLLADGDSVTIIKDLK	2072.1	K	V	4.2	0.5	33.7	17.6
P0AFJ1	12327.5	S	U	T	B	CID	LIT	2	27.9	LVEGDHNIDCK	1299.6	R	I	3.7	0.8	38.7	12.6
P0AFJ1	12327.5	S	U	T	C	CID	LIT	2	27.9	DANGNLLADGDSVTIIKDLK	2072.1	K	V	4.0	0.4	42.0	17.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFJ1	12327.5	S	U	T	C	CID	LIT	2	27.9	LVEGDHNIDCK	1299.6	R	I	3.3	0.7	51.1	11.8
P0AFJ1	12327.5	S	U	T	B	ETD	LIT	2	18.0	LVEGDHNIDCK	1299.6	R	I	4.6	0.7	62.8	11.8
P0AFJ1	12327.5	S	U	T	B	ETD	LIT	2	18.0	VKGSSSMLK	936.5	K	I	1.0	0.4	19.8	16.3
P0AFJ1	12327.5	S	U	T	C	ETD	LIT	3	27.9	DANGNLLADGDSVTIIK	1715.9	K	D	2.3	0.2	55.0	19.0
P0AFJ1	12327.5	S	U	T	C	ETD	LIT	3	27.9	DANGNLLADGDSVTIIKDLK	2072.1	K	V	4.5	0.4	11.5	17.0
P0AFJ1	12327.5	S	U	T	C	ETD	LIT	3	27.9	LVEGDHNIDCK	1299.6	R	I	3.0	0.5	25.8	12.0
P0AFJ1	12327.5	S	U	T	A	ETD+CID	LIT	2	27.9	DANGNLLADGDSVTIIKDLK	2073.1	K	V	4.4	0.5	29.5	18.2
P0AFJ1	12327.5	S	U	T	A	ETD+CID	LIT	2	27.9	LVEGDHNIDCK	1299.6	R	I	4.8	0.6	71.6	12.6
P0A881	12337.6	G	T	T	A	CID	LIT	2	16.7	HQEWLR	868.4	R	F	2.0	0.6	23.6	11.1
P0A881	12337.6	G	T	T	A	CID	LIT	2	16.7	NELGAGIATITR	1215.7	K	G	1.7	0.4	0.0	0.0
P0A881	12337.6	G	T	T	B	CID	LIT	2	16.7	NELGAGIATITR	1215.7	K	G	1.9	0.2	0.0	0.0
P0A881	12337.6	G	T	T	B	CID	LIT	2	16.7	NELGAGIATITRGSNSLK	1802.0	K	A	2.5	0.3	1.3	11.8
P64506	12360.8	G	U	T	A	CID	LIT	2	25.7	MSLAPFIER	1063.6	K	A	2.8	0.5	23.9	13.8
P64506	12360.8	G	U	T	A	CID	LIT	2	25.7	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	5.0	0.7	95.3	13.4
P64506	12360.8	G	T	T	A	CID	LIT	4	36.3	DKWAFNR	936.5	K	E	1.9	0.6	14.3	12.3
P64506	12360.8	G	T	T	A	CID	LIT	4	36.3	FEVGKDK	822.4	R	W	2.1	0.1	15.8	13.8
P64506	12360.8	G	T	T	A	CID	LIT	4	36.3	MSLAPFIER	1063.6	K	A	3.3	0.7	33.4	13.8
P64506	12360.8	G	T	T	A	CID	LIT	4	36.3	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	5.0	0.0	113.0	13.4
P64506	12360.8	G	T	T	B	CID	LIT	2	25.7	MSLAPFIER	1063.6	K	A	1.8	0.3	0.3	14.0
P64506	12360.8	G	T	T	B	CID	LIT	2	25.7	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	5.6	0.0	100.0	12.8
P64506	12360.8	G	T	A	B	CID	LIT	5	65.5	DIAQKEVASGKTNAQPISVIQI	2310.3	N	D	5.2	0.7	63.1	12.8
P64506	12360.8	G	T	A	B	CID	LIT	5	65.5	DKWAFNRE	1065.5	K	E	2.0	0.6	14.1	14.5
P64506	12360.8	G	T	A	B	CID	LIT	5	65.5	DPNNPGEKMSLAPFIERA	1986.0	D	E	4.0	0.0	80.0	14.0
P64506	12360.8	G	T	A	B	CID	LIT	5	65.5	EEVMLTCRPGNALYVINPSTLVQYPLN	3091.6	R	D	3.9	0.0	38.4	15.7
P64506	12360.8	G	T	A	B	CID	LIT	5	65.5	EVMLTCRPGNALYVINPSTLVQYPLN	2962.5	E	D	4.1	0.0	34.6	15.4
P64506	12360.8	S	U	T	B	CID	LIT	3	36.3	FEVGKDKWAFNR	1496.8	R	E	3.2	0.4	24.7	17.3
P64506	12360.8	S	U	T	B	CID	LIT	3	36.3	MSLAPFIER	1063.6	K	A	2.5	0.2	27.4	16.4
P64506	12360.8	S	U	T	B	CID	LIT	3	36.3	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	5.3	0.0	95.7	19.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64506	12360.8	S	U	T	C	CID	LIT	2	25.7	MSLAPFIER	1063.6	K	A	2.8	0.4	37.1	16.4
P64506	12360.8	S	U	T	C	CID	LIT	2	25.7	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	5.1	0.8	88.0	19.0
P64506	12360.8	S	U	T	B	ETD+CID	LIT	2	25.7	MSLAPFIER	1063.6	K	A	0.0	0.0	36.2	16.4
P64506	12360.8	S	U	T	B	ETD+CID	LIT	2	25.7	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	0.0	0.0	106.0	19.4
P64506	12360.8	S	U	T	B	ETD+CID	LIT	2	25.7	MSLAPFIER	1063.6	K	A	2.6	0.7	36.2	16.4
P64506	12360.8	S	U	T	B	ETD+CID	LIT	2	25.7	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	5.9	0.7	106.0	19.4
P64506	12360.8	S	U	T	C	ETD+CID	LIT	2	25.7	MSLAPFIER	1063.6	K	A	3.0	0.4	24.3	16.4
P64506	12360.8	S	U	T	C	ETD+CID	LIT	2	25.7	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	5.3	0.8	95.7	19.0
P64506	12360.8	S	U	T	B	HCD	FT	2	25.7	MSLAPFIER	1063.6	K	A	0.0	0.0	36.2	16.4
P64506	12360.8	S	U	T	B	HCD	FT	2	25.7	TNAQPISVIQIDDPNNPGEK	2150.1	K	M	0.0	0.0	106.0	19.4
P0AB18	12392.8	G	U	T	A	CID	LIT	3	24.8	EIETDTEGYLK	1297.6	K	E	2.5	0.6	25.2	13.0
P0AB18	12392.8	G	U	T	A	CID	LIT	3	24.8	IAGLPKPVK	922.6	K	C	2.4	0.0	30.9	0.0
P0AB18	12392.8	G	U	T	A	CID	LIT	3	24.8	MLIFEGK	837.5	-	E	2.0	0.4	10.8	10.4
P0AB43	12397.1	G	U	T	A	CID	LIT	5	62.0	DDFSRVPEELMK	1465.7	K	G	3.0	0.3	18.4	10.8
P0AB43	12397.1	G	U	T	A	CID	LIT	5	62.0	DQTYLYVEKK	1286.7	R	D	2.4	0.3	9.5	11.8
P0AB43	12397.1	G	U	T	A	CID	LIT	5	62.0	GFGQPQLAMILPLDGR	1712.9	K	K	4.5	0.9	47.5	11.1
P0AB43	12397.1	G	U	T	A	CID	LIT	5	62.0	LVNADIEK	901.5	K	V	2.3	0.6	14.6	11.8
P0AB43	12397.1	G	U	T	A	CID	LIT	5	62.0	QALTEQGYYLQLPPPPEDLLK	2413.3	K	Q	3.7	0.5	37.8	14.0
P0AB43	12397.1	G	T	T	A	CID	LIT	4	25.9	KLVNADIEK	1029.6	K	V	3.1	0.4	27.6	13.8
P0AB43	12397.1	G	T	T	A	CID	LIT	4	25.9	LVNADIEK	901.5	K	V	2.0	0.6	7.2	11.5
P0AB43	12397.1	G	T	T	A	CID	LIT	4	25.9	QHLSVMGQK	1027.5	K	T	2.5	0.7	20.2	11.8
P0AB43	12397.1	G	T	T	A	CID	LIT	4	25.9	RDQTYLYVEK	1314.7	K	K	2.5	0.4	12.3	12.0
P0AB43	12397.1	G	U	T	B	CID	LIT	4	31.5	DQTYLYVEK	1158.6	R	K	2.2	0.7	19.7	11.1
P0AB43	12397.1	G	U	T	B	CID	LIT	4	31.5	GFGQPQLAMILPLDGR	1712.9	K	K	4.1	0.0	33.6	11.5
P0AB43	12397.1	G	U	T	B	CID	LIT	4	31.5	KLVNADIEK	1029.6	K	V	3.3	0.7	33.2	13.8
P0AB43	12397.1	G	U	T	B	CID	LIT	4	31.5	LVNADIEK	901.5	K	V	2.2	0.8	23.3	12.0
P0AB43	12397.1	G	T	A	B	CID	LIT	2	22.2	DLLKQHLSVMGQKT	1597.9	E	D	3.7	0.6	36.0	13.6
P0AB43	12397.1	G	T	A	B	CID	LIT	2	22.2	DQTYLYVEKK	1286.7	R	D	2.2	0.3	21.2	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AB43	12397.1	G	U	A	B	CID	LIT	2	22.2	DLLKQHLSVMGQKT	1597.9	E	D	3.6	0.6	17.5	11.5
P0AB43	12397.1	G	U	A	B	CID	LIT	2	22.2	DQTYLYVEKK	1286.7	R	D	2.8	0.5	30.5	12.0
P0AB43	12397.1	S	U	T	B	CID	LIT	4	53.7	DDFSRVPEELMK	1465.7	K	G	2.9	0.5	15.1	15.4
P0AB43	12397.1	S	U	T	B	CID	LIT	4	53.7	DQTYLYVEK	1158.6	R	K	1.8	0.4	0.0	0.0
P0AB43	12397.1	S	U	T	B	CID	LIT	4	53.7	GFGQPQLAMILPLDGR	1712.9	K	K	3.1	0.4	18.3	16.3
P0AB43	12397.1	S	U	T	B	CID	LIT	4	53.7	QALTEQGYYLQLPPPPEDLLK	2413.3	K	Q	4.2	0.7	48.7	17.9
P0AB43	12397.1	S	U	T	C	CID	LIT	5	54.6	DDFSRVPEELMK	1465.7	K	G	2.7	0.2	23.1	15.3
P0AB43	12397.1	S	U	T	C	CID	LIT	5	54.6	DQTYLYVEK	1158.6	R	K	2.3	0.3	0.0	0.0
P0AB43	12397.1	S	U	T	C	CID	LIT	5	54.6	GFGQPQLAMILPLDGR	1712.9	K	K	4.5	0.6	38.4	16.3
P0AB43	12397.1	S	U	T	C	CID	LIT	5	54.6	GFGQPQLAMILPLDGRK	1841.0	K	K	2.3	0.3	4.0	15.1
P0AB43	12397.1	S	U	T	C	CID	LIT	5	54.6	QALTEQGYYLQLPPPPEDLLK	2413.3	K	Q	3.2	0.0	48.2	17.9
P0AB43	12397.1	S	U	T	B	ETD	LIT	3	48.1	DDFSRVPEELMK	1465.7	K	G	2.3	0.5	27.7	15.4
P0AB43	12397.1	S	U	T	B	ETD	LIT	3	48.1	GFGQPQLAMILPLDGRK	1841.0	K	K	4.1	0.6	26.9	15.2
P0AB43	12397.1	S	U	T	B	ETD	LIT	3	48.1	VKQALTEQGYYLQLPPPPEDLLK	2640.4	K	Q	2.1	0.0	22.3	15.4
P0AB43	12397.1	S	U	T	C	ETD	LIT	4	35.2	DDFSRVPEELMK	1465.7	K	G	2.6	0.5	15.6	15.2
P0AB43	12397.1	S	U	T	C	ETD	LIT	4	35.2	DQTYLYVEK	1158.6	R	K	1.3	0.4	22.9	13.0
P0AB43	12397.1	S	U	T	C	ETD	LIT	4	35.2	GFGQPQLAMILPLDGR	1712.9	K	K	2.2	0.5	23.7	16.5
P0AB43	12397.1	S	U	T	C	ETD	LIT	4	35.2	KDDFSRVPEELMK	1593.8	K	G	2.7	0.4	13.9	17.2
P0AB43	12397.1	S	U	T	B	ETD+CID	LIT	2	26.9	DDFSRVPEELMK	1465.7	K	G	2.5	0.3	0.0	0.0
P0AB43	12397.1	S	U	T	B	ETD+CID	LIT	2	26.9	GFGQPQLAMILPLDGRK	1841.0	K	K	2.4	0.7	0.0	0.0
P0AB43	12397.1	S	U	T	B	ETD+CID	LIT	3	46.3	DDFSRVPEELMK	1465.7	K	G	2.5	0.3	12.6	15.2
P0AB43	12397.1	S	U	T	B	ETD+CID	LIT	3	46.3	GFGQPQLAMILPLDGRK	1841.0	K	K	2.4	0.7	8.0	14.6
P0AB43	12397.1	S	U	T	B	ETD+CID	LIT	3	46.3	QALTEQGYYLQLPPPPEDLLK	2413.3	K	Q	3.8	0.0	51.5	17.5
P0AB43	12397.1	S	U	T	C	ETD+CID	LIT	4	46.3	DDFSRVPEELMK	1465.7	K	G	2.1	0.3	2.4	15.4
P0AB43	12397.1	S	U	T	C	ETD+CID	LIT	4	46.3	GFGQPQLAMILPLDGR	1712.9	K	K	4.4	0.6	38.3	16.6
P0AB43	12397.1	S	U	T	C	ETD+CID	LIT	4	46.3	GFGQPQLAMILPLDGRK	1841.0	K	K	2.7	0.3	0.5	15.1
P0AB43	12397.1	S	U	T	C	ETD+CID	LIT	4	46.3	QALTEQGYYLQLPPPPEDLLK	2413.3	K	Q	3.5	0.6	56.3	18.6
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	EALAEVGITGMTVTEVK	1747.9	R	G	4.6	0.5	82.6	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	GAEYMVDFLPK	1269.6	R	V	2.8	0.8	54.6	11.5
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	IDAIIKPFK	1044.6	K	L	2.3	0.0	33.1	3.0
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	IDAIIKPFKLDDVR	1643.0	K	E	3.0	0.0	32.1	7.8
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	IEIVVPDDIVDTCVDTIIR	2185.1	K	T	4.6	0.0	53.8	11.1
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	IFVFDVAR	966.5	K	V	2.2	0.6	29.1	10.8
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	IGDGKIFVFDVAR	1436.8	K	V	2.1	0.8	3.7	9.5
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	IRTGEEDDAAI	1189.6	R	-	2.4	0.5	40.4	9.5
P0A9Z1	12407.7	G	U	T	A	CID	LIT	9	76.8	KIDAIIKPFK	1172.7	K	L	3.4	0.8	39.9	7.0
P0A9Z1	12407.7	G	U	A	B	CID	LIT	4	24.1	DAIIKPFKL	1044.6	I	D	2.1	0.0	25.0	3.0
P0A9Z1	12407.7	G	U	A	B	CID	LIT	4	24.1	DAIIKPFKLD	1159.7	I	D	2.0	0.7	20.0	12.3
P0A9Z1	12407.7	G	U	A	B	CID	LIT	4	24.1	DTIIRTAQTGKIG	1373.8	V	D	2.3	0.0	15.3	13.8
P0A9Z1	12407.7	G	U	A	B	CID	LIT	4	24.1	MKKIDAIIKPFKLD	1660.0	-	D	2.5	0.0	24.5	3.0
P0A9Z1	12407.7	S	U	T	A	CID	LIT	3	23.2	GAEYMVDFLPK	1269.6	R	V	2.6	0.7	20.7	16.0
P0A9Z1	12407.7	S	U	T	A	CID	LIT	3	23.2	IDAIIKPFKLDDVR	1643.0	K	E	2.1	0.7	0.0	0.0
P0A9Z1	12407.7	S	U	T	A	CID	LIT	3	23.2	KIDAIIKPFKLDDVR	1771.0	K	E	3.4	0.0	18.7	6.0
P0A9Z1	12407.7	S	U	T	B	CID	LIT	2	23.2	GAEYMVDFLPK	1269.6	R	V	2.9	0.7	25.1	16.2
P0A9Z1	12407.7	S	U	T	B	CID	LIT	2	23.2	KIDAIIKPFKLDDVR	1771.0	K	E	4.3	0.0	43.1	7.0
P0A9Z1	12407.7	S	U	T	C	CID	LIT	2	23.2	GAEYMVDFLPK	1269.6	R	V	2.8	0.4	12.2	16.2
P0A9Z1	12407.7	S	U	T	C	CID	LIT	2	23.2	KIDAIIKPFKLDDVR	1771.0	K	E	3.0	0.0	27.1	7.8
P0A9Z1	12407.7	S	U	T	B	CID	FT	2	15.2	IDAIIKPFK	1044.6	K	L	2.4	0.0	21.0	8.5
P0A9Z1	12407.7	S	U	T	B	CID	FT	2	15.2	IFVFDVAR	966.5	K	V	2.5	0.0	30.5	9.5
P0A9Z1	12407.7	S	U	T	A	ETD	LIT	3	29.5	GAEYMVDFLPK	1269.6	R	V	2.2	0.5	17.8	16.2
P0A9Z1	12407.7	S	U	T	A	ETD	LIT	3	29.5	IDAIIKPFKLDDVR	1643.0	K	E	4.6	0.5	48.0	12.3
P0A9Z1	12407.7	S	U	T	A	ETD	LIT	3	29.5	IFVFDVAR	966.5	K	V	2.4	0.7	40.6	13.2
P0A9Z1	12407.7	S	U	T	B	ETD	LIT	2	22.3	GAEYMVDFLPK	1269.6	R	V	2.0	0.6	29.1	16.2
P0A9Z1	12407.7	S	U	T	B	ETD	LIT	2	22.3	IDAIIKPFKLDDVR	1643.0	K	E	2.9	0.4	10.4	11.1
P0A9Z1	12407.7	S	U	T	C	ETD	LIT	3	20.5	IDAIIKPFKLDDVR	1643.0	K	E	5.0	0.6	47.2	11.5
P0A9Z1	12407.7	S	U	T	C	ETD	LIT	3	20.5	IFVFDVAR	966.5	K	V	2.1	0.6	40.3	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9Z1	12407.7	S	U	T	C	ETD	LIT	3	20.5	KIDAIIKPFKLDDVR	1771.0	K	E	4.2	0.0	23.9	6.0
P0A9Z1	12407.7	S	U	T	B	ETD+CID	LIT	2	19.6	IDAIIKPFKLDDVR	1643.0	K	E	0.0	0.0	16.6	12.3
P0A9Z1	12407.7	S	U	T	B	ETD+CID	LIT	2	19.6	IFVFDVAR	966.5	K	V	0.0	0.0	27.9	13.2
P0A9Z1	12407.7	S	U	T	A	ETD+CID	LIT	5	30.4	GAEYMVDFLPK	1269.6	R	V	2.3	0.5	13.6	16.2
P0A9Z1	12407.7	S	U	T	A	ETD+CID	LIT	5	30.4	IDAIIKPFKLDDVR	1643.0	K	E	2.1	0.2	17.2	12.3
P0A9Z1	12407.7	S	U	T	A	ETD+CID	LIT	5	30.4	IFVFDVAR	966.5	K	V	2.1	0.0	43.0	13.2
P0A9Z1	12407.7	S	U	T	A	ETD+CID	LIT	5	30.4	KIDAIIKPFKLDDVR	1771.0	K	E	5.3	0.0	63.8	7.0
P0A9Z1	12407.7	S	U	T	A	ETD+CID	LIT	5	30.4	LLPNKPVEVIDSLLYGKVDGLGVLK	2679.6	-	-	1.4	-0.6	15.4	7.8
P0A9Z1	12407.7	S	U	T	B	ETD+CID	LIT	2	19.6	IDAIIKPFKLDDVR	1643.0	K	E	1.9	0.1	16.6	12.3
P0A9Z1	12407.7	S	U	T	B	ETD+CID	LIT	2	19.6	IFVFDVAR	966.5	K	V	1.9	0.0	27.9	13.2
P0A9Z1	12407.7	S	U	T	C	ETD+CID	LIT	2	22.3	GAEYMVDFLPK	1269.6	R	V	2.4	0.6	14.4	15.7
P0A9Z1	12407.7	S	U	T	C	ETD+CID	LIT	2	22.3	IDAIIKPFKLDDVR	1643.0	K	E	4.4	0.1	30.7	12.3
P0A9Z1	12407.7	S	U	T	B	HCD	FT	2	19.6	IDAIIKPFKLDDVR	1643.0	K	E	0.0	0.0	16.6	12.3
P0A9Z1	12407.7	S	U	T	B	HCD	FT	2	19.6	IFVFDVAR	966.5	K	V	0.0	0.0	27.9	13.2
P0A9Z1	12407.7	S	U	T	B	HCD	FT	2	19.6	IDAIIKPFKLDDVR	1643.0	K	E	4.1	0.0	23.1	11.5
P0A9Z1	12407.7	S	U	T	B	HCD	FT	2	19.6	IFVFDVAR	966.5	K	V	2.1	0.0	36.8	13.2
P64534	12449.0	G	U	T	A	CID	LIT	6	65.2	AYDGEIFYHR	1270.6	K	-	2.8	0.8	29.0	12.3
P64534	12449.0	G	U	T	A	CID	LIT	6	65.2	HFKPGDTVPEMYR	1576.8	K	T	3.5	0.7	33.4	12.0
P64534	12449.0	G	U	T	A	CID	LIT	6	65.2	NLPAPDAGTHWTYMGGAYVLISDTDGK	2850.3	R	I	3.6	0.0	19.5	10.0
P64534	12449.0	G	U	T	A	CID	LIT	6	65.2	TDEYNIK	882.4	R	Q	2.2	0.7	16.9	10.4
P64534	12449.0	G	U	T	A	CID	LIT	6	65.2	TDEYNIKQWQLR	1593.8	R	N	3.1	0.7	37.9	13.0
P64534	12449.0	G	U	T	A	CID	LIT	6	65.2	YELSSFIADFK	1319.7	K	H	2.8	0.8	27.9	11.8
P64534	12449.0	G	T	T	A	CID	LIT	7	41.1	AYDGEIFYHR	1270.6	K	-	2.4	0.4	31.5	12.0
P64534	12449.0	G	T	T	A	CID	LIT	7	41.1	HFKPGDTVPEMYR	1576.8	K	T	3.8	0.8	51.1	11.8
P64534	12449.0	G	T	T	A	CID	LIT	7	41.1	HFKPGDTVPEMYRTDEYNIK	2440.2	K	Q	3.1	0.0	21.7	10.0
P64534	12449.0	G	T	T	A	CID	LIT	7	41.1	QWQLR	730.4	K	N	1.9	0.6	20.2	10.8
P64534	12449.0	G	T	T	A	CID	LIT	7	41.1	TDEYNIK	882.4	R	Q	2.5	0.6	40.0	11.5
P64534	12449.0	G	T	T	A	CID	LIT	7	41.1	TDEYNIKQWQLR	1593.8	R	N	3.3	0.6	35.1	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64534	12449.0	G	T	T	A	CID	LIT	7	41.1	YELSSFIADFK	1319.7	K	H	3.4	0.0	47.1	11.5
P64534	12449.0	G	U	A	A	CID	LIT	4	22.3	DFKHFKPG	975.5	A	D	1.9	0.3	22.3	14.6
P64534	12449.0	G	U	A	A	CID	LIT	4	22.3	DFKHFKPGDTVPEMYRT	2068.0	A	D	4.0	0.5	45.2	14.3
P64534	12449.0	G	U	A	A	CID	LIT	4	22.3	DGEIFYHR	1036.5	Y	-	2.7	0.0	32.7	14.5
P64534	12449.0	G	U	A	A	CID	LIT	4	22.3	DTVPEMYRT	1127.5	G	D	2.3	0.7	25.3	11.1
P64534	12449.0	G	T	A	A	CID	LIT	4	22.3	DFKHFKPG	975.5	A	D	2.2	0.3	20.7	14.6
P64534	12449.0	G	T	A	A	CID	LIT	4	22.3	DFKHFKPGDTVPEMYRT	2068.0	A	D	3.9	0.5	41.6	13.4
P64534	12449.0	G	T	A	A	CID	LIT	4	22.3	DGEIFYHR	1036.5	Y	-	2.6	0.7	40.8	15.8
P64534	12449.0	G	T	A	A	CID	LIT	4	22.3	DTVPEMYRT	1111.5	G	D	2.1	0.6	17.8	14.1
P64534	12449.0	G	U	T	B	CID	LIT	4	34.8	AYDGEIFYHR	1270.6	K	-	2.8	0.7	40.2	12.3
P64534	12449.0	G	U	T	B	CID	LIT	4	34.8	HFKPGDTVPEMYR	1576.8	K	T	3.5	0.0	60.5	12.6
P64534	12449.0	G	U	T	B	CID	LIT	4	34.8	QWQLR	730.4	K	N	1.8	0.6	19.7	13.2
P64534	12449.0	G	U	T	B	CID	LIT	4	34.8	YELSSFIADFK	1319.7	K	H	4.0	0.8	67.4	11.5
P64534	12449.0	G	T	A	B	CID	LIT	6	31.2	DFKHFKPG	975.5	A	D	1.6	0.4	15.4	15.9
P64534	12449.0	G	T	A	B	CID	LIT	6	31.2	DFKHFKPGDTVPEMYRT	2068.0	A	D	3.5	0.4	43.7	12.6
P64534	12449.0	G	T	A	B	CID	LIT	6	31.2	DGEIFYHR	1036.5	Y	-	2.5	0.7	44.5	15.2
P64534	12449.0	G	T	A	B	CID	LIT	6	31.2	DGKIIKAY	907.5	T	D	2.6	0.0	24.0	9.5
P64534	12449.0	G	T	A	B	CID	LIT	6	31.2	DTDGKIIKAY	1123.6	S	D	2.3	0.0	24.8	11.8
P64534	12449.0	G	T	A	B	CID	LIT	6	31.2	DTVPEMYRT	1111.5	G	D	2.2	0.6	24.3	14.1
P64534	12449.0	G	U	A	B	CID	LIT	6	45.5	DEYNIKQWQLRNLPAP	1985.0	T	D	5.1	0.7	36.8	16.1
P64534	12449.0	G	U	A	B	CID	LIT	6	45.5	DFKHFKPG	975.5	A	D	1.3	0.6	10.5	14.8
P64534	12449.0	G	U	A	B	CID	LIT	6	45.5	DFKHFKPGDTVPEMYRT	2068.0	A	D	4.2	0.5	49.9	13.2
P64534	12449.0	G	U	A	B	CID	LIT	6	45.5	DGEIFYHR	1036.5	Y	-	2.9	0.0	33.5	14.5
P64534	12449.0	G	U	A	B	CID	LIT	6	45.5	DTDGKIIKAY	1123.6	S	D	3.3	0.5	29.0	11.8
P64534	12449.0	G	U	A	B	CID	LIT	6	45.5	DTVPEMYRT	1111.5	G	D	2.5	0.7	24.6	12.6
P64534	12449.0	S	U	T	B	CID	LIT	2	17.9	HFKPGDTVPEMYR	1576.8	K	T	3.7	0.6	22.9	17.3
P64534	12449.0	S	U	T	B	CID	LIT	2	17.9	HFKPGDTVPEMYRTDEYNIK	2440.2	K	Q	4.5	0.5	13.0	17.8
P64534	12449.0	S	U	T	C	CID	LIT	4	50.9	AYDGEIFYHR	1270.6	K	-	1.7	0.7	14.0	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64534	12449.0	S	U	T	C	CID	LIT	4	50.9	HFKPGDTVPEMYR	1576.8	K	T	3.1	0.0	31.8	17.6
P64534	12449.0	S	U	T	C	CID	LIT	4	50.9	HFKPGDTVPEMYRTDEYNIK	2440.2	K	Q	4.4	0.6	29.1	17.7
P64534	12449.0	S	U	T	C	CID	LIT	4	50.9	NLPAPDAGTHWTYMGGAYVLISDTDGK	2850.3	R	I	3.3	0.4	0.0	0.0
P64534	12449.0	S	U	T	B	ETD	LIT	3	26.8	AYDGEIFYHR	1270.6	K	-	2.0	0.4	11.2	13.4
P64534	12449.0	S	U	T	B	ETD	LIT	3	26.8	HFKPGDTVPEMYR	1576.8	K	T	5.0	0.0	41.0	16.4
P64534	12449.0	S	U	T	B	ETD	LIT	3	26.8	HFKPGDTVPEMYRTDEYNIK	2440.2	K	Q	4.8	0.0	40.1	17.3
P64534	12449.0	S	U	T	C	ETD	LIT	3	26.8	AYDGEIFYHR	1270.6	K	-	2.4	0.6	33.1	13.6
P64534	12449.0	S	U	T	C	ETD	LIT	3	26.8	HFKPGDTVPEMYR	1576.8	K	T	4.4	0.0	42.2	16.9
P64534	12449.0	S	U	T	C	ETD	LIT	3	26.8	HFKPGDTVPEMYRTDEYNIK	2440.2	K	Q	5.1	0.0	38.3	17.8
P64534	12449.0	S	U	T	C	ETD+CID	LIT	4	50.9	AYDGEIFYHR	1270.6	K	-	1.9	0.5	14.6	13.8
P64534	12449.0	S	U	T	C	ETD+CID	LIT	4	50.9	HFKPGDTVPEMYR	1576.8	K	T	3.2	0.5	31.7	17.2
P64534	12449.0	S	U	T	C	ETD+CID	LIT	4	50.9	HFKPGDTVPEMYRTDEYNIK	2440.2	K	Q	4.0	0.5	24.1	17.8
P64534	12449.0	S	U	T	C	ETD+CID	LIT	4	50.9	NLPAPDAGTHWTYMGGAYVLISDTDGK	2850.3	R	I	3.2	0.4	11.5	17.8
P0AEB7	12475.2	G	U	T	A	CID	LIT	4	45.6	AWDAWVVAGHAPVR	1534.8	K	C	2.5	0.7	0.0	0.0
P0AEB7	12475.2	G	U	T	A	CID	LIT	4	45.6	CTVQAGLMNPK	1218.6	R	Y	3.2	0.7	51.5	11.5
P0AEB7	12475.2	G	U	T	A	CID	LIT	4	45.6	SSILDATIFLADKNDFAAMNK	2285.1	K	A	4.5	0.7	60.3	12.6
P0AEB7	12475.2	G	U	T	A	CID	LIT	4	45.6	YKVEIK	779.5	K	I	1.6	0.1	19.7	8.5
P0AEB7	12475.2	G	T	T	A	CID	LIT	3	36.0	AWDAWVVAGHAPVR	1534.8	K	C	4.8	0.0	71.1	14.1
P0AEB7	12475.2	G	T	T	A	CID	LIT	3	36.0	SSILDATIFLADKNDFAAMNK	2285.1	K	A	4.5	0.6	72.2	12.6
P0AEB7	12475.2	G	T	T	A	CID	LIT	3	36.0	YKVEIK	779.5	K	I	1.6	0.3	21.8	8.5
P0AEB7	12475.2	G	U	A	A	CID	LIT	7	52.6	DAFEQTANTLAQI	1421.7	A	D	3.5	0.7	60.0	14.8
P0AEB7	12475.2	G	U	A	A	CID	LIT	7	52.6	DAVLEKQGSNKSSIL	1588.9	I	D	3.4	0.5	30.6	15.1
P0AEB7	12475.2	G	U	A	A	CID	LIT	7	52.6	DFAAMNKAW	1053.5	N	D	2.8	0.0	30.8	12.8
P0AEB7	12475.2	G	U	A	A	CID	LIT	7	52.6	DKNDFAAMNKAW	1410.6	A	D	4.3	0.6	41.9	13.4
P0AEB7	12475.2	G	U	A	A	CID	LIT	7	52.6	DVVIHNNTLYYTGVPENL	2061.0	S	D	3.0	0.0	29.8	17.0
P0AEB7	12475.2	G	U	A	A	CID	LIT	7	52.6	DVVIHNNTLYYTGVPENLDA	2247.1	S	D	3.2	0.0	43.1	14.8
P0AEB7	12475.2	G	U	A	A	CID	LIT	7	52.6	EKQGSNKSSIL	1190.6	L	D	2.2	0.0	17.9	15.7
P0AEB7	12475.2	G	T	A	A	CID	LIT	5	47.4	DAEARWS	834.4	I	D	2.2	0.8	24.5	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AEB7	12475.2	G	T	A	A	CID	LIT	5	47.4	DAVLEKQGSNKSSIL	1588.9	I	D	2.3	0.7	2.2	14.3
P0AEB7	12475.2	G	T	A	A	CID	LIT	5	47.4	DKNDFAAMNKAW	1410.6	A	D	4.0	0.6	34.3	13.8
P0AEB7	12475.2	G	T	A	A	CID	LIT	5	47.4	DVVIHNNTLYYTGVPENL	2061.0	S	D	2.4	0.6	10.0	17.2
P0AEB7	12475.2	G	T	A	A	CID	LIT	5	47.4	DVVIHNNTLYYTGVPENLDA	2247.1	S	D	2.9	0.0	16.4	14.1
P0AEB7	12475.2	G	T	A	B	CID	LIT	7	55.3	DAFEQTANTLAQI	1421.7	A	D	4.4	0.8	71.3	14.8
P0AEB7	12475.2	G	T	A	B	CID	LIT	7	55.3	DAVLEKQGSNKSSIL	1588.9	I	D	4.0	0.4	41.0	15.1
P0AEB7	12475.2	G	T	A	B	CID	LIT	7	55.3	DFAAMNKAW	1053.5	N	D	2.9	0.0	40.9	12.8
P0AEB7	12475.2	G	T	A	B	CID	LIT	7	55.3	DVVIHNNTLYYTGVPENL	2061.0	S	D	3.2	0.8	43.1	17.2
P0AEB7	12475.2	G	T	A	B	CID	LIT	7	55.3	EKQGSNKSSIL	1190.6	L	D	1.8	0.5	0.0	0.0
P0AEB7	12475.2	G	T	A	B	CID	LIT	7	55.3	MTIVRIDA	918.5	-	E	1.8	0.6	11.2	13.8
P0AEB7	12475.2	G	T	A	B	CID	LIT	7	55.3	TIVRIDA	787.5	M	E	0.0	0.0	24.0	17.6
P0AEB7	12475.2	G	U	A	B	CID	LIT	4	48.2	DAFEQTANTLAQI	1421.7	A	D	3.6	0.5	64.5	14.8
P0AEB7	12475.2	G	U	A	B	CID	LIT	4	48.2	DAVLEKQGSNKSSIL	1588.9	I	D	4.1	0.5	33.6	14.3
P0AEB7	12475.2	G	U	A	B	CID	LIT	4	48.2	DFAAMNKAW	1053.5	N	D	2.9	0.0	30.2	12.8
P0AEB7	12475.2	G	U	A	B	CID	LIT	4	48.2	DVVIHNNTLYYTGVPENL	2061.0	S	D	3.3	0.5	31.5	16.9
P0AEB7	12475.2	S	U	T	A	ETD	LIT	2	17.5	AWDAWVVAGHAPVR	1534.8	K	C	4.8	0.4	54.7	18.0
P0AEB7	12475.2	S	U	T	A	ETD	LIT	2	17.5	IDAEAR	674.3	R	W	1.5	0.0	24.4	19.4
P0AEB7	12475.2	S	U	T	A	ETD+CID	LIT	2	17.5	AWDAWVVAGHAPVR	1534.8	K	C	4.6	0.6	53.2	18.1
P0AEB7	12475.2	S	U	T	A	ETD+CID	LIT	2	17.5	IDAEAR	674.3	R	W	1.6	0.3	21.8	19.4
P0ADS2	12576.4	G	U	T	A	CID	LIT	6	54.1	DALNQAADDLNQR	1443.7	R	L	3.9	0.8	77.2	8.5
P0ADS2	12576.4	G	U	T	A	CID	LIT	6	54.1	DYAASMEQR	1070.5	R	I	2.3	0.0	25.4	3.0
P0ADS2	12576.4	G	U	T	A	CID	LIT	6	54.1	MLQQTIEQALLEQGR	1757.9	R	I	4.4	0.6	82.9	13.0
P0ADS2	12576.4	G	U	T	A	CID	LIT	6	54.1	SAQPVDIQIFGR	1330.7	M	S	0.0	0.0	33.0	13.6
P0ADS2	12576.4	G	U	T	A	CID	LIT	6	54.1	TRDYAASMEQR	1327.6	K	I	3.7	0.8	38.0	11.1
P0ADS2	12576.4	G	U	T	A	CID	LIT	6	54.1	VNCPPDQR	985.5	R	D	2.2	0.0	22.6	7.8
P0ADS2	12576.4	G	T	A	B	CID	LIT	3	33.9	DDLNQRLQ	1001.5	A	D	2.9	0.7	32.3	13.0
P0ADS2	12576.4	G	T	A	B	CID	LIT	3	33.9	DIQIFGRSLRVNCPP	1771.9	V	D	3.0	0.4	0.0	0.0
P0ADS2	12576.4	G	T	A	B	CID	LIT	3	33.9	EQGRITEKTNQNFE	1693.8	L	-	3.9	0.6	28.0	14.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADS2	12576.4	G	U	A	B	CID	LIT	3	33.9	DDLNQRLQ	1001.5	A	D	3.2	0.6	51.4	12.8
P0ADS2	12576.4	G	U	A	B	CID	LIT	3	33.9	DIQIFGRSLRVNCPP	1771.9	V	D	2.6	0.5	26.5	15.2
P0ADS2	12576.4	G	U	A	B	CID	LIT	3	33.9	EQGRITEKTNQNFE	1693.8	L	-	0.0	0.0	36.3	15.3
P0ADS2	12576.4	S	U	T	B	CID	LIT	3	35.8	DALNQAADDLNQR	1443.7	R	L	2.6	0.8	16.9	13.4
P0ADS2	12576.4	S	U	T	B	CID	LIT	3	35.8	MLQQTIEQALLEQGR	1757.9	R	I	4.6	0.6	55.9	17.6
P0ADS2	12576.4	S	U	T	B	CID	LIT	3	35.8	TRDYAASMEQR	1327.6	K	I	2.8	0.4	18.0	13.2
P0ADS2	12576.4	S	U	T	B	ETD	LIT	2	24.8	MLQQTIEQALLEQGR	1757.9	R	I	4.9	0.5	35.3	17.5
P0ADS2	12576.4	S	U	T	B	ETD	LIT	2	24.8	SAQPVDIQIFGR	1330.7	M	S	0.0	0.0	28.0	17.1
P0AB52	12675.2	G	T	T	A	CID	LIT	2	29.1	EQESNLDLR	1103.5	R	L	1.6	0.5	11.6	10.8
P0AB52	12675.2	G	T	T	A	CID	LIT	2	29.1	GQKPGEGYNIQQMLEILTAQNVPVK	2755.4	R	L	4.3	0.0	27.1	9.5
P0A703	12678.4	G	U	A	A	CID	LIT	2	19.5	DCSQVVEIHQH	1351.6	W	D	3.7	0.6	31.5	12.3
P0A703	12678.4	G	U	A	A	CID	LIT	2	19.5	DSLIVKSIEVE	1231.7	G	-	3.3	0.6	32.9	12.3
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	AIAEQLKYTGNK	1335.7	K	D	3.9	0.7	42.5	12.6
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	DVSFDR	738.3	K	S	1.7	0.8	13.4	12.6
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	GIKDVSFDR	1036.5	K	S	2.4	0.7	38.0	12.6
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	HIYAQVIAPNGSEVLVAASTVEK	2396.3	R	A	6.4	0.0	88.6	11.8
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	KLQELGATR	1015.6	R	L	3.0	0.6	50.1	15.6
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	LQELGATR	887.5	K	L	2.8	0.4	40.7	15.2
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	LVVHRTPR	977.6	R	H	1.6	0.0	32.2	4.8
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	SGFQYHGR	951.4	R	V	2.9	0.8	59.1	10.0
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	VQALADAAR	914.5	R	E	3.1	0.7	55.4	11.5
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	VQALADAAREAGLQF	1559.8	R	-	3.9	0.0	32.4	12.0
P0C018	12751.7	G	U	T	A	CID	LIT	11	78.6	YTGNKDAAAAVGK	1265.6	K	A	5.0	0.8	81.5	11.8
P0C018	12751.7	G	T	T	A	CID	LIT	7	46.2	AIAEQLK	772.5	K	Y	1.3	0.6	13.2	15.3
P0C018	12751.7	G	T	T	A	CID	LIT	7	46.2	DVSFDR	738.3	K	S	1.4	0.5	11.4	10.8
P0C018	12751.7	G	T	T	A	CID	LIT	7	46.2	GIKDVSFDR	1036.5	K	S	2.4	0.7	34.7	13.4
P0C018	12751.7	G	T	T	A	CID	LIT	7	46.2	LQELGATR	887.5	K	L	2.1	0.1	20.2	15.2
P0C018	12751.7	G	T	T	A	CID	LIT	7	46.2	SGFQYHGR	951.4	R	V	2.9	0.8	53.6	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C018	12751.7	G	T	T	A	CID	LIT	7	46.2	VQALADAAR	914.5	R	E	2.8	0.6	47.2	12.6
P0C018	12751.7	G	T	T	A	CID	LIT	7	46.2	YTGNKDAAAAVGK	1265.6	K	A	4.2	0.8	65.4	12.8
P0C018	12751.7	G	U	A	A	CID	LIT	7	49.6	DAAAAVGKAVA	943.5	K	E	3.2	0.5	62.0	16.8
P0C018	12751.7	G	U	A	A	CID	LIT	7	49.6	DAAAAVGKAVAERALEKGIK	1968.1	K	D	5.3	0.6	54.0	10.0
P0C018	12751.7	G	U	A	A	CID	LIT	7	49.6	DAAREAGLQF	1077.5	A	-	2.6	0.7	33.1	13.8
P0C018	12751.7	G	U	A	A	CID	LIT	7	49.6	DRSGFQYHGRVQALA	1704.9	F	D	2.3	0.4	0.0	0.0
P0C018	12751.7	G	U	A	A	CID	LIT	7	49.6	DVSFDRSGFQYHGRVQALA	2153.1	K	D	3.6	0.5	12.0	14.5
P0C018	12751.7	G	U	A	A	CID	LIT	7	49.6	EQLKYTGNK	1080.6	A	D	2.1	0.5	21.2	14.6
P0C018	12751.7	G	U	A	A	CID	LIT	7	49.6	ERALEKGIK	1043.6	A	D	3.2	0.7	35.4	9.5
P0C018	12751.7	G	T	A	A	CID	LIT	4	38.5	DAAAAVGKAVAERALEKGIK	1968.1	K	D	2.8	0.7	25.6	9.5
P0C018	12751.7	G	T	A	A	CID	LIT	4	38.5	DAAREAGLQF	1077.5	A	-	2.6	0.7	33.2	13.8
P0C018	12751.7	G	T	A	A	CID	LIT	4	38.5	DRSGFQYHGRVQALA	1704.9	F	D	2.2	0.6	0.0	0.0
P0C018	12751.7	G	T	A	A	CID	LIT	4	38.5	ERALEKGIK	1043.6	A	D	3.3	0.6	27.3	9.5
P0C018	12751.7	G	T	T	B	CID	LIT	4	33.3	GIKDVSFDR	1036.5	K	S	1.8	0.6	6.6	13.4
P0C018	12751.7	G	T	T	B	CID	LIT	4	33.3	SGFQYHGR	951.4	R	V	2.8	0.7	54.0	10.0
P0C018	12751.7	G	T	T	B	CID	LIT	4	33.3	VQALADAAR	914.5	R	E	3.2	0.5	32.7	13.2
P0C018	12751.7	G	T	T	B	CID	LIT	4	33.3	YTGNKDAAAAVGK	1265.6	K	A	4.7	0.8	79.8	12.8
P0C018	12751.7	G	U	T	B	CID	LIT	7	45.3	GIKDVSFDR	1036.5	K	S	2.0	0.7	14.3	13.6
P0C018	12751.7	G	U	T	B	CID	LIT	7	45.3	KLQELGATR	1015.6	R	L	3.1	0.5	52.8	15.6
P0C018	12751.7	G	U	T	B	CID	LIT	7	45.3	LQELGATR	887.5	K	L	3.0	0.4	39.8	15.2
P0C018	12751.7	G	U	T	B	CID	LIT	7	45.3	LVVHR	623.4	R	T	1.6	0.4	15.6	4.8
P0C018	12751.7	G	U	T	B	CID	LIT	7	45.3	SGFQYHGR	951.4	R	V	1.4	0.6	12.3	10.0
P0C018	12751.7	G	U	T	B	CID	LIT	7	45.3	VQALADAAR	914.5	R	E	3.0	0.7	53.7	11.5
P0C018	12751.7	G	U	T	B	CID	LIT	7	45.3	YTGNKDAAAAVGK	1265.6	K	A	4.8	0.0	86.4	12.6
P0C018	12751.7	G	T	A	B	CID	LIT	5	38.5	DAAAAVGKAVA	943.5	K	E	3.2	0.4	53.2	17.4
P0C018	12751.7	G	T	A	B	CID	LIT	5	38.5	DAAAAVGKAVAERALEKGIK	1968.1	K	D	4.3	0.0	61.7	10.8
P0C018	12751.7	G	T	A	B	CID	LIT	5	38.5	DAAREAGLQF	1077.5	A	-	2.3	0.5	17.8	13.8
P0C018	12751.7	G	T	A	B	CID	LIT	5	38.5	DRSGFQYHGRVQALA	1704.9	F	D	2.3	0.5	13.2	16.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C018	12751.7	G	T	A	B	CID	LIT	5	38.5	ERALEKGIK	1043.6	A	D	2.6	0.7	10.9	9.5
P0C018	12751.7	G	U	A	B	CID	LIT	7	46.2	DAAAAVGKAVA	943.5	K	E	3.7	0.5	80.3	17.0
P0C018	12751.7	G	U	A	B	CID	LIT	7	46.2	DAAAAVGKAVAERAL	1412.8	K	E	3.7	0.6	50.5	13.6
P0C018	12751.7	G	U	A	B	CID	LIT	7	46.2	DAAAAVGKAVAERALEKGIK	1968.1	K	D	5.5	0.7	71.9	10.8
P0C018	12751.7	G	U	A	B	CID	LIT	7	46.2	DAAREAGLQF	1077.5	A	-	2.8	0.7	30.1	13.8
P0C018	12751.7	G	U	A	B	CID	LIT	7	46.2	DRSGFQYHGRVQALA	1704.9	F	D	2.2	0.6	19.9	16.2
P0C018	12751.7	G	U	A	B	CID	LIT	7	46.2	EQLKYTGNK	1080.6	A	D	1.9	0.0	19.9	14.6
P0C018	12751.7	G	U	A	B	CID	LIT	7	46.2	ERALEKGIK	1043.6	A	D	3.3	0.0	21.8	9.5
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	AIAEQLKYTGNKDAAAAVGK	2019.1	K	A	5.7	0.6	74.9	16.5
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	DAAAAVGK	702.4	K	A	1.9	0.0	23.2	20.3
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	6.2	0.5	74.8	17.9
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	KLQELGATR	1015.6	R	L	2.6	0.3	35.4	18.2
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	LVVHR	623.4	R	T	1.8	0.4	11.5	4.8
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	RKLQELGATR	1171.7	R	L	3.2	0.7	34.7	15.2
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	SGFQYHGR	951.4	R	V	3.3	0.6	47.3	15.2
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	VQALADAAR	914.5	R	E	3.1	0.6	53.8	14.8
P0C018	12751.7	S	U	T	A	CID	LIT	9	64.1	YTGNKDAAAAVGK	1265.6	K	A	5.2	0.6	69.3	16.2
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	AIAEQLKYTGNKDAAAAVGK	2019.1	K	A	6.1	0.6	66.9	16.5
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	DAAAAVGK	702.4	K	A	2.4	0.3	29.2	20.3
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	6.1	0.8	65.4	18.3
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	KLQELGATR	1015.6	R	L	2.2	0.3	21.3	18.1
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	LQELGATR	887.5	K	L	3.1	0.3	43.8	18.7
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	RKLQELGATR	1171.7	R	L	3.5	0.6	52.8	15.2
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	SGFQYHGR	951.4	R	V	2.8	0.0	43.3	14.5
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	VQALADAAR	914.5	R	E	3.0	0.6	51.0	14.1
P0C018	12751.7	S	U	T	B	CID	LIT	9	59.8	YTGNKDAAAAVGK	1265.6	K	A	4.4	0.8	72.2	15.2
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	DAAAAVGK	702.4	K	A	1.9	0.1	33.2	20.3
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	GIKDVSFDR	1036.5	K	S	2.6	0.6	32.0	16.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	HIYAQVIAPNGSEVLVAASTVEK	2396.3	R	A	4.1	0.7	53.5	16.3
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	KLQELGATR	1015.6	R	L	2.3	0.4	46.9	18.2
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	LQELGATR	887.5	K	L	3.0	0.3	37.6	18.4
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	RKLQELGATR	1171.7	R	L	3.9	0.5	33.0	14.9
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	SGFQYHGR	951.4	R	V	1.9	0.7	30.1	15.2
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	VQALADAAR	914.5	R	E	3.0	0.6	50.8	14.8
P0C018	12751.7	S	U	T	C	CID	LIT	9	61.5	YTGNKDAAAAVGK	1265.6	K	A	4.6	0.7	69.3	15.7
P0C018	12751.7	S	U	T	A	CID	FT	2	19.7	RKLQELGATR	1171.7	R	L	3.3	0.0	26.7	15.2
P0C018	12751.7	S	U	T	A	CID	FT	2	19.7	YTGNKDAAAAVGK	1265.6	K	A	4.4	0.0	62.7	15.2
P0C018	12751.7	S	U	T	B	CID	FT	3	31.6	GIKDVSFDR	1036.5	K	S	2.6	0.0	23.9	16.6
P0C018	12751.7	S	U	T	B	CID	FT	3	31.6	HIYAQVIAPNGSEVLVAASTVEK	2396.3	R	A	3.3	0.0	13.6	16.7
P0C018	12751.7	S	U	T	B	CID	FT	3	31.6	LVVHR	623.4	R	T	1.1	0.3	15.7	4.8
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	AIAEQLKYTGNKDAAAAVGK	2019.1	K	A	3.0	0.3	44.1	16.9
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	DAAAAVGK	702.4	K	A	2.2	0.0	26.8	20.3
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	GIKDVSFDR	1036.5	K	S	3.2	0.4	41.8	15.7
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	HIYAQVIAPNGSEVLVAASTVEK	2396.3	R	A	6.9	0.0	76.3	16.5
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	LQELGATR	887.5	K	L	2.3	0.1	64.6	18.5
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	LVVHR	623.4	R	T	0.0	0.0	26.2	4.8
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	RKLQELGATR	1171.7	R	L	4.9	0.5	61.3	14.6
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	VQALADAAR	914.5	R	E	2.8	0.4	59.6	14.8
P0C018	12751.7	S	U	T	A	ETD	LIT	9	65.0	YTGNKDAAAAVGK	1265.6	K	A	6.2	0.7	80.8	16.2
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	DAAAAVGK	702.4	K	A	2.4	0.1	35.4	20.3
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	GIKDVSFDR	1036.5	K	S	2.9	0.4	0.0	0.0
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	9.3	0.7	88.4	18.1
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	KLQELGATR	1015.6	R	L	2.5	0.2	22.1	18.2
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	LQELGATR	887.5	K	L	0.0	0.0	68.2	18.0
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	LVVHR	623.4	R	T	0.0	0.0	24.7	4.8
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	RKLQELGATR	1171.7	R	L	4.9	0.5	60.9	15.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	SGFQYHGR	951.4	R	V	2.4	0.7	21.9	15.2
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	VQALADAAR	914.5	R	E	2.8	0.4	61.5	13.4
P0C018	12751.7	S	U	T	B	ETD	LIT	10	65.8	YTGNKDAAAAVGK	1265.6	K	A	5.9	0.7	79.0	15.7
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	DAAAAVGK	702.4	K	A	2.2	0.1	28.7	20.3
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	DVSFDR	738.3	K	S	1.8	0.6	39.2	15.3
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	GIKDVSFDR	1036.5	K	S	4.6	0.6	62.4	16.5
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	9.3	0.7	98.3	17.9
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	LQELGATR	887.5	K	L	2.3	0.2	49.1	18.0
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	LVVHR	623.4	R	T	0.0	0.0	24.4	4.8
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	RKLQELGATR	1171.7	R	L	4.9	0.5	73.0	14.9
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	SGFQYHGR	951.4	R	V	2.3	0.7	0.0	0.0
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	VQALADAAR	914.5	R	E	2.7	0.4	59.6	13.4
P0C018	12751.7	S	U	T	C	ETD	LIT	10	65.8	YTGNKDAAAAVGK	1265.6	K	A	6.2	0.7	82.1	15.2
P0C018	12751.7	S	U	T	A	ETD	FT	6	38.5	KLQELGATR	1015.6	R	L	1.8	0.5	17.8	18.2
P0C018	12751.7	S	U	T	A	ETD	FT	6	38.5	LVVHR	623.4	R	T	1.2	0.0	30.6	4.8
P0C018	12751.7	S	U	T	A	ETD	FT	6	38.5	RKLQELGATR	1171.7	R	L	4.1	0.5	80.8	15.2
P0C018	12751.7	S	U	T	A	ETD	FT	6	38.5	SGFQYHGR	951.4	R	V	0.7	0.0	25.4	15.2
P0C018	12751.7	S	U	T	A	ETD	FT	6	38.5	VQALADAAR	914.5	R	E	0.8	0.0	43.0	13.4
P0C018	12751.7	S	U	T	A	ETD	FT	6	38.5	YTGNKDAAAAVGK	1265.6	K	A	3.9	0.0	69.2	15.7
P0C018	12751.7	S	U	T	B	ETD	FT	3	23.9	LVVHR	623.4	R	T	0.8	0.0	23.2	4.8
P0C018	12751.7	S	U	T	B	ETD	FT	3	23.9	RKLQELGATR	1171.7	R	L	4.2	0.5	77.3	14.9
P0C018	12751.7	S	U	T	B	ETD	FT	3	23.9	YTGNKDAAAAVGK	1265.6	K	A	4.1	0.0	69.0	16.2
P0C018	12751.7	S	U	T	C	ETD	FT	3	18.8	LQELGATR	887.5	K	L	0.0	0.0	42.8	18.5
P0C018	12751.7	S	U	T	C	ETD	FT	3	18.8	LVVHR	623.4	R	T	0.0	0.0	27.5	4.8
P0C018	12751.7	S	U	T	C	ETD	FT	3	18.8	VQALADAAR	914.5	R	E	0.0	0.0	61.5	14.8
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	DAAAAVGK	702.4	K	A	0.0	0.0	29.0	20.3
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	0.0	0.0	67.1	18.1
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	LQELGATR	887.5	K	L	0.0	0.0	37.8	18.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	RKLQELGATR	1171.7	R	L	0.0	0.0	59.4	15.2
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	SGFQYHGR	951.4	R	V	0.0	0.0	27.0	14.5
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	VQALADAAR	914.5	R	E	0.0	0.0	42.0	14.1
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	YTGNKDAAAAVGK	1265.6	K	A	0.0	0.0	83.5	16.2
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	DAAAAVGK	702.4	K	A	2.1	0.2	19.1	20.3
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	6.0	0.7	68.4	18.1
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	KLQELGATR	1015.6	R	L	2.4	0.5	31.5	18.2
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	LQELGATR	887.5	K	L	3.1	0.3	42.0	18.7
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	RKLQELGATR	1171.7	R	L	5.0	0.9	70.1	14.9
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	SGFQYHGR	951.4	R	V	3.1	0.0	54.4	14.5
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	VQALADAAR	914.5	R	E	2.9	0.7	48.1	14.1
P0C018	12751.7	S	U	T	A	ETD+CID	LIT	6	53.8	YTGNKDAAAAVGK	1266.6	K	A	4.8	0.6	59.7	16.4
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	2	28.2	HIYAQVIAPNGSEVLVAASTVEK	2396.3	R	A	4.3	0.8	0.0	0.0
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	2	28.2	RKLQELGATR	1171.7	R	L	3.8	0.6	0.0	0.0
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	DAAAAVGK	702.4	K	A	2.3	0.6	29.0	20.3
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	DVFVHFSAIQTNGFK	1710.8	-	-	7.4	0.6	71.3	16.9
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	6.1	0.6	67.1	18.1
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	LQELGATR	887.5	K	L	2.9	0.3	37.8	18.4
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	RKLQELGATR	1171.7	R	L	5.0	0.5	59.4	15.2
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	SGFQYHGR	951.4	R	V	2.5	-0.1	27.0	14.5
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	VQALADAAR	914.5	R	E	3.0	0.7	42.0	14.1
P0C018	12751.7	S	U	T	B	ETD+CID	LIT	5	53.8	YTGNKDAAAAVGK	1265.6	K	A	4.6	0.5	80.7	15.7
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	AEFYSEVLTIVVDGK	1669.9	-	-	1.7	-0.2	25.2	17.2
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	AIAEQLKYTGNKDAAAAVGK	2019.1	K	A	5.5	0.6	58.2	16.4
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	DAAAAVGK	702.4	K	A	1.7	0.0	26.2	20.3
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	GIKDVSFDR	1036.5	K	S	2.7	0.8	23.5	16.5
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	5.0	0.6	72.4	18.1
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	KLQELGATR	1015.6	R	L	2.2	0.2	31.0	18.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	LQELGATR	887.5	K	L	2.9	0.3	41.6	18.7
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	RKLQELGATR	1171.7	R	L	4.9	0.9	55.6	15.2
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	SGFQYHGR	951.4	R	V	1.7	0.3	12.1	15.2
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	VQALADAAR	914.5	R	E	3.1	0.6	49.4	14.1
P0C018	12751.7	S	U	T	C	ETD+CID	LIT	8	67.5	YTGNKDAAAAVGK	1266.6	K	A	4.3	0.6	52.9	14.8
P0C018	12751.7	S	U	T	B	HCD	FT	5	53.8	DAAAAVGK	702.4	K	A	0.0	0.0	29.0	20.3
P0C018	12751.7	S	U	T	B	HCD	FT	5	53.8	HIYAQVIAPNGSEVLVAASTVEK	2397.3	R	A	0.0	0.0	67.1	18.1
P0C018	12751.7	S	U	T	B	HCD	FT	5	53.8	LQELGATR	887.5	K	L	0.0	0.0	37.8	18.4
P0C018	12751.7	S	U	T	B	HCD	FT	5	53.8	RKLQELGATR	1171.7	R	L	0.0	0.0	42.0	15.2
P0C018	12751.7	S	U	T	B	HCD	FT	5	53.8	SGFQYHGR	951.4	R	V	0.0	0.0	27.0	14.5
P0C018	12751.7	S	U	T	B	HCD	FT	5	53.8	VQALADAAR	914.5	R	E	0.0	0.0	42.0	14.1
P0C018	12751.7	S	U	T	B	HCD	FT	5	53.8	YTGNKDAAAAVGK	1265.6	K	A	0.0	0.0	80.7	15.7
P0A8M6	12760.6	G	U	T	A	CID	LIT	4	52.3	GDYEDRVDDYIIK	1600.7	K	N	2.1	0.6	23.4	9.5
P0A8M6	12760.6	G	U	T	A	CID	LIT	4	52.3	METTKPSFQDVLEFVR	1927.0	-	L	3.7	0.9	32.0	12.8
P0A8M6	12760.6	G	U	T	A	CID	LIT	4	52.3	VDDYIIK	865.5	R	N	2.0	0.4	22.3	12.3
P0A8M6	12760.6	G	U	T	A	CID	LIT	4	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	4.7	0.0	37.2	6.0
P0A8M6	12760.6	G	T	T	A	CID	LIT	2	19.3	EIQDVEKK	988.5	R	I	2.6	0.3	25.7	13.6
P0A8M6	12760.6	G	T	T	A	CID	LIT	2	19.3	GDYEDRVDDYIIK	1600.7	K	N	2.0	0.4	15.8	10.0
P0A8M6	12760.6	G	U	A	A	CID	LIT	5	46.8	DDYIIKNA	951.5	V	E	2.5	0.4	7.0	15.9
P0A8M6	12760.6	G	U	A	A	CID	LIT	5	46.8	DISKKLKAMGEMKNGEAK	1994.0	R	-	2.5	0.7	6.1	16.2
P0A8M6	12760.6	G	U	A	A	CID	LIT	5	46.8	DNQKRVLLL	1098.7	R	D	2.0	0.2	16.0	10.4
P0A8M6	12760.6	G	U	A	A	CID	LIT	5	46.8	DVEKKIRDNQKRVLLL	1967.2	Q	D	2.1	0.6	0.3	4.8
P0A8M6	12760.6	G	U	A	A	CID	LIT	5	46.8	METTKPSFQ	1068.5	-	D	2.5	0.5	28.0	13.8
P0A8M6	12760.6	G	T	A	B	CID	LIT	5	42.2	DNQKRVLLL	1098.7	R	D	2.0	0.3	6.9	10.4
P0A8M6	12760.6	G	T	A	B	CID	LIT	5	42.2	DYIKPGMSVEAIQGIIASMKG	2208.1	S	D	2.2	0.6	0.0	0.0
P0A8M6	12760.6	G	T	A	B	CID	LIT	5	42.2	ELSKERR	917.5	A	D	1.6	0.5	15.9	10.4
P0A8M6	12760.6	G	T	A	B	CID	LIT	5	42.2	ETTKPSFQ	937.5	M	D	1.8	0.1	13.8	16.3
P0A8M6	12760.6	G	T	A	B	CID	LIT	5	42.2	METTKPSFQ	1068.5	-	D	2.7	0.4	35.8	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8M6	12760.6	G	U	A	B	CID	LIT	6	66.1	DDYIIKNA	951.5	V	E	2.8	0.8	44.0	16.0
P0A8M6	12760.6	G	U	A	B	CID	LIT	6	66.1	DISKKLKAMGEMKNGEAK	1978.0	R	-	3.7	0.5	25.8	15.1
P0A8M6	12760.6	G	U	A	B	CID	LIT	6	66.1	DNQKRVLLL	1098.7	R	D	2.1	0.5	15.2	10.4
P0A8M6	12760.6	G	U	A	B	CID	LIT	6	66.1	DYIIKNAELSKERR	1735.0	D	D	3.3	0.0	13.7	12.3
P0A8M6	12760.6	G	U	A	B	CID	LIT	6	66.1	DYIKPGMSVEAIQGIIASMKG	2208.1	S	D	3.7	0.7	25.4	15.8
P0A8M6	12760.6	G	U	A	B	CID	LIT	6	66.1	METTKPSFQ	1068.5	-	D	2.7	0.8	26.7	12.8
P0A8M6	12760.6	S	U	T	A	CID	LIT	4	33.9	EIQDVEK	860.4	R	K	2.1	0.3	13.1	16.5
P0A8M6	12760.6	S	U	T	A	CID	LIT	4	33.9	EIQDVEKK	988.5	R	I	2.5	0.3	15.1	16.4
P0A8M6	12760.6	S	U	T	A	CID	LIT	4	33.9	GDYEDRVDDYIIK	1600.7	K	N	2.8	0.2	31.1	14.1
P0A8M6	12760.6	S	U	T	A	CID	LIT	4	33.9	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	35.0	17.4
P0A8M6	12760.6	S	U	T	B	CID	LIT	4	59.6	EIQDVEKK	988.5	R	I	2.6	0.3	26.9	15.6
P0A8M6	12760.6	S	U	T	B	CID	LIT	4	59.6	GDYEDRVDDYIIK	1600.7	K	N	2.6	0.4	28.3	14.3
P0A8M6	12760.6	S	U	T	B	CID	LIT	4	59.6	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	35.1	17.3
P0A8M6	12760.6	S	U	T	B	CID	LIT	4	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	5.9	0.0	52.3	14.8
P0A8M6	12760.6	S	U	T	C	CID	LIT	4	59.6	EIQDVEKK	988.5	R	I	2.6	0.3	28.3	16.4
P0A8M6	12760.6	S	U	T	C	CID	LIT	4	59.6	GDYEDRVDDYIIK	1600.7	K	N	3.0	0.4	30.4	15.1
P0A8M6	12760.6	S	U	T	C	CID	LIT	4	59.6	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	33.6	17.2
P0A8M6	12760.6	S	U	T	C	CID	LIT	4	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	5.5	0.0	48.5	14.8
P0A8M6	12760.6	S	U	T	A	ETD	LIT	4	45.0	EIQDVEKK	988.5	R	I	1.5	0.0	23.1	16.8
P0A8M6	12760.6	S	U	T	A	ETD	LIT	4	45.0	GDYEDRVDDYIIK	1600.7	K	N	3.3	0.8	25.1	14.1
P0A8M6	12760.6	S	U	T	A	ETD	LIT	4	45.0	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	5.0	0.0	32.9	15.1
P0A8M6	12760.6	S	U	T	A	ETD	LIT	4	45.0	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	18.0	15.9
P0A8M6	12760.6	S	U	T	B	ETD	LIT	5	59.6	EIQDVEKK	988.5	R	I	2.0	0.3	37.5	16.4
P0A8M6	12760.6	S	U	T	B	ETD	LIT	5	59.6	GDYEDRVDDYIIK	1600.7	K	N	5.4	0.4	31.9	15.1
P0A8M6	12760.6	S	U	T	B	ETD	LIT	5	59.6	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	52.3	17.9
P0A8M6	12760.6	S	U	T	B	ETD	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	3.5	0.0	26.2	14.8
P0A8M6	12760.6	S	U	T	B	ETD	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	31.8	15.1
P0A8M6	12760.6	S	U	T	C	ETD	LIT	5	59.6	EIQDVEKK	988.5	R	I	1.8	0.3	28.5	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8M6	12760.6	S	U	T	C	ETD	LIT	5	59.6	GDYEDRVDDYIIK	1600.7	K	N	3.4	0.6	25.9	15.1
P0A8M6	12760.6	S	U	T	C	ETD	LIT	5	59.6	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	35.5	17.2
P0A8M6	12760.6	S	U	T	C	ETD	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	4.2	0.0	37.6	14.9
P0A8M6	12760.6	S	U	T	C	ETD	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	20.1	14.9
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	2	52.3	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	38.8	17.7
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	2	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	22.7	15.4
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	GDYEDRVDDYIIK	1600.7	K	N	0.0	0.0	23.4	14.3
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	38.8	17.7
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	0.0	0.0	64.4	14.8
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	22.7	15.4
P0A8M6	12760.6	S	U	T	A	ETD+CID	LIT	5	59.6	EIQDVEKK	988.5	R	I	2.3	0.0	30.8	16.8
P0A8M6	12760.6	S	U	T	A	ETD+CID	LIT	5	59.6	GDYEDRVDDYIIK	1600.7	K	N	2.8	0.3	34.2	14.1
P0A8M6	12760.6	S	U	T	A	ETD+CID	LIT	5	59.6	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	22.7	17.7
P0A8M6	12760.6	S	U	T	A	ETD+CID	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	5.0	0.0	50.2	15.1
P0A8M6	12760.6	S	U	T	A	ETD+CID	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	42.2	15.4
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	GDYEDRVDDYIIK	1600.7	K	N	2.9	0.4	23.4	14.3
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	38.8	17.7
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	5.1	0.0	64.4	14.8
P0A8M6	12760.6	S	U	T	B	ETD+CID	LIT	4	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	22.7	15.4
P0A8M6	12760.6	S	U	T	C	ETD+CID	LIT	5	59.6	EIQDVEKK	988.5	R	I	2.6	0.3	21.7	16.8
P0A8M6	12760.6	S	U	T	C	ETD+CID	LIT	5	59.6	GDYEDRVDDYIIK	1600.7	K	N	3.2	0.4	34.1	14.3
P0A8M6	12760.6	S	U	T	C	ETD+CID	LIT	5	59.6	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	34.9	17.4
P0A8M6	12760.6	S	U	T	C	ETD+CID	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	5.2	0.0	37.0	14.6
P0A8M6	12760.6	S	U	T	C	ETD+CID	LIT	5	59.6	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	28.9	15.4
P0A8M6	12760.6	S	U	T	B	HCD	FT	4	52.3	GDYEDRVDDYIIK	1600.7	K	N	0.0	0.0	23.4	14.3
P0A8M6	12760.6	S	U	T	B	HCD	FT	4	52.3	METTKPSFQDVLEFVR	1943.0	-	L	0.0	0.0	23.1	17.7
P0A8M6	12760.6	S	U	T	B	HCD	FT	4	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMK	3018.6	R	G	0.0	0.0	64.4	14.8
P0A8M6	12760.6	S	U	T	B	HCD	FT	4	52.3	VLLLDNLSDYIKPGMSVEAIQGIIASMKGDYEDRVDDYIIK	4600.4	R	N	0.0	0.0	21.2	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AD49	12766.7	G	U	T	A	CID	LIT	4	38.1	AATSVKDANFVEEVEEE	1866.9	R	-	4.5	0.6	55.0	11.8
P0AD49	12766.7	G	U	T	A	CID	LIT	4	38.1	DANFVEEVEEE	1309.5	K	-	2.7	0.0	36.8	3.0
P0AD49	12766.7	G	U	T	A	CID	LIT	4	38.1	HEDMYTAINELINKLER	2089.0	K	Q	4.7	0.6	38.0	12.8
P0AD49	12766.7	G	U	T	A	CID	LIT	4	38.1	QMEITPAIR	1074.6	K	Q	2.1	0.6	30.9	13.2
P0AD49	12766.7	G	T	T	A	CID	LIT	2	23.0	AATSVKDANFVEEVEEE	1866.9	R	-	4.1	0.6	45.3	11.8
P0AD49	12766.7	G	T	T	A	CID	LIT	2	23.0	QMEITPAIR	1074.6	K	Q	1.9	0.6	12.1	13.2
P0AD49	12766.7	G	U	A	A	CID	LIT	3	52.2	DATINTPNGVLVASGKHE	1822.9	A	D	2.2	0.7	32.7	16.3
P0AD49	12766.7	G	U	A	A	CID	LIT	3	52.2	ERQLNKLQHKGEARRAATSVK	2420.4	L	D	2.4	0.5	0.0	0.0
P0AD49	12766.7	G	U	A	A	CID	LIT	3	52.2	TMNITSKQMEITPAIRQHVA	2285.2	M	D	0.0	0.0	24.3	14.5
P0AD49	12766.7	G	T	T	B	CID	LIT	2	15.9	QHVADRLAK	1037.6	R	L	2.2	0.5	20.5	11.8
P0AD49	12766.7	G	T	T	B	CID	LIT	2	15.9	QMEITPAIR	1058.6	K	Q	3.1	0.5	45.2	13.6
P0AD49	12766.7	G	T	A	B	CID	LIT	3	33.6	DATINTPNGVLVASGKHE	1822.9	A	D	4.0	0.6	63.6	16.3
P0AD49	12766.7	G	T	A	B	CID	LIT	3	33.6	TMNITSKQM	1069.5	M	E	0.0	0.0	25.6	13.8
P0AD49	12766.7	G	T	A	B	CID	LIT	3	33.6	TMNITSKQMEITPAIRQHVA	2269.2	M	D	0.0	0.0	26.0	14.1
P0AD49	12766.7	G	U	A	B	CID	LIT	7	84.1	DATINTPNGVLVASGKHE	1822.9	A	D	3.9	0.8	60.5	16.3
P0AD49	12766.7	G	U	A	B	CID	LIT	7	84.1	DMYTAINELINKL	1537.8	E	E	3.1	0.5	47.7	16.1
P0AD49	12766.7	G	U	A	B	CID	LIT	7	84.1	EITPAIRQHVA	1234.7	M	D	2.3	0.5	17.3	12.3
P0AD49	12766.7	G	U	A	B	CID	LIT	7	84.1	EKWQTHLINPHIILSKEPQGFVA	2685.5	L	D	3.9	0.0	12.5	14.0
P0AD49	12766.7	G	U	A	B	CID	LIT	7	84.1	ELINKL	729.5	N	E	1.8	0.0	19.5	16.9
P0AD49	12766.7	G	U	A	B	CID	LIT	7	84.1	ERQLNKLQHKGEARRAATSVK	2420.4	L	D	3.2	0.6	17.6	12.6
P0AD49	12766.7	G	U	A	B	CID	LIT	7	84.1	TMNITSKQMEITPAIRQHVA	2269.2	M	D	0.0	0.0	58.6	14.9
P0AD49	12766.7	S	U	T	A	CID	LIT	4	48.7	HEDMYTAINELINKLER	2089.0	K	Q	4.7	0.5	51.4	17.6
P0AD49	12766.7	S	U	T	A	CID	LIT	4	48.7	LAKLEK	701.5	R	W	1.7	0.4	11.3	14.5
P0AD49	12766.7	S	U	T	A	CID	LIT	4	48.7	RAATSVKDANFVEEVEEE	2023.0	R	-	4.3	0.6	63.1	18.2
P0AD49	12766.7	S	U	T	A	CID	LIT	4	48.7	WQTHLINPHIILSK	1700.0	K	E	4.3	0.5	35.0	15.3
P0AD49	12766.7	S	U	T	B	CID	LIT	4	46.0	HEDMYTAINELINKLER	2089.0	K	Q	4.7	0.6	41.7	18.1
P0AD49	12766.7	S	U	T	B	CID	LIT	4	46.0	LEKWQTHLINPHIILSK	2070.2	K	E	3.3	0.4	28.4	11.1
P0AD49	12766.7	S	U	T	B	CID	LIT	4	46.0	RAATSVKDANFVEEVEEE	2023.0	R	-	2.8	0.6	25.4	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AD49	12766.7	S	U	T	B	CID	LIT	4	46.0	WQTHLINPHIILSK	1700.0	K	E	3.7	0.0	20.4	14.9
P0AD49	12766.7	S	U	T	C	CID	LIT	3	23.0	LEKWQTHLINPHIILSK	2070.2	K	E	2.8	0.6	8.5	11.1
P0AD49	12766.7	S	U	T	C	CID	LIT	3	23.0	QMEITPAIR	1058.6	K	Q	2.5	0.3	14.7	15.8
P0AD49	12766.7	S	U	T	C	CID	LIT	3	23.0	WQTHLINPHIILSK	1700.0	K	E	2.8	0.4	12.2	15.1
P0AD49	12766.7	S	U	T	A	ETD	LIT	2	30.1	HEDMYTAINELINKLER	2089.0	K	Q	3.8	0.3	28.4	18.1
P0AD49	12766.7	S	U	T	A	ETD	LIT	2	30.1	LEKWQTHLINPHIILSK	2070.2	K	E	4.2	0.4	38.9	12.0
P0AD49	12766.7	S	U	T	B	ETD	LIT	4	38.1	HEDMYTAINELINKLER	2089.0	K	Q	4.3	0.5	30.7	18.1
P0AD49	12766.7	S	U	T	B	ETD	LIT	4	38.1	LEKWQTHLINPHIILSK	2070.2	K	E	6.1	0.0	45.8	11.1
P0AD49	12766.7	S	U	T	B	ETD	LIT	4	38.1	QMEITPAIR	1058.6	K	Q	1.9	0.5	33.2	17.3
P0AD49	12766.7	S	U	T	B	ETD	LIT	4	38.1	WQTHLINPHIILSK	1700.0	K	E	3.1	0.3	17.4	14.9
P0AD49	12766.7	S	U	T	C	ETD	LIT	4	33.6	LEKWQTHLINPHIILSK	2070.2	K	E	3.6	0.5	5.1	11.1
P0AD49	12766.7	S	U	T	C	ETD	LIT	4	33.6	QLNKLQHKGEAR	1421.8	R	R	5.6	0.6	63.5	14.9
P0AD49	12766.7	S	U	T	C	ETD	LIT	4	33.6	QMEITPAIR	1058.6	K	Q	1.4	0.5	28.5	17.6
P0AD49	12766.7	S	U	T	C	ETD	LIT	4	33.6	WQTHLINPHIILSK	1700.0	K	E	3.4	0.4	16.9	15.6
P0AD49	12766.7	S	U	T	A	ETD+CID	LIT	2	27.4	HEDMYTAINELINKLER	2089.0	K	Q	3.5	0.5	33.4	17.8
P0AD49	12766.7	S	U	T	A	ETD+CID	LIT	2	27.4	WQTHLINPHIILSK	1700.0	K	E	2.2	0.3	10.9	14.9
P0AD49	12766.7	S	U	T	B	ETD+CID	LIT	2	27.4	HEDMYTAINELINKLER	2089.0	K	Q	3.7	0.5	24.0	17.7
P0AD49	12766.7	S	U	T	B	ETD+CID	LIT	2	27.4	WQTHLINPHIILSK	1700.0	K	E	3.2	0.5	13.3	15.3
P0AD49	12766.7	S	U	T	C	ETD+CID	LIT	2	23.0	IYNEISKEAWAQWQHK	2031.0	-	-	1.3	-0.2	59.9	17.3
P0AD49	12766.7	S	U	T	C	ETD+CID	LIT	2	23.0	LEKWQTHLINPHIILSK	2070.2	K	E	2.5	0.4	4.6	11.5
P0AD49	12766.7	S	U	T	C	ETD+CID	LIT	2	23.0	QMEITPAIR	1058.6	K	Q	2.6	0.5	24.9	15.8
P0AD49	12766.7	S	U	T	C	HCD	FT	2	20.4	QMEITPAIR	1058.6	K	Q	2.2	0.0	31.7	16.6
P0AD49	12766.7	S	U	T	C	HCD	FT	2	20.4	WQTHLINPHIILSK	1700.0	K	E	4.6	0.9	79.8	15.2
P0AE48	12848.8	G	U	T	A	CID	LIT	3	29.2	IDNATLAELDALR	1414.8	R	T	4.7	0.7	77.4	13.2
P0AE48	12848.8	G	U	T	A	CID	LIT	3	29.2	IFVYGSLR	954.5	R	H	2.5	0.0	39.7	4.8
P0AE48	12848.8	G	U	T	A	CID	LIT	3	29.2	LIESGDWLDRDK	1446.7	K	-	3.6	0.8	42.6	13.0
P0AE48	12848.8	G	U	T	B	CID	LIT	2	20.4	IDNATLAELDALR	1414.8	R	T	4.6	0.6	98.2	14.3
P0AE48	12848.8	G	U	T	B	CID	LIT	2	20.4	LIESGDWLDR	1203.6	K	D	1.8	0.4	8.8	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE48	12848.8	S	U	T	A	CID	LIT	3	29.2	IDNATLAELDALR	1414.8	R	T	3.6	0.6	56.6	17.1
P0AE48	12848.8	S	U	T	A	CID	LIT	3	29.2	IFVYGSLR	954.5	R	H	2.2	0.7	27.8	11.5
P0AE48	12848.8	S	U	T	A	CID	LIT	3	29.2	LIESGDWLDRDK	1446.7	K	-	2.0	0.6	0.0	0.0
P0AE48	12848.8	S	U	T	B	CID	LIT	3	38.1	IFVYGSLR	954.5	R	H	2.1	0.7	21.3	11.5
P0AE48	12848.8	S	U	T	B	CID	LIT	3	38.1	LIESGDWLDRDK	1446.7	K	-	4.0	0.5	35.4	17.6
P0AE48	12848.8	S	U	T	B	CID	LIT	3	38.1	QLIQTPYGSAWMYVYQRPVDGLK	2713.4	R	L	3.5	0.5	0.0	0.0
P0AE48	12848.8	S	U	T	C	CID	LIT	2	22.1	IDNATLAELDALR	1414.8	R	T	2.3	0.2	6.7	16.9
P0AE48	12848.8	S	U	T	C	CID	LIT	2	22.1	LIESGDWLDRDK	1446.7	K	-	3.6	0.5	42.4	17.6
P0AE48	12848.8	S	U	T	B	ETD	LIT	2	22.1	IDNATLAELDALR	1414.8	R	T	1.6	0.5	10.3	17.1
P0AE48	12848.8	S	U	T	B	ETD	LIT	2	22.1	LIESGDWLDRDK	1446.7	K	-	5.4	0.3	35.6	17.2
P0AE48	12848.8	S	U	T	C	ETD	LIT	2	17.7	IFVYGSLR	954.5	R	H	1.9	0.4	14.2	11.5
P0AE48	12848.8	S	U	T	C	ETD	LIT	2	17.7	LIESGDWLDRDK	1446.7	K	-	3.8	0.3	23.5	17.6
P0AC69	12861.1	G	U	T	A	CID	LIT	6	58.3	FAYVDILQNPDIR	1563.8	R	A	4.3	0.8	63.5	13.0
P0AC69	12861.1	G	U	T	A	CID	LIT	6	58.3	GELQQLIK	928.5	R	E	3.2	0.5	51.4	13.4
P0AC69	12861.1	G	U	T	A	CID	LIT	6	58.3	GELQQLIKETAAK	1428.8	R	Y	2.2	0.7	34.2	12.0
P0AC69	12861.1	G	U	T	A	CID	LIT	6	58.3	LPSCGFSAQAVQALAACGER	2093.0	K	F	5.8	0.7	108.0	11.8
P0AC69	12861.1	G	U	T	A	CID	LIT	6	58.3	QIAENPILLYMK	1448.8	R	G	2.8	0.7	20.1	11.1
P0AC69	12861.1	G	U	T	A	CID	LIT	6	58.3	YKSEEPDAE	1067.5	K	-	2.4	0.0	22.7	0.0
P0AC69	12861.1	G	T	T	A	CID	LIT	2	21.7	FAYVDILQNPDIR	1563.8	R	A	3.8	0.9	47.7	13.0
P0AC69	12861.1	G	T	T	A	CID	LIT	2	21.7	QIAENPILLYMK	1432.8	R	G	1.8	0.7	0.0	0.0
P0AC69	12861.1	G	T	T	B	CID	LIT	3	32.2	GELQQLIK	928.5	R	E	2.0	0.1	0.0	0.0
P0AC69	12861.1	G	T	T	B	CID	LIT	3	32.2	LPSCGFSAQAVQALAACGER	2093.0	K	F	6.1	0.0	103.0	10.0
P0AC69	12861.1	G	T	T	B	CID	LIT	3	32.2	STTIEKIQR	1075.6	M	Q	0.0	0.0	27.2	10.0
P0AC69	12861.1	G	U	T	B	CID	LIT	5	53.9	FAYVDILQNPDIR	1563.8	R	A	5.0	0.9	54.0	12.6
P0AC69	12861.1	G	U	T	B	CID	LIT	5	53.9	GELQQLIK	928.5	R	E	3.4	0.6	67.6	13.4
P0AC69	12861.1	G	U	T	B	CID	LIT	5	53.9	LPSCGFSAQAVQALAACGER	2093.0	K	F	5.5	0.0	98.9	11.5
P0AC69	12861.1	G	U	T	B	CID	LIT	5	53.9	QIAENPILLYMK	1432.8	R	G	4.0	0.4	48.8	11.8
P0AC69	12861.1	G	U	T	B	CID	LIT	5	53.9	YKSEEPDAE	1067.5	K	-	2.5	0.0	22.9	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AC69	12861.1	G	T	A	B	CID	LIT	3	34.8	DILQNP	699.4	V	D	1.6	0.0	33.4	12.8
P0AC69	12861.1	G	T	A	B	CID	LIT	3	34.8	DIVIEMYQRG	1223.6	C	E	2.0	0.4	0.0	0.0
P0AC69	12861.1	G	T	A	B	CID	LIT	3	34.8	ELPKYANWPTFPQLWVDGELVGGC	2776.3	A	D	4.6	0.0	32.8	13.4
P0AC69	12861.1	G	U	A	B	CID	LIT	3	40.0	DIVIEMYQRG	1223.6	C	E	2.6	0.6	21.7	14.8
P0AC69	12861.1	G	U	A	B	CID	LIT	3	40.0	ELPKYANWPTFPQLWVDGELVGGC	2776.3	A	D	3.6	0.0	20.0	13.6
P0AC69	12861.1	G	U	A	B	CID	LIT	3	40.0	STTIEKIQRQIA	1387.8	M	E	0.0	0.0	31.8	11.8
P0AC69	12861.1	S	U	T	A	CID	LIT	3	40.0	FAYVDILQNPDIR	1563.8	R	A	2.2	0.6	14.1	16.4
P0AC69	12861.1	S	U	T	A	CID	LIT	3	40.0	GELQQLIKETAAK	1428.8	R	Y	3.1	0.2	22.7	15.6
P0AC69	12861.1	S	U	T	A	CID	LIT	3	40.0	LPSCGFSAQAVQALAACGER	2093.0	K	F	5.4	0.6	97.7	17.1
P0AC69	12861.1	S	U	T	B	CID	LIT	5	40.0	GELQQLIK	928.5	R	E	3.2	0.5	51.4	15.6
P0AC69	12861.1	S	U	T	B	CID	LIT	5	40.0	GELQQLIKETAAK	1428.8	R	Y	3.7	0.4	23.9	16.2
P0AC69	12861.1	S	U	T	B	CID	LIT	5	40.0	GSPKLPSCGFSAQAVQALAACGER	2462.2	K	F	3.4	0.5	10.7	18.6
P0AC69	12861.1	S	U	T	B	CID	LIT	5	40.0	LPSCGFSAQAVQALAACGER	2093.0	K	F	5.8	0.6	94.1	17.0
P0AC69	12861.1	S	U	T	B	CID	LIT	5	40.0	YKSEEPDAE	1067.5	K	-	2.3	0.0	25.5	7.8
P0AC69	12861.1	S	U	T	C	CID	LIT	5	43.5	FAYVDILQNPDIR	1563.8	R	A	2.1	0.6	6.7	15.9
P0AC69	12861.1	S	U	T	C	CID	LIT	5	43.5	GELQQLIK	928.5	R	E	3.2	0.5	50.6	16.8
P0AC69	12861.1	S	U	T	C	CID	LIT	5	43.5	GELQQLIKETAAK	1428.8	R	Y	2.7	0.3	26.0	15.6
P0AC69	12861.1	S	U	T	C	CID	LIT	5	43.5	GSPKLPSCGFSAQAVQALAACGER	2462.2	K	F	5.7	0.6	40.1	18.5
P0AC69	12861.1	S	U	T	C	CID	LIT	5	43.5	LPSCGFSAQAVQALAACGER	2093.0	K	F	4.7	0.5	47.5	17.0
P0AC69	12861.1	S	U	T	B	CID	FT	2	24.3	GELQQLIK	928.5	R	E	2.8	0.0	27.4	15.6
P0AC69	12861.1	S	U	T	B	CID	FT	2	24.3	LPSCGFSAQAVQALAACGER	2093.0	K	F	5.0	0.9	121.0	17.7
P0AC69	12861.1	S	U	T	B	ETD	LIT	4	36.5	FAYVDILQNPDIR	1563.8	R	A	1.6	0.4	20.8	16.6
P0AC69	12861.1	S	U	T	B	ETD	LIT	4	36.5	GELQQLIK	928.5	R	E	1.8	0.5	0.0	0.0
P0AC69	12861.1	S	U	T	B	ETD	LIT	4	36.5	QIAENPILLYMK	1432.8	R	G	2.0	0.4	0.0	0.0
P0AC69	12861.1	S	U	T	B	ETD	LIT	4	36.5	YKSEEPDAE	1067.5	K	-	1.9	0.7	21.5	7.8
P0AC69	12861.1	S	U	T	C	ETD	LIT	4	50.4	FAYVDILQNPDIR	1563.8	R	A	3.1	0.6	50.8	16.3
P0AC69	12861.1	S	U	T	C	ETD	LIT	4	50.4	GELQQLIKETAAK	1428.8	R	Y	2.1	0.6	12.9	16.1
P0AC69	12861.1	S	U	T	C	ETD	LIT	4	50.4	LPSCGFSAQAVQALAACGER	2093.0	K	F	3.7	0.5	13.9	17.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AC69	12861.1	S	U	T	C	ETD	LIT	4	50.4	QIAENPILLYMK	1432.8	R	G	1.8	0.5	6.3	15.8
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	4	36.5	GELQQLIK	928.5	R	E	0.0	0.0	32.4	16.8
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	4	36.5	GELQQLIKETAAK	1428.8	R	Y	0.0	0.0	28.1	16.2
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	4	36.5	LPSCGFSAQAVQALAACGER	2093.0	K	F	0.0	0.0	135.0	17.0
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	4	36.5	YKSEEPDAE	1067.5	K	-	0.0	0.0	30.6	7.8
P0AC69	12861.1	S	U	T	A	ETD+CID	LIT	2	28.7	GELQQLIKETAAK	1428.8	R	Y	2.7	0.3	10.6	16.1
P0AC69	12861.1	S	U	T	A	ETD+CID	LIT	2	28.7	LPSCGFSAQAVQALAACGER	2093.0	K	F	5.6	0.6	126.0	16.9
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	3	21.7	GELQQLIK	928.5	R	E	2.5	0.3	0.0	0.0
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	3	21.7	GELQQLIKETAAK	1428.8	R	Y	3.7	0.4	0.0	0.0
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	3	21.7	QIAENPILLYMK	1432.8	R	G	2.1	0.2	0.0	0.0
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	5	47.0	GELQQLIK	928.5	R	E	2.5	0.3	32.4	16.8
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	5	47.0	GELQQLIKETAAK	1428.8	R	Y	3.7	0.4	28.1	16.2
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	5	47.0	LPSCGFSAQAVQALAACGER	2093.0	K	F	0.0	0.0	135.0	17.0
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	5	47.0	QIAENPILLYMK	1432.8	R	G	2.1	0.2	7.6	16.8
P0AC69	12861.1	S	U	T	B	ETD+CID	LIT	5	47.0	YKSEEPDAE	1067.5	K	-	0.8	0.1	30.6	7.8
P0AC69	12861.1	S	U	T	C	ETD+CID	LIT	5	43.5	FAYVDILQNPDIR	1563.8	R	A	3.9	0.5	49.9	16.6
P0AC69	12861.1	S	U	T	C	ETD+CID	LIT	5	43.5	GELQQLIK	928.5	R	E	3.2	0.5	36.6	16.8
P0AC69	12861.1	S	U	T	C	ETD+CID	LIT	5	43.5	GELQQLIKETAAK	1428.8	R	Y	4.3	0.5	0.0	0.0
P0AC69	12861.1	S	U	T	C	ETD+CID	LIT	5	43.5	GSPKLPSCGFSAQAVQALAACGER	2462.2	K	F	4.3	0.6	50.2	18.3
P0AC69	12861.1	S	U	T	C	ETD+CID	LIT	5	43.5	LPSCGFSAQAVQALAACGER	2093.0	K	F	5.9	0.6	98.1	17.2
P0AC69	12861.1	S	U	T	B	HCD	FT	4	36.5	GELQQLIK	928.5	R	E	0.0	0.0	32.4	16.8
P0AC69	12861.1	S	U	T	B	HCD	FT	4	36.5	GELQQLIKETAAK	1428.8	R	Y	0.0	0.0	28.1	16.2
P0AC69	12861.1	S	U	T	B	HCD	FT	4	36.5	LPSCGFSAQAVQALAACGER	2093.0	K	F	0.0	0.0	135.0	17.0
P0AC69	12861.1	S	U	T	B	HCD	FT	4	36.5	YKSEEPDAE	1067.5	K	-	0.0	0.0	30.6	7.8
P38521	12862.8	G	U	T	A	CID	LIT	2	24.1	FPEGTSEEQIDK	1379.6	R	T	4.0	0.0	73.9	10.8
P38521	12862.8	G	U	T	A	CID	LIT	2	24.1	FPEGTSEEQIDKTVDDFINEVIEPNK	2993.4	R	L	6.1	0.5	70.2	10.0
P38521	12862.8	G	T	A	B	CID	LIT	2	21.3	DEVRTSELF	1095.5	L	D	3.1	0.9	28.1	14.3
P38521	12862.8	G	T	A	B	CID	LIT	2	21.3	DFINEVIEPNKLAF	1648.9	D	D	2.8	0.3	8.6	15.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76170	12891.0	G	T	T	A	CID	LIT	3	34.5	ADAAFDNR	879.4	K	D	2.9	0.0	43.3	9.5
P76170	12891.0	G	T	T	A	CID	LIT	3	34.5	DKCEQSANINAYWEPNTLR	2309.1	R	C	5.1	0.6	35.4	9.0
P76170	12891.0	G	T	T	A	CID	LIT	3	34.5	LVIESGDSAQSR	1261.6	K	Q	3.1	0.4	32.9	12.6
P76170	12891.0	G	T	A	A	CID	LIT	3	42.5	DKCEQSANINAYWEPNTLRCL	2582.2	R	D	5.3	0.0	24.2	10.8
P76170	12891.0	G	T	A	A	CID	LIT	3	42.5	DSAQSRQHAAMEKEQWN	2031.9	G	D	3.2	0.0	23.7	10.0
P76170	12891.0	G	T	A	A	CID	LIT	3	42.5	ETNKLVIESG	1089.6	A	D	2.2	0.5	15.9	15.6
P33219	12943.6	G	T	T	A	CID	LIT	3	30.5	AGMAEYQR	925.4	K	-	2.7	0.0	52.5	9.5
P33219	12943.6	G	T	T	A	CID	LIT	3	30.5	CEDLDAAGIAASVKR	1575.8	K	D	3.2	0.8	47.5	13.0
P33219	12943.6	G	T	T	A	CID	LIT	3	30.5	SADIHYQVSVDCK	1521.7	K	A	4.3	0.6	47.0	10.0
P33219	12943.6	G	U	A	A	CID	LIT	2	26.3	DAAGIAASVKR	1058.6	L	D	3.4	0.4	53.9	16.3
P33219	12943.6	G	U	A	A	CID	LIT	2	26.3	DIQGKDDKWSVPLTVRGKSA	2200.2	Q	D	2.7	0.4	22.2	15.6
P33219	12943.6	G	T	A	A	CID	LIT	6	67.8	DAAGIAASVKR	1058.6	L	D	3.6	0.4	56.4	16.3
P33219	12943.6	G	T	A	A	CID	LIT	6	67.8	DCKAGMAEYQRR	1484.7	V	-	2.1	0.8	19.0	13.6
P33219	12943.6	G	T	A	A	CID	LIT	6	67.8	DDQKIVGQADPVAWVSLQ	1969.0	A	D	3.9	0.6	52.5	15.4
P33219	12943.6	G	T	A	A	CID	LIT	6	67.8	DIHYQVSVDCKAGMAEYQRR	2426.1	A	-	2.7	0.0	11.2	11.8
P33219	12943.6	G	T	A	A	CID	LIT	6	67.8	DIQGKDDKWSVPLTVRGKSA	2200.2	Q	D	4.0	0.6	20.9	15.6
P33219	12943.6	G	T	A	A	CID	LIT	6	67.8	DYQQNRVARWA	1406.7	R	D	1.9	0.7	0.0	0.0
P33219	12943.6	G	T	T	B	CID	LIT	4	31.4	CEDLDAAGIAASVKR	1575.8	K	D	4.3	0.4	61.3	12.3
P33219	12943.6	G	T	T	B	CID	LIT	4	31.4	DYQQNRVAR	1149.6	R	W	2.2	0.6	18.2	13.4
P33219	12943.6	G	T	T	B	CID	LIT	4	31.4	RDYQQNR	979.5	K	V	2.4	0.7	16.7	12.3
P33219	12943.6	G	T	T	B	CID	LIT	4	31.4	SADIHYQVSVDCK	1521.7	K	A	4.3	0.5	43.7	11.1
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DAAGIAASVKR	1058.6	L	D	3.5	0.3	52.3	15.9
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DCKAGMAEYQRR	1500.7	V	-	2.0	0.4	11.1	11.8
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DDKWSVPLTVRGKSA	1658.9	K	D	3.5	0.8	27.1	13.4
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DDQKIVGQA	973.5	A	D	2.7	0.6	36.2	16.2
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DDQKIVGQADPVAWVSLQ	1969.0	A	D	5.3	0.0	58.4	15.3
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DIHYQVSV	960.5	A	D	1.8	0.4	14.5	16.6
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DIQGKDDKWSVPLTVRGKSA	2200.2	Q	D	2.9	0.4	8.7	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DKWSVPLTVRGKSA	1543.9	D	D	3.0	0.5	27.6	11.1
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DQKIVGQA	858.5	D	D	2.5	0.4	35.2	17.6
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DQKIVGQADPVAWVSLQ	1854.0	D	D	4.5	0.7	66.6	15.4
P33219	12943.6	G	T	A	B	CID	LIT	11	67.8	DYQQNRVARWA	1406.7	R	D	1.8	0.6	0.0	0.0
P33219	12943.6	G	U	A	B	CID	LIT	2	19.5	DAAGIAASVKR	1058.6	L	D	3.7	0.3	40.1	16.3
P33219	12943.6	G	U	A	B	CID	LIT	2	19.5	DCKAGMAEYQRR	1484.7	V	-	2.1	0.8	24.1	12.8
P33219	12943.6	S	U	T	A	CID	LIT	2	25.4	IVGQADPVAWVSLQDIQGK	2024.1	K	D	4.4	0.0	40.8	16.7
P33219	12943.6	S	U	T	A	CID	LIT	2	25.4	IVGQADPVAWVSLQDIQGKDDKWSVPLTVR	3320.8	K	G	2.2	0.0	34.5	15.8
P33219	12943.6	S	U	T	B	CID	LIT	2	25.4	IVGQADPVAWVSLQDIQGK	2024.1	K	D	5.0	0.0	55.6	16.4
P33219	12943.6	S	U	T	B	CID	LIT	2	25.4	IVGQADPVAWVSLQDIQGKDDKWSVPLTVR	3320.8	K	G	3.4	0.0	29.0	15.8
P33219	12943.6	S	U	T	C	CID	LIT	4	33.9	CEDLDAAGIAASVKR	1575.8	K	D	3.6	0.6	36.1	17.1
P33219	12943.6	S	U	T	C	CID	LIT	4	33.9	IVGQADPVAWVSLQDIQGK	2024.1	K	D	5.2	0.0	58.9	16.3
P33219	12943.6	S	U	T	C	CID	LIT	4	33.9	SVTFPKCEDLDAAGIAASVK	2079.0	K	R	2.6	0.7	35.1	18.5
P33219	12943.6	S	U	T	C	CID	LIT	4	33.9	SVTFPKCEDLDAAGIAASVKR	2235.1	K	D	4.7	0.4	26.0	18.3
P33219	12943.6	S	U	T	C	ETD	LIT	2	25.4	IVGQADPVAWVSLQDIQGK	2024.1	K	D	1.7	0.5	0.0	0.0
P33219	12943.6	S	U	T	C	ETD	LIT	2	25.4	IVGQADPVAWVSLQDIQGKDDKWSVPLTVR	3320.8	K	G	5.5	0.0	35.6	16.4
P33219	12943.6	S	U	T	C	ETD+CID	LIT	4	43.2	CEDLDAAGIAASVKR	1575.8	K	D	3.6	0.4	30.6	17.2
P33219	12943.6	S	U	T	C	ETD+CID	LIT	4	43.2	IVGQADPVAWVSLQDIQGK	2024.1	K	D	5.3	0.7	0.0	0.0
P33219	12943.6	S	U	T	C	ETD+CID	LIT	4	43.2	IVGQADPVAWVSLQDIQGKDDKWSVPLTVR	3320.8	K	G	1.8	0.0	37.3	15.6
P33219	12943.6	S	U	T	C	ETD+CID	LIT	4	43.2	SVTFPKCEDLDAAGIAASVK	2079.0	K	R	4.2	0.5	28.4	17.6
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	AILAAAGIAEDVK	1241.7	K	I	4.5	0.6	78.3	12.3
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	EISMSIK	807.4	R	R	1.7	0.7	15.6	11.5
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	EISMSIKR	979.5	R	L	1.6	0.7	36.5	15.8
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	FVVEGDLR	934.5	K	R	2.6	0.6	31.8	14.6
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	FVVEGDLRR	1090.6	K	E	1.3	0.6	25.1	12.0
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	GLPVRGQR	882.5	R	T	1.7	0.4	17.9	6.0
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	HAVIALTSIYGVGK	1428.8	K	T	4.2	0.9	61.2	10.4
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	IAGINIPDHK	1077.6	R	H	3.9	0.9	53.3	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	IAGINIPDHKHAVIALTSIYGVGK	2487.4	R	T	6.1	0.0	46.8	3.0
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	ISELSEGQIDTLR	1460.8	K	D	3.9	0.6	52.8	13.8
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.7	0.6	71.1	13.8
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	LMDLGCYR	1027.5	R	G	2.4	0.0	25.3	9.5
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	RGLPVR	697.4	R	G	2.3	0.6	24.5	6.0
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	RLMDLGCYR	1183.6	K	G	2.9	0.5	29.2	10.0
P0A7S9	13082.1	G	U	T	A	CID	LIT	15	77.1	SKAILAAAGIAEDVK	1456.8	R	I	5.2	0.7	84.7	12.0
P0A7S9	13082.1	G	T	T	A	CID	LIT	7	61.0	AILAAAGIAEDVK	1241.7	K	I	3.3	0.6	12.8	12.0
P0A7S9	13082.1	G	T	T	A	CID	LIT	7	61.0	FVVEGDLRR	1090.6	K	E	2.4	0.6	1.2	12.0
P0A7S9	13082.1	G	T	T	A	CID	LIT	7	61.0	HAVIALTSIYGVGK	1428.8	K	T	3.7	0.8	73.4	11.1
P0A7S9	13082.1	G	T	T	A	CID	LIT	7	61.0	IAGINIPDHK	1077.6	R	H	2.5	0.8	7.2	11.8
P0A7S9	13082.1	G	T	T	A	CID	LIT	7	61.0	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.0	0.6	54.7	13.8
P0A7S9	13082.1	G	T	T	A	CID	LIT	7	61.0	RGLPVR	697.4	R	G	1.9	0.0	18.3	6.0
P0A7S9	13082.1	G	T	T	A	CID	LIT	7	61.0	SKAILAAAGIAEDVK	1456.8	R	I	5.1	0.7	69.1	11.5
P0A7S9	13082.1	G	U	A	A	CID	LIT	2	18.6	DEVAKFVVEG	1092.6	R	D	3.0	0.5	30.2	17.2
P0A7S9	13082.1	G	U	A	A	CID	LIT	2	18.6	DVKISELSEGQI	1317.7	E	D	4.1	0.6	34.9	14.0
P0A7S9	13082.1	G	U	T	B	CID	LIT	7	66.1	AILAAAGIAEDVK	1241.7	K	I	4.4	0.7	54.7	12.0
P0A7S9	13082.1	G	U	T	B	CID	LIT	7	66.1	FVVEGDLRR	1090.6	K	E	2.1	0.2	9.7	12.0
P0A7S9	13082.1	G	U	T	B	CID	LIT	7	66.1	HAVIALTSIYGVGK	1428.8	K	T	3.1	0.0	13.4	10.4
P0A7S9	13082.1	G	U	T	B	CID	LIT	7	66.1	IAGINIPDHK	1077.6	R	H	3.8	0.0	48.8	11.8
P0A7S9	13082.1	G	U	T	B	CID	LIT	7	66.1	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.0	0.7	66.2	14.1
P0A7S9	13082.1	G	U	T	B	CID	LIT	7	66.1	LMDLGCYR	1027.5	R	G	2.2	0.0	20.1	7.8
P0A7S9	13082.1	G	U	T	B	CID	LIT	7	66.1	TNARTR	718.4	K	K	1.4	0.5	15.2	12.3
P0A7S9	13082.1	G	T	A	B	CID	LIT	3	22.0	DEVAKFVVEG	1092.6	R	D	2.8	0.4	18.5	17.1
P0A7S9	13082.1	G	T	A	B	CID	LIT	3	22.0	DVKISELSEGQI	1317.7	E	D	4.0	0.8	60.6	13.8
P0A7S9	13082.1	G	T	A	B	CID	LIT	3	22.0	EGQIDTLR	931.5	S	D	1.9	0.0	26.5	16.9
P0A7S9	13082.1	G	U	A	B	CID	LIT	4	29.7	ARIAGINIP	924.6	M	D	0.0	0.0	24.5	3.0
P0A7S9	13082.1	G	U	A	B	CID	LIT	4	29.7	DEVAKFVVEG	1092.6	R	D	2.8	0.5	30.2	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S9	13082.1	G	U	A	B	CID	LIT	4	29.7	DVKISELSEGQI	1317.7	E	D	4.0	0.7	64.8	14.0
P0A7S9	13082.1	G	U	A	B	CID	LIT	4	29.7	EGQIDTLR	931.5	S	D	1.9	0.7	39.4	16.9
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	AILAAAGIAEDVK	1241.7	K	I	2.4	0.3	3.5	16.2
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	4.1	0.7	36.9	15.1
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	FVVEGDLR	934.5	K	R	2.9	0.5	31.5	17.1
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	HAVIALTSIYGVGK	1428.8	K	T	4.4	0.8	60.5	14.8
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	IAGINIPDHK	1077.6	R	H	3.7	0.6	46.1	15.1
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	ISELSEGQIDTLRDEVAK	2003.0	K	F	6.0	0.5	70.1	19.1
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	REISMSIKR	1119.6	R	L	3.3	0.5	35.8	14.0
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	RGLPVR	697.4	R	G	2.1	0.0	20.4	6.0
P0A7S9	13082.1	S	U	T	A	CID	LIT	9	67.8	SKAILAAAGIAEDVK	1456.8	R	I	3.0	0.2	14.2	15.6
P0A7S9	13082.1	S	U	T	B	CID	LIT	6	46.6	AILAAAGIAEDVK	1241.7	K	I	2.6	0.7	0.0	0.0
P0A7S9	13082.1	S	U	T	B	CID	LIT	6	46.6	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	5.6	0.0	49.9	15.2
P0A7S9	13082.1	S	U	T	B	CID	LIT	6	46.6	HAVIALTSIYGVGK	1428.8	K	T	4.2	0.6	56.1	15.1
P0A7S9	13082.1	S	U	T	B	CID	LIT	6	46.6	IAGINIPDHK	1077.6	R	H	3.4	0.0	42.3	15.1
P0A7S9	13082.1	S	U	T	B	CID	LIT	6	46.6	ISELSEGQIDTLR	1460.8	K	D	2.5	0.7	10.7	17.2
P0A7S9	13082.1	S	U	T	B	CID	LIT	6	46.6	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.9	0.6	57.3	18.8
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	4.5	0.8	53.6	14.9
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	FVVEGDLR	934.5	K	R	2.6	0.7	38.1	17.2
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	FVVEGDLRR	1090.6	K	E	1.2	0.6	19.2	15.1
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	HAVIALTSIYGVGK	1428.8	K	T	4.8	0.7	67.2	15.1
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	IAGINIPDHK	1077.6	R	H	4.1	0.7	56.3	15.2
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.6	0.5	76.4	19.0
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	LMDLGCYR	1027.5	R	G	2.5	0.0	20.9	9.5
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	REISMSIKR	1119.6	R	L	3.6	0.6	39.0	14.3
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	RLMDLGCYR	1183.6	K	G	2.9	0.4	27.8	12.8
P0A7S9	13082.1	S	U	T	C	CID	LIT	10	69.5	SKAILAAAGIAEDVK	1456.8	R	I	3.2	0.4	24.8	15.4
P0A7S9	13082.1	S	U	T	A	CID	FT	2	27.1	HAVIALTSIYGVGK	1428.8	K	T	3.3	0.0	58.8	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S9	13082.1	S	U	T	A	CID	FT	2	27.1	ISELSEGQIDTLRDEVAK	2003.0	K	F	4.5	0.0	66.6	18.8
P0A7S9	13082.1	S	U	T	C	CID	FT	3	32.2	HAVIALTSIYGVGK	1428.8	K	T	3.2	0.0	20.2	15.1
P0A7S9	13082.1	S	U	T	C	CID	FT	3	32.2	RLMDLGCYR	1183.6	K	G	2.1	0.0	25.1	14.3
P0A7S9	13082.1	S	U	T	C	CID	FT	3	32.2	SKAILAAAGIAEDVK	1456.8	R	I	4.4	0.0	69.2	15.6
P0A7S9	13082.1	S	U	T	A	ETD	LIT	6	54.2	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	3.2	0.0	45.8	15.3
P0A7S9	13082.1	S	U	T	A	ETD	LIT	6	54.2	FVVEGDLR	934.5	K	R	1.7	0.4	0.0	0.0
P0A7S9	13082.1	S	U	T	A	ETD	LIT	6	54.2	FVVEGDLRR	1090.6	K	E	2.2	0.7	37.5	15.1
P0A7S9	13082.1	S	U	T	A	ETD	LIT	6	54.2	HAVIALTSIYGVGK	1428.8	K	T	2.8	0.7	0.0	0.0
P0A7S9	13082.1	S	U	T	A	ETD	LIT	6	54.2	IAGINIPDHK	1077.6	R	H	4.1	0.6	43.0	15.1
P0A7S9	13082.1	S	U	T	A	ETD	LIT	6	54.2	ISELSEGQIDTLRDEVAK	2003.0	K	F	8.1	0.5	119.0	18.6
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	AILAAAGIAEDVK	1241.7	K	I	3.5	0.3	0.0	0.0
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	0.0	0.0	26.9	14.9
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	FVVEGDLR	934.5	K	R	1.6	0.0	36.9	17.0
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	FVVEGDLRR	1090.6	K	E	3.5	0.4	17.5	15.2
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	HAVIALTSIYGVGK	1428.8	K	T	3.6	0.6	0.0	0.0
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	IAGINIPDHK	1077.6	R	H	4.2	0.7	45.0	15.4
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	ISELSEGQIDTLRDEVAK	2003.0	K	F	7.1	0.4	95.0	18.5
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	LMDLGCYR	1027.5	R	G	1.6	0.6	12.1	10.8
P0A7S9	13082.1	S	U	T	B	ETD	LIT	9	61.9	RLMDLGCYR	1183.6	K	G	1.8	0.5	8.5	14.3
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	AILAAAGIAEDVK	1241.7	K	I	2.4	0.2	18.7	16.1
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	FVVEGDLR	934.5	K	R	1.8	0.0	52.8	17.2
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	FVVEGDLRR	1090.6	K	E	3.6	0.7	21.8	15.2
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	HAVIALTSIYGVGK	1428.8	K	T	3.2	0.6	49.1	14.8
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	IAGINIPDHK	1077.6	R	H	4.0	0.6	0.0	0.0
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.6	0.3	88.5	18.4
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	LMDLGCYR	1027.5	R	G	1.2	0.7	17.6	9.5
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	REISMSIK	963.5	R	R	3.0	0.2	72.8	17.2
P0A7S9	13082.1	S	U	T	C	ETD	LIT	9	67.8	RLMDLGCYR	1183.6	K	G	1.5	0.4	12.6	12.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	4	45.8	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	0.0	0.0	49.3	14.9
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	4	45.8	HAVIALTSIYGVGK	1428.8	K	T	0.0	0.0	50.6	14.6
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	4	45.8	ISELSEGQIDTLRDEVAK	2003.0	K	F	0.0	0.0	55.0	18.8
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	4	45.8	REISMSIKR	1119.6	R	L	0.0	0.0	34.1	12.3
P0A7S9	13082.1	S	U	T	A	ETD+CID	LIT	4	39.8	AILAAAGIAEDVK	1241.7	K	I	2.6	0.7	2.4	15.7
P0A7S9	13082.1	S	U	T	A	ETD+CID	LIT	4	39.8	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	5.4	0.0	59.3	15.2
P0A7S9	13082.1	S	U	T	A	ETD+CID	LIT	4	39.8	HAVIALTSIYGVGK	1428.8	K	T	4.0	0.6	56.8	15.1
P0A7S9	13082.1	S	U	T	A	ETD+CID	LIT	4	39.8	ISELSEGQIDTLRDEVAK	2003.0	K	F	6.0	0.5	75.1	19.1
P0A7S9	13082.1	S	U	T	A	ETD+CID	LIT	4	39.8	SKAILAAAGIAEDVK	1456.8	R	I	2.8	0.3	3.2	15.6
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	2	30.5	AILAAAGIAEDVK	1241.7	K	I	2.1	0.5	0.0	0.0
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	2	30.5	FVVEGDLRR	1090.6	K	E	2.4	0.2	0.0	0.0
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	2	30.5	HAVIALTSIYGVGK	1428.8	K	T	4.0	0.6	0.0	0.0
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	6	52.5	AILAAAGIAEDVK	1241.7	K	I	2.1	0.5	1.7	15.4
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	6	52.5	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	5.2	0.0	42.7	15.1
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	6	52.5	EISMSIK	807.4	R	R	1.6	0.5	10.9	12.3
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	6	52.5	FVVEGDLRR	1090.6	K	E	2.4	0.2	0.0	0.0
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	6	52.5	HAVIALTSIYGVGK	1428.8	K	T	4.0	0.6	37.4	15.3
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	6	52.5	ISELSEGQIDTLRDEVAK	2003.0	K	F	2.9	0.6	48.2	18.9
P0A7S9	13082.1	S	U	T	B	ETD+CID	LIT	6	52.5	REISMSIKR	1119.6	R	L	3.9	0.5	34.1	12.3
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	AILAAAGIAEDVK	1241.7	K	I	2.4	0.6	0.0	0.0
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	5.3	0.0	48.9	15.4
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	FVVEGDLRR	1090.6	K	E	3.1	0.7	25.4	15.2
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	HAVIALTSIYGVGK	1428.8	K	T	4.3	0.8	58.0	15.1
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	IAGINIPDHK	1077.6	R	H	4.1	0.6	57.0	15.2
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.7	0.6	72.5	18.2
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	MNKDEAGGNWK	1249.6	-	-	1.3	-0.3	45.4	13.4
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	RLMDLGCYR	1183.6	K	G	3.0	0.5	29.2	12.8
P0A7S9	13082.1	S	U	T	C	ETD+CID	LIT	7	63.6	SKAILAAAGIAEDVK	1456.8	R	I	4.9	0.6	66.4	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S9	13082.1	S	U	T	B	HCD	FT	4	45.8	AILAAAGIAEDVKISELSEGQIDTLRDEVAK	3225.7	K	F	0.0	0.0	49.3	14.9
P0A7S9	13082.1	S	U	T	B	HCD	FT	4	45.8	HAVIALTSIYGVGK	1428.8	K	T	0.0	0.0	50.6	14.6
P0A7S9	13082.1	S	U	T	B	HCD	FT	4	45.8	ISELSEGQIDTLRDEVAK	2003.0	K	F	0.0	0.0	55.0	18.8
P0A7S9	13082.1	S	U	T	B	HCD	FT	4	45.8	REISMSIKR	1119.6	R	L	0.0	0.0	34.1	12.3
P0A7S9	13082.1	S	U	T	A	HCD	FT	2	27.1	HAVIALTSIYGVGK	1428.8	K	T	3.4	0.8	57.0	14.8
P0A7S9	13082.1	S	U	T	A	HCD	FT	2	27.1	ISELSEGQIDTLRDEVAK	2003.0	K	F	5.0	0.7	82.3	19.1
P0A7S9	13082.1	S	U	T	B	HCD	FT	2	22.0	FVVEGDLR	934.5	K	R	1.6	0.7	34.6	17.2
P0A7S9	13082.1	S	U	T	B	HCD	FT	2	22.0	ISELSEGQIDTLRDEVAK	2003.0	K	F	2.9	0.0	31.3	18.9
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	AKLYYLR	926.5	K	E	2.1	0.7	20.5	6.0
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	GLHSAFTVR	987.5	R	K	2.7	0.7	36.8	14.3
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	GLHSAFTVRK	1115.6	R	I	2.5	0.8	22.0	12.8
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	ISNGEGVER	960.5	K	V	2.9	0.4	41.5	13.2
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	KISNGEGVER	1088.6	R	V	3.2	0.5	48.3	15.1
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	LQAFEGVVIAIR	1315.8	R	N	3.4	0.0	56.8	9.0
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	LYYLRER	1012.6	K	T	2.2	0.0	22.6	10.8
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	NRGLHSAFTVR	1257.7	R	K	2.5	0.7	17.0	15.1
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	QDVPSFRPGDTVEVK	1673.9	K	V	3.1	0.7	39.2	13.4
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	QLEQEQMK	1033.5	K	Q	2.6	0.6	30.7	11.5
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	QLEQEQMKQDVPSFRPGDTVEVK	2704.3	K	V	3.8	0.8	20.6	10.0
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	SNIIKQLEQEQMK	1588.8	M	Q	0.0	0.0	40.0	14.3
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	VFQTHSPVVDSISVK	1642.9	R	R	5.0	0.7	65.2	12.0
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	VFQTHSPVVDSISVKR	1799.0	R	R	5.8	0.8	60.9	10.8
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	VWVVEGSK	903.5	K	K	2.2	0.7	26.1	15.9
P0A7K6	13115.0	G	U	T	A	CID	LIT	16	82.6	VWVVEGSKK	1031.6	K	R	2.4	0.7	25.8	14.9
P0A7K6	13115.0	G	U	T	B	CID	LIT	5	43.5	GLHSAFTVR	987.5	R	K	3.1	0.6	23.3	14.9
P0A7K6	13115.0	G	U	T	B	CID	LIT	5	43.5	KISNGEGVER	1088.6	R	V	1.8	0.4	32.4	14.6
P0A7K6	13115.0	G	U	T	B	CID	LIT	5	43.5	QLEQEQMK	1033.5	K	Q	2.6	0.0	33.6	11.5
P0A7K6	13115.0	G	U	T	B	CID	LIT	5	43.5	VFQTHSPVVDSISVK	1642.9	R	R	4.8	0.0	55.7	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7K6	13115.0	G	U	T	B	CID	LIT	5	43.5	VWVVEGSK	903.5	K	K	2.0	0.0	20.9	15.7
P0A7K6	13115.0	G	U	A	B	CID	LIT	2	12.2	SNIIKQL	815.5	M	E	0.0	0.0	23.8	13.0
P0A7K6	13115.0	G	U	A	B	CID	LIT	2	12.2	SNIIKQLEQEQMKQ	1716.9	M	D	0.0	0.0	59.3	14.3
P0A7K6	13115.0	S	U	T	A	CID	LIT	6	53.0	ISNGEGVER	961.5	K	V	2.6	0.4	12.0	15.6
P0A7K6	13115.0	S	U	T	A	CID	LIT	6	53.0	KISNGEGVER	1089.6	R	V	3.6	0.6	43.4	16.8
P0A7K6	13115.0	S	U	T	A	CID	LIT	6	53.0	LQAFEGVVIAIR	1315.8	R	N	3.6	0.6	47.9	12.6
P0A7K6	13115.0	S	U	T	A	CID	LIT	6	53.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	4.0	0.4	16.5	19.1
P0A7K6	13115.0	S	U	T	A	CID	LIT	6	53.0	RLQAFEGVVIAIR	1471.9	K	N	3.1	0.8	38.3	9.0
P0A7K6	13115.0	S	U	T	A	CID	LIT	6	53.0	VFQTHSPVVDSISVK	1642.9	R	R	4.9	0.6	74.0	17.8
P0A7K6	13115.0	S	U	T	B	CID	LIT	7	53.0	ISNGEGVER	961.5	K	V	2.6	0.5	41.8	15.6
P0A7K6	13115.0	S	U	T	B	CID	LIT	7	53.0	KISNGEGVER	1088.6	R	V	3.3	0.5	60.1	17.3
P0A7K6	13115.0	S	U	T	B	CID	LIT	7	53.0	LQAFEGVVIAIR	1315.8	R	N	3.7	0.7	45.7	12.3
P0A7K6	13115.0	S	U	T	B	CID	LIT	7	53.0	QDVPSFRPGDTVEVK	1673.9	K	V	2.9	0.3	14.6	18.0
P0A7K6	13115.0	S	U	T	B	CID	LIT	7	53.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	3.8	0.2	5.6	19.4
P0A7K6	13115.0	S	U	T	B	CID	LIT	7	53.0	RLQAFEGVVIAIR	1471.9	K	N	2.8	0.7	30.7	8.5
P0A7K6	13115.0	S	U	T	B	CID	LIT	7	53.0	VFQTHSPVVDSISVK	1642.9	R	R	4.6	0.7	75.1	17.0
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	ISNGEGVER	961.5	K	V	2.5	0.5	35.3	15.6
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	KISNGEGVER	1088.6	R	V	3.0	0.5	33.4	17.3
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	LQAFEGVVIAIR	1315.8	R	N	3.5	0.6	50.9	12.6
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	QDVPSFRPGDTVEVK	1673.9	K	V	3.2	0.5	30.9	17.0
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	3.8	0.3	16.0	19.3
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	RLQAFEGVVIAIR	1471.9	K	N	3.1	0.0	27.1	9.0
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	VFQTHSPVVDSISVK	1642.9	R	R	5.0	0.6	65.2	18.1
P0A7K6	13115.0	S	U	T	C	CID	LIT	8	53.9	VFQTHSPVVDSISVKR	1799.0	R	R	5.4	0.6	68.7	15.8
P0A7K6	13115.0	S	U	T	B	CID	FT	3	32.2	KISNGEGVER	1089.6	R	V	3.2	0.0	36.6	15.9
P0A7K6	13115.0	S	U	T	B	CID	FT	3	32.2	LQAFEGVVIAIR	1315.8	R	N	1.7	0.0	39.5	12.6
P0A7K6	13115.0	S	U	T	B	CID	FT	3	32.2	VFQTHSPVVDSISVK	1642.9	R	R	2.8	0.0	52.3	17.6
P0A7K6	13115.0	S	U	T	C	CID	FT	3	33.0	KISNGEGVER	1088.6	R	V	1.3	0.0	22.5	17.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7K6	13115.0	S	U	T	C	CID	FT	3	33.0	LQAFEGVVIAIR	1315.8	R	N	2.3	0.0	37.5	12.3
P0A7K6	13115.0	S	U	T	C	CID	FT	3	33.0	VFQTHSPVVDSISVKR	1799.0	R	R	4.5	0.0	70.7	15.8
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	ISNGEGVER	961.5	K	V	2.8	0.3	39.7	15.8
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	KISNGEGVER	1088.6	R	V	3.3	0.5	45.7	17.2
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	LQAFEGVVIAIR	1315.8	R	N	2.4	0.4	50.7	12.6
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	LYYLR	727.4	K	E	1.9	0.2	31.8	16.3
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	4.0	0.5	38.5	18.5
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	RLQAFEGVVIAIR	1471.9	K	N	3.4	0.9	0.0	0.0
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	VFQTHSPVVDSISVK	1642.9	R	R	5.1	0.5	62.8	17.7
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	VFQTHSPVVDSISVKR	1799.0	R	R	6.3	0.7	67.1	15.8
P0A7K6	13115.0	S	U	T	A	ETD	LIT	9	65.2	VWVVEGSK	903.5	K	K	2.5	0.4	27.1	14.9
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	GLHSAFTVR	987.5	R	K	4.7	0.6	43.2	17.0
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	ISNGEGVER	961.5	K	V	2.5	0.1	28.5	15.6
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	KISNGEGVER	1089.6	R	V	3.6	0.6	48.3	17.2
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	LQAFEGVVIAIR	1315.8	R	N	1.8	0.6	28.4	12.6
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	LYYLR	727.4	K	E	1.4	0.2	30.8	16.3
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	QDVPSFRPGDTVEVK	1673.9	K	V	4.4	0.5	48.0	18.5
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	4.8	0.0	34.3	18.5
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	RLQAFEGVVIAIR	1471.9	K	N	3.1	0.0	50.6	9.0
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	VFQTHSPVVDSISVK	1642.9	R	R	4.9	0.6	65.5	17.2
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	VFQTHSPVVDSISVKR	1799.0	R	R	2.9	0.7	74.6	15.8
P0A7K6	13115.0	S	U	T	B	ETD	LIT	11	73.0	VWVVEGSK	903.5	K	K	0.0	0.0	25.2	16.8
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	ISNGEGVER	961.5	K	V	3.0	0.3	38.4	15.2
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	KISNGEGVER	1089.6	R	V	4.1	0.6	46.3	16.3
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	LQAFEGVVIAIR	1315.8	R	N	1.7	0.6	50.8	12.6
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	LYYLR	727.4	K	E	1.9	0.4	32.0	16.3
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	LYYLRER	1012.6	K	T	1.8	0.4	15.7	13.6
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	QDVPSFRPGDTVEVK	1673.9	K	V	4.5	0.5	41.3	18.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	3.6	0.5	56.3	18.8
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	RLQAFEGVVIAIR	1471.9	K	N	3.0	0.0	40.4	9.0
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	VFQTHSPVVDSISVK	1642.9	R	R	6.2	0.6	78.8	18.1
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	VFQTHSPVVDSISVKR	1799.0	R	R	6.0	0.5	60.8	15.4
P0A7K6	13115.0	S	U	T	C	ETD	LIT	11	67.0	VWVVEGSK	903.5	K	K	2.3	0.6	29.4	16.7
P0A7K6	13115.0	S	U	T	B	ETD	FT	2	12.2	ISNGEGVER	961.5	K	V	1.6	0.0	35.5	15.6
P0A7K6	13115.0	S	U	T	B	ETD	FT	2	12.2	LYYLR	727.4	K	E	1.1	0.0	35.9	9.0
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	3	40.0	KISNGEGVER	1088.6	R	V	0.0	0.0	39.3	17.3
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	3	40.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	0.0	0.0	32.1	18.7
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	3	40.0	RLQAFEGVVIAIR	1471.9	K	N	0.0	0.0	23.8	9.0
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	4	40.0	ISNGEGVER	961.5	K	V	0.0	0.0	37.6	15.6
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	4	40.0	KISNGEGVER	1088.6	R	V	0.0	0.0	39.3	17.3
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	4	40.0	LQAFEGVVIAIR	1315.8	R	N	0.0	0.0	45.9	12.6
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	4	40.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	0.0	0.0	32.1	18.7
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	4	40.0	RLQAFEGVVIAIR	1471.9	K	N	0.0	0.0	31.8	9.0
P0A7K6	13115.0	S	U	T	A	ETD+CID	LIT	5	53.0	ISNGEGVER	961.5	K	V	2.2	0.3	30.9	15.8
P0A7K6	13115.0	S	U	T	A	ETD+CID	LIT	5	53.0	KISNGEGVER	1088.6	R	V	3.0	0.7	19.0	17.3
P0A7K6	13115.0	S	U	T	A	ETD+CID	LIT	5	53.0	LQAFEGVVIAIR	1315.8	R	N	3.7	0.5	44.9	12.6
P0A7K6	13115.0	S	U	T	A	ETD+CID	LIT	5	53.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	4.3	0.5	15.4	18.5
P0A7K6	13115.0	S	U	T	A	ETD+CID	LIT	5	53.0	RLQAFEGVVIAIR	1471.9	K	N	2.4	0.3	8.3	9.0
P0A7K6	13115.0	S	U	T	A	ETD+CID	LIT	5	53.0	VFQTHSPVVDSISVK	1642.9	R	R	4.1	0.4	16.3	17.0
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	5	44.3	ISNGEGVER	961.5	K	V	1.5	0.3	37.6	15.6
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	5	44.3	KISNGEGVER	1088.6	R	V	3.1	0.0	36.1	17.3
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	5	44.3	LQAFEGVVIAIR	1315.8	R	N	3.8	0.6	45.9	12.6
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	5	44.3	LYYLR	727.4	K	E	1.2	0.6	15.0	9.0
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	5	44.3	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	3.9	0.1	25.1	19.4
P0A7K6	13115.0	S	U	T	B	ETD+CID	LIT	5	44.3	RLQAFEGVVIAIR	1471.9	K	N	2.6	0.4	20.7	9.0
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	GLHSAFTVR	987.5	R	K	2.3	0.5	18.3	17.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	ISNGEGVER	961.5	K	V	2.5	0.4	38.9	15.6
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	KISNGEGVER	1088.6	R	V	3.1	0.4	30.5	17.2
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	LQAFEGVVIAIR	1315.8	R	N	3.2	0.4	41.7	12.6
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	QDVPSFRPGDTVEVK	1673.9	K	V	5.0	0.5	59.3	18.0
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	2.8	0.2	9.5	18.5
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	RLQAFEGVVIAIR	1471.9	K	N	4.1	0.8	0.0	0.0
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	VFQTHSPVVDSISVKR	1799.0	R	R	5.1	0.6	60.4	15.3
P0A7K6	13115.0	S	U	T	C	ETD+CID	LIT	8	68.7	VWVVEGSK	903.5	K	K	2.0	0.4	9.5	15.4
P0A7K6	13115.0	S	U	T	B	HCD	FT	4	40.0	ISNGEGVER	961.5	K	V	0.0	0.0	37.6	15.6
P0A7K6	13115.0	S	U	T	B	HCD	FT	4	40.0	KISNGEGVER	1089.6	R	V	0.0	0.0	43.1	16.0
P0A7K6	13115.0	S	U	T	B	HCD	FT	4	40.0	LQAFEGVVIAIR	1315.8	R	N	0.0	0.0	45.9	12.6
P0A7K6	13115.0	S	U	T	B	HCD	FT	4	40.0	QLEQEQMKQDVPSFRPGDTVEVK	2688.3	K	V	0.0	0.0	25.1	19.4
P0A7K6	13115.0	S	U	T	B	HCD	FT	4	40.0	RLQAFEGVVIAIR	1471.9	K	N	0.0	0.0	31.8	9.0
P0A7K6	13115.0	S	U	T	C	HCD	FT	2	21.7	GLHSAFTVR	987.5	R	K	2.8	0.5	26.1	14.9
P0A7K6	13115.0	S	U	T	C	HCD	FT	2	21.7	VFQTHSPVVDSISVKR	1799.0	R	R	2.4	0.0	52.7	15.3
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	EAQLLER	858.5	K	H	1.8	0.5	16.8	14.9
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	4.7	0.0	65.2	4.8
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	GEREPVTEAER	1272.6	R	V	3.5	0.6	33.8	12.8
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	HGDFTIK	817.4	R	E	2.7	0.6	27.0	12.6
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	HGDFTIKEAQLLER	1656.9	R	H	3.8	0.8	57.3	12.6
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	HGYAFNELDLGK	1363.7	R	R	5.0	0.9	72.3	14.1
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	HGYAFNELDLGKR	1519.8	R	E	4.8	0.8	56.3	15.3
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	4.3	0.0	70.8	6.0
P0ADN2	13115.7	G	U	T	A	CID	LIT	9	62.5	YFDNKHYPR	1239.6	R	G	3.4	0.6	52.7	12.3
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	AESFTTTNR	1026.5	M	Y	0.0	0.0	29.8	4.8
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	EAQLLER	858.5	K	H	2.0	0.4	18.5	14.9
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	EPVTEAER	930.5	R	V	1.8	0.6	33.9	9.5
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	4.8	0.0	59.4	3.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	GEREPVTEAER	1272.6	R	V	3.5	0.6	33.2	11.8
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	HGDFTIK	817.4	R	E	2.4	0.6	24.6	14.9
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	HGYAFNELDLGK	1363.7	R	R	3.0	0.7	12.3	14.1
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	LFVAVCR	864.5	K	G	1.6	0.5	12.1	9.5
P0ADN2	13115.7	G	T	T	A	CID	LIT	9	67.9	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	4.3	0.0	57.3	3.0
P0ADN2	13115.7	G	U	A	A	CID	LIT	3	30.4	AESFTTTNRYF	1336.6	M	D	0.0	0.0	48.2	15.2
P0ADN2	13115.7	G	U	A	A	CID	LIT	3	30.4	DNKHYPRGFSRHG	1570.8	F	D	1.9	0.7	0.0	0.0
P0ADN2	13115.7	G	U	A	A	CID	LIT	3	30.4	ERHGYAFNEL	1235.6	L	D	2.6	0.2	25.8	14.8
P0ADN2	13115.7	G	T	T	B	CID	LIT	2	16.1	GEREPVTEAER	1272.6	R	V	3.2	0.4	31.4	13.0
P0ADN2	13115.7	G	T	T	B	CID	LIT	2	16.1	HGDFTIK	817.4	R	E	2.8	0.4	15.3	14.9
P0ADN2	13115.7	G	U	T	B	CID	LIT	2	17.9	AESFTTTNR	1026.5	M	Y	0.0	0.0	33.1	4.8
P0ADN2	13115.7	G	U	T	B	CID	LIT	2	17.9	GEREPVTEAER	1272.6	R	V	3.2	0.0	28.7	12.8
P0ADN2	13115.7	G	T	A	B	CID	LIT	4	36.6	AESFTTTNRYF	1336.6	M	D	0.0	0.0	21.9	14.9
P0ADN2	13115.7	G	T	A	B	CID	LIT	4	36.6	DFTIKEAQLL	1177.6	G	E	1.9	0.5	0.0	0.0
P0ADN2	13115.7	G	T	A	B	CID	LIT	4	36.6	DLGKREPVTE	1143.6	L	E	2.3	0.8	14.6	14.6
P0ADN2	13115.7	G	T	A	B	CID	LIT	4	36.6	ERHGYAFNEL	1235.6	L	D	3.1	0.4	30.8	14.8
P0ADN2	13115.7	G	U	A	B	CID	LIT	4	27.7	AESFTTTNRYF	1336.6	M	D	0.0	0.0	39.5	15.1
P0ADN2	13115.7	G	U	A	B	CID	LIT	4	27.7	DFTIKEAQLL	1177.6	G	E	2.9	0.6	36.8	12.8
P0ADN2	13115.7	G	U	A	B	CID	LIT	4	27.7	EAQLLERHGYAFNEL	1789.9	K	D	4.3	0.9	32.0	14.8
P0ADN2	13115.7	G	U	A	B	CID	LIT	4	27.7	ERHGYAFNEL	1235.6	L	D	3.0	0.3	18.1	15.1
P0ADN2	13115.7	S	U	T	A	CID	LIT	7	64.3	AESFTTTNR	1026.5	M	Y	0.0	0.0	31.5	10.8
P0ADN2	13115.7	S	U	T	A	CID	LIT	7	64.3	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	5.8	0.0	73.2	11.1
P0ADN2	13115.7	S	U	T	A	CID	LIT	7	64.3	GEREPVTEAER	1272.6	R	V	3.1	0.7	34.0	14.0
P0ADN2	13115.7	S	U	T	A	CID	LIT	7	64.3	HGYAFNELDLGK	1363.7	R	R	4.4	0.7	51.8	17.1
P0ADN2	13115.7	S	U	T	A	CID	LIT	7	64.3	HGYAFNELDLGKR	1519.8	R	E	4.2	0.7	74.3	18.7
P0ADN2	13115.7	S	U	T	A	CID	LIT	7	64.3	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	5.6	0.6	42.2	17.5
P0ADN2	13115.7	S	U	T	A	CID	LIT	7	64.3	YFDNKHYPR	1239.6	R	G	2.4	0.6	24.1	14.8
P0ADN2	13115.7	S	U	T	B	CID	LIT	7	62.5	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	5.5	0.0	62.4	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADN2	13115.7	S	U	T	B	CID	LIT	7	62.5	GEREPVTEAER	1272.6	R	V	2.8	0.7	20.3	13.4
P0ADN2	13115.7	S	U	T	B	CID	LIT	7	62.5	HGYAFNELDLGK	1363.7	R	R	4.6	0.8	59.1	16.4
P0ADN2	13115.7	S	U	T	B	CID	LIT	7	62.5	HGYAFNELDLGKR	1519.8	R	E	4.0	0.6	51.4	18.4
P0ADN2	13115.7	S	U	T	B	CID	LIT	7	62.5	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	6.1	0.6	53.6	17.8
P0ADN2	13115.7	S	U	T	B	CID	LIT	7	62.5	LFVAVCR	864.5	K	G	2.1	0.6	32.3	9.5
P0ADN2	13115.7	S	U	T	B	CID	LIT	7	62.5	YFDNKHYPR	1239.6	R	G	3.3	0.5	38.9	14.0
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	5.9	0.8	60.8	10.8
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	GEREPVTEAER	1272.6	R	V	2.5	0.5	18.0	13.8
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	GEREPVTEAERVWSK	1772.9	R	Y	3.3	0.3	14.4	16.6
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	HGYAFNELDLGK	1363.7	R	R	4.7	0.6	52.3	17.1
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	HGYAFNELDLGKR	1519.8	R	E	4.7	0.7	60.6	18.3
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	5.7	0.6	51.6	17.8
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	LFVAVCRGEREPVTEAER	2118.1	K	V	2.8	0.4	3.6	18.3
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	REPVTEEEK	1116.6	K	L	2.0	0.2	10.8	16.2
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	REPVTEEEKLFVAVCR	1962.0	K	G	3.6	0.5	18.6	18.6
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	4.4	0.7	65.1	13.2
P0ADN2	13115.7	S	U	T	C	CID	LIT	11	67.0	YFDNKHYPR	1239.6	R	G	3.2	0.5	44.6	15.4
P0ADN2	13115.7	S	U	T	A	CID	FT	3	32.1	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	3.3	0.0	38.8	10.0
P0ADN2	13115.7	S	U	T	A	CID	FT	3	32.1	HGYAFNELDLGKR	1519.8	R	E	2.7	0.0	19.3	18.6
P0ADN2	13115.7	S	U	T	A	CID	FT	3	32.1	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	3.1	0.0	42.7	13.2
P0ADN2	13115.7	S	U	T	B	CID	FT	2	29.5	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	3.3	0.0	22.9	11.1
P0ADN2	13115.7	S	U	T	B	CID	FT	2	29.5	GEREPVTEAER	1272.6	R	V	2.9	0.0	23.2	13.8
P0ADN2	13115.7	S	U	T	C	CID	FT	4	48.2	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	4.1	0.0	63.8	10.0
P0ADN2	13115.7	S	U	T	C	CID	FT	4	48.2	HGYAFNELDLGKR	1519.8	R	E	3.3	0.8	55.2	17.8
P0ADN2	13115.7	S	U	T	C	CID	FT	4	48.2	LFVAVCRGEREPVTEAER	2118.1	K	V	2.8	0.0	13.9	18.2
P0ADN2	13115.7	S	U	T	C	CID	FT	4	48.2	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	3.3	0.0	18.7	13.0
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	GEREPVTEAER	1272.6	R	V	4.5	0.5	50.7	13.8
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	GEREPVTEAERVWSK	1772.9	R	Y	5.4	0.6	16.3	16.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	HGYAFNELDLGK	1363.7	R	R	2.1	0.4	16.1	17.1
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	HGYAFNELDLGKR	1519.8	R	E	2.1	0.6	0.0	0.0
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	7.3	0.0	52.2	17.8
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	LFVAVCRGEREPVTEAER	2118.1	K	V	4.2	0.6	0.0	0.0
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	0.0	0.0	49.9	12.8
P0ADN2	13115.7	S	U	T	A	ETD	LIT	8	67.0	YFDNKHYPR	1239.6	R	G	3.2	0.4	33.7	14.0
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	GEREPVTEAER	1272.6	R	V	3.7	0.5	57.7	13.8
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	GEREPVTEAERVWSK	1772.9	R	Y	4.5	0.6	31.2	16.0
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	HGYAFNELDLGK	1363.7	R	R	2.3	0.4	22.1	17.1
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	HGYAFNELDLGKR	1519.8	R	E	5.7	0.6	0.0	0.0
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	0.0	0.0	40.3	18.1
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	LFVAVCR	864.5	K	G	1.5	0.6	28.8	10.0
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	LFVAVCRGEREPVTEAER	2118.1	K	V	3.1	0.4	12.2	18.2
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	2.7	0.0	18.9	13.2
P0ADN2	13115.7	S	U	T	B	ETD	LIT	9	67.0	YFDNKHYPR	1239.6	R	G	2.7	0.2	25.3	14.0
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	4.2	0.0	49.5	10.8
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	GEREPVTEAER	1272.6	R	V	3.8	0.4	47.6	14.3
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	GEREPVTEAERVWSK	1772.9	R	Y	4.5	0.5	33.9	16.0
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	HGYAFNELDLGK	1363.7	R	R	2.6	0.4	21.5	15.8
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	HGYAFNELDLGKR	1519.8	R	E	5.1	0.5	43.3	17.9
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	4.7	0.5	47.7	17.7
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	LFVAVCRGEREPVTEAER	2118.1	K	V	5.1	0.5	49.3	18.1
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	5.6	0.6	42.0	13.2
P0ADN2	13115.7	S	U	T	C	ETD	LIT	9	67.0	YFDNKHYPR	1239.6	R	G	2.5	0.4	3.7	14.3
P0ADN2	13115.7	S	U	T	C	ETD	FT	3	47.3	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	2.4	0.0	18.0	10.8
P0ADN2	13115.7	S	U	T	C	ETD	FT	3	47.3	HGYAFNELDLGKR	1519.8	R	E	2.5	0.0	39.3	18.4
P0ADN2	13115.7	S	U	T	C	ETD	FT	3	47.3	LFVAVCRGEREPVTEAER	2118.1	K	V	3.4	0.0	33.2	18.1
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	5	49.1	GEREPVTEAER	1272.6	R	V	0.0	0.0	17.0	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	5	49.1	HGYAFNELDLGK	1363.7	R	R	0.0	0.0	69.5	17.0
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	5	49.1	HGYAFNELDLGKR	1519.8	R	E	0.0	0.0	67.7	18.8
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	5	49.1	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	0.0	0.0	20.8	17.9
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	5	49.1	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	0.0	0.0	40.6	13.2
P0ADN2	13115.7	S	U	T	A	ETD+CID	LIT	7	57.1	FHTLSGGKPQVEGAEDYTDSDD	2368.0	R	-	5.7	0.0	60.5	10.8
P0ADN2	13115.7	S	U	T	A	ETD+CID	LIT	7	57.1	GEREPVTEAER	1272.6	R	V	3.1	0.7	24.5	14.0
P0ADN2	13115.7	S	U	T	A	ETD+CID	LIT	7	57.1	HGYAFNELDLGK	1363.7	R	R	3.9	0.6	42.7	16.4
P0ADN2	13115.7	S	U	T	A	ETD+CID	LIT	7	57.1	HGYAFNELDLGKR	1519.8	R	E	3.9	0.6	67.0	18.3
P0ADN2	13115.7	S	U	T	A	ETD+CID	LIT	7	57.1	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	3.4	0.6	5.2	17.7
P0ADN2	13115.7	S	U	T	A	ETD+CID	LIT	7	57.1	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	3.1	0.6	0.0	0.0
P0ADN2	13115.7	S	U	T	A	ETD+CID	LIT	7	57.1	YFDNKHYPR	1239.6	R	G	1.6	0.4	15.3	14.0
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	2	18.8	HGYAFNELDLGKR	1519.8	R	E	3.3	0.4	0.0	0.0
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	2	18.8	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	3.9	0.6	0.0	0.0
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	6	57.1	GEREPVTEAER	1272.6	R	V	2.6	0.8	17.0	13.4
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	6	57.1	HGYAFNELDLGK	1363.7	R	R	4.6	0.6	69.5	17.0
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	6	57.1	HGYAFNELDLGKR	1519.8	R	E	5.8	0.7	67.7	18.8
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	6	57.1	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	3.9	0.6	20.8	17.9
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	6	57.1	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	1.2	0.0	40.6	13.2
P0ADN2	13115.7	S	U	T	B	ETD+CID	LIT	6	57.1	YFDNKHYPR	1239.6	R	G	3.2	0.2	9.5	14.6
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	EPVTEEEKLFVAVCR	1805.9	R	G	2.5	0.5	55.1	18.5
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	GEREPVTEAER	1272.6	R	V	2.7	0.4	26.4	15.4
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	GEREPVTEAERVWSK	1772.9	R	Y	2.0	0.6	18.3	15.6
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	HGYAFNELDLGK	1363.7	R	R	4.7	0.6	47.8	17.1
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	HGYAFNELDLGKR	1519.8	R	E	4.1	0.6	57.7	18.5
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	IAHWVGQGATISDR	1510.8	-	-	2.7	0.4	25.1	16.8
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	2.9	0.6	39.5	13.4
P0ADN2	13115.7	S	U	T	C	ETD+CID	LIT	8	67.0	YFDNKHYPR	1239.6	R	G	3.2	0.5	11.4	14.0
P0ADN2	13115.7	S	U	T	B	HCD	FT	5	49.1	GEREPVTEAER	1272.6	R	V	0.0	0.0	17.0	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADN2	13115.7	S	U	T	B	HCD	FT	5	49.1	HGYAFNELDLGK	1363.7	R	R	0.0	0.0	69.5	17.0
P0ADN2	13115.7	S	U	T	B	HCD	FT	5	49.1	HGYAFNELDLGKR	1519.8	R	E	0.0	0.0	67.7	18.8
P0ADN2	13115.7	S	U	T	B	HCD	FT	5	49.1	HGYAFNELDLGKREPVTEEEK	2461.2	R	L	0.0	0.0	20.8	17.9
P0ADN2	13115.7	S	U	T	B	HCD	FT	5	49.1	RFHTLSGGKPQVEGAEDYTDSDD	2524.1	K	-	0.0	0.0	40.6	13.2
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	AEETIFSK	924.5	M	I	0.0	0.0	51.1	10.4
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	DISPQAPTHILIIPNILIPTVNDVSAEHEQALGR	3672.0	R	M	6.0	0.0	59.9	6.0
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	EIPSDIVYQDDLVTAFR	1981.0	R	D	4.4	0.9	67.6	12.8
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	HGGQEVYHIHMHLLGGRPLGPMLAHK	2885.5	R	G	4.5	0.7	9.6	10.4
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	IAEQEGIAEDGYR	1450.7	K	L	4.1	0.7	54.7	11.1
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	LIMNTNR	861.5	R	H	2.5	0.4	37.0	16.0
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	MITVAAK	733.4	R	I	2.1	0.5	20.8	10.8
P0ACE7	13223.7	G	U	T	A	CID	LIT	8	95.0	REIPSDIVYQDDLVTAFR	2137.1	R	D	5.1	0.0	66.7	13.6
P0ACE7	13223.7	G	U	A	A	CID	LIT	2	25.2	DDLVTAFR	936.5	Q	D	2.7	0.4	26.9	15.3
P0ACE7	13223.7	G	U	A	A	CID	LIT	2	25.2	DISPQAPTHILIIPNILIPTVN	2379.4	R	D	3.3	0.0	23.4	8.5
P0ACE7	13223.7	G	T	A	B	CID	LIT	2	25.2	DDLVTAFR	936.5	Q	D	2.1	0.2	22.4	15.3
P0ACE7	13223.7	G	T	A	B	CID	LIT	2	25.2	DISPQAPTHILIIPNILIPTVN	2379.4	R	D	3.4	0.0	25.4	9.5
P0ACE7	13223.7	G	U	A	B	CID	LIT	2	25.2	DDLVTAFR	936.5	Q	D	2.1	0.2	13.3	15.3
P0ACE7	13223.7	G	U	A	B	CID	LIT	2	25.2	DISPQAPTHILIIPNILIPTVN	2379.4	R	D	2.7	0.0	24.0	10.4
P0ACE7	13223.7	S	U	T	A	CID	LIT	3	43.7	DISPQAPTHILIIPNILIPTVNDVSAEHEQALGR	3672.0	R	M	3.7	0.0	25.9	14.3
P0ACE7	13223.7	S	U	T	A	CID	LIT	3	43.7	EIPSDIVYQDDLVTAFR	1981.0	R	D	4.6	0.8	56.4	17.6
P0ACE7	13223.7	S	U	T	A	CID	LIT	3	43.7	REIPSDIVYQDDLVTAFR	2137.1	R	D	5.4	0.6	55.4	18.1
P0ACE7	13223.7	S	U	T	B	CID	LIT	2	42.9	DISPQAPTHILIIPNILIPTVNDVSAEHEQALGR	3672.0	R	M	2.6	0.0	35.1	14.3
P0ACE7	13223.7	S	U	T	B	CID	LIT	2	42.9	EIPSDIVYQDDLVTAFR	1981.0	R	D	5.5	0.8	67.8	18.0
P0ACE7	13223.7	S	U	T	C	CID	LIT	3	26.1	EIPSDIVYQDDLVTAFR	1981.0	R	D	3.9	0.8	53.9	18.0
P0ACE7	13223.7	S	U	T	C	CID	LIT	3	26.1	IAEQEGIAEDGYR	1450.7	K	L	3.9	0.5	59.1	15.6
P0ACE7	13223.7	S	U	T	C	CID	LIT	3	26.1	REIPSDIVYQDDLVTAFR	2137.1	R	D	3.7	0.6	29.8	18.4
P0ACE7	13223.7	S	U	T	A	ETD	LIT	2	42.9	DISPQAPTHILIIPNILIPTVNDVSAEHEQALGR	3672.0	R	M	6.8	0.0	52.6	14.8
P0ACE7	13223.7	S	U	T	A	ETD	LIT	2	42.9	EIPSDIVYQDDLVTAFR	1981.0	R	D	0.0	0.0	71.5	17.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACE7	13223.7	S	U	T	B	ETD	LIT	4	54.6	DISPQAPTHILIIPNILIPTVNDVSAEHEQALGR	3672.0	R	M	4.6	0.0	46.1	14.9
P0ACE7	13223.7	S	U	T	B	ETD	LIT	4	54.6	EIPSDIVYQDDLVTAFR	1981.0	R	D	3.1	0.5	0.0	0.0
P0ACE7	13223.7	S	U	T	B	ETD	LIT	4	54.6	IAEQEGIAEDGYR	1450.7	K	L	2.4	0.7	80.1	16.3
P0ACE7	13223.7	S	U	T	B	ETD	LIT	4	54.6	REIPSDIVYQDDLVTAFR	2137.1	R	D	4.2	0.6	28.2	19.0
P0ACE7	13223.7	S	U	T	C	ETD	LIT	3	26.1	EIPSDIVYQDDLVTAFR	1981.0	R	D	0.0	0.0	29.1	17.6
P0ACE7	13223.7	S	U	T	C	ETD	LIT	3	26.1	IAEQEGIAEDGYR	1450.7	K	L	2.8	0.6	78.3	16.3
P0ACE7	13223.7	S	U	T	C	ETD	LIT	3	26.1	REIPSDIVYQDDLVTAFR	2137.1	R	D	4.3	0.6	62.8	19.0
P0ACE7	13223.7	S	U	T	A	ETD+CID	LIT	2	15.1	EIPSDIVYQDDLVTAFR	1981.0	R	D	4.8	0.7	60.9	18.0
P0ACE7	13223.7	S	U	T	A	ETD+CID	LIT	2	15.1	REIPSDIVYQDDLVTAFR	2137.1	R	D	4.4	0.6	71.6	18.2
P0ACE7	13223.7	S	U	T	C	ETD+CID	LIT	2	25.2	EIPSDIVYQDDLVTAFR	1981.0	R	D	4.0	0.6	40.9	18.0
P0ACE7	13223.7	S	U	T	C	ETD+CID	LIT	2	25.2	IAEQEGIAEDGYR	1450.7	K	L	3.6	0.5	50.5	16.2
P77667	13282.0	G	T	T	A	CID	LIT	3	29.5	EGLNQIFK	948.5	R	F	1.8	0.5	19.0	13.4
P77667	13282.0	G	T	T	A	CID	LIT	3	29.5	LFVPLQAMPFIDGTEVDFVR	2294.2	K	E	2.8	0.5	15.1	11.8
P77667	13282.0	G	T	T	A	CID	LIT	3	29.5	QPGMVGVR	843.5	K	L	2.1	0.3	16.2	7.8
P77667	13282.0	G	T	A	B	CID	LIT	2	25.4	DGAKLFVPLQAMPFIDGTEV	2148.1	H	D	3.1	0.4	41.2	15.1
P77667	13282.0	G	T	A	B	CID	LIT	2	25.4	MDMHSGTFNPQ	1264.5	-	D	1.9	0.2	11.6	4.8
P0AAQ6	13300.4	G	U	T	A	CID	LIT	2	25.6	AEENEEVVFSWIEYPSK	2056.0	K	E	3.4	0.0	56.8	9.5
P0AAQ6	13300.4	G	U	T	A	CID	LIT	2	25.6	IVECWASDVPDGK	1475.7	R	V	2.9	0.0	24.6	8.5
P0AAQ2	13346.2	G	U	T	A	CID	LIT	4	42.6	EFVYSNLR	1027.5	R	E	2.6	0.0	36.4	13.4
P0AAQ2	13346.2	G	U	T	A	CID	LIT	4	42.6	IYPWVCGR	1050.5	K	C	1.4	0.6	16.4	13.0
P0AAQ2	13346.2	G	U	T	A	CID	LIT	4	42.6	YNPFADLK	967.5	K	A	2.1	0.0	52.7	10.8
P0AAQ2	13346.2	G	U	T	A	CID	LIT	4	42.6	YTEADQYGTTVIAGEDAQKDVGEAK	2659.2	K	Y	4.4	0.0	53.2	10.8
P0AAQ2	13346.2	G	U	A	A	CID	LIT	6	40.0	DAQKDVGEAKYNPFA	1652.8	E	D	3.6	0.7	19.9	14.3
P0AAQ2	13346.2	G	U	A	A	CID	LIT	6	40.0	DHEHSKYTEA	1216.5	H	D	2.2	0.0	14.8	12.6
P0AAQ2	13346.2	G	U	A	A	CID	LIT	6	40.0	DLKAMMNKKK	1206.7	A	-	2.3	0.7	0.0	0.0
P0AAQ2	13346.2	G	U	A	A	CID	LIT	6	40.0	DQYGTTVIAGE	1153.5	A	D	2.9	0.7	27.9	14.8
P0AAQ2	13346.2	G	U	A	A	CID	LIT	6	40.0	DQYGTTVIAGEDAQK	1595.8	A	D	5.0	0.8	97.6	14.1
P0AAQ2	13346.2	G	U	A	A	CID	LIT	6	40.0	DVGEAKYNPFA	1210.6	K	D	2.9	0.8	24.2	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAQ2	13346.2	G	T	A	A	CID	LIT	2	21.7	DHEHSKYTEA	1216.5	H	D	2.4	0.0	19.7	10.8
P0AAQ2	13346.2	G	T	A	A	CID	LIT	2	21.7	DQYGTTVIAGEDAQK	1595.8	A	D	4.6	0.6	47.0	14.1
P0AAQ2	13346.2	S	U	T	A	CID	LIT	2	13.9	IYPWVCGR	1050.5	K	C	1.4	0.0	28.7	16.6
P0AAQ2	13346.2	S	U	T	A	CID	LIT	2	13.9	LESGYREK	981.5	R	A	1.7	0.7	0.4	12.6
P0AAQ2	13346.2	S	U	T	A	ETD+CID	LIT	2	13.9	IYPWVCGR	1050.5	K	C	1.6	0.0	31.2	16.6
P0AAQ2	13346.2	S	U	T	A	ETD+CID	LIT	2	13.9	YNPFADLK	967.5	K	A	2.0	0.5	28.8	12.3
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	EQYLAELAQHEQEGK	1772.8	R	R	4.7	0.8	70.5	11.8
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	EQYLAELAQHEQEGKR	1928.9	R	L	2.5	0.0	33.9	13.0
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	ILVDR	615.4	R	L	1.3	0.5	26.3	17.8
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	KAFHGEVVDYATFR	1639.8	R	E	4.3	0.8	57.4	13.2
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	KQPLTLLYSAK	1261.8	K	N	2.5	0.0	23.5	4.8
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	NTTQNHALVLADWLR	1751.9	K	S	3.8	0.7	46.7	12.3
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	RLADIAK	786.5	K	K	2.5	0.2	26.4	17.5
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	RVYDPAEQSDGYR	1555.7	K	I	3.0	0.6	12.8	8.5
P76243	13368.7	G	U	T	A	CID	LIT	9	69.6	VYDPAEQSDGYR	1399.6	R	I	2.9	0.7	25.6	8.5
P76243	13368.7	G	T	T	A	CID	LIT	3	28.7	EQYLAELAQHEQEGK	1772.8	R	R	4.2	0.8	52.8	11.8
P76243	13368.7	G	T	T	A	CID	LIT	3	28.7	KQPLTLLYSAK	1261.8	K	N	2.8	0.0	26.0	4.8
P76243	13368.7	G	T	T	A	CID	LIT	3	28.7	RLADIAK	786.5	K	K	2.1	0.0	25.1	17.5
P76243	13368.7	G	U	A	A	CID	LIT	4	35.7	DPAEQSDGYRILV	1462.7	Y	D	3.9	0.0	38.5	17.5
P76243	13368.7	G	U	A	A	CID	LIT	4	35.7	DWLRSL	789.4	A	-	2.0	0.2	13.2	14.8
P76243	13368.7	G	U	A	A	CID	LIT	4	35.7	ELAQHEQEGKRLA	1508.8	A	D	3.0	0.0	33.6	15.1
P76243	13368.7	G	U	A	A	CID	LIT	4	35.7	MNIQCKRVY	1211.6	-	D	2.9	0.4	35.2	14.1
P76243	13368.7	G	U	A	B	CID	LIT	6	62.6	DGYRILV	835.5	S	D	1.5	0.3	12.8	14.5
P76243	13368.7	G	U	A	B	CID	LIT	6	62.6	DIAKKQPLTLLYSAKNTTQNHALVLA	2851.6	A	D	4.5	0.0	22.9	10.4
P76243	13368.7	G	U	A	B	CID	LIT	6	62.6	DWLRSL	789.4	A	-	2.2	0.2	14.8	14.8
P76243	13368.7	G	U	A	B	CID	LIT	6	62.6	DYATFREQYLA	1376.6	V	E	2.6	0.0	19.3	13.6
P76243	13368.7	G	U	A	B	CID	LIT	6	62.6	ELAQHEQEGKRLA	1508.8	A	D	3.3	0.0	48.8	14.6
P76243	13368.7	G	U	A	B	CID	LIT	6	62.6	MNIQCKRVY	1211.6	-	D	2.5	0.3	10.8	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76243	13368.7	S	U	T	A	CID	LIT	4	40.9	KQPLTLLYSAK	1261.8	K	N	3.0	0.4	74.8	9.0
P76243	13368.7	S	U	T	A	CID	LIT	4	40.9	KTDLALDEWDKEITPSTELR	2360.2	K	K	4.3	0.6	19.3	19.3
P76243	13368.7	S	U	T	A	CID	LIT	4	40.9	NTTQNHALVLADWLR	1751.9	K	S	4.6	0.6	45.5	16.7
P76243	13368.7	S	U	T	A	CID	LIT	4	40.9	TDLALDEWDKEITPSTELRK	2360.2	K	A	2.6	0.2	0.0	0.0
P76243	13368.7	S	U	T	B	CID	LIT	3	40.0	KQPLTLLYSAK	1261.8	K	N	3.0	0.4	57.3	9.0
P76243	13368.7	S	U	T	B	CID	LIT	3	40.0	KTDLALDEWDKEITPSTELR	2360.2	K	K	2.7	0.3	18.2	19.0
P76243	13368.7	S	U	T	B	CID	LIT	3	40.0	NTTQNHALVLADWLR	1751.9	K	S	3.4	0.4	36.6	16.5
P76243	13368.7	S	U	T	C	CID	LIT	4	53.9	EQYLAELAQHEQEGKR	1928.9	R	L	4.5	0.6	57.3	17.9
P76243	13368.7	S	U	T	C	CID	LIT	4	53.9	KQPLTLLYSAK	1261.8	K	N	2.6	0.3	39.1	9.0
P76243	13368.7	S	U	T	C	CID	LIT	4	53.9	KTDLALDEWDKEITPSTELR	2360.2	K	K	2.4	0.5	0.0	0.0
P76243	13368.7	S	U	T	C	CID	LIT	4	53.9	NTTQNHALVLADWLR	1751.9	K	S	3.9	0.4	45.9	16.5
P76243	13368.7	S	U	T	A	ETD	LIT	4	53.9	EQYLAELAQHEQEGKR	1928.9	R	L	2.7	0.0	28.2	17.9
P76243	13368.7	S	U	T	A	ETD	LIT	4	53.9	KQPLTLLYSAK	1261.8	K	N	3.0	0.0	25.1	9.0
P76243	13368.7	S	U	T	A	ETD	LIT	4	53.9	KTDLALDEWDKEITPSTELR	2360.2	K	K	6.9	0.5	63.3	19.5
P76243	13368.7	S	U	T	A	ETD	LIT	4	53.9	NTTQNHALVLADWLR	1751.9	K	S	6.0	0.6	67.2	16.5
P76243	13368.7	S	U	T	B	ETD	LIT	2	30.4	KTDLALDEWDKEITPSTELR	2360.2	K	K	6.1	0.5	50.6	19.0
P76243	13368.7	S	U	T	B	ETD	LIT	2	30.4	NTTQNHALVLADWLR	1751.9	K	S	5.5	0.6	64.0	16.5
P76243	13368.7	S	U	T	C	ETD	LIT	3	44.3	EQYLAELAQHEQEGKR	1928.9	R	L	2.9	0.0	47.7	18.1
P76243	13368.7	S	U	T	C	ETD	LIT	3	44.3	KTDLALDEWDKEITPSTELR	2360.2	K	K	4.9	0.5	29.8	19.4
P76243	13368.7	S	U	T	C	ETD	LIT	3	44.3	NTTQNHALVLADWLR	1751.9	K	S	3.5	0.5	13.6	16.5
P76243	13368.7	S	U	T	B	ETD+CID	LIT	3	40.0	KQPLTLLYSAK	1261.8	K	N	0.0	0.0	39.4	9.5
P76243	13368.7	S	U	T	B	ETD+CID	LIT	3	40.0	KTDLALDEWDKEITPSTELR	2360.2	K	K	0.0	0.0	25.2	19.1
P76243	13368.7	S	U	T	B	ETD+CID	LIT	3	40.0	NTTQNHALVLADWLR	1751.9	K	S	0.0	0.0	24.7	16.5
P76243	13368.7	S	U	T	A	ETD+CID	LIT	3	40.0	KQPLTLLYSAK	1261.8	K	N	2.6	0.3	26.8	9.0
P76243	13368.7	S	U	T	A	ETD+CID	LIT	3	40.0	KTDLALDEWDKEITPSTELR	2360.2	K	K	3.8	0.1	0.0	0.0
P76243	13368.7	S	U	T	A	ETD+CID	LIT	3	40.0	NTTQNHALVLADWLR	1751.9	K	S	4.0	0.6	46.5	16.7
P76243	13368.7	S	U	T	B	ETD+CID	LIT	3	40.0	KQPLTLLYSAK	1261.8	K	N	2.6	0.4	39.4	9.5
P76243	13368.7	S	U	T	B	ETD+CID	LIT	3	40.0	KTDLALDEWDKEITPSTELR	2360.2	K	K	3.8	0.5	25.2	19.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76243	13368.7	S	U	T	B	ETD+CID	LIT	3	40.0	NTTQNHALVLADWLR	1751.9	K	S	3.2	0.4	24.7	16.5
P76243	13368.7	S	U	T	C	ETD+CID	LIT	2	22.6	KQPLTLLYSAK	1261.8	K	N	2.4	0.2	30.3	9.0
P76243	13368.7	S	U	T	C	ETD+CID	LIT	2	22.6	NTTQNHALVLADWLR	1751.9	K	S	4.6	0.5	48.3	16.5
P76243	13368.7	S	U	T	B	HCD	FT	3	40.0	KQPLTLLYSAK	1261.8	K	N	0.0	0.0	39.4	9.5
P76243	13368.7	S	U	T	B	HCD	FT	3	40.0	KTDLALDEWDKEITPSTELR	2360.2	K	K	0.0	0.0	25.2	19.1
P76243	13368.7	S	U	T	B	HCD	FT	3	40.0	NTTQNHALVLADWLR	1751.9	K	S	0.0	0.0	24.7	16.5
P76243	13368.7	S	U	T	B	HCD	FT	2	17.4	ILVDRLWPR	1167.7	R	G	1.4	0.0	20.3	7.8
P76243	13368.7	S	U	T	B	HCD	FT	2	17.4	KQPLTLLYSAK	1261.8	K	N	2.3	0.0	27.9	9.0
P76569	13381.0	G	T	T	B	CID	LIT	2	30.3	ELNLADSSLSEEALIQAMVDNPK	2487.2	K	L	4.2	0.5	42.2	12.0
P76569	13381.0	G	T	T	B	CID	LIT	2	30.3	IGRPPEQVLEIVG	1406.8	R	-	2.2	0.0	16.5	10.0
P76569	13381.0	G	T	A	B	CID	LIT	4	34.5	DLLKILGMNSAR	1330.8	R	E	3.2	0.6	37.6	14.0
P76569	13381.0	G	T	A	B	CID	LIT	4	34.5	DLYKELNLA	1078.6	E	D	2.7	0.0	19.2	15.2
P76569	13381.0	G	T	A	B	CID	LIT	4	34.5	DNPKLM	717.4	V	E	1.7	0.3	6.1	12.8
P76569	13381.0	G	T	A	B	CID	LIT	4	34.5	DSSLSEEALIQAMV	1492.7	A	D	2.1	0.0	22.8	14.9
P0AA57	13392.1	G	T	T	A	CID	LIT	2	16.1	ITGPKNENIK	1113.6	K	T	3.2	0.7	27.8	11.8
P0AA57	13392.1	G	T	T	A	CID	LIT	2	16.1	TKGHYTFSVK	1167.6	K	-	3.2	0.5	14.9	12.8
P76001	13396.7	G	T	T	A	CID	LIT	6	27.9	DDRYFGVDGK	1171.5	R	R	2.9	0.0	25.1	8.5
P76001	13396.7	G	T	T	A	CID	LIT	6	27.9	KYLGEK	737.4	R	A	2.2	0.3	24.1	12.6
P76001	13396.7	G	T	T	A	CID	LIT	6	27.9	MLFMCRE	986.4	K	-	2.3	0.0	34.9	4.8
P76001	13396.7	G	T	T	A	CID	LIT	6	27.9	SGKINQTTTK	1077.6	R	M	2.3	0.0	28.0	11.1
P76001	13396.7	G	T	T	A	CID	LIT	6	27.9	YFGVDGK	785.4	R	R	1.9	0.7	27.4	9.5
P76001	13396.7	G	T	T	A	CID	LIT	6	27.9	YFGVDGKR	941.5	R	S	2.1	0.0	30.6	12.3
P76001	13396.7	G	T	A	A	CID	LIT	4	29.5	DAGGLQSPACGVVC	1390.6	N	D	2.8	0.6	11.4	13.0
P76001	13396.7	G	T	A	A	CID	LIT	4	29.5	DPSEFTFANGVFC	1490.6	Y	D	2.2	0.0	17.6	11.1
P76001	13396.7	G	T	A	A	CID	LIT	4	29.5	DVKEKLCR	1047.6	C	D	2.3	0.8	36.8	13.0
P76001	13396.7	G	T	A	A	CID	LIT	4	29.5	DVKEKLCRD	1162.6	C	D	2.2	0.7	29.2	13.2
P76001	13396.7	G	T	T	B	CID	LIT	2	11.5	INQTTTK	805.4	K	M	1.9	0.4	9.5	9.0
P76001	13396.7	G	T	T	B	CID	LIT	2	11.5	MLFMCRE	986.4	K	-	2.3	0.0	26.9	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	DAGGLQSPACGVVC	1390.6	N	D	3.2	0.0	26.0	12.3
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	DDRYFGV	871.4	R	D	2.2	0.8	19.9	13.2
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	DGKRSGKINQTTTKMLFMCRE	2501.2	V	-	3.2	0.7	28.1	12.6
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	DPSEFTFANGVFC	1490.6	Y	D	3.6	0.0	59.3	11.1
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	DPYICVNS	967.4	C	D	1.5	0.4	17.9	13.0
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	DVKEKLCR	1047.6	C	D	1.9	0.0	31.6	13.0
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	DVKEKLCRD	1162.6	C	D	2.2	0.0	15.4	13.2
P76001	13396.7	G	T	A	B	CID	LIT	8	68.9	EKAAENLQSLQGY	1450.7	G	D	3.3	0.7	24.6	16.0
P76001	13396.7	S	U	T	C	CID	LIT	2	32.0	AAENLQSLQGYDPSEFTFANGVFCDVKEK	3264.5	K	L	5.3	0.8	84.8	17.9
P76001	13396.7	S	U	T	C	CID	LIT	2	32.0	DDRYFGVDGK	1171.5	R	R	2.0	0.6	4.3	11.8
P76001	13396.7	S	U	T	C	ETD+CID	LIT	2	32.0	AAENLQSLQGYDPSEFTFANGVFCDVKEK	3265.5	K	L	6.3	0.0	62.5	17.7
P76001	13396.7	S	U	T	C	ETD+CID	LIT	2	32.0	DDRYFGVDGK	1171.5	R	R	2.3	0.2	8.5	12.3
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	AGQYAYR	828.4	K	D	2.5	0.0	20.5	9.5
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	AGQYAYRDR	1099.5	K	R	2.0	0.2	11.2	11.1
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	ASVEIDR	789.4	K	K	1.7	0.6	15.7	14.1
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	ASVEIDRK	917.5	K	I	2.9	0.3	46.6	13.6
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	FINGLKK	819.5	K	A	2.2	0.3	21.0	7.8
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	ILADIAVFDK	1104.6	K	V	3.5	0.0	71.9	11.8
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	KILADIAVFDK	1232.7	R	V	3.5	0.9	47.6	7.8
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	QLWIAR	786.5	R	I	1.6	0.7	13.8	10.8
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	VAFQAVIK	875.5	R	A	2.2	0.0	34.7	10.0
P0A7L3	13479.6	G	U	T	A	CID	LIT	10	48.3	VAFTALVEK	977.6	K	A	2.9	0.8	47.0	9.5
P0A7L3	13479.6	G	U	T	B	CID	LIT	3	20.3	ASVEIDR	789.4	K	K	2.3	0.3	50.2	14.1
P0A7L3	13479.6	G	U	T	B	CID	LIT	3	20.3	VAFQAVIK	875.5	R	A	2.5	0.3	40.8	10.0
P0A7L3	13479.6	G	U	T	B	CID	LIT	3	20.3	VAFTALVEK	977.6	K	A	1.9	0.8	23.5	9.5
P0A7L3	13479.6	S	U	T	B	CID	LIT	3	23.7	ASVEIDRK	917.5	K	I	2.6	0.1	42.2	17.6
P0A7L3	13479.6	S	U	T	B	CID	LIT	3	23.7	ILADIAVFDKVAFTALVEK	2063.2	K	A	2.2	0.6	0.0	0.0
P0A7L3	13479.6	S	U	T	B	CID	LIT	3	23.7	KASVEIDRK	1045.6	K	I	2.9	0.4	25.5	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7L3	13479.6	S	U	T	B	ETD	LIT	2	23.7	ILADIAVFDKVAFTALVEK	2063.2	K	A	0.0	0.0	21.4	12.3
P0A7L3	13479.6	S	U	T	B	ETD	LIT	2	23.7	KASVEIDRK	1045.6	K	I	3.7	0.4	61.2	15.6
P0A7L3	13479.6	S	U	T	B	ETD+CID	LIT	2	23.7	ILADIAVFDKVAFTALVEK	2063.2	K	A	0.0	0.0	21.4	12.6
P0A7L3	13479.6	S	U	T	B	ETD+CID	LIT	2	23.7	KASVEIDRK	1045.6	K	I	0.0	0.0	36.7	15.6
P0A7L3	13479.6	S	U	T	B	ETD+CID	LIT	2	23.7	ILADIAVFDKVAFTALVEK	2063.2	K	A	3.8	0.8	0.0	0.0
P0A7L3	13479.6	S	U	T	B	ETD+CID	LIT	2	23.7	KASVEIDRK	1045.6	K	I	2.8	0.3	36.7	15.6
P0AF50	13501.4	G	U	T	A	CID	LIT	5	55.9	EVENRPAVSLK	1241.7	K	T	2.8	0.8	23.5	11.5
P0AF50	13501.4	G	U	T	A	CID	LIT	5	55.9	MTISELLQYCMAKPGAEQSVHNDWK	2936.4	-	A	4.7	0.0	36.2	9.5
P0AF50	13501.4	G	U	T	A	CID	LIT	5	55.9	QQHSDVRPSR	1209.6	R	H	3.3	0.5	27.3	13.2
P0AF50	13501.4	G	U	T	A	CID	LIT	5	55.9	TSPELAELLR	1128.6	K	Q	3.0	0.7	61.1	11.8
P0AF50	13501.4	G	U	T	A	CID	LIT	5	55.9	VEDVLFAMVK	1150.6	K	E	3.3	0.8	52.7	10.8
P0AF50	13501.4	G	U	A	A	CID	LIT	3	45.8	DASYQQAVNLLPEEKRKLLVQL	2555.4	V	-	3.8	0.0	46.5	12.0
P0AF50	13501.4	G	U	A	A	CID	LIT	3	45.8	DWKATQIKVE	1217.7	N	D	2.3	0.6	14.7	17.3
P0AF50	13501.4	G	U	A	A	CID	LIT	3	45.8	MTISELLQYCMAKPGAEQSVHN	2507.2	-	D	3.3	0.0	47.3	12.3
P0AF50	13501.4	G	U	T	B	CID	LIT	2	17.8	EVENRPAVSLK	1241.7	K	T	2.6	0.0	20.9	10.8
P0AF50	13501.4	G	U	T	B	CID	LIT	2	17.8	QQHSDVRPSR	1209.6	R	H	2.8	0.6	15.4	12.8
P0AF50	13501.4	G	T	A	B	CID	LIT	2	27.1	DASYQQAVNLLPEEKRKLLVQL	2555.4	V	-	3.9	0.0	32.6	10.8
P0AF50	13501.4	G	T	A	B	CID	LIT	2	27.1	DWKATQIKVE	1217.7	N	D	3.4	0.2	19.0	17.3
P0AF50	13501.4	G	U	A	B	CID	LIT	5	66.9	DASYQQAVNLLPEEKRKLLVQL	2555.4	V	-	2.9	0.0	41.2	12.6
P0AF50	13501.4	G	U	A	B	CID	LIT	5	66.9	DSQIYYLV	1000.5	P	D	2.3	0.6	21.1	13.6
P0AF50	13501.4	G	U	A	B	CID	LIT	5	66.9	DWKATQIKVE	1217.7	N	D	3.4	0.4	22.3	17.3
P0AF50	13501.4	G	U	A	B	CID	LIT	5	66.9	EVENRPAVSLKTSPELA	1840.0	K	E	3.1	0.5	20.6	15.1
P0AF50	13501.4	G	U	A	B	CID	LIT	5	66.9	MTISELLQYCMAKPGAEQSVHN	2507.2	-	D	3.4	0.0	52.0	12.0
P0AF50	13501.4	S	U	T	A	CID	LIT	3	21.2	ATQIKVEDVLFAMVK	1691.9	K	E	2.3	0.8	0.0	0.0
P0AF50	13501.4	S	U	T	A	CID	LIT	3	21.2	TSPELAELLR	1128.6	K	Q	3.1	0.4	45.4	15.6
P0AF50	13501.4	S	U	T	A	CID	LIT	3	21.2	VEDVLFAMVK	1150.6	K	E	1.8	0.4	0.0	0.0
P0AF50	13501.4	S	U	T	B	CID	LIT	3	42.4	ATQIKVEDVLFAMVK	1691.9	K	E	4.1	0.5	44.3	13.6
P0AF50	13501.4	S	U	T	B	CID	LIT	3	42.4	MTISELLQYCMAKPGAEQSVHNDWK	2936.4	-	A	4.9	0.6	26.2	18.9

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		digestion	lysis	protease	replicate												
P0AF50	13501.4	S	U	T	B	CID	LIT	3	42.4	TSPELAELLR	1128.6	K	Q	2.9	0.8	52.3	15.6
P0AF50	13501.4	S	U	T	C	CID	LIT	2	21.2	ATQIKVEDVLFAMVK	1691.9	K	E	3.8	0.4	24.5	13.8
P0AF50	13501.4	S	U	T	C	CID	LIT	2	21.2	TSPELAELLR	1128.6	K	Q	3.4	0.5	38.8	15.6
P0AF50	13501.4	S	U	T	A	ETD	LIT	2	21.2	ATQIKVEDVLFAMVK	1691.9	K	E	3.4	0.6	0.0	0.0
P0AF50	13501.4	S	U	T	A	ETD	LIT	2	21.2	TSPELAELLR	1128.6	K	Q	2.4	0.7	50.1	15.6
P0AF50	13501.4	S	U	T	B	ETD	LIT	5	51.7	ATQIKVEDVLFAMVK	1691.9	K	E	3.8	0.5	0.0	0.0
P0AF50	13501.4	S	U	T	B	ETD	LIT	5	51.7	EVENRPAVSLK	1241.7	K	T	4.2	0.5	53.9	13.8
P0AF50	13501.4	S	U	T	B	ETD	LIT	5	51.7	MTISELLQYCMAKPGAEQSVHNDWK	2936.4	-	A	5.4	0.0	39.5	18.4
P0AF50	13501.4	S	U	T	B	ETD	LIT	5	51.7	TSPELAELLR	1128.6	K	Q	2.0	0.6	37.0	14.8
P0AF50	13501.4	S	U	T	B	ETD	LIT	5	51.7	VEDVLFAMVK	1150.6	K	E	1.7	0.4	12.6	14.0
P0AF50	13501.4	S	U	T	C	ETD	LIT	4	51.7	ATQIKVEDVLFAMVK	1691.9	K	E	3.2	0.4	0.0	0.0
P0AF50	13501.4	S	U	T	C	ETD	LIT	4	51.7	EVENRPAVSLK	1241.7	K	T	3.7	0.5	42.2	13.8
P0AF50	13501.4	S	U	T	C	ETD	LIT	4	51.7	MTISELLQYCMAKPGAEQSVHNDWK	2936.4	-	A	5.7	0.0	38.5	18.1
P0AF50	13501.4	S	U	T	C	ETD	LIT	4	51.7	TSPELAELLR	1128.6	K	Q	2.3	0.4	0.0	0.0
P0AF50	13501.4	S	U	T	B	ETD+CID	LIT	2	42.4	ATQIKVEDVLFAMVK	1691.9	K	E	0.0	0.0	18.1	14.3
P0AF50	13501.4	S	U	T	B	ETD+CID	LIT	2	42.4	MTISELLQYCMAKPGAEQSVHNDWK	2936.4	-	A	0.0	0.0	24.1	18.8
P0AF50	13501.4	S	U	T	B	ETD+CID	LIT	2	42.4	TSPELAELLR	1128.6	K	Q	0.0	0.0	55.6	15.6
P0AF50	13501.4	S	U	T	B	ETD+CID	LIT	2	42.4	ATQIKVEDVLFAMVK	1691.9	K	E	2.5	0.6	0.0	0.0
P0AF50	13501.4	S	U	T	B	ETD+CID	LIT	2	42.4	MTISELLQYCMAKPGAEQSVHNDWK	2936.4	-	A	4.1	0.4	24.1	18.8
P0AF50	13501.4	S	U	T	B	ETD+CID	LIT	2	42.4	TSPELAELLR	1128.6	K	Q	2.8	0.7	0.0	0.0
P0AF50	13501.4	S	U	T	B	HCD	FT	2	29.7	MTISELLQYCMAKPGAEQSVHNDWK	2936.4	-	A	0.0	0.0	24.1	18.8
P0AF50	13501.4	S	U	T	B	HCD	FT	2	29.7	TSPELAELLR	1128.6	K	Q	0.0	0.0	55.6	15.6
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	ELRSEK	761.4	R	F	2.1	0.4	13.0	15.8
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	3.5	0.7	25.9	13.8
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	IFGPVTR	789.5	R	E	1.7	0.7	25.2	15.1
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	ITIKEAIPR	1040.6	K	G	2.7	0.6	54.0	4.8
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	MIQEQTMLNVADNSGAR	1877.9	-	R	4.8	0.8	110.0	10.0
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	RPDGSVIR	899.5	R	F	3.2	0.8	39.3	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	RYAGVGDIIK	1091.6	R	I	3.4	0.8	38.6	12.6
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	VLGGSHR	725.4	K	R	1.7	0.0	34.7	8.5
P0ADY3	13523.2	G	U	T	A	CID	LIT	9	68.3	YAGVGDIIK	935.5	R	I	2.8	0.4	41.2	14.0
P0ADY3	13523.2	G	T	T	B	CID	LIT	2	22.0	MIQEQTMLNVADNSGAR	1877.9	-	R	5.6	0.8	96.1	11.1
P0ADY3	13523.2	G	T	T	B	CID	LIT	2	22.0	RYAGVGDIIK	1091.6	R	I	2.3	0.3	6.1	12.6
P0ADY3	13523.2	G	U	T	B	CID	LIT	6	48.8	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	5.1	0.0	45.8	11.5
P0ADY3	13523.2	G	U	T	B	CID	LIT	6	48.8	IFGPVTR	789.5	R	E	1.4	0.5	15.1	15.1
P0ADY3	13523.2	G	U	T	B	CID	LIT	6	48.8	MIQEQTMLNVADNSGAR	1877.9	-	R	5.4	0.7	104.0	9.0
P0ADY3	13523.2	G	U	T	B	CID	LIT	6	48.8	RVMCIK	806.4	R	V	2.1	0.3	4.0	12.0
P0ADY3	13523.2	G	U	T	B	CID	LIT	6	48.8	RYAGVGDIIK	1091.6	R	I	2.5	0.6	17.9	12.6
P0ADY3	13523.2	G	U	T	B	CID	LIT	6	48.8	YAGVGDIIK	935.5	R	I	2.8	0.4	23.6	14.0
P0ADY3	13523.2	G	U	A	B	CID	LIT	4	41.5	DGNACVLLNNNS	1290.6	F	E	2.2	0.6	26.2	13.0
P0ADY3	13523.2	G	U	A	B	CID	LIT	4	41.5	DGNACVLLNNNSEQPIGTRIFGPVTR	2842.4	F	E	2.9	0.0	53.9	15.7
P0ADY3	13523.2	G	U	A	B	CID	LIT	4	41.5	EKFMKIISLAPEVL	1617.9	S	-	2.9	0.8	19.0	10.8
P0ADY3	13523.2	G	U	A	B	CID	LIT	4	41.5	MIQEQTMLNVA	1277.6	-	D	3.0	0.7	23.8	14.9
P0ADY3	13523.2	S	U	T	A	CID	LIT	5	44.7	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	5.1	0.6	88.2	18.3
P0ADY3	13523.2	S	U	T	A	CID	LIT	5	44.7	MIQEQTMLNVADNSGAR	1877.9	-	R	5.2	0.6	79.2	15.7
P0ADY3	13523.2	S	U	T	A	CID	LIT	5	44.7	RPDGSVIR	899.5	R	F	3.0	0.5	32.2	12.6
P0ADY3	13523.2	S	U	T	A	CID	LIT	5	44.7	RYAGVGDIIK	1091.6	R	I	3.3	0.8	36.5	14.8
P0ADY3	13523.2	S	U	T	A	CID	LIT	5	44.7	YAGVGDIIK	935.5	R	I	2.7	0.2	36.6	14.6
P0ADY3	13523.2	S	U	T	B	CID	LIT	5	50.4	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	4.8	0.6	93.4	18.3
P0ADY3	13523.2	S	U	T	B	CID	LIT	5	50.4	IFGPVTR	789.5	R	E	1.3	0.6	17.8	15.9
P0ADY3	13523.2	S	U	T	B	CID	LIT	5	50.4	MIQEQTMLNVADNSGAR	1877.9	-	R	6.2	0.6	98.9	16.1
P0ADY3	13523.2	S	U	T	B	CID	LIT	5	50.4	RPDGSVIR	899.5	R	F	2.9	0.4	31.5	12.6
P0ADY3	13523.2	S	U	T	B	CID	LIT	5	50.4	RYAGVGDIIK	1091.6	R	I	4.0	0.8	41.4	14.6
P0ADY3	13523.2	S	U	T	C	CID	LIT	5	44.7	FDGNACVLLNNNSEQPIGTR	2220.0	R	I	4.3	0.6	87.6	17.3
P0ADY3	13523.2	S	U	T	C	CID	LIT	5	44.7	MIQEQTMLNVADNSGAR	1877.9	-	R	6.2	0.7	84.1	16.1
P0ADY3	13523.2	S	U	T	C	CID	LIT	5	44.7	RPDGSVIR	899.5	R	F	2.8	0.4	34.3	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADY3	13523.2	S	U	T	C	CID	LIT	5	44.7	RYAGVGDIIK	1091.6	R	I	3.5	0.8	35.8	14.6
P0ADY3	13523.2	S	U	T	C	CID	LIT	5	44.7	YAGVGDIIK	935.5	R	I	2.8	0.1	33.5	16.0
P0ADY3	13523.2	S	U	T	A	CID	FT	2	23.6	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	4.0	0.0	68.9	18.3
P0ADY3	13523.2	S	U	T	A	CID	FT	2	23.6	YAGVGDIIK	935.5	R	I	2.1	0.2	32.9	16.0
P0ADY3	13523.2	S	U	T	A	ETD	LIT	5	51.2	FDGNACVLLNNNSEQPIGTR	2220.0	R	I	1.7	0.7	24.0	17.1
P0ADY3	13523.2	S	U	T	A	ETD	LIT	5	51.2	IFGPVTR	789.5	R	E	2.2	0.0	41.8	13.6
P0ADY3	13523.2	S	U	T	A	ETD	LIT	5	51.2	IISLAPEVL	954.6	K	-	2.2	0.2	28.6	9.5
P0ADY3	13523.2	S	U	T	A	ETD	LIT	5	51.2	MIQEQTMLNVADNSGAR	1877.9	-	R	2.4	0.5	35.3	16.2
P0ADY3	13523.2	S	U	T	A	ETD	LIT	5	51.2	RYAGVGDIIK	1091.6	R	I	3.3	0.7	47.8	14.6
P0ADY3	13523.2	S	U	T	A	ETD	LIT	5	51.2	YAGVGDIIK	935.5	R	I	2.7	0.3	45.3	16.0
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	3.6	0.6	41.9	18.3
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	IFGPVTR	789.5	R	E	2.0	0.3	35.2	13.6
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	IISLAPEVL	954.6	K	-	2.8	0.3	28.8	9.5
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	MIQEQTMLNVADNSGAR	1877.9	-	R	4.7	0.4	34.2	16.1
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	MIQEQTMLNVADNSGARR	2034.0	-	V	1.8	0.0	39.2	17.2
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	RPDGSVIR	899.5	R	F	2.2	0.5	14.4	12.6
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	RVMCIK	806.4	R	V	1.9	0.7	8.4	14.1
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	RYAGVGDIIK	1091.6	R	I	3.0	0.0	23.5	14.8
P0ADY3	13523.2	S	U	T	B	ETD	LIT	9	62.6	YAGVGDIIK	935.5	R	I	2.7	0.3	33.3	15.8
P0ADY3	13523.2	S	U	T	C	ETD	LIT	7	52.0	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	1.9	0.6	14.7	18.9
P0ADY3	13523.2	S	U	T	C	ETD	LIT	7	52.0	IFGPVTR	789.5	R	E	2.4	0.2	38.4	16.7
P0ADY3	13523.2	S	U	T	C	ETD	LIT	7	52.0	IISLAPEVL	954.6	K	-	2.0	0.0	23.2	9.5
P0ADY3	13523.2	S	U	T	C	ETD	LIT	7	52.0	MIQEQTMLNVADNSGAR	1877.9	-	R	2.1	0.4	0.0	0.0
P0ADY3	13523.2	S	U	T	C	ETD	LIT	7	52.0	MIQEQTMLNVADNSGARR	2034.0	-	V	0.0	0.0	59.5	17.3
P0ADY3	13523.2	S	U	T	C	ETD	LIT	7	52.0	RYAGVGDIIK	1091.6	R	I	3.1	0.7	51.8	14.6
P0ADY3	13523.2	S	U	T	C	ETD	LIT	7	52.0	YAGVGDIIK	935.5	R	I	1.9	0.2	17.2	16.0
P0ADY3	13523.2	S	U	T	B	ETD+CID	LIT	3	36.6	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	0.0	0.0	101.0	18.8
P0ADY3	13523.2	S	U	T	B	ETD+CID	LIT	3	36.6	MIQEQTMLNVADNSGAR	1877.9	-	R	0.0	0.0	107.0	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADY3	13523.2	S	U	T	B	ETD+CID	LIT	3	36.6	RPDGSVIR	899.5	R	F	0.0	0.0	35.9	12.6
P0ADY3	13523.2	S	U	T	A	ETD+CID	LIT	3	30.1	FDGNACVLLNNNSEQPIGTR	2220.0	R	I	0.0	0.0	88.0	17.5
P0ADY3	13523.2	S	U	T	A	ETD+CID	LIT	3	30.1	NKDGIPAVVERLEYDPNR	2085.1	-	-	1.0	-0.8	33.2	17.8
P0ADY3	13523.2	S	U	T	A	ETD+CID	LIT	3	30.1	RPDGSVIR	899.5	R	F	3.0	0.4	34.9	12.6
P0ADY3	13523.2	S	U	T	A	ETD+CID	LIT	3	30.1	YAGVGDIIK	935.5	R	I	2.7	0.1	36.6	14.6
P0ADY3	13523.2	S	U	T	B	ETD+CID	LIT	4	44.7	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	0.0	0.0	101.0	18.8
P0ADY3	13523.2	S	U	T	B	ETD+CID	LIT	4	44.7	MIQEQTMLNVADNSGAR	1877.9	-	R	6.1	0.6	107.0	16.3
P0ADY3	13523.2	S	U	T	B	ETD+CID	LIT	4	44.7	RPDGSVIR	899.5	R	F	1.8	0.1	35.9	12.6
P0ADY3	13523.2	S	U	T	B	ETD+CID	LIT	4	44.7	RYAGVGDIIK	1091.6	R	I	2.1	0.6	12.9	14.5
P0ADY3	13523.2	S	U	T	C	ETD+CID	LIT	6	50.4	FDGNACVLLNNNSEQPIGTR	2220.0	R	I	4.9	0.7	92.5	17.3
P0ADY3	13523.2	S	U	T	C	ETD+CID	LIT	6	50.4	IFGPVTR	789.5	R	E	1.0	0.5	10.9	15.7
P0ADY3	13523.2	S	U	T	C	ETD+CID	LIT	6	50.4	MIQEQTMLNVADNSGAR	1877.9	-	R	6.8	0.6	93.1	16.2
P0ADY3	13523.2	S	U	T	C	ETD+CID	LIT	6	50.4	RPDGSVIR	899.5	R	F	3.0	0.5	29.7	12.6
P0ADY3	13523.2	S	U	T	C	ETD+CID	LIT	6	50.4	RYAGVGDIIK	1091.6	R	I	2.3	0.2	11.5	14.6
P0ADY3	13523.2	S	U	T	C	ETD+CID	LIT	6	50.4	YAGVGDIIK	935.5	R	I	2.7	0.2	43.0	15.7
P0ADY3	13523.2	S	U	T	B	HCD	FT	3	36.6	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	0.0	0.0	101.0	18.8
P0ADY3	13523.2	S	U	T	B	HCD	FT	3	36.6	MIQEQTMLNVADNSGAR	1877.9	-	R	0.0	0.0	107.0	16.3
P0ADY3	13523.2	S	U	T	B	HCD	FT	3	36.6	RPDGSVIR	899.5	R	F	0.0	0.0	35.9	12.6
P0ADY3	13523.2	S	U	T	C	HCD	FT	2	23.6	FDGNACVLLNNNSEQPIGTR	2219.1	R	I	3.4	0.0	52.9	18.3
P0ADY3	13523.2	S	U	T	C	HCD	FT	2	23.6	YAGVGDIIK	935.5	R	I	2.3	0.0	28.5	16.0
P24178	13583.4	G	U	T	A	CID	LIT	4	33.9	ITDAASAAALMTEMPAIIK	1918.0	K	R	4.6	0.6	47.4	13.6
P24178	13583.4	G	U	T	A	CID	LIT	4	33.9	MVTLYGIK	924.5	-	N	2.3	0.0	31.8	11.1
P24178	13583.4	G	U	T	A	CID	LIT	4	33.9	NKITDAASAAALMTEMPAIIK	2160.1	R	R	3.0	0.8	34.8	12.3
P24178	13583.4	G	U	T	A	CID	LIT	4	33.9	RWLEANNIDYR	1449.7	R	F	2.7	0.8	17.2	12.3
P24178	13583.4	G	U	A	B	CID	LIT	3	17.8	DSSYQQFFHEV	1386.6	S	-	3.2	0.0	25.7	11.1
P24178	13583.4	G	U	A	B	CID	LIT	3	17.8	MVTLYGIKNC	1198.6	-	D	3.3	0.6	35.5	13.2
P24178	13583.4	G	U	A	B	CID	LIT	3	17.8	VTLYGIKNC	1067.6	M	D	0.0	0.0	36.3	13.0
P24178	13583.4	S	U	T	B	CID	LIT	4	32.2	ITDAASAAALMTEMPAIIK	1918.0	K	R	3.7	0.6	50.3	17.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P24178	13583.4	S	U	T	B	CID	LIT	4	32.2	MVTLYGIK	924.5	-	N	2.5	0.8	27.7	13.2
P24178	13583.4	S	U	T	B	CID	LIT	4	32.2	RWLEANNIDYR	1449.7	R	F	3.0	0.6	35.7	16.5
P24178	13583.4	S	U	T	B	CID	LIT	4	32.2	WLEANNIDYR	1294.6	R	F	3.1	0.6	25.0	16.5
P24178	13583.4	S	U	T	C	CID	LIT	5	33.9	ITDAASAAALMTEMPAIIK	1918.0	K	R	2.6	0.8	50.0	17.4
P24178	13583.4	S	U	T	C	CID	LIT	5	33.9	MVTLYGIK	924.5	-	N	2.4	0.0	32.0	13.2
P24178	13583.4	S	U	T	C	CID	LIT	5	33.9	NKITDAASAAALMTEMPAIIK	2160.1	R	R	4.6	0.7	48.5	16.9
P24178	13583.4	S	U	T	C	CID	LIT	5	33.9	RWLEANNIDYR	1449.7	R	F	3.4	0.7	19.0	16.2
P24178	13583.4	S	U	T	C	CID	LIT	5	33.9	WLEANNIDYR	1293.6	R	F	1.9	0.5	12.6	15.8
P24178	13583.4	S	U	T	C	ETD	LIT	2	16.1	MVTLYGIK	924.5	-	N	2.6	0.0	25.8	13.2
P24178	13583.4	S	U	T	C	ETD	LIT	2	16.1	RWLEANNIDYR	1449.7	R	F	2.8	0.6	20.7	16.5
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	ITDAASAAALMTEMPAIIK	1918.0	K	R	0.0	0.0	59.0	19.1
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	MVTLYGIK	924.5	-	N	0.0	0.0	34.0	13.2
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	RWLEANNIDYR	1449.7	R	F	0.0	0.0	41.4	16.5
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	WLEANNIDYR	1294.6	R	F	0.0	0.0	23.5	16.5
P24178	13583.4	S	U	T	A	ETD+CID	LIT	3	16.1	MVTLYGIK	924.5	-	N	1.8	0.6	1.6	13.2
P24178	13583.4	S	U	T	A	ETD+CID	LIT	3	16.1	RWLEANNIDYR	1449.7	R	F	2.8	0.5	22.2	16.5
P24178	13583.4	S	U	T	A	ETD+CID	LIT	3	16.1	WLEANNIDYR	1293.6	R	F	3.0	0.5	0.0	0.0
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	ITDAASAAALMTEMPAIIK	1918.0	K	R	3.8	0.6	59.0	19.1
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	MVTLYGIK	924.5	-	N	2.3	0.6	34.0	13.2
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	RWLEANNIDYR	1449.7	R	F	3.0	0.6	41.4	16.5
P24178	13583.4	S	U	T	B	ETD+CID	LIT	4	32.2	WLEANNIDYR	1294.6	R	F	2.7	0.6	23.5	16.5
P24178	13583.4	S	U	T	C	ETD+CID	LIT	3	16.1	MVTLYGIK	924.5	-	N	2.6	0.8	26.1	7.0
P24178	13583.4	S	U	T	C	ETD+CID	LIT	3	16.1	RWLEANNIDYR	1449.7	R	F	2.0	0.6	0.0	0.0
P24178	13583.4	S	U	T	C	ETD+CID	LIT	3	16.1	WLEANNIDYR	1293.6	R	F	2.9	0.7	47.7	16.1
P24178	13583.4	S	U	T	B	HCD	FT	4	32.2	ITDAASAAALMTEMPAIIK	1918.0	K	R	0.0	0.0	59.0	19.1
P24178	13583.4	S	U	T	B	HCD	FT	4	32.2	MVTLYGIK	924.5	-	N	0.0	0.0	34.0	13.2
P24178	13583.4	S	U	T	B	HCD	FT	4	32.2	RWLEANNIDYR	1449.7	R	F	0.0	0.0	41.4	16.5
P24178	13583.4	S	U	T	B	HCD	FT	4	32.2	WLEANNIDYR	1294.6	R	F	0.0	0.0	23.5	16.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	AIVEAAGLK	871.5	K	V	2.7	0.7	38.6	13.2
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	AIVEAAGLKVGDIVK	1482.9	K	T	5.0	0.0	79.3	4.8
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	4.0	0.0	83.9	7.8
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	IEIEAIAVR	1013.6	K	-	3.1	0.6	32.2	9.0
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	IEIEAIAVRR	1169.7	K	-	3.1	0.5	33.3	8.5
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	SCVEVAR	820.4	R	L	2.3	0.7	43.7	14.0
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	SCVEVARLPK	1158.6	R	D	2.0	0.5	2.1	12.8
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3781.0	M	T	0.0	0.0	60.9	6.0
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	TGEVPADVAAQAR	1284.7	K	Q	3.8	0.0	87.5	10.8
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	TIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3549.9	K	T	5.2	0.0	53.0	11.5
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	TTVFVK	694.4	K	D	1.8	0.5	17.2	6.0
P0AF93	13593.4	G	U	T	A	CID	LIT	12	91.4	VGDIVK	630.4	K	T	2.1	0.4	27.5	18.1
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	AIVEAAGLK	871.5	K	V	2.5	0.8	45.0	13.2
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	AIVEAAGLKVGDIVK	1482.9	K	T	5.6	0.0	77.6	4.8
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	5.0	0.0	77.0	7.8
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	DVKIEIEAIAVR	1355.8	K	-	4.0	0.5	54.7	8.5
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	IEIEAIAVR	1013.6	K	-	2.9	0.7	12.7	9.0
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	IEIEAIAVRR	1169.7	K	-	2.6	0.5	18.7	8.5
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	QSLDNVK	803.4	R	A	2.7	0.3	25.6	16.2
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	SCVEVAR	820.4	R	L	2.1	0.6	42.2	13.4
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	SCVEVARLPK	1158.6	R	D	2.3	0.6	22.7	12.8
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	57.4	7.0
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	TGEVPADVAAQAR	1284.7	K	Q	4.2	0.8	67.4	10.4
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	TIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3549.9	K	T	2.7	0.8	13.0	11.1
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	TTVFVK	694.4	K	D	1.8	0.6	0.0	0.0
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	TTVFVKDLNDFATVNATYEAFFTEHNATFPAR	3637.8	K	S	6.2	0.0	61.5	9.0
P0AF93	13593.4	G	T	T	A	CID	LIT	15	99.2	VGDIVK	630.4	K	T	2.5	0.7	47.3	18.1
P0AF93	13593.4	G	U	A	A	CID	LIT	5	50.0	DFATVNATY	1001.5	N	E	2.0	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AF93	13593.4	G	U	A	A	CID	LIT	5	50.0	DIVKTTVFVK	1149.7	G	D	2.9	0.0	28.2	4.8
P0AF93	13593.4	G	U	A	A	CID	LIT	5	50.0	DNVKAIVEAAGLKVG	1483.8	L	D	3.8	0.4	37.8	9.0
P0AF93	13593.4	G	U	A	A	CID	LIT	5	50.0	DVAAQARQSL	1058.6	A	D	3.8	0.6	57.4	15.4
P0AF93	13593.4	G	U	A	A	CID	LIT	5	50.0	SKTIATENAPAAIGPYVQGV	1987.1	M	D	0.0	0.0	57.3	14.9
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DFATVNATY	1001.5	N	E	3.7	0.0	55.1	12.0
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DIVKTTVFVK	1149.7	G	D	3.1	0.0	39.4	4.8
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DIVKTTVFVKDLN	1491.8	G	D	2.8	0.5	17.1	11.1
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DLNDFATVNATY	1343.6	K	E	2.8	0.0	29.0	11.1
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DNVKAIVEAAGLKVG	1483.8	L	D	4.2	0.6	59.3	8.5
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DNVKAIVEAAGLKVGDIVKTTVFVK	2614.5	L	D	5.0	0.0	41.8	7.0
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DVAAQARQSL	1058.6	A	D	3.8	0.6	64.3	15.2
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DVAAQARQSLDNVKAIVEAAGLKVG	2523.4	A	D	4.2	0.6	31.1	12.6
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	DVKIEIEAIAVRR	1511.9	K	-	1.9	0.7	27.5	6.0
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	EAFFTEHNATFPARSCVEVARLPK	2777.4	Y	D	3.4	0.0	34.3	12.3
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	EVARLPK	812.5	V	D	2.3	0.6	3.5	6.0
P0AF93	13593.4	G	T	A	A	CID	LIT	12	81.2	SKTIATENAPAAIGPYVQGV	1987.1	M	D	0.0	0.0	57.2	15.3
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	AIVEAAGLK	871.5	K	V	2.0	0.5	17.7	13.2
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	5.5	0.0	49.7	10.4
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	IEIEAIAVR	1013.6	K	-	3.1	0.0	68.9	9.0
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	IEIEAIAVRR	1169.7	K	-	1.1	0.0	19.4	8.5
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	SCVEVAR	820.4	R	L	2.3	0.5	39.8	13.4
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	SCVEVARLPK	1158.6	R	D	2.9	0.5	64.0	12.8
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	62.7	9.0
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	TGEVPADVAAQAR	1284.7	K	Q	3.9	0.7	63.0	11.1
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	TGEVPADVAAQARQSLDNVK	2069.1	K	A	5.4	0.0	56.0	13.4
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	TIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3549.9	K	T	3.5	0.0	13.5	10.8
P0AF93	13593.4	G	T	T	B	CID	LIT	11	92.2	VGDIVK	630.4	K	T	2.4	0.5	23.2	18.1
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	DFATVNATY	1001.5	N	E	3.6	0.0	43.8	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	DIVKTTVFVK	1149.7	G	D	3.0	0.0	38.1	4.8
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	DLGNMIITSGQIPVNPKTGEVPA	2351.2	V	D	4.3	0.6	30.3	14.0
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	DNVKAIVEAAGLKVG	1483.8	L	D	4.8	0.5	62.8	7.0
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	DVAAQARQSL	1058.6	A	D	3.6	0.6	61.2	16.0
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	DVKIEIEAIAVRR	1511.9	K	-	1.9	0.5	23.1	6.0
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	EAFFTEHNATFPARSCV	1983.9	Y	E	3.9	0.0	61.3	9.0
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	EAFFTEHNATFPARSCVEVARLPK	2777.4	Y	D	2.8	0.0	20.9	12.3
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	EAIAVRR	814.5	I	-	1.9	0.5	11.8	13.6
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	EVARLPK	812.5	V	D	2.0	0.0	34.1	6.0
P0AF93	13593.4	G	T	A	B	CID	LIT	11	96.9	SKTIATENAPAAIGPYVQGV	1987.1	M	D	0.0	0.0	57.8	15.3
P0AF93	13593.4	G	U	A	B	CID	LIT	7	86.7	DFATVNATY	1001.5	N	E	3.2	0.0	33.8	12.0
P0AF93	13593.4	G	U	A	B	CID	LIT	7	86.7	DIVKTTVFVK	1149.7	G	D	2.8	0.9	22.7	4.8
P0AF93	13593.4	G	U	A	B	CID	LIT	7	86.7	DLGNMIITSGQIPVNPKTGEVPA	2351.2	V	D	3.7	0.7	33.6	14.3
P0AF93	13593.4	G	U	A	B	CID	LIT	7	86.7	DNVKAIVEAAGLKVG	1483.8	L	D	3.9	0.6	46.3	7.8
P0AF93	13593.4	G	U	A	B	CID	LIT	7	86.7	DVAAQARQSL	1058.6	A	D	3.8	0.6	67.5	16.0
P0AF93	13593.4	G	U	A	B	CID	LIT	7	86.7	EAFFTEHNATFPARSCVEVARLPK	2777.4	Y	D	2.7	0.4	8.8	12.0
P0AF93	13593.4	G	U	A	B	CID	LIT	7	86.7	SKTIATENAPAAIGPYVQGV	1987.1	M	D	0.0	0.0	49.1	15.3
P0AF93	13593.4	S	U	T	A	CID	LIT	7	69.5	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	4.5	0.6	39.7	16.9
P0AF93	13593.4	S	U	T	A	CID	LIT	7	69.5	DVKIEIEAIAVR	1355.8	K	-	3.8	0.5	44.8	13.2
P0AF93	13593.4	S	U	T	A	CID	LIT	7	69.5	IEIEAIAVR	1013.6	K	-	2.9	0.0	53.6	13.2
P0AF93	13593.4	S	U	T	A	CID	LIT	7	69.5	IEIEAIAVRR	1169.7	K	-	2.7	0.3	6.6	12.0
P0AF93	13593.4	S	U	T	A	CID	LIT	7	69.5	QSLDNVK	803.4	R	A	2.5	0.4	40.8	18.7
P0AF93	13593.4	S	U	T	A	CID	LIT	7	69.5	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	63.0	16.4
P0AF93	13593.4	S	U	T	A	CID	LIT	7	69.5	VGDIVK	630.4	K	T	2.3	0.6	26.2	19.6
P0AF93	13593.4	S	U	T	B	CID	LIT	4	58.6	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	3.7	0.6	30.4	16.6
P0AF93	13593.4	S	U	T	B	CID	LIT	4	58.6	DVKIEIEAIAVR	1355.8	K	-	3.6	0.5	39.4	13.2
P0AF93	13593.4	S	U	T	B	CID	LIT	4	58.6	IEIEAIAVR	1013.6	K	-	3.0	0.6	46.6	13.0
P0AF93	13593.4	S	U	T	B	CID	LIT	4	58.6	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	65.3	16.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AF93	13593.4	S	U	T	C	CID	LIT	6	75.8	AIVEAAGLK	871.5	K	V	2.2	0.6	30.6	16.0
P0AF93	13593.4	S	U	T	C	CID	LIT	6	75.8	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	4.1	0.0	26.5	16.6
P0AF93	13593.4	S	U	T	C	CID	LIT	6	75.8	DVKIEIEAIAVR	1355.8	K	-	3.0	0.5	19.8	12.3
P0AF93	13593.4	S	U	T	C	CID	LIT	6	75.8	IEIEAIAVR	1013.6	K	-	2.0	0.5	11.4	13.2
P0AF93	13593.4	S	U	T	C	CID	LIT	6	75.8	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	66.8	16.4
P0AF93	13593.4	S	U	T	C	CID	LIT	6	75.8	TGEVPADVAAQAR	1284.7	K	Q	3.1	0.4	14.2	14.3
P0AF93	13593.4	S	U	T	A	ETD	LIT	4	68.8	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	0.0	0.0	26.9	16.6
P0AF93	13593.4	S	U	T	A	ETD	LIT	4	68.8	DVKIEIEAIAVR	1355.8	K	-	4.1	0.5	0.0	0.0
P0AF93	13593.4	S	U	T	A	ETD	LIT	4	68.8	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	61.1	16.4
P0AF93	13593.4	S	U	T	A	ETD	LIT	4	68.8	TGEVPADVAAQAR	1284.7	K	Q	2.8	0.8	49.9	12.6
P0AF93	13593.4	S	U	T	B	ETD	LIT	3	48.4	DVKIEIEAIAVR	1355.8	K	-	2.8	0.4	24.3	13.2
P0AF93	13593.4	S	U	T	B	ETD	LIT	3	48.4	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	54.0	17.0
P0AF93	13593.4	S	U	T	B	ETD	LIT	3	48.4	TGEVPADVAAQAR	1284.7	K	Q	3.0	0.9	66.9	14.3
P0AF93	13593.4	S	U	T	C	ETD	LIT	5	55.5	AIVEAAGLK	871.5	K	V	2.5	0.3	31.7	16.0
P0AF93	13593.4	S	U	T	C	ETD	LIT	5	55.5	DVKIEIEAIAVR	1355.8	K	-	3.5	0.5	25.6	13.2
P0AF93	13593.4	S	U	T	C	ETD	LIT	5	55.5	IEIEAIAVR	1013.6	K	-	2.2	0.4	43.5	13.2
P0AF93	13593.4	S	U	T	C	ETD	LIT	5	55.5	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	44.6	17.0
P0AF93	13593.4	S	U	T	C	ETD	LIT	5	55.5	TGEVPADVAAQAR	1284.7	K	Q	2.9	0.8	67.0	14.3
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	0.0	0.0	27.6	16.6
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	DVKIEIEAIAVR	1355.8	K	-	0.0	0.0	30.0	13.2
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	IEIEAIAVR	1013.6	K	-	0.0	0.0	47.9	13.2
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	62.9	17.3
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	TGEVPADVAAQAR	1284.7	K	Q	0.0	0.0	60.2	14.3
P0AF93	13593.4	S	U	T	A	ETD+CID	LIT	5	59.4	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	5.0	0.7	40.6	16.8
P0AF93	13593.4	S	U	T	A	ETD+CID	LIT	5	59.4	DVKIEIEAIAVR	1355.8	K	-	3.3	0.4	50.0	13.2
P0AF93	13593.4	S	U	T	A	ETD+CID	LIT	5	59.4	IEIEAIAVR	1013.6	K	-	3.3	0.0	57.9	13.0
P0AF93	13593.4	S	U	T	A	ETD+CID	LIT	5	59.4	IEIEAIAVRR	1169.7	K	-	2.1	0.2	0.0	0.0
P0AF93	13593.4	S	U	T	A	ETD+CID	LIT	5	59.4	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	60.9	17.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	3	29.7	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	5.6	0.6	0.0	0.0
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	3	29.7	DVKIEIEAIAVR	1355.8	K	-	3.0	0.4	0.0	0.0
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	3	29.7	IEIEAIAVR	1013.6	K	-	3.3	0.5	0.0	0.0
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	5.6	0.6	0.0	0.0
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	DVKIEIEAIAVR	1355.8	K	-	3.5	0.6	0.0	0.0
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	IEIEAIAVR	1013.6	K	-	3.3	0.5	47.9	13.2
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	62.9	17.3
P0AF93	13593.4	S	U	T	B	ETD+CID	LIT	5	68.8	TGEVPADVAAQAR	1284.7	K	Q	4.1	0.8	60.2	14.3
P0AF93	13593.4	S	U	T	C	ETD+CID	LIT	5	65.6	AIVEAAGLK	871.5	K	V	2.2	0.4	17.2	16.0
P0AF93	13593.4	S	U	T	C	ETD+CID	LIT	5	65.6	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	4.2	0.6	12.6	16.8
P0AF93	13593.4	S	U	T	C	ETD+CID	LIT	5	65.6	DVKIEIEAIAVR	1355.8	K	-	3.2	0.6	33.0	13.2
P0AF93	13593.4	S	U	T	C	ETD+CID	LIT	5	65.6	IEIEAIAVR	1013.6	K	-	2.2	0.0	20.5	13.2
P0AF93	13593.4	S	U	T	C	ETD+CID	LIT	5	65.6	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	66.8	16.2
P0AF93	13593.4	S	U	T	B	HCD	FT	5	68.8	DLNDFATVNATYEAFFTEHNATFPAR	2962.4	K	S	0.0	0.0	27.6	16.6
P0AF93	13593.4	S	U	T	B	HCD	FT	5	68.8	DVKIEIEAIAVR	1355.8	K	-	0.0	0.0	30.0	13.2
P0AF93	13593.4	S	U	T	B	HCD	FT	5	68.8	IEIEAIAVR	1013.6	K	-	0.0	0.0	47.9	13.2
P0AF93	13593.4	S	U	T	B	HCD	FT	5	68.8	SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPK	3765.0	M	T	0.0	0.0	62.9	17.3
P0AF93	13593.4	S	U	T	B	HCD	FT	5	68.8	TGEVPADVAAQAR	1284.7	K	Q	0.0	0.0	60.2	14.3
P64488	13593.5	G	U	T	A	CID	LIT	4	34.5	HLDKGTRPGVYPR	1495.8	R	L	2.3	0.6	9.9	11.5
P64488	13593.5	G	U	T	A	CID	LIT	4	34.5	LSVMHGAVK	941.5	R	Y	2.9	0.9	45.4	10.8
P64488	13593.5	G	U	T	A	CID	LIT	4	34.5	MLQIPQNYIHTR	1513.8	-	S	2.9	0.5	35.2	14.1
P64488	13593.5	G	U	T	A	CID	LIT	4	34.5	STPFWNK	879.4	R	Q	1.8	0.7	8.4	14.1
P64488	13593.5	G	T	T	A	CID	LIT	3	23.5	GTRPGVYPR	1002.5	K	L	2.7	0.8	15.1	12.8
P64488	13593.5	G	T	T	A	CID	LIT	3	23.5	LSVMHGAVK	941.5	R	Y	2.5	0.6	21.5	10.8
P64488	13593.5	G	T	T	A	CID	LIT	3	23.5	QTAPAGIFER	1089.6	K	H	2.1	0.6	13.9	14.6
P64488	13593.5	S	U	T	A	CID	LIT	2	21.0	HLDKGTRPGVYPR	1495.8	R	L	2.8	0.4	8.3	15.9
P64488	13593.5	S	U	T	A	CID	LIT	2	21.0	MLQIPQNYIHTR	1513.8	-	S	2.2	0.2	10.4	16.4
P0ADK8	13678.4	G	U	T	A	CID	LIT	4	35.8	ATLEAEIAR	973.5	K	L	2.8	0.7	18.8	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADK8	13678.4	G	U	T	A	CID	LIT	4	35.8	EMGLQEMTGFSK	1357.6	R	T	2.5	0.0	45.6	7.0
P0ADK8	13678.4	G	U	T	A	CID	LIT	4	35.8	GLVVVHPMTALGR	1365.8	R	E	1.7	0.5	12.2	10.0
P0ADK8	13678.4	G	U	T	A	CID	LIT	4	35.8	LSDRLDAIR	1058.6	R	H	1.5	0.6	28.8	15.3
P0ADK8	13678.4	G	T	T	A	CID	LIT	3	28.3	ATLEAEIAR	973.5	K	L	2.0	0.3	0.0	0.0
P0ADK8	13678.4	G	T	T	A	CID	LIT	3	28.3	EMGLQEMTGFSK	1389.6	R	T	2.7	0.7	31.8	3.0
P0ADK8	13678.4	G	T	T	A	CID	LIT	3	28.3	GLVVVHPMTALGR	1349.8	R	E	3.4	0.0	27.1	7.8
P0ADK8	13678.4	G	T	T	B	CID	LIT	2	14.2	ATLEAEIAR	973.5	K	L	2.6	0.3	30.0	15.1
P0ADK8	13678.4	G	T	T	B	CID	LIT	2	14.2	LREVHSQK	996.6	R	L	2.0	0.7	6.2	10.8
P0ADK8	13678.4	G	T	A	B	CID	LIT	2	14.2	DAIRHQQA	938.5	L	D	1.8	0.7	14.2	15.3
P0ADK8	13678.4	G	T	A	B	CID	LIT	2	14.2	EVHSQKLSK	1055.6	R	E	2.0	0.8	18.6	12.6
P0ADK8	13678.4	S	U	T	C	CID	LIT	4	43.3	ATLEAEIAR	973.5	K	L	2.6	0.4	19.5	17.4
P0ADK8	13678.4	S	U	T	C	CID	LIT	4	43.3	EMGLQEMTGFSK	1357.6	R	T	2.7	0.0	36.2	11.1
P0ADK8	13678.4	S	U	T	C	CID	LIT	4	43.3	HQQADLSLVEAADKYAELEKEK	2515.3	R	A	5.8	0.4	38.6	18.6
P0ADK8	13678.4	S	U	T	C	CID	LIT	4	43.3	LSDRLDAIR	1058.6	R	H	1.6	0.4	20.8	18.0
P0ADK8	13678.4	S	U	T	C	ETD+CID	LIT	3	25.8	HQQADLSLVEAADKYAELEKEK	2515.3	R	A	4.8	0.7	46.6	18.3
P0ADK8	13678.4	S	U	T	C	ETD+CID	LIT	3	25.8	LSDRLDAIR	1058.6	R	H	2.6	0.2	13.8	18.0
P0AEQ1	13718.6	G	T	T	A	CID	LIT	3	32.8	AAAAVLAK	714.5	K	-	2.9	0.2	27.2	15.2
P0AEQ1	13718.6	G	T	T	A	CID	LIT	3	32.8	MDDCAPIAAYISQEK	1711.8	R	A	4.1	0.0	52.4	8.5
P0AEQ1	13718.6	G	T	T	A	CID	LIT	3	32.8	VILSQQMASAIIAAGQEEAQK	2186.1	K	N	5.7	0.8	84.2	11.5
P0AEQ1	13718.6	G	T	A	A	CID	LIT	2	19.4	DAQVAKAAAAVLAK	1326.8	Q	-	3.7	0.6	43.6	13.0
P0AEQ1	13718.6	G	T	A	A	CID	LIT	2	19.4	DDGGHLLALSRM	1284.6	A	D	3.4	0.7	16.9	12.0
P0AEQ1	13718.6	G	T	A	B	CID	LIT	3	32.1	DAQVAKAAAAVLAK	1326.8	Q	-	4.2	0.6	54.5	13.0
P0AEQ1	13718.6	G	T	A	B	CID	LIT	3	32.1	DDGGHLLALSRM	1284.6	A	D	3.2	0.8	37.9	13.0
P0AEQ1	13718.6	G	T	A	B	CID	LIT	3	32.1	DGQIIGAVGVSGLTGAQ	1542.8	V	D	4.3	0.9	60.3	14.6
P0AEQ1	13718.6	G	U	A	B	CID	LIT	2	19.4	DAQVAKAAAAVLAK	1326.8	Q	-	3.7	0.6	61.6	13.0
P0AEQ1	13718.6	G	U	A	B	CID	LIT	2	19.4	DDGGHLLALSRM	1284.6	A	D	2.4	0.7	13.7	13.8
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	ATVNQLVR	900.5	M	K	0.0	0.0	43.7	15.3
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	GALDCSGVK	906.4	R	D	2.7	0.7	54.1	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	GALDCSGVKDR	1177.6	R	K	2.8	0.6	52.3	10.0
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	KPNSALR	785.5	K	K	2.3	0.5	23.5	11.8
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	SNVPALEACPQK	1313.7	K	R	3.0	0.0	47.1	10.8
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	SNVPALEACPQKR	1469.8	K	G	2.3	0.7	40.8	10.0
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	VYTTTPK	809.4	R	K	1.6	0.6	13.5	11.5
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	VYTTTPKKPNSALR	1575.9	R	K	2.9	0.0	40.0	11.1
P0A7S3	13718.7	G	U	T	A	CID	LIT	9	41.1	YHTVR	675.4	R	G	1.4	0.6	18.4	13.2
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	ATVNQLVR	900.5	M	K	0.0	0.0	46.1	15.4
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	GALDCSGVK	906.4	R	D	2.5	0.6	12.3	13.0
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	GALDCSGVKDR	1177.6	R	K	2.7	0.7	49.9	10.8
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	KPNSALR	785.5	K	K	2.6	0.4	26.1	11.8
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	SNVPALEACPQK	1313.7	K	R	3.7	0.0	46.6	10.4
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	SNVPALEACPQKR	1469.8	K	G	3.3	0.0	49.6	10.0
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	VYTTTPK	809.4	R	K	1.3	0.6	22.0	13.0
P0A7S3	13718.7	G	T	T	A	CID	LIT	8	41.1	YHTVR	675.4	R	G	1.7	0.6	23.8	13.2
P0A7S3	13718.7	G	T	T	B	CID	LIT	3	25.8	ATVNQLVR	900.5	M	K	0.0	0.0	50.3	15.3
P0A7S3	13718.7	G	T	T	B	CID	LIT	3	25.8	GALDCSGVKDR	1177.6	R	K	2.3	0.3	37.1	10.4
P0A7S3	13718.7	G	T	T	B	CID	LIT	3	25.8	SNVPALEACPQKR	1469.8	K	G	1.7	0.0	37.0	9.5
P0A7S3	13718.7	G	U	T	B	CID	LIT	2	8.9	GALDCSGVK	906.4	R	D	2.7	0.7	46.1	13.0
P0A7S3	13718.7	G	U	T	B	CID	LIT	2	8.9	GALDCSGVKDR	1177.6	R	K	2.9	0.6	60.7	10.0
P0A7S3	13718.7	S	U	T	A	CID	LIT	3	36.3	GALDCSGVKDR	1177.6	R	K	2.6	0.6	52.1	14.1
P0A7S3	13718.7	S	U	T	A	CID	LIT	3	36.3	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	5.9	0.7	78.3	17.5
P0A7S3	13718.7	S	U	T	A	CID	LIT	3	36.3	VYTTTPK	809.4	R	K	1.7	0.4	22.7	13.0
P0A7S3	13718.7	S	U	T	B	CID	LIT	4	36.3	GALDCSGVK	906.4	R	D	2.6	0.6	32.8	17.4
P0A7S3	13718.7	S	U	T	B	CID	LIT	4	36.3	GALDCSGVKDR	1177.6	R	K	3.1	0.6	43.8	14.5
P0A7S3	13718.7	S	U	T	B	CID	LIT	4	36.3	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	5.3	0.6	81.0	17.6
P0A7S3	13718.7	S	U	T	B	CID	LIT	4	36.3	VYTTTPK	809.4	R	K	1.2	0.6	26.4	13.0
P0A7S3	13718.7	S	U	T	C	CID	LIT	6	53.2	ATVNQLVR	901.5	M	K	0.0	0.0	34.5	20.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S3	13718.7	S	U	T	C	CID	LIT	6	53.2	GALDCSGVKDR	1177.6	R	K	2.6	0.5	40.8	14.5
P0A7S3	13718.7	S	U	T	C	CID	LIT	6	53.2	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	4.3	0.6	67.6	17.3
P0A7S3	13718.7	S	U	T	C	CID	LIT	6	53.2	SNVPALEACPQK	1313.7	K	R	2.0	0.3	0.0	0.0
P0A7S3	13718.7	S	U	T	C	CID	LIT	6	53.2	SNVPALEACPQKR	1469.8	K	G	2.3	0.5	0.0	0.0
P0A7S3	13718.7	S	U	T	C	CID	LIT	6	53.2	VYTTTPK	809.4	R	K	1.7	0.4	20.1	13.0
P0A7S3	13718.7	S	U	T	B	CID	FT	2	14.5	GALDCSGVKDR	1177.6	R	K	2.4	0.7	55.1	13.6
P0A7S3	13718.7	S	U	T	B	CID	FT	2	14.5	VYTTTPK	809.4	R	K	1.6	0.0	24.7	13.0
P0A7S3	13718.7	S	U	T	A	ETD	LIT	6	46.8	GALDCSGVK	906.4	R	D	2.4	0.3	11.9	17.1
P0A7S3	13718.7	S	U	T	A	ETD	LIT	6	46.8	GALDCSGVKDR	1177.6	R	K	4.8	0.6	51.9	13.8
P0A7S3	13718.7	S	U	T	A	ETD	LIT	6	46.8	GALDCSGVKDRK	1305.7	R	Q	5.8	0.7	46.4	14.9
P0A7S3	13718.7	S	U	T	A	ETD	LIT	6	46.8	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	6.3	0.0	59.9	17.2
P0A7S3	13718.7	S	U	T	A	ETD	LIT	6	46.8	SNVPALEACPQK	1313.7	K	R	1.2	0.6	18.9	14.6
P0A7S3	13718.7	S	U	T	A	ETD	LIT	6	46.8	VYTTTPK	809.4	R	K	1.9	0.5	23.1	13.0
P0A7S3	13718.7	S	U	T	B	ETD	LIT	5	42.7	ATVNQLVR	900.5	M	K	0.0	0.0	51.6	17.4
P0A7S3	13718.7	S	U	T	B	ETD	LIT	5	42.7	GALDCSGVK	906.4	R	D	2.3	0.3	17.3	17.1
P0A7S3	13718.7	S	U	T	B	ETD	LIT	5	42.7	GALDCSGVKDR	1177.6	R	K	2.8	0.5	30.5	13.4
P0A7S3	13718.7	S	U	T	B	ETD	LIT	5	42.7	LTNGFEVTSYIGGEGHNLQEHSVILIR	2983.5	R	G	5.7	0.0	53.2	17.4
P0A7S3	13718.7	S	U	T	B	ETD	LIT	5	42.7	VYTTTPK	809.4	R	K	1.8	0.4	23.9	12.8
P0A7S3	13718.7	S	U	T	C	ETD	LIT	7	53.2	ATVNQLVR	900.5	M	K	0.0	0.0	51.7	17.2
P0A7S3	13718.7	S	U	T	C	ETD	LIT	7	53.2	GALDCSGVK	906.4	R	D	2.3	0.4	12.3	17.1
P0A7S3	13718.7	S	U	T	C	ETD	LIT	7	53.2	GALDCSGVKDR	1177.6	R	K	4.4	0.7	31.0	13.8
P0A7S3	13718.7	S	U	T	C	ETD	LIT	7	53.2	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	7.9	0.0	56.2	17.4
P0A7S3	13718.7	S	U	T	C	ETD	LIT	7	53.2	SNVPALEACPQK	1313.7	K	R	1.9	0.6	10.8	14.6
P0A7S3	13718.7	S	U	T	C	ETD	LIT	7	53.2	SNVPALEACPQKR	1469.8	K	G	4.8	0.5	38.4	15.3
P0A7S3	13718.7	S	U	T	C	ETD	LIT	7	53.2	VYTTTPK	809.4	R	K	1.6	0.6	20.7	13.0
P0A7S3	13718.7	S	U	T	B	ETD	FT	2	14.5	GALDCSGVKDR	1177.6	R	K	1.7	0.0	24.1	14.0
P0A7S3	13718.7	S	U	T	B	ETD	FT	2	14.5	VYTTTPK	809.4	R	K	1.7	0.6	29.2	12.8
P0A7S3	13718.7	S	U	T	C	ETD	FT	2	16.9	ATVNQLVR	900.5	M	K	0.0	0.0	66.3	17.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7S3	13718.7	S	U	T	C	ETD	FT	2	16.9	SNVPALEACPQKR	1469.8	K	G	3.4	0.0	46.2	15.3
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	ATVNQLVR	901.5	M	K	0.0	0.0	25.7	20.0
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	GALDCSGVK	906.4	R	D	0.0	0.0	49.6	17.0
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	GALDCSGVKDR	1177.6	R	K	0.0	0.0	39.0	14.1
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	0.0	0.0	64.1	17.5
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	VYTTTPK	809.4	R	K	0.0	0.0	21.2	12.8
P0A7S3	13718.7	S	U	T	A	ETD+CID	LIT	3	36.3	GALDCSGVK	906.4	R	D	2.8	0.6	34.4	17.3
P0A7S3	13718.7	S	U	T	A	ETD+CID	LIT	3	36.3	GALDCSGVKDR	1177.6	R	K	2.8	0.5	46.3	14.8
P0A7S3	13718.7	S	U	T	A	ETD+CID	LIT	3	36.3	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	4.5	0.5	66.4	17.9
P0A7S3	13718.7	S	U	T	A	ETD+CID	LIT	3	36.3	VYTTTPK	809.4	R	K	2.0	0.3	14.6	13.0
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	ATVNQLVR	901.5	M	K	0.0	0.0	25.7	20.0
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	GALDCSGVK	906.4	R	D	2.9	0.7	49.6	17.0
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	GALDCSGVKDR	1177.6	R	K	2.5	0.4	39.0	14.1
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	3.4	0.5	66.5	18.1
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	VKIATEDRETK	1289.7	-	-	2.9	0.3	25.6	16.0
P0A7S3	13718.7	S	U	T	B	ETD+CID	LIT	4	42.7	VYTTTPK	809.4	R	K	1.8	0.3	21.2	12.8
P0A7S3	13718.7	S	U	T	C	ETD+CID	LIT	4	46.8	ATVNQLVR	901.5	M	K	0.0	0.0	35.1	20.0
P0A7S3	13718.7	S	U	T	C	ETD+CID	LIT	4	46.8	AVEHLVK	795.5	-	-	1.9	0.2	4.7	9.0
P0A7S3	13718.7	S	U	T	C	ETD+CID	LIT	4	46.8	GALDCSGVK	906.4	R	D	0.0	0.0	45.3	16.1
P0A7S3	13718.7	S	U	T	C	ETD+CID	LIT	4	46.8	GALDCSGVKDR	1177.6	R	K	0.0	0.0	45.9	14.1
P0A7S3	13718.7	S	U	T	C	ETD+CID	LIT	4	46.8	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	7.2	0.0	79.6	17.5
P0A7S3	13718.7	S	U	T	C	ETD+CID	LIT	4	46.8	SNVPALEACPQK	1313.7	K	R	0.0	0.0	61.8	15.6
P0A7S3	13718.7	S	U	T	B	HCD	FT	4	42.7	ATVNQLVR	901.5	M	K	0.0	0.0	25.7	20.0
P0A7S3	13718.7	S	U	T	B	HCD	FT	4	42.7	GALDCSGVK	906.4	R	D	0.0	0.0	49.6	17.0
P0A7S3	13718.7	S	U	T	B	HCD	FT	4	42.7	GALDCSGVKDR	1177.6	R	K	0.0	0.0	39.0	14.1
P0A7S3	13718.7	S	U	T	B	HCD	FT	4	42.7	LTNGFEVTSYIGGEGHNLQEHSVILIR	2984.5	R	G	0.0	0.0	68.2	17.6
P0A7S3	13718.7	S	U	T	B	HCD	FT	4	42.7	VYTTTPK	809.4	R	K	0.0	0.0	21.2	12.8
P09996	13769.0	G	T	A	B	CID	LIT	2	18.9	DALSPQGEVSPQANN	1526.7	I	D	3.4	0.5	44.5	15.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P09996	13769.0	G	T	A	B	CID	LIT	2	18.9	DEVVGAFLKG	1034.6	F	D	3.0	0.6	44.2	15.7
P0A6T9	13793.2	G	U	T	A	CID	LIT	3	14.0	EHEWLRK	997.5	K	E	2.2	0.7	14.4	11.8
P0A6T9	13793.2	G	U	T	A	CID	LIT	3	14.0	SNVPAELK	857.5	M	Y	0.0	0.0	38.1	12.6
P0A6T9	13793.2	G	U	T	A	CID	LIT	3	14.0	YSKEHEWLR	1247.6	K	K	3.1	0.8	37.7	14.1
P0A6T9	13793.2	G	U	A	A	CID	LIT	4	51.2	DDCAVAESVKAAS	1322.6	G	D	3.0	0.7	65.0	13.0
P0A6T9	13793.2	G	U	A	A	CID	LIT	4	51.2	DGTYTVGITEHAQELLG	1803.9	A	D	3.1	0.4	28.5	13.2
P0A6T9	13793.2	G	U	A	A	CID	LIT	4	51.2	DIYAPVSGEIVAVN	1446.7	S	D	3.4	0.9	28.8	14.9
P0A6T9	13793.2	G	U	A	A	CID	LIT	4	51.2	DSPELVNSEPYAGGWIFKIKAS	2408.2	S	D	2.6	0.4	6.8	16.2
P0A6T9	13793.2	G	T	A	B	CID	LIT	4	51.2	DDCAVAESVKAAS	1322.6	G	D	3.0	0.5	50.7	14.0
P0A6T9	13793.2	G	T	A	B	CID	LIT	4	51.2	DGTYTVGITEHAQELLG	1803.9	A	D	1.8	0.5	11.3	13.6
P0A6T9	13793.2	G	T	A	B	CID	LIT	4	51.2	DIYAPVSGEIVAVN	1446.7	S	D	2.8	0.6	18.0	15.2
P0A6T9	13793.2	G	T	A	B	CID	LIT	4	51.2	DSPELVNSEPYAGGWIFKIKAS	2408.2	S	D	3.6	0.5	20.2	15.7
P0A6T9	13793.2	G	U	A	B	CID	LIT	6	60.5	DDCAVAESVKAAS	1322.6	G	D	2.8	0.3	46.6	13.0
P0A6T9	13793.2	G	U	A	B	CID	LIT	6	60.5	DGTYTVGITEHAQ	1391.6	A	E	3.0	0.0	22.4	14.0
P0A6T9	13793.2	G	U	A	B	CID	LIT	6	60.5	DGTYTVGITEHAQELLG	1803.9	A	D	2.9	0.4	17.3	13.6
P0A6T9	13793.2	G	U	A	B	CID	LIT	6	60.5	DIYAPVSGEIVAVN	1446.7	S	D	3.2	0.7	47.3	15.2
P0A6T9	13793.2	G	U	A	B	CID	LIT	6	60.5	DLPEVGATVSAG	1115.6	V	D	1.7	0.5	11.7	15.9
P0A6T9	13793.2	G	U	A	B	CID	LIT	6	60.5	DSPELVNSEPYAGGWIFKIKAS	2408.2	S	D	3.2	0.4	23.5	16.1
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	ALNAAGFR	819.4	R	I	2.6	0.7	52.4	12.3
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	CADAVKEYGIK	1253.6	R	N	3.4	0.6	46.0	12.6
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	GPGPGRESTIR	1126.6	K	A	1.6	0.6	11.8	13.0
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	5.8	0.7	71.8	12.3
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	KSTPFAAQVAAER	1375.7	R	C	3.8	0.8	68.3	12.8
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	NLEVMVK	848.5	K	G	1.8	0.7	16.3	13.6
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	NLEVMVKGPGPGR	1353.7	K	E	3.5	0.0	49.5	10.4
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	QGNALGWATAGGSGFR	1549.8	R	G	4.0	0.7	67.9	10.8
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	QGNALGWATAGGSGFRGSR	1849.9	R	K	2.2	0.7	18.9	12.0
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	3.8	0.6	33.2	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R9	13827.0	G	U	T	A	CID	LIT	11	72.1	STPFAAQVAAER	1247.6	K	C	3.5	0.8	62.4	14.9
P0A7R9	13827.0	G	T	T	A	CID	LIT	2	16.3	ALNAAGFR	819.4	R	I	2.8	0.6	37.2	12.0
P0A7R9	13827.0	G	T	T	A	CID	LIT	2	16.3	KSTPFAAQVAAER	1375.7	R	C	4.2	0.4	44.2	12.6
P0A7R9	13827.0	G	T	T	B	CID	LIT	2	16.3	ALNAAGFR	819.4	R	I	2.2	0.3	13.1	12.3
P0A7R9	13827.0	G	T	T	B	CID	LIT	2	16.3	KSTPFAAQVAAER	1375.7	R	C	3.4	0.4	48.1	13.6
P0A7R9	13827.0	G	U	T	B	CID	LIT	3	16.3	ALNAAGFR	819.4	R	I	2.2	0.7	16.6	7.8
P0A7R9	13827.0	G	U	T	B	CID	LIT	3	16.3	KSTPFAAQVAAER	1375.7	R	C	3.4	0.5	51.3	11.8
P0A7R9	13827.0	G	U	T	B	CID	LIT	3	16.3	STPFAAQVAAER	1247.6	K	C	2.6	0.6	39.0	15.2
P0A7R9	13827.0	G	T	A	B	CID	LIT	3	50.4	DAVKEYGIKNL	1249.7	A	E	2.3	0.3	16.4	14.0
P0A7R9	13827.0	G	T	A	B	CID	LIT	3	50.4	DGVAHIHASFNNTIVTIT	1910.0	S	D	3.1	0.6	28.8	15.3
P0A7R9	13827.0	G	T	A	B	CID	LIT	3	50.4	DRQGNALGWATAGGSGFRGSRKSTPFAAQVAAERCA	3708.8	T	D	3.3	0.0	10.1	10.4
P0A7R9	13827.0	G	U	A	B	CID	LIT	3	50.4	DAVKEYGIKNL	1249.7	A	E	3.2	0.5	46.8	14.0
P0A7R9	13827.0	G	U	A	B	CID	LIT	3	50.4	DGVAHIHASFNNTIVTIT	1910.0	S	D	2.5	0.0	49.4	15.7
P0A7R9	13827.0	G	U	A	B	CID	LIT	3	50.4	DRQGNALGWATAGGSGFRGSRKSTPFAAQVAAERCA	3708.8	T	D	3.2	0.0	12.1	10.4
P0A7R9	13827.0	S	U	T	A	CID	LIT	7	66.7	ITNITDVTPIPHNGCRPPK	2132.1	R	K	2.0	0.4	11.1	18.1
P0A7R9	13827.0	S	U	T	A	CID	LIT	7	66.7	ITNITDVTPIPHNGCRPPKK	2259.2	R	R	3.0	0.7	47.5	17.6
P0A7R9	13827.0	S	U	T	A	CID	LIT	7	66.7	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	5.4	0.8	71.6	18.1
P0A7R9	13827.0	S	U	T	A	CID	LIT	7	66.7	KSTPFAAQVAAER	1375.7	R	C	1.8	0.5	2.1	17.2
P0A7R9	13827.0	S	U	T	A	CID	LIT	7	66.7	NLEVMVKGPGPGR	1353.7	K	E	2.8	0.6	43.7	15.2
P0A7R9	13827.0	S	U	T	A	CID	LIT	7	66.7	QGNALGWATAGGSGFR	1549.8	R	G	4.5	0.8	68.9	16.0
P0A7R9	13827.0	S	U	T	A	CID	LIT	7	66.7	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	4.1	0.5	35.2	18.3
P0A7R9	13827.0	S	U	T	B	CID	LIT	7	58.9	ITNITDVTPIPHNGCRPPK	2131.1	R	K	3.6	0.6	64.6	18.5
P0A7R9	13827.0	S	U	T	B	CID	LIT	7	58.9	ITNITDVTPIPHNGCRPPKK	2259.2	R	R	4.3	0.6	33.3	18.0
P0A7R9	13827.0	S	U	T	B	CID	LIT	7	58.9	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	4.7	0.7	52.6	18.0
P0A7R9	13827.0	S	U	T	B	CID	LIT	7	58.9	NLEVMVKGPGPGR	1353.7	K	E	2.2	0.4	0.0	0.0
P0A7R9	13827.0	S	U	T	B	CID	LIT	7	58.9	QGNALGWATAGGSGFR	1550.7	R	G	3.6	0.7	58.2	16.1
P0A7R9	13827.0	S	U	T	B	CID	LIT	7	58.9	QGNALGWATAGGSGFRGSR	1849.9	R	K	1.9	0.3	10.1	17.4
P0A7R9	13827.0	S	U	T	B	CID	LIT	7	58.9	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	3.7	0.5	29.7	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	ALNAAGFR	820.4	R	I	2.0	0.4	17.1	17.0
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	ITNITDVTPIPHNGCRPPK	2131.1	R	K	3.1	0.7	53.2	19.1
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	ITNITDVTPIPHNGCRPPKK	2259.2	R	R	4.9	0.6	40.7	17.6
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	5.7	0.7	65.7	18.2
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	KSTPFAAQVAAER	1375.7	R	C	3.8	0.7	62.3	16.3
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	NLEVMVK	832.5	K	G	2.4	0.5	34.0	13.0
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	NLEVMVKGPGPGR	1353.7	K	E	2.5	0.5	12.2	14.8
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	QGNALGWATAGGSGFR	1550.7	R	G	4.2	0.8	78.1	17.2
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	3.9	0.3	30.3	18.3
P0A7R9	13827.0	S	U	T	C	CID	LIT	10	72.9	STPFAAQVAAER	1247.6	K	C	3.6	0.5	50.4	18.6
P0A7R9	13827.0	S	U	T	A	CID	FT	3	45.7	ITNITDVTPIPHNGCRPPK	2131.1	R	K	3.8	0.0	44.9	18.3
P0A7R9	13827.0	S	U	T	A	CID	FT	3	45.7	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	5.0	0.0	59.0	18.0
P0A7R9	13827.0	S	U	T	A	CID	FT	3	45.7	QGNALGWATAGGSGFR	1549.8	R	G	3.5	0.0	73.3	16.2
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	ITNITDVTPIPHNGCRPPK	2131.1	R	K	0.0	0.0	44.2	18.6
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	ITNITDVTPIPHNGCRPPKK	2259.2	R	R	3.7	0.5	32.9	17.6
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	0.0	0.0	71.8	18.2
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	NLEVMVK	832.5	K	G	1.4	0.4	18.8	16.0
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	QGNALGWATAGGSGFR	1550.7	R	G	3.4	0.6	113.0	15.3
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	QGNALGWATAGGSGFRGSR	1849.9	R	K	5.3	0.4	81.9	17.6
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	5.1	0.0	43.2	18.5
P0A7R9	13827.0	S	U	T	A	ETD	LIT	8	63.6	STPFAAQVAAER	1247.6	K	C	0.0	0.0	26.5	17.3
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	ALNAAGFR	819.4	R	I	2.2	0.7	64.6	15.6
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	ITNITDVTPIPHNGCRPPK	2131.1	R	K	4.6	0.5	44.3	18.6
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	7.1	0.0	76.7	18.5
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	KSTPFAAQVAAER	1375.7	R	C	6.2	0.6	78.6	17.2
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	QGNALGWATAGGSGFR	1550.7	R	G	3.5	0.6	87.0	15.8
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	QGNALGWATAGGSGFRGSR	1849.9	R	K	3.6	0.4	82.5	18.4
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	0.0	0.0	45.2	18.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R9	13827.0	S	U	T	B	ETD	LIT	8	64.3	STPFAAQVAAER	1247.6	K	C	2.3	0.1	23.6	17.4
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	ITNITDVTPIPHNGCRPPK	2131.1	R	K	6.8	0.0	40.2	18.9
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	ITNITDVTPIPHNGCRPPKK	2259.2	R	R	3.7	0.4	24.0	17.8
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	0.0	0.0	87.5	18.5
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	KSTPFAAQVAAER	1375.7	R	C	6.0	0.6	70.1	16.2
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	QGNALGWATAGGSGFR	1549.8	R	G	3.4	0.0	100.0	16.5
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	QGNALGWATAGGSGFRGSR	1849.9	R	K	1.8	0.5	85.9	17.5
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	0.0	0.0	36.3	18.4
P0A7R9	13827.0	S	U	T	C	ETD	LIT	8	58.9	STPFAAQVAAER	1247.6	K	C	0.0	0.0	43.5	17.4
P0A7R9	13827.0	S	U	T	C	ETD	FT	2	15.5	KSTPFAAQVAAER	1375.7	R	C	2.1	0.0	42.9	15.8
P0A7R9	13827.0	S	U	T	C	ETD	FT	2	15.5	NLEVMVK	832.5	K	G	0.0	0.0	21.4	13.2
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	2	18.6	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	0.0	0.0	27.5	18.1
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	2	18.6	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	0.0	0.0	32.2	18.3
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	ITNITDVTPIPHNGCRPPK	2132.1	R	K	0.0	0.0	45.0	18.1
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	0.0	0.0	77.8	18.4
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	QGNALGWATAGGSGFR	1550.7	R	G	0.0	0.0	88.3	15.8
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	0.0	0.0	32.2	18.3
P0A7R9	13827.0	S	U	T	A	ETD+CID	LIT	4	51.9	ALNAAGFR	819.4	R	I	2.5	0.7	36.0	14.9
P0A7R9	13827.0	S	U	T	A	ETD+CID	LIT	4	51.9	ITNITDVTPIPHNGCRPPK	2132.1	R	K	3.3	0.6	45.4	18.3
P0A7R9	13827.0	S	U	T	A	ETD+CID	LIT	4	51.9	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	6.4	0.8	73.6	18.1
P0A7R9	13827.0	S	U	T	A	ETD+CID	LIT	4	51.9	QGNALGWATAGGSGFR	1550.7	R	G	3.9	0.8	72.8	17.0
P0A7R9	13827.0	S	U	T	A	ETD+CID	LIT	4	51.9	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	3.6	0.5	15.0	18.5
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	2	18.6	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	3.4	0.8	0.0	0.0
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	2	18.6	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	3.5	0.3	0.0	0.0
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	ITNITDVTPIPHNGCRPPK	2132.1	R	K	0.0	0.0	45.0	18.1
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	6.4	0.7	77.8	18.4
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	QGNALGWATAGGSGFR	1550.7	R	G	3.3	0.6	42.0	15.8
P0A7R9	13827.0	S	U	T	B	ETD+CID	LIT	3	45.7	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	3.3	0.5	37.1	18.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	ALNAAGFR	820.4	R	I	2.2	0.6	34.0	17.1
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	ITNITDVTPIPHNGCRPPK	2131.1	R	K	0.0	0.0	46.4	18.1
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	6.7	0.8	0.0	0.0
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	KSTPFAAQVAAER	1375.7	R	C	3.5	0.3	0.0	0.0
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	NLEVMVKGPGPGR	1353.7	K	E	1.8	0.5	0.0	0.0
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	QGNALGWATAGGSGFR	1550.7	R	G	4.5	0.9	65.7	16.1
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	3.1	0.4	0.0	0.0
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	STPFAAQVAAER	1247.6	K	C	3.1	0.4	0.0	0.0
P0A7R9	13827.0	S	U	T	C	ETD+CID	LIT	8	72.1	VHVHVEEGSPK	1217.6	-	-	3.7	0.5	33.0	16.8
P0A7R9	13827.0	S	U	T	B	HCD	FT	3	45.7	ITNITDVTPIPHNGCRPPK	2132.1	R	K	0.0	0.0	45.0	18.1
P0A7R9	13827.0	S	U	T	B	HCD	FT	3	45.7	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	0.0	0.0	77.8	18.4
P0A7R9	13827.0	S	U	T	B	HCD	FT	3	45.7	QGNALGWATAGGSGFR	1550.7	R	G	0.0	0.0	88.3	15.8
P0A7R9	13827.0	S	U	T	B	HCD	FT	3	45.7	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	0.0	0.0	37.1	18.0
P0A7R9	13827.0	S	U	T	A	HCD	FT	4	45.7	ITNITDVTPIPHNGCRPPK	2131.1	R	K	2.4	0.0	34.7	18.8
P0A7R9	13827.0	S	U	T	A	HCD	FT	4	45.7	KQVSDGVAHIHASFNNTIVTITDR	2623.4	R	Q	3.2	0.0	28.9	18.3
P0A7R9	13827.0	S	U	T	A	HCD	FT	4	45.7	QGNALGWATAGGSGFR	1550.7	R	G	2.9	0.0	64.8	17.0
P0A7R9	13827.0	S	U	T	A	HCD	FT	4	45.7	QVSDGVAHIHASFNNTIVTITDR	2495.3	K	Q	2.3	0.0	34.8	18.5
P0A7R9	13827.0	S	U	T	B	HCD	FT	2	27.1	ITNITDVTPIPHNGCRPPK	2131.1	R	K	3.0	0.0	37.9	18.6
P0A7R9	13827.0	S	U	T	B	HCD	FT	2	27.1	QGNALGWATAGGSGFR	1550.7	R	G	2.3	0.0	61.4	16.5
P0ACD4	13830.9	G	U	T	A	CID	LIT	5	41.4	AAIADYK	751.4	K	S	2.3	0.0	27.7	13.8
P0ACD4	13830.9	G	U	T	A	CID	LIT	5	41.4	IHCSILAEDAIK	1369.7	K	A	3.7	0.5	19.8	14.0
P0ACD4	13830.9	G	U	T	A	CID	LIT	5	41.4	NTDIAEELELPPVK	1567.8	K	I	3.0	0.7	38.3	11.5
P0ACD4	13830.9	G	U	T	A	CID	LIT	5	41.4	VIDHYENPR	1142.6	K	N	3.3	0.0	34.3	11.8
P0ACD4	13830.9	G	U	T	A	CID	LIT	5	41.4	VNDEGIIEDAR	1230.6	K	F	3.7	0.8	57.4	13.0
P0ACD4	13830.9	G	T	T	A	CID	LIT	6	39.1	AAIADYK	751.4	K	S	2.2	0.6	27.0	15.7
P0ACD4	13830.9	G	T	T	A	CID	LIT	6	39.1	GKSLDEAQAIK	1159.6	K	N	3.3	0.5	22.2	14.0
P0ACD4	13830.9	G	T	T	A	CID	LIT	6	39.1	IHCSILAEDAIK	1369.7	K	A	2.8	0.7	32.3	12.6
P0ACD4	13830.9	G	T	T	A	CID	LIT	6	39.1	SLDEAQAIK	974.5	K	N	2.7	0.2	7.5	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACD4	13830.9	G	T	T	A	CID	LIT	6	39.1	VIDHYENPR	1142.6	K	N	3.0	0.0	40.5	11.8
P0ACD4	13830.9	G	T	T	A	CID	LIT	6	39.1	VNDEGIIEDAR	1230.6	K	F	3.5	0.0	50.5	12.3
P0ACD4	13830.9	G	U	A	A	CID	LIT	7	43.8	AYSEKVI	809.4	M	D	0.0	0.0	31.2	12.8
P0ACD4	13830.9	G	U	A	A	CID	LIT	7	43.8	DEAQAIKNT	989.5	L	D	2.7	0.4	50.2	16.2
P0ACD4	13830.9	G	U	A	A	CID	LIT	7	43.8	DENVGSGMVGAPACG	1420.6	N	D	3.0	0.7	43.2	7.0
P0ACD4	13830.9	G	U	A	A	CID	LIT	7	43.8	DHYENPRNVGSF	1434.6	I	D	2.6	0.7	20.2	11.8
P0ACD4	13830.9	G	U	A	A	CID	LIT	7	43.8	DHYENPRNVGSFDNN	1777.8	I	D	4.6	0.7	40.3	7.8
P0ACD4	13830.9	G	U	A	A	CID	LIT	7	43.8	DVMKLQIKVN	1187.7	G	D	2.3	0.7	0.0	0.0
P0ACD4	13830.9	G	U	A	A	CID	LIT	7	43.8	ENPRNVGSFDNN	1362.6	Y	D	3.6	0.0	30.8	12.3
P0ACD4	13830.9	G	T	A	A	CID	LIT	3	18.8	DEAQAIKNT	989.5	L	D	2.9	0.3	41.8	16.3
P0ACD4	13830.9	G	T	A	A	CID	LIT	3	18.8	DHYENPRNVGSF	1434.6	I	D	3.1	0.6	28.3	11.8
P0ACD4	13830.9	G	T	A	A	CID	LIT	3	18.8	DHYENPRNVGSFDNN	1777.8	I	D	4.4	0.6	44.0	7.0
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	AAIADYK	751.4	K	S	1.6	0.5	14.2	15.9
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	AYSEKVIDHYENPR	1720.8	M	N	0.0	0.0	66.6	12.3
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	GKSLDEAQAIK	1159.6	K	N	3.1	0.4	13.8	13.6
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	IHCSILAEDAIK	1369.7	K	A	3.1	0.7	23.2	12.3
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	NVGSFDNNDENVGSGMVGAPACGDVMK	2741.2	R	L	5.2	0.0	53.0	4.8
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	SLDEAQAIK	974.5	K	N	3.1	0.3	36.5	15.2
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	TYGCGSAIASSSLVTEWVK	2016.0	K	G	5.7	0.0	85.2	10.8
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	VIDHYENPR	1142.6	K	N	3.3	0.8	30.6	11.1
P0ACD4	13830.9	G	T	T	B	CID	LIT	9	78.9	VNDEGIIEDAR	1230.6	K	F	3.2	0.5	15.0	12.0
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	AYSEKVI	809.4	M	D	0.0	0.0	36.7	12.8
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DAIKAAIA	772.5	E	D	2.3	0.1	21.2	17.3
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DARFKTYGCGSAIASSSLVTEWVKGKSL	3018.5	E	D	5.0	0.5	33.8	15.4
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DEAQAIKNT	989.5	L	D	2.8	0.5	56.4	16.3
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DEAQAIKNTDIA	1288.6	L	E	2.6	0.3	17.7	13.8
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DENVGSGMVGAPACG	1420.6	N	D	3.3	0.7	38.7	7.0
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DHYENPRNVGSF	1434.6	I	D	3.2	0.7	39.9	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DHYENPRNVGSFDNN	1777.8	I	D	4.0	0.5	43.7	7.0
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DVMKLQIKVN	1187.7	G	D	1.9	0.7	0.0	0.0
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	DYKSKREAK	1124.6	A	-	1.9	0.6	17.0	10.8
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	ENPRNVGSF	1019.5	Y	D	1.9	0.6	24.2	15.2
P0ACD4	13830.9	G	T	A	B	CID	LIT	12	81.2	ENPRNVGSFDNN	1362.6	Y	D	3.3	0.0	27.8	12.0
P0ACD4	13830.9	G	U	A	B	CID	LIT	4	24.2	DEAQAIKNT	989.5	L	D	3.0	0.5	60.3	16.2
P0ACD4	13830.9	G	U	A	B	CID	LIT	4	24.2	DHYENPRNVGSF	1434.6	I	D	2.3	0.5	36.8	12.0
P0ACD4	13830.9	G	U	A	B	CID	LIT	4	24.2	DVMKLQIKVN	1187.7	G	D	2.7	0.6	19.6	10.8
P0ACD4	13830.9	G	U	A	B	CID	LIT	4	24.2	ENPRNVGSF	1019.5	Y	D	2.0	0.0	22.9	15.2
P0ACD4	13830.9	S	U	T	B	CID	LIT	3	32.8	NTDIAEELELPPVK	1567.8	K	I	2.2	0.5	11.5	14.9
P0ACD4	13830.9	S	U	T	B	CID	LIT	3	32.8	SLDEAQAIKNTDIAEELELPPVK	2523.3	K	I	4.3	0.6	49.0	17.7
P0ACD4	13830.9	S	U	T	B	CID	LIT	3	32.8	TYGCGSAIASSSLVTEWVK	2016.0	K	G	4.5	0.6	57.1	17.6
P0ACD4	13830.9	S	U	T	C	CID	LIT	6	71.9	IHCSILAEDAIK	1369.7	K	A	2.0	0.7	6.1	16.9
P0ACD4	13830.9	S	U	T	C	CID	LIT	6	71.9	NTDIAEELELPPVK	1567.8	K	I	3.3	0.7	31.7	14.9
P0ACD4	13830.9	S	U	T	C	CID	LIT	6	71.9	NVGSFDNNDENVGSGMVGAPACGDVMK	2741.2	R	L	3.5	0.0	44.0	7.8
P0ACD4	13830.9	S	U	T	C	CID	LIT	6	71.9	SLDEAQAIKNTDIAEELELPPVK	2523.3	K	I	3.3	0.3	50.3	17.5
P0ACD4	13830.9	S	U	T	C	CID	LIT	6	71.9	TYGCGSAIASSSLVTEWVK	2016.0	K	G	4.4	0.6	55.2	17.2
P0ACD4	13830.9	S	U	T	C	CID	LIT	6	71.9	VNDEGIIEDAR	1230.6	K	F	3.9	0.6	51.3	15.2
P0ACD4	13830.9	S	U	T	B	ETD	LIT	3	28.9	IHCSILAEDAIK	1369.7	K	A	2.1	0.6	32.5	15.4
P0ACD4	13830.9	S	U	T	B	ETD	LIT	3	28.9	NTDIAEELELPPVK	1567.8	K	I	1.9	0.0	36.7	15.3
P0ACD4	13830.9	S	U	T	B	ETD	LIT	3	28.9	VNDEGIIEDAR	1230.6	K	F	3.1	0.5	32.8	15.7
P0ACD4	13830.9	S	U	T	C	ETD	LIT	5	52.3	FKTYGCGSAIASSSLVTEWVK	2291.1	R	G	4.8	0.6	51.5	18.1
P0ACD4	13830.9	S	U	T	C	ETD	LIT	5	52.3	IHCSILAEDAIK	1369.7	K	A	1.5	0.3	23.6	16.9
P0ACD4	13830.9	S	U	T	C	ETD	LIT	5	52.3	NTDIAEELELPPVK	1567.8	K	I	2.0	0.8	49.1	15.2
P0ACD4	13830.9	S	U	T	C	ETD	LIT	5	52.3	SLDEAQAIKNTDIAEELELPPVK	2523.3	K	I	4.5	0.0	21.0	17.9
P0ACD4	13830.9	S	U	T	C	ETD	LIT	5	52.3	VNDEGIIEDAR	1230.6	K	F	3.8	0.6	38.2	15.7
P0ACD4	13830.9	S	U	T	B	ETD+CID	LIT	2	25.8	NTDIAEELELPPVK	1567.8	K	I	0.0	0.0	24.0	15.9
P0ACD4	13830.9	S	U	T	B	ETD+CID	LIT	2	25.8	TYGCGSAIASSSLVTEWVK	2016.0	K	G	0.0	0.0	84.3	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACD4	13830.9	S	U	T	B	ETD+CID	LIT	2	25.8	NTDIAEELELPPVK	1567.8	K	I	2.6	0.7	24.0	15.9
P0ACD4	13830.9	S	U	T	B	ETD+CID	LIT	2	25.8	TYGCGSAIASSSLVTEWVK	2016.0	K	G	4.9	0.7	84.3	17.6
P0ACD4	13830.9	S	U	T	C	ETD+CID	LIT	5	64.8	IHCSILAEDAIK	1369.7	K	A	3.4	0.7	57.5	16.2
P0ACD4	13830.9	S	U	T	C	ETD+CID	LIT	5	64.8	NTDIAEELELPPVK	1567.8	K	I	3.7	0.8	43.8	14.9
P0ACD4	13830.9	S	U	T	C	ETD+CID	LIT	5	64.8	NVGSFDNNDENVGSGMVGAPACGDVMK	2741.2	R	L	3.8	0.0	45.2	10.4
P0ACD4	13830.9	S	U	T	C	ETD+CID	LIT	5	64.8	TYGCGSAIASSSLVTEWVK	2016.0	K	G	4.2	0.6	60.8	17.6
P0ACD4	13830.9	S	U	T	C	ETD+CID	LIT	5	64.8	VNDEGIIEDAR	1230.6	K	F	3.8	0.6	41.4	15.6
P0ACD4	13830.9	S	U	T	B	HCD	FT	2	25.8	NTDIAEELELPPVK	1567.8	K	I	0.0	0.0	24.0	15.9
P0ACD4	13830.9	S	U	T	B	HCD	FT	2	25.8	TYGCGSAIASSSLVTEWVK	2016.0	K	G	0.0	0.0	84.3	17.6
P42616	13888.3	G	T	A	B	CID	LIT	2	23.8	DGLNKALSEVRANCS	1633.8	I	D	3.9	0.6	40.0	15.3
P42616	13888.3	G	T	A	B	CID	LIT	2	23.8	EISYAEKHQNQNRI	1729.9	K	D	2.5	0.0	24.7	14.3
P0A8E5	13923.0	G	U	T	A	CID	LIT	2	11.7	DITGVVK	731.4	R	V	1.7	0.3	10.6	15.4
P0A8E5	13923.0	G	U	T	A	CID	LIT	2	11.7	MDYEFLR	973.4	-	D	2.3	0.7	26.6	4.8
P0AGL2	13989.0	G	T	T	A	CID	LIT	2	20.2	DVKLEIEAIAVR	1355.8	K	S	4.0	0.5	54.7	8.5
P0AGL2	13989.0	G	T	T	A	CID	LIT	2	20.2	LEIEAIAVR	1013.6	K	S	2.9	0.7	12.7	9.0
P0AGL2	13989.0	G	T	T	A	CID	LIT	2	20.2	LSLENVK	802.5	R	A	1.9	0.4	13.7	15.4
P0AGL2	13989.0	G	T	T	A	CID	LIT	2	20.2	SCVQVAR	819.4	R	L	1.9	0.8	43.8	13.2
P0ADU5	13992.4	G	U	T	A	CID	LIT	5	33.1	DASGTINVDIDHK	1384.7	K	R	3.7	0.5	35.6	11.5
P0ADU5	13992.4	G	U	T	A	CID	LIT	5	33.1	DASGTINVDIDHKR	1540.8	K	W	3.8	0.6	69.0	13.0
P0ADU5	13992.4	G	U	T	A	CID	LIT	5	33.1	ISDDLYVFK	1099.6	R	D	2.1	0.8	14.4	10.0
P0ADU5	13992.4	G	U	T	A	CID	LIT	5	33.1	SLRDDTWVTLR	1361.7	K	G	2.6	0.6	29.7	13.0
P0ADU5	13992.4	G	U	T	A	CID	LIT	5	33.1	WNGVTVTPK	1001.5	R	D	2.6	0.7	37.8	15.3
P0ADU5	13992.4	G	T	T	A	CID	LIT	6	49.2	DASGTINVDIDHK	1384.7	K	R	4.4	0.6	67.3	11.8
P0ADU5	13992.4	G	T	T	A	CID	LIT	6	49.2	DASGTINVDIDHKR	1540.8	K	W	4.1	0.5	93.4	12.6
P0ADU5	13992.4	G	T	T	A	CID	LIT	6	49.2	DTVEIQGEVDKDWNSVEIDVK	2418.2	K	Q	5.1	0.5	42.4	12.8
P0ADU5	13992.4	G	T	T	A	CID	LIT	6	49.2	ISDDLYVFK	1099.6	R	D	3.1	0.8	37.8	10.4
P0ADU5	13992.4	G	T	T	A	CID	LIT	6	49.2	SLRDDTWVTLR	1361.7	K	G	4.1	0.4	30.9	12.6
P0ADU5	13992.4	G	T	T	A	CID	LIT	6	49.2	WNGVTVTPK	1001.5	R	D	3.0	0.7	39.1	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADU5	13992.4	G	U	A	A	CID	LIT	4	30.8	DDLYVFK	899.5	S	D	2.7	0.0	25.9	13.8
P0ADU5	13992.4	G	U	A	A	CID	LIT	4	30.8	DDTWVTLRGNIVERIS	1874.0	R	D	1.8	0.6	0.0	0.0
P0ADU5	13992.4	G	U	A	A	CID	LIT	4	30.8	DVKQIRKVNP	1196.7	I	-	2.7	0.4	20.6	4.8
P0ADU5	13992.4	G	U	A	A	CID	LIT	4	30.8	DWNSVEIDVKQIRKVNP	2040.1	K	-	2.8	0.0	19.8	14.9
P0ADU5	13992.4	G	T	A	A	CID	LIT	5	30.8	DDLYVFK	899.5	S	D	2.9	0.7	29.2	13.8
P0ADU5	13992.4	G	T	A	A	CID	LIT	5	30.8	DDTWVTLRGNIVERIS	1874.0	R	D	3.6	0.7	38.2	14.6
P0ADU5	13992.4	G	T	A	A	CID	LIT	5	30.8	DLYVFK	784.4	D	D	1.7	0.7	8.8	11.1
P0ADU5	13992.4	G	T	A	A	CID	LIT	5	30.8	DVKQIRKVNP	1196.7	I	-	2.1	0.6	18.4	4.8
P0ADU5	13992.4	G	T	A	A	CID	LIT	5	30.8	DWNSVEIDVKQIRKVNP	2040.1	K	-	3.5	0.5	32.3	15.3
P0ADU5	13992.4	G	T	A	B	CID	LIT	5	48.5	DASGTINVDIDHKRWNGVTVTPK	2523.3	K	D	3.1	0.0	12.9	14.0
P0ADU5	13992.4	G	T	A	B	CID	LIT	5	48.5	DDLYVFK	899.5	S	D	2.7	0.0	29.1	13.8
P0ADU5	13992.4	G	T	A	B	CID	LIT	5	48.5	DDTWVTLRGNIVERIS	1874.0	R	D	2.7	0.3	2.7	15.1
P0ADU5	13992.4	G	T	A	B	CID	LIT	5	48.5	DVKQIRKVNP	1196.7	I	-	2.5	0.4	30.3	4.8
P0ADU5	13992.4	G	T	A	B	CID	LIT	5	48.5	DWNSVEIDVKQIRKVNP	2040.1	K	-	3.9	0.7	25.6	14.9
P0ADU5	13992.4	G	U	A	B	CID	LIT	2	13.1	DDLYVFK	899.5	S	D	2.6	0.0	16.8	13.8
P0ADU5	13992.4	G	U	A	B	CID	LIT	2	13.1	DVKQIRKVNP	1196.7	I	-	2.5	0.0	33.9	4.8
P0ADU5	13992.4	S	U	T	A	CID	LIT	2	13.1	GNIVER	687.4	R	I	1.9	0.4	32.0	18.4
P0ADU5	13992.4	S	U	T	A	CID	LIT	2	13.1	SLRDDTWVTLR	1361.7	K	G	4.0	0.4	35.5	17.2
P0ADU5	13992.4	S	U	T	C	ETD	LIT	2	15.4	ISDDLYVFK	1099.6	R	D	2.4	0.7	31.9	14.0
P0ADU5	13992.4	S	U	T	C	ETD	LIT	2	15.4	SLRDDTWVTLR	1361.7	K	G	1.9	0.4	13.7	16.8
P0ADU5	13992.4	S	U	T	A	ETD+CID	LIT	2	15.4	ISDDLYVFK	1099.6	R	D	2.8	0.7	39.7	14.1
P0ADU5	13992.4	S	U	T	A	ETD+CID	LIT	2	15.4	SLRDDTWVTLR	1361.7	K	G	3.4	0.4	34.2	17.2
P0ADU5	13992.4	S	U	T	B	ETD+CID	LIT	3	22.3	ISDDLYVFK	1099.6	R	D	2.6	0.7	39.5	14.0
P0ADU5	13992.4	S	U	T	B	ETD+CID	LIT	3	22.3	SLRDDTWVTLR	1361.7	K	G	2.4	0.2	6.1	17.2
P0ADU5	13992.4	S	U	T	B	ETD+CID	LIT	3	22.3	WNGVTVTPK	1001.5	R	D	2.7	0.3	10.1	17.2
P31130	14103.3	G	T	T	A	CID	LIT	5	47.7	EVQPDQMINISGSLDKK	1902.0	R	S	3.5	0.7	32.0	13.4
P31130	14103.3	G	T	T	A	CID	LIT	5	47.7	GNLISHKGEDR	1225.6	R	Y	3.0	0.8	28.7	11.8
P31130	14103.3	G	T	T	A	CID	LIT	5	47.7	MTVDFAK	811.4	K	T	1.4	0.5	14.6	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P31130	14103.3	G	T	T	A	CID	LIT	5	47.7	SGEINVVIPAAVFDGR	1643.9	K	E	3.1	0.0	37.5	14.0
P31130	14103.3	G	T	T	A	CID	LIT	5	47.7	TMHDGASVSLR	1189.6	K	G	2.7	0.7	23.3	11.5
P31130	14103.3	G	T	A	A	CID	LIT	2	14.6	DAAPPPPHAIE	1114.6	Q	D	1.9	0.2	22.8	14.5
P31130	14103.3	G	T	A	A	CID	LIT	2	14.6	DDQGGLKQ	860.4	A	D	2.3	0.6	24.0	16.6
P31130	14103.3	G	T	T	B	CID	LIT	2	10.8	KSAPAVVR	827.5	K	V	1.9	0.2	0.0	0.0
P31130	14103.3	G	T	T	B	CID	LIT	2	10.8	SAPAVVRVTHLQK	1405.8	K	-	2.5	0.2	14.3	7.0
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DAAPPPPHAIE	1114.6	Q	D	2.1	0.4	20.4	14.5
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DDQGGLKQ	860.4	A	D	2.5	0.7	40.9	16.6
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DFAKTMH	849.4	V	D	2.0	0.0	33.1	12.3
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DGASVSLRGNLISHKGE	1739.9	H	D	3.2	0.7	33.6	15.3
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DGYRGTD	783.3	E	D	2.2	0.0	20.0	11.1
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DKKSAPAVVRVTHLQK	1777.0	L	-	3.6	0.0	38.2	4.8
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DKSGEINVVIPAAVF	1558.8	R	D	2.8	0.0	35.8	14.3
P31130	14103.3	G	T	A	B	CID	LIT	8	66.9	DRYVFR	855.4	E	D	2.6	0.0	24.2	12.8
P31130	14103.3	S	U	T	B	ETD+CID	LIT	2	24.6	DKSGEINVVIPAAVFDGR	1887.0	R	E	2.3	0.2	7.1	17.9
P31130	14103.3	S	U	T	B	ETD+CID	LIT	2	24.6	GTDDAKKMTVDFAK	1526.8	R	T	2.4	0.6	0.0	0.0
P0A7W7	14108.9	G	U	T	A	CID	LIT	7	55.4	AAVTMPSSK	891.5	K	L	2.5	0.8	19.1	13.8
P0A7W7	14108.9	G	U	T	A	CID	LIT	7	55.4	AVVESIQR	901.5	K	V	2.6	0.7	41.7	17.3
P0A7W7	14108.9	G	U	T	A	CID	LIT	7	55.4	IRNGQAANK	971.5	R	A	1.8	0.7	4.0	13.6
P0A7W7	14108.9	G	U	T	A	CID	LIT	7	55.4	QAGLGGEIICYVA	1350.7	R	-	2.3	0.8	18.7	12.6
P0A7W7	14108.9	G	U	T	A	CID	LIT	7	55.4	SMQDPIADMLTR	1377.7	M	I	0.0	0.0	60.8	7.8
P0A7W7	14108.9	G	U	T	A	CID	LIT	7	55.4	VMAGLGIAVVSTSK	1332.8	K	G	4.9	0.7	62.4	13.2
P0A7W7	14108.9	G	U	T	A	CID	LIT	7	55.4	VSRPGLR	784.5	R	I	1.8	0.5	11.2	8.5
P0A7W7	14108.9	G	T	T	A	CID	LIT	2	16.9	AVVESIQR	901.5	K	V	2.3	0.1	19.7	17.3
P0A7W7	14108.9	G	T	T	A	CID	LIT	2	16.9	VMAGLGIAVVSTSK	1348.8	K	G	3.8	0.6	46.7	14.0
P0A7W7	14108.9	G	T	T	B	CID	LIT	4	25.4	AAVTMPSSK	891.5	K	L	2.0	0.3	16.3	13.6
P0A7W7	14108.9	G	T	T	B	CID	LIT	4	25.4	AVVESIQR	901.5	K	V	2.5	0.3	20.5	17.3
P0A7W7	14108.9	G	T	T	B	CID	LIT	4	25.4	GVMTDRAAR	976.5	K	Q	2.0	0.0	16.7	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7W7	14108.9	G	T	T	B	CID	LIT	4	25.4	VSRPGLR	784.5	R	I	1.7	0.5	6.1	8.5
P0A7W7	14108.9	G	U	T	B	CID	LIT	3	25.4	AVVESIQR	901.5	K	V	2.6	0.4	40.5	17.3
P0A7W7	14108.9	G	U	T	B	CID	LIT	3	25.4	QAGLGGEIICYVA	1350.7	R	-	2.2	0.7	14.3	11.8
P0A7W7	14108.9	G	U	T	B	CID	LIT	3	25.4	SMQDPIADMLTR	1377.7	M	I	0.0	0.0	44.5	7.8
P0A7W7	14108.9	S	U	T	A	CID	LIT	2	5.4	KDELPK	729.4	R	V	2.0	0.2	24.3	12.8
P0A7W7	14108.9	S	U	T	A	CID	LIT	2	5.4	RKDELPK	885.5	K	V	2.6	0.4	22.5	16.1
P0A7W7	14108.9	S	U	T	B	CID	LIT	6	65.4	AAVTMPSSK	891.5	K	L	1.9	0.5	10.5	15.8
P0A7W7	14108.9	S	U	T	B	CID	LIT	6	65.4	KDELPK	729.4	R	V	1.6	0.4	13.6	12.8
P0A7W7	14108.9	S	U	T	B	CID	LIT	6	65.4	QAGLGGEIICYVA	1350.7	R	-	2.2	0.8	15.6	16.0
P0A7W7	14108.9	S	U	T	B	CID	LIT	6	65.4	SMQDPIADMLTR	1377.7	M	I	0.0	0.0	32.4	14.1
P0A7W7	14108.9	S	U	T	B	CID	LIT	6	65.4	VAIANVLKEEGFIEDFKVEGDTKPELELTLK	3474.9	K	Y	3.5	0.0	39.7	14.8
P0A7W7	14108.9	S	U	T	B	CID	LIT	6	65.4	VMAGLGIAVVSTSK	1332.8	K	G	3.3	0.5	18.5	15.3
P0A7W7	14108.9	S	U	T	C	CID	LIT	2	11.5	AAVTMPSSK	891.5	K	L	2.4	0.7	19.6	16.7
P0A7W7	14108.9	S	U	T	C	CID	LIT	2	11.5	KDELPK	729.4	R	V	1.9	0.5	23.6	12.8
P0A7W7	14108.9	S	U	T	A	ETD	LIT	2	28.5	KDELPK	729.4	R	V	1.8	0.6	10.8	12.8
P0A7W7	14108.9	S	U	T	A	ETD	LIT	2	28.5	VAIANVLKEEGFIEDFKVEGDTKPELELTLK	3474.9	K	Y	5.1	0.0	22.3	14.5
P0A7W7	14108.9	S	U	T	B	ETD	LIT	3	20.0	GVMTDR	678.3	K	A	1.2	0.1	29.0	17.8
P0A7W7	14108.9	S	U	T	B	ETD	LIT	3	20.0	KDELPK	729.4	R	V	1.8	0.6	14.7	12.8
P0A7W7	14108.9	S	U	T	B	ETD	LIT	3	20.0	VMAGLGIAVVSTSK	1332.8	K	G	2.0	0.4	6.3	15.2
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	3	20.8	AAVTMPSSK	891.5	K	L	0.0	0.0	24.3	15.8
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	3	20.8	KDELPK	729.4	R	V	0.0	0.0	23.9	12.8
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	3	20.8	SMQDPIADMLTR	1377.7	M	I	0.0	0.0	35.7	14.1
P0A7W7	14108.9	S	U	T	A	ETD+CID	LIT	2	5.4	KDELPK	729.4	R	V	0.6	-0.7	23.7	12.8
P0A7W7	14108.9	S	U	T	A	ETD+CID	LIT	2	5.4	RKDELPK	885.5	K	V	2.3	0.7	24.2	16.1
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	2	11.5	AAVTMPSSK	891.5	K	L	2.8	0.7	0.0	0.0
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	2	11.5	KDELPK	729.4	R	V	1.8	0.5	0.0	0.0
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	4	31.5	AAVTMPSSK	891.5	K	L	2.8	0.7	24.3	15.8
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	4	31.5	KDELPK	729.4	R	V	1.8	0.5	23.9	12.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	4	31.5	SMQDPIADMLTR	1377.7	M	I	0.0	0.0	35.7	14.1
P0A7W7	14108.9	S	U	T	B	ETD+CID	LIT	4	31.5	VMAGLGIAVVSTSK	1332.8	K	G	2.4	0.6	0.0	0.0
P0A7W7	14108.9	S	U	T	C	ETD+CID	LIT	3	35.4	AAVTMPSSK	891.5	K	L	2.6	0.7	20.3	16.0
P0A7W7	14108.9	S	U	T	C	ETD+CID	LIT	3	35.4	KDELPK	729.4	R	V	2.1	0.1	24.4	12.8
P0A7W7	14108.9	S	U	T	C	ETD+CID	LIT	3	35.4	VAIANVLKEEGFIEDFKVEGDTKPELELTLK	3474.9	K	Y	1.2	-0.7	15.0	14.1
P0A7W7	14108.9	S	U	T	B	HCD	FT	3	20.8	AAVTMPSSK	891.5	K	L	0.0	0.0	24.3	15.8
P0A7W7	14108.9	S	U	T	B	HCD	FT	3	20.8	KDELPK	729.4	R	V	0.0	0.0	23.9	12.8
P0A7W7	14108.9	S	U	T	B	HCD	FT	3	20.8	SMQDPIADMLTR	1377.7	M	I	0.0	0.0	35.7	14.1
P25738	14241.1	G	U	T	A	CID	LIT	2	18.5	AAADEWDER	1062.4	R	-	2.8	0.0	68.4	4.8
P25738	14241.1	G	U	T	A	CID	LIT	2	18.5	TMYATLEEAIDAAR	1554.7	M	E	0.0	0.0	79.4	11.5
P25738	14241.1	G	U	A	A	CID	LIT	3	21.0	DAAREEFLA	1021.5	I	D	2.4	0.2	16.1	15.8
P25738	14241.1	G	U	A	A	CID	LIT	3	21.0	DANVQQFNAQKYVLQ	1765.9	E	D	4.2	0.7	63.3	16.2
P25738	14241.1	G	U	A	A	CID	LIT	3	21.0	DANVQQFNAQKYVLQDG	1937.9	E	D	3.3	0.6	57.2	16.0
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	AANDDLLNSFWLLDSEK	1950.9	K	G	5.0	0.7	87.4	13.2
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	4.3	0.7	64.9	11.5
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	AGYAEDEVVAVSK	1337.7	K	L	4.5	0.7	89.9	14.5
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	ETLEDAVK	904.5	R	H	1.9	0.6	16.3	12.0
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	ETLEDAVKHPEK	1395.7	R	Y	3.9	0.8	53.9	11.1
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	EVPVEVKPEVR	1280.7	R	V	3.2	0.7	43.7	9.0
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	FNSLTPEQQR	1219.6	R	D	3.3	0.5	29.6	12.6
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	FNSLTPEQQRDVIAR	1773.9	R	T	3.2	0.5	34.4	13.8
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	HPEKYPQLTIR	1381.8	K	V	2.7	0.7	37.3	11.5
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	LGDIEYR	865.4	K	E	2.7	0.4	53.9	13.4
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	LGDIEYREVPVEVKPEVR	2127.1	K	V	3.9	0.6	31.8	9.5
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	MITGIQITK	1004.6	-	A	3.0	0.6	46.7	10.8
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	RETLEDAVK	1060.6	R	H	2.7	0.6	37.1	14.8
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	VEGGQHLNVNVLR	1434.8	R	R	4.5	0.5	62.9	13.0
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	VEGGQHLNVNVLRR	1590.9	R	E	2.7	0.0	25.1	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	VSGYAVR	751.4	R	F	2.2	0.6	50.1	14.5
P68066	14266.0	G	U	T	A	CID	LIT	17	91.3	YPQLTIR	890.5	K	V	2.0	0.7	29.5	14.5
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	AANDDLLNSFWLLDSEK	1950.9	K	G	4.6	0.7	66.7	13.4
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	4.7	0.9	95.2	11.5
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	AGYAEDEVVAVSK	1337.7	K	L	4.1	0.7	86.8	14.8
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	ETLEDAVK	904.5	R	H	2.2	0.6	22.6	12.0
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	ETLEDAVKHPEK	1395.7	R	Y	2.5	0.0	48.1	11.1
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	EVPVEVKPEVR	1280.7	R	V	3.1	0.7	36.8	9.0
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	FNSLTPEQQR	1219.6	R	D	3.1	0.5	47.2	12.3
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	HPEKYPQLTIR	1381.8	K	V	2.2	0.5	33.5	10.8
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	ITGIQITK	873.5	M	A	0.0	0.0	30.4	10.0
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	LGDIEYR	865.4	K	E	2.8	0.4	54.2	14.3
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	LGDIEYREVPVEVKPEVR	2127.1	K	V	5.6	0.0	25.5	9.0
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	MITGIQITK	1004.6	-	A	3.1	0.6	44.7	10.8
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	RETLEDAVK	1060.6	R	H	3.2	0.2	32.8	15.2
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	VEGGQHLNVNVLR	1434.8	R	R	4.3	0.5	71.1	12.8
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	VEGGQHLNVNVLRR	1590.9	R	E	0.9	0.0	36.1	8.5
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	VSGYAVR	751.4	R	F	2.3	0.8	33.6	14.6
P68066	14266.0	G	T	T	A	CID	LIT	17	87.4	YPQLTIR	890.5	K	V	1.5	0.3	11.4	14.5
P68066	14266.0	G	U	A	A	CID	LIT	7	44.1	DDLLNSFWLL	1235.6	N	D	3.1	0.4	48.2	17.2
P68066	14266.0	G	U	A	A	CID	LIT	7	44.1	DEVVAVSKLG	1016.6	E	D	3.7	0.6	59.4	16.0
P68066	14266.0	G	U	A	A	CID	LIT	7	44.1	DVIARTFTESL	1251.7	R	-	4.0	0.7	62.2	14.0
P68066	14266.0	G	U	A	A	CID	LIT	7	44.1	EARCIVAKAGYAE	1437.7	G	D	2.9	0.5	34.1	13.4
P68066	14266.0	G	U	A	A	CID	LIT	7	44.1	ITGIQITKAAN	1129.7	M	D	0.0	0.0	58.9	10.8
P68066	14266.0	G	U	A	A	CID	LIT	7	44.1	MITGIQITKAAN	1260.7	-	D	4.4	0.6	74.0	12.6
P68066	14266.0	G	U	A	A	CID	LIT	7	44.1	MITGIQITKAAND	1375.7	-	D	4.7	0.6	49.6	15.9
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	DDLLNSFWLL	1235.6	N	D	3.3	0.5	49.3	17.8
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	DEVVAVSKLG	1016.6	E	D	2.9	0.7	59.0	16.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	DVIARTFTESL	1251.7	R	-	3.1	0.5	20.4	13.4
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	EARCIVAKAGYAE	1437.7	G	D	3.3	0.0	36.0	14.0
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	EVVAVSKLG	901.5	D	D	3.0	0.7	39.3	13.0
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	ITGIQITKAAN	1129.7	M	D	0.0	0.0	69.5	10.8
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	MITGIQITKAAN	1260.7	-	D	4.7	0.6	71.5	14.3
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	MITGIQITKAAND	1375.7	-	D	4.9	0.6	66.7	15.9
P68066	14266.0	G	T	A	A	CID	LIT	9	44.1	MITGIQITKAANDDLLNSFWLL	2493.3	-	D	0.0	0.0	51.7	13.6
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	AGYAEDEVVAVSK	1337.7	K	L	4.6	0.6	89.7	14.8
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	AGYAEDEVVAVSKLGDIEYR	2184.1	K	E	3.9	0.8	56.4	12.8
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	EVPVEVKPEVR	1280.7	R	V	3.3	0.8	25.3	9.0
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	FNSLTPEQQR	1219.6	R	D	3.2	0.4	32.2	12.3
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	FNSLTPEQQRDVIAR	1773.9	R	T	3.0	0.4	18.4	13.8
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	HPEKYPQLTIR	1381.8	K	V	1.8	0.5	22.1	11.5
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	LGDIEYR	865.4	K	E	2.5	0.4	33.8	13.4
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	LGDIEYREVPVEVKPEVR	2127.1	K	V	2.8	0.8	0.3	9.0
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	MITGIQITK	1004.6	-	A	2.8	0.8	34.6	10.8
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	RETLEDAVK	1060.6	R	H	2.5	0.1	13.8	14.5
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	VEGGQHLNVNVLR	1434.8	R	R	4.2	0.5	88.6	11.8
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	VEGGQHLNVNVLRR	1590.9	R	E	2.9	0.4	9.0	10.0
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	VSGYAVR	751.4	R	F	2.1	0.7	26.9	14.8
P68066	14266.0	G	T	T	B	CID	LIT	14	74.8	VSGYAVRFNSLTPEQQR	1952.0	R	D	3.4	0.8	25.9	12.0
P68066	14266.0	G	U	T	B	CID	LIT	4	29.9	AGYAEDEVVAVSK	1337.7	K	L	4.5	0.0	72.3	14.8
P68066	14266.0	G	U	T	B	CID	LIT	4	29.9	EVPVEVKPEVR	1280.7	R	V	1.5	0.7	11.8	9.0
P68066	14266.0	G	U	T	B	CID	LIT	4	29.9	LGDIEYR	865.4	K	E	2.5	0.4	52.2	13.4
P68066	14266.0	G	U	T	B	CID	LIT	4	29.9	VSGYAVR	751.4	R	F	2.4	0.8	37.1	14.6
P68066	14266.0	G	T	A	B	CID	LIT	7	44.1	DDLLNSFWLL	1235.6	N	D	2.7	0.7	34.0	17.8
P68066	14266.0	G	T	A	B	CID	LIT	7	44.1	DEVVAVSKLG	1016.6	E	D	2.8	0.6	47.1	16.0
P68066	14266.0	G	T	A	B	CID	LIT	7	44.1	DVIARTFTESL	1251.7	R	-	3.8	0.7	53.1	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68066	14266.0	G	T	A	B	CID	LIT	7	44.1	EARCIVAKAGYAE	1437.7	G	D	2.7	0.7	30.3	13.4
P68066	14266.0	G	T	A	B	CID	LIT	7	44.1	ITGIQITKAAN	1129.7	M	D	0.0	0.0	51.7	10.8
P68066	14266.0	G	T	A	B	CID	LIT	7	44.1	MITGIQITKAAN	1260.7	-	D	4.5	0.6	67.8	12.8
P68066	14266.0	G	T	A	B	CID	LIT	7	44.1	MITGIQITKAAND	1375.7	-	D	4.7	0.6	64.2	14.5
P68066	14266.0	G	U	A	B	CID	LIT	6	37.0	DEVVAVSKLG	1016.6	E	D	2.7	0.0	39.5	16.0
P68066	14266.0	G	U	A	B	CID	LIT	6	37.0	DVIARTFTESL	1251.7	R	-	3.5	0.7	46.6	13.4
P68066	14266.0	G	U	A	B	CID	LIT	6	37.0	EARCIVAKAGYAE	1437.7	G	D	3.1	0.0	32.6	14.0
P68066	14266.0	G	U	A	B	CID	LIT	6	37.0	ITGIQITKAAN	1129.7	M	D	0.0	0.0	53.4	10.8
P68066	14266.0	G	U	A	B	CID	LIT	6	37.0	MITGIQITKAAN	1260.7	-	D	4.0	0.5	72.3	13.8
P68066	14266.0	G	U	A	B	CID	LIT	6	37.0	MITGIQITKAAND	1375.7	-	D	4.2	0.7	51.5	14.5
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	AANDDLLNSFWLLDSEK	1950.9	K	G	5.6	0.7	91.2	17.8
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	5.5	0.7	96.0	18.2
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	AGYAEDEVVAVSK	1337.7	K	L	5.2	0.6	78.3	16.7
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	3.9	0.5	66.1	15.7
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	EVPVEVKPEVR	1280.7	R	V	2.8	0.0	24.7	11.5
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	MITGIQITK	1004.6	-	A	3.0	0.0	40.6	13.0
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	VEGGQHLNVNVLR	1434.8	R	R	1.5	0.5	33.3	16.1
P68066	14266.0	S	U	T	A	CID	LIT	7	73.2	VSGYAVR	751.4	R	F	1.9	0.7	27.9	15.7
P68066	14266.0	S	U	T	B	CID	LIT	6	64.6	AANDDLLNSFWLLDSEKGEAR	2365.1	K	C	4.3	0.6	64.9	18.5
P68066	14266.0	S	U	T	B	CID	LIT	6	64.6	AGYAEDEVVAVSK	1337.7	K	L	5.1	0.6	87.1	16.6
P68066	14266.0	S	U	T	B	CID	LIT	6	64.6	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	3.7	0.8	55.2	15.7
P68066	14266.0	S	U	T	B	CID	LIT	6	64.6	LGDIEYR	865.4	K	E	2.9	0.4	54.2	17.4
P68066	14266.0	S	U	T	B	CID	LIT	6	64.6	MITGIQITK	1004.6	-	A	2.9	0.8	38.7	13.0
P68066	14266.0	S	U	T	B	CID	LIT	6	64.6	VEGGQHLNVNVLR	1434.8	R	R	2.9	0.5	11.9	16.9
P68066	14266.0	S	U	T	C	CID	LIT	7	68.5	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	5.3	0.7	94.8	18.0
P68066	14266.0	S	U	T	C	CID	LIT	7	68.5	AGYAEDEVVAVSK	1337.7	K	L	4.6	0.6	79.7	16.6
P68066	14266.0	S	U	T	C	CID	LIT	7	68.5	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	3.4	0.7	59.5	15.6
P68066	14266.0	S	U	T	C	CID	LIT	7	68.5	EVPVEVKPEVR	1280.7	R	V	2.5	0.7	16.8	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68066	14266.0	S	U	T	C	CID	LIT	7	68.5	MITGIQITK	1004.6	-	A	3.2	0.4	34.6	13.0
P68066	14266.0	S	U	T	C	CID	LIT	7	68.5	VEGGQHLNVNVLR	1434.8	R	R	3.9	0.5	76.2	16.9
P68066	14266.0	S	U	T	C	CID	LIT	7	68.5	VEGGQHLNVNVLRR	1590.9	R	E	3.0	0.3	15.0	15.2
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	0.0	0.0	88.6	18.4
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	AGYAEDEVVAVSK	1337.7	K	L	3.7	0.7	0.0	0.0
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	0.0	0.0	55.4	15.9
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	EVPVEVKPEVR	1280.7	R	V	4.2	0.9	55.2	11.8
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	FNSLTPEQQR	1220.6	R	D	0.0	0.0	30.0	16.6
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	HPEKYPQLTIR	1381.8	K	V	4.1	0.9	34.5	14.9
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	LGDIEYR	865.4	K	E	2.3	0.3	39.5	16.2
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	LGDIEYREVPVEVKPEVR	2127.1	K	V	5.2	0.3	46.4	16.3
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	MITGIQITK	1004.6	-	A	2.5	0.8	34.4	13.0
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	VEGGQHLNVNVLR	1434.8	R	R	2.9	0.4	36.1	16.4
P68066	14266.0	S	U	T	A	ETD	LIT	10	81.9	VEGGQHLNVNVLRR	1590.9	R	E	6.3	0.7	60.9	15.6
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	6.0	0.6	64.6	18.1
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	6.4	0.5	54.1	15.8
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	EVPVEVKPEVR	1280.7	R	V	4.3	0.6	32.5	11.8
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	FNSLTPEQQR	1219.6	R	D	1.3	0.5	23.4	15.4
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	HPEKYPQLTIR	1381.8	K	V	4.0	0.6	41.5	14.3
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	LGDIEYR	865.4	K	E	2.2	0.3	0.0	0.0
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	MITGIQITK	1004.6	-	A	2.5	0.5	24.6	13.0
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	VEGGQHLNVNVLR	1434.8	R	R	5.8	0.6	0.0	0.0
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	VEGGQHLNVNVLRR	1590.9	R	E	2.8	0.4	50.5	16.4
P68066	14266.0	S	U	T	B	ETD	LIT	10	77.2	VSGYAVR	751.4	R	F	2.1	0.6	28.5	15.7
P68066	14266.0	S	U	T	C	ETD	LIT	7	58.3	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	5.8	0.6	63.2	18.4
P68066	14266.0	S	U	T	C	ETD	LIT	7	58.3	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	5.4	0.5	45.2	15.9
P68066	14266.0	S	U	T	C	ETD	LIT	7	58.3	EVPVEVKPEVR	1280.7	R	V	1.9	0.3	5.4	11.8
P68066	14266.0	S	U	T	C	ETD	LIT	7	58.3	HPEKYPQLTIR	1381.8	K	V	4.2	0.0	39.2	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68066	14266.0	S	U	T	C	ETD	LIT	7	58.3	MITGIQITK	1004.6	-	A	2.5	0.4	14.2	13.0
P68066	14266.0	S	U	T	C	ETD	LIT	7	58.3	VEGGQHLNVNVLR	1434.8	R	R	3.8	0.6	59.5	16.9
P68066	14266.0	S	U	T	C	ETD	LIT	7	58.3	VEGGQHLNVNVLRR	1590.9	R	E	3.2	0.3	36.8	16.3
P68066	14266.0	S	U	T	C	ETD	FT	3	29.9	AGYAEDEVVAVSK	1337.7	K	L	1.4	0.0	42.2	16.3
P68066	14266.0	S	U	T	C	ETD	FT	3	29.9	EVPVEVKPEVR	1280.7	R	V	1.8	0.0	40.7	12.6
P68066	14266.0	S	U	T	C	ETD	FT	3	29.9	VEGGQHLNVNVLRR	1590.9	R	E	4.7	0.0	66.1	16.4
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	AANDDLLNSFWLLDSEKGEAR	2365.1	K	C	0.0	0.0	95.1	18.4
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	AGYAEDEVVAVSK	1337.7	K	L	0.0	0.0	52.8	17.1
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	0.0	0.0	43.3	15.7
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	LGDIEYR	865.4	K	E	0.0	0.0	49.2	17.6
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	MITGIQITK	1004.6	-	A	0.0	0.0	41.4	13.0
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	5.0	0.8	80.2	18.6
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	AGYAEDEVVAVSKLGDIEYR	2184.1	K	E	2.2	0.3	5.3	17.8
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	5.4	0.0	54.7	15.6
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	FNSLTPEQQR	1219.6	R	D	3.2	0.6	51.9	16.1
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	LGDIEYREVPVEVKPEVR	2127.1	K	V	2.2	0.4	0.0	0.0
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	MITGIQITK	1004.6	-	A	3.1	0.7	26.5	13.0
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	TRPGQHHR	988.5	-	-	1.8	0.2	6.6	16.6
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	VEGGQHLNVNVLR	1434.8	R	R	5.6	0.7	72.1	16.3
P68066	14266.0	S	U	T	A	ETD+CID	LIT	8	81.9	VEGGQHLNVNVLRR	1591.9	R	E	2.7	0.4	6.9	16.7
P68066	14266.0	S	U	T	B	ETD+CID	LIT	4	47.2	AANDDLLNSFWLLDSEKGEAR	2364.1	K	C	3.7	0.8	0.0	0.0
P68066	14266.0	S	U	T	B	ETD+CID	LIT	4	47.2	AGYAEDEVVAVSK	1337.7	K	L	3.8	0.6	0.0	0.0
P68066	14266.0	S	U	T	B	ETD+CID	LIT	4	47.2	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	3.5	0.8	0.0	0.0
P68066	14266.0	S	U	T	B	ETD+CID	LIT	4	47.2	LGDIEYR	865.4	K	E	2.6	0.4	0.0	0.0
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	AANDDLLNSFWLLDSEKGEAR	2365.1	K	C	4.9	0.6	95.1	18.4
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	AGYAEDEVVAVSK	1337.7	K	L	3.8	0.6	52.8	17.1
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	3.4	0.8	43.9	16.1
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	LGDIEYR	865.4	K	E	2.6	0.4	49.2	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P68066	14266.0	S	U	T	B	ETD+CID	LIT	5	54.3	MITGIQITK	1004.6	-	A	2.8	0.7	41.4	13.0
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	AANDDLLNSFWLLDSEKGEAR	2365.1	K	C	4.6	0.6	63.2	18.2
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	AGYAEDEVVAVSK	1337.7	K	L	4.8	0.7	0.0	0.0
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	4.1	0.7	62.3	15.8
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	EVPVEVKPEVR	1280.7	R	V	3.7	0.8	23.9	10.4
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	HPEKYPQLTIR	1381.8	K	V	4.4	0.0	39.2	14.3
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	LGDIEYR	865.4	K	E	2.7	0.4	48.5	17.4
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	MITGIQITK	1004.6	-	A	3.1	0.7	39.8	13.0
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	VEGGQHLNVNVLR	1434.8	R	R	4.4	0.5	69.6	15.9
P68066	14266.0	S	U	T	C	ETD+CID	LIT	9	74.0	VEGGQHLNVNVLRR	1590.9	R	E	2.6	0.4	17.8	15.2
P68066	14266.0	S	U	T	B	HCD	FT	5	54.3	AANDDLLNSFWLLDSEKGEAR	2365.1	K	C	0.0	0.0	95.1	18.4
P68066	14266.0	S	U	T	B	HCD	FT	5	54.3	AGYAEDEVVAVSK	1337.7	K	L	0.0	0.0	52.8	17.1
P68066	14266.0	S	U	T	B	HCD	FT	5	54.3	ETLEDAVKHPEKYPQLTIR	2267.2	R	V	0.0	0.0	43.9	16.1
P68066	14266.0	S	U	T	B	HCD	FT	5	54.3	LGDIEYR	865.4	K	E	0.0	0.0	49.2	17.6
P68066	14266.0	S	U	T	B	HCD	FT	5	54.3	MITGIQITK	1004.6	-	A	0.0	0.0	41.4	13.0
P68066	14266.0	S	U	T	A	HCD	FT	2	12.6	LGDIEYR	865.4	K	E	2.2	0.3	0.0	0.0
P68066	14266.0	S	U	T	A	HCD	FT	2	12.6	MITGIQITK	1004.6	-	A	1.1	0.6	23.9	14.1
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	AGDNAPMAYIELVDR	1634.8	R	S	3.8	0.9	83.6	12.0
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	AGDNAPMAYIELVDRSEK	1979.0	R	A	2.5	0.7	23.8	11.8
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	AGGYTR	624.3	R	I	2.2	0.0	35.2	10.8
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	HEIIKTTLPK	1179.7	R	A	2.7	0.8	32.6	7.0
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	LFNELGPR	945.5	K	F	3.1	0.8	52.5	15.2
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	NMAGSLVR	863.4	R	H	2.1	0.5	12.4	14.8
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	QAMFR	652.3	R	N	1.6	0.4	10.7	10.0
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	RLAFAR	733.4	R	T	2.5	0.7	23.9	9.5
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	RVVEPLITLAK	1238.8	R	T	3.6	0.0	64.2	0.0
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	SEKAEAAAE	905.4	R	-	2.4	0.7	17.2	7.0
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	TDSVANR	762.4	K	R	2.1	0.0	30.1	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	TDSVANRR	918.5	K	L	1.3	0.5	12.7	14.0
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	TRDNEIVAK	1045.6	R	L	3.0	0.5	27.8	14.8
P0AG44	14347.2	G	U	T	A	CID	LIT	14	74.0	VVEPLITLAK	1082.7	R	T	3.1	0.0	54.1	7.0
P0AG44	14347.2	G	T	T	A	CID	LIT	4	24.4	LFNELGPR	945.5	K	F	2.5	0.4	37.5	15.3
P0AG44	14347.2	G	T	T	A	CID	LIT	4	24.4	NMAGSLVR	863.4	R	H	2.1	0.5	32.2	15.3
P0AG44	14347.2	G	T	T	A	CID	LIT	4	24.4	RLAFAR	733.4	R	T	2.0	0.5	11.4	9.5
P0AG44	14347.2	G	T	T	A	CID	LIT	4	24.4	TRDNEIVAK	1045.6	R	L	3.2	0.5	25.4	14.8
P0AG44	14347.2	G	U	T	B	CID	LIT	5	39.4	AGDNAPMAYIELVDR	1634.8	R	S	3.7	0.0	66.5	12.3
P0AG44	14347.2	G	U	T	B	CID	LIT	5	39.4	LFNELGPR	945.5	K	F	2.9	0.4	42.3	15.3
P0AG44	14347.2	G	U	T	B	CID	LIT	5	39.4	NMAGSLVR	847.4	R	H	2.0	0.5	10.3	13.6
P0AG44	14347.2	G	U	T	B	CID	LIT	5	39.4	SEKAEAAAE	905.4	R	-	2.3	0.8	13.6	7.0
P0AG44	14347.2	G	U	T	B	CID	LIT	5	39.4	VVEPLITLAK	1082.7	R	T	3.4	0.0	41.3	7.0
P0AG44	14347.2	G	U	A	B	CID	LIT	2	17.3	DNAPMAYIELV	1235.6	G	D	2.2	0.0	16.4	16.3
P0AG44	14347.2	G	U	A	B	CID	LIT	2	17.3	DRSEKAEAAAE	1176.5	V	-	2.5	0.6	0.0	0.0
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	AGDNAPMAYIELVDR	1650.8	R	S	3.9	0.5	64.7	17.3
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	4.1	0.4	34.4	17.1
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	DNEIVAK	788.4	R	L	2.3	0.3	22.5	18.5
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	HEIIK	639.4	R	T	1.9	0.1	26.0	11.1
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	LFNELGPR	945.5	K	F	3.2	0.7	50.6	18.0
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	RVVEPLITLAK	1238.8	R	T	4.0	0.0	54.7	4.8
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	TRDNEIVAK	1045.6	R	L	2.6	0.4	24.7	17.7
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	TRDNEIVAKLFNELGPR	1972.1	R	F	2.7	0.6	15.0	17.6
P0AG44	14347.2	S	U	T	A	CID	LIT	9	44.9	VVEPLITLAK	1082.7	R	T	2.1	0.0	25.7	3.0
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	AGDNAPMAYIELVDR	1650.8	R	S	4.0	0.5	56.2	16.8
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	AGDNAPMAYIELVDRSEK	1979.0	R	A	3.7	0.5	37.0	17.6
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	4.7	0.5	35.7	17.2
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	LFNELGPR	945.5	K	F	3.0	0.4	50.2	18.8
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	RVVEPLITLAK	1238.8	R	T	2.9	0.3	16.0	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	RVVEPLITLAKTDSVANR	1982.1	R	R	3.9	0.8	34.7	12.6
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	TRDNEIVAK	1045.6	R	L	2.8	0.4	28.8	17.6
P0AG44	14347.2	S	U	T	B	CID	LIT	8	46.5	VVEPLITLAK	1082.7	R	T	2.2	0.0	22.6	7.8
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	AGDNAPMAYIELVDR	1634.8	R	S	3.4	0.5	39.5	17.0
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	AGDNAPMAYIELVDRSEK	1979.0	R	A	3.0	0.5	34.5	17.4
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	4.3	0.4	23.4	17.2
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	HEIIK	639.4	R	T	2.0	0.2	22.3	11.1
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	LFNELGPR	945.5	K	F	3.2	0.5	41.1	18.8
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	RVVEPLITLAK	1238.8	R	T	2.9	0.0	33.7	4.8
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	TRDNEIVAK	1045.6	R	L	3.0	0.4	25.9	17.7
P0AG44	14347.2	S	U	T	C	CID	LIT	8	44.9	VVEPLITLAK	1082.7	R	T	2.3	0.8	32.2	7.8
P0AG44	14347.2	S	U	T	C	CID	FT	2	15.0	LFNELGPR	945.5	K	F	1.9	0.0	24.9	18.8
P0AG44	14347.2	S	U	T	C	CID	FT	2	15.0	RVVEPLITLAK	1238.8	R	T	4.2	0.0	31.0	3.0
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	AGDNAPMAYIELVDR	1634.8	R	S	2.5	0.0	57.8	16.9
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	AGDNAPMAYIELVDRSEK	1979.0	R	A	5.7	0.5	53.9	17.6
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	5.5	0.6	43.7	17.1
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	HEIIK	639.4	R	T	1.5	0.6	28.8	11.1
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	LFNELGPR	946.5	K	F	1.6	0.5	26.2	18.8
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	RVVEPLITLAK	1238.8	R	T	4.3	0.0	44.4	4.8
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	TRDNEIVAK	1045.6	R	L	3.9	0.4	54.0	17.6
P0AG44	14347.2	S	U	T	A	ETD	LIT	8	44.9	VVEPLITLAK	1082.7	R	T	2.4	0.3	23.1	7.8
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	AGDNAPMAYIELVDR	1634.8	R	S	2.0	0.2	37.8	17.8
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	AGDNAPMAYIELVDRSEK	1979.0	R	A	2.4	0.4	0.0	0.0
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	4.2	0.0	31.2	17.5
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	HEIIK	639.4	R	T	1.4	0.4	20.2	11.1
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	LFNELGPR	945.5	K	F	2.0	0.0	39.7	18.8
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	NMAGSLVR	847.4	R	H	2.0	0.6	30.9	16.7
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	RVVEPLITLAK	1238.8	R	T	4.1	0.0	41.0	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	TRDNEIVAK	1045.6	R	L	4.0	0.5	52.1	17.7
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	TRDNEIVAKLFNELGPR	1972.1	R	F	2.9	0.0	19.2	16.5
P0AG44	14347.2	S	U	T	B	ETD	LIT	10	51.2	VVEPLITLAK	1082.7	R	T	3.5	0.4	26.7	7.8
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	AGDNAPMAYIELVDR	1634.8	R	S	2.3	0.3	0.0	0.0
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	AGDNAPMAYIELVDRSEK	1979.0	R	A	4.2	0.5	23.6	17.6
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	5.3	0.6	0.0	0.0
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	HEIIK	639.4	R	T	2.0	0.4	30.5	11.1
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	LFNELGPR	945.5	K	F	0.0	0.0	35.2	18.8
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	NMAGSLVR	847.4	R	H	2.2	0.4	59.3	12.6
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	RVVEPLITLAK	1238.8	R	T	0.0	0.0	33.2	4.8
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	TRDNEIVAK	1045.6	R	L	3.8	0.4	55.0	17.6
P0AG44	14347.2	S	U	T	C	ETD	LIT	9	51.2	VVEPLITLAK	1082.7	R	T	3.2	0.4	0.0	0.0
P0AG44	14347.2	S	U	T	A	ETD	FT	3	22.0	LFNELGPR	945.5	K	F	1.0	0.0	23.6	18.8
P0AG44	14347.2	S	U	T	A	ETD	FT	3	22.0	RVVEPLITLAK	1238.8	R	T	2.2	0.0	54.4	4.8
P0AG44	14347.2	S	U	T	A	ETD	FT	3	22.0	TRDNEIVAK	1045.6	R	L	2.2	0.2	39.1	17.7
P0AG44	14347.2	S	U	T	B	ETD	FT	3	22.0	LFNELGPR	945.5	K	F	0.8	0.0	23.8	18.8
P0AG44	14347.2	S	U	T	B	ETD	FT	3	22.0	RVVEPLITLAK	1238.8	R	T	1.9	0.8	34.1	4.8
P0AG44	14347.2	S	U	T	B	ETD	FT	3	22.0	TRDNEIVAK	1045.6	R	L	2.6	0.4	59.4	17.6
P0AG44	14347.2	S	U	T	C	ETD	FT	2	12.6	LFNELGPR	945.5	K	F	0.0	0.0	21.8	18.8
P0AG44	14347.2	S	U	T	C	ETD	FT	2	12.6	NMAGSLVR	847.4	R	H	0.0	0.0	43.7	16.2
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	7	40.9	AGDNAPMAYIELVDR	1650.8	R	S	0.0	0.0	57.3	17.5
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	7	40.9	AGDNAPMAYIELVDRSEK	1979.0	R	A	0.0	0.0	49.6	17.4
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	7	40.9	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	0.0	0.0	32.5	17.9
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	7	40.9	LFNELGPR	945.5	K	F	0.0	0.0	46.6	18.8
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	7	40.9	RVVEPLITLAK	1238.8	R	T	0.0	0.0	64.8	3.0
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	7	40.9	TRDNEIVAK	1045.6	R	L	0.0	0.0	26.1	17.7
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	7	40.9	VVEPLITLAK	1082.7	R	T	0.0	0.0	24.0	7.8
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	AGDNAPMAYIELVDR	1634.8	R	S	4.2	0.6	71.2	16.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	AGDNAPMAYIELVDRSEK	1979.0	R	A	2.3	0.5	18.1	17.6
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	4.7	0.4	26.6	17.5
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	HEIIK	639.4	R	T	0.6	-0.6	25.1	11.1
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	LFNELGPR	946.5	K	F	2.4	0.6	35.2	18.8
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	MFQQEVTITAPNGLHTRPAAQFVK	2685.4	-	-	5.4	-0.1	35.7	18.1
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	TRDNEIVAK	1045.6	R	L	3.0	0.4	25.2	17.7
P0AG44	14347.2	S	U	T	A	ETD+CID	LIT	8	44.1	VVEPLITLAK	1082.7	R	T	2.5	0.0	26.7	7.8
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	3	18.9	AGDNAPMAYIELVDR	1634.8	R	S	3.6	0.6	0.0	0.0
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	3	18.9	AGDNAPMAYIELVDRSEK	1979.0	R	A	2.2	0.7	0.0	0.0
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	3	18.9	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	5.3	0.4	0.0	0.0
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	AGDNAPMAYIELVDR	1650.8	R	S	3.1	0.4	57.3	17.5
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	AGDNAPMAYIELVDRSEK	1979.0	R	A	4.1	0.5	49.6	17.4
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	5.3	0.4	32.5	17.9
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	HEIIK	639.4	R	T	1.8	0.3	20.3	11.1
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	LFNELGPR	945.5	K	F	3.2	0.5	46.6	18.8
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	MPVADGERLRVTGK	1528.8	-	-	2.3	0.5	6.3	16.8
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	RVVEPLITLAK	1238.8	R	T	3.9	0.0	64.8	3.0
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	TRDNEIVAK	1045.6	R	L	2.3	0.2	26.1	17.7
P0AG44	14347.2	S	U	T	B	ETD+CID	LIT	9	44.9	VVEPLITLAK	1082.7	R	T	2.2	0.0	24.0	7.8
P0AG44	14347.2	S	U	T	C	ETD+CID	LIT	7	44.1	AGDNAPMAYIELVDR	1634.8	R	S	3.8	0.7	0.0	0.0
P0AG44	14347.2	S	U	T	C	ETD+CID	LIT	7	44.1	AGDNAPMAYIELVDRSEK	1979.0	R	A	4.2	0.6	36.7	18.2
P0AG44	14347.2	S	U	T	C	ETD+CID	LIT	7	44.1	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	4.5	0.4	27.3	17.1
P0AG44	14347.2	S	U	T	C	ETD+CID	LIT	7	44.1	HEIIK	639.4	R	T	1.9	0.0	23.8	11.1
P0AG44	14347.2	S	U	T	C	ETD+CID	LIT	7	44.1	LFNELGPR	945.5	K	F	3.2	0.5	0.0	0.0
P0AG44	14347.2	S	U	T	C	ETD+CID	LIT	7	44.1	TRDNEIVAK	1045.6	R	L	3.1	0.3	30.0	17.9
P0AG44	14347.2	S	U	T	C	ETD+CID	LIT	7	44.1	VVEPLITLAK	1082.7	R	T	2.3	0.0	22.3	7.8
P0AG44	14347.2	S	U	T	B	HCD	FT	7	40.9	AGDNAPMAYIELVDR	1650.8	R	S	0.0	0.0	57.3	17.5
P0AG44	14347.2	S	U	T	B	HCD	FT	7	40.9	AGDNAPMAYIELVDRSEK	1979.0	R	A	0.0	0.0	49.6	17.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG44	14347.2	S	U	T	B	HCD	FT	7	40.9	AGDNAPMAYIELVDRSEKAEAAAE	2521.2	R	-	0.0	0.0	32.5	17.9
P0AG44	14347.2	S	U	T	B	HCD	FT	7	40.9	LFNELGPR	945.5	K	F	0.0	0.0	46.6	18.8
P0AG44	14347.2	S	U	T	B	HCD	FT	7	40.9	RVVEPLITLAK	1238.8	R	T	0.0	0.0	64.8	3.0
P0AG44	14347.2	S	U	T	B	HCD	FT	7	40.9	TRDNEIVAK	1045.6	R	L	0.0	0.0	26.1	17.7
P0AG44	14347.2	S	U	T	B	HCD	FT	7	40.9	VVEPLITLAK	1082.7	R	T	0.0	0.0	24.0	7.8
P0ADX1	14498.4	G	U	T	A	CID	LIT	2	17.9	AVNITHSYEVVAA	1373.7	K	-	1.7	0.5	14.4	14.5
P0ADX1	14498.4	G	U	T	A	CID	LIT	2	17.9	GRQDVVDCEVK	1304.6	K	L	3.4	0.0	30.6	9.0
P76549	14535.9	G	T	A	B	CID	LIT	2	16.9	DRLPCLFAAGVVA	1388.7	E	D	2.3	0.5	10.7	16.2
P76549	14535.9	G	T	A	B	CID	LIT	2	16.9	DYAWKHVKE	1175.6	R	D	2.3	0.0	24.2	14.9
P39332	14572.2	G	T	T	A	CID	LIT	3	21.4	EDGTPEPDFQQQVR	1645.7	R	L	3.1	0.5	48.2	8.5
P39332	14572.2	G	T	T	A	CID	LIT	3	21.4	HSLYAEHR	1012.5	R	Y	2.4	0.6	27.1	11.5
P39332	14572.2	G	T	T	A	CID	LIT	3	21.4	YSAAIR	680.4	R	S	1.7	0.6	27.1	14.9
P75874	14683.3	G	U	T	A	CID	LIT	4	45.3	DAGLNVVMDR	1089.5	R	C	3.4	0.7	48.8	13.0
P75874	14683.3	G	U	T	A	CID	LIT	4	45.3	GYGTLADVPEKVDMVDVFR	2111.0	K	N	5.1	0.7	36.5	13.2
P75874	14683.3	G	U	T	A	CID	LIT	4	45.3	NSEAAWGVAQEAIAIGAK	1785.9	R	T	4.8	0.6	69.9	12.6
P75874	14683.3	G	U	T	A	CID	LIT	4	45.3	YLLDQGYHVIPVSPK	1728.9	K	V	4.2	0.8	58.8	11.1
P75874	14683.3	G	T	T	A	CID	LIT	2	18.2	DAGLNVVMDR	1089.5	R	C	3.3	0.8	26.1	13.0
P75874	14683.3	G	T	T	A	CID	LIT	2	18.2	YLLDQGYHVIPVSPK	1728.9	K	V	3.0	0.4	21.9	10.4
P75874	14683.3	G	U	A	A	CID	LIT	2	31.4	DQGYHVIPVSPKVAGKTLLGQKGYGTLA	2897.6	L	D	4.4	0.0	27.9	12.8
P75874	14683.3	G	U	A	A	CID	LIT	2	31.4	DRCPAIEIPRLGLAK	1709.0	M	-	3.1	0.7	0.0	0.0
P75874	14683.3	G	T	T	B	CID	LIT	3	25.5	DAGLNVVMDR	1089.5	R	C	3.0	0.3	43.5	13.8
P75874	14683.3	G	T	T	B	CID	LIT	3	25.5	VAGKTLLGQK	1014.6	K	G	2.6	0.5	7.6	11.1
P75874	14683.3	G	T	T	B	CID	LIT	3	25.5	YLLDQGYHVIPVSPK	1728.9	K	V	3.8	0.6	23.6	10.0
P75874	14683.3	G	T	A	B	CID	LIT	4	54.7	DIAGILTSTHTIALVGAS	1740.0	T	D	2.3	0.4	18.2	12.8
P75874	14683.3	G	T	A	B	CID	LIT	4	54.7	DQGYHVIPVSPKVAGKTLLGQKGYGTLA	2897.6	L	D	3.3	0.0	24.4	13.2
P75874	14683.3	G	T	A	B	CID	LIT	4	54.7	DRCPAIEIPRLGLAK	1709.0	M	-	4.0	0.6	20.0	10.0
P75874	14683.3	G	T	A	B	CID	LIT	4	54.7	DVFRNSEAAWGVAQ	1549.7	V	E	3.2	0.6	26.8	13.8
P75874	14683.3	G	U	A	B	CID	LIT	3	41.6	DQGYHVIPVSPKVAGKTLLGQKGYGTLA	2897.6	L	D	3.4	0.0	28.8	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P75874	14683.3	G	U	A	B	CID	LIT	3	41.6	DRCPAIEIPRLGLAK	1709.0	M	-	2.6	0.0	27.3	10.0
P75874	14683.3	G	U	A	B	CID	LIT	3	41.6	DVFRNSEAAWGVAQ	1549.7	V	E	3.5	0.7	15.5	13.6
P75874	14683.3	S	U	T	A	CID	LIT	4	51.1	DAGLNVVMDRCPAIEIPR	2026.0	R	L	1.8	0.6	10.6	18.2
P75874	14683.3	S	U	T	A	CID	LIT	4	51.1	GYGTLADVPEKVDMVDVFR	2111.0	K	N	3.5	0.6	26.4	18.1
P75874	14683.3	S	U	T	A	CID	LIT	4	51.1	NSEAAWGVAQEAIAIGAK	1785.9	R	T	2.1	0.6	0.0	0.0
P75874	14683.3	S	U	T	A	CID	LIT	4	51.1	YLLDQGYHVIPVSPK	1728.9	K	V	2.7	0.5	24.0	17.1
P75874	14683.3	S	U	T	B	CID	LIT	4	60.6	GYGTLADVPEKVDMVDVFR	2111.0	K	N	3.9	0.4	45.0	18.1
P75874	14683.3	S	U	T	B	CID	LIT	4	60.6	MKETDIAGILTSTHTIALVGASDKPDRPSYR	3343.7	-	V	2.0	0.3	23.3	17.6
P75874	14683.3	S	U	T	B	CID	LIT	4	60.6	NSEAAWGVAQEAIAIGAK	1785.9	R	T	3.5	0.2	12.1	17.9
P75874	14683.3	S	U	T	B	CID	LIT	4	60.6	YLLDQGYHVIPVSPK	1728.9	K	V	1.3	0.6	35.1	15.8
P75874	14683.3	S	U	T	C	CID	LIT	2	24.1	NSEAAWGVAQEAIAIGAK	1785.9	R	T	3.1	0.3	2.9	17.9
P75874	14683.3	S	U	T	C	CID	LIT	2	24.1	YLLDQGYHVIPVSPK	1728.9	K	V	2.2	0.5	9.2	17.1
P75874	14683.3	S	U	T	A	ETD	LIT	2	24.1	NSEAAWGVAQEAIAIGAK	1785.9	R	T	2.0	0.0	32.4	17.9
P75874	14683.3	S	U	T	A	ETD	LIT	2	24.1	YLLDQGYHVIPVSPK	1728.9	K	V	4.2	0.6	29.7	17.1
P75874	14683.3	S	U	T	B	ETD	LIT	2	24.8	GYGTLADVPEKVDMVDVFR	2111.0	K	N	3.1	0.6	22.7	17.6
P75874	14683.3	S	U	T	B	ETD	LIT	2	24.8	YLLDQGYHVIPVSPK	1728.9	K	V	3.6	0.0	18.6	17.1
P75874	14683.3	S	U	T	A	ETD+CID	LIT	2	37.2	DAGLNVVMDRCPAIEIPR	2026.0	R	L	2.8	0.6	22.3	17.7
P75874	14683.3	S	U	T	A	ETD+CID	LIT	2	37.2	NSEAAWGVAQEAIAIGAK	1785.9	R	T	4.6	0.5	0.0	0.0
P75874	14683.3	S	U	T	A	ETD+CID	LIT	2	37.2	YLLDQGYHVIPVSPK	1728.9	K	V	3.9	0.6	28.4	15.8
Q46864	14685.1	G	U	T	A	CID	LIT	2	20.6	VLDKHPELLNEIR	1575.9	R	-	3.8	0.8	38.0	11.1
Q46864	14685.1	G	U	T	A	CID	LIT	2	20.6	YEKGNAQPHPSTIK	1569.8	R	L	4.0	0.8	26.7	13.0
Q46864	14685.1	S	U	T	C	CID	LIT	2	21.4	ASVNAETVAPEFIVK	1574.8	R	V	3.0	0.4	12.1	16.6
Q46864	14685.1	S	U	T	C	CID	LIT	2	21.4	VLDKHPELLNEIR	1575.9	R	-	3.8	0.4	23.1	14.0
Q46864	14685.1	S	U	T	C	ETD+CID	LIT	2	21.4	ASVNAETVAPEFIVK	1574.8	R	V	2.7	0.2	3.2	16.5
Q46864	14685.1	S	U	T	C	ETD+CID	LIT	2	21.4	VLDKHPELLNEIR	1575.9	R	-	2.9	0.4	22.7	14.5
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	AENQYYGTGR	1158.5	M	R	0.0	0.0	50.0	4.8
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	AGFVTR	650.4	K	D	1.7	0.3	35.9	17.1
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	ALMEYDESLR	1242.6	R	S	2.7	0.6	35.3	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	ALMEYDESLRSELR	1711.8	R	K	2.0	0.8	19.6	11.5
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	GGGISGQAGAIR	1043.6	K	H	4.2	0.9	67.9	12.6
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	IVINQR	742.5	K	S	1.9	0.7	28.7	11.1
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	LDLYITVK	964.6	K	G	2.7	0.6	24.4	7.0
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	MVVRQPLELVDMVEK	1786.0	R	L	4.6	0.6	52.7	13.0
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	QPLELVDMVEK	1300.7	R	L	2.7	0.8	55.3	11.1
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	RPQFSKR	918.5	R	-	2.8	0.7	28.2	12.6
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	SLEQYFGR	999.5	R	E	2.7	0.0	42.5	11.1
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	SLEQYFGRETAR	1456.7	R	M	1.6	0.6	12.7	10.8
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	VFIKPGNGK	959.6	R	I	2.3	0.7	24.3	12.8
P0A7X3	14838.6	G	U	T	A	CID	LIT	14	76.2	VFIKPGNGKIVINQR	1683.0	R	S	3.0	0.0	30.3	3.0
P0A7X3	14838.6	G	T	T	A	CID	LIT	4	27.7	AENQYYGTGR	1158.5	M	R	0.0	0.0	50.9	4.8
P0A7X3	14838.6	G	T	T	A	CID	LIT	4	27.7	GGGISGQAGAIR	1043.6	K	H	3.7	0.6	53.9	12.6
P0A7X3	14838.6	G	T	T	A	CID	LIT	4	27.7	IVINQR	742.5	K	S	1.9	0.6	24.3	12.3
P0A7X3	14838.6	G	T	T	A	CID	LIT	4	27.7	SLEQYFGR	999.5	R	E	2.1	0.0	41.8	10.8
P0A7X3	14838.6	G	T	T	B	CID	LIT	3	22.3	AENQYYGTGR	1158.5	M	R	0.0	0.0	46.4	4.8
P0A7X3	14838.6	G	T	T	B	CID	LIT	3	22.3	GGGISGQAGAIR	1043.6	K	H	3.2	0.4	44.6	13.0
P0A7X3	14838.6	G	T	T	B	CID	LIT	3	22.3	RPQFSKR	918.5	R	-	1.8	0.7	19.6	12.6
P0A7X3	14838.6	G	U	T	B	CID	LIT	3	23.1	AENQYYGTGR	1158.5	M	R	0.0	0.0	55.5	4.8
P0A7X3	14838.6	G	U	T	B	CID	LIT	3	23.1	GGGISGQAGAIR	1043.6	K	H	3.6	0.5	54.1	14.1
P0A7X3	14838.6	G	U	T	B	CID	LIT	3	23.1	SLEQYFGR	999.5	R	E	2.7	0.8	24.7	11.1
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	AENQYYGTGR	1158.5	M	R	0.0	0.0	46.6	9.5
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	AGFVTR	650.4	K	D	1.5	0.2	28.5	17.3
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	ALMEYDESLRSELR	1711.8	R	K	2.6	0.4	18.6	16.6
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	GGGISGQAGAIR	1043.6	K	H	3.8	0.6	63.8	15.8
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	KAGFVTR	778.5	R	D	2.2	0.6	20.5	14.6
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	QPLELVDMVEK	1300.7	R	L	2.7	0.6	11.9	16.9
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	RRPQFSKR	1074.6	R	-	2.6	0.8	21.6	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	SLEQYFGR	999.5	R	E	3.0	0.4	31.4	14.5
P0A7X3	14838.6	S	U	T	A	CID	LIT	9	60.8	VFIKPGNGK	959.6	R	I	1.9	0.2	9.0	15.6
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	AENQYYGTGR	1158.5	M	R	0.0	0.0	51.8	9.5
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	ALMEYDESLR	1226.6	R	S	2.7	0.8	40.8	14.0
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	ALMEYDESLRSELR	1711.8	R	K	2.6	0.3	8.4	17.0
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	GGGISGQAGAIR	1043.6	K	H	3.5	0.7	57.2	15.8
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	KAGFVTR	778.5	R	D	1.9	0.7	22.5	14.6
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	QPLELVDMVEK	1300.7	R	L	3.1	0.0	19.2	16.9
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	RRPQFSKR	1074.6	R	-	2.3	0.8	6.6	11.8
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	SLEQYFGRETAR	1456.7	R	M	1.8	0.6	0.0	0.0
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	VFIKPGNGK	960.6	R	I	2.4	0.6	21.0	12.6
P0A7X3	14838.6	S	U	T	B	CID	LIT	10	68.5	VFIKPGNGKIVINQR	1684.0	R	S	3.3	0.5	33.8	9.0
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	AENQYYGTGR	1158.5	M	R	0.0	0.0	55.2	9.5
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	ALMEYDESLRSELR	1711.8	R	K	2.5	0.3	12.0	17.1
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	GGGISGQAGAIR	1043.6	K	H	3.6	0.6	53.3	15.8
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	KAGFVTR	778.5	R	D	2.0	0.6	16.0	14.6
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	MVVRQPLELVDMVEK	1786.0	R	L	3.9	0.5	12.9	17.2
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	QPLELVDMVEK	1300.7	R	L	3.3	0.0	28.0	16.9
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	RRPQFSKR	1074.6	R	-	2.2	0.7	0.0	0.0
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	SLEQYFGR	999.5	R	E	2.9	0.4	42.5	14.5
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	VFIKPGNGK	960.6	R	I	2.7	0.4	23.7	17.3
P0A7X3	14838.6	S	U	T	C	CID	LIT	10	68.5	VFIKPGNGKIVINQR	1683.0	R	S	3.0	0.0	19.1	7.0
P0A7X3	14838.6	S	U	T	B	CID	FT	2	16.9	KAGFVTR	778.5	R	D	2.1	0.0	27.4	14.6
P0A7X3	14838.6	S	U	T	B	CID	FT	2	16.9	VFIKPGNGKIVINQR	1684.0	R	S	2.7	0.0	41.4	10.0
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	AENQYYGTGR	1158.5	M	R	0.0	0.0	39.3	9.5
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	ALMEYDESLR	1226.6	R	S	1.8	0.7	0.0	0.0
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	ALMEYDESLRSELR	1711.8	R	K	2.2	0.5	0.0	0.0
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	GGGISGQAGAIR	1043.6	K	H	3.4	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	KAGFVTR	778.5	R	D	2.4	0.3	24.5	14.6
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	MVVRQPLELVDMVEK	1786.0	R	L	3.5	0.4	34.5	17.2
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	QPLELVDMVEK	1300.7	R	L	2.0	0.7	28.5	16.9
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	RRPQFSK	918.5	R	-	2.7	0.6	22.9	15.7
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	RRPQFSKR	1074.6	R	-	2.4	0.5	12.9	11.8
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	SLEQYFGR	999.5	R	E	1.9	0.5	39.3	12.8
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	SLEQYFGRETAR	1456.7	R	M	4.0	0.6	35.6	14.3
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	VFIKPGNGK	960.6	R	I	3.0	0.5	34.9	12.6
P0A7X3	14838.6	S	U	T	A	ETD	LIT	13	71.5	VFIKPGNGKIVINQR	1684.0	R	S	5.7	0.6	46.3	9.5
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	AENQYYGTGR	1158.5	M	R	0.0	0.0	48.8	9.5
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	AENQYYGTGRR	1314.6	M	K	0.0	0.0	58.7	13.8
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	AGFVTR	650.4	K	D	1.3	0.2	30.3	17.3
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	ALMEYDESLR	1226.6	R	S	1.8	0.7	29.9	13.6
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	ALMEYDESLRSELR	1711.8	R	K	2.1	0.7	36.0	16.6
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	GGGISGQAGAIR	1043.6	K	H	3.4	0.6	68.6	14.8
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	KAGFVTR	778.5	R	D	2.0	0.4	21.9	14.3
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	MVVRQPLELVDMVEK	1786.0	R	L	0.0	0.0	46.7	17.3
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	QPLELVDMVEK	1300.7	R	L	2.3	0.6	25.7	15.8
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	RRPQFSK	918.5	R	-	2.1	0.5	16.4	15.8
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	RRPQFSKR	1074.6	R	-	2.2	0.2	0.0	0.0
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	SLEQYFGR	999.5	R	E	1.7	0.7	0.0	0.0
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	SLEQYFGRETAR	1456.7	R	M	3.9	0.6	46.6	14.8
P0A7X3	14838.6	S	U	T	B	ETD	LIT	14	72.3	VFIKPGNGKIVINQR	1684.0	R	S	5.1	0.7	44.9	10.0
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	AENQYYGTGR	1158.5	M	R	0.0	0.0	62.5	9.5
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	ALMEYDESLR	1226.6	R	S	2.0	0.8	26.5	14.0
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	ALMEYDESLRSELR	1711.8	R	K	2.0	0.6	36.3	16.6
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	GGGISGQAGAIR	1043.6	K	H	3.2	0.6	70.8	15.2
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	KAGFVTR	778.5	R	D	2.4	0.4	33.3	14.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	QPLELVDMVEK	1300.7	R	L	2.8	0.0	27.3	15.8
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	RRPQFSK	918.5	R	-	2.5	0.6	21.0	15.7
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	RRPQFSKR	1074.6	R	-	3.2	0.2	35.2	12.3
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	SLEQYFGR	999.5	R	E	1.8	0.4	30.3	14.6
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	SLEQYFGRETAR	1456.7	R	M	2.3	0.3	9.2	15.2
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	VFIKPGNGK	960.6	R	I	2.5	0.2	18.2	17.3
P0A7X3	14838.6	S	U	T	C	ETD	LIT	12	68.5	VFIKPGNGKIVINQR	1684.0	R	S	4.2	0.0	38.5	9.5
P0A7X3	14838.6	S	U	T	A	ETD	FT	6	40.0	AENQYYGTGR	1158.5	M	R	0.0	0.0	65.1	9.5
P0A7X3	14838.6	S	U	T	A	ETD	FT	6	40.0	GGGISGQAGAIR	1043.6	K	H	2.3	0.3	69.3	15.8
P0A7X3	14838.6	S	U	T	A	ETD	FT	6	40.0	KAGFVTR	778.5	R	D	1.5	0.0	28.8	14.6
P0A7X3	14838.6	S	U	T	A	ETD	FT	6	40.0	RRPQFSK	918.5	R	-	1.6	0.0	29.2	15.7
P0A7X3	14838.6	S	U	T	A	ETD	FT	6	40.0	RRPQFSKR	1074.6	R	-	1.8	0.0	26.0	11.8
P0A7X3	14838.6	S	U	T	A	ETD	FT	6	40.0	VFIKPGNGKIVINQR	1684.0	R	S	4.2	0.5	38.0	10.0
P0A7X3	14838.6	S	U	T	B	ETD	FT	3	13.8	AENQYYGTGR	1158.5	M	R	0.0	0.0	67.8	9.5
P0A7X3	14838.6	S	U	T	B	ETD	FT	3	13.8	RRPQFSK	918.5	R	-	2.0	0.4	33.0	15.7
P0A7X3	14838.6	S	U	T	B	ETD	FT	3	13.8	RRPQFSKR	1074.6	R	-	2.3	0.3	36.7	11.8
P0A7X3	14838.6	S	U	T	C	ETD	FT	3	21.5	RRPQFSK	918.5	R	-	1.9	0.0	29.5	15.8
P0A7X3	14838.6	S	U	T	C	ETD	FT	3	21.5	SLEQYFGRETAR	1456.7	R	M	0.7	0.0	23.2	14.8
P0A7X3	14838.6	S	U	T	C	ETD	FT	3	21.5	VFIKPGNGK	960.6	R	I	1.9	0.6	18.2	13.4
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	4	27.7	AENQYYGTGR	1158.5	M	R	0.0	0.0	52.3	9.5
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	4	27.7	QPLELVDMVEK	1300.7	R	L	0.0	0.0	30.1	16.9
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	4	27.7	RRPQFSK	918.5	R	-	0.0	0.0	20.1	15.7
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	4	27.7	SLEQYFGR	999.5	R	E	0.0	0.0	41.7	12.8
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	AENQYYGTGR	1158.5	M	R	0.0	0.0	52.2	9.5
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	ALMEYDESLRSELR	1711.8	R	K	3.0	0.4	0.0	0.0
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	KAGFVTR	778.5	R	D	2.1	0.0	18.8	14.6
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	QPLELVDMVEK	1300.7	R	L	2.6	0.6	27.4	16.9
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	RRPQFSK	918.5	R	-	2.9	0.8	24.4	15.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	RRPQFSKR	1074.6	R	-	2.9	0.0	14.6	11.8
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	SLEQYFGR	999.5	R	E	2.7	0.7	0.0	0.0
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	SLEQYFGRETAR	1456.7	R	M	2.8	0.6	11.3	15.2
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	VFIKPGNGK	960.6	R	I	2.8	0.7	17.8	13.4
P0A7X3	14838.6	S	U	T	A	ETD+CID	LIT	10	59.2	VFIKPGNGKIVINQR	1683.0	R	S	2.4	0.6	22.0	8.5
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	AENQYYGTGR	1158.5	M	R	0.0	0.0	52.3	9.5
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	ALMEYDESLRSELR	1711.8	R	K	2.5	0.5	13.5	16.6
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	KAGFVTR	778.5	R	D	2.1	0.0	19.1	14.6
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	QPLELVDMVEK	1300.7	R	L	2.9	0.0	30.1	16.9
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	RRPQFSK	918.5	R	-	3.0	0.6	20.1	15.7
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	RRPQFSKR	1074.6	R	-	1.8	0.3	12.1	11.8
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	SLEQYFGR	999.5	R	E	3.0	0.0	41.7	12.8
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	SLEQYFGRETAR	1456.7	R	M	2.5	0.6	7.4	14.8
P0A7X3	14838.6	S	U	T	B	ETD+CID	LIT	9	54.6	VFIKPGNGK	960.6	R	I	2.5	0.7	14.8	12.6
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	AENQYYGTGR	1158.5	M	R	0.0	0.0	52.4	9.5
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	ALMEYDESLR	1242.6	R	S	2.1	0.3	0.0	0.0
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	ALMEYDESLRSELR	1711.8	R	K	2.6	0.3	0.0	0.0
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	KAGFVTR	778.5	R	D	2.2	0.5	22.0	14.6
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	QPLELVDMVEK	1300.7	R	L	2.9	0.0	19.6	16.9
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	RRPQFSK	918.5	R	-	2.8	0.7	11.8	15.7
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	RRPQFSKR	1074.6	R	-	2.3	0.3	25.7	13.0
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	SLEQYFGR	999.5	R	E	2.9	0.4	44.6	14.5
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	SLEQYFGRETAR	1456.7	R	M	2.3	0.6	16.5	14.8
P0A7X3	14838.6	S	U	T	C	ETD+CID	LIT	10	54.6	VFIKPGNGK	960.6	R	I	2.4	0.7	30.4	13.4
P0A7X3	14838.6	S	U	T	B	HCD	FT	3	22.3	AENQYYGTGR	1158.5	M	R	0.0	0.0	52.3	9.5
P0A7X3	14838.6	S	U	T	B	HCD	FT	3	22.3	QPLELVDMVEK	1300.7	R	L	0.0	0.0	30.1	16.9
P0A7X3	14838.6	S	U	T	B	HCD	FT	3	22.3	SLEQYFGR	999.5	R	E	0.0	0.0	41.7	12.8
P0A7J7	14857.5	G	U	T	A	CID	LIT	6	38.7	AADMTGADIEAMTR	1452.6	K	S	3.6	0.8	48.0	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7J7	14857.5	G	U	T	A	CID	LIT	6	38.7	AQLQEIAQTK	1129.6	R	A	3.5	0.6	53.2	13.6
P0A7J7	14857.5	G	U	T	A	CID	LIT	6	38.7	GLPIPVVITVYADR	1512.9	K	S	2.9	0.8	31.4	9.5
P0A7J7	14857.5	G	U	T	A	CID	LIT	6	38.7	SFTFVTK	829.4	R	T	2.2	0.0	23.4	7.8
P0A7J7	14857.5	G	U	T	A	CID	LIT	6	38.7	TPPAAVLLK	909.6	K	K	2.3	0.0	45.1	0.0
P0A7J7	14857.5	G	U	T	A	CID	LIT	6	38.7	TPPAAVLLKK	1037.7	K	A	2.2	0.6	30.9	4.8
P0A7J7	14857.5	G	T	T	A	CID	LIT	4	33.1	AADMTGADIEAMTR	1484.6	K	S	3.8	0.8	60.9	7.0
P0A7J7	14857.5	G	T	T	A	CID	LIT	4	33.1	AQLQEIAQTK	1129.6	R	A	3.2	0.5	37.9	13.2
P0A7J7	14857.5	G	T	T	A	CID	LIT	4	33.1	GLPIPVVITVYADR	1512.9	K	S	3.5	0.0	69.9	9.5
P0A7J7	14857.5	G	T	T	A	CID	LIT	4	33.1	TPPAAVLLK	909.6	K	K	2.1	0.0	18.2	0.0
P0A7J7	14857.5	G	U	A	A	CID	LIT	4	29.6	DKVGKISRAQLQ	1342.8	K	E	4.3	0.8	52.4	9.5
P0A7J7	14857.5	G	U	A	A	CID	LIT	4	29.6	DKVGKISRAQLQEIAQTKAA	2155.2	K	D	4.5	0.6	58.2	11.5
P0A7J7	14857.5	G	U	A	A	CID	LIT	4	29.6	DSIEKGLPIPVVITVYA	1814.0	T	D	2.9	0.0	27.4	11.8
P0A7J7	14857.5	G	U	A	A	CID	LIT	4	29.6	EIAQTKAADMTGA	1306.6	Q	D	2.3	0.3	15.6	15.4
P0A7J7	14857.5	G	T	T	B	CID	LIT	4	28.2	AADMTGADIEAMTR	1452.6	K	S	4.2	0.7	66.3	9.0
P0A7J7	14857.5	G	T	T	B	CID	LIT	4	28.2	AQLQEIAQTK	1129.6	R	A	3.4	0.6	45.3	13.2
P0A7J7	14857.5	G	T	T	B	CID	LIT	4	28.2	SIEGTAR	733.4	R	S	1.5	0.6	21.2	14.6
P0A7J7	14857.5	G	T	T	B	CID	LIT	4	28.2	TPPAAVLLK	909.6	K	K	1.9	0.0	22.5	0.0
P0A7J7	14857.5	G	U	T	B	CID	LIT	4	28.2	AQLQEIAQTK	1129.6	R	A	3.0	0.4	40.4	13.2
P0A7J7	14857.5	G	U	T	B	CID	LIT	4	28.2	GLPIPVVITVYADR	1512.9	K	S	3.4	0.0	54.8	8.5
P0A7J7	14857.5	G	U	T	B	CID	LIT	4	28.2	SFTFVTK	829.4	R	T	2.0	0.4	12.3	10.8
P0A7J7	14857.5	G	U	T	B	CID	LIT	4	28.2	TPPAAVLLK	909.6	K	K	2.6	0.0	27.5	0.0
P0A7J7	14857.5	G	T	A	B	CID	LIT	5	48.6	DKVGKISRAQLQ	1342.8	K	E	3.7	0.7	51.5	9.5
P0A7J7	14857.5	G	T	A	B	CID	LIT	5	48.6	DKVGKISRAQLQEIAQTKAA	2155.2	K	D	3.1	0.7	25.1	11.1
P0A7J7	14857.5	G	T	A	B	CID	LIT	5	48.6	DRSFTFVTKTPPAAVLLKKAAGIKSGSGKPNK	3314.9	A	D	3.7	0.0	17.2	7.8
P0A7J7	14857.5	G	T	A	B	CID	LIT	5	48.6	DSIEKGLPIPVVITVYA	1814.0	T	D	3.3	0.7	40.7	12.0
P0A7J7	14857.5	G	T	A	B	CID	LIT	5	48.6	EIAQTKAA	831.5	Q	D	2.5	0.7	32.4	17.3
P0A7J7	14857.5	G	U	A	B	CID	LIT	4	48.6	DKVGKISRAQLQ	1342.8	K	E	2.9	0.6	31.1	9.5
P0A7J7	14857.5	G	U	A	B	CID	LIT	4	48.6	DKVGKISRAQLQEIAQTKAA	2155.2	K	D	3.4	0.7	41.6	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7J7	14857.5	G	U	A	B	CID	LIT	4	48.6	DRSFTFVTKTPPAAVLLKKAAGIKSGSGKPNK	3314.9	A	D	3.6	0.0	18.5	7.0
P0A7J7	14857.5	G	U	A	B	CID	LIT	4	48.6	DSIEKGLPIPVVITVYA	1814.0	T	D	4.2	0.6	49.7	12.0
P0A7J7	14857.5	S	U	T	A	CID	LIT	3	26.1	AADMTGADIEAMTR	1452.6	K	S	3.7	0.4	39.8	14.1
P0A7J7	14857.5	S	U	T	A	CID	LIT	3	26.1	GLPIPVVITVYADR	1512.9	K	S	2.7	0.8	24.6	15.1
P0A7J7	14857.5	S	U	T	A	CID	LIT	3	26.1	TPPAAVLLK	909.6	K	K	2.5	0.0	49.1	7.0
P0A7J7	14857.5	S	U	T	B	CID	LIT	2	16.2	AADMTGADIEAMTR	1452.6	K	S	2.7	0.7	28.4	14.1
P0A7J7	14857.5	S	U	T	B	CID	LIT	2	16.2	TPPAAVLLK	909.6	K	K	2.1	0.0	36.5	7.0
P0A7J7	14857.5	S	U	T	C	CID	LIT	4	35.9	AADMTGADIEAMTR	1452.6	K	S	2.4	0.5	6.4	14.1
P0A7J7	14857.5	S	U	T	C	CID	LIT	4	35.9	GLPIPVVITVYADR	1512.9	K	S	4.0	0.9	88.3	13.8
P0A7J7	14857.5	S	U	T	C	CID	LIT	4	35.9	SFTFVTK	829.4	R	T	1.3	0.6	23.0	13.4
P0A7J7	14857.5	S	U	T	C	CID	LIT	4	35.9	SIEGTAR	733.4	R	S	1.3	0.4	21.0	18.1
P0A7J7	14857.5	S	U	T	C	CID	LIT	4	35.9	TPPAAVLLK	909.6	K	K	2.3	0.0	35.5	7.0
P0A7J7	14857.5	S	U	T	A	ETD	LIT	4	28.9	GLPIPVVITVYADR	1512.9	K	S	3.1	0.7	67.7	14.8
P0A7J7	14857.5	S	U	T	A	ETD	LIT	4	28.9	SFTFVTK	829.4	R	T	1.7	0.6	20.4	13.4
P0A7J7	14857.5	S	U	T	A	ETD	LIT	4	28.9	SGSGKPNKDKVGK	1301.7	K	I	3.1	0.0	28.0	15.6
P0A7J7	14857.5	S	U	T	A	ETD	LIT	4	28.9	SIEGTAR	733.4	R	S	2.2	0.0	50.2	16.9
P0A7J7	14857.5	S	U	T	B	ETD	LIT	2	12.0	AQLQEIAQTK	1129.6	R	A	0.0	0.0	34.8	17.6
P0A7J7	14857.5	S	U	T	B	ETD	LIT	2	12.0	SFTFVTK	829.4	R	T	2.2	0.0	22.8	7.8
P0A7J7	14857.5	S	U	T	C	ETD	LIT	4	33.8	AADMTGADIEAMTR	1452.6	K	S	2.3	0.8	70.0	14.1
P0A7J7	14857.5	S	U	T	C	ETD	LIT	4	33.8	GLPIPVVITVYADR	1512.9	K	S	2.7	0.8	59.4	13.6
P0A7J7	14857.5	S	U	T	C	ETD	LIT	4	33.8	SGSGKPNKDKVGK	1301.7	K	I	2.7	0.6	24.5	16.0
P0A7J7	14857.5	S	U	T	C	ETD	LIT	4	33.8	SIEGTAR	733.4	R	S	1.6	0.5	50.0	16.9
P0A7J7	14857.5	S	U	T	C	ETD	FT	2	12.0	SFTFVTK	829.4	R	T	1.1	0.0	23.8	13.4
P0A7J7	14857.5	S	U	T	C	ETD	FT	2	12.0	TPPAAVLLKK	1037.7	K	A	2.5	0.0	42.6	4.8
P0A7J7	14857.5	S	U	T	B	ETD+CID	LIT	2	19.7	AADMTGADIEAMTR	1452.6	K	S	0.0	0.0	89.5	14.1
P0A7J7	14857.5	S	U	T	B	ETD+CID	LIT	2	19.7	GLPIPVVITVYADR	1512.9	K	S	0.0	0.0	83.8	13.8
P0A7J7	14857.5	S	U	T	A	ETD+CID	LIT	3	24.6	AADMTGADIEAMTR	1452.6	K	S	3.2	0.7	60.5	14.1
P0A7J7	14857.5	S	U	T	A	ETD+CID	LIT	3	24.6	GLPIPVVITVYADR	1512.9	K	S	1.7	0.7	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7J7	14857.5	S	U	T	A	ETD+CID	LIT	3	24.6	SIEGTAR	733.4	R	S	1.7	0.0	25.1	16.9
P0A7J7	14857.5	S	U	T	B	ETD+CID	LIT	2	19.7	AADMTGADIEAMTR	1452.6	K	S	4.0	0.8	89.5	14.1
P0A7J7	14857.5	S	U	T	B	ETD+CID	LIT	2	19.7	GLPIPVVITVYADR	1512.9	K	S	3.9	0.0	83.8	13.8
P0A7J7	14857.5	S	U	T	C	ETD+CID	LIT	4	35.9	AADMTGADIEAMTR	1452.6	K	S	4.6	0.7	81.8	14.1
P0A7J7	14857.5	S	U	T	C	ETD+CID	LIT	4	35.9	GLPIPVVITVYADR	1512.9	K	S	4.3	0.0	89.8	13.8
P0A7J7	14857.5	S	U	T	C	ETD+CID	LIT	4	35.9	SFTFVTK	829.4	R	T	0.0	0.0	31.1	15.4
P0A7J7	14857.5	S	U	T	C	ETD+CID	LIT	4	35.9	SIEGTAR	733.4	R	S	1.4	0.5	19.7	18.1
P0A7J7	14857.5	S	U	T	C	ETD+CID	LIT	4	35.9	TPPAAVLLK	909.6	K	K	2.3	0.0	52.4	7.0
P0A7J7	14857.5	S	U	T	B	HCD	FT	2	19.7	AADMTGADIEAMTR	1452.6	K	S	0.0	0.0	89.5	14.1
P0A7J7	14857.5	S	U	T	B	HCD	FT	2	19.7	GLPIPVVITVYADR	1512.9	K	S	0.0	0.0	83.8	13.8
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	GHSSAQYSGEIK	1263.6	K	G	3.6	0.0	53.4	9.5
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	GYDYDTYTFYAK	1506.6	K	K	3.9	0.0	63.3	3.0
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	KGHSSAQYSGEIK	1391.7	R	G	3.6	0.6	31.3	13.0
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	KYNVDIQIK	1120.6	K	-	2.3	0.8	27.4	7.8
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	NVNVEFR	877.5	K	K	1.5	0.3	13.7	10.0
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	NVNVEFRK	1005.5	K	G	2.1	0.7	19.3	14.0
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	4.8	0.0	53.0	9.5
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	YNVDIQIK	992.5	K	-	2.5	0.3	29.8	14.1
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	YSPELDSHGQYSLPASGK	1935.9	R	Y	4.3	0.0	78.5	12.6
P76002	14888.6	G	U	T	A	CID	LIT	10	67.7	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	4.3	0.0	47.6	11.8
P76002	14888.6	G	T	T	A	CID	LIT	7	42.1	GHSSAQYSGEIK	1263.6	K	G	3.4	0.0	43.3	9.5
P76002	14888.6	G	T	T	A	CID	LIT	7	42.1	GYDYDTYTFYAK	1506.6	K	K	3.4	0.0	65.0	6.0
P76002	14888.6	G	T	T	A	CID	LIT	7	42.1	KGHSSAQYSGEIK	1391.7	R	G	4.0	0.8	30.7	13.0
P76002	14888.6	G	T	T	A	CID	LIT	7	42.1	KYNVDIQIK	1120.6	K	-	3.2	0.0	39.8	7.8
P76002	14888.6	G	T	T	A	CID	LIT	7	42.1	YNVDIQIK	992.5	K	-	2.4	0.0	31.5	14.6
P76002	14888.6	G	T	T	A	CID	LIT	7	42.1	YSPELDSHGQYSLPASGK	1935.9	R	Y	4.5	0.8	80.6	11.8
P76002	14888.6	G	T	T	A	CID	LIT	7	42.1	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	3.7	0.0	44.2	11.5
P76002	14888.6	G	U	A	A	CID	LIT	2	12.8	DARKNKTKKYNV	1464.8	N	D	3.3	0.8	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76002	14888.6	G	U	A	A	CID	LIT	2	12.8	DARKNKTKKYNVDIQIK	2062.2	N	-	3.5	0.7	36.3	8.5
P76002	14888.6	G	U	A	B	CID	LIT	5	50.4	DLSRYSPEL	1079.5	V	D	1.9	0.3	4.9	15.4
P76002	14888.6	G	U	A	B	CID	LIT	5	50.4	DSHGQYSLPASGKY	1509.7	L	E	3.3	0.6	31.9	14.5
P76002	14888.6	G	U	A	B	CID	LIT	5	50.4	DSHGQYSLPASGKYELRVLQTRN	2619.3	L	D	2.5	0.8	12.3	15.7
P76002	14888.6	G	U	A	B	CID	LIT	5	50.4	DTYLFGPGIDDSV	1398.6	A	D	2.3	0.7	11.6	12.0
P76002	14888.6	G	U	A	B	CID	LIT	5	50.4	DTYTFYAKKGQKVHVSISNEGA	2443.2	Y	D	5.5	0.6	46.2	14.1
P76002	14888.6	S	U	T	A	CID	LIT	4	46.6	KGHSSAQYSGEIK	1391.7	R	G	2.8	0.6	19.6	15.9
P76002	14888.6	S	U	T	A	CID	LIT	4	46.6	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	5.5	0.7	33.3	18.7
P76002	14888.6	S	U	T	A	CID	LIT	4	46.6	YSPELDSHGQYSLPASGK	1935.9	R	Y	4.6	0.8	65.4	17.2
P76002	14888.6	S	U	T	A	CID	LIT	4	46.6	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	3.2	0.0	56.0	18.3
P76002	14888.6	S	U	T	B	CID	LIT	5	53.4	KGHSSAQYSGEIK	1391.7	R	G	2.3	0.5	0.0	0.0
P76002	14888.6	S	U	T	B	CID	LIT	5	53.4	KYNVDIQIK	1120.6	K	-	2.5	0.6	27.3	13.2
P76002	14888.6	S	U	T	B	CID	LIT	5	53.4	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	5.4	0.0	31.8	18.7
P76002	14888.6	S	U	T	B	CID	LIT	5	53.4	YSPELDSHGQYSLPASGK	1935.9	R	Y	5.8	0.7	67.5	17.1
P76002	14888.6	S	U	T	B	CID	LIT	5	53.4	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	3.6	0.8	44.7	18.5
P76002	14888.6	S	U	T	C	CID	LIT	5	53.4	KGHSSAQYSGEIK	1391.7	R	G	4.9	0.6	51.3	15.9
P76002	14888.6	S	U	T	C	CID	LIT	5	53.4	KYNVDIQIK	1120.6	K	-	2.8	0.5	25.9	13.2
P76002	14888.6	S	U	T	C	CID	LIT	5	53.4	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	5.8	0.7	44.7	18.6
P76002	14888.6	S	U	T	C	CID	LIT	5	53.4	YSPELDSHGQYSLPASGK	1935.9	R	Y	5.5	0.7	79.6	17.2
P76002	14888.6	S	U	T	C	CID	LIT	5	53.4	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	3.9	0.6	45.1	18.3
P76002	14888.6	S	U	T	A	ETD	LIT	3	26.3	KGHSSAQYSGEIK	1391.7	R	G	5.7	0.7	60.8	16.8
P76002	14888.6	S	U	T	A	ETD	LIT	3	26.3	YSPELDSHGQYSLPASGK	1935.9	R	Y	5.9	0.6	77.1	17.2
P76002	14888.6	S	U	T	A	ETD	LIT	3	26.3	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	4.9	0.0	52.3	18.5
P76002	14888.6	S	U	T	B	ETD	LIT	5	51.9	KGHSSAQYSGEIK	1391.7	R	G	3.0	0.8	27.0	15.9
P76002	14888.6	S	U	T	B	ETD	LIT	5	51.9	NVNVEFR	877.5	K	K	1.9	0.4	43.2	17.6
P76002	14888.6	S	U	T	B	ETD	LIT	5	51.9	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	0.0	0.0	26.5	18.7
P76002	14888.6	S	U	T	B	ETD	LIT	5	51.9	YSPELDSHGQYSLPASGK	1935.9	R	Y	5.1	0.0	56.0	16.8
P76002	14888.6	S	U	T	B	ETD	LIT	5	51.9	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	6.6	0.0	55.4	18.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76002	14888.6	S	U	T	C	ETD	LIT	5	53.4	KGHSSAQYSGEIK	1391.7	R	G	7.2	0.7	79.0	15.1
P76002	14888.6	S	U	T	C	ETD	LIT	5	53.4	KYNVDIQIK	1120.6	K	-	2.4	0.5	19.0	13.2
P76002	14888.6	S	U	T	C	ETD	LIT	5	53.4	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	0.0	0.0	22.0	18.9
P76002	14888.6	S	U	T	C	ETD	LIT	5	53.4	YSPELDSHGQYSLPASGK	1935.9	R	Y	5.8	0.6	51.8	17.2
P76002	14888.6	S	U	T	C	ETD	LIT	5	53.4	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	5.5	0.7	66.4	18.3
P76002	14888.6	S	U	T	B	ETD	FT	2	23.3	KGHSSAQYSGEIK	1391.7	R	G	3.8	0.6	80.8	16.8
P76002	14888.6	S	U	T	B	ETD	FT	2	23.3	YSPELDSHGQYSLPASGK	1935.9	R	Y	2.3	0.0	50.5	17.2
P76002	14888.6	S	U	T	C	ETD	FT	2	20.3	KYNVDIQIK	1120.6	K	-	1.3	0.0	27.5	13.2
P76002	14888.6	S	U	T	C	ETD	FT	2	20.3	YSPELDSHGQYSLPASGK	1935.9	R	Y	2.3	0.0	44.7	16.7
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	GYDYDTYTFYAK	1506.6	K	K	0.0	0.0	22.6	9.5
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	KYNVDIQIK	1120.6	K	-	0.0	0.0	50.5	13.2
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	0.0	0.0	33.0	18.9
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	YSPELDSHGQYSLPASGK	1935.9	R	Y	0.0	0.0	24.8	16.7
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	0.0	0.0	56.9	18.3
P76002	14888.6	S	U	T	A	ETD+CID	LIT	4	53.4	KGHSSAQYSGEIK	1391.7	R	G	6.2	0.7	62.2	16.8
P76002	14888.6	S	U	T	A	ETD+CID	LIT	4	53.4	KYNVDIQIK	1120.6	K	-	3.0	0.6	19.0	13.2
P76002	14888.6	S	U	T	A	ETD+CID	LIT	4	53.4	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	5.7	0.0	23.9	18.6
P76002	14888.6	S	U	T	A	ETD+CID	LIT	4	53.4	YSPELDSHGQYSLPASGK	1935.9	R	Y	1.9	0.7	26.9	16.7
P76002	14888.6	S	U	T	A	ETD+CID	LIT	4	53.4	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	3.5	0.8	47.5	18.3
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	DVFVHFSAIQGNGFK	1666.8	-	-	5.0	0.5	66.4	17.7
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	GYDYDTYTFYAK	1506.6	K	K	2.8	0.4	22.6	9.5
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	KYNVDIQIK	1120.6	K	-	3.3	0.5	50.5	13.2
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	5.4	0.8	33.0	18.9
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	YSPELDSHGQYSLPASGK	1935.9	R	Y	1.7	0.7	24.8	16.7
P76002	14888.6	S	U	T	B	ETD+CID	LIT	5	52.6	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	3.5	0.0	56.9	18.3
P76002	14888.6	S	U	T	C	ETD+CID	LIT	6	62.4	GYDYDTYTFYAK	1506.6	K	K	1.9	0.3	11.6	9.5
P76002	14888.6	S	U	T	C	ETD+CID	LIT	6	62.4	KGHSSAQYSGEIK	1391.7	R	G	4.2	0.5	49.6	15.9
P76002	14888.6	S	U	T	C	ETD+CID	LIT	6	62.4	KYNVDIQIK	1120.6	K	-	3.4	0.8	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P76002	14888.6	S	U	T	C	ETD+CID	LIT	6	62.4	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	5.2	0.9	44.8	18.7
P76002	14888.6	S	U	T	C	ETD+CID	LIT	6	62.4	YNVDIQIK	992.5	K	-	2.2	0.3	22.4	16.9
P76002	14888.6	S	U	T	C	ETD+CID	LIT	6	62.4	YSPELDSHGQYSLPASGK	1935.9	R	Y	5.4	0.7	78.5	17.2
P76002	14888.6	S	U	T	C	ETD+CID	LIT	6	62.4	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	5.1	0.6	55.2	18.5
P76002	14888.6	S	U	T	B	HCD	FT	5	52.6	GYDYDTYTFYAK	1506.6	K	K	0.0	0.0	22.6	9.5
P76002	14888.6	S	U	T	B	HCD	FT	5	52.6	KYNVDIQIK	1120.6	K	-	0.0	0.0	50.5	13.2
P76002	14888.6	S	U	T	B	HCD	FT	5	52.6	VHVSISNEGADTYLFGPGIDDSVDLSR	2863.4	K	Y	0.0	0.0	33.0	18.9
P76002	14888.6	S	U	T	B	HCD	FT	5	52.6	YSPELDSHGQYSLPASGK	1935.9	R	Y	0.0	0.0	24.8	16.7
P76002	14888.6	S	U	T	B	HCD	FT	5	52.6	YSPELDSHGQYSLPASGKYELR	2497.2	R	V	0.0	0.0	56.9	18.3
P0AC81	14902.2	G	T	T	A	CID	LIT	4	23.0	IELIEEKDAGR	1272.7	K	G	3.3	0.8	48.7	13.4
P0AC81	14902.2	G	T	T	A	CID	LIT	4	23.0	LLHTMLR	899.5	R	V	2.2	0.6	22.6	11.5
P0AC81	14902.2	G	T	T	A	CID	LIT	4	23.0	SIDFYTK	873.4	R	V	2.2	0.6	29.1	12.3
P0AC81	14902.2	G	T	T	A	CID	LIT	4	23.0	VGDLQR	687.4	R	S	2.1	0.3	22.5	17.8
P0AFW4	14909.3	G	U	A	A	CID	LIT	3	25.7	DILLEQPAYAGLPIA	1583.9	I	D	2.6	0.5	17.2	12.3
P0AFW4	14909.3	G	U	A	A	CID	LIT	3	25.7	DLDAERI	831.4	N	D	2.0	0.4	11.1	18.8
P0AFW4	14909.3	G	U	A	A	CID	LIT	3	25.7	DRAQMCSPEEMPH	1587.6	L	D	2.8	0.0	20.5	4.8
P0AFW4	14909.3	G	T	T	B	CID	LIT	2	8.8	FRNLSDGEVR	1192.6	K	V	2.7	0.4	36.0	13.6
P0AFW4	14909.3	G	T	T	B	CID	LIT	2	8.8	NLSDGEVRVR	1144.6	R	T	2.5	0.3	30.2	14.8
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	DILLEQPAYAGLPIA	1583.9	I	D	3.8	0.6	52.6	12.3
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	DRAQMCSPEEMPH	1587.6	L	D	3.7	0.0	38.2	4.8
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	DSIHWELPGGVATHL	1631.8	G	E	3.3	0.0	35.7	14.6
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	DSIHWELPGGVATHLEVL	1973.0	G	E	3.4	0.6	17.2	16.7
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	DSNTQLSVMAPVGAALLGLRVG	2169.2	T	D	5.6	0.7	72.6	14.1
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	ELEYQPEAAG	1106.5	L	D	2.2	0.7	18.9	15.1
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	SRPTIIIN	913.5	M	D	0.0	0.0	21.1	13.4
P0AFW4	14909.3	G	T	A	B	CID	LIT	8	64.7	SRPTIIINDL	1141.7	M	D	0.0	0.0	28.3	12.0
P0AFW4	14909.3	G	U	A	B	CID	LIT	3	31.6	DILLEQPAYAGLPIA	1583.9	I	D	3.1	0.0	47.1	12.3
P0AFW4	14909.3	G	U	A	B	CID	LIT	3	31.6	DRAQMCSPEEMPH	1587.6	L	D	2.9	0.8	30.2	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFW4	14909.3	G	U	A	B	CID	LIT	3	31.6	DSIHWELPGGVATHL	1631.8	G	E	3.6	0.0	22.5	14.6
P0ADW3	14943.3	G	T	T	A	CID	LIT	3	34.1	DYSEGASGLLR	1167.6	R	T	3.3	0.8	55.2	11.1
P0ADW3	14943.3	G	T	T	A	CID	LIT	3	34.1	LAESEASNDQAPVQMPR	1842.9	R	D	4.2	0.0	61.0	7.0
P0ADW3	14943.3	G	T	T	A	CID	LIT	3	34.1	SSSSLLPELSAEANPFR	1804.9	K	N	3.7	0.0	39.0	14.1
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	AAIEAAGGKIEE	1158.6	R	-	3.5	0.6	40.8	11.8
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	AANIIGIQIEFAK	1387.8	K	V	2.3	0.4	3.5	12.3
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	FGFTSRK	842.5	K	A	1.9	0.7	16.1	11.5
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	GFEGGQMPLYR	1254.6	R	R	2.6	0.6	19.5	12.0
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	GIGSGLGK	688.4	R	T	2.3	0.5	30.0	18.4
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	KAAITAEIR	972.6	R	L	3.0	0.7	46.0	13.0
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	LGRGIGSGLGK	1014.6	R	T	3.0	0.8	21.8	11.5
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	LNTLSPAEGSK	1116.6	R	K	3.2	0.6	42.2	13.2
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	LNTLSPAEGSKK	1244.7	R	A	3.0	0.4	38.1	12.3
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	MRLNTLSPAEGSK	1403.7	-	K	4.4	0.6	46.2	14.3
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	RGFEGGQMPLYR	1410.7	R	R	4.0	0.5	33.1	13.4
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	VEGGVVDLNTLK	1243.7	K	A	4.3	0.8	52.7	12.3
P02413	14963.1	G	U	T	A	CID	LIT	13	71.5	VILAGEVTTPVTVR	1454.9	K	G	4.9	0.0	83.7	3.0
P02413	14963.1	G	T	T	A	CID	LIT	2	18.1	AAIEAAGGKIEE	1158.6	R	-	3.1	0.7	41.6	11.8
P02413	14963.1	G	T	T	A	CID	LIT	2	18.1	VILAGEVTTPVTVR	1454.9	K	G	3.2	0.0	35.0	3.0
P02413	14963.1	G	U	T	B	CID	LIT	5	40.3	AAIEAAGGKIEE	1158.6	R	-	3.3	0.0	46.7	11.8
P02413	14963.1	G	U	T	B	CID	LIT	5	40.3	KAAITAEIR	972.6	R	L	2.8	0.7	40.9	12.3
P02413	14963.1	G	U	T	B	CID	LIT	5	40.3	LNTLSPAEGSK	1116.6	R	K	2.6	0.4	22.1	13.6
P02413	14963.1	G	U	T	B	CID	LIT	5	40.3	VEGGVVDLNTLK	1243.7	K	A	3.6	0.3	12.0	12.3
P02413	14963.1	G	U	T	B	CID	LIT	5	40.3	VILAGEVTTPVTVR	1454.9	K	G	4.5	0.0	55.5	4.8
P02413	14963.1	S	U	T	A	CID	LIT	4	37.5	AANIIGIQIEFAK	1387.8	K	V	3.8	0.5	31.4	13.6
P02413	14963.1	S	U	T	A	CID	LIT	4	37.5	KAAITAEIR	972.6	R	L	3.3	0.7	69.7	16.3
P02413	14963.1	S	U	T	A	CID	LIT	4	37.5	LSDLAKVEGGVVDLNTLK	1871.0	R	A	3.8	0.4	22.5	14.0
P02413	14963.1	S	U	T	A	CID	LIT	4	37.5	VILAGEVTTPVTVR	1454.9	K	G	3.2	0.8	26.4	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02413	14963.1	S	U	T	B	CID	LIT	5	45.1	AANIIGIQIEFAK	1387.8	K	V	3.5	0.6	24.5	13.8
P02413	14963.1	S	U	T	B	CID	LIT	5	45.1	GFEGGQMPLYR	1254.6	R	R	3.3	0.7	20.8	14.6
P02413	14963.1	S	U	T	B	CID	LIT	5	45.1	KAAITAEIR	972.6	R	L	2.3	0.5	33.2	16.3
P02413	14963.1	S	U	T	B	CID	LIT	5	45.1	LSDLAKVEGGVVDLNTLK	1871.0	R	A	5.4	0.5	32.7	14.0
P02413	14963.1	S	U	T	B	CID	LIT	5	45.1	VILAGEVTTPVTVR	1454.9	K	G	4.6	0.9	93.6	10.8
P02413	14963.1	S	U	T	C	CID	LIT	7	54.2	AAIEAAGGKIEE	1158.6	R	-	2.8	0.4	29.5	15.3
P02413	14963.1	S	U	T	C	CID	LIT	7	54.2	AANIIGIQIEFAK	1387.8	K	V	2.5	0.4	8.2	13.8
P02413	14963.1	S	U	T	C	CID	LIT	7	54.2	GFEGGQMPLYR	1254.6	R	R	3.6	0.6	33.1	14.5
P02413	14963.1	S	U	T	C	CID	LIT	7	54.2	KAAITAEIR	972.6	R	L	2.7	0.6	41.6	16.0
P02413	14963.1	S	U	T	C	CID	LIT	7	54.2	LSDLAKVEGGVVDLNTLK	1871.0	R	A	4.3	0.5	18.6	14.0
P02413	14963.1	S	U	T	C	CID	LIT	7	54.2	RGFEGGQMPLYR	1410.7	R	R	4.0	0.5	43.8	16.4
P02413	14963.1	S	U	T	C	CID	LIT	7	54.2	VILAGEVTTPVTVR	1454.9	K	G	4.9	0.0	76.1	10.4
P02413	14963.1	S	U	T	B	CID	FT	2	20.1	GFEGGQMPLYR	1254.6	R	R	2.7	0.0	14.8	14.8
P02413	14963.1	S	U	T	B	CID	FT	2	20.1	LSDLAKVEGGVVDLNTLK	1871.0	R	A	3.0	0.0	19.6	14.0
P02413	14963.1	S	U	T	A	ETD	LIT	6	45.1	AAIEAAGGKIEE	1158.6	R	-	2.7	0.4	0.0	0.0
P02413	14963.1	S	U	T	A	ETD	LIT	6	45.1	GFEGGQMPLYR	1254.6	R	R	2.4	0.4	16.7	14.5
P02413	14963.1	S	U	T	A	ETD	LIT	6	45.1	KAAITAEIR	972.6	R	L	2.4	0.3	29.7	16.0
P02413	14963.1	S	U	T	A	ETD	LIT	6	45.1	LSDLAKVEGGVVDLNTLK	1871.0	R	A	6.5	0.5	76.8	13.0
P02413	14963.1	S	U	T	A	ETD	LIT	6	45.1	RGFEGGQMPLYR	1410.7	R	R	2.9	0.0	24.3	17.2
P02413	14963.1	S	U	T	A	ETD	LIT	6	45.1	VILAGEVTTPVTVR	1454.9	K	G	0.0	0.0	66.3	10.8
P02413	14963.1	S	U	T	B	ETD	LIT	5	44.4	AAIEAAGGKIEE	1158.6	R	-	4.1	0.5	0.0	0.0
P02413	14963.1	S	U	T	B	ETD	LIT	5	44.4	GFEGGQMPLYR	1254.6	R	R	2.7	0.0	23.9	14.1
P02413	14963.1	S	U	T	B	ETD	LIT	5	44.4	KAAITAEIR	972.6	R	L	2.4	0.1	30.2	16.0
P02413	14963.1	S	U	T	B	ETD	LIT	5	44.4	LSDLAKVEGGVVDLNTLK	1871.0	R	A	5.4	0.5	44.2	13.8
P02413	14963.1	S	U	T	B	ETD	LIT	5	44.4	VILAGEVTTPVTVR	1454.9	K	G	3.5	0.0	61.9	10.4
P02413	14963.1	S	U	T	C	ETD	LIT	7	52.8	AAIEAAGGKIEE	1158.6	R	-	3.1	0.3	37.5	15.7
P02413	14963.1	S	U	T	C	ETD	LIT	7	52.8	GFEGGQMPLYR	1254.6	R	R	1.9	0.6	33.3	14.8
P02413	14963.1	S	U	T	C	ETD	LIT	7	52.8	KAAITAEIR	972.6	R	L	2.7	0.3	27.8	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02413	14963.1	S	U	T	C	ETD	LIT	7	52.8	LNTLSPAEGSK	1116.6	R	K	2.9	0.5	30.7	16.1
P02413	14963.1	S	U	T	C	ETD	LIT	7	52.8	LSDLAKVEGGVVDLNTLK	1871.0	R	A	2.7	0.9	26.8	14.0
P02413	14963.1	S	U	T	C	ETD	LIT	7	52.8	RGFEGGQMPLYR	1410.7	R	R	3.8	0.5	43.2	17.3
P02413	14963.1	S	U	T	C	ETD	LIT	7	52.8	VILAGEVTTPVTVR	1454.9	K	G	3.5	0.0	66.1	10.8
P02413	14963.1	S	U	T	A	ETD	FT	2	14.6	KAAITAEIR	972.6	R	L	1.8	0.0	40.9	16.3
P02413	14963.1	S	U	T	A	ETD	FT	2	14.6	RGFEGGQMPLYR	1410.7	R	R	2.0	0.0	27.5	17.2
P02413	14963.1	S	U	T	C	ETD	FT	2	8.3	GFEGGQMPLYR	1254.6	R	R	1.8	0.0	19.0	14.5
P02413	14963.1	S	U	T	C	ETD	FT	2	8.3	RGFEGGQMPLYR	1410.7	R	R	2.0	0.3	33.9	16.4
P02413	14963.1	S	U	T	B	ETD+CID	LIT	4	36.1	GFEGGQMPLYR	1254.6	R	R	0.0	0.0	20.7	15.1
P02413	14963.1	S	U	T	B	ETD+CID	LIT	4	36.1	KAAITAEIR	972.6	R	L	0.0	0.0	47.4	16.3
P02413	14963.1	S	U	T	B	ETD+CID	LIT	4	36.1	LSDLAKVEGGVVDLNTLK	1871.0	R	A	0.0	0.0	51.3	14.0
P02413	14963.1	S	U	T	B	ETD+CID	LIT	4	36.1	VILAGEVTTPVTVR	1454.9	K	G	0.0	0.0	30.8	10.4
P02413	14963.1	S	U	T	A	ETD+CID	LIT	4	38.9	AANIIGIQIEFAK	1387.8	K	V	3.5	0.8	25.8	13.6
P02413	14963.1	S	U	T	A	ETD+CID	LIT	4	38.9	DANDTGSTEVQVALLTAQINHLQGHFAEHK	3245.6	-	-	5.7	0.0	47.4	19.8
P02413	14963.1	S	U	T	A	ETD+CID	LIT	4	38.9	GFEGGQMPLYR	1254.6	R	R	2.2	0.6	13.8	15.4
P02413	14963.1	S	U	T	A	ETD+CID	LIT	4	38.9	LSDLAKVEGGVVDLNTLK	1871.0	R	A	4.4	0.5	21.9	14.0
P02413	14963.1	S	U	T	A	ETD+CID	LIT	4	38.9	VILAGEVTTPVTVR	1454.9	K	G	4.8	0.9	0.0	0.0
P02413	14963.1	S	U	T	B	ETD+CID	LIT	5	45.1	AANIIGIQIEFAK	1387.8	K	V	3.4	0.5	0.0	0.0
P02413	14963.1	S	U	T	B	ETD+CID	LIT	5	45.1	GFEGGQMPLYR	1254.6	R	R	3.1	0.0	20.7	15.1
P02413	14963.1	S	U	T	B	ETD+CID	LIT	5	45.1	KAAITAEIR	972.6	R	L	0.0	0.0	47.4	16.3
P02413	14963.1	S	U	T	B	ETD+CID	LIT	5	45.1	LSDLAKVEGGVVDLNTLK	1871.0	R	A	4.6	0.5	51.3	14.0
P02413	14963.1	S	U	T	B	ETD+CID	LIT	5	45.1	VILAGEVTTPVTVR	1454.9	K	G	3.4	0.0	30.8	10.4
P02413	14963.1	S	U	T	C	ETD+CID	LIT	7	54.2	AAIEAAGGKIEE	1158.6	R	-	0.0	0.0	41.3	15.3
P02413	14963.1	S	U	T	C	ETD+CID	LIT	7	54.2	AANIIGIQIEFAK	1387.8	K	V	3.1	0.5	30.9	13.8
P02413	14963.1	S	U	T	C	ETD+CID	LIT	7	54.2	GFEGGQMPLYR	1254.6	R	R	4.0	0.7	53.7	14.8
P02413	14963.1	S	U	T	C	ETD+CID	LIT	7	54.2	KAAITAEIR	972.6	R	L	2.5	0.6	50.4	16.0
P02413	14963.1	S	U	T	C	ETD+CID	LIT	7	54.2	LSDLAKVEGGVVDLNTLK	1871.0	R	A	3.3	0.4	11.6	14.1
P02413	14963.1	S	U	T	C	ETD+CID	LIT	7	54.2	RGFEGGQMPLYR	1410.7	R	R	3.3	0.4	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02413	14963.1	S	U	T	C	ETD+CID	LIT	7	54.2	VILAGEVTTPVTVR	1454.9	K	G	2.0	0.2	8.3	10.4
P02413	14963.1	S	U	T	B	HCD	FT	4	36.1	GFEGGQMPLYR	1254.6	R	R	0.0	0.0	20.7	15.1
P02413	14963.1	S	U	T	B	HCD	FT	4	36.1	KAAITAEIR	972.6	R	L	0.0	0.0	47.4	16.3
P02413	14963.1	S	U	T	B	HCD	FT	4	36.1	LSDLAKVEGGVVDLNTLK	1871.0	R	A	0.0	0.0	51.3	14.0
P02413	14963.1	S	U	T	B	HCD	FT	4	36.1	VILAGEVTTPVTVR	1454.9	K	G	0.0	0.0	30.8	10.4
P31063	14965.5	G	U	A	A	CID	LIT	3	21.2	DGMTMERV	938.4	Y	D	2.0	0.6	4.3	15.1
P31063	14965.5	G	U	A	A	CID	LIT	3	21.2	DKAPLPTPLP	1048.6	L	-	2.2	0.6	11.8	7.8
P31063	14965.5	G	U	A	A	CID	LIT	3	21.2	DRPTAECAAAL	1174.6	V	D	2.3	0.7	34.4	16.6
P31063	14965.5	G	U	T	B	CID	LIT	4	42.3	ALVSPEAIGSLIVTK	1497.9	R	E	4.7	0.0	84.8	3.0
P31063	14965.5	G	U	T	B	CID	LIT	4	42.3	DGNTIEYDGMTMER	1631.7	R	V	3.1	0.0	42.5	0.0
P31063	14965.5	G	U	T	B	CID	LIT	4	42.3	ELYEVER	937.5	R	D	2.0	0.0	20.9	9.0
P31063	14965.5	G	U	T	B	CID	LIT	4	42.3	VDRPTAECAAALDKAPLPTPLP	2303.2	R	-	3.5	0.0	26.2	12.6
P31063	14965.5	G	U	A	B	CID	LIT	4	30.7	DDLTNVTVKRELY	1565.8	S	E	2.6	0.0	23.2	13.8
P31063	14965.5	G	U	A	B	CID	LIT	4	30.7	DGMTMERV	938.4	Y	D	2.2	0.0	22.5	15.1
P31063	14965.5	G	U	A	B	CID	LIT	4	30.7	DKAPLPTPLP	1048.6	L	-	2.2	0.8	15.5	7.8
P31063	14965.5	G	U	A	B	CID	LIT	4	30.7	DRPTAECAAAL	1174.6	V	D	2.4	0.0	36.8	16.1
P31063	14965.5	S	U	T	C	ETD	LIT	2	27.0	ALVSPEAIGSLIVTK	1497.9	R	E	2.4	0.1	26.2	12.3
P31063	14965.5	S	U	T	C	ETD	LIT	2	27.0	VDRPTAECAAALDKAPLPTPLP	2303.2	R	-	5.2	0.7	27.6	18.2
P0A6E6	15050.4	G	U	T	A	CID	LIT	7	69.1	AEEHISSSHGDVDYAQASAELAK	2415.1	K	A	7.2	0.8	61.0	10.0
P0A6E6	15050.4	G	U	T	A	CID	LIT	7	69.1	AIAQLR	671.4	K	V	1.8	0.4	26.9	14.0
P0A6E6	15050.4	G	U	T	A	CID	LIT	7	69.1	AMTYHLDVVSAEQQMFSGLVEK	2483.2	M	I	0.0	0.0	74.9	10.4
P0A6E6	15050.4	G	U	T	A	CID	LIT	7	69.1	GQDLDEAR	903.4	R	A	2.2	0.4	12.0	7.8
P0A6E6	15050.4	G	U	T	A	CID	LIT	7	69.1	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	5.3	0.0	67.0	4.8
P0A6E6	15050.4	G	U	T	A	CID	LIT	7	69.1	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	6.3	0.8	40.4	7.8
P0A6E6	15050.4	G	U	T	A	CID	LIT	7	69.1	VIELTKK	830.5	R	A	2.1	0.3	6.3	9.0
P0A6E6	15050.4	G	T	A	B	CID	LIT	3	21.6	DEARAMEAKRKA	1375.7	L	E	2.3	0.5	6.3	15.1
P0A6E6	15050.4	G	T	A	B	CID	LIT	3	21.6	DTAIRGQDL	988.5	A	D	2.9	0.6	31.4	16.5
P0A6E6	15050.4	G	T	A	B	CID	LIT	3	21.6	EAKRKAEEHISSSHG	1665.8	M	D	2.1	0.8	12.6	15.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6E6	15050.4	G	U	A	B	CID	LIT	3	23.0	DEARAMEAKRKA	1375.7	L	E	1.6	0.5	14.5	15.1
P0A6E6	15050.4	G	U	A	B	CID	LIT	3	23.0	DTAIRGQDL	988.5	A	D	2.9	0.0	38.1	17.2
P0A6E6	15050.4	G	U	A	B	CID	LIT	3	23.0	EVQPGNVTVLA	1126.6	L	D	2.5	0.0	36.2	11.8
P0A6E6	15050.4	S	U	T	A	CID	LIT	2	38.1	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	4.5	0.0	42.8	13.2
P0A6E6	15050.4	S	U	T	A	CID	LIT	2	38.1	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	5.9	0.7	65.7	17.7
P0A6E6	15050.4	S	U	T	B	CID	LIT	3	43.9	GQDLDEAR	903.4	R	A	2.5	0.0	23.1	14.0
P0A6E6	15050.4	S	U	T	B	CID	LIT	3	43.9	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	3.7	0.0	64.2	14.0
P0A6E6	15050.4	S	U	T	B	CID	LIT	3	43.9	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	6.0	0.6	68.5	16.9
P0A6E6	15050.4	S	U	T	C	CID	LIT	3	43.9	GQDLDEAR	903.4	R	A	2.4	0.3	19.4	14.0
P0A6E6	15050.4	S	U	T	C	CID	LIT	3	43.9	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	4.8	0.0	53.5	13.2
P0A6E6	15050.4	S	U	T	C	CID	LIT	3	43.9	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	7.1	0.7	58.0	17.0
P0A6E6	15050.4	S	U	T	A	ETD	LIT	2	38.1	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	3.1	0.0	37.8	14.0
P0A6E6	15050.4	S	U	T	A	ETD	LIT	2	38.1	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	7.4	0.0	64.4	16.7
P0A6E6	15050.4	S	U	T	B	ETD	LIT	3	43.9	GQDLDEAR	903.4	R	A	1.3	0.4	41.1	14.0
P0A6E6	15050.4	S	U	T	B	ETD	LIT	3	43.9	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	4.3	0.0	37.2	14.0
P0A6E6	15050.4	S	U	T	B	ETD	LIT	3	43.9	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	5.8	0.0	34.1	17.1
P0A6E6	15050.4	S	U	T	B	ETD+CID	LIT	2	26.6	GQDLDEAR	903.4	R	A	0.0	0.0	25.5	14.0
P0A6E6	15050.4	S	U	T	B	ETD+CID	LIT	2	26.6	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	0.0	0.0	48.7	13.0
P0A6E6	15050.4	S	U	T	A	ETD+CID	LIT	2	38.1	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	3.6	0.0	49.0	14.1
P0A6E6	15050.4	S	U	T	A	ETD+CID	LIT	2	38.1	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	5.9	0.7	60.4	16.9
P0A6E6	15050.4	S	U	T	B	ETD+CID	LIT	2	26.6	GQDLDEAR	903.4	R	A	2.5	0.3	25.5	14.0
P0A6E6	15050.4	S	U	T	B	ETD+CID	LIT	2	26.6	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	4.7	0.0	48.7	13.0
P0A6E6	15050.4	S	U	T	C	ETD+CID	LIT	3	43.9	GQDLDEAR	903.4	R	A	2.4	0.0	19.9	14.0
P0A6E6	15050.4	S	U	T	C	ETD+CID	LIT	3	43.9	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	4.2	0.0	75.6	13.2
P0A6E6	15050.4	S	U	T	C	ETD+CID	LIT	3	43.9	KAEEHISSSHGDVDYAQASAELAK	2543.2	R	A	7.1	0.6	66.1	16.6
P0A6E6	15050.4	S	U	T	B	HCD	FT	2	26.6	GQDLDEAR	903.4	R	A	0.0	0.0	25.5	14.0
P0A6E6	15050.4	S	U	T	B	HCD	FT	2	26.6	IQVTGSEGELGIYPGHAPLLTAIKPGMIR	3018.6	K	I	0.0	0.0	48.7	13.0
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	AEITLDYQLK	1193.6	K	-	2.9	0.0	23.9	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	AEITLDYQLKS	1280.7	K	-	2.6	0.6	34.4	12.6
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	AGCPVSQVLK	1058.6	K	A	2.6	0.0	32.3	13.0
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	AKAGCPVSQVLK	1257.7	K	A	3.9	0.5	43.3	12.0
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	GKGTVSTESGVLNQQPYGFNTR	2340.2	R	F	5.6	0.9	35.8	11.5
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	GQAHWEGDIK	1140.5	K	R	2.4	0.7	12.1	12.0
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	GQAHWEGDIKR	1296.6	K	G	4.2	0.8	44.4	11.8
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	6.3	0.7	78.0	10.4
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	IALKSEVAVPGIDASTFDGIIQK	2372.3	K	A	5.1	0.0	76.3	7.0
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	KGQAHWEGDIK	1268.6	K	R	3.9	0.8	40.5	10.8
P0C0L2	15070.5	G	U	T	A	CID	LIT	11	55.9	SEVAVPGIDASTFDGIIQK	1947.0	K	A	4.0	0.8	77.0	13.0
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	AEITLDYQLK	1193.6	K	-	3.2	0.0	37.8	10.0
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	AEITLDYQLKS	1280.7	K	-	3.6	0.7	44.3	13.0
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	AGCPVSQVLK	1058.6	K	A	2.0	0.6	28.8	13.0
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	AKAGCPVSQVLK	1257.7	K	A	3.0	0.5	28.3	12.0
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	GKGTVSTESGVLNQQPYGFNTR	2340.2	R	F	4.7	0.8	21.2	11.8
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	GQAHWEGDIK	1140.5	K	R	3.0	0.7	28.8	12.0
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	GQAHWEGDIKR	1296.6	K	G	3.7	0.8	48.5	12.8
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	6.3	0.7	72.2	10.4
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	IALKSEVAVPGIDASTFDGIIQK	2372.3	K	A	3.8	0.0	26.8	7.0
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	KGQAHWEGDIK	1268.6	K	R	3.3	0.8	31.5	11.5
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	SEVAVPGIDASTFDGIIQK	1947.0	K	A	4.1	0.8	21.9	13.2
P0C0L2	15070.5	G	T	T	A	CID	LIT	12	62.2	VDAGFAITK	921.5	K	I	3.2	0.4	47.8	15.6
P0C0L2	15070.5	G	U	A	A	CID	LIT	3	25.2	DGIIQKAKAGCPVSQVLKAEITL	2439.4	F	D	3.3	0.5	16.8	11.8
P0C0L2	15070.5	G	U	A	A	CID	LIT	3	25.2	DVSLDKV	775.4	A	D	2.0	0.5	16.6	17.2
P0C0L2	15070.5	G	U	A	A	CID	LIT	3	25.2	DYQLKS	753.4	L	-	1.9	0.5	27.5	11.8
P0C0L2	15070.5	G	T	A	B	CID	LIT	4	46.2	DAGFAITKIALKSEVAVPGIDASTF	2521.4	V	D	4.0	0.0	20.4	11.5
P0C0L2	15070.5	G	T	A	B	CID	LIT	4	46.2	DGIIQKAKAGCPVSQVLKAEITL	2439.4	F	D	3.9	0.5	22.3	11.8
P0C0L2	15070.5	G	T	A	B	CID	LIT	4	46.2	DYQLKS	753.4	L	-	1.8	0.6	19.3	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C0L2	15070.5	G	T	A	B	CID	LIT	4	46.2	TIHKKGQAHWEG	1391.7	M	D	0.0	0.0	28.0	15.3
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	AEITLDYQLKS	1280.7	K	-	2.6	0.6	0.0	0.0
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	4.5	0.5	25.9	19.0
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	GQAHWEGDIKR	1296.6	K	G	3.4	0.5	41.8	14.5
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	6.1	0.7	68.2	17.2
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	GTVSTESGVLNQQPYGFNTRFEGEK	2745.3	K	G	3.4	0.8	8.0	17.9
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	KGQAHWEGDIK	1268.6	K	R	2.6	0.7	12.9	14.6
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	KGQAHWEGDIKR	1424.7	K	G	2.6	0.4	28.5	16.1
P0C0L2	15070.5	S	U	T	A	CID	LIT	8	48.3	SEVAVPGIDASTFDGIIQK	1947.0	K	A	4.7	0.5	44.4	17.9
P0C0L2	15070.5	S	U	T	B	CID	LIT	7	40.6	GKGTVSTESGVLNQQPYGFNTR	2340.2	R	F	6.5	0.7	72.1	17.7
P0C0L2	15070.5	S	U	T	B	CID	LIT	7	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	2.6	0.4	17.5	18.7
P0C0L2	15070.5	S	U	T	B	CID	LIT	7	40.6	GQAHWEGDIKR	1296.6	K	G	2.5	0.5	40.2	15.8
P0C0L2	15070.5	S	U	T	B	CID	LIT	7	40.6	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	6.3	0.8	86.6	17.1
P0C0L2	15070.5	S	U	T	B	CID	LIT	7	40.6	KGQAHWEGDIK	1268.6	K	R	2.5	0.6	25.1	15.2
P0C0L2	15070.5	S	U	T	B	CID	LIT	7	40.6	KGQAHWEGDIKR	1424.7	K	G	4.0	0.6	38.4	16.2
P0C0L2	15070.5	S	U	T	B	CID	LIT	7	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	5.4	0.5	47.9	17.4
P0C0L2	15070.5	S	U	T	C	CID	LIT	6	40.6	GKGTVSTESGVLNQQPYGFNTR	2340.2	R	F	5.8	0.7	82.3	18.3
P0C0L2	15070.5	S	U	T	C	CID	LIT	6	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	2.4	0.3	28.8	18.9
P0C0L2	15070.5	S	U	T	C	CID	LIT	6	40.6	GTVSTESGVLNQQPYGFNTRFEGEK	2745.3	K	G	3.5	0.0	21.7	17.9
P0C0L2	15070.5	S	U	T	C	CID	LIT	6	40.6	KGQAHWEGDIK	1268.6	K	R	4.0	0.6	29.0	14.8
P0C0L2	15070.5	S	U	T	C	CID	LIT	6	40.6	KGQAHWEGDIKR	1424.7	K	G	3.5	0.4	23.1	15.8
P0C0L2	15070.5	S	U	T	C	CID	LIT	6	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	4.6	0.5	42.3	17.9
P0C0L2	15070.5	S	U	T	A	ETD	LIT	6	40.6	GKGTVSTESGVLNQQPYGFNTR	2340.2	R	F	6.1	0.0	83.4	18.0
P0C0L2	15070.5	S	U	T	A	ETD	LIT	6	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	7.2	0.6	82.0	18.6
P0C0L2	15070.5	S	U	T	A	ETD	LIT	6	40.6	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	1.9	0.8	8.5	16.7
P0C0L2	15070.5	S	U	T	A	ETD	LIT	6	40.6	KGQAHWEGDIK	1268.6	K	R	5.1	0.5	37.3	16.4
P0C0L2	15070.5	S	U	T	A	ETD	LIT	6	40.6	KGQAHWEGDIKR	1424.7	K	G	3.5	0.5	36.8	15.7
P0C0L2	15070.5	S	U	T	A	ETD	LIT	6	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	3.7	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C0L2	15070.5	S	U	T	B	ETD	LIT	3	37.1	GKGTVSTESGVLNQQPYGFNTR	2340.2	R	F	6.8	0.0	70.3	18.1
P0C0L2	15070.5	S	U	T	B	ETD	LIT	3	37.1	KGQAHWEGDIKR	1424.7	K	G	4.0	0.6	30.2	15.4
P0C0L2	15070.5	S	U	T	B	ETD	LIT	3	37.1	SEVAVPGIDASTFDGIIQK	1947.0	K	A	3.6	0.6	53.6	17.6
P0C0L2	15070.5	S	U	T	C	ETD	LIT	3	37.1	GKGTVSTESGVLNQQPYGFNTR	2340.2	R	F	6.1	0.0	54.7	18.0
P0C0L2	15070.5	S	U	T	C	ETD	LIT	3	37.1	KGQAHWEGDIKR	1424.7	K	G	4.7	0.6	56.0	15.7
P0C0L2	15070.5	S	U	T	C	ETD	LIT	3	37.1	SEVAVPGIDASTFDGIIQK	1947.0	K	A	2.9	0.5	35.8	17.9
P0C0L2	15070.5	S	U	T	A	ETD	FT	2	8.4	KGQAHWEGDIK	1268.6	K	R	2.3	0.3	40.6	14.8
P0C0L2	15070.5	S	U	T	A	ETD	FT	2	8.4	KGQAHWEGDIKR	1424.7	K	G	3.0	0.0	53.8	15.4
P0C0L2	15070.5	S	U	T	B	ETD	FT	2	8.4	KGQAHWEGDIK	1268.6	K	R	3.5	0.5	57.5	14.8
P0C0L2	15070.5	S	U	T	B	ETD	FT	2	8.4	KGQAHWEGDIKR	1424.7	K	G	2.5	0.0	42.8	15.6
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	0.0	0.0	60.9	19.0
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	GQAHWEGDIKR	1296.6	K	G	0.0	0.0	38.0	16.4
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	0.0	0.0	79.0	16.8
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	KGQAHWEGDIK	1268.6	K	R	0.0	0.0	40.0	14.9
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	KGQAHWEGDIKR	1424.7	K	G	0.0	0.0	39.2	15.7
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	0.0	0.0	70.2	18.2
P0C0L2	15070.5	S	U	T	A	ETD+CID	LIT	6	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	3.9	0.0	35.6	18.7
P0C0L2	15070.5	S	U	T	A	ETD+CID	LIT	6	40.6	GQAHWEGDIKR	1296.6	K	G	3.6	0.7	35.6	16.4
P0C0L2	15070.5	S	U	T	A	ETD+CID	LIT	6	40.6	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	6.2	0.7	0.0	0.0
P0C0L2	15070.5	S	U	T	A	ETD+CID	LIT	6	40.6	KGQAHWEGDIK	1268.6	K	R	3.9	0.7	40.4	14.9
P0C0L2	15070.5	S	U	T	A	ETD+CID	LIT	6	40.6	KGQAHWEGDIKR	1424.7	K	G	4.1	0.5	38.3	16.2
P0C0L2	15070.5	S	U	T	A	ETD+CID	LIT	6	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	5.0	0.6	68.9	18.1
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	4.4	0.6	35.9	18.8
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	GQAHWEGDIKR	1296.6	K	G	3.3	0.6	38.0	16.4
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	6.0	0.0	79.0	16.8
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	KGQAHWEGDIK	1268.6	K	R	3.7	0.0	40.0	14.9
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	KGQAHWEGDIKR	1424.7	K	G	4.5	0.6	39.2	15.7
P0C0L2	15070.5	S	U	T	B	ETD+CID	LIT	6	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	5.5	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C0L2	15070.5	S	U	T	C	ETD+CID	LIT	5	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	6.7	0.0	70.8	18.8
P0C0L2	15070.5	S	U	T	C	ETD+CID	LIT	5	40.6	GQAHWEGDIKR	1296.6	K	G	3.2	0.6	39.9	16.3
P0C0L2	15070.5	S	U	T	C	ETD+CID	LIT	5	40.6	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	2.8	0.7	0.0	0.0
P0C0L2	15070.5	S	U	T	C	ETD+CID	LIT	5	40.6	IGNRFDLVLVAAR	1443.8	-	-	0.9	-0.7	24.0	10.4
P0C0L2	15070.5	S	U	T	C	ETD+CID	LIT	5	40.6	KGQAHWEGDIK	1268.6	K	R	2.6	0.6	17.9	14.5
P0C0L2	15070.5	S	U	T	C	ETD+CID	LIT	5	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	5.0	0.5	0.0	0.0
P0C0L2	15070.5	S	U	T	B	HCD	FT	6	40.6	GKGTVSTESGVLNQQPYGFNTRFEGEK	2930.4	R	G	0.0	0.0	35.9	18.8
P0C0L2	15070.5	S	U	T	B	HCD	FT	6	40.6	GQAHWEGDIKR	1296.6	K	G	0.0	0.0	38.0	16.4
P0C0L2	15070.5	S	U	T	B	HCD	FT	6	40.6	GTVSTESGVLNQQPYGFNTR	2155.0	K	F	0.0	0.0	79.0	16.8
P0C0L2	15070.5	S	U	T	B	HCD	FT	6	40.6	KGQAHWEGDIK	1268.6	K	R	0.0	0.0	40.0	14.9
P0C0L2	15070.5	S	U	T	B	HCD	FT	6	40.6	KGQAHWEGDIKR	1424.7	K	G	0.0	0.0	39.2	15.7
P0C0L2	15070.5	S	U	T	B	HCD	FT	6	40.6	SEVAVPGIDASTFDGIIQK	1947.0	K	A	0.0	0.0	70.2	18.2
P0A6Z6	15075.5	G	U	T	A	CID	LIT	3	36.1	HGHLQCLPKED	1333.6	R	-	3.2	0.8	36.2	11.8
P0A6Z6	15075.5	G	U	T	A	CID	LIT	3	36.1	SALAQEATQQHGTQGFAVLSYVYEHEKR	3148.5	R	D	2.6	0.0	19.3	11.5
P0A6Z6	15075.5	G	U	T	A	CID	LIT	3	36.1	SEAIRDILR	1072.6	R	S	2.3	0.4	27.9	13.2
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	DKGEFFAK	941.5	K	S	2.7	0.8	28.2	9.0
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	DRSEVDLK	961.5	R	R	2.4	0.4	29.1	15.1
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	EVQEISPNLR	1184.6	K	Y	3.0	0.6	32.3	11.1
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	FKYPR	710.4	K	Q	1.6	0.7	20.2	11.8
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	HLESVVTNK	1026.6	R	I	3.2	0.8	32.9	11.1
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	HLESVVTNKISEIEADLEK	2154.1	R	L	3.7	0.0	27.0	12.3
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	ILDDLR	744.4	K	H	1.8	0.2	33.2	17.3
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	ILDDLRHLESVVTNK	1752.0	K	I	3.7	0.8	41.0	10.8
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	ISEIEADLEK	1146.6	K	L	3.5	0.8	49.1	13.6
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	ISEIEADLEKLTR	1516.8	K	-	3.4	0.8	56.7	14.0
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	IYFQKDK	941.5	K	G	2.2	0.3	10.9	12.3
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	KILDDLR	872.5	R	H	2.8	0.2	43.7	15.4
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	KTVVADGVGQGYK	1321.7	R	E	4.6	0.6	78.8	12.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	QEANNDILK	1044.5	R	I	3.0	0.7	16.4	13.0
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	SEVDLKR	846.5	R	K	1.8	0.6	30.6	15.2
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	SLGITNPEEIDR	1343.7	K	Y	3.6	0.8	44.0	12.0
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	SLGITNPEEIDRYSLR	1863.0	K	Q	3.0	0.0	21.9	11.1
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	TVVADGVGQGYK	1193.6	K	E	4.0	0.8	62.4	12.8
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	4.5	0.7	76.2	10.0
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	YIIDELDQICQR	1565.8	R	D	4.7	0.6	75.5	12.8
P62768	15079.0	G	U	T	A	CID	LIT	21	90.6	YSLRQEANNDILK	1563.8	R	I	4.5	0.6	24.6	13.0
P62768	15079.0	G	T	T	A	CID	LIT	2	15.6	DKGEFFAK	941.5	K	S	2.1	0.6	3.5	9.0
P62768	15079.0	G	T	T	A	CID	LIT	2	15.6	SLGITNPEEIDR	1343.7	K	Y	3.0	0.7	28.6	12.0
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DELDQICQR	1176.5	I	D	2.5	0.3	9.9	13.0
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DGVGQGYKEVQ	1179.6	A	E	3.9	0.8	55.4	14.3
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DGVGQGYKEVQEISPNLRYII	2378.2	A	D	4.4	0.5	73.2	15.9
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DILKIYFQK	1167.7	N	D	2.5	0.0	22.2	6.0
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DKGEFFAKSVKFKYPRQRKTVVA	2729.5	K	D	2.5	0.0	22.2	10.0
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DLEKLTRK	1002.6	A	-	2.0	0.5	18.1	11.8
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DLKRKIL	885.6	V	D	1.7	0.4	8.0	4.8
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DLKRKILD	1000.6	V	D	1.7	0.6	12.2	10.0
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DNLKSLGITNPEEI	1542.8	Y	D	3.5	0.5	29.2	13.8
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DQICQRDRSEV	1405.6	L	D	2.1	0.3	7.4	13.4
P62768	15079.0	G	U	A	A	CID	LIT	11	75.8	DRSEVDLKRKIL	1471.9	R	D	2.4	0.8	7.0	9.0
P62768	15079.0	G	U	T	B	CID	LIT	4	32.8	HLESVVTNK	1026.6	R	I	3.0	0.0	24.1	11.1
P62768	15079.0	G	U	T	B	CID	LIT	4	32.8	ISEIEADLEK	1146.6	K	L	2.3	0.3	11.4	15.4
P62768	15079.0	G	U	T	B	CID	LIT	4	32.8	KTVVADGVGQGYK	1321.7	R	E	3.6	0.5	32.9	12.0
P62768	15079.0	G	U	T	B	CID	LIT	4	32.8	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	3.5	0.0	19.1	11.1
P62768	15079.0	G	T	A	B	CID	LIT	4	32.8	DGVGQGYKEVQ	1179.6	A	E	2.7	0.7	26.3	14.9
P62768	15079.0	G	T	A	B	CID	LIT	4	32.8	DILKIYFQK	1167.7	N	D	2.4	0.0	15.1	7.0
P62768	15079.0	G	T	A	B	CID	LIT	4	32.8	DLEKLTRK	1002.6	A	-	1.8	0.5	13.6	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62768	15079.0	G	T	A	B	CID	LIT	4	32.8	DNLKSLGITNPEEI	1542.8	Y	D	3.8	0.6	63.4	14.0
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	DGVGQGYKEVQ	1179.6	A	E	2.0	0.7	7.5	14.8
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	DGVGQGYKEVQEISPNLRYII	2378.2	A	D	4.2	0.7	50.6	15.8
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	DILKIYFQK	1167.7	N	D	2.9	0.0	35.0	6.0
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	DLEKLTRK	1002.6	A	-	1.2	0.3	10.4	11.8
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	DNLKSLGITNPEEI	1542.8	Y	D	3.8	0.4	54.3	13.8
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	DRSEV	605.3	R	D	1.5	0.0	26.2	16.9
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	DRYSLRQEANN	1365.7	I	D	1.5	0.5	16.2	14.5
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	EISPNLRYII	1217.7	Q	D	2.3	0.0	28.3	10.0
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	EKLTRK	774.5	L	-	1.6	0.1	19.0	3.0
P62768	15079.0	G	U	A	B	CID	LIT	10	63.3	ESVVTNKISEIEA	1418.7	L	D	3.2	0.5	21.9	17.4
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	DRSEVDLKR	1117.6	R	K	2.2	0.2	7.3	16.7
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	EVQEISPNLR	1184.6	K	Y	2.6	0.4	28.7	13.4
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	HLESVVTNK	1026.6	R	I	2.8	0.0	32.9	14.1
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	ISEIEADLEK	1146.6	K	L	1.8	0.6	7.3	16.7
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	ISEIEADLEKLTR	1516.8	K	-	3.0	0.4	29.5	16.8
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	4.3	0.6	37.0	16.9
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	SLGITNPEEIDR	1343.7	K	Y	2.8	0.4	13.9	15.9
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	2.5	0.6	7.9	19.2
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	4.2	0.6	71.9	17.2
P62768	15079.0	S	U	T	A	CID	LIT	10	71.1	YIIDELDQICQR	1565.8	R	D	2.8	0.4	5.6	17.6
P62768	15079.0	S	U	T	B	CID	LIT	7	54.7	EVQEISPNLR	1184.6	K	Y	2.4	0.4	5.7	13.4
P62768	15079.0	S	U	T	B	CID	LIT	7	54.7	ISEIEADLEK	1146.6	K	L	2.4	0.0	23.3	17.0
P62768	15079.0	S	U	T	B	CID	LIT	7	54.7	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	5.6	0.7	50.7	16.9
P62768	15079.0	S	U	T	B	CID	LIT	7	54.7	SLGITNPEEIDR	1343.7	K	Y	2.4	0.2	13.6	16.0
P62768	15079.0	S	U	T	B	CID	LIT	7	54.7	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	3.5	0.7	20.0	19.4
P62768	15079.0	S	U	T	B	CID	LIT	7	54.7	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	5.0	0.5	84.4	17.7
P62768	15079.0	S	U	T	B	CID	LIT	7	54.7	YIIDELDQICQR	1565.8	R	D	4.4	0.7	51.5	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	EVQEISPNLR	1184.6	K	Y	2.6	0.3	17.4	13.0
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	ISEIEADLEK	1146.6	K	L	2.3	0.7	24.3	16.6
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	ISEIEADLEKLTR	1516.8	K	-	2.7	0.2	24.8	16.8
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	IYFQKDKGEFFAK	1620.8	K	S	3.4	0.7	13.9	17.0
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	4.8	0.0	65.9	17.1
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	4.5	0.4	8.5	19.4
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	4.2	0.5	68.8	17.6
P62768	15079.0	S	U	T	C	CID	LIT	8	67.2	YIIDELDQICQR	1565.8	R	D	4.3	0.7	58.0	17.5
P62768	15079.0	S	U	T	A	CID	FT	3	28.1	IYFQKDKGEFFAK	1620.8	K	S	2.5	0.3	6.7	17.8
P62768	15079.0	S	U	T	A	CID	FT	3	28.1	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	4.9	0.0	64.2	16.8
P62768	15079.0	S	U	T	A	CID	FT	3	28.1	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	2.6	0.0	80.8	18.3
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	EVQEISPNLR	1184.6	K	Y	2.7	0.0	29.1	13.4
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	HLESVVTNK	1026.6	R	I	2.1	0.6	34.6	12.8
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	ISEIEADLEKLTR	1516.8	K	-	5.9	0.5	56.6	17.3
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	IYFQKDKGEFFAK	1620.8	K	S	2.6	0.2	13.7	17.1
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	6.8	0.6	76.1	16.6
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	6.1	0.0	60.2	19.2
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	4.7	0.0	61.6	17.8
P62768	15079.0	S	U	T	A	ETD	LIT	7	74.2	YIIDELDQICQR	1565.8	R	D	1.5	0.0	25.7	16.7
P62768	15079.0	S	U	T	B	ETD	LIT	7	57.8	EVQEISPNLR	1184.6	K	Y	2.3	0.3	32.6	12.8
P62768	15079.0	S	U	T	B	ETD	LIT	7	57.8	ISEIEADLEK	1146.6	K	L	3.0	0.3	0.0	0.0
P62768	15079.0	S	U	T	B	ETD	LIT	7	57.8	ISEIEADLEKLTR	1516.8	K	-	5.8	0.4	61.9	17.3
P62768	15079.0	S	U	T	B	ETD	LIT	7	57.8	IYFQKDKGEFFAK	1620.8	K	S	2.4	0.0	27.1	17.2
P62768	15079.0	S	U	T	B	ETD	LIT	7	57.8	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	7.2	0.7	66.7	17.1
P62768	15079.0	S	U	T	B	ETD	LIT	7	57.8	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	3.6	0.0	30.9	19.1
P62768	15079.0	S	U	T	B	ETD	LIT	7	57.8	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	5.3	0.0	34.9	17.3
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	EVQEISPNLR	1184.6	K	Y	1.5	0.0	41.8	12.8
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	ISEIEADLEK	1146.6	K	L	3.2	0.2	21.6	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	ISEIEADLEKLTR	1516.8	K	-	3.4	0.4	42.5	17.0
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	IYFQKDKGEFFAK	1620.8	K	S	5.1	0.4	43.8	17.1
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	5.3	0.6	51.6	17.0
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	5.8	0.0	66.4	19.1
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	6.1	0.6	43.7	17.5
P62768	15079.0	S	U	T	C	ETD	LIT	8	67.2	YIIDELDQICQR	1565.8	R	D	0.0	0.0	54.7	17.1
P62768	15079.0	S	U	T	B	ETD+CID	LIT	5	57.0	ISEIEADLEKLTR	1516.8	K	-	0.0	0.0	49.5	16.8
P62768	15079.0	S	U	T	B	ETD+CID	LIT	5	57.0	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	0.0	0.0	81.6	17.0
P62768	15079.0	S	U	T	B	ETD+CID	LIT	5	57.0	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	0.0	0.0	20.2	19.2
P62768	15079.0	S	U	T	B	ETD+CID	LIT	5	57.0	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	0.0	0.0	82.1	17.2
P62768	15079.0	S	U	T	B	ETD+CID	LIT	5	57.0	YIIDELDQICQR	1565.8	R	D	0.0	0.0	55.5	17.2
P62768	15079.0	S	U	T	A	ETD+CID	LIT	6	57.8	EVQEISPNLR	1184.6	K	Y	1.8	0.2	13.0	13.2
P62768	15079.0	S	U	T	A	ETD+CID	LIT	6	57.8	ISEIEADLEKLTR	1516.8	K	-	3.1	0.5	30.2	16.8
P62768	15079.0	S	U	T	A	ETD+CID	LIT	6	57.8	IYFQKDKGEFFAK	1620.8	K	S	4.1	0.5	41.4	16.8
P62768	15079.0	S	U	T	A	ETD+CID	LIT	6	57.8	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	5.6	0.7	83.7	16.9
P62768	15079.0	S	U	T	A	ETD+CID	LIT	6	57.8	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	0.8	-0.9	63.4	19.2
P62768	15079.0	S	U	T	A	ETD+CID	LIT	6	57.8	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	5.0	0.6	73.5	17.3
P62768	15079.0	S	U	T	B	ETD+CID	LIT	6	57.0	ISEIEADLEK	1146.6	K	L	2.3	0.6	18.9	17.2
P62768	15079.0	S	U	T	B	ETD+CID	LIT	6	57.0	ISEIEADLEKLTR	1516.8	K	-	5.0	0.7	49.5	16.8
P62768	15079.0	S	U	T	B	ETD+CID	LIT	6	57.0	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	5.0	0.6	81.6	17.0
P62768	15079.0	S	U	T	B	ETD+CID	LIT	6	57.0	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	3.6	0.5	20.2	19.2
P62768	15079.0	S	U	T	B	ETD+CID	LIT	6	57.0	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	4.5	0.6	82.1	17.2
P62768	15079.0	S	U	T	B	ETD+CID	LIT	6	57.0	YIIDELDQICQR	1565.8	R	D	4.7	0.7	55.5	17.2
P62768	15079.0	S	U	T	C	ETD+CID	LIT	7	68.0	ISEIEADLEKLTR	1516.8	K	-	6.2	0.5	59.6	17.1
P62768	15079.0	S	U	T	C	ETD+CID	LIT	7	68.0	ISEIEADLEKLTRK	1644.9	K	-	2.4	0.6	9.5	14.6
P62768	15079.0	S	U	T	C	ETD+CID	LIT	7	68.0	IYFQKDKGEFFAK	1620.8	K	S	3.3	0.4	19.4	17.0
P62768	15079.0	S	U	T	C	ETD+CID	LIT	7	68.0	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	5.3	0.7	54.1	17.2
P62768	15079.0	S	U	T	C	ETD+CID	LIT	7	68.0	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	3.8	0.7	15.9	19.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62768	15079.0	S	U	T	C	ETD+CID	LIT	7	68.0	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	4.8	0.5	71.2	18.2
P62768	15079.0	S	U	T	C	ETD+CID	LIT	7	68.0	YIIDELDQICQR	1565.8	R	D	4.3	0.6	46.5	17.1
P62768	15079.0	S	U	T	B	HCD	FT	4	46.9	KTVVADGVGQGYKEVQEISPNLR	2487.3	R	Y	0.0	0.0	81.6	17.0
P62768	15079.0	S	U	T	B	HCD	FT	4	46.9	SLGITNPEEIDRYSLRQEANNDILK	2888.5	K	I	0.0	0.0	20.2	19.2
P62768	15079.0	S	U	T	B	HCD	FT	4	46.9	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	0.0	0.0	82.1	17.2
P62768	15079.0	S	U	T	B	HCD	FT	4	46.9	YIIDELDQICQR	1565.8	R	D	0.0	0.0	55.5	17.2
P62768	15079.0	S	U	T	B	HCD	FT	2	25.0	ISEIEADLEK	1146.6	K	L	1.5	0.0	21.2	17.2
P62768	15079.0	S	U	T	B	HCD	FT	2	25.0	TVVADGVGQGYKEVQEISPNLR	2359.2	K	Y	3.3	0.0	70.2	17.5
P62768	15079.0	S	U	T	C	HCD	FT	2	18.0	ISEIEADLEK	1146.6	K	L	2.0	0.5	24.9	17.0
P62768	15079.0	S	U	T	C	HCD	FT	2	18.0	IYFQKDKGEFFAK	1620.8	K	S	3.3	0.0	49.3	16.8
P0A7G2	15136.8	G	U	T	A	CID	LIT	6	54.1	ALQEASGFIR	1091.6	K	S	2.3	0.3	18.1	15.7
P0A7G2	15136.8	G	U	T	A	CID	LIT	6	54.1	IVPELTFFYDNSLVEGMR	2130.1	R	M	4.5	0.0	69.2	11.8
P0A7G2	15136.8	G	U	T	A	CID	LIT	6	54.1	LGMMTTVSGVEMSR	1498.7	R	D	3.5	0.0	63.2	11.1
P0A7G2	15136.8	G	U	T	A	CID	LIT	6	54.1	MSNLVTSVVK	1077.6	R	H	3.2	0.5	42.5	12.8
P0A7G2	15136.8	G	U	T	A	CID	LIT	6	54.1	MSNLVTSVVKHDEER	1743.9	R	R	4.6	0.8	108.0	11.5
P0A7G2	15136.8	G	U	T	A	CID	LIT	6	54.1	VYVTFLNDKDEDAVK	1755.9	K	A	4.1	0.7	80.0	13.8
P0A7G2	15136.8	G	U	A	B	CID	LIT	3	39.1	DNSLVEGMRMSNLVTSVVKH	2216.1	Y	D	3.8	0.8	15.5	15.6
P0A7G2	15136.8	G	U	A	B	CID	LIT	3	39.1	DPRLGMMTTVSGVEMSR	1866.9	K	D	3.2	0.0	25.6	11.1
P0A7G2	15136.8	G	U	A	B	CID	LIT	3	39.1	EMQKEIALILQREIK	1842.1	Q	D	2.9	0.0	22.0	7.8
P0A7G2	15136.8	S	U	T	A	CID	LIT	2	13.5	EIALILQR	955.6	K	E	2.5	0.5	32.7	11.5
P0A7G2	15136.8	S	U	T	A	CID	LIT	2	13.5	MSNLVTSVVK	1077.6	R	H	2.8	0.7	25.0	15.2
P0A7G2	15136.8	S	U	T	C	CID	LIT	3	24.8	ALQEASGFIR	1091.6	K	S	2.8	0.4	32.2	17.5
P0A7G2	15136.8	S	U	T	C	CID	LIT	3	24.8	EIALILQR	955.6	K	E	1.8	0.6	22.8	11.5
P0A7G2	15136.8	S	U	T	C	CID	LIT	3	24.8	MSNLVTSVVKHDEER	1743.9	R	R	4.6	0.6	94.1	17.0
P0A7G2	15136.8	S	U	T	B	ETD	LIT	3	28.6	EIALILQR	955.6	K	E	1.9	0.3	16.4	11.5
P0A7G2	15136.8	S	U	T	B	ETD	LIT	3	28.6	MSNLVTSVVKHDEER	1743.9	R	R	5.0	0.6	46.8	17.6
P0A7G2	15136.8	S	U	T	B	ETD	LIT	3	28.6	VYVTFLNDKDEDAVK	1755.9	K	A	4.7	0.5	84.8	17.3
P0A7G2	15136.8	S	U	T	C	ETD	LIT	3	17.3	EIALILQR	955.6	K	E	2.1	0.7	41.5	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7G2	15136.8	S	U	T	C	ETD	LIT	3	17.3	MSNLVTSVVK	1077.6	R	H	1.9	0.4	25.6	15.2
P0A7G2	15136.8	S	U	T	C	ETD	LIT	3	17.3	MSNLVTSVVKHDEER	1743.9	R	R	5.4	0.0	52.5	17.4
P0A7G2	15136.8	S	U	T	B	ETD+CID	LIT	2	24.8	IVPELTFFYDNSLVEGMR	2130.1	R	M	2.7	0.4	0.0	0.0
P0A7G2	15136.8	S	U	T	B	ETD+CID	LIT	2	24.8	VYVTFLNDKDEDAVK	1755.9	K	A	4.8	0.7	76.0	17.4
P0A7G2	15136.8	S	U	T	C	ETD+CID	LIT	3	30.1	ALQEASGFIR	1091.6	K	S	2.9	0.4	38.1	17.5
P0A7G2	15136.8	S	U	T	C	ETD+CID	LIT	3	30.1	MSNLVTSVVKHDEER	1743.9	R	R	4.5	0.6	39.8	17.5
P0A7G2	15136.8	S	U	T	C	ETD+CID	LIT	3	30.1	VYVTFLNDKDEDAVK	1755.9	K	A	5.2	0.6	86.9	17.3
P0A8I1	15168.9	G	U	T	A	CID	LIT	2	15.9	ITGTARPLPAIK	1237.8	R	A	3.3	0.0	31.1	6.0
P0A8I1	15168.9	G	U	T	A	CID	LIT	2	15.9	SGLFEQGGYR	1113.5	R	A	3.0	0.7	33.3	10.0
P0AAA9	15181.5	G	T	T	A	CID	LIT	4	34.8	EMENLR	791.4	K	Q	1.6	0.5	10.1	14.1
P0AAA9	15181.5	G	T	T	A	CID	LIT	4	34.8	IHNDFYAQSSALQQQLVTK	2191.1	K	R	4.3	0.8	18.4	12.8
P0AAA9	15181.5	G	T	T	A	CID	LIT	4	34.8	QSLDELR	860.4	R	V	2.0	0.4	29.0	14.8
P0AAA9	15181.5	G	T	T	A	CID	LIT	4	34.8	RYEYNALLAANPPDSSK	1908.9	K	I	3.1	0.7	11.0	10.4
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	EAFKLAAAK	948.6	R	L	3.0	0.5	43.8	12.0
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	GKGNVEYWVALIQPGK	1759.0	K	V	4.8	0.6	61.5	11.1
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	GLAQGTDVSFGSFGLK	1583.8	R	A	5.1	0.7	80.9	12.0
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	GLAQGTDVSFGSFGLKAVGR	1967.0	R	G	2.2	0.7	13.9	12.6
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	GNVEYWVALIQPGK	1573.8	K	V	3.9	0.8	60.2	12.6
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	LAAAKLPIK	924.6	K	T	2.5	0.7	31.2	6.0
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	LPIKTTFVTK	1147.7	K	T	2.5	0.0	40.1	0.0
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	NRGLAQGTDVSFGSFGLK	1854.0	R	A	6.4	0.7	91.5	13.0
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	TTFVTK	696.4	K	T	1.0	0.5	13.3	8.5
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	VFPDKPITEKPLAVR	1710.0	R	M	3.1	0.0	50.4	4.8
P0ADY7	15263.6	G	U	T	A	CID	LIT	11	63.2	VLYEMDGVPEELAR	1636.8	K	E	3.6	0.5	63.1	12.6
P0ADY7	15263.6	G	U	T	B	CID	LIT	4	33.8	GKGNVEYWVALIQPGK	1759.0	K	V	4.7	0.0	72.2	10.4
P0ADY7	15263.6	G	U	T	B	CID	LIT	4	33.8	GLAQGTDVSFGSFGLK	1583.8	R	A	5.3	0.7	68.6	12.3
P0ADY7	15263.6	G	U	T	B	CID	LIT	4	33.8	GNVEYWVALIQPGK	1573.8	K	V	4.1	0.9	51.6	12.6
P0ADY7	15263.6	G	U	T	B	CID	LIT	4	33.8	VLYEMDGVPEELAR	1620.8	K	E	3.7	0.5	60.6	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADY7	15263.6	S	U	T	A	CID	LIT	7	46.3	GKGNVEYWVALIQPGK	1759.0	K	V	4.8	0.8	77.6	16.8
P0ADY7	15263.6	S	U	T	A	CID	LIT	7	46.3	GLAQGTDVSFGSFGLK	1583.8	R	A	5.3	0.6	91.4	16.8
P0ADY7	15263.6	S	U	T	A	CID	LIT	7	46.3	GNVEYWVALIQPGK	1573.8	K	V	4.5	0.8	64.0	16.5
P0ADY7	15263.6	S	U	T	A	CID	LIT	7	46.3	GNVEYWVALIQPGKVLYEMDGVPEELAR	3175.6	K	E	4.7	0.6	33.2	18.0
P0ADY7	15263.6	S	U	T	A	CID	LIT	7	46.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	6.2	0.8	73.7	17.0
P0ADY7	15263.6	S	U	T	A	CID	LIT	7	46.3	VFPDKPITEKPLAVR	1710.0	R	M	3.2	0.0	48.3	11.8
P0ADY7	15263.6	S	U	T	A	CID	LIT	7	46.3	VLYEMDGVPEELAR	1620.8	K	E	3.8	0.4	24.2	17.3
P0ADY7	15263.6	S	U	T	B	CID	LIT	6	46.3	GKGNVEYWVALIQPGK	1759.0	K	V	4.0	0.6	43.5	15.9
P0ADY7	15263.6	S	U	T	B	CID	LIT	6	46.3	GLAQGTDVSFGSFGLK	1583.8	R	A	5.7	0.7	70.9	16.4
P0ADY7	15263.6	S	U	T	B	CID	LIT	6	46.3	GNVEYWVALIQPGKVLYEMDGVPEELAR	3175.6	K	E	3.6	0.0	26.9	18.1
P0ADY7	15263.6	S	U	T	B	CID	LIT	6	46.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	5.9	0.6	51.9	16.7
P0ADY7	15263.6	S	U	T	B	CID	LIT	6	46.3	VFPDKPITEKPLAVR	1710.0	R	M	2.5	0.7	33.1	11.5
P0ADY7	15263.6	S	U	T	B	CID	LIT	6	46.3	VLYEMDGVPEELAR	1620.8	K	E	4.2	0.6	52.7	17.6
P0ADY7	15263.6	S	U	T	C	CID	LIT	5	35.3	GKGNVEYWVALIQPGK	1759.0	K	V	4.0	0.8	43.9	15.8
P0ADY7	15263.6	S	U	T	C	CID	LIT	5	35.3	GLAQGTDVSFGSFGLK	1583.8	R	A	5.6	0.8	83.2	15.6
P0ADY7	15263.6	S	U	T	C	CID	LIT	5	35.3	GNVEYWVALIQPGK	1573.8	K	V	4.2	0.7	62.2	16.5
P0ADY7	15263.6	S	U	T	C	CID	LIT	5	35.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	6.4	0.7	66.3	16.7
P0ADY7	15263.6	S	U	T	C	CID	LIT	5	35.3	VLYEMDGVPEELAR	1620.8	K	E	3.1	0.4	23.8	18.0
P0ADY7	15263.6	S	U	T	B	CID	FT	2	18.4	GLAQGTDVSFGSFGLK	1583.8	R	A	4.5	0.7	78.2	17.3
P0ADY7	15263.6	S	U	T	B	CID	FT	2	18.4	LAAAKLPIK	924.6	K	T	3.2	0.0	27.7	6.0
P0ADY7	15263.6	S	U	T	A	ETD	LIT	6	46.3	GKGNVEYWVALIQPGK	1759.0	K	V	6.9	0.6	103.0	16.4
P0ADY7	15263.6	S	U	T	A	ETD	LIT	6	46.3	GLAQGTDVSFGSFGLK	1583.8	R	A	4.9	0.7	50.6	16.4
P0ADY7	15263.6	S	U	T	A	ETD	LIT	6	46.3	GNVEYWVALIQPGK	1573.8	K	V	3.0	0.4	26.0	16.6
P0ADY7	15263.6	S	U	T	A	ETD	LIT	6	46.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	6.7	0.5	104.0	17.7
P0ADY7	15263.6	S	U	T	A	ETD	LIT	6	46.3	VFPDKPITEKPLAVR	1710.0	R	M	2.1	0.2	4.2	10.8
P0ADY7	15263.6	S	U	T	A	ETD	LIT	6	46.3	VLYEMDGVPEELAR	1620.8	K	E	2.8	0.7	48.0	16.9
P0ADY7	15263.6	S	U	T	B	ETD	LIT	7	52.9	GKGNVEYWVALIQPGK	1759.0	K	V	5.9	0.6	49.0	15.9
P0ADY7	15263.6	S	U	T	B	ETD	LIT	7	52.9	GLAQGTDVSFGSFGLK	1583.8	R	A	4.4	0.7	62.8	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADY7	15263.6	S	U	T	B	ETD	LIT	7	52.9	GNVEYWVALIQPGK	1573.8	K	V	4.9	0.6	48.6	16.6
P0ADY7	15263.6	S	U	T	B	ETD	LIT	7	52.9	LAAAKLPIK	924.6	K	T	1.8	0.5	14.5	6.0
P0ADY7	15263.6	S	U	T	B	ETD	LIT	7	52.9	NRGLAQGTDVSFGSFGLK	1854.0	R	A	5.9	0.6	86.1	17.1
P0ADY7	15263.6	S	U	T	B	ETD	LIT	7	52.9	VFPDKPITEKPLAVR	1710.0	R	M	4.7	0.4	43.5	11.8
P0ADY7	15263.6	S	U	T	B	ETD	LIT	7	52.9	VLYEMDGVPEELAR	1620.8	K	E	1.4	0.1	45.3	17.7
P0ADY7	15263.6	S	U	T	C	ETD	LIT	5	35.3	GKGNVEYWVALIQPGK	1759.0	K	V	6.4	0.6	61.2	15.2
P0ADY7	15263.6	S	U	T	C	ETD	LIT	5	35.3	GLAQGTDVSFGSFGLK	1583.8	R	A	3.4	0.4	55.4	16.4
P0ADY7	15263.6	S	U	T	C	ETD	LIT	5	35.3	GNVEYWVALIQPGK	1573.8	K	V	5.0	0.6	38.7	16.7
P0ADY7	15263.6	S	U	T	C	ETD	LIT	5	35.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	2.5	0.8	41.0	16.8
P0ADY7	15263.6	S	U	T	C	ETD	LIT	5	35.3	VLYEMDGVPEELAR	1620.8	K	E	2.6	0.6	0.0	0.0
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	GKGNVEYWVALIQPGK	1759.0	K	V	0.0	0.0	60.4	15.6
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	GLAQGTDVSFGSFGLK	1583.8	R	A	0.0	0.0	78.9	16.5
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	GNVEYWVALIQPGK	1573.8	K	V	0.0	0.0	69.4	17.2
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	0.0	0.0	41.7	17.4
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	VLYEMDGVPEELAR	1620.8	K	E	0.0	0.0	45.7	17.6
P0ADY7	15263.6	S	U	T	A	ETD+CID	LIT	5	35.3	GKGNVEYWVALIQPGK	1759.0	K	V	4.3	0.8	63.0	15.9
P0ADY7	15263.6	S	U	T	A	ETD+CID	LIT	5	35.3	GLAQGTDVSFGSFGLK	1583.8	R	A	5.8	0.7	85.5	16.4
P0ADY7	15263.6	S	U	T	A	ETD+CID	LIT	5	35.3	GNVEYWVALIQPGK	1573.8	K	V	4.7	0.8	0.0	0.0
P0ADY7	15263.6	S	U	T	A	ETD+CID	LIT	5	35.3	GNVEYWVALIQPGKVLYEMDGVPEELAR	3175.6	K	E	3.6	0.0	43.7	17.9
P0ADY7	15263.6	S	U	T	A	ETD+CID	LIT	5	35.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	6.7	0.7	106.0	16.7
P0ADY7	15263.6	S	U	T	A	ETD+CID	LIT	5	35.3	VLYEMDGVPEELAR	1620.8	K	E	4.0	0.0	60.4	16.9
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	GKGNVEYWVALIQPGK	1759.0	K	V	4.1	0.7	60.4	15.6
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	GLAQGTDVSFGSFGLK	1583.8	R	A	5.2	0.7	0.0	0.0
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	GNVEYWVALIQPGK	1573.8	K	V	4.7	0.8	69.4	17.2
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	5.8	0.6	0.0	0.0
P0ADY7	15263.6	S	U	T	B	ETD+CID	LIT	4	35.3	VLYEMDGVPEELAR	1620.8	K	E	4.2	0.6	45.7	17.6
P0ADY7	15263.6	S	U	T	C	ETD+CID	LIT	4	35.3	GKGNVEYWVALIQPGK	1759.0	K	V	4.7	0.7	55.0	15.6
P0ADY7	15263.6	S	U	T	C	ETD+CID	LIT	4	35.3	GLAQGTDVSFGSFGLK	1583.8	R	A	5.6	0.7	75.1	16.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADY7	15263.6	S	U	T	C	ETD+CID	LIT	4	35.3	GNVEYWVALIQPGK	1573.8	K	V	3.5	0.5	20.1	16.7
P0ADY7	15263.6	S	U	T	C	ETD+CID	LIT	4	35.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	5.6	0.7	77.8	17.2
P0ADY7	15263.6	S	U	T	C	ETD+CID	LIT	4	35.3	VLYEMDGVPEELAR	1620.8	K	E	4.4	0.8	57.2	17.7
P0ADY7	15263.6	S	U	T	B	HCD	FT	4	35.3	GKGNVEYWVALIQPGK	1759.0	K	V	0.0	0.0	60.4	15.6
P0ADY7	15263.6	S	U	T	B	HCD	FT	4	35.3	GLAQGTDVSFGSFGLK	1583.8	R	A	0.0	0.0	78.9	16.5
P0ADY7	15263.6	S	U	T	B	HCD	FT	4	35.3	GNVEYWVALIQPGK	1573.8	K	V	0.0	0.0	69.4	17.2
P0ADY7	15263.6	S	U	T	B	HCD	FT	4	35.3	NRGLAQGTDVSFGSFGLK	1854.0	R	A	0.0	0.0	41.7	17.4
P0ADY7	15263.6	S	U	T	B	HCD	FT	4	35.3	VLYEMDGVPEELAR	1620.8	K	E	0.0	0.0	45.7	17.6
P0ADY7	15263.6	S	U	T	B	HCD	FT	2	14.7	QIEAAR	687.4	R	R	1.8	0.0	33.8	18.4
P0ADY7	15263.6	S	U	T	B	HCD	FT	2	14.7	VLYEMDGVPEELAR	1620.8	K	E	3.0	0.0	40.4	17.7
P04982	15274.2	G	U	T	A	CID	LIT	6	57.6	HHNPQLHETLLTHLEQLQK	2316.2	K	H	2.5	0.6	3.2	12.6
P04982	15274.2	G	U	T	A	CID	LIT	6	57.6	HQGNTIEIR	1067.6	K	Y	2.8	0.4	52.7	13.0
P04982	15274.2	G	U	T	A	CID	LIT	6	57.6	KGTVLNSDISSVISR	1575.9	K	L	5.0	0.0	105.0	10.0
P04982	15274.2	G	U	T	A	CID	LIT	6	57.6	LGHTDTLVVCDAGLPIPK	1906.0	R	S	5.0	0.0	63.2	10.8
P04982	15274.2	G	U	T	A	CID	LIT	6	57.6	QQTAESQAVIR	1230.6	K	S	3.4	0.5	29.5	13.0
P04982	15274.2	G	U	T	A	CID	LIT	6	57.6	YTTHEQFK	1053.5	R	Q	2.4	0.7	25.8	10.0
P04982	15274.2	G	U	A	B	CID	LIT	2	18.0	DAGLPIPKSTTRI	1368.8	C	D	2.1	0.3	6.9	9.5
P04982	15274.2	G	U	A	B	CID	LIT	2	18.0	DISSVISRLGHT	1284.7	S	D	2.0	0.0	27.0	11.8
P04982	15274.2	S	U	T	A	CID	LIT	2	23.0	GTVLNSDISSVISR	1447.8	K	L	1.9	0.5	0.0	0.0
P04982	15274.2	S	U	T	A	CID	LIT	2	23.0	LGHTDTLVVCDAGLPIPK	1906.0	R	S	5.5	0.7	65.3	16.8
P04982	15274.2	S	U	T	C	CID	LIT	2	23.0	GTVLNSDISSVISR	1447.8	K	L	3.5	0.4	40.9	16.6
P04982	15274.2	S	U	T	C	CID	LIT	2	23.0	LGHTDTLVVCDAGLPIPK	1906.0	R	S	3.5	0.0	30.4	17.2
P04982	15274.2	S	U	T	C	ETD	LIT	2	23.0	GTVLNSDISSVISR	1447.8	K	L	1.4	0.3	36.8	18.1
P04982	15274.2	S	U	T	C	ETD	LIT	2	23.0	LGHTDTLVVCDAGLPIPK	1906.0	R	S	3.4	0.8	33.7	17.6
P0ACG1	15330.0	G	U	T	A	CID	LIT	5	48.5	ADGINPEELLGNSSAAAPR	1881.9	K	A	5.0	0.7	60.0	13.6
P0ACG1	15330.0	G	U	T	A	CID	LIT	5	48.5	EFSIDVLEEMLEK	1581.8	R	F	3.1	0.0	62.1	11.5
P0ACG1	15330.0	G	U	T	A	CID	LIT	5	48.5	ISTWLELMK	1120.6	K	A	2.4	0.8	35.5	13.6
P0ACG1	15330.0	G	U	T	A	CID	LIT	5	48.5	SVMLQSLNNIR	1274.7	M	T	0.0	0.0	45.9	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACG1	15330.0	G	U	T	A	CID	LIT	5	48.5	TPKPIAQALAEGK	1323.8	R	S	3.5	0.6	42.2	9.0
P0ACG1	15330.0	S	U	T	A	CID	LIT	2	20.9	ADGINPEELLGNSSAAAPR	1881.9	K	A	5.4	0.7	61.6	18.1
P0ACG1	15330.0	S	U	T	A	CID	LIT	2	20.9	FTDVNGETK	1011.5	K	T	2.3	0.6	19.6	13.0
P0ACG1	15330.0	S	U	T	C	CID	LIT	3	37.3	ADGINPEELLGNSSAAAPR	1881.9	K	A	5.9	0.6	60.9	18.1
P0ACG1	15330.0	S	U	T	C	CID	LIT	3	37.3	SVMLQSLNNIR	1274.7	M	T	0.0	0.0	52.1	16.8
P0ACG1	15330.0	S	U	T	C	CID	LIT	3	37.3	TPKPIAQALAEGK	1323.8	R	S	3.2	0.7	36.8	11.8
P0ACG1	15330.0	S	U	T	C	CID	LIT	3	37.3	TWTGQGR	805.4	K	T	1.5	0.3	12.1	16.6
P0ACG1	15330.0	S	U	T	A	ETD	LIT	3	35.8	ADGINPEELLGNSSAAAPR	1881.9	K	A	2.4	0.6	71.0	18.2
P0ACG1	15330.0	S	U	T	A	ETD	LIT	3	35.8	ISTWLELMK	1120.6	K	A	1.2	0.6	16.5	14.8
P0ACG1	15330.0	S	U	T	A	ETD	LIT	3	35.8	TPKPIAQALAEGK	1323.8	R	S	4.8	0.6	71.5	11.8
P0ACG1	15330.0	S	U	T	A	ETD	LIT	3	35.8	TWTGQGR	805.4	K	T	2.2	0.5	36.1	16.6
P0ACG1	15330.0	S	U	T	B	ETD	LIT	2	26.1	ADGINPEELLGNSSAAAPR	1881.9	K	A	2.7	0.4	0.0	0.0
P0ACG1	15330.0	S	U	T	B	ETD	LIT	2	26.1	FTDVNGETK	1011.5	K	T	2.4	0.7	28.2	13.0
P0ACG1	15330.0	S	U	T	B	ETD	LIT	2	26.1	TWTGQGR	805.4	K	T	2.2	0.6	35.8	16.6
P0ACG1	15330.0	S	U	T	C	ETD	LIT	4	44.0	ADGINPEELLGNSSAAAPR	1881.9	K	A	2.1	0.6	62.1	18.1
P0ACG1	15330.0	S	U	T	C	ETD	LIT	4	44.0	ISTWLELMK	1120.6	K	A	2.0	0.0	28.3	15.3
P0ACG1	15330.0	S	U	T	C	ETD	LIT	4	44.0	SVMLQSLNNIR	1274.7	M	T	0.0	0.0	43.1	16.0
P0ACG1	15330.0	S	U	T	C	ETD	LIT	4	44.0	TPKPIAQALAEGK	1323.8	R	S	4.2	0.6	52.3	12.3
P0ACG1	15330.0	S	U	T	C	ETD	LIT	4	44.0	TWTGQGR	805.4	K	T	2.1	0.7	35.1	16.6
P0ACG1	15330.0	S	U	T	B	ETD+CID	LIT	2	22.4	ADGINPEELLGNSSAAAPR	1881.9	K	A	0.0	0.0	48.4	18.1
P0ACG1	15330.0	S	U	T	B	ETD+CID	LIT	2	22.4	SVMLQSLNNIR	1274.7	M	T	0.0	0.0	32.6	16.7
P0ACG1	15330.0	S	U	T	B	ETD+CID	LIT	2	22.4	ADGINPEELLGNSSAAAPR	1881.9	K	A	5.2	0.5	48.4	18.1
P0ACG1	15330.0	S	U	T	B	ETD+CID	LIT	2	22.4	SVMLQSLNNIR	1274.7	M	T	0.0	0.0	32.6	16.7
P0ACG1	15330.0	S	U	T	C	ETD+CID	LIT	5	53.7	ADGINPEELLGNSSAAAPR	1881.9	K	A	6.0	0.7	67.5	18.2
P0ACG1	15330.0	S	U	T	C	ETD+CID	LIT	5	53.7	EFSIDVLEEMLEK	1581.8	R	F	2.7	0.4	18.2	15.9
P0ACG1	15330.0	S	U	T	C	ETD+CID	LIT	5	53.7	FTDVNGETK	1011.5	K	T	2.2	0.7	22.8	13.2
P0ACG1	15330.0	S	U	T	C	ETD+CID	LIT	5	53.7	SVMLQSLNNIR	1274.7	M	T	0.0	0.0	29.4	14.6
P0ACG1	15330.0	S	U	T	C	ETD+CID	LIT	5	53.7	TPKPIAQALAEGK	1323.8	R	S	3.0	0.6	22.3	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACG1	15330.0	S	U	T	C	ETD+CID	LIT	5	53.7	TWTGQGR	805.4	K	T	1.8	0.5	9.9	14.8
P0ACG1	15330.0	S	U	T	B	HCD	FT	2	22.4	ADGINPEELLGNSSAAAPR	1881.9	K	A	0.0	0.0	48.4	18.1
P0ACG1	15330.0	S	U	T	B	HCD	FT	2	22.4	SVMLQSLNNIR	1274.7	M	T	0.0	0.0	32.6	16.7
P0A746	15433.2	G	U	T	A	CID	LIT	5	52.6	ANKPSAEELKK	1214.7	M	N	0.0	0.0	33.1	13.6
P0A746	15433.2	G	U	T	A	CID	LIT	5	52.6	DGVYHCLICDAPLFHSQTK	2261.0	R	Y	4.2	0.0	21.4	10.0
P0A746	15433.2	G	U	T	A	CID	LIT	5	52.6	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	4.4	0.0	36.3	9.5
P0A746	15433.2	G	U	T	A	CID	LIT	5	52.6	YCVNSASLR	1069.5	R	F	2.6	0.8	32.2	7.0
P0A746	15433.2	G	U	T	A	CID	LIT	5	52.6	YIKDLSHGMQR	1347.7	R	I	2.7	0.5	40.9	12.3
P0A746	15433.2	G	T	T	A	CID	LIT	4	36.5	ANKPSAEELKK	1214.7	M	N	0.0	0.0	41.5	13.6
P0A746	15433.2	G	T	T	A	CID	LIT	4	36.5	DLSHGMQR	943.4	K	I	1.9	0.6	22.5	7.8
P0A746	15433.2	G	T	T	A	CID	LIT	4	36.5	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	3.2	0.0	31.4	10.0
P0A746	15433.2	G	T	T	A	CID	LIT	4	36.5	YCVNSASLR	1069.5	R	F	2.5	0.0	28.6	7.0
P0A746	15433.2	G	U	A	A	CID	LIT	2	14.6	DAHLGHVFP	992.5	C	D	1.8	0.6	14.8	14.6
P0A746	15433.2	G	U	A	A	CID	LIT	2	14.6	DAPLFHSQTKY	1306.6	C	D	2.2	0.6	13.9	16.9
P0A746	15433.2	G	T	A	A	CID	LIT	2	14.6	DAHLGHVFP	992.5	C	D	1.9	0.7	13.5	14.5
P0A746	15433.2	G	T	A	A	CID	LIT	2	14.6	DAPLFHSQTKY	1306.6	C	D	1.9	0.7	6.1	16.3
P0A746	15433.2	G	T	T	B	CID	LIT	6	51.8	ANKPSAEELKK	1214.7	M	N	0.0	0.0	40.4	14.1
P0A746	15433.2	G	T	T	B	CID	LIT	6	51.8	FTDGENGEEING	1281.5	R	-	3.3	0.0	29.6	3.0
P0A746	15433.2	G	T	T	B	CID	LIT	6	51.8	LLHNKR	780.5	R	D	1.6	0.4	36.1	10.4
P0A746	15433.2	G	T	T	B	CID	LIT	6	51.8	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	3.0	0.0	33.0	12.3
P0A746	15433.2	G	T	T	B	CID	LIT	6	51.8	YCVNSASLR	1069.5	R	F	2.2	0.6	15.9	7.0
P0A746	15433.2	G	T	T	B	CID	LIT	6	51.8	YIKDLSHGMQR	1347.7	R	I	3.0	0.4	43.7	13.2
P0A746	15433.2	G	T	A	B	CID	LIT	7	58.4	ANKPSAEELKKNLS	1528.8	M	E	0.0	0.0	22.0	14.0
P0A746	15433.2	G	T	A	B	CID	LIT	7	58.4	DAHLGHVFP	992.5	C	D	2.0	0.7	22.1	14.5
P0A746	15433.2	G	T	A	B	CID	LIT	7	58.4	DAPLFHSQTKY	1306.6	C	D	2.7	0.8	19.7	15.6
P0A746	15433.2	G	T	A	B	CID	LIT	7	58.4	DLSHGMQRI	1056.5	K	E	1.9	0.4	10.0	14.6
P0A746	15433.2	G	T	A	B	CID	LIT	7	58.4	EESIRYIK	1037.6	S	D	2.0	0.6	7.3	13.8
P0A746	15433.2	G	T	A	B	CID	LIT	7	58.4	EMQFYVTQNHGTEPPFTGRLLHNKR	3016.5	S	D	1.4	0.0	33.4	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A746	15433.2	G	T	A	B	CID	LIT	7	58.4	EPVSEESIRYIK	1449.8	Y	D	2.9	0.6	26.6	16.2
P0A746	15433.2	G	U	A	B	CID	LIT	5	49.6	DAHLGHVFP	992.5	C	D	1.4	0.3	18.1	15.1
P0A746	15433.2	G	U	A	B	CID	LIT	5	49.6	DAPLFHSQTKY	1306.6	C	D	2.7	0.7	12.0	15.7
P0A746	15433.2	G	U	A	B	CID	LIT	5	49.6	DGPQPTGERYCVNSASLRFT	2255.1	P	D	2.7	0.8	0.0	0.0
P0A746	15433.2	G	U	A	B	CID	LIT	5	49.6	DLSHGMQRIEIRCGNC	1945.9	K	D	2.3	0.0	19.2	7.0
P0A746	15433.2	G	U	A	B	CID	LIT	5	49.6	EPVSEESIRYIK	1449.8	Y	D	2.8	0.8	32.1	16.3
P0A746	15433.2	S	U	T	A	CID	LIT	2	30.7	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	4.1	0.6	25.7	16.7
P0A746	15433.2	S	U	T	A	CID	LIT	2	30.7	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	3.8	0.7	49.4	9.5
P0A746	15433.2	S	U	T	B	CID	LIT	3	44.5	DGVYHCLICDAPLFHSQTK	2261.0	R	Y	4.1	0.0	33.2	16.6
P0A746	15433.2	S	U	T	B	CID	LIT	3	44.5	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	4.6	0.9	65.5	16.6
P0A746	15433.2	S	U	T	B	CID	LIT	3	44.5	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	4.1	0.7	57.5	10.0
P0A746	15433.2	S	U	T	C	CID	LIT	3	38.7	ANKPSAEELKK	1214.7	M	N	0.0	0.0	35.9	16.9
P0A746	15433.2	S	U	T	C	CID	LIT	3	38.7	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	3.7	0.6	39.8	16.3
P0A746	15433.2	S	U	T	C	CID	LIT	3	38.7	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	3.6	0.6	45.1	10.0
P0A746	15433.2	S	U	T	B	ETD	LIT	3	29.9	DGVYHCLICDAPLFHSQTK	2261.0	R	Y	3.0	0.0	19.8	16.5
P0A746	15433.2	S	U	T	B	ETD	LIT	3	29.9	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	4.7	0.0	53.7	16.3
P0A746	15433.2	S	U	T	B	ETD+CID	LIT	3	44.5	DGVYHCLICDAPLFHSQTK	2261.0	R	Y	0.0	0.0	49.8	16.6
P0A746	15433.2	S	U	T	B	ETD+CID	LIT	3	44.5	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	0.0	0.0	37.4	16.9
P0A746	15433.2	S	U	T	B	ETD+CID	LIT	3	44.5	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	0.0	0.0	59.5	9.5
P0A746	15433.2	S	U	T	A	ETD+CID	LIT	2	30.7	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	2.8	0.7	24.6	16.7
P0A746	15433.2	S	U	T	A	ETD+CID	LIT	2	30.7	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	0.0	0.0	59.3	10.8
P0A746	15433.2	S	U	T	B	ETD+CID	LIT	3	44.5	DGVYHCLICDAPLFHSQTK	2261.0	R	Y	3.9	0.6	49.8	16.6
P0A746	15433.2	S	U	T	B	ETD+CID	LIT	3	44.5	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	3.2	0.0	37.4	16.9
P0A746	15433.2	S	U	T	B	ETD+CID	LIT	3	44.5	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	4.0	0.6	59.5	9.5
P0A746	15433.2	S	U	T	C	ETD+CID	LIT	3	44.5	DGVYHCLICDAPLFHSQTK	2261.0	R	Y	4.3	0.0	31.3	16.5
P0A746	15433.2	S	U	T	C	ETD+CID	LIT	3	44.5	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	4.9	0.0	71.4	16.3
P0A746	15433.2	S	U	T	C	ETD+CID	LIT	3	44.5	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	3.9	0.5	49.4	10.0
P0A746	15433.2	S	U	T	B	HCD	FT	3	44.5	DGVYHCLICDAPLFHSQTK	2261.0	R	Y	0.0	0.0	49.8	16.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A746	15433.2	S	U	T	B	HCD	FT	3	44.5	NLSEMQFYVTQNHGTEPPFTGR	2553.2	K	L	0.0	0.0	37.4	16.9
P0A746	15433.2	S	U	T	B	HCD	FT	3	44.5	YDSGCGWPSFYEPVSEESIR	2365.0	K	Y	0.0	0.0	59.5	9.5
P76341	15441.9	S	U	T	C	ETD+CID	LIT	2	23.4	ADNGWLQLNTAKTDKDGR	2005.0	K	I	1.5	0.4	11.9	15.7
P76341	15441.9	S	U	T	C	ETD+CID	LIT	2	23.4	ALWPEQTATTGDYR	1608.8	K	V	2.2	0.3	32.8	16.7
P0A763	15445.6	G	U	T	A	CID	LIT	5	46.2	ADYADSLTENGTHGSDSVESAAR	2353.0	R	E	4.1	0.0	36.6	4.8
P0A763	15445.6	G	U	T	A	CID	LIT	5	46.2	DLLGATNPANALAGTLR	1667.9	R	A	4.9	0.8	85.9	10.4
P0A763	15445.6	G	U	T	A	CID	LIT	5	46.2	EIAYFFGEGEVCPR	1673.8	R	T	3.7	0.0	57.3	10.0
P0A763	15445.6	G	U	T	A	CID	LIT	5	46.2	HRDLLGATNPANALAGTLR	1961.1	R	A	6.1	0.6	76.1	13.0
P0A763	15445.6	G	U	T	A	CID	LIT	5	46.2	MLHLTVEQAR	1197.6	K	G	3.3	0.0	30.5	10.4
P0A763	15445.6	G	T	T	B	CID	LIT	4	41.3	ADYADSLTENGTHGSDSVESAAR	2353.0	R	E	3.8	0.0	29.5	4.8
P0A763	15445.6	G	T	T	B	CID	LIT	4	41.3	EIAYFFGEGEVCPR	1673.8	R	T	3.0	0.0	43.1	10.4
P0A763	15445.6	G	T	T	B	CID	LIT	4	41.3	FEAAGFKIVGTK	1267.7	R	M	1.8	0.2	0.0	0.0
P0A763	15445.6	G	T	T	B	CID	LIT	4	41.3	MLHLTVEQAR	1197.6	K	G	2.0	0.2	0.0	0.0
P0A763	15445.6	G	T	A	B	CID	LIT	2	23.8	DLLGATNPANALAGTLRA	1738.9	R	D	5.7	0.6	70.7	14.5
P0A763	15445.6	G	T	A	B	CID	LIT	2	23.8	EIAYFFGEGEVCPRTR	1930.9	R	-	1.9	0.6	21.0	13.6
P0A763	15445.6	G	U	A	B	CID	LIT	2	23.8	DLLGATNPANALAGTLRA	1738.9	R	D	5.5	0.6	65.2	14.5
P0A763	15445.6	G	U	A	B	CID	LIT	2	23.8	EIAYFFGEGEVCPRTR	1930.9	R	-	3.0	0.0	25.8	13.4
P0A763	15445.6	S	U	T	A	CID	LIT	3	39.2	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	5.5	0.0	85.4	9.0
P0A763	15445.6	S	U	T	A	CID	LIT	3	39.2	EIAYFFGEGEVCPR	1673.8	R	T	3.7	0.7	64.0	14.6
P0A763	15445.6	S	U	T	A	CID	LIT	3	39.2	HRDLLGATNPANALAGTLR	1961.1	R	A	3.5	0.6	40.7	16.4
P0A763	15445.6	S	U	T	B	CID	LIT	4	39.2	ADYADSLTENGTHGSDSVESAAR	2353.0	R	E	5.8	0.7	79.8	11.1
P0A763	15445.6	S	U	T	B	CID	LIT	4	39.2	DLLGATNPANALAGTLR	1667.9	R	A	4.5	0.7	75.3	14.8
P0A763	15445.6	S	U	T	B	CID	LIT	4	39.2	EIAYFFGEGEVCPR	1673.8	R	T	3.1	0.6	30.0	14.5
P0A763	15445.6	S	U	T	B	CID	LIT	4	39.2	HRDLLGATNPANALAGTLR	1961.1	R	A	5.3	0.5	32.7	16.3
P0A763	15445.6	S	U	T	C	CID	LIT	6	54.5	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	5.1	0.0	83.2	8.5
P0A763	15445.6	S	U	T	C	CID	LIT	6	54.5	DLLGATNPANALAGTLR	1667.9	R	A	2.2	0.3	8.7	15.4
P0A763	15445.6	S	U	T	C	CID	LIT	6	54.5	EIAYFFGEGEVCPR	1673.8	R	T	3.9	0.0	45.6	14.5
P0A763	15445.6	S	U	T	C	CID	LIT	6	54.5	HRDLLGATNPANALAGTLR	1961.1	R	A	4.4	0.6	28.7	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A763	15445.6	S	U	T	C	CID	LIT	6	54.5	MLHLTVEQAR	1197.6	K	G	2.0	0.2	12.5	15.2
P0A763	15445.6	S	U	T	C	CID	LIT	6	54.5	TFSIIKPNAVAK	1288.8	R	N	2.8	0.8	17.6	7.8
P0A763	15445.6	S	U	T	A	ETD	LIT	2	25.9	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	4.0	0.0	49.6	9.0
P0A763	15445.6	S	U	T	A	ETD	LIT	2	25.9	EIAYFFGEGEVCPR	1673.8	R	T	1.2	0.0	26.8	14.3
P0A763	15445.6	S	U	T	B	ETD	LIT	3	37.8	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	1.4	0.0	40.2	9.0
P0A763	15445.6	S	U	T	B	ETD	LIT	3	37.8	DLLGATNPANALAGTLR	1667.9	R	A	1.9	0.0	30.2	15.4
P0A763	15445.6	S	U	T	B	ETD	LIT	3	37.8	EIAYFFGEGEVCPR	1673.8	R	T	0.0	0.0	28.1	14.6
P0A763	15445.6	S	U	T	C	ETD	LIT	4	46.2	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	3.8	0.0	44.2	8.5
P0A763	15445.6	S	U	T	C	ETD	LIT	4	46.2	DLLGATNPANALAGTLR	1667.9	R	A	3.6	0.5	0.0	0.0
P0A763	15445.6	S	U	T	C	ETD	LIT	4	46.2	EIAYFFGEGEVCPR	1673.8	R	T	1.5	0.6	20.1	14.6
P0A763	15445.6	S	U	T	C	ETD	LIT	4	46.2	TFSIIKPNAVAK	1288.8	R	N	2.9	0.0	29.5	7.8
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	0.0	0.0	36.0	8.5
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	DLLGATNPANALAGTLR	1667.9	R	A	0.0	0.0	74.1	15.1
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	EIAYFFGEGEVCPR	1673.8	R	T	0.0	0.0	60.7	14.5
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	HRDLLGATNPANALAGTLR	1961.1	R	A	0.0	0.0	40.4	16.9
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	MLHLTVEQAR	1197.6	K	G	0.0	0.0	23.9	13.2
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	TFSIIKPNAVAK	1289.7	R	N	0.0	0.0	21.4	12.3
P0A763	15445.6	S	U	T	A	ETD+CID	LIT	4	39.2	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	5.7	0.0	89.6	9.0
P0A763	15445.6	S	U	T	A	ETD+CID	LIT	4	39.2	DLLGATNPANALAGTLR	1667.9	R	A	4.2	0.7	62.8	15.4
P0A763	15445.6	S	U	T	A	ETD+CID	LIT	4	39.2	EIAYFFGEGEVCPR	1673.8	R	T	3.0	0.4	23.6	14.6
P0A763	15445.6	S	U	T	A	ETD+CID	LIT	4	39.2	HRDLLGATNPANALAGTLR	1961.1	R	A	4.5	0.5	28.8	16.5
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	3.7	0.0	36.0	8.5
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	DLLGATNPANALAGTLR	1667.9	R	A	4.9	0.7	74.1	15.1
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	EIAYFFGEGEVCPR	1673.8	R	T	0.0	0.0	60.7	14.5
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	HRDLLGATNPANALAGTLR	1961.1	R	A	3.3	0.7	40.4	16.9
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	MLHLTVEQAR	1197.6	K	G	2.6	0.4	23.9	13.2
P0A763	15445.6	S	U	T	B	ETD+CID	LIT	6	54.5	TFSIIKPNAVAK	1289.7	R	N	3.1	0.5	21.4	12.3
P0A763	15445.6	S	U	T	C	ETD+CID	LIT	6	54.5	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	5.2	0.0	79.2	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A763	15445.6	S	U	T	C	ETD+CID	LIT	6	54.5	DLLGATNPANALAGTLR	1667.9	R	A	4.7	0.6	68.7	15.4
P0A763	15445.6	S	U	T	C	ETD+CID	LIT	6	54.5	EIAYFFGEGEVCPR	1673.8	R	T	0.0	0.0	32.9	14.6
P0A763	15445.6	S	U	T	C	ETD+CID	LIT	6	54.5	HRDLLGATNPANALAGTLR	1961.1	R	A	4.8	0.7	39.6	16.4
P0A763	15445.6	S	U	T	C	ETD+CID	LIT	6	54.5	MLHLTVEQAR	1197.6	K	G	1.9	0.2	22.1	13.2
P0A763	15445.6	S	U	T	C	ETD+CID	LIT	6	54.5	TFSIIKPNAVAK	1288.8	R	N	3.0	0.7	20.3	7.8
P0A763	15445.6	S	U	T	B	HCD	FT	6	54.5	ADYADSLTENGTHGSDSVESAAR	2354.0	R	E	0.0	0.0	36.0	8.5
P0A763	15445.6	S	U	T	B	HCD	FT	6	54.5	DLLGATNPANALAGTLR	1667.9	R	A	0.0	0.0	74.1	15.1
P0A763	15445.6	S	U	T	B	HCD	FT	6	54.5	EIAYFFGEGEVCPR	1673.8	R	T	0.0	0.0	60.7	14.5
P0A763	15445.6	S	U	T	B	HCD	FT	6	54.5	HRDLLGATNPANALAGTLR	1961.1	R	A	0.0	0.0	40.4	16.9
P0A763	15445.6	S	U	T	B	HCD	FT	6	54.5	MLHLTVEQAR	1197.6	K	G	0.0	0.0	23.9	13.2
P0A763	15445.6	S	U	T	B	HCD	FT	6	54.5	TFSIIKPNAVAK	1289.7	R	N	0.0	0.0	21.4	12.3
P0AEN8	15456.0	G	T	A	B	CID	LIT	2	24.3	DAHFPAHSMGPQVIRA	1733.9	S	D	1.6	0.7	12.9	15.1
P0AEN8	15456.0	G	T	A	B	CID	LIT	2	24.3	MLKTISPLISPELLKVLA	1966.2	-	E	3.0	0.0	22.8	0.0
P0ABV2	15509.3	G	T	A	B	CID	LIT	2	8.5	DETMITALNALT	1292.6	T	E	2.0	0.6	10.4	16.5
P0ABV2	15509.3	G	T	A	B	CID	LIT	2	8.5	ETMITALNALT	1177.6	D	E	1.9	0.4	4.6	13.8
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	AQRPAKYSYVDENGETK	1955.9	R	T	2.4	0.0	31.4	11.5
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	ECTLETLEEMLEK	1624.7	R	L	3.3	0.6	58.2	13.0
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	4.0	0.7	12.6	12.3
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	EEESAAAAEVEER	1419.6	R	T	3.6	0.9	87.5	7.8
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	6.2	0.6	89.1	10.0
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	KAMDEQGK	906.4	K	S	2.4	0.6	36.1	13.0
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	KLQQYR	835.5	R	E	2.2	0.7	28.8	12.8
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	LEVVVNER	957.5	K	R	2.9	0.6	39.3	15.3
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	LEVVVNERR	1113.6	K	E	2.5	0.2	34.8	13.2
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	REEESAAAAEVEER	1575.7	R	T	5.3	0.6	84.8	9.0
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	SLDDFLIK	950.5	K	-	2.8	0.7	36.5	11.5
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	SLDDFLIKQ	1078.6	K	-	3.2	0.5	52.2	12.8
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	TPAVIK	628.4	R	K	2.3	0.4	35.7	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	TPAVIKK	756.5	R	A	2.6	0.2	36.1	10.8
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	YSYVDENGETK	1304.6	K	T	3.3	0.0	38.3	4.8
P0ACF8	15522.0	G	U	T	A	CID	LIT	16	79.6	YSYVDENGETKTWTGQGR	2090.9	K	T	4.3	0.0	88.3	3.0
P0ACF8	15522.0	G	T	T	A	CID	LIT	3	24.1	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	6.8	0.7	84.2	10.0
P0ACF8	15522.0	G	T	T	A	CID	LIT	3	24.1	KLQQYR	835.5	R	E	1.8	0.4	24.3	12.8
P0ACF8	15522.0	G	T	T	A	CID	LIT	3	24.1	TPAVIK	628.4	R	K	2.4	0.3	27.4	10.4
P0ACF8	15522.0	G	T	T	B	CID	LIT	6	44.5	EEESAAAAEVEER	1419.6	R	T	3.9	0.0	83.7	6.0
P0ACF8	15522.0	G	T	T	B	CID	LIT	6	44.5	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	6.9	0.6	96.5	9.0
P0ACF8	15522.0	G	T	T	B	CID	LIT	6	44.5	KLQQYR	835.5	R	E	2.4	0.3	27.0	12.8
P0ACF8	15522.0	G	T	T	B	CID	LIT	6	44.5	REEESAAAAEVEER	1575.7	R	T	5.8	0.6	74.5	7.8
P0ACF8	15522.0	G	T	T	B	CID	LIT	6	44.5	SEALKILNNIR	1270.7	M	T	0.0	0.0	24.2	10.8
P0ACF8	15522.0	G	T	T	B	CID	LIT	6	44.5	SLDDFLIKQ	1078.6	K	-	2.8	0.4	20.9	13.0
P0ACF8	15522.0	G	T	A	B	CID	LIT	3	27.0	DDFLIKQ	878.5	L	-	2.7	0.7	35.2	16.1
P0ACF8	15522.0	G	T	A	B	CID	LIT	3	27.0	DENGETKTWTGQGRTPAVIKKAM	2518.3	V	D	2.7	0.5	0.0	0.0
P0ACF8	15522.0	G	T	A	B	CID	LIT	3	27.0	EEMLEKL	891.4	L	E	2.1	0.3	25.6	16.8
P0ACF8	15522.0	G	U	A	B	CID	LIT	3	27.0	DDFLIKQ	878.5	L	-	2.4	0.0	35.4	16.1
P0ACF8	15522.0	G	U	A	B	CID	LIT	3	27.0	DENGETKTWTGQGRTPAVIKKAM	2518.3	V	D	2.2	0.7	0.0	0.0
P0ACF8	15522.0	G	U	A	B	CID	LIT	3	27.0	EEMLEKL	907.4	L	E	1.7	0.7	2.6	13.2
P0ACF8	15522.0	S	U	T	A	CID	LIT	6	41.6	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	4.0	0.3	41.6	19.0
P0ACF8	15522.0	S	U	T	A	CID	LIT	6	41.6	KLQQYR	835.5	R	E	1.4	0.3	10.9	15.2
P0ACF8	15522.0	S	U	T	A	CID	LIT	6	41.6	REEESAAAAEVEER	1575.7	R	T	5.3	0.6	74.3	13.8
P0ACF8	15522.0	S	U	T	A	CID	LIT	6	41.6	SLDDFLIKQ	1078.6	K	-	3.4	0.5	24.0	16.1
P0ACF8	15522.0	S	U	T	A	CID	LIT	6	41.6	TPAVIK	628.4	R	K	1.9	0.3	21.3	10.4
P0ACF8	15522.0	S	U	T	A	CID	LIT	6	41.6	TPAVIKK	756.5	R	A	2.7	0.2	24.8	11.8
P0ACF8	15522.0	S	U	T	B	CID	LIT	6	52.6	ECTLETLEEMLEK	1624.7	R	L	3.4	0.6	61.6	15.4
P0ACF8	15522.0	S	U	T	B	CID	LIT	6	52.6	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	3.9	0.3	37.2	19.0
P0ACF8	15522.0	S	U	T	B	CID	LIT	6	52.6	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	7.1	0.6	94.0	17.2
P0ACF8	15522.0	S	U	T	B	CID	LIT	6	52.6	REEESAAAAEVEER	1575.7	R	T	3.1	0.5	14.5	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF8	15522.0	S	U	T	B	CID	LIT	6	52.6	SLDDFLIKQ	1078.6	K	-	2.4	0.3	24.2	16.1
P0ACF8	15522.0	S	U	T	B	CID	LIT	6	52.6	TPAVIKK	756.5	R	A	2.6	0.2	24.4	11.8
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	ECTLETLEEMLEK	1624.7	R	L	2.2	0.0	20.0	15.6
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	4.5	0.4	45.6	19.0
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	7.4	0.6	103.0	18.0
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	ILNNIR	742.5	K	T	1.7	0.6	26.0	12.6
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	KLQQYR	835.5	R	E	1.9	0.2	26.5	14.8
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	LQQYR	707.4	K	E	1.3	0.4	13.0	17.2
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	REEESAAAAEVEER	1575.7	R	T	2.8	0.4	6.6	14.3
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	TPAVIKK	756.5	R	A	2.7	0.2	30.5	11.8
P0ACF8	15522.0	S	U	T	C	CID	LIT	9	59.9	TWTGQGR	805.4	K	T	1.5	0.3	12.1	16.6
P0ACF8	15522.0	S	U	T	B	CID	FT	2	6.6	SLDDFLIK	950.5	K	-	2.3	0.0	27.1	14.0
P0ACF8	15522.0	S	U	T	B	CID	FT	2	6.6	SLDDFLIKQ	1078.6	K	-	3.6	0.9	38.2	16.1
P0ACF8	15522.0	S	U	T	A	ETD	LIT	5	40.9	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	4.1	0.0	23.0	19.1
P0ACF8	15522.0	S	U	T	A	ETD	LIT	5	40.9	LQQYR	707.4	K	E	0.9	0.0	24.1	17.2
P0ACF8	15522.0	S	U	T	A	ETD	LIT	5	40.9	REEESAAAAEVEER	1575.7	R	T	2.1	0.8	13.1	14.0
P0ACF8	15522.0	S	U	T	A	ETD	LIT	5	40.9	SLDDFLIKQ	1078.6	K	-	2.2	0.6	37.4	16.1
P0ACF8	15522.0	S	U	T	A	ETD	LIT	5	40.9	TWTGQGR	805.4	K	T	2.2	0.5	36.1	16.6
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	ECTLETLEEMLEK	1624.7	R	L	1.7	0.8	24.7	15.8
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	4.8	0.0	44.5	19.0
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	2.4	0.0	55.3	17.1
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	ILNNIR	743.4	K	T	0.0	0.0	26.1	19.4
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	REEESAAAAEVEER	1575.7	R	T	4.8	0.4	0.0	0.0
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	SLDDFLIKQ	1078.6	K	-	1.9	0.6	17.8	16.1
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	TPAVIK	628.4	R	K	1.6	0.7	13.3	10.4
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	TPAVIKK	756.5	R	A	1.6	0.4	19.9	11.8
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	TWTGQGR	805.4	K	T	2.2	0.6	35.8	16.6
P0ACF8	15522.0	S	U	T	B	ETD	LIT	10	70.1	YSYVDENGETK	1305.5	K	T	1.9	0.0	33.2	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	4.3	0.0	37.5	19.0
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	1.7	0.0	26.5	17.1
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	KLQQYR	835.5	R	E	1.6	0.6	12.6	14.9
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	REEESAAAAEVEER	1575.7	R	T	2.4	0.4	0.0	0.0
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	SLDDFLIKQ	1078.6	K	-	2.2	0.5	19.4	15.9
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	TPAVIKK	756.5	R	A	1.8	0.1	19.3	11.8
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	TWTGQGR	805.4	K	T	2.1	0.7	35.1	16.6
P0ACF8	15522.0	S	U	T	C	ETD	LIT	8	70.1	YSYVDENGETK	1304.6	K	T	3.5	0.0	33.8	9.5
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	6	46.7	ECTLETLEEMLEK	1624.7	R	L	0.0	0.0	44.1	15.2
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	6	46.7	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	0.0	0.0	49.0	19.0
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	6	46.7	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	0.0	0.0	66.7	16.9
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	6	46.7	KLQQYR	835.5	R	E	0.0	0.0	26.2	14.8
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	6	46.7	SLDDFLIKQ	1078.6	K	-	0.0	0.0	21.3	16.1
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	6	46.7	TPAVIKK	756.5	R	A	0.0	0.0	33.6	11.8
P0ACF8	15522.0	S	U	T	A	ETD+CID	LIT	6	59.9	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	5.1	0.4	44.8	19.0
P0ACF8	15522.0	S	U	T	A	ETD+CID	LIT	6	59.9	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	6.6	0.6	85.1	17.2
P0ACF8	15522.0	S	U	T	A	ETD+CID	LIT	6	59.9	KLQQYR	835.5	R	E	1.9	0.6	0.0	0.0
P0ACF8	15522.0	S	U	T	A	ETD+CID	LIT	6	59.9	SLDDFLIKQ	1078.6	K	-	3.1	0.4	30.0	16.1
P0ACF8	15522.0	S	U	T	A	ETD+CID	LIT	6	59.9	TPAVIKK	756.5	R	A	1.8	0.0	22.7	11.8
P0ACF8	15522.0	S	U	T	A	ETD+CID	LIT	6	59.9	YSYVDENGETKTWTGQGR	2091.9	K	T	4.1	0.4	50.7	10.8
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	ECTLETLEEMLEK	1624.7	R	L	3.3	0.5	44.1	15.2
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	0.0	0.0	49.0	19.0
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	7.3	0.6	75.9	16.8
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	KLQQYR	835.5	R	E	2.1	0.0	26.2	14.8
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	LQQYR	707.4	K	E	1.2	0.3	13.6	17.4
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	REEESAAAAEVEER	1575.7	R	T	2.7	0.6	14.9	14.0
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	SLDDFLIKQ	1078.6	K	-	3.0	0.4	21.3	16.1
P0ACF8	15522.0	S	U	T	B	ETD+CID	LIT	8	56.9	TPAVIKK	756.5	R	A	2.8	0.0	33.6	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACF8	15522.0	S	U	T	C	ETD+CID	LIT	6	46.0	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	3.5	0.3	41.6	19.1
P0ACF8	15522.0	S	U	T	C	ETD+CID	LIT	6	46.0	LQQYR	707.4	K	E	1.4	0.3	12.8	17.2
P0ACF8	15522.0	S	U	T	C	ETD+CID	LIT	6	46.0	REEESAAAAEVEER	1575.7	R	T	3.2	0.4	0.0	0.0
P0ACF8	15522.0	S	U	T	C	ETD+CID	LIT	6	46.0	SLDDFLIKQ	1078.6	K	-	2.3	0.4	5.5	16.1
P0ACF8	15522.0	S	U	T	C	ETD+CID	LIT	6	46.0	TPAVIKK	756.5	R	A	2.7	0.0	29.6	11.8
P0ACF8	15522.0	S	U	T	C	ETD+CID	LIT	6	46.0	TWTGQGR	805.4	K	T	1.8	0.5	9.9	14.8
P0ACF8	15522.0	S	U	T	B	HCD	FT	6	46.7	ECTLETLEEMLEK	1624.7	R	L	0.0	0.0	44.1	15.2
P0ACF8	15522.0	S	U	T	B	HCD	FT	6	46.7	ECTLETLEEMLEKLEVVVNER	2563.3	R	R	0.0	0.0	49.0	19.0
P0ACF8	15522.0	S	U	T	B	HCD	FT	6	46.7	EMLIADGIDPNELLNSLAAVK	2226.2	R	S	0.0	0.0	75.9	16.8
P0ACF8	15522.0	S	U	T	B	HCD	FT	6	46.7	KLQQYR	835.5	R	E	0.0	0.0	26.2	14.8
P0ACF8	15522.0	S	U	T	B	HCD	FT	6	46.7	SLDDFLIKQ	1078.6	K	-	0.0	0.0	21.3	16.1
P0ACF8	15522.0	S	U	T	B	HCD	FT	6	46.7	TPAVIKK	756.5	R	A	0.0	0.0	33.6	11.8
P0AGG4	15536.9	G	U	T	A	CID	LIT	3	25.9	IPDDRIEDAAK	1242.6	R	C	2.8	0.0	18.9	10.4
P0AGG4	15536.9	G	U	T	A	CID	LIT	3	25.9	NFAPIFEDVAQER	1535.7	R	S	3.7	0.0	52.6	11.8
P0AGG4	15536.9	G	U	T	A	CID	LIT	3	25.9	VNTEAERELSSR	1390.7	K	F	3.0	0.8	36.0	10.4
P0AGG4	15536.9	G	T	A	B	CID	LIT	2	17.3	DGEVINATGETL	1218.6	F	D	1.7	0.4	0.0	0.0
P0AGG4	15536.9	G	T	A	B	CID	LIT	2	17.3	DMLNGAVPKAPF	1259.6	V	D	2.6	0.4	7.0	13.2
P0A905	15582.6	G	T	T	A	CID	LIT	6	38.7	DDGNTIMVVQK	1219.6	K	Q	2.5	0.8	36.7	9.5
P0A905	15582.6	G	T	T	A	CID	LIT	6	38.7	KDDGNTIMVVQK	1347.7	R	Q	4.8	0.8	81.2	11.1
P0A905	15582.6	G	T	T	A	CID	LIT	6	38.7	SLATAAGAVAGGVAGQGVQSAMNK	2116.1	R	T	7.4	0.8	116.0	12.3
P0A905	15582.6	G	T	T	A	CID	LIT	6	38.7	TQGVELEIR	1044.6	K	K	2.5	0.7	20.7	14.6
P0A905	15582.6	G	T	T	A	CID	LIT	6	38.7	TQGVELEIRK	1172.7	K	D	2.1	0.7	30.1	12.6
P0A905	15582.6	G	T	T	A	CID	LIT	6	38.7	VVLASNGSQVTVSPR	1513.8	R	-	3.8	0.8	43.8	13.0
P0A905	15582.6	G	U	T	B	CID	LIT	3	29.0	KDDGNTIMVVQK	1347.7	R	Q	5.1	0.9	74.4	11.1
P0A905	15582.6	G	U	T	B	CID	LIT	3	29.0	SLATAAGAVAGGVAGQGVQSAMNK	2116.1	R	T	6.5	0.8	87.3	12.6
P0A905	15582.6	G	U	T	B	CID	LIT	3	29.0	TQGVELEIR	1044.6	K	K	2.4	0.0	20.9	14.6
P0A780	15671.5	G	U	T	A	CID	LIT	4	36.0	ELLAGVATNTAYLDGLMKPYLSR	2512.3	R	L	2.5	0.3	0.0	0.0
P0A780	15671.5	G	U	T	A	CID	LIT	4	36.0	LLEELGQVEK	1157.6	R	A	3.1	0.8	55.8	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A780	15671.5	G	U	T	A	CID	LIT	4	36.0	SDVPYKVAINEAIELAK	1860.0	R	S	2.7	0.0	21.1	9.5
P0A780	15671.5	G	U	T	A	CID	LIT	4	36.0	VAINEAIELAK	1170.7	K	S	3.1	0.6	37.8	12.3
P0A780	15671.5	G	U	A	A	CID	LIT	2	15.8	DKAAPVIRPNKK	1336.8	L	-	3.2	0.0	35.6	0.0
P0A780	15671.5	G	U	A	A	CID	LIT	2	15.8	DVEYQFLAEQ	1241.6	A	D	2.4	0.7	0.0	0.0
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	5.7	0.8	58.2	12.3
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	FNDAVIR	834.4	R	S	2.9	0.6	61.4	16.8
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	HAVTEASPMVK	1169.6	K	A	3.3	0.7	46.1	10.8
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	6.2	0.0	49.9	9.5
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	IHRLEDWGR	1181.6	K	R	2.3	0.8	25.9	12.3
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	LEDWGR	775.4	R	R	2.0	0.2	29.2	11.1
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	LEDWGRR	931.5	R	Q	1.2	0.6	15.1	11.8
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	QLAYPINK	946.5	R	L	2.3	0.6	20.7	14.6
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	RDDFANETADDAEAGDSEEEEEE	2573.0	R	-	5.5	0.0	138.0	0.0
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	RQLAYPINK	1102.6	R	L	2.8	0.8	29.2	10.4
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	TKHAVTEASPMVK	1398.7	R	A	3.9	0.6	63.8	13.8
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	YTAAITGAEGK	1081.6	R	I	3.8	0.8	54.7	11.5
P02358	15685.3	G	U	T	A	CID	LIT	13	86.7	YTAAITGAEGKIHR	1487.8	R	L	2.8	0.0	43.0	14.3
P02358	15685.3	G	T	T	A	CID	LIT	5	29.6	FNDAVIR	834.4	R	S	1.9	0.6	19.2	13.4
P02358	15685.3	G	T	T	A	CID	LIT	5	29.6	HAVTEASPMVK	1185.6	K	A	2.4	0.7	16.4	11.8
P02358	15685.3	G	T	T	A	CID	LIT	5	29.6	RQLAYPINK	1102.6	R	L	2.4	0.8	29.6	10.0
P02358	15685.3	G	T	T	A	CID	LIT	5	29.6	TKHAVTEASPMVK	1398.7	R	A	3.8	0.8	32.4	13.0
P02358	15685.3	G	T	T	A	CID	LIT	5	29.6	YTAAITGAEGK	1081.6	R	I	3.3	0.8	38.0	11.5
P02358	15685.3	G	U	A	A	CID	LIT	2	12.6	DELETTFRFN	1271.6	I	D	3.7	0.0	58.6	14.1
P02358	15685.3	G	U	A	A	CID	LIT	2	12.6	DERRERR	1016.5	K	D	1.5	0.5	10.6	15.9
P02358	15685.3	G	T	T	B	CID	LIT	4	23.0	FNDAVIR	834.4	R	S	2.3	0.2	60.8	16.7
P02358	15685.3	G	T	T	B	CID	LIT	4	23.0	HAVTEASPMVK	1169.6	K	A	3.5	0.6	51.2	10.8
P02358	15685.3	G	T	T	B	CID	LIT	4	23.0	TKHAVTEASPMVK	1398.7	R	A	4.4	0.5	49.7	13.0
P02358	15685.3	G	T	T	B	CID	LIT	4	23.0	YTAAITGAEGK	1081.6	R	I	2.9	0.4	16.8	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02358	15685.3	G	U	T	B	CID	LIT	3	19.3	LEDWGR	775.4	R	R	1.9	0.0	16.2	12.0
P02358	15685.3	G	U	T	B	CID	LIT	3	19.3	RQLAYPINK	1102.6	R	L	2.6	0.6	9.7	10.4
P02358	15685.3	G	U	T	B	CID	LIT	3	19.3	YTAAITGAEGK	1081.6	R	I	3.2	0.0	55.6	11.5
P02358	15685.3	G	T	A	B	CID	LIT	2	25.9	DAVIRSMVMRTKHAVTEASPMVKAK	2756.5	N	D	3.2	0.5	0.0	0.0
P02358	15685.3	G	T	A	B	CID	LIT	2	25.9	DELETTFRFN	1271.6	I	D	3.4	0.6	43.2	14.5
P02358	15685.3	G	U	A	B	CID	LIT	3	31.9	DAVIRSMVMRTKHAVTEASPMVKAK	2756.5	N	D	3.5	0.4	17.9	12.0
P02358	15685.3	G	U	A	B	CID	LIT	3	31.9	DDFANETA	882.3	R	D	1.8	0.0	31.3	9.0
P02358	15685.3	G	U	A	B	CID	LIT	3	31.9	DELETTFRFN	1271.6	I	D	3.7	0.0	55.1	14.5
P02358	15685.3	S	U	T	A	CID	LIT	4	51.1	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	6.8	0.7	50.3	19.3
P02358	15685.3	S	U	T	A	CID	LIT	4	51.1	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	4.2	0.5	19.5	18.3
P02358	15685.3	S	U	T	A	CID	LIT	4	51.1	TKHAVTEASPMVK	1398.7	R	A	3.9	0.6	37.2	15.3
P02358	15685.3	S	U	T	A	CID	LIT	4	51.1	YTAAITGAEGK	1081.6	R	I	3.4	0.6	38.5	14.0
P02358	15685.3	S	U	T	B	CID	LIT	4	43.0	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	8.3	0.7	52.5	19.0
P02358	15685.3	S	U	T	B	CID	LIT	4	43.0	HAVTEASPMVK	1169.6	K	A	3.5	0.8	56.8	13.8
P02358	15685.3	S	U	T	B	CID	LIT	4	43.0	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	5.5	0.7	44.1	18.0
P02358	15685.3	S	U	T	B	CID	LIT	4	43.0	TKHAVTEASPMVK	1398.7	R	A	4.3	0.7	65.3	15.6
P02358	15685.3	S	U	T	C	CID	LIT	5	57.8	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	5.6	0.7	86.2	19.4
P02358	15685.3	S	U	T	C	CID	LIT	5	57.8	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	4.2	0.5	30.8	18.3
P02358	15685.3	S	U	T	C	CID	LIT	5	57.8	IHRLEDWGR	1181.6	K	R	2.1	0.2	14.5	15.9
P02358	15685.3	S	U	T	C	CID	LIT	5	57.8	QLAYPINKLHK	1324.8	R	A	2.2	0.4	0.0	0.0
P02358	15685.3	S	U	T	C	CID	LIT	5	57.8	TKHAVTEASPMVK	1398.7	R	A	4.4	0.6	61.4	15.6
P02358	15685.3	S	U	T	A	ETD	LIT	4	40.0	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	4.6	0.0	47.4	19.1
P02358	15685.3	S	U	T	A	ETD	LIT	4	40.0	IHRLEDWGR	1181.6	K	R	2.0	0.0	24.9	14.6
P02358	15685.3	S	U	T	A	ETD	LIT	4	40.0	LEDWGRR	931.5	R	Q	2.1	0.1	20.2	15.9
P02358	15685.3	S	U	T	A	ETD	LIT	4	40.0	QLAYPINK	946.5	R	L	1.7	0.3	13.6	17.3
P02358	15685.3	S	U	T	A	ETD	LIT	4	40.0	TKHAVTEASPMVK	1398.7	R	A	4.3	0.5	53.5	16.0
P02358	15685.3	S	U	T	B	ETD	LIT	6	45.2	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	4.6	0.0	48.3	19.5
P02358	15685.3	S	U	T	B	ETD	LIT	6	45.2	FNDAVIR	834.4	R	S	0.0	0.0	32.4	18.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02358	15685.3	S	U	T	B	ETD	LIT	6	45.2	IHRLEDWGR	1181.6	K	R	2.1	0.2	0.0	0.0
P02358	15685.3	S	U	T	B	ETD	LIT	6	45.2	QLAYPINK	946.5	R	L	2.2	0.5	19.3	15.3
P02358	15685.3	S	U	T	B	ETD	LIT	6	45.2	RQLAYPINK	1102.6	R	L	2.6	0.6	0.0	0.0
P02358	15685.3	S	U	T	B	ETD	LIT	6	45.2	TKHAVTEASPMVK	1398.7	R	A	5.0	0.7	70.1	14.6
P02358	15685.3	S	U	T	C	ETD	LIT	6	48.1	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	5.7	0.0	56.7	19.1
P02358	15685.3	S	U	T	C	ETD	LIT	6	48.1	HAVTEASPMVK	1169.6	K	A	2.7	0.7	27.5	13.6
P02358	15685.3	S	U	T	C	ETD	LIT	6	48.1	IHRLEDWGR	1181.6	K	R	3.1	0.7	37.8	14.5
P02358	15685.3	S	U	T	C	ETD	LIT	6	48.1	RQLAYPINK	1102.6	R	L	2.6	0.5	29.7	13.4
P02358	15685.3	S	U	T	C	ETD	LIT	6	48.1	TKHAVTEASPMVK	1398.7	R	A	5.3	0.6	71.8	14.8
P02358	15685.3	S	U	T	C	ETD	LIT	6	48.1	YTAAITGAEGK	1081.6	R	I	3.0	0.7	25.8	13.4
P02358	15685.3	S	U	T	C	ETD	FT	3	20.0	FNDAVIR	834.4	R	S	0.8	0.0	42.3	18.3
P02358	15685.3	S	U	T	C	ETD	FT	3	20.0	IHRLEDWGR	1181.6	K	R	3.1	0.0	43.8	14.5
P02358	15685.3	S	U	T	C	ETD	FT	3	20.0	YTAAITGAEGK	1081.6	R	I	1.7	0.0	24.7	13.4
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	0.0	0.0	44.7	19.3
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	HAVTEASPMVK	1169.6	K	A	0.0	0.0	30.9	15.3
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	0.0	0.0	29.6	18.0
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	TKHAVTEASPMVK	1398.7	R	A	0.0	0.0	68.5	16.4
P02358	15685.3	S	U	T	A	ETD+CID	LIT	4	61.5	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	6.0	0.8	41.3	19.3
P02358	15685.3	S	U	T	A	ETD+CID	LIT	4	61.5	ERRDDFANETADDAEAGDSEEEEEE	2858.1	R	-	3.5	0.0	86.6	0.0
P02358	15685.3	S	U	T	A	ETD+CID	LIT	4	61.5	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	3.4	0.6	12.1	18.6
P02358	15685.3	S	U	T	A	ETD+CID	LIT	4	61.5	TKHAVTEASPMVK	1398.7	R	A	5.0	0.5	69.9	15.3
P02358	15685.3	S	U	T	B	ETD+CID	LIT	2	26.7	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	7.3	0.7	0.0	0.0
P02358	15685.3	S	U	T	B	ETD+CID	LIT	2	26.7	TKHAVTEASPMVK	1398.7	R	A	4.2	0.6	0.0	0.0
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	7.3	0.7	44.7	19.3
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	HAVTEASPMVK	1169.6	K	A	3.4	0.7	30.9	15.3
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	4.6	0.5	29.6	18.0
P02358	15685.3	S	U	T	B	ETD+CID	LIT	4	43.0	TKHAVTEASPMVK	1398.7	R	A	4.2	0.6	62.7	15.6
P02358	15685.3	S	U	T	C	ETD+CID	LIT	3	43.0	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	7.1	0.8	38.0	19.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02358	15685.3	S	U	T	C	ETD+CID	LIT	3	43.0	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	5.3	0.6	34.0	18.0
P02358	15685.3	S	U	T	C	ETD+CID	LIT	3	43.0	TKHAVTEASPMVK	1398.7	R	A	4.3	0.7	65.2	14.6
P02358	15685.3	S	U	T	B	HCD	FT	4	43.0	AHYVLMNVEAPQEVIDELETTFR	2704.3	K	F	0.0	0.0	44.7	19.3
P02358	15685.3	S	U	T	B	HCD	FT	4	43.0	HAVTEASPMVK	1169.6	K	A	0.0	0.0	30.9	15.3
P02358	15685.3	S	U	T	B	HCD	FT	4	43.0	HYEIVFMVHPDQSEQVPGMIER	2641.3	R	Y	0.0	0.0	29.6	18.0
P02358	15685.3	S	U	T	B	HCD	FT	4	43.0	TKHAVTEASPMVK	1398.7	R	A	0.0	0.0	62.7	15.6
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	AEKINALETVTIASK	1587.9	R	A	5.1	0.6	70.9	10.4
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	AGDEGKLFGSIGTR	1407.7	K	D	4.7	0.6	77.2	12.0
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	AVPATKK	714.5	K	N	1.5	0.6	27.9	15.2
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	DIADAVTAAGVEVAK	1429.8	R	S	4.9	0.6	80.2	13.2
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	DIADAVTAAGVEVAKSEVR	1901.0	R	L	3.3	0.0	40.9	11.8
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	INALETVTIASK	1259.7	K	A	3.9	0.9	55.5	11.1
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	KNIEFFEAR	1153.6	K	R	3.3	0.9	59.3	10.4
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	LAEVLAAANAR	1098.6	K	A	4.1	0.5	93.5	10.4
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	LFGSIGTR	850.5	K	D	2.4	0.7	40.9	15.1
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	LPNGVLR	768.5	R	T	2.2	0.3	33.3	9.0
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	MQVILLDK	959.6	-	V	1.7	0.7	19.0	12.6
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	MQVILLDKVANLGSLGDQVNVK	2354.3	-	A	6.9	0.0	96.7	4.8
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	NIEFFEAR	1025.5	K	R	2.2	0.3	25.3	11.5
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	NIEFFEARR	1181.6	K	A	1.7	0.7	17.4	12.0
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	SEVRLPNGVLR	1239.7	K	T	3.0	0.7	35.7	9.0
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	TTGEHEVSFQVHSEVFAK	2032.0	R	V	5.7	0.8	48.6	13.2
P0A7R1	15750.7	G	U	T	A	CID	LIT	17	81.9	VANLGSLGDQVNVK	1413.8	K	A	4.7	0.6	76.1	13.2
P0A7R1	15750.7	G	T	T	A	CID	LIT	7	58.4	AEKINALETVTIASK	1587.9	R	A	4.3	0.4	41.7	10.4
P0A7R1	15750.7	G	T	T	A	CID	LIT	7	58.4	AGDEGKLFGSIGTR	1407.7	K	D	3.4	0.8	25.3	11.5
P0A7R1	15750.7	G	T	T	A	CID	LIT	7	58.4	DIADAVTAAGVEVAK	1429.8	R	S	4.5	0.6	79.8	12.8
P0A7R1	15750.7	G	T	T	A	CID	LIT	7	58.4	INALETVTIASK	1259.7	K	A	3.3	0.0	45.5	7.0
P0A7R1	15750.7	G	T	T	A	CID	LIT	7	58.4	LAEVLAAANAR	1098.6	K	A	4.4	0.5	66.9	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R1	15750.7	G	T	T	A	CID	LIT	7	58.4	TTGEHEVSFQVHSEVFAK	2032.0	R	V	5.2	0.9	49.3	13.2
P0A7R1	15750.7	G	T	T	A	CID	LIT	7	58.4	VANLGSLGDQVNVK	1413.8	K	A	3.8	0.5	46.6	13.0
P0A7R1	15750.7	G	U	A	A	CID	LIT	6	31.5	DEGKLFGSIGTR	1279.7	G	D	3.3	0.8	46.2	15.2
P0A7R1	15750.7	G	U	A	A	CID	LIT	6	31.5	DEGKLFGSIGTRDIA	1578.8	G	D	3.8	0.7	22.2	16.6
P0A7R1	15750.7	G	U	A	A	CID	LIT	6	31.5	DKVANLGSLG	973.5	L	D	3.5	0.6	47.7	17.3
P0A7R1	15750.7	G	U	A	A	CID	LIT	6	31.5	EKINALETVTIASKAG	1644.9	A	D	4.7	0.8	63.8	11.8
P0A7R1	15750.7	G	U	A	A	CID	LIT	6	31.5	ETVTIASKAG	976.5	L	D	2.9	0.5	40.6	10.8
P0A7R1	15750.7	G	U	A	A	CID	LIT	6	31.5	MQVILLDKVANLGSLG	1671.0	-	D	4.0	0.8	50.6	11.5
P0A7R1	15750.7	G	T	A	A	CID	LIT	2	14.8	DEGKLFGSIGTR	1279.7	G	D	2.2	0.0	29.0	15.2
P0A7R1	15750.7	G	T	A	A	CID	LIT	2	14.8	DKVANLGSLG	973.5	L	D	3.2	0.5	31.7	18.0
P0A7R1	15750.7	G	T	T	B	CID	LIT	5	40.3	DIADAVTAAGVEVAK	1429.8	R	S	2.2	0.7	0.0	0.0
P0A7R1	15750.7	G	T	T	B	CID	LIT	5	40.3	INALETVTIASK	1259.7	K	A	3.5	0.5	55.3	7.0
P0A7R1	15750.7	G	T	T	B	CID	LIT	5	40.3	LAEVLAAANAR	1098.6	K	A	4.1	0.5	75.9	10.4
P0A7R1	15750.7	G	T	T	B	CID	LIT	5	40.3	MQVILLDK	959.6	-	V	2.3	0.3	12.8	12.6
P0A7R1	15750.7	G	T	T	B	CID	LIT	5	40.3	VANLGSLGDQVNVK	1413.8	K	A	4.6	0.5	72.2	13.2
P0A7R1	15750.7	G	U	T	B	CID	LIT	5	36.9	DIADAVTAAGVEVAK	1429.8	R	S	4.4	0.6	50.0	13.8
P0A7R1	15750.7	G	U	T	B	CID	LIT	5	36.9	LAEVLAAANAR	1098.6	K	A	3.8	0.5	45.1	10.4
P0A7R1	15750.7	G	U	T	B	CID	LIT	5	36.9	LPNGVLR	768.5	R	T	1.8	0.0	27.9	9.0
P0A7R1	15750.7	G	U	T	B	CID	LIT	5	36.9	MQVILLDK	959.6	-	V	2.6	0.3	34.1	12.6
P0A7R1	15750.7	G	U	T	B	CID	LIT	5	36.9	VANLGSLGDQVNVK	1413.8	K	A	3.6	0.6	40.5	13.2
P0A7R1	15750.7	G	T	A	B	CID	LIT	4	42.3	DEGKLFGSIGTR	1279.7	G	D	3.3	0.5	33.7	15.6
P0A7R1	15750.7	G	T	A	B	CID	LIT	4	42.3	DKVANLGSLG	973.5	L	D	3.3	0.6	43.2	17.3
P0A7R1	15750.7	G	T	A	B	CID	LIT	4	42.3	DQVNVKAGYARNFLVPQGKAVPATKKNIEFF	3449.9	G	E	3.9	0.0	10.5	11.5
P0A7R1	15750.7	G	T	A	B	CID	LIT	4	42.3	ETVTIASKAG	976.5	L	D	1.7	0.5	1.3	10.8
P0A7R1	15750.7	G	U	A	B	CID	LIT	5	53.0	DEGKLFGSIGTR	1279.7	G	D	2.5	0.6	12.4	15.8
P0A7R1	15750.7	G	U	A	B	CID	LIT	5	53.0	DKVANLGSLG	973.5	L	D	3.2	0.5	42.6	17.3
P0A7R1	15750.7	G	U	A	B	CID	LIT	5	53.0	DQVNVKAGYARNFLVPQGKAVPATKKNIEFF	3449.9	G	E	3.6	0.0	11.9	12.0
P0A7R1	15750.7	G	U	A	B	CID	LIT	5	53.0	EKINALETVTIASKAG	1644.9	A	D	4.8	0.7	67.8	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R1	15750.7	G	U	A	B	CID	LIT	5	53.0	EVLAAANARA	985.5	A	E	2.4	0.0	38.7	7.0
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	DIADAVTAAGVEVAKSEVR	1901.0	R	L	5.6	0.6	68.7	18.1
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	DIADAVTAAGVEVAKSEVRLPNGVLR	2651.4	R	T	2.2	0.0	28.4	15.2
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	INALETVTIASK	1259.7	K	A	2.2	0.8	5.5	12.8
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	KNIEFFEAR	1153.6	K	R	2.7	0.4	32.1	14.5
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	NFLVPQGK	902.5	R	A	1.5	0.5	11.8	15.9
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	NIEFFEAR	1025.5	K	R	2.2	0.1	20.5	15.7
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	RAELEAK	816.5	R	L	2.1	0.2	0.0	19.5
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	RAELEAKLAEVLAAANAR	1896.1	R	A	3.7	0.6	29.0	11.8
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	SEVRLPNGVLR	1240.7	K	T	3.2	0.5	24.9	12.8
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	TTGEHEVSFQVHSEVFAK	2032.0	R	V	2.6	0.7	0.0	0.0
P0A7R1	15750.7	S	U	T	A	CID	LIT	11	70.5	VANLGSLGDQVNVK	1413.8	K	A	4.2	0.6	58.5	15.7
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	AGDEGKLFGSIGTR	1407.7	K	D	3.2	0.6	33.0	16.8
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	DIADAVTAAGVEVAK	1429.8	R	S	5.2	0.6	84.0	17.2
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	DIADAVTAAGVEVAKSEVR	1901.0	R	L	5.4	0.6	67.1	17.4
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	KNIEFFEAR	1153.6	K	R	3.2	0.4	42.7	14.5
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	LAEVLAAANAR	1098.6	K	A	4.5	0.5	51.3	12.6
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	LFGSIGTR	850.5	K	D	1.8	0.5	26.8	16.2
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	MQVILLDKVANLGSLGDQVNVK	2354.3	-	A	5.7	0.7	46.2	13.6
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	NIEFFEAR	1025.5	K	R	2.4	0.2	24.1	14.8
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	SEVRLPNGVLR	1240.7	K	T	2.7	0.4	20.5	12.0
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	TTGEHEVSFQVHSEVFAK	2032.0	R	V	2.4	0.5	0.0	0.0
P0A7R1	15750.7	S	U	T	B	CID	LIT	11	67.1	VANLGSLGDQVNVK	1413.8	K	A	4.5	0.6	57.5	15.7
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	AEKINALETVTIASK	1587.9	R	A	2.5	0.3	0.0	0.0
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	AGDEGKLFGSIGTR	1407.7	K	D	2.1	0.4	27.1	16.8
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	DIADAVTAAGVEVAK	1429.8	R	S	4.8	0.7	79.3	16.9
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	DIADAVTAAGVEVAKSEVR	1901.0	R	L	5.4	0.6	76.3	18.1
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	INALETVTIASK	1259.7	K	A	3.6	0.6	52.5	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	KNIEFFEAR	1153.6	K	R	2.4	0.7	26.3	14.5
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	LFGSIGTR	850.5	K	D	1.7	0.5	25.6	16.0
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	LPNGVLR	769.5	R	T	1.8	0.4	18.3	12.0
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	NFLVPQGK	902.5	R	A	1.9	0.5	8.2	13.2
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	SEVRLPNGVLR	1240.7	K	T	3.0	0.5	29.5	12.0
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	TTGEHEVSFQVHSEVFAK	2032.0	R	V	2.7	0.5	0.0	0.0
P0A7R1	15750.7	S	U	T	C	CID	LIT	12	69.8	VANLGSLGDQVNVK	1413.8	K	A	4.3	0.5	57.8	15.7
P0A7R1	15750.7	S	U	T	A	CID	FT	2	17.4	DIADAVTAAGVEVAK	1429.8	R	S	3.0	0.0	32.0	17.0
P0A7R1	15750.7	S	U	T	A	CID	FT	2	17.4	LAEVLAAANAR	1098.6	K	A	1.6	0.0	27.6	12.6
P0A7R1	15750.7	S	U	T	C	CID	FT	3	22.8	KNIEFFEAR	1153.6	K	R	2.2	0.0	30.0	14.6
P0A7R1	15750.7	S	U	T	C	CID	FT	3	22.8	SEVRLPNGVLR	1240.7	K	T	2.6	0.0	38.0	13.2
P0A7R1	15750.7	S	U	T	C	CID	FT	3	22.8	VANLGSLGDQVNVK	1413.8	K	A	3.8	0.0	49.6	15.7
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	AGDEGKLFGSIGTR	1407.7	K	D	6.7	0.5	57.4	16.8
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	DIADAVTAAGVEVAK	1429.8	R	S	2.8	0.3	0.0	0.0
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	DIADAVTAAGVEVAKSEVR	1901.0	R	L	3.5	0.3	31.2	17.9
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	KNIEFFEAR	1153.6	K	R	2.7	0.4	23.3	14.5
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	MQVILLDK	959.6	-	V	2.4	0.3	21.1	15.1
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	MQVILLDKVANLGSLGDQVNVK	2354.3	-	A	4.2	0.0	49.3	14.0
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	NFLVPQGK	902.5	R	A	1.6	0.6	22.1	18.6
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	NIEFFEAR	1025.5	K	R	2.1	0.2	43.1	15.1
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	RAELEAK	816.5	R	L	2.1	0.3	43.3	19.5
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	SEVRLPNGVLR	1240.7	K	T	2.8	0.5	0.0	0.0
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	TTGEHEVSFQVHSEVFAK	2032.0	R	V	0.0	0.0	69.1	17.2
P0A7R1	15750.7	S	U	T	A	ETD	LIT	12	69.8	VANLGSLGDQVNVK	1413.8	K	A	3.1	0.2	47.5	15.7
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	AGDEGKLFGSIGTR	1407.7	K	D	5.1	0.3	42.3	16.8
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	DIADAVTAAGVEVAK	1429.8	R	S	2.0	0.5	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	DIADAVTAAGVEVAKSEVR	1901.0	R	L	5.2	0.3	45.4	18.5
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	KNIEFFEAR	1153.6	K	R	2.4	0.3	19.3	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	LFGSIGTR	850.5	K	D	2.0	0.2	29.7	16.2
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	MQVILLDK	959.6	-	V	1.9	0.0	22.4	15.1
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	NFLVPQGK	902.5	R	A	1.9	0.5	22.7	15.9
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	RAELEAK	816.5	R	L	1.4	0.3	19.5	19.5
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	SEVRLPNGVLR	1240.7	K	T	0.0	0.0	29.9	12.0
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	TTGEHEVSFQVHSEVFAK	2032.0	R	V	0.0	0.0	85.4	17.2
P0A7R1	15750.7	S	U	T	B	ETD	LIT	11	69.8	VANLGSLGDQVNVK	1413.8	K	A	3.8	0.2	0.0	0.0
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	AGDEGKLFGSIGTR	1407.7	K	D	4.5	0.3	39.4	15.9
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	DIADAVTAAGVEVAK	1429.8	R	S	2.9	0.4	42.8	17.0
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	DIADAVTAAGVEVAKSEVR	1901.0	R	L	3.0	0.7	30.5	17.7
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	INALETVTIASK	1259.7	K	A	1.7	0.4	27.7	13.0
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	KNIEFFEAR	1153.6	K	R	2.2	0.3	29.3	14.5
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	LFGSIGTR	850.5	K	D	2.0	0.2	0.0	0.0
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	MQVILLDK	959.6	-	V	2.5	0.3	20.2	15.1
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	TTGEHEVSFQVHSEVFAK	2032.0	R	V	5.3	0.7	0.0	0.0
P0A7R1	15750.7	S	U	T	C	ETD	LIT	9	63.1	VANLGSLGDQVNVK	1413.8	K	A	3.3	0.3	51.0	15.3
P0A7R1	15750.7	S	U	T	B	ETD	FT	2	14.8	LAEVLAAANAR	1098.6	K	A	1.3	0.0	22.9	12.0
P0A7R1	15750.7	S	U	T	B	ETD	FT	2	14.8	SEVRLPNGVLR	1240.7	K	T	2.5	0.0	35.0	12.8
P0A7R1	15750.7	S	U	T	C	ETD	FT	2	7.4	LPNGVLR	769.5	R	T	1.1	0.3	23.3	12.0
P0A7R1	15750.7	S	U	T	C	ETD	FT	2	7.4	SEVRLPNGVLR	1240.7	K	T	2.4	0.0	34.2	12.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	2	21.5	AGDEGKLFGSIGTR	1407.7	K	D	0.0	0.0	59.3	16.8
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	2	21.5	TTGEHEVSFQVHSEVFAK	2032.0	R	V	0.0	0.0	63.0	16.9
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	AGDEGKLFGSIGTR	1407.7	K	D	0.0	0.0	59.3	16.8
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	DIADAVTAAGVEVAK	1429.8	R	S	0.0	0.0	82.2	17.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	DIADAVTAAGVEVAKSEVR	1901.0	R	L	0.0	0.0	49.8	18.1
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	INALETVTIASK	1259.7	K	A	0.0	0.0	28.7	13.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	MQVILLDK	959.6	-	V	0.0	0.0	39.3	15.1
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	RAELEAK	816.5	R	L	0.0	0.0	21.7	19.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	TTGEHEVSFQVHSEVFAK	2032.0	R	V	0.0	0.0	63.0	16.9
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	VANLGSLGDQVNVK	1413.8	K	A	0.0	0.0	59.4	15.7
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	AGDEGKLFGSIGTR	1407.7	K	D	5.7	0.3	38.5	16.8
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	DIADAVTAAGVEVAK	1429.8	R	S	5.5	0.6	80.2	17.2
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	DIADAVTAAGVEVAKSEVR	1901.0	R	L	5.2	0.6	70.3	18.1
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	INALETVTIASK	1259.7	K	A	3.6	0.6	39.0	13.0
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	LAEVLAAANAR	1098.6	K	A	2.3	0.8	0.0	0.0
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	MQVILLDK	959.6	-	V	2.8	0.4	38.4	15.1
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	NFLVPQGK	902.5	R	A	2.1	0.2	12.6	18.0
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	RAELEAKLAEVLAAANAR	1896.1	R	A	3.8	0.6	29.4	11.8
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	SEVRLPNGVLR	1240.7	K	T	3.0	0.5	22.9	12.0
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	TTGEHEVSFQVHSEVFAK	2032.0	R	V	5.3	0.5	44.6	17.2
P0A7R1	15750.7	S	U	T	A	ETD+CID	LIT	11	79.2	VANLGSLGDQVNVK	1413.8	K	A	4.5	0.6	71.7	15.7
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	4	30.2	AGDEGKLFGSIGTR	1407.7	K	D	6.2	0.5	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	4	30.2	DIADAVTAAGVEVAK	1429.8	R	S	4.9	0.6	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	4	30.2	DIADAVTAAGVEVAKSEVR	1901.0	R	L	4.1	0.6	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	4	30.2	INALETVTIASK	1259.7	K	A	2.2	0.6	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	4	30.2	KDDPQFKK	1005.5	-	-	2.0	0.3	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	AGDEGKLFGSIGTR	1407.7	K	D	6.2	0.5	59.3	16.8
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	DIADAVTAAGVEVAK	1429.8	R	S	4.9	0.6	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	DIADAVTAAGVEVAKSEVR	1901.0	R	L	4.1	0.6	49.8	18.1
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	INALETVTIASK	1259.7	K	A	2.1	0.7	0.0	0.0
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	KDDPQFKK	1005.5	-	-	2.0	0.3	21.8	18.1
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	MQVILLDK	959.6	-	V	2.4	0.5	39.3	15.1
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	RAELEAK	816.5	R	L	2.0	0.3	21.7	19.5
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	TTGEHEVSFQVHSEVFAK	2032.0	R	V	5.1	0.6	63.0	16.9
P0A7R1	15750.7	S	U	T	B	ETD+CID	LIT	8	61.7	VANLGSLGDQVNVK	1413.8	K	A	4.2	0.6	59.4	15.7
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	AGDEGKLFGSIGTR	1407.7	K	D	5.6	0.3	35.6	16.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	DIADAVTAAGVEVAK	1429.8	R	S	1.9	0.5	0.0	0.0
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	DIADAVTAAGVEVAKSEVR	1901.0	R	L	5.0	0.6	72.9	18.1
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	INALETVTIASK	1259.7	K	A	0.0	0.0	51.8	15.1
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	KNIEFFEAR	1153.6	K	R	2.7	0.7	35.5	14.1
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	LFGSIGTR	850.5	K	D	1.8	0.6	26.6	16.3
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	LPNGVLR	769.5	R	T	1.4	0.0	28.0	12.3
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	SEVRLPNGVLR	1240.7	K	T	3.2	0.5	0.0	0.0
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	SGFQYHGR	951.4	-	-	2.7	-0.5	41.5	14.5
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	TTGEHEVSFQVHSEVFAK	2032.0	R	V	3.0	0.8	0.0	0.0
P0A7R1	15750.7	S	U	T	C	ETD+CID	LIT	11	62.4	VANLGSLGDQVNVK	1413.8	K	A	4.3	0.6	57.6	15.7
P0A7R1	15750.7	S	U	T	B	HCD	FT	7	52.3	DIADAVTAAGVEVAK	1429.8	R	S	0.0	0.0	82.2	17.0
P0A7R1	15750.7	S	U	T	B	HCD	FT	7	52.3	DIADAVTAAGVEVAKSEVR	1901.0	R	L	0.0	0.0	49.8	18.1
P0A7R1	15750.7	S	U	T	B	HCD	FT	7	52.3	INALETVTIASK	1259.7	K	A	0.0	0.0	28.7	13.0
P0A7R1	15750.7	S	U	T	B	HCD	FT	7	52.3	MQVILLDK	959.6	-	V	0.0	0.0	39.3	15.1
P0A7R1	15750.7	S	U	T	B	HCD	FT	7	52.3	RAELEAK	816.5	R	L	0.0	0.0	21.7	19.5
P0A7R1	15750.7	S	U	T	B	HCD	FT	7	52.3	TTGEHEVSFQVHSEVFAK	2032.0	R	V	0.0	0.0	24.4	17.2
P0A7R1	15750.7	S	U	T	B	HCD	FT	7	52.3	VANLGSLGDQVNVK	1413.8	K	A	0.0	0.0	59.4	15.7
P0A7R1	15750.7	S	U	T	B	HCD	FT	2	12.1	RAELEAK	816.5	R	L	2.3	0.1	35.7	19.5
P0A7R1	15750.7	S	U	T	B	HCD	FT	2	12.1	SEVRLPNGVLR	1240.7	K	T	3.0	0.0	53.7	12.8
P0A7R1	15750.7	S	U	T	C	HCD	FT	2	14.8	LAEVLAAANAR	1098.6	K	A	2.1	0.0	22.2	12.6
P0A7R1	15750.7	S	U	T	C	HCD	FT	2	14.8	SEVRLPNGVLR	1240.7	K	T	3.1	0.0	43.3	12.0
P0C054	15756.2	G	U	T	A	CID	LIT	4	21.9	FQLAENIHVR	1226.7	K	G	3.3	0.0	41.8	9.0
P0C054	15756.2	G	U	T	A	CID	LIT	4	21.9	KFQLAENIHVR	1354.8	R	G	5.0	0.8	65.8	10.4
P0C054	15756.2	G	U	T	A	CID	LIT	4	21.9	NFDLSPLYR	1124.6	R	S	2.9	0.7	19.0	12.3
P0C054	15756.2	G	U	T	A	CID	LIT	4	21.9	TYLYQGIAER	1213.6	R	N	3.0	0.0	48.5	10.8
P0C054	15756.2	S	U	T	A	CID	LIT	2	29.2	LFNHLENNQSQSNGGYPPYNVELVDENHYR	3547.6	R	I	5.7	0.0	46.5	17.8
P0C054	15756.2	S	U	T	A	CID	LIT	2	29.2	TYLYQGIAER	1213.6	R	N	3.2	0.4	29.5	14.9
P0C054	15756.2	S	U	T	B	CID	LIT	2	29.2	LFNHLENNQSQSNGGYPPYNVELVDENHYR	3548.6	R	I	4.1	0.6	20.6	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0C054	15756.2	S	U	T	B	CID	LIT	2	29.2	TYLYQGIAER	1213.6	R	N	3.1	0.4	23.9	14.9
P0C054	15756.2	S	U	T	A	ETD+CID	LIT	2	29.2	LFNHLENNQSQSNGGYPPYNVELVDENHYR	3548.6	R	I	3.5	0.0	27.1	17.2
P0C054	15756.2	S	U	T	A	ETD+CID	LIT	2	29.2	TYLYQGIAER	1213.6	R	N	3.1	0.5	26.7	15.2
P0C054	15756.2	S	U	T	B	ETD+CID	LIT	2	29.2	LFNHLENNQSQSNGGYPPYNVELVDENHYR	3548.6	R	I	3.9	0.6	23.0	17.3
P0C054	15756.2	S	U	T	B	ETD+CID	LIT	2	29.2	TYLYQGIAER	1213.6	R	N	3.1	0.5	18.3	14.9
P0C054	15756.2	S	U	T	C	ETD+CID	LIT	2	29.2	LFNHLENNQSQSNGGYPPYNVELVDENHYR	3547.6	R	I	3.2	0.5	0.0	0.0
P0C054	15756.2	S	U	T	C	ETD+CID	LIT	2	29.2	TYLYQGIAER	1213.6	R	N	2.8	0.2	10.8	15.2
P03817	15790.5	G	T	A	B	CID	LIT	4	42.9	DIPDNLSPFYEALQ	1621.8	G	E	2.6	0.0	29.5	12.3
P03817	15790.5	G	T	A	B	CID	LIT	4	42.9	DKLEAELKNSGAKQTG	1688.9	I	E	1.9	0.6	19.6	16.1
P03817	15790.5	G	T	A	B	CID	LIT	4	42.9	DLPASGIWLVISSTHGAG	1780.9	E	D	2.6	0.8	7.8	13.8
P03817	15790.5	G	T	A	B	CID	LIT	4	42.9	DPAEEWLGSWVNLLK	1756.9	E	-	3.8	0.0	45.8	16.1
P0AB96	15836.0	G	T	A	B	CID	LIT	2	28.4	EMIRNSGTEPTIIHYLETPPTR	2555.3	L	D	3.2	0.0	15.6	15.7
P0AB96	15836.0	G	T	A	B	CID	LIT	2	28.4	SNITIYHNPACGTSRNTL	2019.0	M	E	0.0	0.0	42.5	14.0
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	DEVNELAEELGADVVVIGSR	2114.1	R	N	4.8	0.8	105.0	12.8
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	FAADVR	678.4	R	R	2.1	0.6	32.2	14.9
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	FAADVRR	834.5	R	F	2.1	0.6	21.8	15.3
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	FEEHLQHEAQER	1552.7	R	L	4.1	0.7	40.9	10.8
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	5.8	0.6	82.1	12.3
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	5.1	0.9	53.3	10.8
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	HANLPVLVVR	1117.7	R	-	3.2	0.0	48.1	0.0
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	IKQHVR	780.5	R	F	1.9	0.6	25.8	10.4
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	LQTMVSHFTIDPSR	1631.8	R	I	3.8	0.9	79.2	12.6
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	LQTMVSHFTIDPSRIK	1873.0	R	Q	3.2	0.6	5.9	11.5
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	NPSISTHLLGSNASSVIR	1853.0	R	H	5.9	0.7	90.7	10.0
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	RFEEHLQHEAQER	1708.8	R	L	5.4	0.6	78.0	12.3
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	TIIMPVDVFEMELSDK	1866.9	K	A	4.1	0.8	64.2	10.0
P39177	15916.8	G	U	T	A	CID	LIT	14	97.9	TIIMPVDVFEMELSDKAVR	2193.1	K	H	4.7	0.8	102.0	11.5
P39177	15916.8	G	T	T	A	CID	LIT	5	43.0	FAADVR	678.4	R	R	1.8	0.6	13.7	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P39177	15916.8	G	T	T	A	CID	LIT	5	43.0	HANLPVLVVR	1117.7	R	-	2.8	0.0	20.1	0.0
P39177	15916.8	G	T	T	A	CID	LIT	5	43.0	LQTMVSHFTIDPSR	1631.8	R	I	3.5	0.8	58.2	13.2
P39177	15916.8	G	T	T	A	CID	LIT	5	43.0	NPSISTHLLGSNASSVIR	1853.0	R	H	3.9	0.0	31.0	10.0
P39177	15916.8	G	T	T	A	CID	LIT	5	43.0	RFEEHLQHEAQER	1708.8	R	L	3.4	0.6	15.3	12.0
P39177	15916.8	G	U	A	A	CID	LIT	6	67.6	DDGVIHLLHVLPGSASLSLHRFAA	2525.4	Q	D	3.8	0.6	17.9	13.2
P39177	15916.8	G	U	A	A	CID	LIT	6	67.6	DKAVRHAEFLAQ	1384.7	S	D	3.3	0.6	48.0	13.0
P39177	15916.8	G	U	A	A	CID	LIT	6	67.6	DKAVRHAEFLAQD	1499.8	S	D	3.6	0.6	26.8	13.2
P39177	15916.8	G	U	A	A	CID	LIT	6	67.6	DPSRIKQHVRFGSVR	1782.0	I	D	1.5	0.0	27.1	12.3
P39177	15916.8	G	U	A	A	CID	LIT	6	67.6	DVVVIGSRNPSISTHLLGSNASSVIRHANLPVLVVR	3777.1	A	-	2.6	0.0	10.7	9.5
P39177	15916.8	G	U	A	A	CID	LIT	6	67.6	MYKTIIMPV	1095.6	-	D	2.5	0.7	27.7	10.0
P39177	15916.8	G	T	T	B	CID	LIT	6	47.2	FAADVR	678.4	R	R	2.1	0.4	14.4	14.9
P39177	15916.8	G	T	T	B	CID	LIT	6	47.2	HANLPVLVVR	1117.7	R	-	2.6	0.0	40.2	0.0
P39177	15916.8	G	T	T	B	CID	LIT	6	47.2	IKQHVR	780.5	R	F	2.1	0.2	26.2	10.4
P39177	15916.8	G	T	T	B	CID	LIT	6	47.2	LQTMVSHFTIDPSR	1631.8	R	I	2.9	0.7	18.7	12.6
P39177	15916.8	G	T	T	B	CID	LIT	6	47.2	NPSISTHLLGSNASSVIR	1853.0	R	H	4.4	0.6	56.8	9.0
P39177	15916.8	G	T	T	B	CID	LIT	6	47.2	RFEEHLQHEAQER	1708.8	R	L	4.4	0.5	56.4	12.8
P39177	15916.8	G	U	T	B	CID	LIT	6	54.2	FAADVR	678.4	R	R	1.9	0.0	20.9	14.9
P39177	15916.8	G	U	T	B	CID	LIT	6	54.2	HANLPVLVVR	1117.7	R	-	3.3	0.0	32.3	0.0
P39177	15916.8	G	U	T	B	CID	LIT	6	54.2	LQTMVSHFTIDPSR	1631.8	R	I	2.8	0.7	24.6	12.6
P39177	15916.8	G	U	T	B	CID	LIT	6	54.2	NPSISTHLLGSNASSVIR	1853.0	R	H	5.6	0.0	83.4	10.0
P39177	15916.8	G	U	T	B	CID	LIT	6	54.2	RFEEHLQHEAQER	1708.8	R	L	3.0	0.8	23.1	11.8
P39177	15916.8	G	U	T	B	CID	LIT	6	54.2	TIIMPVDVFEMELSDK	1866.9	K	A	2.8	0.0	55.4	10.0
P39177	15916.8	G	T	A	B	CID	LIT	7	34.5	DEVNELA	789.4	R	E	1.8	0.2	16.5	15.1
P39177	15916.8	G	T	A	B	CID	LIT	7	34.5	DKAVRHAEFLAQ	1384.7	S	D	3.9	0.7	42.1	14.5
P39177	15916.8	G	T	A	B	CID	LIT	7	34.5	DKAVRHAEFLAQD	1499.8	S	D	3.7	0.0	36.6	14.0
P39177	15916.8	G	T	A	B	CID	LIT	7	34.5	DVFEMELS	969.4	V	D	1.5	0.3	13.8	11.5
P39177	15916.8	G	T	A	B	CID	LIT	7	34.5	ERLQTMVSHFTI	1461.8	Q	D	2.1	0.6	13.3	16.6
P39177	15916.8	G	T	A	B	CID	LIT	7	34.5	MYKTIIMPV	1095.6	-	D	2.0	0.8	24.3	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P39177	15916.8	G	T	A	B	CID	LIT	7	34.5	MYKTIIMPVDVF	1456.8	-	E	2.2	0.5	9.6	15.6
P39177	15916.8	G	U	A	B	CID	LIT	6	42.3	DDGVIHLLHVLPGSASLSLHRFAA	2525.4	Q	D	4.4	0.0	22.6	13.4
P39177	15916.8	G	U	A	B	CID	LIT	6	42.3	DKAVRHAEFLAQ	1384.7	S	D	3.0	0.7	44.0	13.0
P39177	15916.8	G	U	A	B	CID	LIT	6	42.3	DKAVRHAEFLAQD	1499.8	S	D	3.5	0.0	24.1	13.2
P39177	15916.8	G	U	A	B	CID	LIT	6	42.3	ERLQTMVSHFTI	1461.8	Q	D	2.3	0.8	25.0	16.6
P39177	15916.8	G	U	A	B	CID	LIT	6	42.3	MYKTIIMPV	1095.6	-	D	2.4	0.0	28.6	10.0
P39177	15916.8	G	U	A	B	CID	LIT	6	42.3	MYKTIIMPVDVF	1456.8	-	E	2.8	0.8	24.3	15.6
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	FEEHLQHEAQER	1552.7	R	L	4.5	0.5	45.8	15.3
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	6.4	0.6	73.4	19.0
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	4.4	0.0	56.5	16.5
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	HANLPVLVVR	1117.7	R	-	3.2	0.8	30.5	10.0
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	LQTMVSHFTIDPSR	1631.8	R	I	4.1	0.5	83.9	17.4
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	LQTMVSHFTIDPSRIK	1873.0	R	Q	2.9	0.4	7.2	17.1
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	NPSISTHLLGSNASSVIR	1853.0	R	H	5.6	0.7	104.0	14.9
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	RFEEHLQHEAQER	1708.8	R	L	4.8	0.7	41.7	17.1
P39177	15916.8	S	U	T	A	CID	LIT	9	88.7	TIIMPVDVFEMELSDK	1866.9	K	A	4.2	0.5	60.2	17.5
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	DEVNELAEELGADVVVIGSR	2114.1	R	N	2.5	0.3	0.0	0.0
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	FEEHLQHEAQER	1552.7	R	L	4.2	0.6	32.6	15.1
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	5.7	0.5	87.1	18.9
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	4.2	0.7	65.2	16.2
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	HANLPVLVVR	1117.7	R	-	2.3	0.3	10.0	10.0
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	LQTMVSHFTIDPSR	1631.8	R	I	3.9	0.5	79.3	17.4
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	NPSISTHLLGSNASSVIR	1853.0	R	H	5.5	0.7	104.0	15.7
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	RFEEHLQHEAQER	1708.8	R	L	5.3	0.5	73.8	17.1
P39177	15916.8	S	U	T	B	CID	LIT	9	87.3	TIIMPVDVFEMELSDK	1866.9	K	A	4.2	0.8	76.8	17.9
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	FEEHLQHEAQER	1552.7	R	L	2.9	0.7	30.8	14.8
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	4.2	0.5	45.6	19.1
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	4.0	0.0	60.5	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	HANLPVLVVR	1117.7	R	-	2.5	0.5	12.7	10.0
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	LQTMVSHFTIDPSR	1647.8	R	I	3.5	0.5	41.5	17.5
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	NPSISTHLLGSNASSVIR	1853.0	R	H	5.9	0.7	107.0	14.9
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	RFEEHLQHEAQER	1708.8	R	L	5.5	0.6	87.9	17.1
P39177	15916.8	S	U	T	C	CID	LIT	8	87.3	TIIMPVDVFEMELSDK	1866.9	K	A	4.2	0.6	64.7	17.5
P39177	15916.8	S	U	T	A	CID	FT	2	22.5	LQTMVSHFTIDPSR	1647.8	R	I	3.5	0.0	55.1	16.8
P39177	15916.8	S	U	T	A	CID	FT	2	22.5	NPSISTHLLGSNASSVIR	1854.0	R	H	2.6	0.0	60.7	17.1
P39177	15916.8	S	U	T	A	ETD	LIT	6	69.7	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	0.0	0.0	49.0	16.2
P39177	15916.8	S	U	T	A	ETD	LIT	6	69.7	HANLPVLVVR	1117.7	R	-	2.3	0.7	0.0	0.0
P39177	15916.8	S	U	T	A	ETD	LIT	6	69.7	LQTMVSHFTIDPSR	1647.8	R	I	3.2	0.5	32.8	17.7
P39177	15916.8	S	U	T	A	ETD	LIT	6	69.7	NPSISTHLLGSNASSVIR	1854.0	R	H	6.8	0.0	86.2	16.6
P39177	15916.8	S	U	T	A	ETD	LIT	6	69.7	RFEEHLQHEAQER	1708.8	R	L	4.8	0.7	65.6	17.4
P39177	15916.8	S	U	T	A	ETD	LIT	6	69.7	TIIMPVDVFEMELSDK	1866.9	K	A	3.8	0.1	25.4	17.5
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	FEEHLQHEAQER	1552.7	R	L	4.0	0.5	21.7	15.2
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	0.0	0.0	54.9	18.9
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	0.0	0.0	54.5	15.6
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	HANLPVLVVR	1117.7	R	-	1.9	0.6	0.0	0.0
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	LQTMVSHFTIDPSR	1631.8	R	I	3.2	0.3	0.0	0.0
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	NPSISTHLLGSNASSVIR	1853.0	R	H	7.4	0.6	88.6	15.7
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	RFEEHLQHEAQER	1708.8	R	L	5.1	0.7	0.0	0.0
P39177	15916.8	S	U	T	B	ETD	LIT	8	87.3	TIIMPVDVFEMELSDK	1866.9	K	A	4.2	0.3	22.1	17.3
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	FEEHLQHEAQER	1552.7	R	L	4.4	0.0	34.0	15.2
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	3.7	0.0	36.5	19.0
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	FGSVRDEVNELAEELGADVVVIGSRNPSISTHLLGSNASSVIR	4494.3	R	H	0.0	0.0	21.1	17.0
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	0.0	0.0	56.2	16.2
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	HANLPVLVVR	1117.7	R	-	2.9	0.8	17.0	10.0
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	LQTMVSHFTIDPSR	1631.8	R	I	4.7	0.3	52.9	16.9
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	NPSISTHLLGSNASSVIR	1853.0	R	H	3.8	0.7	91.1	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	RFEEHLQHEAQER	1708.8	R	L	4.0	0.0	45.2	17.7
P39177	15916.8	S	U	T	C	ETD	LIT	9	87.3	TIIMPVDVFEMELSDK	1866.9	K	A	4.5	0.3	27.7	17.5
P39177	15916.8	S	U	T	A	ETD	FT	2	16.2	HANLPVLVVR	1117.7	R	-	1.7	0.0	37.6	10.0
P39177	15916.8	S	U	T	A	ETD	FT	2	16.2	RFEEHLQHEAQER	1708.8	R	L	4.5	0.0	62.8	17.3
P39177	15916.8	S	U	T	B	ETD+CID	LIT	4	61.3	FGSVRDEVNELAEELGADVVVIGSRNPSISTHLLGSNASSVIR	4494.3	R	H	0.0	0.0	18.2	16.7
P39177	15916.8	S	U	T	B	ETD+CID	LIT	4	61.3	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	0.0	0.0	33.0	16.6
P39177	15916.8	S	U	T	B	ETD+CID	LIT	4	61.3	NPSISTHLLGSNASSVIR	1853.0	R	H	0.0	0.0	82.4	15.3
P39177	15916.8	S	U	T	B	ETD+CID	LIT	4	61.3	TIIMPVDVFEMELSDK	1866.9	K	A	0.0	0.0	25.5	17.4
P39177	15916.8	S	U	T	B	ETD+CID	LIT	7	78.2	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	0.0	0.0	75.3	19.4
P39177	15916.8	S	U	T	B	ETD+CID	LIT	7	78.2	FGSVRDEVNELAEELGADVVVIGSRNPSISTHLLGSNASSVIR	4494.3	R	H	0.0	0.0	18.2	16.7
P39177	15916.8	S	U	T	B	ETD+CID	LIT	7	78.2	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	0.0	0.0	61.5	16.5
P39177	15916.8	S	U	T	B	ETD+CID	LIT	7	78.2	HANLPVLVVR	1117.7	R	-	0.0	0.0	51.9	10.0
P39177	15916.8	S	U	T	B	ETD+CID	LIT	7	78.2	LQTMVSHFTIDPSR	1631.8	R	I	0.0	0.0	47.0	17.0
P39177	15916.8	S	U	T	B	ETD+CID	LIT	7	78.2	NPSISTHLLGSNASSVIR	1853.0	R	H	0.0	0.0	107.0	15.9
P39177	15916.8	S	U	T	B	ETD+CID	LIT	7	78.2	TIIMPVDVFEMELSDK	1866.9	K	A	0.0	0.0	25.5	17.4
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	FEEHLQHEAQER	1552.7	R	L	4.2	0.0	26.4	15.2
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	6.6	0.6	84.5	19.4
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	FGSVRDEVNELAEELGADVVVIGSRNPSISTHLLGSNASSVIR	4494.3	R	H	5.3	0.0	66.3	16.1
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	3.9	0.0	61.5	16.5
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	HANLPVLVVR	1117.7	R	-	2.9	0.0	38.5	10.0
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	LQTMVSHFTIDPSR	1631.8	R	I	3.6	0.5	74.0	17.6
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	LQTMVSHFTIDPSRIK	1873.0	R	Q	2.4	0.2	20.7	17.0
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	NPSISTHLLGSNASSVIR	1853.0	R	H	5.2	0.7	107.0	15.7
P39177	15916.8	S	U	T	A	ETD+CID	LIT	9	77.5	RFEEHLQHEAQER	1708.8	R	L	4.0	0.7	30.5	17.1
P39177	15916.8	S	U	T	B	ETD+CID	LIT	2	37.3	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	3.6	0.5	0.0	0.0
P39177	15916.8	S	U	T	B	ETD+CID	LIT	2	37.3	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	5.1	0.9	0.0	0.0
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	6.6	0.6	75.3	19.4
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	FGSVRDEVNELAEELGADVVVIGSRNPSISTHLLGSNASSVIR	4494.3	R	H	0.0	0.0	18.2	16.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	4.3	0.8	61.5	16.5
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	HANLPVLVVR	1117.7	R	-	2.9	0.4	31.3	10.0
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	LQTMVSHFTIDPSR	1631.8	R	I	2.7	0.6	47.0	17.0
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	LQTMVSHFTIDPSRIK	1873.0	R	Q	2.6	0.4	4.5	17.0
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	NPSISTHLLGSNASSVIR	1853.0	R	H	5.8	0.7	107.0	15.9
P39177	15916.8	S	U	T	B	ETD+CID	LIT	8	79.6	TIIMPVDVFEMELSDK	1866.9	K	A	4.4	0.2	25.5	17.4
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	FEEHLQHEAQER	1552.7	R	L	3.1	0.5	16.1	15.1
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	6.3	0.7	72.8	18.9
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	4.5	0.5	21.7	16.5
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	HANLPVLVVR	1117.7	R	-	3.6	0.0	47.7	10.0
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	LQTMVSHFTIDPSR	1631.8	R	I	5.0	0.4	0.0	0.0
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	NPSISTHLLGSNASSVIR	1854.0	R	H	5.9	0.8	94.5	16.5
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	RFEEHLQHEAQER	1708.8	R	L	5.3	0.6	81.3	17.4
P39177	15916.8	S	U	T	C	ETD+CID	LIT	8	87.3	TIIMPVDVFEMELSDK	1866.9	K	A	1.8	0.3	0.0	0.0
P39177	15916.8	S	U	T	B	HCD	FT	5	66.9	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	0.0	0.0	75.3	19.4
P39177	15916.8	S	U	T	B	HCD	FT	5	66.9	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	0.0	0.0	61.5	16.5
P39177	15916.8	S	U	T	B	HCD	FT	5	66.9	HANLPVLVVR	1117.7	R	-	0.0	0.0	51.9	10.0
P39177	15916.8	S	U	T	B	HCD	FT	5	66.9	LQTMVSHFTIDPSR	1631.8	R	I	0.0	0.0	47.0	17.0
P39177	15916.8	S	U	T	B	HCD	FT	5	66.9	NPSISTHLLGSNASSVIR	1853.0	R	H	0.0	0.0	107.0	15.9
P39177	15916.8	S	U	T	A	HCD	FT	3	47.2	FGSVRDEVNELAEELGADVVVIGSR	2660.4	R	N	5.0	0.0	108.0	19.1
P39177	15916.8	S	U	T	A	HCD	FT	3	47.2	HAEFLAQDDGVIHLLHVLPGSASLSLHR	3032.6	R	F	7.0	0.0	22.3	15.6
P39177	15916.8	S	U	T	A	HCD	FT	3	47.2	LQTMVSHFTIDPSR	1631.8	R	I	3.9	0.0	77.4	16.6
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	FKLPTDR	876.5	K	V	2.0	0.2	18.9	14.9
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	HAECSVLVVR	1169.6	R	-	2.9	0.5	33.8	12.8
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	SQLEEIIK	959.5	K	K	2.0	0.0	30.5	12.6
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	SQLEEIIKK	1087.6	K	F	2.6	0.7	34.5	11.5
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	TILVPIDISDSELTQR	1800.0	R	V	4.2	0.8	89.3	14.1
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	VHVHVEEGSPK	1217.6	R	D	3.9	0.5	29.6	12.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	VHVHVEEGSPKDR	1488.8	R	I	4.5	0.7	51.2	13.4
P37903	15998.9	G	U	T	A	CID	LIT	8	45.1	VISHVEEEAK	1140.6	R	I	3.3	0.5	49.2	11.8
P37903	15998.9	G	T	T	A	CID	LIT	2	9.0	VHVHVEEGSPK	1217.6	R	D	3.1	0.5	26.0	12.8
P37903	15998.9	G	T	T	A	CID	LIT	2	9.0	VHVHVEEGSPKDR	1488.8	R	I	3.9	0.0	27.5	13.0
P37903	15998.9	G	T	T	B	CID	LIT	3	20.1	HAECSVLVVR	1169.6	R	-	2.6	0.4	27.3	12.6
P37903	15998.9	G	T	T	B	CID	LIT	3	20.1	SQLEEIIK	959.5	K	K	2.4	0.3	29.2	13.6
P37903	15998.9	G	T	T	B	CID	LIT	3	20.1	VHVHVEEGSPK	1217.6	R	D	3.0	0.5	30.5	13.6
P37903	15998.9	G	T	A	B	CID	LIT	2	17.4	DRVHVHVEEGSPK	1488.8	T	D	3.4	0.7	21.0	16.4
P37903	15998.9	G	T	A	B	CID	LIT	2	17.4	MNRTILVPIDIS	1371.8	-	D	2.3	0.7	17.2	12.3
P37903	15998.9	G	U	A	B	CID	LIT	2	16.0	DDLKAEAKSQL	1217.6	M	E	1.7	0.0	23.4	15.3
P37903	15998.9	G	U	A	B	CID	LIT	2	16.0	MNRTILVPIDIS	1371.8	-	D	2.2	0.0	17.2	12.3
P37903	15998.9	S	U	T	A	CID	LIT	4	26.4	SQLEEIIKK	1087.6	K	F	2.6	0.5	22.1	14.1
P37903	15998.9	S	U	T	A	CID	LIT	4	26.4	TILVPIDISDSELTQR	1800.0	R	V	4.7	0.5	27.0	16.8
P37903	15998.9	S	U	T	A	CID	LIT	4	26.4	VHVHVEEGSPK	1217.6	R	D	3.1	0.8	32.2	17.1
P37903	15998.9	S	U	T	A	CID	LIT	4	26.4	VHVHVEEGSPKDR	1488.8	R	I	4.3	0.5	55.6	17.4
P37903	15998.9	S	U	T	B	CID	LIT	4	25.0	SQLEEIIK	959.5	K	K	2.3	0.5	24.5	16.6
P37903	15998.9	S	U	T	B	CID	LIT	4	25.0	SQLEEIIKK	1087.6	K	F	2.8	0.5	21.0	14.1
P37903	15998.9	S	U	T	B	CID	LIT	4	25.0	TILVPIDISDSELTQR	1800.0	R	V	4.6	0.7	84.8	16.9
P37903	15998.9	S	U	T	B	CID	LIT	4	25.0	VHVHVEEGSPK	1217.6	R	D	3.7	0.7	48.8	17.1
P37903	15998.9	S	U	T	C	CID	LIT	4	31.9	SQLEEIIKK	1087.6	K	F	2.5	0.6	22.8	14.1
P37903	15998.9	S	U	T	C	CID	LIT	4	31.9	TILVPIDISDSELTQR	1800.0	R	V	3.9	0.8	82.2	16.8
P37903	15998.9	S	U	T	C	CID	LIT	4	31.9	VHVHVEEGSPK	1217.6	R	D	3.5	0.7	33.3	16.8
P37903	15998.9	S	U	T	C	CID	LIT	4	31.9	VISHVEEEAK	1140.6	R	I	3.1	0.4	30.6	14.5
P37903	15998.9	S	U	T	A	ETD	LIT	2	16.7	SQLEEIIK	959.5	K	K	2.6	0.2	19.5	17.3
P37903	15998.9	S	U	T	A	ETD	LIT	2	16.7	TILVPIDISDSELTQR	1800.0	R	V	3.3	0.8	0.0	0.0
P37903	15998.9	S	U	T	B	ETD	LIT	3	39.6	KIPAHMIIIASHRPDITTYLLGSNAAAVVR	3228.8	K	H	0.0	0.0	33.6	9.0
P37903	15998.9	S	U	T	B	ETD	LIT	3	39.6	TILVPIDISDSELTQR	1800.0	R	V	4.2	0.6	37.4	16.7
P37903	15998.9	S	U	T	B	ETD	LIT	3	39.6	VHVHVEEGSPK	1217.6	R	D	4.8	0.5	43.0	17.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P37903	15998.9	S	U	T	C	ETD	LIT	5	52.1	KIPAHMIIIASHRPDITTYLLGSNAAAVVR	3228.8	K	H	0.0	0.0	27.1	8.5
P37903	15998.9	S	U	T	C	ETD	LIT	5	52.1	SQLEEIIK	959.5	K	K	2.5	0.1	25.4	16.6
P37903	15998.9	S	U	T	C	ETD	LIT	5	52.1	TILVPIDISDSELTQR	1800.0	R	V	5.3	0.6	57.8	16.6
P37903	15998.9	S	U	T	C	ETD	LIT	5	52.1	VHVHVEEGSPK	1217.6	R	D	5.0	0.5	38.8	16.8
P37903	15998.9	S	U	T	C	ETD	LIT	5	52.1	VISHVEEEAK	1140.6	R	I	3.6	0.8	36.9	13.6
P37903	15998.9	S	U	T	B	ETD	FT	2	13.9	SQLEEIIKK	1087.6	K	F	1.7	0.6	32.3	14.0
P37903	15998.9	S	U	T	B	ETD	FT	2	13.9	VHVHVEEGSPK	1217.6	R	D	4.1	0.6	40.5	17.0
P37903	15998.9	S	U	T	B	ETD+CID	LIT	2	25.0	SQLEEIIKK	1087.6	K	F	0.0	0.0	30.4	14.0
P37903	15998.9	S	U	T	B	ETD+CID	LIT	2	25.0	TILVPIDISDSELTQR	1800.0	R	V	0.0	0.0	84.6	16.8
P37903	15998.9	S	U	T	B	ETD+CID	LIT	2	25.0	VHVHVEEGSPK	1217.6	R	D	0.0	0.0	42.3	17.1
P37903	15998.9	S	U	T	A	ETD+CID	LIT	3	25.7	SQLEEIIK	959.5	K	K	2.1	0.0	25.7	17.3
P37903	15998.9	S	U	T	A	ETD+CID	LIT	3	25.7	TILVPIDISDSELTQR	1800.0	R	V	4.5	0.6	72.2	16.8
P37903	15998.9	S	U	T	A	ETD+CID	LIT	3	25.7	VHVHVEEGSPK	1217.6	R	D	3.7	0.7	46.6	17.1
P37903	15998.9	S	U	T	A	ETD+CID	LIT	3	25.7	VHVHVEEGSPKDR	1488.8	R	I	4.1	0.4	31.5	17.4
P37903	15998.9	S	U	T	B	ETD+CID	LIT	2	25.0	SQLEEIIKK	1087.6	K	F	2.3	0.7	30.4	14.0
P37903	15998.9	S	U	T	B	ETD+CID	LIT	2	25.0	TILVPIDISDSELTQR	1800.0	R	V	4.3	0.8	84.6	16.8
P37903	15998.9	S	U	T	B	ETD+CID	LIT	2	25.0	VHVHVEEGSPK	1217.6	R	D	4.0	0.8	45.8	15.8
P37903	15998.9	S	U	T	B	HCD	FT	2	25.0	SQLEEIIKK	1087.6	K	F	0.0	0.0	30.4	14.0
P37903	15998.9	S	U	T	B	HCD	FT	2	25.0	TILVPIDISDSELTQR	1800.0	R	V	0.0	0.0	84.6	16.8
P37903	15998.9	S	U	T	B	HCD	FT	2	25.0	VHVHVEEGSPK	1217.6	R	D	0.0	0.0	45.8	15.8
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	5.9	0.7	91.7	12.6
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	5.2	0.0	42.6	10.4
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	DWYVVDATGK	1153.6	R	T	3.1	0.7	32.3	10.4
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	DWYVVDATGKTLGR	1580.8	R	L	3.9	0.8	54.3	14.0
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	GMLPKGPLGR	1025.6	K	A	2.1	0.0	31.6	6.0
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	5.6	0.0	51.4	12.0
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	LATELAR	773.5	R	R	2.2	0.5	34.7	17.9
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	LATELARR	929.6	R	L	2.4	0.2	17.2	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.4	0.7	32.8	12.0
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	MKTFTAKPETVK	1380.8	-	R	2.6	0.4	16.0	12.6
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	QATFEEMIAR	1211.6	K	R	3.0	0.6	49.7	10.4
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	RDWYVVDATGK	1309.7	K	T	3.8	0.7	66.0	12.3
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	RPERVIEIAVK	1309.8	R	G	1.8	0.6	10.9	7.0
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	TDKVYYHHTGHIGGIK	1825.9	R	Q	4.4	0.8	56.3	10.4
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	TFTAKPETVK	1121.6	K	R	2.6	0.8	30.6	13.2
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	TFTAKPETVKR	1277.7	K	D	2.6	0.7	27.0	10.4
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	VAVTGNKR	844.5	K	T	1.6	0.4	23.8	14.9
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	VIEIAVK	771.5	R	G	2.4	0.6	32.4	7.8
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.2	0.7	48.5	11.8
P0AA10	16000.7	G	U	T	A	CID	LIT	20	93.7	VYYHHTGHIGGIK	1481.8	K	Q	4.6	0.6	53.9	11.8
P0AA10	16000.7	G	T	T	A	CID	LIT	3	19.7	LATELAR	773.5	R	R	2.5	0.3	24.6	17.9
P0AA10	16000.7	G	T	T	A	CID	LIT	3	19.7	RDWYVVDATGK	1309.7	K	T	3.6	0.5	33.7	12.6
P0AA10	16000.7	G	T	T	A	CID	LIT	3	19.7	TFTAKPETVKR	1277.7	K	D	2.5	0.7	14.5	10.4
P0AA10	16000.7	G	U	A	A	CID	LIT	5	31.0	DKVAVTGNKRT	1188.7	A	D	2.7	0.7	31.7	12.6
P0AA10	16000.7	G	U	A	A	CID	LIT	5	31.0	DYIIVLNADKVAVTGNKRT	2090.2	G	D	3.9	0.0	16.0	12.6
P0AA10	16000.7	G	U	A	A	CID	LIT	5	31.0	EHNHAAQQPQVL	1371.7	N	D	2.3	0.3	25.9	12.0
P0AA10	16000.7	G	U	A	A	CID	LIT	5	31.0	KTFTAKPETVKR	1405.8	M	D	0.0	0.0	40.7	7.0
P0AA10	16000.7	G	U	A	A	CID	LIT	5	31.0	MKTFTAKPETVKR	1536.9	-	D	4.2	0.7	64.5	6.0
P0AA10	16000.7	G	T	T	B	CID	LIT	4	24.6	LATELAR	773.5	R	R	2.5	0.3	28.5	17.9
P0AA10	16000.7	G	T	T	B	CID	LIT	4	24.6	RDWYVVDATGK	1309.7	K	T	2.1	0.6	9.8	12.6
P0AA10	16000.7	G	T	T	B	CID	LIT	4	24.6	TFTAKPETVKR	1277.7	K	D	3.2	0.8	35.9	10.4
P0AA10	16000.7	G	T	T	B	CID	LIT	4	24.6	VIEIAVK	771.5	R	G	2.3	0.3	13.0	7.8
P0AA10	16000.7	G	U	T	B	CID	LIT	2	12.0	LATELAR	773.5	R	R	2.5	0.3	51.9	17.9
P0AA10	16000.7	G	U	T	B	CID	LIT	2	12.0	TFTAKPETVK	1121.6	K	R	2.3	0.0	22.0	13.2
P0AA10	16000.7	G	T	A	B	CID	LIT	3	30.3	DKVAVTGNKRT	1188.7	A	D	2.0	0.5	14.4	12.6
P0AA10	16000.7	G	T	A	B	CID	LIT	3	30.3	DKVYYHHTGHIGGIKQATF	2172.1	T	E	3.1	0.4	11.8	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	G	T	A	B	CID	LIT	3	30.3	MKTFTAKPETVKR	1536.9	-	D	4.7	0.0	60.4	7.8
P0AA10	16000.7	G	U	A	B	CID	LIT	3	30.3	DKVAVTGNKRT	1188.7	A	D	2.0	0.6	20.5	12.6
P0AA10	16000.7	G	U	A	B	CID	LIT	3	30.3	DKVYYHHTGHIGGIKQATF	2172.1	T	E	5.8	0.7	56.0	14.9
P0AA10	16000.7	G	U	A	B	CID	LIT	3	30.3	MKTFTAKPETVKR	1536.9	-	D	2.1	0.7	19.0	7.8
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	5.8	0.7	63.5	18.5
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	6.4	0.0	64.8	18.6
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	2.6	0.4	22.3	18.9
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	DWYVVDATGK	1153.6	R	T	1.9	0.4	0.0	0.0
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	4.8	0.6	41.8	18.8
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	3.8	0.0	41.3	17.6
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	LATELAR	773.5	R	R	2.0	0.3	35.2	20.6
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.9	0.6	46.8	18.5
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	MKTFTAKPETVKR	1536.9	-	D	1.8	0.6	12.4	14.0
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	RDWYVVDATGK	1309.7	K	T	3.9	0.7	58.0	15.7
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	RTDKVYYHHTGHIGGIK	1982.0	K	Q	2.6	0.8	0.0	0.0
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	TDKVYYHHTGHIGGIK	1825.9	R	Q	4.2	0.8	60.4	16.7
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	TFTAKPETVK	1121.6	K	R	3.0	0.4	29.8	16.0
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	TFTAKPETVKR	1277.7	K	D	2.9	0.0	28.3	14.9
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.4	0.8	42.3	18.0
P0AA10	16000.7	S	U	T	A	CID	LIT	16	68.3	VYYHHTGHIGGIK	1481.8	K	Q	4.5	0.6	46.8	16.1
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	5.5	0.7	100.0	18.5
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	6.3	0.0	66.9	18.6
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	2.9	0.4	24.0	18.9
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	DWYVVDATGK	1153.6	R	T	2.7	0.4	23.5	14.5
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	3.9	0.4	29.5	18.7
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	2.2	0.7	31.7	17.6
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	LATELAR	773.5	R	R	1.8	0.3	34.3	20.6
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.7	0.0	43.0	18.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	MKTFTAKPETVKR	1536.9	-	D	4.4	0.8	64.8	14.0
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	RDWYVVDATGK	1309.7	K	T	4.1	0.8	62.0	15.7
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	TDKVYYHHTGHIGGIK	1825.9	R	Q	2.9	0.5	17.2	17.1
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	TFTAKPETVK	1121.6	K	R	2.7	0.3	35.3	15.6
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	TFTAKPETVKR	1277.7	K	D	3.0	0.0	28.1	14.9
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.0	0.8	44.9	18.0
P0AA10	16000.7	S	U	T	B	CID	LIT	15	68.3	VYYHHTGHIGGIK	1481.8	K	Q	4.5	0.7	50.6	16.5
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	5.3	0.7	75.5	19.3
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	5.2	0.0	56.0	18.5
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3060.6	K	T	4.1	0.8	32.0	19.1
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	DWYVVDATGK	1153.6	R	T	3.0	0.4	24.7	14.5
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	4.8	0.5	42.2	19.1
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	5.0	0.0	44.3	17.3
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	LATELAR	773.5	R	R	1.6	0.3	42.6	20.6
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.9	0.6	41.0	18.8
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	MKTFTAKPETVKR	1536.9	-	D	4.4	0.8	55.5	14.5
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	QATFEEMIAR	1195.6	K	R	2.9	0.4	58.4	15.8
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	RDWYVVDATGK	1309.7	K	T	4.2	0.6	72.8	15.6
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	RTDKVYYHHTGHIGGIK	1982.0	K	Q	2.8	0.4	0.0	0.0
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	TDKVYYHHTGHIGGIK	1825.9	R	Q	2.9	0.0	18.3	17.3
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	TFTAKPETVK	1121.6	K	R	3.1	0.5	28.9	16.0
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	TFTAKPETVKR	1277.7	K	D	2.9	0.8	31.7	14.9
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	VIEIAVK	771.5	R	G	2.6	0.5	39.3	13.0
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.1	0.9	38.3	17.9
P0AA10	16000.7	S	U	T	C	CID	LIT	18	80.3	VYYHHTGHIGGIK	1481.8	K	Q	2.9	0.7	42.1	16.1
P0AA10	16000.7	S	U	T	A	CID	FT	3	28.9	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	6.0	0.0	24.3	18.6
P0AA10	16000.7	S	U	T	A	CID	FT	3	28.9	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	3.9	0.0	13.1	18.7
P0AA10	16000.7	S	U	T	A	CID	FT	3	28.9	TFTAKPETVKR	1277.7	K	D	2.5	0.0	33.2	14.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	S	U	T	B	CID	FT	2	33.8	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	7.6	0.0	41.0	18.0
P0AA10	16000.7	S	U	T	B	CID	FT	2	33.8	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	2.8	0.0	23.0	17.9
P0AA10	16000.7	S	U	T	C	CID	FT	4	29.6	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.4	0.0	36.7	18.6
P0AA10	16000.7	S	U	T	C	CID	FT	4	29.6	RDWYVVDATGK	1309.7	K	T	2.1	0.0	45.8	15.6
P0AA10	16000.7	S	U	T	C	CID	FT	4	29.6	TFTAKPETVKR	1277.7	K	D	2.5	0.0	21.9	15.4
P0AA10	16000.7	S	U	T	C	CID	FT	4	29.6	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	2.3	0.0	23.4	17.6
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	2.4	0.4	5.8	18.5
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	4.8	0.0	39.5	18.5
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	0.0	0.0	56.6	18.2
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	DWYVVDATGK	1153.6	R	T	0.0	0.0	22.6	14.5
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	4.7	0.0	50.7	17.9
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	KTFTAKPETVKR	1405.8	M	D	0.0	0.0	76.8	10.0
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	5.9	0.7	42.8	19.0
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	MKTFTAKPETVKR	1536.9	-	D	6.1	0.6	75.2	15.1
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	QATFEEMIAR	1195.6	K	R	2.1	0.6	0.0	0.0
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	RDWYVVDATGK	1309.7	K	T	2.9	0.6	0.0	0.0
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	RTDKVYYHHTGHIGGIK	1982.0	K	Q	2.6	0.0	25.9	16.6
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	TFTAKPETVK	1121.6	K	R	4.3	0.5	41.4	16.0
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	TFTAKPETVKR	1277.7	K	D	4.7	0.8	60.6	15.2
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	VIEIAVK	771.5	R	G	1.6	0.3	12.0	13.0
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	6.6	0.4	0.0	0.0
P0AA10	16000.7	S	U	T	A	ETD	LIT	16	75.4	VYYHHTGHIGGIK	1481.8	K	Q	4.6	0.6	19.8	16.4
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	3.8	0.0	41.6	19.3
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	3.1	0.0	26.1	18.5
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3060.6	K	T	0.0	0.0	43.3	19.8
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	DWYVVDATGK	1153.6	R	T	2.4	0.6	11.8	15.1
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	6.1	0.0	54.8	18.6
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	0.0	0.0	22.7	18.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	KTFTAKPETVKR	1405.8	M	D	0.0	0.0	26.6	10.0
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	LATELAR	773.5	R	R	1.8	0.3	38.0	20.6
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	MKTFTAKPETVKR	1536.9	-	D	4.6	0.5	43.1	15.1
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	QATFEEMIAR	1195.6	K	R	2.2	0.5	43.6	14.9
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	RDWYVVDATGK	1309.7	K	T	2.9	0.4	36.8	15.4
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	RTDKVYYHHTGHIGGIK	1982.0	K	Q	2.6	0.4	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	TDKVYYHHTGHIGGIK	1825.9	R	Q	2.4	0.5	15.8	17.2
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	TFTAKPETVKR	1277.7	K	D	4.8	0.6	39.7	15.9
P0AA10	16000.7	S	U	T	B	ETD	LIT	15	73.9	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	6.2	0.4	65.1	17.6
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	6.2	0.6	52.9	18.6
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	0.0	0.0	103.0	18.5
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	0.0	0.0	36.4	18.5
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	0.0	0.0	31.1	18.1
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	LATELAR	773.5	R	R	2.0	0.2	31.4	20.6
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	5.0	0.0	25.7	18.7
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	MKTFTAKPETVKR	1536.9	-	D	5.7	0.6	57.5	14.5
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	QATFEEMIAR	1195.6	K	R	1.8	0.0	24.3	15.8
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	RDWYVVDATGK	1309.7	K	T	2.6	0.5	31.4	15.2
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	RTDKVYYHHTGHIGGIK	1982.0	K	Q	3.5	0.0	32.3	16.2
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	TFTAKPETVK	1121.6	K	R	2.4	0.8	23.0	16.0
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	TFTAKPETVKR	1277.7	K	D	5.6	0.7	40.8	14.9
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	VIEIAVK	771.5	R	G	1.9	0.2	25.2	13.0
P0AA10	16000.7	S	U	T	C	ETD	LIT	14	80.3	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	7.0	0.4	53.4	17.6
P0AA10	16000.7	S	U	T	A	ETD	FT	6	38.7	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	4.5	0.0	38.5	18.6
P0AA10	16000.7	S	U	T	A	ETD	FT	6	38.7	RDWYVVDATGK	1309.7	K	T	3.0	0.0	23.7	14.9
P0AA10	16000.7	S	U	T	A	ETD	FT	6	38.7	TFTAKPETVK	1121.6	K	R	1.4	0.0	16.6	16.0
P0AA10	16000.7	S	U	T	A	ETD	FT	6	38.7	TFTAKPETVKR	1277.7	K	D	2.4	0.0	46.0	14.9
P0AA10	16000.7	S	U	T	A	ETD	FT	6	38.7	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.3	0.4	20.7	17.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	S	U	T	A	ETD	FT	6	38.7	VYYHHTGHIGGIK	1481.8	K	Q	5.5	0.7	55.2	15.8
P0AA10	16000.7	S	U	T	B	ETD	FT	3	22.5	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	5.3	0.0	41.8	18.6
P0AA10	16000.7	S	U	T	B	ETD	FT	3	22.5	RDWYVVDATGK	1309.7	K	T	2.6	0.0	34.1	15.2
P0AA10	16000.7	S	U	T	B	ETD	FT	3	22.5	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.8	0.3	39.2	17.7
P0AA10	16000.7	S	U	T	C	ETD	FT	4	34.5	MKTFTAKPETVKR	1536.9	-	D	5.0	0.0	54.3	15.1
P0AA10	16000.7	S	U	T	C	ETD	FT	4	34.5	RDWYVVDATGK	1309.7	K	T	2.0	0.0	16.0	15.1
P0AA10	16000.7	S	U	T	C	ETD	FT	4	34.5	VIEIAVK	771.5	R	G	1.3	0.0	22.0	13.0
P0AA10	16000.7	S	U	T	C	ETD	FT	4	34.5	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	1.6	0.0	43.9	17.9
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	5	41.5	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	0.0	0.0	22.4	18.5
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	5	41.5	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	0.0	0.0	57.2	18.7
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	5	41.5	MKTFTAKPETVKR	1536.9	-	D	0.0	0.0	81.2	14.1
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	5	41.5	RTDKVYYHHTGHIGGIK	1982.0	K	Q	0.0	0.0	24.8	15.3
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	5	41.5	TFTAKPETVKR	1277.7	K	D	0.0	0.0	57.2	15.1
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	0.0	0.0	69.3	18.8
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	0.0	0.0	72.2	18.6
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	0.0	0.0	34.4	18.6
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	DWYVVDATGK	1153.6	R	T	0.0	0.0	31.0	14.5
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	0.0	0.0	57.2	18.7
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	0.0	0.0	32.3	18.8
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	MKTFTAKPETVKR	1536.9	-	D	0.0	0.0	81.2	14.1
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	QATFEEMIAR	1195.6	K	R	0.0	0.0	50.2	15.8
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	RTDKVYYHHTGHIGGIK	1982.0	K	Q	0.0	0.0	24.8	15.3
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	TFTAKPETVK	1121.6	K	R	0.0	0.0	32.4	14.9
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	TFTAKPETVKR	1277.7	K	D	0.0	0.0	57.2	15.1
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	0.0	0.0	45.4	17.4
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	VYYHHTGHIGGIK	1481.8	K	Q	0.0	0.0	29.7	16.7
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	6.4	0.7	104.0	19.0
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	5.1	0.0	50.6	18.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	3.0	0.8	0.0	0.0
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	DWYVVDATGK	1153.6	R	T	3.4	0.5	0.0	0.0
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	5.0	0.6	56.7	18.9
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	0.0	0.0	50.2	17.7
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.7	0.6	40.0	18.9
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	MKTFTAKPETVKR	1536.9	-	D	6.1	0.9	71.9	13.2
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	QATFEEMIAR	1195.6	K	R	3.1	0.6	72.7	14.9
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	RDWYVVDATGK	1309.7	K	T	4.1	0.8	58.5	15.7
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	RTDKVYYHHTGHIGGIK	1982.0	K	Q	3.1	0.7	0.0	0.0
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	TDKVYYHHTGHIGGIK	1825.9	R	Q	2.3	0.7	2.9	16.4
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	TFTAKPETVK	1121.6	K	R	2.6	0.4	27.2	14.9
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	TFTAKPETVKR	1277.7	K	D	5.7	0.7	55.3	15.9
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.0	0.7	0.0	0.0
P0AA10	16000.7	S	U	T	A	ETD+CID	LIT	16	70.4	VYYHHTGHIGGIK	1481.8	K	Q	2.2	0.7	15.1	16.7
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	4	28.2	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	4.7	0.6	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	4	28.2	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	4.2	0.6	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	4	28.2	DWYVVDATGK	1153.6	R	T	3.1	0.5	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	4	28.2	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	4.6	0.5	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	5.0	0.6	69.3	18.8
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	6.5	0.0	72.2	18.6
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	4.2	0.6	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	DWYVVDATGK	1153.6	R	T	3.1	0.5	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	4.6	0.5	48.6	19.1
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.5	0.0	32.3	18.8
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	MKTFTAKPETVKR	1536.9	-	D	5.6	0.7	81.2	14.1
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	QATFEEMIAR	1195.6	K	R	2.7	0.6	50.2	15.8
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	RTDKVYYHHTGHIGGIK	1982.0	K	Q	2.9	0.3	0.0	0.0
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	TFTAKPETVK	1121.6	K	R	2.8	0.4	32.4	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	TFTAKPETVKR	1277.7	K	D	5.9	0.9	57.2	15.1
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.2	0.8	45.4	17.4
P0AA10	16000.7	S	U	T	B	ETD+CID	LIT	13	70.4	VYYHHTGHIGGIK	1481.8	K	Q	1.7	0.5	29.7	16.7
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	5.7	0.7	69.7	18.6
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	7.0	0.7	73.8	18.6
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	3.0	0.8	0.0	0.0
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	DWYVVDATGK	1153.6	R	T	2.4	0.1	0.0	0.0
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	8.1	0.0	81.3	18.9
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	HKAEYTPHVDTGDYIIVLNADKVAVTGNK	3168.6	K	R	5.8	0.0	32.5	17.6
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	3.4	0.6	38.3	18.6
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	MKTFTAKPETVKR	1536.9	-	D	5.8	0.9	75.4	14.1
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	QATFEEMIAR	1195.6	K	R	2.9	0.4	42.1	15.4
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	RDWYVVDATGK	1309.7	K	T	4.1	0.6	57.7	15.2
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	RTDKVYYHHTGHIGGIK	1982.0	K	Q	2.9	0.7	8.8	15.3
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	TDKVYYHHTGHIGGIK	1825.9	R	Q	2.7	0.5	0.0	0.0
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	TFTAKPETVK	1121.6	K	R	2.7	0.5	31.1	14.9
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	TFTAKPETVKR	1277.7	K	D	3.0	0.0	36.4	15.4
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	VIEIAVK	771.5	R	G	2.5	0.3	26.5	13.0
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.4	0.6	43.9	17.4
P0AA10	16000.7	S	U	T	C	ETD+CID	LIT	17	75.4	VYYHHTGHIGGIK	1481.8	K	Q	1.7	0.7	16.3	16.8
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	AEYTPHVDTGDYIIVLNADK	2234.1	K	V	0.0	0.0	69.3	18.8
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	AEYTPHVDTGDYIIVLNADKVAVTGNK	2903.5	K	R	0.0	0.0	72.2	18.6
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	AEYTPHVDTGDYIIVLNADKVAVTGNKR	3059.6	K	T	0.0	0.0	34.4	18.6
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	DWYVVDATGK	1153.6	R	T	0.0	0.0	31.0	14.5
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	HKAEYTPHVDTGDYIIVLNADK	2499.3	K	V	0.0	0.0	48.6	19.1
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	LKVYAGNEHNHAAQQPQVLDI	2345.2	K	-	0.0	0.0	32.3	18.8
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	MKTFTAKPETVKR	1536.9	-	D	0.0	0.0	60.4	13.2
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	QATFEEMIAR	1195.6	K	R	0.0	0.0	50.2	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	TFTAKPETVK	1121.6	K	R	0.0	0.0	32.4	14.9
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	TFTAKPETVKR	1277.7	K	D	0.0	0.0	32.7	15.9
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	0.0	0.0	45.4	17.4
P0AA10	16000.7	S	U	T	B	HCD	FT	12	68.3	VYYHHTGHIGGIK	1481.8	K	Q	0.0	0.0	29.7	16.7
P0AA10	16000.7	S	U	T	B	HCD	FT	2	21.1	RDWYVVDATGK	1309.7	K	T	3.2	0.7	50.4	15.1
P0AA10	16000.7	S	U	T	B	HCD	FT	2	21.1	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	3.2	0.0	21.2	18.1
P0AA10	16000.7	S	U	T	C	HCD	FT	2	21.1	RDWYVVDATGK	1309.7	K	T	3.1	0.0	47.7	15.4
P0AA10	16000.7	S	U	T	C	HCD	FT	2	21.1	VYAGNEHNHAAQQPQVLDI	2104.0	K	-	2.8	0.0	21.7	17.5
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	ATVTGDGLSQEAK	1276.6	K	E	4.3	0.8	88.3	13.0
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	ATVTGDGLSQEAKEK	1533.8	K	I	4.3	0.7	81.1	12.8
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	IFEANKPMLK	1206.7	K	S	3.2	0.5	29.5	12.0
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	ILVAVGNISGIASVDDQVK	1898.1	K	T	6.6	0.0	95.5	8.5
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	IYPGQVLR	945.6	K	I	1.8	0.6	20.4	14.6
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	KVQEHLNK	995.6	K	T	3.0	0.4	30.1	9.0
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	LWDAVTGQHDKDDQAK	1826.9	K	K	3.3	0.9	17.5	10.8
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	QVYGNANLYNK	1283.6	K	I	3.2	0.0	28.4	10.0
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	SGDTLSAISK	978.5	K	Q	2.3	0.7	16.4	11.8
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	SPDKIYPGQVLR	1372.8	K	I	3.7	0.7	60.2	13.0
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	TATPATASQFYTVK	1485.8	K	S	3.9	0.8	61.6	13.2
P0ADE6	16045.4	G	U	T	A	CID	LIT	12	88.6	TGIPDADKVNIQIADGK	1754.9	K	A	4.6	0.6	50.2	12.8
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	ATVTGDGLSQEAK	1276.6	K	E	3.8	0.8	72.6	13.0
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	ATVTGDGLSQEAKEK	1533.8	K	I	3.6	0.7	44.5	13.2
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	IFEANKPMLK	1190.7	K	S	2.4	0.5	15.8	13.4
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	ILVAVGNISGIASVDDQVK	1898.1	K	T	6.6	0.0	86.4	9.5
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	IYPGQVLR	945.6	K	I	1.7	0.6	8.3	12.8
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	KVQEHLNK	995.6	K	T	2.3	0.4	11.9	9.0
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	SGDTLSAISK	978.5	K	Q	3.3	0.7	45.8	11.1
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	SPDKIYPGQVLR	1372.8	K	I	4.3	0.7	60.9	12.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	TATPATASQFYTVK	1485.8	K	S	4.3	0.8	80.8	13.6
P0ADE6	16045.4	G	T	T	A	CID	LIT	10	70.5	TGIPDADKVNIQIADGK	1754.9	K	A	4.5	0.6	39.1	12.3
P0ADE6	16045.4	G	U	A	A	CID	LIT	7	57.0	DAGEKLW	818.4	K	D	2.5	0.4	34.8	15.2
P0ADE6	16045.4	G	U	A	A	CID	LIT	7	57.0	DAVTGQHDKD	1085.5	W	D	2.4	0.7	10.3	14.0
P0ADE6	16045.4	G	U	A	A	CID	LIT	7	57.0	DKIYPGQVLRIPEE	1656.9	P	-	3.8	0.6	29.0	13.8
P0ADE6	16045.4	G	U	A	A	CID	LIT	7	57.0	DKVNIQIA	900.5	A	D	2.5	0.1	28.0	15.7
P0ADE6	16045.4	G	U	A	A	CID	LIT	7	57.0	DKVNIQIADGKATVTG	1629.9	A	D	3.9	0.5	26.0	13.4
P0ADE6	16045.4	G	U	A	A	CID	LIT	7	57.0	DQAKKVQEHLNKTGIPDA	1992.1	D	D	4.3	0.6	40.2	16.3
P0ADE6	16045.4	G	U	A	A	CID	LIT	7	57.0	DQVKTATPATASQFYTVKSG	2100.1	D	D	2.4	0.8	3.0	15.4
P0ADE6	16045.4	G	T	A	A	CID	LIT	2	18.8	DKVNIQIA	900.5	A	D	1.8	0.6	11.2	15.8
P0ADE6	16045.4	G	T	A	A	CID	LIT	2	18.8	DQVKTATPATASQFYTVKSG	2100.1	D	D	4.9	0.6	63.6	15.8
P0ADE6	16045.4	G	U	A	B	CID	LIT	3	23.5	DAGEKLW	818.4	K	D	1.8	0.5	10.2	15.2
P0ADE6	16045.4	G	U	A	B	CID	LIT	3	23.5	DKVNIQIA	900.5	A	D	2.1	0.0	16.5	15.8
P0ADE6	16045.4	G	U	A	B	CID	LIT	3	23.5	DQVKTATPATASQFYTVKSG	2100.1	D	D	5.1	0.8	51.3	15.8
P0ADE6	16045.4	S	U	T	A	CID	LIT	7	64.4	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	5.2	0.4	33.9	16.9
P0ADE6	16045.4	S	U	T	A	CID	LIT	7	64.4	IFEANKPMLK	1190.7	K	S	2.6	0.4	13.5	15.9
P0ADE6	16045.4	S	U	T	A	CID	LIT	7	64.4	ILVAVGNISGIASVDDQVK	1898.1	K	T	5.4	0.7	62.2	15.9
P0ADE6	16045.4	S	U	T	A	CID	LIT	7	64.4	IYPGQVLR	945.6	K	I	1.5	0.7	13.4	13.8
P0ADE6	16045.4	S	U	T	A	CID	LIT	7	64.4	SPDKIYPGQVLRIPEE	1841.0	K	-	4.5	0.8	49.1	16.3
P0ADE6	16045.4	S	U	T	A	CID	LIT	7	64.4	TGIPDADKVNIQIADGK	1754.9	K	A	4.3	0.5	39.0	17.2
P0ADE6	16045.4	S	U	T	A	CID	LIT	7	64.4	TGIPDADKVNIQIADGKATVTGDGLSQEAK	3012.5	K	E	3.8	0.4	11.8	18.6
P0ADE6	16045.4	S	U	T	B	CID	LIT	3	38.3	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	3.2	0.8	32.0	16.5
P0ADE6	16045.4	S	U	T	B	CID	LIT	3	38.3	ILVAVGNISGIASVDDQVK	1898.1	K	T	4.1	0.5	25.7	15.9
P0ADE6	16045.4	S	U	T	B	CID	LIT	3	38.3	TGIPDADKVNIQIADGK	1754.9	K	A	4.5	0.6	40.9	17.2
P0ADE6	16045.4	S	U	T	C	CID	LIT	7	50.3	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	3.6	0.6	29.4	16.3
P0ADE6	16045.4	S	U	T	C	CID	LIT	7	50.3	IFEANKPMLK	1190.7	K	S	2.4	0.4	23.5	15.3
P0ADE6	16045.4	S	U	T	C	CID	LIT	7	50.3	LWDAVTGQHDKDDQAK	1826.9	K	K	5.5	0.6	56.6	15.4
P0ADE6	16045.4	S	U	T	C	CID	LIT	7	50.3	QVYGNANLYNK	1283.6	K	I	3.0	0.4	37.4	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADE6	16045.4	S	U	T	C	CID	LIT	7	50.3	SPDKIYPGQVLR	1372.8	K	I	3.2	0.6	23.6	15.6
P0ADE6	16045.4	S	U	T	C	CID	LIT	7	50.3	SPDKIYPGQVLRIPEE	1841.0	K	-	3.1	0.6	14.9	16.4
P0ADE6	16045.4	S	U	T	C	CID	LIT	7	50.3	TGIPDADKVNIQIADGK	1754.9	K	A	4.6	0.6	45.8	17.0
P0ADE6	16045.4	S	U	T	A	CID	FT	3	34.2	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	4.0	0.0	32.5	16.6
P0ADE6	16045.4	S	U	T	A	CID	FT	3	34.2	SPDKIYPGQVLRIPEE	1841.0	K	-	2.5	0.0	35.9	16.3
P0ADE6	16045.4	S	U	T	A	CID	FT	3	34.2	TATPATASQFYTVK	1485.8	K	S	1.3	0.0	30.8	18.0
P0ADE6	16045.4	S	U	T	A	ETD	LIT	6	49.0	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	4.2	0.6	23.5	16.7
P0ADE6	16045.4	S	U	T	A	ETD	LIT	6	49.0	ILVAVGNISGIASVDDQVK	1898.1	K	T	0.0	0.0	30.3	15.7
P0ADE6	16045.4	S	U	T	A	ETD	LIT	6	49.0	LWDAVTGQHDKDDQAK	1826.9	K	K	2.8	0.7	45.0	16.1
P0ADE6	16045.4	S	U	T	A	ETD	LIT	6	49.0	SPDKIYPGQVLR	1372.8	K	I	3.0	0.3	8.0	16.2
P0ADE6	16045.4	S	U	T	A	ETD	LIT	6	49.0	SPDKIYPGQVLRIPEE	1841.0	K	-	4.9	0.4	64.9	16.8
P0ADE6	16045.4	S	U	T	A	ETD	LIT	6	49.0	TGIPDADKVNIQIADGK	1754.9	K	A	6.5	0.5	52.6	18.1
P0ADE6	16045.4	S	U	T	B	ETD	LIT	6	57.0	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	0.0	0.0	79.1	16.6
P0ADE6	16045.4	S	U	T	B	ETD	LIT	6	57.0	IFEANKPMLK	1190.7	K	S	1.9	0.1	16.8	16.6
P0ADE6	16045.4	S	U	T	B	ETD	LIT	6	57.0	QVYGNANLYNK	1283.6	K	I	2.1	0.3	15.8	14.0
P0ADE6	16045.4	S	U	T	B	ETD	LIT	6	57.0	SPDKIYPGQVLR	1372.8	K	I	4.4	0.5	45.2	16.2
P0ADE6	16045.4	S	U	T	B	ETD	LIT	6	57.0	TATPATASQFYTVK	1485.8	K	S	1.9	0.4	27.6	16.5
P0ADE6	16045.4	S	U	T	B	ETD	LIT	6	57.0	TGIPDADKVNIQIADGK	1754.9	K	A	3.9	0.5	47.2	17.0
P0ADE6	16045.4	S	U	T	C	ETD	LIT	6	59.1	ATVTGDGLSQEAK	1276.6	K	E	2.0	0.5	16.9	16.8
P0ADE6	16045.4	S	U	T	C	ETD	LIT	6	59.1	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	6.9	0.0	68.0	16.6
P0ADE6	16045.4	S	U	T	C	ETD	LIT	6	59.1	QVYGNANLYNK	1283.6	K	I	2.0	0.4	16.1	14.0
P0ADE6	16045.4	S	U	T	C	ETD	LIT	6	59.1	SPDKIYPGQVLR	1372.8	K	I	4.7	0.4	40.1	16.1
P0ADE6	16045.4	S	U	T	C	ETD	LIT	6	59.1	TATPATASQFYTVK	1485.8	K	S	2.2	0.4	37.7	17.4
P0ADE6	16045.4	S	U	T	C	ETD	LIT	6	59.1	TGIPDADKVNIQIADGK	1754.9	K	A	2.5	0.4	37.8	16.9
P0ADE6	16045.4	S	U	T	B	ETD+CID	LIT	3	38.3	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	0.0	0.0	21.1	16.4
P0ADE6	16045.4	S	U	T	B	ETD+CID	LIT	3	38.3	ILVAVGNISGIASVDDQVK	1898.1	K	T	0.0	0.0	27.4	15.7
P0ADE6	16045.4	S	U	T	B	ETD+CID	LIT	3	38.3	TGIPDADKVNIQIADGK	1754.9	K	A	0.0	0.0	49.2	17.4
P0ADE6	16045.4	S	U	T	A	ETD+CID	LIT	5	57.7	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	5.7	0.6	67.4	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADE6	16045.4	S	U	T	A	ETD+CID	LIT	5	57.7	ILVAVGNISGIASVDDQVK	1898.1	K	T	5.5	0.7	62.1	15.9
P0ADE6	16045.4	S	U	T	A	ETD+CID	LIT	5	57.7	SPDKIYPGQVLRIPEE	1841.0	K	-	4.7	0.7	56.2	16.3
P0ADE6	16045.4	S	U	T	A	ETD+CID	LIT	5	57.7	TGIPDADKVNIQIADGK	1754.9	K	A	4.6	0.5	32.4	16.9
P0ADE6	16045.4	S	U	T	A	ETD+CID	LIT	5	57.7	TGIPDADKVNIQIADGKATVTGDGLSQEAK	3012.5	K	E	4.4	0.6	17.5	19.7
P0ADE6	16045.4	S	U	T	B	ETD+CID	LIT	3	38.3	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	2.9	0.7	21.1	16.4
P0ADE6	16045.4	S	U	T	B	ETD+CID	LIT	3	38.3	ILVAVGNISGIASVDDQVK	1898.1	K	T	4.9	0.6	27.4	15.7
P0ADE6	16045.4	S	U	T	B	ETD+CID	LIT	3	38.3	TGIPDADKVNIQIADGK	1754.9	K	A	4.6	0.5	49.2	17.4
P0ADE6	16045.4	S	U	T	C	ETD+CID	LIT	4	40.3	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	5.0	0.5	51.5	17.1
P0ADE6	16045.4	S	U	T	C	ETD+CID	LIT	4	40.3	IFEANKPMLK	1190.7	K	S	2.7	0.3	25.9	15.3
P0ADE6	16045.4	S	U	T	C	ETD+CID	LIT	4	40.3	SPDKIYPGQVLR	1372.8	K	I	3.8	0.5	36.6	15.6
P0ADE6	16045.4	S	U	T	C	ETD+CID	LIT	4	40.3	TGIPDADKVNIQIADGK	1754.9	K	A	4.0	0.4	34.8	17.4
P0ADE6	16045.4	S	U	T	B	HCD	FT	3	38.3	DAGEKLWDAVTGQHDKDDQAK	2327.1	K	K	0.0	0.0	21.1	16.4
P0ADE6	16045.4	S	U	T	B	HCD	FT	3	38.3	ILVAVGNISGIASVDDQVK	1898.1	K	T	0.0	0.0	27.4	15.7
P0ADE6	16045.4	S	U	T	B	HCD	FT	3	38.3	TGIPDADKVNIQIADGK	1754.9	K	A	0.0	0.0	49.2	17.4
P0AED0	16048.5	G	U	T	A	CID	LIT	6	45.1	AVSMARPYNAK	1223.6	K	V	2.9	0.8	45.4	12.0
P0AED0	16048.5	G	U	T	A	CID	LIT	6	45.1	AYKHILIAVDLSPESK	1784.0	M	V	0.0	0.0	57.0	10.8
P0AED0	16048.5	G	U	T	A	CID	LIT	6	45.1	HILIAVDLSPESK	1421.8	K	V	4.5	0.6	87.2	8.5
P0AED0	16048.5	G	U	T	A	CID	LIT	6	45.1	KYDMDLVVCGHHQDFWSK	2265.0	K	L	4.8	0.0	59.1	7.8
P0AED0	16048.5	G	U	T	A	CID	LIT	6	45.1	QLINTVHVDMLIVPLRDEEE	2363.2	R	-	4.7	0.6	26.9	12.3
P0AED0	16048.5	G	U	T	A	CID	LIT	6	45.1	YDMDLVVCGHHQDFWSK	2136.9	K	L	3.1	0.0	21.8	6.0
P0AED0	16048.5	G	T	T	A	CID	LIT	2	16.7	AVSMARPYNAK	1223.6	K	V	2.0	0.5	15.0	12.6
P0AED0	16048.5	G	T	T	A	CID	LIT	2	16.7	HILIAVDLSPESK	1421.8	K	V	4.3	0.6	70.4	8.5
P0AED0	16048.5	G	U	A	A	CID	LIT	7	23.6	AYKHILIAV	1027.6	M	D	0.0	0.0	24.8	9.0
P0AED0	16048.5	G	U	A	A	CID	LIT	7	23.6	DAIKKY	737.4	V	D	1.5	0.7	10.6	9.0
P0AED0	16048.5	G	U	A	A	CID	LIT	7	23.6	DAIKKYDM	983.5	V	D	2.3	0.7	27.2	13.6
P0AED0	16048.5	G	U	A	A	CID	LIT	7	23.6	DAIKKYDMDLVVCGHHQ	2029.0	V	D	3.0	0.4	0.0	0.0
P0AED0	16048.5	G	U	A	A	CID	LIT	7	23.6	DLVVCGHHQ	1064.5	M	D	2.5	0.7	28.4	16.5
P0AED0	16048.5	G	U	A	A	CID	LIT	7	23.6	DMDLVVCGHHQ	1310.6	Y	D	3.5	0.7	34.8	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AED0	16048.5	G	U	A	A	CID	LIT	7	23.6	DMLIVPLR	972.6	V	D	2.6	0.7	25.0	14.5
P0AED0	16048.5	G	T	T	B	CID	LIT	2	11.1	AVSMARPYNAK	1207.6	K	V	3.7	0.4	32.7	14.8
P0AED0	16048.5	G	T	T	B	CID	LIT	2	11.1	VLVEKAVSMARPYNAK	1776.0	K	V	2.9	0.5	19.6	10.0
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	AYKHILIAV	1027.6	M	D	0.0	0.0	25.2	9.0
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	DAIKKY	737.4	V	D	1.5	0.7	19.4	9.0
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	DLGQVLV	743.4	G	D	2.1	0.1	32.0	17.1
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	DLSPESKVLV	1086.6	V	E	2.3	0.5	15.4	15.8
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	DLSPESKVLVEKAVSMARPYNAKVSLIHV	3180.7	V	D	3.6	0.0	29.1	12.6
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	DLVVCGHHQ	1064.5	M	D	2.8	0.7	28.6	16.5
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	DMLIVPLR	956.6	V	D	2.0	0.7	19.1	10.8
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	DMQKRISEETHHALT	1795.9	G	E	2.9	0.5	16.1	15.6
P0AED0	16048.5	G	T	A	B	CID	LIT	9	70.1	ELSTNAGYPITETLSGSG	1796.9	T	D	3.0	0.0	42.5	13.8
P0AED0	16048.5	G	U	A	B	CID	LIT	4	34.7	DLVVCGHHQ	1064.5	M	D	2.5	0.5	19.4	16.5
P0AED0	16048.5	G	U	A	B	CID	LIT	4	34.7	DMLIVPLR	972.6	V	D	2.1	0.6	20.1	14.5
P0AED0	16048.5	G	U	A	B	CID	LIT	4	34.7	DMQKRISEETHHALT	1795.9	G	E	2.6	0.6	16.0	15.2
P0AED0	16048.5	G	U	A	B	CID	LIT	4	34.7	ELSTNAGYPITETLSGSG	1796.9	T	D	3.3	0.0	39.6	13.8
P0AED0	16048.5	S	U	T	B	CID	LIT	3	30.6	AVSMARPYNAK	1207.6	K	V	3.0	0.3	22.0	16.3
P0AED0	16048.5	S	U	T	B	CID	LIT	3	30.6	HILIAVDLSPESK	1421.8	K	V	3.6	0.5	39.9	13.6
P0AED0	16048.5	S	U	T	B	CID	LIT	3	30.6	QLINTVHVDMLIVPLRDEEE	2363.2	R	-	3.3	0.2	0.0	0.0
P0AED0	16048.5	S	U	T	C	CID	LIT	3	30.6	AVSMARPYNAK	1207.6	K	V	3.1	0.4	40.6	15.1
P0AED0	16048.5	S	U	T	C	CID	LIT	3	30.6	HILIAVDLSPESK	1421.8	K	V	4.1	0.5	63.1	12.3
P0AED0	16048.5	S	U	T	C	CID	LIT	3	30.6	QLINTVHVDMLIVPLRDEEE	2363.2	R	-	3.5	0.5	9.4	18.5
P0AED0	16048.5	S	U	T	A	ETD	LIT	2	16.7	AVSMARPYNAK	1207.6	K	V	2.6	0.6	22.1	17.3
P0AED0	16048.5	S	U	T	A	ETD	LIT	2	16.7	HILIAVDLSPESK	1421.8	K	V	2.2	0.5	13.8	13.6
P0AED0	16048.5	S	U	T	B	ETD	LIT	2	36.1	HILIAVDLSPESK	1421.8	K	V	2.2	0.5	19.7	14.9
P0AED0	16048.5	S	U	T	B	ETD	LIT	2	36.1	ISEETHHALTELSTNAGYPITETLSGSGDLGQVLVDAIK	4067.0	R	K	0.0	0.0	18.3	16.5
P0AED0	16048.5	S	U	T	B	ETD+CID	LIT	3	29.2	AVSMARPYNAK	1207.6	K	V	0.0	0.0	35.6	16.9
P0AED0	16048.5	S	U	T	B	ETD+CID	LIT	3	29.2	HILIAVDLSPESK	1421.8	K	V	0.0	0.0	39.2	13.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AED0	16048.5	S	U	T	B	ETD+CID	LIT	3	29.2	KYDMDLVVCGHHQDFWSK	2265.0	K	L	0.0	0.0	22.8	14.1
P0AED0	16048.5	S	U	T	B	ETD+CID	LIT	4	43.1	AVSMARPYNAK	1207.6	K	V	3.4	0.3	35.6	16.9
P0AED0	16048.5	S	U	T	B	ETD+CID	LIT	4	43.1	HILIAVDLSPESK	1421.8	K	V	4.0	0.4	0.0	0.0
P0AED0	16048.5	S	U	T	B	ETD+CID	LIT	4	43.1	KYDMDLVVCGHHQDFWSK	2265.0	K	L	0.7	-0.8	22.8	14.1
P0AED0	16048.5	S	U	T	B	ETD+CID	LIT	4	43.1	QLINTVHVDMLIVPLRDEEE	2363.2	R	-	2.7	0.3	10.7	18.5
P0AED0	16048.5	S	U	T	C	ETD+CID	LIT	2	9.0	HILIAVDLSPESK	1421.8	K	V	3.1	0.5	0.0	0.0
P0AED0	16048.5	S	U	T	B	HCD	FT	2	16.7	AVSMARPYNAK	1207.6	K	V	0.0	0.0	35.6	16.9
P0AED0	16048.5	S	U	T	B	HCD	FT	2	16.7	HILIAVDLSPESK	1421.8	K	V	0.0	0.0	39.2	13.6
P0AEM0	16063.5	G	U	T	A	CID	LIT	2	19.5	LDDGTTAESTR	1165.5	K	N	3.2	0.6	50.6	10.8
P0AEM0	16063.5	G	U	T	A	CID	LIT	2	19.5	LGDASLSEGLEQHLLGLK	1880.0	R	V	3.6	0.0	34.4	10.4
P0AEM0	16063.5	G	T	A	B	CID	LIT	2	20.8	DASLSEGLEQHLLGLKVG	1866.0	G	D	4.0	0.5	35.6	13.6
P0AEM0	16063.5	G	T	A	B	CID	LIT	2	20.8	DFNHPLAGQTVHF	1482.7	V	D	2.5	0.8	8.3	16.5
P0AEM0	16063.5	G	U	A	B	CID	LIT	2	21.5	DASLSEGLEQHLLGLKVG	1866.0	G	D	3.6	0.7	26.1	13.4
P0AEM0	16063.5	G	U	A	B	CID	LIT	2	21.5	DGSEMPGVIREING	1473.7	M	D	3.1	0.7	26.3	12.6
P0AEM0	16063.5	S	U	T	C	CID	LIT	2	19.5	LDDGTTAESTR	1165.5	K	N	3.1	0.6	54.1	13.6
P0AEM0	16063.5	S	U	T	C	CID	LIT	2	19.5	LGDASLSEGLEQHLLGLK	1880.0	R	V	2.6	0.5	24.6	16.2
P0AEM0	16063.5	S	U	T	B	ETD	LIT	2	19.5	LDDGTTAESTR	1165.5	K	N	1.4	0.0	32.9	13.6
P0AEM0	16063.5	S	U	T	B	ETD	LIT	2	19.5	LGDASLSEGLEQHLLGLK	1880.0	R	V	7.0	0.0	74.0	16.2
P0AEM0	16063.5	S	U	T	C	ETD	LIT	2	19.5	LDDGTTAESTR	1165.5	K	N	1.8	0.0	30.2	13.6
P0AEM0	16063.5	S	U	T	C	ETD	LIT	2	19.5	LGDASLSEGLEQHLLGLK	1880.0	R	V	6.8	0.7	83.3	16.2
P0AEM0	16063.5	S	U	T	C	ETD+CID	LIT	2	19.5	LDDGTTAESTR	1165.5	K	N	2.7	0.4	39.0	13.0
P0AEM0	16063.5	S	U	T	C	ETD+CID	LIT	2	19.5	LGDASLSEGLEQHLLGLK	1880.0	R	V	3.2	0.5	34.4	17.0
P06968	16137.8	G	U	A	A	CID	LIT	5	43.7	DATDRGEGGFGHSGRQ	1646.7	F	-	3.5	0.7	32.5	10.8
P06968	16137.8	G	U	A	A	CID	LIT	5	43.7	DAVELAPGDTTLVPTGLAIHIA	2174.2	N	D	3.7	0.0	21.4	16.0
P06968	16137.8	G	U	A	A	CID	LIT	5	43.7	DLRACLN	861.4	L	D	2.4	0.5	35.5	15.9
P06968	16137.8	G	U	A	A	CID	LIT	5	43.7	DPRVGKEFPLPTYATSGSAGL	2163.1	L	D	2.8	0.4	13.4	15.1
P06968	16137.8	G	U	A	A	CID	LIT	5	43.7	DRGEGGFGHSGRQ	1359.6	T	-	2.8	0.6	57.4	10.0
P06968	16137.8	G	T	A	B	CID	LIT	2	28.5	DAVELAPGDTTLVPTGLAIHIA	2174.2	N	D	2.8	0.7	35.3	16.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P06968	16137.8	G	T	A	B	CID	LIT	2	28.5	DPRVGKEFPLPTYATSGSAGL	2163.1	L	D	2.3	0.7	21.5	15.1
P06968	16137.8	G	U	A	B	CID	LIT	2	14.6	DAVELAPGDTTLVPTGLAIHIA	2174.2	N	D	2.7	0.2	1.5	15.4
P06968	16137.8	G	U	A	B	CID	LIT	2	14.6	DTTLVPTGLAIHIA	1421.8	G	D	2.3	0.4	13.9	9.5
P06968	16137.8	S	U	T	A	CID	LIT	2	13.9	EFPLPTYATSGSAGLDLR	1895.0	K	A	4.3	0.6	37.7	18.6
P06968	16137.8	S	U	T	A	CID	LIT	2	13.9	VGKEFPLPTYATSGSAGLDLR	2179.1	R	A	2.2	0.3	15.3	18.4
P61714	16138.9	G	U	T	A	CID	LIT	6	48.1	AGNKGAEAALTALEMINVLK	2014.1	K	A	6.7	0.7	106.0	11.5
P61714	16138.9	G	U	T	A	CID	LIT	6	48.1	FNNFINDSLLEGAIDALKR	2150.1	R	I	3.7	0.0	45.1	12.6
P61714	16138.9	G	U	T	A	CID	LIT	6	48.1	GAEAALTALEMINVLK	1643.9	K	A	4.4	0.7	84.4	10.4
P61714	16138.9	G	U	T	A	CID	LIT	6	48.1	MNIIEANVATPDAR	1514.8	-	V	4.1	0.5	70.2	11.1
P61714	16138.9	G	U	T	A	CID	LIT	6	48.1	TGKYDAVIALGTVIR	1576.9	K	G	3.8	0.5	34.8	7.8
P61714	16138.9	G	U	T	A	CID	LIT	6	48.1	VAITIAR	743.5	R	F	2.2	0.6	29.0	15.3
P61714	16138.9	S	U	T	A	CID	LIT	2	12.2	FNNFINDSLLEGAIDALK	1994.0	R	R	4.1	0.5	27.1	17.9
P61714	16138.9	S	U	T	A	CID	LIT	2	12.2	FNNFINDSLLEGAIDALKR	2151.1	R	I	4.6	0.7	24.0	17.9
P61714	16138.9	S	U	T	C	ETD	LIT	2	22.4	FNNFINDSLLEGAIDALKR	2150.1	R	I	4.0	0.6	51.9	17.3
P61714	16138.9	S	U	T	C	ETD	LIT	2	22.4	GAEAALTALEMINVLK	1643.9	K	A	3.4	0.3	41.6	17.2
P16681	16153.6	G	T	T	A	CID	LIT	7	68.7	ASYSGFTLVLDSQQVEEGKR	2214.1	K	W	5.1	0.9	70.5	13.6
P16681	16153.6	G	T	T	A	CID	LIT	7	68.7	FGVPWMINVVK	1305.7	K	Q	1.8	0.5	7.3	13.2
P16681	16153.6	G	T	T	A	CID	LIT	7	68.7	IAGSDIMMSDAMPSGK	1658.7	R	A	3.1	0.0	61.0	3.0
P16681	16153.6	G	T	T	A	CID	LIT	7	68.7	IEMAWQETFWAHGFGK	1953.9	K	V	4.2	0.0	17.8	7.8
P16681	16153.6	G	T	T	A	CID	LIT	7	68.7	ISFGEMPK	908.5	K	S	2.4	0.0	39.2	10.4
P16681	16153.6	G	T	T	A	CID	LIT	7	68.7	SAQDSAENCPSGMQFPDTAIAHANVR	2774.2	K	I	4.3	0.0	71.4	7.0
P16681	16153.6	G	T	T	A	CID	LIT	7	68.7	VTDKFGVPWMINVVK	1732.9	K	Q	4.2	0.6	34.8	11.1
P16681	16153.6	G	T	A	A	CID	LIT	6	50.3	DAMPSGKASYSGFTLVL	1759.9	S	D	2.6	0.5	17.0	15.7
P16681	16153.6	G	T	A	A	CID	LIT	6	50.3	DKFGVPWMINVVKQQPTQ	2115.1	T	-	3.2	0.0	14.9	14.6
P16681	16153.6	G	T	A	A	CID	LIT	6	50.3	DSAENCPSGMQFP	1455.6	Q	D	2.7	0.5	31.8	3.0
P16681	16153.6	G	T	A	A	CID	LIT	6	50.3	DSAENCPSGMQFPDTAIAHANVRIAGS	2832.3	Q	D	3.1	0.0	37.1	8.5
P16681	16153.6	G	T	A	A	CID	LIT	6	50.3	DSQQVEEGKRWF	1508.7	L	D	2.3	0.3	19.9	14.6
P16681	16153.6	G	T	A	A	CID	LIT	6	50.3	DTAIAHANVRIAGS	1395.7	P	D	2.7	0.4	24.7	13.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P16681	16153.6	G	T	A	B	CID	LIT	2	20.4	DKFGVPWMINVVKQQPTQ	2115.1	T	-	3.1	0.5	19.7	14.3
P16681	16153.6	G	T	A	B	CID	LIT	2	20.4	DSQQVEEGKRWF	1508.7	L	D	2.1	0.7	1.9	15.1
P65367	16256.3	G	T	A	B	CID	LIT	4	40.3	DALLQEQSAQRVGEMLLI	2014.1	F	D	2.7	0.7	30.1	15.8
P65367	16256.3	G	T	A	B	CID	LIT	4	40.3	DKYVLVVTSTTGQG	1467.8	Q	D	3.9	0.0	29.2	14.3
P65367	16256.3	G	T	A	B	CID	LIT	4	40.3	DSIVPLFQGIK	1216.7	P	D	2.4	0.0	20.3	12.6
P65367	16256.3	G	T	A	B	CID	LIT	4	40.3	DSLGFQPNLRYGVIALG	1820.0	K	D	1.9	0.4	9.9	15.7
P65367	16256.3	G	U	A	B	CID	LIT	4	42.3	DALLQEQSAQRVGEMLLI	2014.1	F	D	3.1	0.8	32.4	15.8
P65367	16256.3	G	U	A	B	CID	LIT	4	42.3	DKYVLVVTSTTGQG	1467.8	Q	D	3.7	0.7	28.1	15.3
P65367	16256.3	G	U	A	B	CID	LIT	4	42.3	DSLGFQPNLRYGVIALG	1820.0	K	D	3.7	0.0	32.9	15.2
P65367	16256.3	G	U	A	B	CID	LIT	4	42.3	DSSYVNFCNGGKQF	1622.7	G	D	3.0	0.0	29.9	7.0
P0AAB8	16276.2	G	U	T	A	CID	LIT	7	55.6	ALELAR	672.4	K	H	1.8	0.1	33.6	17.2
P0AAB8	16276.2	G	U	T	A	CID	LIT	7	55.6	AYKHIGVAISGNEEDALLVNK	2241.2	M	A	0.0	0.0	66.8	10.8
P0AAB8	16276.2	G	U	T	A	CID	LIT	7	55.6	EQCDLLVCGHHHSFINR	2122.0	K	L	3.4	0.7	38.3	9.0
P0AAB8	16276.2	G	U	T	A	CID	LIT	7	55.6	GEMPETLLEIMQK	1518.8	R	E	3.2	0.0	34.4	12.0
P0AAB8	16276.2	G	U	T	A	CID	LIT	7	55.6	IERGEMPETLLEIMQK	1917.0	R	E	3.7	0.8	5.2	12.6
P0AAB8	16276.2	G	U	T	A	CID	LIT	7	55.6	MSADLLIVPFIDK	1461.8	K	-	3.9	0.6	59.2	13.8
P0AAB8	16276.2	G	U	T	A	CID	LIT	7	55.6	NIQWPK	785.4	K	T	1.9	0.5	8.9	8.5
P0AAB8	16276.2	G	U	A	A	CID	LIT	4	33.1	AYKHIGVAISGNEE	1487.7	M	D	0.0	0.0	41.8	15.4
P0AAB8	16276.2	G	U	A	A	CID	LIT	4	33.1	DALLVNKALELARHN	1676.9	E	D	3.4	0.0	42.1	7.8
P0AAB8	16276.2	G	U	A	A	CID	LIT	4	33.1	DLLIVPFIDK	1172.7	A	-	2.4	0.0	32.3	11.1
P0AAB8	16276.2	G	U	A	A	CID	LIT	4	33.1	EIMQKEQC	1065.5	L	D	2.4	0.8	20.3	13.0
P0AAB8	16276.2	G	T	A	B	CID	LIT	3	20.4	AYKHIGVAISGNEE	1487.7	M	D	0.0	0.0	37.1	15.4
P0AAB8	16276.2	G	T	A	B	CID	LIT	3	20.4	DALLVNKAL	956.6	E	E	2.6	0.3	35.8	11.5
P0AAB8	16276.2	G	T	A	B	CID	LIT	3	20.4	DALLVNKALELARHN	1676.9	E	D	4.7	0.6	44.2	7.8
P0AAB8	16276.2	G	U	A	B	CID	LIT	5	33.1	AYKHIGVAISGNEE	1487.7	M	D	0.0	0.0	62.6	15.9
P0AAB8	16276.2	G	U	A	B	CID	LIT	5	33.1	DALLVNKAL	956.6	E	E	2.2	0.3	18.3	11.5
P0AAB8	16276.2	G	U	A	B	CID	LIT	5	33.1	DALLVNKALELARHN	1676.9	E	D	4.9	0.0	44.6	8.5
P0AAB8	16276.2	G	U	A	B	CID	LIT	5	33.1	DILQLLKNKS	1171.7	E	D	2.8	0.5	21.5	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAB8	16276.2	G	U	A	B	CID	LIT	5	33.1	EIMQKEQC	1065.5	L	D	2.2	0.0	20.2	13.0
P0ABL3	16277.9	G	T	T	A	CID	LIT	3	13.4	ISPTHFMDSDGK	1334.6	R	V	3.6	0.8	50.9	10.0
P0ABL3	16277.9	G	T	T	A	CID	LIT	3	13.4	ISPTHFMDSDGKVGAEVAPR	2114.0	R	R	3.3	0.8	42.3	12.3
P0ABL3	16277.9	G	T	T	A	CID	LIT	3	13.4	VGAEVAPR	798.4	K	R	3.0	0.9	53.3	12.8
P0A8W2	16335.9	G	U	T	A	CID	LIT	6	45.8	AEILHGISAEELEQLITLIAK	2291.3	R	L	4.1	0.0	18.8	6.0
P0A8W2	16335.9	G	U	T	A	CID	LIT	6	45.8	AEPLISEMEAVINK	1543.8	K	T	4.8	0.6	62.2	12.8
P0A8W2	16335.9	G	U	T	A	CID	LIT	6	45.8	AIGIEQPSLVR	1182.7	K	T	3.5	0.8	43.8	10.0
P0A8W2	16335.9	G	U	T	A	CID	LIT	6	45.8	LEHNIIELQAK	1307.7	K	-	3.9	0.8	55.6	7.0
P0A8W2	16335.9	G	U	T	A	CID	LIT	6	45.8	LEHNIIELQAKG	1364.8	K	-	3.4	0.9	19.5	10.8
P0A8W2	16335.9	G	U	T	A	CID	LIT	6	45.8	TLDQLEEK	975.5	R	G	2.4	0.6	38.2	13.0
P0A8W2	16335.9	G	U	A	B	CID	LIT	2	26.4	DQLEEKGLISRQTCAS	1834.9	L	D	3.2	0.0	47.4	17.1
P0A8W2	16335.9	G	U	A	B	CID	LIT	2	26.4	DQSQIQLAKAIGIEQPSLVRTL	2408.4	P	D	4.6	0.6	26.8	9.0
P0ADX7	16605.9	G	T	T	A	CID	LIT	5	37.0	GMLNQQLK	931.5	K	T	2.2	0.6	20.6	15.3
P0ADX7	16605.9	G	T	T	A	CID	LIT	5	37.0	MQTQMQTQQIQQK	1620.8	R	G	4.8	0.0	100.0	11.8
P0ADX7	16605.9	G	T	T	A	CID	LIT	5	37.0	TQTQLQQQHLENQINNNSQR	2422.2	K	V	5.0	0.9	48.3	9.5
P0ADX7	16605.9	G	T	T	A	CID	LIT	5	37.0	VLQSQPGER	1013.5	R	N	2.9	0.8	36.7	12.3
P0ADX7	16605.9	G	T	T	A	CID	LIT	5	37.0	VLQSQPGERNPAR	1451.8	R	Q	2.9	0.8	20.6	12.3
P0ADX7	16605.9	G	T	T	B	CID	LIT	3	22.6	TQTQLQQQHLENQINNNSQR	2422.2	K	V	4.4	0.6	37.8	9.5
P0ADX7	16605.9	G	T	T	B	CID	LIT	3	22.6	VLQSQPGER	1013.5	R	N	2.3	0.0	34.3	12.3
P0ADX7	16605.9	G	T	T	B	CID	LIT	3	22.6	VLQSQPGERNPAR	1451.8	R	Q	3.4	0.0	28.2	10.8
P0ADX7	16605.9	G	T	A	B	CID	LIT	2	17.1	DIPLKTIGP	953.6	P	-	2.2	0.7	23.6	9.5
P0ADX7	16605.9	G	T	A	B	CID	LIT	2	17.1	DSSLNQQHMLPERRNG	1881.9	P	D	2.0	0.4	21.9	13.4
P0ABD8	16669.0	G	U	T	A	CID	LIT	4	38.5	AFIEVGQK	891.5	K	V	2.3	0.2	42.5	14.8
P0ABD8	16669.0	G	U	T	A	CID	LIT	4	38.5	AILVESGQPVEFDEPLVVIE	2183.1	K	-	3.0	0.0	75.4	10.8
P0ABD8	16669.0	G	U	T	A	CID	LIT	4	38.5	LIELVEESGISELEISEGEESVR	2546.3	K	I	4.6	0.0	49.6	12.6
P0ABD8	16669.0	G	U	T	A	CID	LIT	4	38.5	SPMVGTFYR	1057.5	R	T	3.0	0.8	47.5	10.0
P0ABD8	16669.0	G	T	T	A	CID	LIT	3	23.7	AFIEVGQK	891.5	K	V	2.6	0.3	41.4	14.8
P0ABD8	16669.0	G	T	T	A	CID	LIT	3	23.7	AILVESGQPVEFDEPLVVIE	2183.1	K	-	2.7	0.4	10.2	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABD8	16669.0	G	T	T	A	CID	LIT	3	23.7	SPMVGTFYR	1073.5	R	T	2.6	0.7	30.3	9.0
P0ABD8	16669.0	G	U	A	A	CID	LIT	2	21.8	DAKAFIEVGQKVNVG	1574.9	P	D	4.2	0.4	35.3	14.6
P0ABD8	16669.0	G	U	A	A	CID	LIT	2	21.8	DKSGTVKAILVESGQPVEF	2004.1	A	D	4.5	0.0	60.3	14.5
P0ABD8	16669.0	G	T	T	B	CID	LIT	3	15.4	AFIEVGQK	891.5	K	V	2.0	0.0	17.2	13.0
P0ABD8	16669.0	G	T	T	B	CID	LIT	3	15.4	SPMVGTFYR	1057.5	R	T	3.1	0.0	38.3	11.1
P0ABD8	16669.0	G	T	T	B	CID	LIT	3	15.4	SPMVGTFYRTPSPDAK	1753.9	R	A	4.6	0.7	59.5	11.8
P0ABD8	16669.0	G	T	A	B	CID	LIT	3	35.3	DAKAFIEVGQKVNVG	1574.9	P	D	2.3	0.5	28.0	14.6
P0ABD8	16669.0	G	T	A	B	CID	LIT	3	35.3	DKSGTVKAILVESGQPVEF	2004.1	A	D	4.5	0.6	40.6	14.3
P0ABD8	16669.0	G	T	A	B	CID	LIT	3	35.3	EISGHIVRSPMVGTFYRTPSP	2331.2	A	D	2.7	0.8	0.0	0.0
P0ABD8	16669.0	G	U	A	B	CID	LIT	2	21.8	DAKAFIEVGQKVNVG	1574.9	P	D	3.8	0.5	25.9	14.6
P0ABD8	16669.0	G	U	A	B	CID	LIT	2	21.8	DKSGTVKAILVESGQPVEF	2004.1	A	D	3.5	0.0	17.1	14.3
P0ABD8	16669.0	S	U	T	C	CID	LIT	2	10.9	AFIEVGQK	891.5	K	V	2.5	0.2	42.3	17.2
P0ABD8	16669.0	S	U	T	C	CID	LIT	2	10.9	SPMVGTFYR	1057.5	R	T	3.2	0.7	37.8	14.0
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	AGLKVTLPR	954.6	K	L	3.0	0.0	46.5	4.8
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	4.5	0.8	32.8	14.9
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	4.4	0.0	34.4	10.8
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	LIDMGEEIGLATVYR	1679.9	R	V	4.6	0.6	65.2	11.1
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	LKILEVLQEPDNHHVSAEDLYK	2590.4	R	R	4.2	0.0	35.0	10.8
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	LTNHSLYLYGHCAEGDCREDEHAHEGK	3198.4	R	-	6.4	0.0	25.3	0.0
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	SVFELTQQHHHDHLICLDCGK	2574.2	K	V	4.4	0.0	29.9	7.0
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	VIEFSDDSIEAR	1380.7	K	Q	3.0	0.8	47.2	12.3
P0A9A9	16776.9	G	U	T	A	CID	LIT	9	81.1	VLNQFDDAGIVTR	1447.8	R	H	3.8	0.8	58.9	11.1
P0A9A9	16776.9	G	U	A	A	CID	LIT	2	6.8	DCGKVIEFS	1054.5	L	D	2.4	0.8	36.6	13.6
P0A9A9	16776.9	G	U	A	A	CID	LIT	2	6.8	DCGKVIEFSD	1169.5	L	D	2.2	0.7	10.9	10.4
P0A9A9	16776.9	G	T	T	B	CID	LIT	2	16.9	VIEFSDDSIEAR	1380.7	K	Q	2.5	0.8	23.3	12.6
P0A9A9	16776.9	G	T	T	B	CID	LIT	2	16.9	VLNQFDDAGIVTR	1447.8	R	H	3.0	0.5	30.5	13.0
P0A9A9	16776.9	G	T	A	B	CID	LIT	2	18.2	DCGKVIEFS	1054.5	L	D	2.3	0.0	20.9	13.6
P0A9A9	16776.9	G	T	A	B	CID	LIT	2	18.2	DDAGIVTRHNFEGGKSVF	1949.0	F	E	2.5	0.0	16.9	12.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9A9	16776.9	S	U	T	A	CID	LIT	5	24.3	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	4.0	0.4	38.2	19.8
P0A9A9	16776.9	S	U	T	A	CID	LIT	5	24.3	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	2.7	0.4	13.0	18.5
P0A9A9	16776.9	S	U	T	A	CID	LIT	5	24.3	LKILEVLQEPDNHHVSAEDLYK	2590.4	R	R	3.1	0.0	16.1	17.9
P0A9A9	16776.9	S	U	T	A	CID	LIT	5	24.3	LKILEVLQEPDNHHVSAEDLYKR	2746.5	R	L	3.0	0.5	16.4	17.1
P0A9A9	16776.9	S	U	T	A	CID	LIT	5	24.3	VLNQFDDAGIVTR	1447.8	R	H	2.5	0.6	7.4	16.3
P0A9A9	16776.9	S	U	T	B	CID	LIT	5	32.4	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	3.0	0.4	24.7	20.0
P0A9A9	16776.9	S	U	T	B	CID	LIT	5	32.4	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	3.0	0.5	13.1	18.5
P0A9A9	16776.9	S	U	T	B	CID	LIT	5	32.4	LKILEVLQEPDNHHVSAEDLYKR	2746.5	R	L	3.5	0.5	3.3	16.9
P0A9A9	16776.9	S	U	T	B	CID	LIT	5	32.4	VIEFSDDSIEAR	1380.7	K	Q	2.7	0.5	20.6	16.4
P0A9A9	16776.9	S	U	T	B	CID	LIT	5	32.4	VLNQFDDAGIVTR	1447.8	R	H	3.5	0.6	73.3	16.7
P0A9A9	16776.9	S	U	T	C	CID	LIT	4	31.1	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	3.5	0.3	16.5	19.6
P0A9A9	16776.9	S	U	T	C	CID	LIT	4	31.1	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	3.6	0.7	25.6	18.0
P0A9A9	16776.9	S	U	T	C	CID	LIT	4	31.1	VIEFSDDSIEAR	1380.7	K	Q	2.7	0.7	20.3	15.9
P0A9A9	16776.9	S	U	T	C	CID	LIT	4	31.1	VLNQFDDAGIVTR	1447.8	R	H	3.0	0.7	42.6	16.4
P0A9A9	16776.9	S	U	T	A	ETD	LIT	3	23.0	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	6.9	0.2	37.2	19.5
P0A9A9	16776.9	S	U	T	A	ETD	LIT	3	23.0	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	3.8	0.0	20.0	18.3
P0A9A9	16776.9	S	U	T	A	ETD	LIT	3	23.0	VLNQFDDAGIVTR	1447.8	R	H	1.3	0.0	29.1	16.4
P0A9A9	16776.9	S	U	T	B	ETD	LIT	3	23.0	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	6.4	0.2	38.6	19.8
P0A9A9	16776.9	S	U	T	B	ETD	LIT	3	23.0	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	3.1	0.0	21.2	18.5
P0A9A9	16776.9	S	U	T	B	ETD	LIT	3	23.0	VLNQFDDAGIVTR	1447.8	R	H	2.9	0.4	68.1	17.1
P0A9A9	16776.9	S	U	T	C	ETD	LIT	3	30.4	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	6.1	0.3	42.2	19.8
P0A9A9	16776.9	S	U	T	C	ETD	LIT	3	30.4	VIEFSDDSIEAR	1380.7	K	Q	2.1	0.2	39.3	16.2
P0A9A9	16776.9	S	U	T	C	ETD	LIT	3	30.4	VLNQFDDAGIVTR	1447.8	R	H	2.9	0.4	72.2	16.4
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	0.0	0.0	25.0	19.8
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	0.0	0.0	17.2	18.5
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	VIEFSDDSIEAR	1380.7	K	Q	0.0	0.0	45.5	15.9
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	VLNQFDDAGIVTR	1447.8	R	H	0.0	0.0	61.3	16.3
P0A9A9	16776.9	S	U	T	A	ETD+CID	LIT	4	23.6	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	4.6	0.5	33.6	20.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9A9	16776.9	S	U	T	A	ETD+CID	LIT	4	23.6	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	2.6	0.3	10.6	18.5
P0A9A9	16776.9	S	U	T	A	ETD+CID	LIT	4	23.6	LKILEVLQEPDNHHVSAEDLYK	2590.4	R	R	0.0	0.0	15.9	17.9
P0A9A9	16776.9	S	U	T	A	ETD+CID	LIT	4	23.6	VIEFSDDSIEAR	1380.7	K	Q	3.1	0.7	0.0	0.0
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	3.9	0.5	25.0	19.8
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	2.9	0.5	17.2	18.5
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	VIEFSDDSIEAR	1380.7	K	Q	2.5	0.4	45.5	15.9
P0A9A9	16776.9	S	U	T	B	ETD+CID	LIT	4	31.1	VLNQFDDAGIVTR	1447.8	R	H	3.0	0.5	61.3	16.3
P0A9A9	16776.9	S	U	T	C	ETD+CID	LIT	5	32.4	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	3.8	0.4	24.7	19.4
P0A9A9	16776.9	S	U	T	C	ETD+CID	LIT	5	32.4	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	3.1	0.4	23.0	18.5
P0A9A9	16776.9	S	U	T	C	ETD+CID	LIT	5	32.4	LKILEVLQEPDNHHVSAEDLYK	2590.4	R	R	2.9	0.6	13.2	18.4
P0A9A9	16776.9	S	U	T	C	ETD+CID	LIT	5	32.4	VIEFSDDSIEAR	1380.7	K	Q	3.2	0.6	35.3	16.1
P0A9A9	16776.9	S	U	T	C	ETD+CID	LIT	5	32.4	VLNQFDDAGIVTR	1447.8	R	H	4.1	0.7	76.0	16.4
P0A9A9	16776.9	S	U	T	B	HCD	FT	4	31.1	ILEVLQEPDNHHVSAEDLYK	2349.2	K	R	0.0	0.0	25.0	19.8
P0A9A9	16776.9	S	U	T	B	HCD	FT	4	31.1	ILEVLQEPDNHHVSAEDLYKR	2505.3	K	L	0.0	0.0	17.2	18.5
P0A9A9	16776.9	S	U	T	B	HCD	FT	4	31.1	VIEFSDDSIEAR	1380.7	K	Q	0.0	0.0	45.5	15.9
P0A9A9	16776.9	S	U	T	B	HCD	FT	4	31.1	VLNQFDDAGIVTR	1447.8	R	H	0.0	0.0	61.3	16.3
P0AF67	16835.4	G	U	T	A	CID	LIT	2	19.6	VIPLPDEQATLDLGER	1765.9	R	V	2.9	0.0	19.9	13.2
P0AF67	16835.4	G	U	T	A	CID	LIT	2	19.6	VSAVSSAGELLLAR	1372.8	R	L	4.3	0.5	76.0	12.8
P0AF96	16847.5	S	U	T	B	CID	LIT	2	22.7	LFYLISEDMTEPYEAR	1976.9	R	R	3.3	0.5	31.2	16.9
P0AF96	16847.5	S	U	T	B	CID	LIT	2	22.7	MIIGNIHNLQPWLPQELR	2172.2	-	Q	3.2	0.5	13.3	14.6
P0AF96	16847.5	S	U	T	B	ETD+CID	LIT	2	22.7	LFYLISEDMTEPYEAR	1976.9	R	R	3.1	0.5	32.4	16.6
P0AF96	16847.5	S	U	T	B	ETD+CID	LIT	2	22.7	MIIGNIHNLQPWLPQELR	2172.2	-	Q	2.8	0.4	0.0	0.0
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	AAFNQMVQGHK	1246.6	K	L	3.1	0.8	28.4	10.4
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	AAFNQMVQGHKLPAWVMK	2056.1	K	G	3.3	0.7	37.2	11.1
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	5.0	0.0	41.6	4.8
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	IAVMWSEK	963.5	R	S	1.7	0.6	17.7	14.5
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	LPAWVMK	844.5	K	G	2.2	0.6	43.0	16.4
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	LTWLNVNDALSIDGK	1658.9	K	T	3.9	0.7	64.7	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	SNQMTGLFSTIDEK	1586.7	K	T	4.0	0.7	84.4	10.0
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	TSQEKLTWLNVNDALSIDGK	2232.2	K	T	5.3	0.7	61.3	12.8
P0AD59	16854.5	G	U	T	A	CID	LIT	9	72.0	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	4.4	0.9	32.4	10.4
P0AD59	16854.5	G	U	A	A	CID	LIT	3	21.7	DEKTSQEKLTWLNVN	1804.9	I	D	3.0	0.5	25.6	17.1
P0AD59	16854.5	G	U	A	A	CID	LIT	3	21.7	DETYQVMSACKPH	1565.7	G	D	3.9	0.0	62.3	8.5
P0AD59	16854.5	G	U	A	A	CID	LIT	3	21.7	DGFNFK	727.3	P	-	1.7	0.6	16.6	13.2
P0AD59	16854.5	G	T	A	B	CID	LIT	4	36.3	DALSIDGKTVLFAALTGSLENHP	2369.2	N	D	3.7	0.0	22.0	13.8
P0AD59	16854.5	G	T	A	B	CID	LIT	4	36.3	DEKTSQEKLTWLNVN	1804.9	I	D	2.5	0.6	18.5	16.4
P0AD59	16854.5	G	T	A	B	CID	LIT	4	36.3	DETYQVMSACKPH	1565.7	G	D	3.8	0.0	47.9	9.0
P0AD59	16854.5	G	T	A	B	CID	LIT	4	36.3	DGFNFK	727.3	P	-	1.9	0.4	24.7	10.0
P0AD59	16854.5	G	U	A	B	CID	LIT	4	36.3	DALSIDGKTVLFAALTGSLENHP	2369.2	N	D	4.0	0.0	32.0	14.0
P0AD59	16854.5	G	U	A	B	CID	LIT	4	36.3	DEKTSQEKLTWLNVN	1804.9	I	D	3.0	0.6	19.9	16.4
P0AD59	16854.5	G	U	A	B	CID	LIT	4	36.3	DETYQVMSACKPH	1565.7	G	D	3.2	0.0	61.4	10.0
P0AD59	16854.5	G	U	A	B	CID	LIT	4	36.3	DGFNFK	727.3	P	-	2.3	0.7	31.0	10.0
P0AD59	16854.5	S	U	T	A	CID	LIT	5	57.3	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	4.2	0.6	62.7	13.8
P0AD59	16854.5	S	U	T	A	CID	LIT	5	57.3	IAVMWSEK	963.5	R	S	2.0	0.6	26.2	15.9
P0AD59	16854.5	S	U	T	A	CID	LIT	5	57.3	LTWLNVNDALSIDGK	1658.9	K	T	3.9	0.5	24.2	18.3
P0AD59	16854.5	S	U	T	A	CID	LIT	5	57.3	SNQMTGLFSTIDEK	1570.7	K	T	4.2	0.9	78.8	14.3
P0AD59	16854.5	S	U	T	A	CID	LIT	5	57.3	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	5.9	0.5	101.0	19.0
P0AD59	16854.5	S	U	T	B	CID	LIT	6	61.8	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	4.0	0.0	56.7	14.5
P0AD59	16854.5	S	U	T	B	CID	LIT	6	61.8	IAVMWSEK	963.5	R	S	2.2	0.8	29.3	12.6
P0AD59	16854.5	S	U	T	B	CID	LIT	6	61.8	LPAWVMK	844.5	K	G	1.8	0.5	19.2	18.5
P0AD59	16854.5	S	U	T	B	CID	LIT	6	61.8	LTWLNVNDALSIDGK	1658.9	K	T	3.7	0.5	42.9	17.2
P0AD59	16854.5	S	U	T	B	CID	LIT	6	61.8	SNQMTGLFSTIDEK	1586.7	K	T	4.2	0.6	64.6	14.1
P0AD59	16854.5	S	U	T	B	CID	LIT	6	61.8	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	5.5	0.6	106.0	18.9
P0AD59	16854.5	S	U	T	C	CID	LIT	6	63.7	AAFNQMVQGHKLPAWVMK	2056.1	K	G	3.0	0.5	7.9	17.7
P0AD59	16854.5	S	U	T	C	CID	LIT	6	63.7	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	4.4	0.0	46.9	13.4
P0AD59	16854.5	S	U	T	C	CID	LIT	6	63.7	LPAWVMK	844.5	K	G	2.2	0.5	29.8	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AD59	16854.5	S	U	T	C	CID	LIT	6	63.7	LTWLNVNDALSIDGK	1658.9	K	T	4.3	0.5	33.7	17.2
P0AD59	16854.5	S	U	T	C	CID	LIT	6	63.7	SNQMTGLFSTIDEK	1586.7	K	T	4.1	0.6	46.7	13.0
P0AD59	16854.5	S	U	T	C	CID	LIT	6	63.7	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	4.9	0.6	93.0	19.0
P0AD59	16854.5	S	U	T	A	ETD	LIT	5	57.3	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	3.9	0.0	32.8	14.1
P0AD59	16854.5	S	U	T	A	ETD	LIT	5	57.3	IAVMWSEK	963.5	R	S	2.4	0.5	0.0	0.0
P0AD59	16854.5	S	U	T	A	ETD	LIT	5	57.3	LTWLNVNDALSIDGK	1658.9	K	T	3.1	0.3	22.0	18.3
P0AD59	16854.5	S	U	T	A	ETD	LIT	5	57.3	SNQMTGLFSTIDEK	1570.7	K	T	3.1	0.6	57.9	14.5
P0AD59	16854.5	S	U	T	A	ETD	LIT	5	57.3	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	6.8	0.6	0.0	0.0
P0AD59	16854.5	S	U	T	B	ETD	LIT	6	63.7	AAFNQMVQGHK	1231.6	K	L	3.3	0.7	0.0	0.0
P0AD59	16854.5	S	U	T	B	ETD	LIT	6	63.7	AAFNQMVQGHKLPAWVMK	2056.1	K	G	6.1	0.6	78.2	17.9
P0AD59	16854.5	S	U	T	B	ETD	LIT	6	63.7	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	0.0	0.0	37.1	13.2
P0AD59	16854.5	S	U	T	B	ETD	LIT	6	63.7	LTWLNVNDALSIDGK	1658.9	K	T	3.1	0.4	38.2	17.2
P0AD59	16854.5	S	U	T	B	ETD	LIT	6	63.7	SNQMTGLFSTIDEK	1570.7	K	T	1.9	0.6	30.1	15.2
P0AD59	16854.5	S	U	T	B	ETD	LIT	6	63.7	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	4.8	0.8	30.5	18.6
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	AAFNQMVQGHK	1230.6	K	L	4.5	0.7	37.8	14.6
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	AAFNQMVQGHKLPAWVMK	2056.1	K	G	6.7	0.8	80.6	17.6
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	0.0	0.0	51.5	13.6
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	IAVMWSEK	963.5	R	S	2.3	0.6	0.0	0.0
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	LPAWVMK	844.5	K	G	1.8	0.6	20.1	18.5
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	LTWLNVNDALSIDGK	1658.9	K	T	3.0	0.3	0.0	0.0
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	SNQMTGLFSTIDEK	1570.7	K	T	2.1	0.5	26.7	14.3
P0AD59	16854.5	S	U	T	C	ETD	LIT	8	68.8	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	2.6	0.3	0.0	0.0
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	0.0	0.0	53.5	13.8
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	IAVMWSEK	963.5	R	S	0.0	0.0	35.2	13.0
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	LTWLNVNDALSIDGK	1658.9	K	T	0.0	0.0	36.9	18.3
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	SNQMTGLFSTIDEK	1586.7	K	T	0.0	0.0	68.8	13.2
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	0.0	0.0	97.5	18.6
P0AD59	16854.5	S	U	T	A	ETD+CID	LIT	6	64.3	AAFNQMVQGHK	1231.6	K	L	2.2	0.2	11.5	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AD59	16854.5	S	U	T	A	ETD+CID	LIT	6	64.3	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	4.0	0.0	43.6	14.1
P0AD59	16854.5	S	U	T	A	ETD+CID	LIT	6	64.3	IAVMWSEK	963.5	R	S	2.1	0.8	26.0	15.7
P0AD59	16854.5	S	U	T	A	ETD+CID	LIT	6	64.3	LTWLNVNDALSIDGK	1658.9	K	T	4.4	0.6	0.0	0.0
P0AD59	16854.5	S	U	T	A	ETD+CID	LIT	6	64.3	SNQMTGLFSTIDEK	1570.7	K	T	4.7	0.7	81.0	14.5
P0AD59	16854.5	S	U	T	A	ETD+CID	LIT	6	64.3	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	4.7	0.6	110.0	19.0
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	5.1	0.0	53.5	13.8
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	IAVMWSEK	963.5	R	S	2.6	0.7	35.2	13.0
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	LTWLNVNDALSIDGK	1658.9	K	T	4.2	0.5	0.0	0.0
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	SNQMTGLFSTIDEK	1586.7	K	T	4.1	0.8	68.8	13.2
P0AD59	16854.5	S	U	T	B	ETD+CID	LIT	5	57.3	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	6.0	0.5	97.5	18.6
P0AD59	16854.5	S	U	T	C	ETD+CID	LIT	7	68.8	AAFNQMVQGHKLPAWVMK	2056.1	K	G	2.2	0.7	0.0	0.0
P0AD59	16854.5	S	U	T	C	ETD+CID	LIT	7	68.8	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	4.9	0.0	59.5	14.1
P0AD59	16854.5	S	U	T	C	ETD+CID	LIT	7	68.8	IAVMWSEK	963.5	R	S	2.3	0.8	0.0	0.0
P0AD59	16854.5	S	U	T	C	ETD+CID	LIT	7	68.8	LPAWVMK	844.5	K	G	1.7	0.0	26.1	17.6
P0AD59	16854.5	S	U	T	C	ETD+CID	LIT	7	68.8	LTWLNVNDALSIDGK	1658.9	K	T	3.3	0.5	0.0	0.0
P0AD59	16854.5	S	U	T	C	ETD+CID	LIT	7	68.8	SNQMTGLFSTIDEK	1570.7	K	T	4.6	0.8	0.0	0.0
P0AD59	16854.5	S	U	T	C	ETD+CID	LIT	7	68.8	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	4.2	0.6	37.4	19.1
P0AD59	16854.5	S	U	T	B	HCD	FT	5	57.3	GGTYTPAQTVTLGDETYQVMSACKPHDCGSQR	3515.6	K	I	0.0	0.0	43.2	13.2
P0AD59	16854.5	S	U	T	B	HCD	FT	5	57.3	IAVMWSEK	963.5	R	S	0.0	0.0	35.2	13.0
P0AD59	16854.5	S	U	T	B	HCD	FT	5	57.3	LTWLNVNDALSIDGK	1658.9	K	T	0.0	0.0	36.9	18.3
P0AD59	16854.5	S	U	T	B	HCD	FT	5	57.3	SNQMTGLFSTIDEK	1586.7	K	T	0.0	0.0	68.8	13.2
P0AD59	16854.5	S	U	T	B	HCD	FT	5	57.3	TVLFAALTGSLENHPDGFNFK	2278.2	K	-	0.0	0.0	97.5	18.6
P69828	16889.7	G	U	T	A	CID	LIT	5	28.0	GVVHDTWPQALIAR	1562.8	K	E	2.7	0.5	31.9	12.6
P69828	16889.7	G	U	T	A	CID	LIT	5	28.0	SEVLTHIGNEMLAK	1541.8	R	G	4.1	0.6	43.7	14.5
P69828	16889.7	G	U	T	A	CID	LIT	5	28.0	SGISFVDR	880.5	R	S	2.3	0.3	33.5	14.6
P69828	16889.7	G	U	T	A	CID	LIT	5	28.0	SGISFVDRSEVLTHIGNEMLAK	2403.2	R	G	4.1	0.0	26.1	12.0
P69828	16889.7	G	U	T	A	CID	LIT	5	28.0	TNLFVR	749.4	M	S	0.0	0.0	49.3	14.5
P69828	16889.7	S	U	T	B	ETD+CID	LIT	2	22.0	GVVHDTWPQALIAR	1562.8	K	E	3.9	0.5	29.3	17.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69828	16889.7	S	U	T	B	ETD+CID	LIT	2	22.0	LQQPDIVETLITLPETQLK	2179.2	K	E	2.8	0.5	7.9	13.4
P0A731	16900.8	G	U	T	A	CID	LIT	3	12.5	HIALVAHDHCK	1300.7	K	Q	4.2	0.9	66.2	13.0
P0A731	16900.8	G	U	T	A	CID	LIT	3	12.5	KHIALVAHDHCK	1428.8	R	Q	4.3	0.8	60.1	10.4
P0A731	16900.8	G	U	T	A	CID	LIT	3	12.5	YLADRLK	878.5	R	-	1.6	0.5	10.5	13.6
P0A731	16900.8	G	U	A	A	CID	LIT	2	14.5	DFIIQSPHFN	1217.6	A	D	2.5	0.7	17.2	15.2
P0A731	16900.8	G	U	A	A	CID	LIT	2	14.5	DILIPDYQRYLA	1479.8	V	D	2.3	0.3	13.6	14.3
P0A731	16900.8	G	T	A	B	CID	LIT	2	11.2	DFIIQSPHFN	1217.6	A	D	3.1	0.8	29.6	15.9
P0A731	16900.8	G	T	A	B	CID	LIT	2	11.2	DYQRYLA	928.5	P	D	2.3	0.8	26.4	14.0
P0A731	16900.8	S	U	T	B	CID	LIT	2	21.7	HIALVAHDHCK	1300.7	K	Q	3.6	0.7	30.8	15.6
P0A731	16900.8	S	U	T	B	CID	LIT	2	21.7	HQPLLEQHVLYATGTTGNLISR	2448.3	R	A	4.3	0.6	33.5	17.2
P0A731	16900.8	S	U	T	C	CID	LIT	2	21.7	HIALVAHDHCK	1300.7	K	Q	2.9	0.5	16.8	15.3
P0A731	16900.8	S	U	T	C	CID	LIT	2	21.7	HQPLLEQHVLYATGTTGNLISR	2448.3	R	A	5.7	0.7	54.7	17.2
P0A731	16900.8	S	U	T	B	ETD+CID	LIT	2	21.7	HIALVAHDHCK	1300.7	K	Q	0.0	0.0	22.6	15.3
P0A731	16900.8	S	U	T	B	ETD+CID	LIT	2	21.7	HQPLLEQHVLYATGTTGNLISR	2448.3	R	A	0.0	0.0	50.0	17.3
P0A731	16900.8	S	U	T	B	ETD+CID	LIT	2	21.7	HIALVAHDHCK	1300.7	K	Q	2.7	0.6	22.6	15.3
P0A731	16900.8	S	U	T	B	ETD+CID	LIT	2	21.7	HQPLLEQHVLYATGTTGNLISR	2448.3	R	A	4.8	0.7	50.0	17.3
P0A731	16900.8	S	U	T	C	ETD+CID	LIT	2	21.7	HIALVAHDHCK	1300.7	K	Q	2.7	0.6	29.2	15.3
P0A731	16900.8	S	U	T	C	ETD+CID	LIT	2	21.7	HQPLLEQHVLYATGTTGNLISR	2448.3	R	A	5.3	0.8	60.3	17.3
P0A731	16900.8	S	U	T	B	HCD	FT	2	21.7	HIALVAHDHCK	1300.7	K	Q	0.0	0.0	22.6	15.3
P0A731	16900.8	S	U	T	B	HCD	FT	2	21.7	HQPLLEQHVLYATGTTGNLISR	2448.3	R	A	0.0	0.0	50.0	17.3
P0A8D3	16951.8	G	U	A	A	CID	LIT	2	19.7	DNEIVRQCEAG	1290.6	A	D	3.5	0.6	38.5	13.0
P0A8D3	16951.8	G	U	A	A	CID	LIT	2	19.7	DTLRASGIQTGGPDSLSQR	1959.0	M	D	4.8	0.8	52.2	15.1
P0A8D3	16951.8	G	T	A	B	CID	LIT	2	18.4	DACPNVIK	916.5	A	E	1.8	0.6	7.3	13.4
P0A8D3	16951.8	G	T	A	B	CID	LIT	2	18.4	DIPLAAEAIEKGAAALNPRG	1977.1	A	E	2.9	0.7	9.6	14.0
P0A9M5	16952.7	G	U	T	A	CID	LIT	4	39.5	GGLVPGALLAR	1023.6	R	E	2.0	0.0	31.0	3.0
P0A9M5	16952.7	G	U	T	A	CID	LIT	4	39.5	GIIAVSR	715.4	K	G	1.8	0.0	34.5	18.5
P0A9M5	16952.7	G	U	T	A	CID	LIT	4	39.5	HVDTVCISSYDHDNQR	1945.8	R	E	5.3	0.0	34.3	7.0
P0A9M5	16952.7	G	U	T	A	CID	LIT	4	39.5	RAEGDGEGFIVIDDLVDTGGTAVAIR	2646.3	K	E	4.3	0.0	26.8	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P30749	16962.7	G	U	T	A	CID	LIT	4	46.7	ALAEIVDEAR	1086.6	K	N	3.3	0.8	40.6	12.3
P30749	16962.7	G	U	T	A	CID	LIT	4	46.7	EATPEGDRWVEAR	1515.7	R	E	2.2	0.4	21.3	12.3
P30749	16962.7	G	U	T	A	CID	LIT	4	46.7	IVVGPQPFSVGEEYPWLAERDEDGAVVTFTGK	3492.7	K	V	3.5	0.0	43.4	11.1
P30749	16962.7	G	U	T	A	CID	LIT	4	46.7	SSAFEAGQFIMDYLK	1706.8	R	T	3.1	0.0	34.5	12.3
P30749	16962.7	G	U	A	A	CID	LIT	2	18.7	DEDGAVVTFTGKVRNHNLG	2029.0	R	D	3.7	0.5	12.6	16.2
P30749	16962.7	G	U	A	A	CID	LIT	2	18.7	DRWVEARES	1147.5	G	D	2.0	0.2	14.1	15.6
P30749	16962.7	S	U	T	A	CID	LIT	2	36.0	IVVGPQPFSVGEEYPWLAERDEDGAVVTFTGK	3492.7	K	V	2.7	0.0	43.8	19.0
P30749	16962.7	S	U	T	A	CID	LIT	2	36.0	NHNLGDSVNALTLEHYPGMTEK	2440.2	R	A	4.1	0.7	33.7	17.5
P12994	17067.0	G	T	A	B	CID	LIT	3	24.1	DFGKTGY	787.4	T	D	1.2	0.7	18.5	13.6
P12994	17067.0	G	T	A	B	CID	LIT	3	24.1	DTRVLPQGFGSGLVAMPDGVLQTRT	2615.4	A	D	4.4	0.5	31.3	15.1
P12994	17067.0	G	T	A	B	CID	LIT	3	24.1	MKLISN	705.4	-	D	1.8	0.2	17.9	8.5
P12994	17067.0	S	U	T	B	CID	LIT	2	22.8	TGYDGAAPPKGETHR	1556.7	K	Y	3.4	0.0	55.0	16.0
P12994	17067.0	S	U	T	B	CID	LIT	2	22.8	VLPQGFGSGLVAMPDGVLQTR	2142.1	R	T	4.0	0.6	35.5	17.2
P0AAR3	17075.5	G	U	T	A	CID	LIT	3	21.4	FADIAR	692.4	K	R	1.6	0.5	10.2	15.9
P0AAR3	17075.5	G	U	T	A	CID	LIT	3	21.4	GLDIELAAGDLAK	1285.7	R	I	3.4	0.7	75.3	12.8
P0AAR3	17075.5	G	U	T	A	CID	LIT	3	21.4	STGYLVGGISPLGQK	1476.8	R	K	3.2	0.0	19.1	11.5
P0AE91	17090.1	G	U	T	A	CID	LIT	5	36.3	IVVEAFDDPDVK	1346.7	K	N	3.8	0.0	60.7	10.0
P0AE91	17090.1	G	U	T	A	CID	LIT	5	36.3	NAISAVPVMPWRQ	1468.8	K	-	3.3	0.8	29.0	14.1
P0AE91	17090.1	G	U	T	A	CID	LIT	5	36.3	NALAYLAYSDKVVEGSPK	1925.0	R	N	4.7	0.5	61.9	9.5
P0AE91	17090.1	G	U	T	A	CID	LIT	5	36.3	NVTCYVSR	998.5	K	A	2.0	0.0	30.8	11.5
P0AE91	17090.1	G	U	T	A	CID	LIT	5	36.3	TSLVFK	694.4	R	S	1.4	0.5	14.3	10.8
P0AE91	17090.1	G	U	A	B	CID	LIT	3	31.8	DAAISCQQVGPIELS	1587.8	S	D	2.9	0.7	48.2	13.0
P0AE91	17090.1	G	U	A	B	CID	LIT	3	31.8	DAKRNALAYLAYS	1455.8	Y	D	2.5	0.5	19.4	15.2
P0AE91	17090.1	G	U	A	B	CID	LIT	3	31.8	DKVVEGSPKNAISAVPVMPWRQ	2408.3	S	-	2.3	0.4	0.0	0.0
P0AE91	17090.1	S	U	T	C	CID	LIT	2	28.7	GGLGLAEDTSDAAISCQQVGPIELSDR	2759.3	K	I	4.7	0.6	43.4	18.0
P0AE91	17090.1	S	U	T	C	CID	LIT	2	28.7	NALAYLAYSDKVVEGSPK	1925.0	R	N	4.7	0.5	33.8	17.5
P0AE91	17090.1	S	U	T	C	ETD	LIT	2	19.7	NAISAVPVMPWRQ	1468.8	K	-	2.9	0.4	19.0	15.9
P0AE91	17090.1	S	U	T	C	ETD	LIT	2	19.7	NALAYLAYSDKVVEGSPK	1925.0	R	N	2.1	0.6	26.1	17.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	ALEKRPVSSDDVEMAINHIK	2252.2	R	S	5.7	0.7	47.1	12.6
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	FTTFEVAELVMPR	1555.8	R	V	2.3	0.0	31.2	10.4
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	LVGEGSSVR	903.5	R	R	2.5	0.6	36.6	14.0
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	LVGEGSSVRR	1059.6	R	R	2.6	0.3	19.3	12.8
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	MIGNLVMEQLK	1275.7	K	K	3.5	0.0	69.2	13.0
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	QCLVCNER	1078.5	R	F	2.5	0.7	18.7	6.0
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	SFEDIKEFGEEIAR	1669.8	R	L	3.4	0.7	40.2	12.8
P0A8D0	17210.8	G	U	T	A	CID	LIT	8	59.1	SNDVREPFNEEK	1463.7	K	L	3.6	0.4	33.8	10.0
P0ABA0	17246.5	S	U	T	C	ETD+CID	LIT	2	18.6	RQKEIADGLASAER	1544.8	K	A	2.3	0.8	0.0	0.0
P0ABA0	17246.5	S	U	T	C	ETD+CID	LIT	2	18.6	SQILDEAKAEAEQER	1716.8	R	T	3.8	0.5	38.5	17.2
P0AG86	17259.1	S	U	T	B	CID	LIT	2	32.3	DISFEAPNAPHVFQK	1699.8	K	D	4.4	0.5	23.0	17.6
P0AG86	17259.1	S	U	T	B	CID	LIT	2	32.3	GTFPQLNLAPVNFDALFMNYLQQQAGEGTEEHQDA	3893.8	R	-	6.6	0.0	62.3	18.1
P0AG86	17259.1	S	U	T	B	ETD+CID	LIT	2	32.3	DISFEAPNAPHVFQK	1699.8	K	D	4.4	0.4	18.8	17.2
P0AG86	17259.1	S	U	T	B	ETD+CID	LIT	2	32.3	GTFPQLNLAPVNFDALFMNYLQQQAGEGTEEHQDA	3893.8	R	-	7.4	0.0	84.0	18.0
P0AGK8	17318.7	S	U	T	B	CID	LIT	3	19.8	CLTHALWR	1056.5	K	D	1.9	0.4	23.8	14.0
P0AGK8	17318.7	S	U	T	B	CID	LIT	3	19.8	GPGGGYLLGK	918.5	R	D	3.1	0.0	37.8	17.0
P0AGK8	17318.7	S	U	T	B	CID	LIT	3	19.8	QGISLSYLEQLFSR	1640.9	R	L	2.9	0.8	22.0	16.1
P0AGK8	17318.7	S	U	T	C	CID	LIT	2	14.8	GPGGGYLLGK	918.5	R	D	3.3	0.6	28.7	17.2
P0AGK8	17318.7	S	U	T	C	CID	LIT	2	14.8	QGISLSYLEQLFSR	1640.9	R	L	1.8	0.7	0.0	0.0
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	ACDLVLK	818.4	K	Q	2.9	0.6	32.2	14.3
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	DGQQLNLDNIGTTPLAEK	1927.0	K	V	4.4	0.0	92.9	12.6
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	LASVTDAENIK	1160.6	K	N	2.7	0.6	32.8	14.1
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	LASVTDAENIKNQVLEK	1872.0	K	L	5.7	0.8	85.9	10.8
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	LGLNSEEQKEDTNYLDGIQGLLK	2577.3	K	T	6.1	0.7	35.2	13.2
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	QKLASVTDAENIK	1416.8	K	N	3.1	0.8	33.8	11.8
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	TKACDLVLK	1047.6	K	Q	2.4	0.7	21.3	12.6
P18390	17335.3	G	T	T	A	CID	LIT	8	43.3	TKDGQQLNLDNIGTTPLAEK	2156.1	K	V	5.2	0.7	85.6	12.0
P18390	17335.3	G	T	A	A	CID	LIT	2	13.4	DGIQGLLKTK	1072.6	L	D	2.3	0.7	12.6	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P18390	17335.3	G	T	A	A	CID	LIT	2	13.4	DLVLKQGLNFIS	1346.8	C	-	3.3	0.0	40.2	10.4
P18390	17335.3	G	T	T	B	CID	LIT	4	22.0	ACDLVLK	818.4	K	Q	2.0	0.2	2.7	14.3
P18390	17335.3	G	T	T	B	CID	LIT	4	22.0	ACDLVLKQGLNFIS	1577.8	K	-	2.8	0.4	22.5	12.6
P18390	17335.3	G	T	T	B	CID	LIT	4	22.0	DGQQLNLDNIGTTPLAEKVK	2154.1	K	T	3.8	0.4	30.6	12.8
P18390	17335.3	G	T	T	B	CID	LIT	4	22.0	TKACDLVLK	1047.6	K	Q	2.7	0.4	24.4	12.6
P18390	17335.3	G	T	A	B	CID	LIT	6	67.7	DAENIKNQVL	1143.6	T	E	1.9	0.1	17.0	13.8
P18390	17335.3	G	T	A	B	CID	LIT	6	67.7	DALSSAASELGNQNSTTQEGGWSLASLTNLLSSGNQALSA	3950.9	K	D	5.2	0.0	57.3	9.5
P18390	17335.3	G	T	A	B	CID	LIT	6	67.7	DGIQGLLKTK	1072.6	L	D	2.7	0.0	44.5	10.4
P18390	17335.3	G	T	A	B	CID	LIT	6	67.7	DLVLKQGLNFIS	1346.8	C	-	3.1	0.8	27.9	10.4
P18390	17335.3	G	T	A	B	CID	LIT	6	67.7	DNIGTTPLAEKVKTKAC	1846.0	L	D	4.1	0.9	55.3	14.5
P18390	17335.3	G	T	A	B	CID	LIT	6	67.7	DNMNNAAGILQYCAKQKLASVT	2410.2	A	D	3.9	0.4	23.0	14.3
P0A8R0	17342.4	G	U	T	A	CID	LIT	4	19.9	ASFGGQIITVK	1120.6	R	C	2.9	0.7	30.1	7.8
P0A8R0	17342.4	G	U	T	A	CID	LIT	4	19.9	RALVDAELAR	1113.6	R	L	3.1	0.2	35.5	13.2
P0A8R0	17342.4	G	U	T	A	CID	LIT	4	19.9	VLVVDGGGSVR	1057.6	R	R	3.1	0.7	30.4	13.6
P0A8R0	17342.4	G	U	T	A	CID	LIT	4	19.9	VLVVDGGGSVRR	1213.7	R	A	1.5	0.6	19.2	11.5
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	AAQEEEFSLELR	1421.7	R	N	4.2	0.8	60.8	12.8
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	ILEAWR	787.4	R	N	1.8	0.7	32.5	12.0
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	KTSSLSILAIAGVEPYQEKPGEEYMNEAQLAHFR	3806.9	R	R	3.9	0.0	35.6	11.1
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	KVEDEDFGYCESCGVEIGIR	2362.0	K	R	5.5	0.9	37.8	6.0
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	LEARPTADLCIDCK	1661.8	R	T	4.2	0.8	36.0	13.0
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	NQLRDEVDR	1144.6	R	T	1.4	0.6	18.1	12.0
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	RILEAWR	943.5	R	N	2.9	0.3	27.5	14.0
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	RLEARPTADLCIDCK	1817.9	R	T	2.0	0.7	12.9	14.5
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	TLAEIR	702.4	K	E	1.8	0.5	22.6	16.6
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	TLAEIREK	959.6	K	Q	2.1	0.2	16.4	14.9
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	TSSLSILAIAGVEPYQEKPGEEYMNEAQLAHFR	3678.8	K	R	4.9	0.0	18.3	10.4
P0ABS1	17510.1	G	U	T	A	CID	LIT	12	81.5	TVTHMQDEAANFPDPVDR	2042.9	R	A	4.1	0.0	59.8	7.0
P0ABS1	17510.1	G	U	A	A	CID	LIT	5	19.9	DEVDRTVTHMQ	1330.6	R	D	2.9	0.7	31.9	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABS1	17510.1	G	U	A	A	CID	LIT	5	19.9	DLCIDCKTLA	1208.6	A	E	2.8	0.8	31.5	13.8
P0ABS1	17510.1	G	U	A	A	CID	LIT	5	19.9	DLCIDCKTLAEIR	1606.8	A	E	3.2	0.4	54.1	15.9
P0ABS1	17510.1	G	U	A	A	CID	LIT	5	19.9	DRTVTHMQ	987.5	V	D	2.4	0.0	24.6	13.4
P0ABS1	17510.1	G	U	A	A	CID	LIT	5	19.9	EIREKQMAG	1061.5	A	-	2.3	0.6	8.7	14.0
P0ABS1	17510.1	G	U	A	B	CID	LIT	3	20.5	DEAANFPDPV	1074.5	Q	D	2.8	0.4	29.5	12.6
P0ABS1	17510.1	G	U	A	B	CID	LIT	3	20.5	DEVDRTVTHMQ	1330.6	R	D	2.3	0.5	11.5	12.6
P0ABS1	17510.1	G	U	A	B	CID	LIT	3	20.5	DLCIDCKTLA	1208.6	A	E	2.6	0.0	29.5	13.8
P0ABS1	17510.1	S	U	T	A	CID	LIT	3	26.5	RILEAWR	943.5	R	N	2.8	0.2	27.1	15.4
P0ABS1	17510.1	S	U	T	A	CID	LIT	3	26.5	RLEARPTADLCIDCK	1817.9	R	T	3.1	0.4	20.5	18.1
P0ABS1	17510.1	S	U	T	A	CID	LIT	3	26.5	TVTHMQDEAANFPDPVDR	2042.9	R	A	5.4	0.6	58.8	12.6
P0ABS1	17510.1	S	U	T	B	CID	LIT	6	53.6	AAQEEEFSLELR	1421.7	R	N	2.8	0.3	9.3	15.2
P0ABS1	17510.1	S	U	T	B	CID	LIT	6	53.6	KVEDEDFGYCESCGVEIGIR	2362.0	K	R	3.7	0.7	0.0	0.0
P0ABS1	17510.1	S	U	T	B	CID	LIT	6	53.6	NQLRDEVDR	1144.6	R	T	2.9	0.5	27.9	14.5
P0ABS1	17510.1	S	U	T	B	CID	LIT	6	53.6	RILEAWR	943.5	R	N	2.6	0.0	26.6	15.4
P0ABS1	17510.1	S	U	T	B	CID	LIT	6	53.6	RLEARPTADLCIDCK	1817.9	R	T	3.1	0.4	27.5	18.1
P0ABS1	17510.1	S	U	T	B	CID	LIT	6	53.6	TVTHMQDEAANFPDPVDR	2042.9	R	A	4.2	0.6	51.4	13.2
P0ABS1	17510.1	S	U	T	C	CID	LIT	2	21.9	RLEARPTADLCIDCK	1817.9	R	T	2.5	0.7	11.2	18.2
P0ABS1	17510.1	S	U	T	C	CID	LIT	2	21.9	TVTHMQDEAANFPDPVDR	2042.9	R	A	4.9	0.6	54.3	12.6
P0ABS1	17510.1	S	U	T	B	CID	FT	2	19.9	AAQEEEFSLELR	1421.7	R	N	2.5	0.0	46.3	16.3
P0ABS1	17510.1	S	U	T	B	CID	FT	2	19.9	TVTHMQDEAANFPDPVDR	2042.9	R	A	4.3	0.0	57.0	12.3
P0ABS1	17510.1	S	U	T	A	ETD	LIT	3	37.7	NQLRDEVDR	1144.6	R	T	2.2	0.2	17.4	14.5
P0ABS1	17510.1	S	U	T	A	ETD	LIT	3	37.7	RLEARPTADLCIDCK	1817.9	R	T	1.7	0.4	13.0	18.1
P0ABS1	17510.1	S	U	T	A	ETD	LIT	3	37.7	TSSLSILAIAGVEPYQEKPGEEYMNEAQLAHFR	3678.8	K	R	0.0	0.0	29.1	19.1
P0ABS1	17510.1	S	U	T	B	ETD	LIT	2	16.6	RILEAWR	943.5	R	N	1.9	0.1	27.1	15.4
P0ABS1	17510.1	S	U	T	B	ETD	LIT	2	16.6	TVTHMQDEAANFPDPVDR	2042.9	R	A	2.4	0.0	29.7	12.3
P0ABS1	17510.1	S	U	T	C	ETD	LIT	3	26.5	RILEAWR	943.5	R	N	2.1	0.2	33.2	16.8
P0ABS1	17510.1	S	U	T	C	ETD	LIT	3	26.5	RLEARPTADLCIDCK	1817.9	R	T	3.9	0.0	41.1	18.2
P0ABS1	17510.1	S	U	T	C	ETD	LIT	3	26.5	TVTHMQDEAANFPDPVDR	2042.9	R	A	4.6	0.6	52.5	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	3	32.5	NQLRDEVDR	1144.6	R	T	0.0	0.0	35.7	14.5
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	3	32.5	RILEAWR	943.5	R	N	0.0	0.0	35.8	12.3
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	3	32.5	RLEARPTADLCIDCK	1817.9	R	T	0.0	0.0	40.4	17.9
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	3	32.5	TVTHMQDEAANFPDPVDR	2042.9	R	A	0.0	0.0	67.5	12.3
P0ABS1	17510.1	S	U	T	A	ETD+CID	LIT	2	17.9	NQLRDEVDR	1144.6	R	T	1.8	0.5	28.5	14.5
P0ABS1	17510.1	S	U	T	A	ETD+CID	LIT	2	17.9	TVTHMQDEAANFPDPVDR	2042.9	R	A	5.3	0.6	59.5	12.3
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	2	12.6	AAQEEEFSLELR	1421.7	R	N	2.1	0.2	0.0	0.0
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	2	12.6	RILEAWR	943.5	R	N	2.9	0.2	0.0	0.0
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	4	40.4	AAQEEEFSLELR	1421.7	R	N	2.1	0.2	0.0	0.0
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	4	40.4	NQLRDEVDR	1144.6	R	T	2.8	0.4	35.7	14.5
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	4	40.4	RILEAWR	943.5	R	N	2.9	0.2	35.8	12.3
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	4	40.4	RLEARPTADLCIDCK	1817.9	R	T	1.1	0.2	40.4	17.9
P0ABS1	17510.1	S	U	T	B	ETD+CID	LIT	4	40.4	TVTHMQDEAANFPDPVDR	2042.9	R	A	5.3	0.6	67.5	12.3
P0ABS1	17510.1	S	U	T	C	ETD+CID	LIT	3	38.4	RILEAWR	943.5	R	N	2.0	0.2	2.5	16.2
P0ABS1	17510.1	S	U	T	C	ETD+CID	LIT	3	38.4	TSSLSILAIAGVEPYQEKPGEEYMNEAQLAHFR	3678.8	K	R	4.6	0.0	40.8	19.2
P0ABS1	17510.1	S	U	T	C	ETD+CID	LIT	3	38.4	TVTHMQDEAANFPDPVDR	2042.9	R	A	5.4	0.6	59.6	11.8
P0ABS1	17510.1	S	U	T	B	HCD	FT	3	22.5	NQLRDEVDR	1144.6	R	T	0.0	0.0	35.7	14.5
P0ABS1	17510.1	S	U	T	B	HCD	FT	3	22.5	RILEAWR	943.5	R	N	0.0	0.0	35.8	12.3
P0ABS1	17510.1	S	U	T	B	HCD	FT	3	22.5	TVTHMQDEAANFPDPVDR	2042.9	R	A	0.0	0.0	67.5	12.3
P0A6G3	17563.3	G	T	T	A	CID	LIT	2	14.5	GFVTYSNEAK	1115.5	R	A	2.8	0.7	26.5	8.5
P0A6G3	17563.3	G	T	T	A	CID	LIT	2	14.5	VITDIAGSSAWFER	1551.8	K	G	4.7	0.8	84.5	12.8
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	AREVPAAIQK	1082.6	K	A	2.8	0.8	38.8	9.0
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	ATIDGLENMNSPEMVAAK	1890.9	R	R	4.7	0.8	66.8	9.5
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	ATIDGLENMNSPEMVAAKR	2047.0	R	G	5.1	0.9	78.7	12.3
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	AVLEVAGVHNVLAK	1419.8	R	A	5.1	0.6	70.9	7.0
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	AYGSTNPINVVR	1290.7	K	A	4.3	0.8	66.5	15.6
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	EVPAAIQK	855.5	R	A	1.7	0.6	29.8	12.0
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	GKSVEEILGK	1059.6	R	-	3.3	0.6	50.0	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	IFSFTALTVVGDGNGR	1653.9	R	V	4.2	0.0	79.0	9.5
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	LIAVNR	685.4	K	V	1.8	0.7	19.7	14.0
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	LIAVNRVSK	999.6	K	T	2.5	0.0	29.6	7.8
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	SVEEILGK	874.5	K	-	2.2	0.7	16.3	13.0
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	VFMQPASEGTGIIAGGAMR	1892.9	R	A	5.3	0.9	98.3	10.8
P0A7W1	17585.0	G	U	T	A	CID	LIT	13	69.5	VGFGYGK	727.4	R	A	1.7	0.8	18.2	10.0
P0A7W1	17585.0	G	T	T	A	CID	LIT	5	35.9	ATIDGLENMNSPEMVAAK	1890.9	R	R	3.7	0.5	48.0	10.0
P0A7W1	17585.0	G	T	T	A	CID	LIT	5	35.9	AVLEVAGVHNVLAK	1419.8	R	A	3.7	0.5	42.4	7.8
P0A7W1	17585.0	G	T	T	A	CID	LIT	5	35.9	AYGSTNPINVVR	1290.7	K	A	2.7	0.7	25.3	14.8
P0A7W1	17585.0	G	T	T	A	CID	LIT	5	35.9	GKSVEEILGK	1059.6	R	-	2.8	0.3	15.6	13.0
P0A7W1	17585.0	G	T	T	A	CID	LIT	5	35.9	LIAVNR	685.4	K	V	1.8	0.4	7.1	14.1
P0A7W1	17585.0	G	T	T	B	CID	LIT	3	20.4	AVLEVAGVHNVLAK	1419.8	R	A	1.8	0.5	0.0	0.0
P0A7W1	17585.0	G	T	T	B	CID	LIT	3	20.4	AYGSTNPINVVR	1290.7	K	A	3.7	0.7	51.4	14.8
P0A7W1	17585.0	G	T	T	B	CID	LIT	3	20.4	QAGELQEK	902.5	K	L	1.9	0.2	7.9	12.3
P0A7W1	17585.0	G	U	T	B	CID	LIT	5	28.1	AVLEVAGVHNVLAK	1419.8	R	A	4.2	0.6	44.1	7.8
P0A7W1	17585.0	G	U	T	B	CID	LIT	5	28.1	AYGSTNPINVVR	1290.7	K	A	3.5	0.6	57.0	14.5
P0A7W1	17585.0	G	U	T	B	CID	LIT	5	28.1	LIAVNR	685.4	K	V	1.7	0.4	10.1	14.0
P0A7W1	17585.0	G	U	T	B	CID	LIT	5	28.1	QAGELQEK	902.5	K	L	2.0	0.5	14.0	12.3
P0A7W1	17585.0	G	U	T	B	CID	LIT	5	28.1	VGFGYGK	727.4	R	A	1.8	0.0	16.6	9.0
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	ATIDGLENMNSPEMVAAK	1890.9	R	R	4.2	0.5	27.1	17.4
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	AVLEVAGVHNVLAK	1419.8	R	A	3.3	0.5	22.3	11.1
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	AYGSTNPINVVR	1290.7	K	A	2.8	0.4	26.7	18.2
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	EVPAAIQK	855.5	R	A	1.6	0.6	13.4	12.8
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	IFSFTALTVVGDGNGR	1653.9	R	V	4.6	0.5	62.1	16.4
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	QAGELQEK	902.5	K	L	2.3	0.4	33.2	16.7
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	RNMINVALNNGTLQHPVK	2019.1	R	G	5.0	0.5	40.5	17.2
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	SVEEILGK	874.5	K	-	2.4	0.2	36.7	17.5
P0A7W1	17585.0	S	U	T	A	CID	LIT	9	72.5	VFMQPASEGTGIIAGGAMR	1892.9	R	A	4.0	0.0	67.0	17.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	ATIDGLENMNSPEMVAAK	1906.9	R	R	3.6	0.8	40.0	15.8
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	ATIDGLENMNSPEMVAAKR	2047.0	R	G	2.6	0.6	19.6	18.4
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	AVLEVAGVHNVLAK	1420.8	R	A	2.1	0.2	0.0	0.0
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	AYGSTNPINVVR	1290.7	K	A	4.2	0.0	68.3	17.9
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	IFSFTALTVVGDGNGR	1654.8	R	V	3.8	0.6	56.7	15.7
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	LIAVNRVSK	999.6	K	T	2.0	0.0	25.0	12.3
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	NMINVALNNGTLQHPVKGVHTGSR	2558.3	R	V	2.8	0.5	18.7	17.3
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	RNMINVALNNGTLQHPVK	2020.1	R	G	6.0	0.6	62.3	17.4
P0A7W1	17585.0	S	U	T	B	CID	LIT	9	68.3	VFMQPASEGTGIIAGGAMR	1892.9	R	A	5.8	0.7	112.0	17.9
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	AREVPAAIQK	1082.6	K	A	2.1	0.3	24.8	11.1
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	ATIDGLENMNSPEMVAAK	1890.9	R	R	3.6	0.5	30.8	17.5
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	ATIDGLENMNSPEMVAAKR	2047.0	R	G	5.0	0.6	105.0	18.3
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	AVLEVAGVHNVLAK	1420.8	R	A	2.6	0.4	0.0	0.0
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	AYGSTNPINVVR	1290.7	K	A	2.1	0.4	0.0	0.0
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	GKSVEEILGK	1059.6	R	-	2.8	0.6	42.5	16.4
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	IFSFTALTVVGDGNGR	1653.9	R	V	4.3	0.6	66.7	16.4
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	QAGELQEK	902.5	K	L	2.1	0.4	25.8	16.7
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	RNMINVALNNGTLQHPVK	2020.1	R	G	5.3	0.6	45.3	17.5
P0A7W1	17585.0	S	U	T	C	CID	LIT	10	75.4	VFMQPASEGTGIIAGGAMR	1892.9	R	A	4.6	0.6	53.3	17.8
P0A7W1	17585.0	S	U	T	C	CID	FT	2	17.4	AYGSTNPINVVR	1290.7	K	A	2.8	0.0	47.3	16.8
P0A7W1	17585.0	S	U	T	C	CID	FT	2	17.4	NMINVALNNGTLQHPVK	1864.0	R	G	2.5	0.4	9.2	17.5
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	AREVPAAIQK	1082.6	K	A	2.7	0.4	47.7	11.8
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	ATIDGLENMNSPEMVAAK	1890.9	R	R	2.7	0.3	29.1	17.6
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	AVLEVAGVHNVLAK	1419.8	R	A	6.8	0.7	87.5	11.1
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	AYGSTNPINVVR	1290.7	K	A	1.7	0.6	56.3	18.6
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	EVPAAIQK	855.5	R	A	2.0	0.2	23.4	12.8
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	GKSVEEILGK	1059.6	R	-	2.9	0.1	11.5	16.2
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	IFSFTALTVVGDGNGR	1654.8	R	V	3.1	0.5	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	QAGELQEK	902.5	K	L	1.7	0.1	25.3	16.7
P0A7W1	17585.0	S	U	T	A	ETD	LIT	9	64.1	VFMQPASEGTGIIAGGAMR	1892.9	R	A	5.0	0.6	44.4	18.3
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	ATIDGLENMNSPEMVAAK	1890.9	R	R	2.6	0.0	35.5	17.0
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	AVLEVAGVHNVLAK	1419.8	R	A	5.8	0.6	79.8	11.5
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	AYGSTNPINVVR	1290.7	K	A	2.1	0.6	40.9	16.8
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	IFSFTALTVVGDGNGR	1654.8	R	V	2.0	0.5	0.0	0.0
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	NMINVALNNGTLQHPVK	1863.0	R	G	3.1	0.3	12.4	16.9
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	QAGELQEK	902.5	K	L	2.2	0.2	26.2	16.7
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	RNMINVALNNGTLQHPVK	2019.1	R	G	4.7	0.5	75.3	16.8
P0A7W1	17585.0	S	U	T	B	ETD	LIT	8	62.9	VFMQPASEGTGIIAGGAMR	1892.9	R	A	3.6	0.7	114.0	18.3
P0A7W1	17585.0	S	U	T	C	ETD	LIT	7	59.3	ATIDGLENMNSPEMVAAK	1890.9	R	R	2.8	0.2	48.0	17.2
P0A7W1	17585.0	S	U	T	C	ETD	LIT	7	59.3	AVLEVAGVHNVLAK	1419.8	R	A	5.1	0.7	62.0	11.1
P0A7W1	17585.0	S	U	T	C	ETD	LIT	7	59.3	AYGSTNPINVVR	1290.7	K	A	0.0	0.0	36.0	16.8
P0A7W1	17585.0	S	U	T	C	ETD	LIT	7	59.3	GKSVEEILGK	1059.6	R	-	1.9	0.4	11.4	16.3
P0A7W1	17585.0	S	U	T	C	ETD	LIT	7	59.3	QAGELQEK	902.5	K	L	2.0	0.2	28.0	16.7
P0A7W1	17585.0	S	U	T	C	ETD	LIT	7	59.3	RNMINVALNNGTLQHPVK	2019.1	R	G	3.1	0.7	35.1	16.9
P0A7W1	17585.0	S	U	T	C	ETD	LIT	7	59.3	VFMQPASEGTGIIAGGAMR	1892.9	R	A	5.0	0.5	32.9	17.8
P0A7W1	17585.0	S	U	T	C	ETD	FT	3	10.2	GKSVEEILGK	1059.6	R	-	1.6	0.0	20.3	15.1
P0A7W1	17585.0	S	U	T	C	ETD	FT	3	10.2	SVEEILGK	874.5	K	-	0.9	0.0	24.3	16.6
P0A7W1	17585.0	S	U	T	C	ETD	FT	3	10.2	VGFGYGK	727.4	R	A	1.1	0.0	24.7	10.4
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	AREVPAAIQK	1082.6	K	A	0.0	0.0	30.5	11.5
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	ATIDGLENMNSPEMVAAK	1890.9	R	R	0.0	0.0	20.9	17.6
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	AVLEVAGVHNVLAK	1419.8	R	A	0.0	0.0	28.4	11.1
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	IFSFTALTVVGDGNGR	1653.9	R	V	0.0	0.0	32.5	16.2
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	QAGELQEK	902.5	K	L	0.0	0.0	29.1	16.7
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	RNMINVALNNGTLQHPVK	2020.1	R	G	0.0	0.0	52.4	17.4
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	VFMQPASEGTGIIAGGAMR	1892.9	R	A	0.0	0.0	93.9	18.4
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	AREVPAAIQK	1082.6	K	A	2.2	0.4	21.5	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	ATIDGLENMNSPEMVAAK	1906.9	R	R	4.5	0.7	42.2	15.7
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	AVLEVAGVHNVLAK	1419.8	R	A	4.8	0.0	71.6	10.8
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	IFSFTALTVVGDGNGR	1653.9	R	V	5.3	0.6	0.0	0.0
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	NMINVALNNGTLQHPVKGVHTGSR	2558.3	R	V	4.0	0.6	36.0	17.9
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	QAGELQEK	902.5	K	L	2.2	0.5	32.8	16.7
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	RNMINVALNNGTLQHPVK	2020.1	R	G	4.6	0.5	37.5	16.7
P0A7W1	17585.0	S	U	T	A	ETD+CID	LIT	8	65.9	VFMQPASEGTGIIAGGAMR	1892.9	R	A	5.3	0.8	96.2	17.9
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	4	34.7	AREVPAAIQK	1082.6	K	A	2.5	0.5	0.0	0.0
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	4	34.7	ATIDGLENMNSPEMVAAK	1890.9	R	R	4.1	0.4	0.0	0.0
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	4	34.7	AVLEVAGVHNVLAK	1419.8	R	A	4.0	0.6	0.0	0.0
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	4	34.7	IFSFTALTVVGDGNGR	1654.8	R	V	3.2	0.4	0.0	0.0
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	AREVPAAIQK	1082.6	K	A	2.5	0.5	30.5	11.5
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	ATIDGLENMNSPEMVAAK	1890.9	R	R	4.1	0.4	20.9	17.6
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	AVLEVAGVHNVLAK	1419.8	R	A	4.0	0.6	28.4	11.1
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	IFSFTALTVVGDGNGR	1653.9	R	V	3.6	0.6	32.5	16.2
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	QAGELQEK	902.5	K	L	2.0	0.3	29.1	16.7
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	RNMINVALNNGTLQHPVK	2020.1	R	G	4.8	0.5	52.4	17.4
P0A7W1	17585.0	S	U	T	B	ETD+CID	LIT	7	61.7	VFMQPASEGTGIIAGGAMR	1892.9	R	A	5.0	0.7	93.9	18.4
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	AREVPAAIQK	1082.6	K	A	2.8	0.6	27.2	11.5
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	ATIDGLENMNSPEMVAAK	1890.9	R	R	3.6	0.4	21.9	17.5
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	AVLEVAGVHNVLAK	1419.8	R	A	4.6	0.6	45.1	11.5
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	AYGSTNPINVVR	1290.7	K	A	2.6	0.8	34.0	16.9
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	GKSVEEILGK	1059.6	R	-	0.0	0.0	48.8	16.3
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	IFSFTALTVVGDGNGR	1653.9	R	V	4.5	0.6	40.3	16.4
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	NMINVALNNGTLQHPVKGVHTGSR	2557.3	R	V	2.7	0.2	28.2	17.7
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	QAGELQEK	902.5	K	L	2.0	0.4	22.2	16.7
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	RNMINVALNNGTLQHPVK	2020.1	R	G	4.0	0.3	20.1	17.4
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	SVEEILGK	874.5	K	-	2.6	0.2	25.8	17.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7W1	17585.0	S	U	T	C	ETD+CID	LIT	11	79.0	VFMQPASEGTGIIAGGAMR	1892.9	R	A	5.6	0.7	95.5	17.8
P0A7W1	17585.0	S	U	T	B	HCD	FT	7	61.7	AREVPAAIQK	1082.6	K	A	0.0	0.0	30.5	11.5
P0A7W1	17585.0	S	U	T	B	HCD	FT	7	61.7	ATIDGLENMNSPEMVAAK	1890.9	R	R	0.0	0.0	20.9	17.6
P0A7W1	17585.0	S	U	T	B	HCD	FT	7	61.7	AVLEVAGVHNVLAK	1419.8	R	A	0.0	0.0	28.4	11.1
P0A7W1	17585.0	S	U	T	B	HCD	FT	7	61.7	IFSFTALTVVGDGNGR	1653.9	R	V	0.0	0.0	32.5	16.2
P0A7W1	17585.0	S	U	T	B	HCD	FT	7	61.7	QAGELQEK	902.5	K	L	0.0	0.0	29.1	16.7
P0A7W1	17585.0	S	U	T	B	HCD	FT	7	61.7	RNMINVALNNGTLQHPVK	2020.1	R	G	0.0	0.0	52.4	17.4
P0A7W1	17585.0	S	U	T	B	HCD	FT	7	61.7	VFMQPASEGTGIIAGGAMR	1892.9	R	A	0.0	0.0	93.9	18.4
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	AGVDVLGISTDKPEK	1528.8	K	L	4.3	0.6	68.3	12.3
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	AGVDVLGISTDKPEKLSR	1885.0	K	F	2.9	0.0	39.5	9.5
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	AMTPGCTVQACGLR	1521.7	K	D	4.3	0.6	64.4	9.5
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	DNMDELKK	992.5	R	A	2.3	0.6	30.8	11.8
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	4.6	0.9	68.4	7.8
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	ISFLIDADGKIEHVFDDFK	2209.1	R	T	2.2	0.8	6.3	11.1
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	KAGVDVLGISTDKPEK	1656.9	K	L	3.1	0.5	13.6	10.4
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	MNPLKAGDIAPK	1254.7	-	F	3.3	0.0	28.6	11.1
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	TSNHHDVVLNWLK	1562.8	K	E	3.3	0.0	43.2	11.8
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	TYDGIHR	861.4	K	I	2.3	0.7	30.7	13.8
P0AE52	17616.2	G	U	T	A	CID	LIT	11	76.3	VLVYFYPK	1028.6	R	A	2.6	0.8	33.1	13.0
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DADGKIEHVF	1130.5	I	D	3.1	0.8	22.0	14.3
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DDFKTSNHH	1100.5	F	D	2.5	0.0	15.4	7.8
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DELKKAGV	859.5	M	D	1.8	0.2	26.6	16.7
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DELKKAGVDVLGIST	1544.9	M	D	3.2	0.0	28.2	14.3
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DGIHRISFLI	1170.7	Y	D	2.0	0.5	15.9	13.8
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DGIHRISFLIDA	1356.7	Y	D	1.9	0.6	29.5	14.5
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DGKIEHVF	944.5	A	D	2.6	0.8	18.6	13.2
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DGKIEHVFD	1059.5	A	D	2.0	0.6	18.8	14.3
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DNMDELKKAGV	1219.6	R	D	2.7	0.4	11.7	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE52	17616.2	G	U	A	A	CID	LIT	10	37.2	DVVLNWLKEHA	1323.7	H	-	3.3	0.5	45.3	9.5
P0AE52	17616.2	G	T	T	B	CID	LIT	3	24.4	AGVDVLGISTDKPEKLSR	1885.0	K	F	3.1	0.0	36.9	9.5
P0AE52	17616.2	G	T	T	B	CID	LIT	3	24.4	MNPLKAGDIAPK	1254.7	-	F	2.9	0.8	18.1	11.1
P0AE52	17616.2	G	T	T	B	CID	LIT	3	24.4	VLVYFYPK	1028.6	R	A	2.1	0.6	32.0	13.0
P0AE52	17616.2	G	T	A	B	CID	LIT	2	11.5	DELKKAGV	859.5	M	D	1.6	0.4	16.1	16.8
P0AE52	17616.2	G	T	A	B	CID	LIT	2	11.5	DGIHRISFLI	1170.7	Y	D	2.5	0.3	19.9	13.8
P0AE52	17616.2	S	U	T	A	CID	LIT	4	34.6	AGVDVLGISTDKPEK	1528.8	K	L	4.5	0.6	54.4	16.8
P0AE52	17616.2	S	U	T	A	CID	LIT	4	34.6	AGVDVLGISTDKPEKLSR	1885.0	K	F	2.9	0.7	28.2	14.8
P0AE52	17616.2	S	U	T	A	CID	LIT	4	34.6	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	4.4	0.8	66.4	16.5
P0AE52	17616.2	S	U	T	A	CID	LIT	4	34.6	TSNHHDVVLNWLKEHA	1899.9	K	-	3.4	0.2	23.0	17.4
P0AE52	17616.2	S	U	T	B	CID	LIT	6	46.8	AGVDVLGISTDKPEK	1528.8	K	L	4.5	0.6	57.4	15.9
P0AE52	17616.2	S	U	T	B	CID	LIT	6	46.8	AMTPGCTVQACGLR	1521.7	K	D	3.4	0.0	51.5	14.5
P0AE52	17616.2	S	U	T	B	CID	LIT	6	46.8	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	5.0	0.7	96.9	16.2
P0AE52	17616.2	S	U	T	B	CID	LIT	6	46.8	TSNHHDVVLNWLK	1562.8	K	E	4.0	0.6	42.9	17.0
P0AE52	17616.2	S	U	T	B	CID	LIT	6	46.8	TSNHHDVVLNWLKEHA	1899.9	K	-	4.2	0.4	10.8	18.1
P0AE52	17616.2	S	U	T	B	CID	LIT	6	46.8	VLVYFYPK	1028.6	R	A	2.7	0.8	50.8	15.3
P0AE52	17616.2	S	U	T	C	CID	LIT	5	44.2	AGVDVLGISTDKPEK	1528.8	K	L	4.5	0.6	50.2	16.8
P0AE52	17616.2	S	U	T	C	CID	LIT	5	44.2	AMTPGCTVQACGLR	1521.7	K	D	3.5	0.0	67.4	14.0
P0AE52	17616.2	S	U	T	C	CID	LIT	5	44.2	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	4.8	0.7	82.4	16.1
P0AE52	17616.2	S	U	T	C	CID	LIT	5	44.2	MNPLKAGDIAPK	1254.7	-	F	2.3	0.5	0.0	0.0
P0AE52	17616.2	S	U	T	C	CID	LIT	5	44.2	VLVYFYPK	1028.6	R	A	1.9	0.5	19.2	15.6
P0AE52	17616.2	S	U	T	A	ETD	LIT	3	16.0	AGDIAPK	671.4	K	F	1.9	0.5	9.0	10.4
P0AE52	17616.2	S	U	T	A	ETD	LIT	3	16.0	AGVDVLGISTDKPEK	1528.8	K	L	3.2	0.4	67.4	16.6
P0AE52	17616.2	S	U	T	A	ETD	LIT	3	16.0	AGVDVLGISTDKPEKLSR	1885.0	K	F	5.5	0.4	98.8	14.8
P0AE52	17616.2	S	U	T	B	ETD	LIT	3	32.7	AGVDVLGISTDKPEK	1528.8	K	L	1.4	0.5	42.2	15.9
P0AE52	17616.2	S	U	T	B	ETD	LIT	3	32.7	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	1.8	0.6	15.9	16.4
P0AE52	17616.2	S	U	T	B	ETD	LIT	3	32.7	TSNHHDVVLNWLKEHA	1899.9	K	-	4.0	0.0	20.9	18.0
P0AE52	17616.2	S	U	T	C	ETD	LIT	4	36.5	AGVDVLGISTDKPEK	1528.8	K	L	2.3	0.5	70.8	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE52	17616.2	S	U	T	C	ETD	LIT	4	36.5	AMTPGCTVQACGLR	1521.7	K	D	2.1	0.7	25.1	14.0
P0AE52	17616.2	S	U	T	C	ETD	LIT	4	36.5	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	1.9	0.7	0.0	0.0
P0AE52	17616.2	S	U	T	C	ETD	LIT	4	36.5	VLVYFYPK	1028.6	R	A	2.5	0.3	13.9	15.3
P0AE52	17616.2	S	U	T	B	ETD+CID	LIT	2	22.4	AGVDVLGISTDKPEK	1528.8	K	L	0.0	0.0	46.5	15.9
P0AE52	17616.2	S	U	T	B	ETD+CID	LIT	2	22.4	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	0.0	0.0	66.3	16.1
P0AE52	17616.2	S	U	T	A	ETD+CID	LIT	4	29.5	AGVDVLGISTDKPEK	1528.8	K	L	4.6	0.6	54.6	15.9
P0AE52	17616.2	S	U	T	A	ETD+CID	LIT	4	29.5	AGVDVLGISTDKPEKLSR	1885.0	K	F	3.1	0.6	23.7	15.4
P0AE52	17616.2	S	U	T	A	ETD+CID	LIT	4	29.5	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	4.8	0.8	83.6	16.4
P0AE52	17616.2	S	U	T	A	ETD+CID	LIT	4	29.5	VLVYFYPK	1028.6	R	A	2.1	0.4	0.0	0.0
P0AE52	17616.2	S	U	T	B	ETD+CID	LIT	3	32.7	AGVDVLGISTDKPEK	1528.8	K	L	4.9	0.6	46.5	15.9
P0AE52	17616.2	S	U	T	B	ETD+CID	LIT	3	32.7	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	5.4	0.7	66.3	16.1
P0AE52	17616.2	S	U	T	B	ETD+CID	LIT	3	32.7	TSNHHDVVLNWLKEHA	1899.9	K	-	3.6	0.5	11.9	17.6
P0AE52	17616.2	S	U	T	C	ETD+CID	LIT	4	38.5	AGVDVLGISTDKPEKLSR	1885.0	K	F	4.6	0.4	62.2	16.1
P0AE52	17616.2	S	U	T	C	ETD+CID	LIT	4	38.5	AMTPGCTVQACGLR	1521.7	K	D	3.6	0.5	68.6	14.0
P0AE52	17616.2	S	U	T	C	ETD+CID	LIT	4	38.5	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	4.5	0.6	65.4	16.1
P0AE52	17616.2	S	U	T	C	ETD+CID	LIT	4	38.5	VLVYFYPK	1028.6	R	A	2.0	0.7	14.0	15.3
P0AE52	17616.2	S	U	T	B	HCD	FT	2	22.4	AGVDVLGISTDKPEK	1528.8	K	L	0.0	0.0	46.5	15.9
P0AE52	17616.2	S	U	T	B	HCD	FT	2	22.4	FSLPDQDGEQVNLTDFQGQR	2294.1	K	V	0.0	0.0	66.3	16.1
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	EHGDLKENAEYHAAR	1739.8	R	E	3.5	0.0	38.8	9.0
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	EQQGFCEGR	1110.5	R	I	2.8	0.0	34.4	3.0
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	GLIGKEEDDVVVIK	1513.8	R	T	4.6	0.6	55.3	11.8
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	IVGDDEADFKQNLISVNSPIAR	2401.2	R	G	4.8	0.6	45.2	11.8
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	LREELDFLK	1162.6	K	S	4.0	0.4	25.6	13.2
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	LSNAQVIDVTK	1187.7	K	M	4.2	0.8	58.6	12.6
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	MQAIPMTLR	1060.6	-	G	1.7	0.6	18.6	14.8
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	RPEIIAAIAEAR	1309.8	R	E	3.8	0.8	61.2	9.5
P0A6W5	17623.1	G	U	T	A	CID	LIT	9	65.8	SVRRPEIIAAIAEAR	1652.0	K	E	3.7	0.0	23.6	7.0
P0A6W5	17623.1	G	T	T	A	CID	LIT	2	11.4	LREELDFLK	1162.6	K	S	3.6	0.5	18.0	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6W5	17623.1	G	T	T	A	CID	LIT	2	11.4	MQAIPMTLR	1060.6	-	G	2.7	0.3	22.1	14.8
P0A6W5	17623.1	G	T	T	B	CID	LIT	7	44.3	EQQGFCEGR	1110.5	R	I	2.6	0.0	33.0	4.8
P0A6W5	17623.1	G	T	T	B	CID	LIT	7	44.3	IVGDDEADFKQNLISVNSPIAR	2401.2	R	G	3.0	0.4	0.0	0.0
P0A6W5	17623.1	G	T	T	B	CID	LIT	7	44.3	LREELDFLK	1162.6	K	S	1.7	0.3	10.6	13.2
P0A6W5	17623.1	G	T	T	B	CID	LIT	7	44.3	LSNAQVIDVTK	1187.7	K	M	3.5	0.7	47.9	12.6
P0A6W5	17623.1	G	T	T	B	CID	LIT	7	44.3	LSNAQVIDVTKMPNNGR	1857.0	K	V	3.4	0.0	43.3	12.0
P0A6W5	17623.1	G	T	T	B	CID	LIT	7	44.3	MQAIPMTLR	1060.6	-	G	2.5	0.4	28.8	15.7
P0A6W5	17623.1	G	T	T	B	CID	LIT	7	44.3	MQAIPMTLRGAEK	1445.8	-	L	2.7	0.4	24.7	14.3
P0A6W5	17623.1	G	T	A	B	CID	LIT	4	36.1	DFKQNLISVNSPIARGLIGKEE	2428.3	A	D	4.8	0.0	31.9	13.8
P0A6W5	17623.1	G	T	A	B	CID	LIT	4	36.1	DIEAKLSNAQVI	1300.7	K	D	2.9	0.7	40.5	14.0
P0A6W5	17623.1	G	T	A	B	CID	LIT	4	36.1	DLKENAEYHAAR	1416.7	G	E	3.4	0.8	57.2	12.6
P0A6W5	17623.1	G	T	A	B	CID	LIT	4	36.1	EYHAAREQQGFCEGRIK	2079.0	A	D	3.3	0.7	9.7	14.3
P0A6W5	17623.1	S	U	T	A	CID	LIT	4	27.2	EHGDLKENAEYHAAR	1739.8	R	E	4.6	0.8	44.7	14.1
P0A6W5	17623.1	S	U	T	A	CID	LIT	4	27.2	IKDIEAK	816.5	R	L	2.3	0.0	19.9	18.9
P0A6W5	17623.1	S	U	T	A	CID	LIT	4	27.2	LREELDFLK	1162.6	K	S	1.8	0.3	9.5	15.6
P0A6W5	17623.1	S	U	T	A	CID	LIT	4	27.2	RPEIIAAIAEAR	1309.8	R	E	3.6	0.7	38.2	11.5
P0A6W5	17623.1	S	U	T	B	CID	LIT	3	23.4	GLIGKEEDDVVVIK	1513.8	R	T	4.1	0.5	51.5	15.1
P0A6W5	17623.1	S	U	T	B	CID	LIT	3	23.4	LSNAQVIDVTK	1187.7	K	M	3.7	0.6	76.3	16.3
P0A6W5	17623.1	S	U	T	B	CID	LIT	3	23.4	RPEIIAAIAEAR	1309.8	R	E	3.4	0.8	44.5	11.5
P0A6W5	17623.1	S	U	T	C	CID	LIT	4	31.6	EHGDLKENAEYHAAR	1739.8	R	E	2.4	0.4	17.3	14.9
P0A6W5	17623.1	S	U	T	C	CID	LIT	4	31.6	EQQGFCEGR	1110.5	R	I	2.0	0.0	27.0	7.0
P0A6W5	17623.1	S	U	T	C	CID	LIT	4	31.6	GLIGKEEDDVVVIK	1513.8	R	T	3.6	0.4	32.3	15.6
P0A6W5	17623.1	S	U	T	C	CID	LIT	4	31.6	RPEIIAAIAEAR	1309.8	R	E	3.6	0.8	37.2	11.1
P0A6W5	17623.1	S	U	T	A	ETD	LIT	2	13.3	LREELDFLK	1162.6	K	S	1.8	0.5	24.3	15.6
P0A6W5	17623.1	S	U	T	A	ETD	LIT	2	13.3	RPEIIAAIAEAR	1309.8	R	E	2.1	0.4	20.3	11.1
P0A6W5	17623.1	S	U	T	B	ETD	LIT	2	17.1	EHGDLKENAEYHAAR	1739.8	R	E	7.6	0.7	54.3	14.9
P0A6W5	17623.1	S	U	T	B	ETD	LIT	2	17.1	RPEIIAAIAEAR	1309.8	R	E	3.0	0.4	34.9	11.1
P0A6W5	17623.1	S	U	T	C	ETD	LIT	3	20.3	LREELDFLK	1162.6	K	S	2.3	0.5	37.2	15.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6W5	17623.1	S	U	T	C	ETD	LIT	3	20.3	LSNAQVIDVTK	1187.7	K	M	2.3	0.2	37.2	16.1
P0A6W5	17623.1	S	U	T	C	ETD	LIT	3	20.3	RPEIIAAIAEAR	1309.8	R	E	2.7	0.5	26.8	11.1
P0A6W5	17623.1	S	U	T	B	ETD+CID	LIT	3	24.1	GLIGKEEDDVVVIK	1513.8	R	T	0.0	0.0	63.2	15.1
P0A6W5	17623.1	S	U	T	B	ETD+CID	LIT	3	24.1	QNLISVNSPIAR	1311.7	K	G	0.0	0.0	35.2	13.4
P0A6W5	17623.1	S	U	T	B	ETD+CID	LIT	3	24.1	RPEIIAAIAEAR	1309.8	R	E	0.0	0.0	30.3	11.1
P0A6W5	17623.1	S	U	T	A	ETD+CID	LIT	3	30.4	GLIGKEEDDVVVIK	1513.8	R	T	3.3	0.5	24.2	15.2
P0A6W5	17623.1	S	U	T	A	ETD+CID	LIT	3	30.4	IVGDDEADFKQNLISVNSPIAR	2401.2	R	G	3.4	0.2	3.5	18.1
P0A6W5	17623.1	S	U	T	A	ETD+CID	LIT	3	30.4	RPEIIAAIAEAR	1309.8	R	E	3.0	0.6	24.0	11.1
P0A6W5	17623.1	S	U	T	B	ETD+CID	LIT	4	33.5	EHGDLKENAEYHAAR	1739.8	R	E	2.3	0.6	14.6	14.9
P0A6W5	17623.1	S	U	T	B	ETD+CID	LIT	4	33.5	GLIGKEEDDVVVIK	1513.8	R	T	4.2	0.4	63.2	15.1
P0A6W5	17623.1	S	U	T	B	ETD+CID	LIT	4	33.5	QNLISVNSPIAR	1311.7	K	G	3.2	0.0	35.2	13.4
P0A6W5	17623.1	S	U	T	B	ETD+CID	LIT	4	33.5	RPEIIAAIAEAR	1309.8	R	E	3.0	0.8	30.3	11.1
P0A6W5	17623.1	S	U	T	C	ETD+CID	LIT	5	36.7	GLIGKEEDDVVVIK	1513.8	R	T	3.9	0.5	58.9	15.1
P0A6W5	17623.1	S	U	T	C	ETD+CID	LIT	5	36.7	LREELDFLK	1162.6	K	S	2.7	0.3	22.0	15.1
P0A6W5	17623.1	S	U	T	C	ETD+CID	LIT	5	36.7	LSNAQVIDVTK	1187.7	K	M	2.5	0.4	22.4	16.3
P0A6W5	17623.1	S	U	T	C	ETD+CID	LIT	5	36.7	QNLISVNSPIAR	1311.7	K	G	2.8	0.6	32.7	13.4
P0A6W5	17623.1	S	U	T	C	ETD+CID	LIT	5	36.7	RPEIIAAIAEAR	1309.8	R	E	4.2	0.0	36.3	11.1
P0A6W5	17623.1	S	U	T	B	HCD	FT	4	33.5	EHGDLKENAEYHAAR	1739.8	R	E	0.0	0.0	14.6	14.9
P0A6W5	17623.1	S	U	T	B	HCD	FT	4	33.5	GLIGKEEDDVVVIK	1513.8	R	T	0.0	0.0	63.2	15.1
P0A6W5	17623.1	S	U	T	B	HCD	FT	4	33.5	QNLISVNSPIAR	1311.7	K	G	0.0	0.0	35.2	13.4
P0A6W5	17623.1	S	U	T	B	HCD	FT	4	33.5	RPEIIAAIAEAR	1309.8	R	E	0.0	0.0	30.3	11.1
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	ALMVHVGGDNMSDQPKPLGGGGER	2454.2	K	Y	4.0	0.0	45.3	10.8
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	ALPPGEHGFHIHAK	1510.8	K	G	2.6	0.0	28.0	11.8
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	ASAAESAGGHLDPQNTGK	1710.8	K	H	4.5	0.8	60.4	10.0
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	ASAAESAGGHLDPQNTGKHEGPEGAGHLGDLPALVVNNDGK	3987.9	K	A	4.2	0.0	24.6	11.5
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	ATDAVIAPR	913.5	K	L	3.3	0.0	50.6	12.6
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	DGKASAAESAGGHLDPQNTGK	2010.9	K	H	5.0	0.8	80.3	11.5
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	GSCQPATK	848.4	K	D	2.1	0.6	22.1	9.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	HEGPEGAGHLGDLPALVVNNDGK	2296.1	K	A	4.9	0.0	32.2	13.0
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	LKSLDEIK	945.6	R	D	2.9	0.4	15.0	13.8
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	SLDEIKDK	947.5	K	A	2.9	0.4	41.7	14.6
P0AGD1	17663.0	G	T	T	A	CID	LIT	11	67.1	YACGVIK	810.4	R	-	2.0	0.6	0.0	0.0
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DAVIAPRLKSL	1182.7	T	D	2.7	0.0	30.4	9.0
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DGKASAAESAGGHL	1270.6	K	D	3.3	0.7	22.8	14.6
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DGKATDAVIAPRLKSL	1654.9	N	D	3.2	0.0	15.9	8.5
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DKALMVHVGGDNMS	1473.7	K	D	4.0	0.6	56.5	14.0
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DLPALVVNNDGKAT	1426.8	G	D	2.7	0.6	25.8	13.0
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DLPALVVNNDGKATDAVIAPRLKSL	2590.5	G	D	3.2	0.0	27.9	12.0
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DPQNTGKHEGPEGAGHLG	1800.8	L	D	3.4	0.7	56.2	11.8
P0AGD1	17663.0	G	T	A	A	CID	LIT	8	52.0	DQPKPLGGGGERYACGVIK	2002.0	S	-	2.6	0.7	0.0	0.0
P0AGD1	17663.0	G	T	T	B	CID	LIT	5	27.7	ALMVHVGGDNMSDQPKPLGGGGER	2422.2	K	Y	4.9	0.0	50.0	9.0
P0AGD1	17663.0	G	T	T	B	CID	LIT	5	27.7	ALMVHVGGDNMSDQPKPLGGGGERYACGVIK	3213.6	K	-	2.8	0.3	4.0	12.3
P0AGD1	17663.0	G	T	T	B	CID	LIT	5	27.7	ATDAVIAPR	913.5	K	L	2.6	0.6	36.7	12.6
P0AGD1	17663.0	G	T	T	B	CID	LIT	5	27.7	SLDEIKDK	947.5	K	A	2.3	0.1	16.9	14.6
P0AGD1	17663.0	G	T	T	B	CID	LIT	5	27.7	YACGVIK	810.4	R	-	2.0	0.6	27.6	12.8
P0AGD1	17663.0	G	T	A	B	CID	LIT	7	60.7	DAVIAPRLKSL	1182.7	T	D	2.6	0.0	26.1	9.0
P0AGD1	17663.0	G	T	A	B	CID	LIT	7	60.7	DGKASAAESAGGHL	1270.6	K	D	4.0	0.6	60.8	13.2
P0AGD1	17663.0	G	T	A	B	CID	LIT	7	60.7	DKALMVHVGG	1026.5	K	D	3.6	0.6	4.0	8.5
P0AGD1	17663.0	G	T	A	B	CID	LIT	7	60.7	DKGLEFSP	892.4	T	D	2.2	0.2	25.1	17.2
P0AGD1	17663.0	G	T	A	B	CID	LIT	7	60.7	DLKALPPGEHGFHIHAKGSCQPATK	2696.4	P	D	2.6	0.8	16.8	14.8
P0AGD1	17663.0	G	T	A	B	CID	LIT	7	60.7	DPQNTGKHEGPEGAGHLG	1800.8	L	D	3.6	0.0	53.7	11.5
P0AGD1	17663.0	G	T	A	B	CID	LIT	7	60.7	DQPKPLGGGGERYACGVIK	2002.0	S	-	3.1	0.0	31.7	15.2
P0AEU7	17670.4	G	U	T	A	CID	LIT	7	54.7	AQAFEQDR	964.4	K	A	2.5	0.6	33.7	12.8
P0AEU7	17670.4	G	U	T	A	CID	LIT	7	54.7	IAIVNMGSLFQQVAQK	1763.0	K	T	4.4	0.6	76.6	11.8
P0AEU7	17670.4	G	U	T	A	CID	LIT	7	54.7	LEKDVMAQR	1105.6	K	Q	3.1	0.7	48.8	12.0
P0AEU7	17670.4	G	U	T	A	CID	LIT	7	54.7	METDLQAK	935.5	R	M	2.1	0.8	7.5	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AEU7	17670.4	G	U	T	A	CID	LIT	7	54.7	SVANSQDIDLVVDANAVAYNSSDVKDITADVLK	3449.7	K	Q	5.4	0.0	68.6	10.4
P0AEU7	17670.4	G	U	T	A	CID	LIT	7	54.7	TGVSNTLENEFK	1338.7	K	G	3.4	0.4	40.6	10.4
P0AEU7	17670.4	G	U	T	A	CID	LIT	7	54.7	TGVSNTLENEFKGR	1551.8	K	A	4.1	0.8	84.3	13.6
P0AEU7	17670.4	G	T	T	A	CID	LIT	5	28.0	AQAFEQDR	964.4	K	A	1.9	0.6	28.1	12.8
P0AEU7	17670.4	G	T	T	A	CID	LIT	5	28.0	DITADVLK	874.5	K	Q	2.0	0.6	4.5	13.0
P0AEU7	17670.4	G	T	T	A	CID	LIT	5	28.0	LEKDVMAQR	1105.6	K	Q	2.8	0.7	48.5	12.0
P0AEU7	17670.4	G	T	T	A	CID	LIT	5	28.0	METDLQAK	935.5	R	M	2.2	0.5	3.0	10.4
P0AEU7	17670.4	G	T	T	A	CID	LIT	5	28.0	TGVSNTLENEFK	1338.7	K	G	3.5	0.6	44.6	10.4
P0AEU7	17670.4	G	U	A	A	CID	LIT	3	23.6	DANAVAYNSSDVK	1353.6	V	D	3.2	0.9	60.8	14.6
P0AEU7	17670.4	G	U	A	A	CID	LIT	3	23.6	DVLKQVK	829.5	A	-	1.8	0.5	5.5	13.6
P0AEU7	17670.4	G	U	A	A	CID	LIT	3	23.6	DVMAQRQTFAQKAQAFEQ	2097.0	K	D	5.0	0.7	64.8	15.2
P0AEU7	17670.4	G	T	A	A	CID	LIT	3	21.7	DANAVAYNSS	1011.4	V	D	1.8	0.4	7.5	10.4
P0AEU7	17670.4	G	T	A	A	CID	LIT	3	21.7	DVLKQVK	829.5	A	-	1.9	0.4	18.0	13.6
P0AEU7	17670.4	G	T	A	A	CID	LIT	3	21.7	DVMAQRQTFAQKAQAFEQ	2097.0	K	D	4.7	0.6	48.5	15.2
P0AEU7	17670.4	G	T	T	B	CID	LIT	2	13.7	AQAFEQDR	964.4	K	A	2.4	0.5	26.7	12.8
P0AEU7	17670.4	G	T	T	B	CID	LIT	2	13.7	TGVSNTLENEFKGR	1551.8	K	A	2.3	0.4	13.5	13.6
P0AEU7	17670.4	G	T	A	B	CID	LIT	3	25.5	DLQAKMKKLQSMKAGS	1764.0	T	D	3.1	0.7	16.9	13.0
P0AEU7	17670.4	G	T	A	B	CID	LIT	3	25.5	DVLKQVK	829.5	A	-	1.8	0.6	14.7	13.6
P0AEU7	17670.4	G	T	A	B	CID	LIT	3	25.5	DVMAQRQTFAQKAQAFEQ	2097.0	K	D	4.4	0.6	42.0	16.0
P0AEU7	17670.4	G	U	A	B	CID	LIT	3	25.5	DLQAKMKKLQSMKAGS	1764.0	T	D	2.9	0.0	16.9	13.4
P0AEU7	17670.4	G	U	A	B	CID	LIT	3	25.5	DVLKQVK	829.5	A	-	1.8	0.3	13.8	13.6
P0AEU7	17670.4	G	U	A	B	CID	LIT	3	25.5	DVMAQRQTFAQKAQAFEQ	2097.0	K	D	4.9	0.7	37.4	16.0
P0AEU7	17670.4	S	U	T	A	CID	LIT	3	18.6	IAIVNMGSLFQQVAQK	1747.0	K	T	4.2	0.4	37.0	15.3
P0AEU7	17670.4	S	U	T	A	CID	LIT	3	18.6	TGVSNTLENEFK	1338.7	K	G	3.3	0.5	36.3	16.8
P0AEU7	17670.4	S	U	T	A	CID	LIT	3	18.6	TGVSNTLENEFKGR	1551.8	K	A	2.9	0.7	30.6	17.0
P0AEU7	17670.4	S	U	T	B	CID	LIT	3	32.9	IAIVNMGSLFQQVAQK	1747.0	K	T	5.7	0.6	73.0	15.6
P0AEU7	17670.4	S	U	T	B	CID	LIT	3	32.9	SVANSQDIDLVVDANAVAYNSSDVK	2594.3	K	D	3.6	0.3	14.5	18.5
P0AEU7	17670.4	S	U	T	B	CID	LIT	3	32.9	TGVSNTLENEFK	1338.7	K	G	3.6	0.5	50.6	15.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AEU7	17670.4	S	U	T	C	CID	LIT	6	44.1	IAIVNMGSLFQQVAQK	1747.0	K	T	5.8	0.6	85.3	15.4
P0AEU7	17670.4	S	U	T	C	CID	LIT	6	44.1	METDLQAK	935.5	R	M	2.1	0.4	27.1	15.2
P0AEU7	17670.4	S	U	T	C	CID	LIT	6	44.1	SVANSQDIDLVVDANAVAYNSSDVK	2594.3	K	D	4.3	0.4	22.4	19.1
P0AEU7	17670.4	S	U	T	C	CID	LIT	6	44.1	SVANSQDIDLVVDANAVAYNSSDVKDITADVLK	3449.7	K	Q	3.1	0.0	31.1	18.9
P0AEU7	17670.4	S	U	T	C	CID	LIT	6	44.1	TGVSNTLENEFK	1338.7	K	G	3.8	0.6	45.5	15.2
P0AEU7	17670.4	S	U	T	C	CID	LIT	6	44.1	TGVSNTLENEFKGR	1551.8	K	A	3.6	0.0	28.4	17.2
P0AEU7	17670.4	S	U	T	A	ETD	LIT	3	21.1	ASELQR	703.4	R	M	1.2	0.0	31.5	19.0
P0AEU7	17670.4	S	U	T	A	ETD	LIT	3	21.1	IAIVNMGSLFQQVAQK	1747.0	K	T	3.3	0.4	43.9	15.6
P0AEU7	17670.4	S	U	T	A	ETD	LIT	3	21.1	TGVSNTLENEFK	1338.7	K	G	3.4	0.5	30.7	15.2
P0AEU7	17670.4	S	U	T	B	ETD	LIT	4	23.6	AQAFEQDR	964.4	K	A	0.0	0.0	29.1	14.8
P0AEU7	17670.4	S	U	T	B	ETD	LIT	4	23.6	IAIVNMGSLFQQVAQK	1747.0	K	T	2.1	0.4	47.1	15.4
P0AEU7	17670.4	S	U	T	B	ETD	LIT	4	23.6	TGVSNTLENEFK	1338.7	K	G	3.0	0.6	31.8	16.8
P0AEU7	17670.4	S	U	T	B	ETD	LIT	4	23.6	TGVSNTLENEFKGR	1551.8	K	A	1.8	0.6	46.2	17.0
P0AEU7	17670.4	S	U	T	C	ETD	LIT	4	23.6	IAIVNMGSLFQQVAQK	1747.0	K	T	2.9	0.5	0.0	0.0
P0AEU7	17670.4	S	U	T	C	ETD	LIT	4	23.6	METDLQAK	935.5	R	M	2.3	0.2	36.5	14.6
P0AEU7	17670.4	S	U	T	C	ETD	LIT	4	23.6	TGVSNTLENEFK	1338.7	K	G	3.5	0.5	41.5	16.7
P0AEU7	17670.4	S	U	T	C	ETD	LIT	4	23.6	TGVSNTLENEFKGR	1551.8	K	A	2.8	0.4	61.8	17.1
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	2	30.4	IAIVNMGSLFQQVAQK	1747.0	K	T	0.0	0.0	82.9	15.6
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	2	30.4	SVANSQDIDLVVDANAVAYNSSDVKDITADVLK	3449.7	K	Q	0.0	0.0	29.7	19.1
P0AEU7	17670.4	S	U	T	A	ETD+CID	LIT	3	30.4	IAIVNMGSLFQQVAQK	1747.0	K	T	5.9	0.5	65.1	16.3
P0AEU7	17670.4	S	U	T	A	ETD+CID	LIT	3	30.4	SVANSQDIDLVVDANAVAYNSSDVK	2594.3	K	D	4.6	0.6	0.0	0.0
P0AEU7	17670.4	S	U	T	A	ETD+CID	LIT	3	30.4	SVANSQDIDLVVDANAVAYNSSDVKDITADVLK	3449.7	K	Q	3.6	0.7	0.0	0.0
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	6	44.1	AQAFEQDR	964.4	K	A	2.1	0.0	19.8	14.8
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	6	44.1	IAIVNMGSLFQQVAQK	1747.0	K	T	5.2	0.5	82.9	15.6
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	6	44.1	METDLQAK	935.5	R	M	2.0	0.4	19.3	14.6
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	6	44.1	QTFAQK	722.4	R	A	1.9	0.5	14.3	17.3
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	6	44.1	SVANSQDIDLVVDANAVAYNSSDVK	2594.3	K	D	3.0	0.4	0.0	0.0
P0AEU7	17670.4	S	U	T	B	ETD+CID	LIT	6	44.1	SVANSQDIDLVVDANAVAYNSSDVKDITADVLK	3449.7	K	Q	1.8	0.0	29.7	19.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AEU7	17670.4	S	U	T	C	ETD+CID	LIT	4	35.4	IAIVNMGSLFQQVAQK	1747.0	K	T	5.1	0.5	49.6	15.8
P0AEU7	17670.4	S	U	T	C	ETD+CID	LIT	4	35.4	METDLQAK	935.5	R	M	2.3	0.3	0.0	0.0
P0AEU7	17670.4	S	U	T	C	ETD+CID	LIT	4	35.4	SVANSQDIDLVVDANAVAYNSSDVK	2594.3	K	D	3.4	0.5	0.0	0.0
P0AEU7	17670.4	S	U	T	C	ETD+CID	LIT	4	35.4	SVANSQDIDLVVDANAVAYNSSDVKDITADVLK	3449.7	K	Q	2.9	0.0	24.2	18.8
P0AEU7	17670.4	S	U	T	B	HCD	FT	2	30.4	IAIVNMGSLFQQVAQK	1747.0	K	T	0.0	0.0	82.9	15.6
P0AEU7	17670.4	S	U	T	B	HCD	FT	2	30.4	SVANSQDIDLVVDANAVAYNSSDVKDITADVLK	3449.7	K	Q	0.0	0.0	29.7	19.1
P0A8N0	17675.8	G	U	T	A	CID	LIT	4	18.0	HFNAEHQHTR	1276.6	R	K	3.5	0.0	44.6	9.5
P0A8N0	17675.8	G	U	T	A	CID	LIT	4	18.0	HMNPELVNR	1109.6	K	M	2.0	0.6	9.5	13.2
P0A8N0	17675.8	G	U	T	A	CID	LIT	4	18.0	LAGLAQR	728.4	R	R	2.2	0.7	43.2	13.8
P0A8N0	17675.8	G	U	T	A	CID	LIT	4	18.0	RHFNAEHQHTR	1432.7	K	K	4.2	0.9	24.8	11.1
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	AAAFEGELIPASQIDR	1687.9	K	L	3.2	0.5	50.4	12.0
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	ALNLQDKQAIVAEVSEVAK	2026.1	M	G	0.0	0.0	81.9	9.5
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	ANAKFEVK	906.5	K	A	2.4	0.6	36.2	14.1
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	DAFVGPTLIAYSMEHPGAAAR	2174.1	K	L	2.6	0.6	13.8	12.6
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	GALSAVVADSR	1045.6	K	G	3.9	0.5	94.9	14.8
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	GVTVDKMTELR	1248.7	R	K	3.2	0.7	64.2	10.0
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	LATLPTYEEAIAR	1447.8	R	L	3.3	0.8	60.7	11.1
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	LFKEFAK	882.5	R	A	2.2	0.7	29.5	11.1
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	LMATMK	694.4	R	E	1.6	0.7	21.7	13.2
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	LMATMKEASAGK	1237.6	R	L	3.3	0.7	59.6	13.0
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	QAIVAEVSEVAK	1243.7	K	G	2.9	0.0	29.1	13.8
P0A7J3	17693.8	G	U	T	A	CID	LIT	12	75.2	TLAAVR	630.4	R	D	1.7	0.5	12.1	19.1
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	AAAFEGELIPASQIDR	1687.9	K	L	3.0	0.4	10.1	12.0
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	ALNLQDKQAIVAEVSEVAK	2026.1	M	G	0.0	0.0	73.2	9.5
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	ANAKFEVK	906.5	K	A	1.9	0.4	3.8	14.5
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	AVEGTPFECLK	1250.6	R	D	2.4	0.5	30.1	12.3
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	DAFVGPTLIAYSMEHPGAAAR	2190.1	K	L	2.2	0.8	9.0	13.0
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	GALSAVVADSR	1045.6	K	G	3.8	0.5	75.7	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	GVTVDKMTELR	1248.7	R	K	3.3	0.6	55.8	13.0
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	LATLPTYEEAIAR	1447.8	R	L	2.7	0.7	41.4	11.1
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	MTELR	649.3	K	K	1.6	0.5	14.8	16.3
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	QAIVAEVSEVAK	1243.7	K	G	3.6	0.8	53.2	12.3
P0A7J3	17693.8	G	T	T	A	CID	LIT	11	67.3	RAVEGTPFECLK	1406.7	R	D	4.1	0.5	40.5	12.6
P0A7J3	17693.8	G	U	A	A	CID	LIT	3	17.6	DKQAIVAEVS	1059.6	Q	E	2.4	0.3	28.0	18.4
P0A7J3	17693.8	G	U	A	A	CID	LIT	3	17.6	DKQAIVAEVSEVAKGALSAVVA	2155.2	Q	D	5.0	0.6	69.6	12.0
P0A7J3	17693.8	G	U	A	A	CID	LIT	3	17.6	DSRGVTV	733.4	A	D	2.0	0.5	21.6	16.1
P0A7J3	17693.8	G	T	A	A	CID	LIT	4	17.6	DKQAIVAEVS	1059.6	Q	E	2.5	0.7	40.1	18.0
P0A7J3	17693.8	G	T	A	A	CID	LIT	4	17.6	DKQAIVAEVSEVAKGALSAVVA	2155.2	Q	D	5.5	0.6	95.7	12.0
P0A7J3	17693.8	G	T	A	A	CID	LIT	4	17.6	DSRGVTV	733.4	A	D	1.9	0.7	19.1	16.1
P0A7J3	17693.8	G	T	A	A	CID	LIT	4	17.6	EVAKGALSAVVA	1114.6	S	D	2.1	0.6	20.3	12.8
P0A7J3	17693.8	G	T	T	B	CID	LIT	6	41.8	AAAFEGELIPASQIDR	1687.9	K	L	2.1	0.2	21.8	12.0
P0A7J3	17693.8	G	T	T	B	CID	LIT	6	41.8	ALNLQDKQAIVAEVSEVAK	2026.1	M	G	0.0	0.0	38.8	7.8
P0A7J3	17693.8	G	T	T	B	CID	LIT	6	41.8	GALSAVVADSR	1045.6	K	G	3.6	0.4	72.3	14.1
P0A7J3	17693.8	G	T	T	B	CID	LIT	6	41.8	GVTVDKMTELR	1264.7	R	K	3.2	0.7	41.1	13.2
P0A7J3	17693.8	G	T	T	B	CID	LIT	6	41.8	QAIVAEVSEVAK	1243.7	K	G	3.7	0.8	57.3	12.3
P0A7J3	17693.8	G	T	T	B	CID	LIT	6	41.8	RAVEGTPFECLK	1406.7	R	D	2.3	0.5	0.0	0.0
P0A7J3	17693.8	G	U	T	B	CID	LIT	7	47.9	AAAFEGELIPASQIDR	1687.9	K	L	3.3	0.6	25.8	12.0
P0A7J3	17693.8	G	U	T	B	CID	LIT	7	47.9	EAGVYMR	825.4	R	V	1.5	0.7	21.2	12.8
P0A7J3	17693.8	G	U	T	B	CID	LIT	7	47.9	EFAKANAK	878.5	K	F	1.9	0.1	0.0	0.0
P0A7J3	17693.8	G	U	T	B	CID	LIT	7	47.9	GALSAVVADSR	1045.6	K	G	3.7	0.6	66.0	14.1
P0A7J3	17693.8	G	U	T	B	CID	LIT	7	47.9	LATLPTYEEAIAR	1447.8	R	L	2.8	0.0	40.2	11.5
P0A7J3	17693.8	G	U	T	B	CID	LIT	7	47.9	QAIVAEVSEVAK	1243.7	K	G	3.4	0.8	38.0	13.8
P0A7J3	17693.8	G	U	T	B	CID	LIT	7	47.9	RAVEGTPFECLK	1406.7	R	D	3.3	0.4	22.4	12.6
P0A7J3	17693.8	G	T	A	B	CID	LIT	6	23.0	DKQAIVAEVS	1059.6	Q	E	2.4	0.6	31.1	18.0
P0A7J3	17693.8	G	T	A	B	CID	LIT	6	23.0	DKQAIVAEVSEVAKGALSAVVA	2155.2	Q	D	5.1	0.6	73.8	12.6
P0A7J3	17693.8	G	T	A	B	CID	LIT	6	23.0	DRLATLPTY	1049.6	I	E	2.3	0.5	14.9	13.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7J3	17693.8	G	T	A	B	CID	LIT	6	23.0	DSRGVTV	733.4	A	D	1.6	0.2	10.1	16.1
P0A7J3	17693.8	G	T	A	B	CID	LIT	6	23.0	EVAKGALSAVVA	1114.6	S	D	3.6	0.8	48.3	12.8
P0A7J3	17693.8	G	T	A	B	CID	LIT	6	23.0	EVSEVAKGALSAVVA	1429.8	A	D	2.5	0.4	0.0	0.0
P0A7J3	17693.8	G	U	A	B	CID	LIT	4	23.0	DKQAIVAEVS	1059.6	Q	E	2.2	0.5	25.0	18.0
P0A7J3	17693.8	G	U	A	B	CID	LIT	4	23.0	DRLATLPTY	1049.6	I	E	2.1	0.2	8.1	13.2
P0A7J3	17693.8	G	U	A	B	CID	LIT	4	23.0	DSRGVTV	733.4	A	D	1.6	0.6	19.7	14.5
P0A7J3	17693.8	G	U	A	B	CID	LIT	4	23.0	EVAKGALSAVVA	1114.6	S	D	2.4	0.4	28.3	12.8
P0A7J3	17693.8	S	U	T	A	CID	LIT	5	41.8	AAAFEGELIPASQIDR	1687.9	K	L	3.4	0.7	38.8	17.3
P0A7J3	17693.8	S	U	T	A	CID	LIT	5	41.8	ANAKFEVK	906.5	K	A	2.2	0.3	26.9	16.5
P0A7J3	17693.8	S	U	T	A	CID	LIT	5	41.8	DAFVGPTLIAYSMEHPGAAAR	2174.1	K	L	4.1	0.0	69.9	18.1
P0A7J3	17693.8	S	U	T	A	CID	LIT	5	41.8	GALSAVVADSR	1045.6	K	G	3.6	0.5	76.2	18.1
P0A7J3	17693.8	S	U	T	A	CID	LIT	5	41.8	LATLPTYEEAIAR	1447.8	R	L	2.7	0.0	54.5	16.0
P0A7J3	17693.8	S	U	T	B	CID	LIT	5	44.2	AAAFEGELIPASQIDR	1687.9	K	L	3.6	0.3	35.5	17.9
P0A7J3	17693.8	S	U	T	B	CID	LIT	5	44.2	DAFVGPTLIAYSMEHPGAAAR	2174.1	K	L	4.9	0.0	55.8	18.1
P0A7J3	17693.8	S	U	T	B	CID	LIT	5	44.2	GALSAVVADSR	1045.6	K	G	3.8	0.5	76.4	17.7
P0A7J3	17693.8	S	U	T	B	CID	LIT	5	44.2	LATLPTYEEAIAR	1447.8	R	L	2.5	0.7	2.2	16.8
P0A7J3	17693.8	S	U	T	B	CID	LIT	5	44.2	RAVEGTPFECLK	1406.7	R	D	3.6	0.7	39.6	15.6
P0A7J3	17693.8	S	U	T	C	CID	LIT	6	46.1	DAFVGPTLIAYSMEHPGAAAR	2174.1	K	L	4.1	0.8	50.3	18.2
P0A7J3	17693.8	S	U	T	C	CID	LIT	6	46.1	GALSAVVADSR	1045.6	K	G	3.7	0.5	50.7	17.9
P0A7J3	17693.8	S	U	T	C	CID	LIT	6	46.1	GVTVDKMTELR	1248.7	R	K	2.8	0.0	37.1	14.3
P0A7J3	17693.8	S	U	T	C	CID	LIT	6	46.1	LATLPTYEEAIAR	1447.8	R	L	2.6	0.5	16.1	16.8
P0A7J3	17693.8	S	U	T	C	CID	LIT	6	46.1	MALNLQDK	948.5	-	Q	0.0	0.0	27.4	16.4
P0A7J3	17693.8	S	U	T	C	CID	LIT	6	46.1	RAVEGTPFECLK	1406.7	R	D	3.3	0.4	9.2	15.9
P0A7J3	17693.8	S	U	T	A	ETD	LIT	3	24.2	AAAFEGELIPASQIDR	1687.9	K	L	3.4	0.0	70.3	17.6
P0A7J3	17693.8	S	U	T	A	ETD	LIT	3	24.2	GVTVDKMTELR	1248.7	R	K	2.5	0.3	29.1	14.8
P0A7J3	17693.8	S	U	T	A	ETD	LIT	3	24.2	LATLPTYEEAIAR	1447.8	R	L	0.0	0.0	55.0	17.1
P0A7J3	17693.8	S	U	T	B	ETD	LIT	4	31.5	AAAFEGELIPASQIDR	1687.9	K	L	2.8	0.4	0.0	0.0
P0A7J3	17693.8	S	U	T	B	ETD	LIT	4	31.5	GVTVDKMTELR	1248.7	R	K	2.5	0.4	31.5	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7J3	17693.8	S	U	T	B	ETD	LIT	4	31.5	LATLPTYEEAIAR	1447.8	R	L	2.0	0.7	0.0	0.0
P0A7J3	17693.8	S	U	T	B	ETD	LIT	4	31.5	RAVEGTPFECLK	1406.7	R	D	1.8	0.5	0.0	0.0
P0A7J3	17693.8	S	U	T	C	ETD	LIT	3	24.2	AAAFEGELIPASQIDR	1687.9	K	L	3.2	0.5	65.3	17.9
P0A7J3	17693.8	S	U	T	C	ETD	LIT	3	24.2	GVTVDKMTELR	1248.7	R	K	1.8	0.0	26.5	14.8
P0A7J3	17693.8	S	U	T	C	ETD	LIT	3	24.2	LATLPTYEEAIAR	1447.8	R	L	2.4	0.6	37.2	16.8
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	AAAFEGELIPASQIDR	1687.9	K	L	0.0	0.0	36.7	17.3
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	GALSAVVADSR	1045.6	K	G	0.0	0.0	35.2	17.9
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	GVTVDKMTELR	1248.7	R	K	0.0	0.0	33.3	14.8
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	LATLPTYEEAIAR	1447.8	R	L	0.0	0.0	45.2	16.3
P0A7J3	17693.8	S	U	T	A	ETD+CID	LIT	4	37.0	AAAFEGELIPASQIDR	1687.9	K	L	3.6	0.4	62.0	17.9
P0A7J3	17693.8	S	U	T	A	ETD+CID	LIT	4	37.0	DAFVGPTLIAYSMEHPGAAAR	2174.1	K	L	5.0	0.7	55.9	18.5
P0A7J3	17693.8	S	U	T	A	ETD+CID	LIT	4	37.0	GVTVDKMTELR	1248.7	R	K	2.6	0.4	36.7	17.1
P0A7J3	17693.8	S	U	T	A	ETD+CID	LIT	4	37.0	LATLPTYEEAIAR	1447.8	R	L	3.1	0.8	0.0	0.0
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	2	17.6	AAAFEGELIPASQIDR	1687.9	K	L	3.4	0.4	0.0	0.0
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	2	17.6	LATLPTYEEAIAR	1447.8	R	L	2.3	0.7	0.0	0.0
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	AAAFEGELIPASQIDR	1687.9	K	L	3.4	0.4	36.7	17.3
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	GALSAVVADSR	1045.6	K	G	2.8	0.3	35.2	17.9
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	GVTVDKMTELR	1248.7	R	K	2.5	0.0	33.3	14.8
P0A7J3	17693.8	S	U	T	B	ETD+CID	LIT	4	30.9	LATLPTYEEAIAR	1447.8	R	L	2.3	0.7	45.2	16.3
P0A7J3	17693.8	S	U	T	C	ETD+CID	LIT	5	43.6	AAAFEGELIPASQIDR	1687.9	K	L	3.2	0.3	33.5	17.6
P0A7J3	17693.8	S	U	T	C	ETD+CID	LIT	5	43.6	DAFVGPTLIAYSMEHPGAAAR	2174.1	K	L	5.1	0.0	39.1	18.1
P0A7J3	17693.8	S	U	T	C	ETD+CID	LIT	5	43.6	GALSAVVADSR	1045.6	K	G	3.4	0.4	29.3	17.9
P0A7J3	17693.8	S	U	T	C	ETD+CID	LIT	5	43.6	GVTVDKMTELR	1248.7	R	K	3.0	0.4	38.0	14.5
P0A7J3	17693.8	S	U	T	C	ETD+CID	LIT	5	43.6	LATLPTYEEAIAR	1447.8	R	L	2.4	0.7	64.8	16.0
P0A7J3	17693.8	S	U	T	B	HCD	FT	4	30.9	AAAFEGELIPASQIDR	1687.9	K	L	0.0	0.0	36.7	17.3
P0A7J3	17693.8	S	U	T	B	HCD	FT	4	30.9	GALSAVVADSR	1045.6	K	G	0.0	0.0	35.2	17.9
P0A7J3	17693.8	S	U	T	B	HCD	FT	4	30.9	GVTVDKMTELR	1248.7	R	K	0.0	0.0	33.3	14.8
P0A7J3	17693.8	S	U	T	B	HCD	FT	4	30.9	LATLPTYEEAIAR	1447.8	R	L	0.0	0.0	45.2	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P37182	17733.4	G	T	T	A	CID	LIT	5	29.9	DHLIIADAIVSK	1294.7	R	K	2.8	0.0	24.0	7.0
P37182	17733.4	G	T	T	A	CID	LIT	5	29.9	DHLIIADAIVSKK	1422.8	R	N	4.4	0.0	80.8	6.0
P37182	17733.4	G	T	T	A	CID	LIT	5	29.9	ESGVEAIPR	957.5	R	E	1.8	0.4	38.0	13.2
P37182	17733.4	G	T	T	A	CID	LIT	5	29.9	ILVLGVGNILLTDEAIGVR	1965.2	R	I	2.6	0.0	21.9	3.0
P37182	17733.4	G	T	T	A	CID	LIT	5	29.9	IVEALEQR	957.5	R	Y	3.4	0.4	43.2	14.9
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	AQTFTLVAK	978.6	K	D	2.6	0.3	38.2	11.5
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	AQTFTLVAKDLSDVTLGQFAGK	2310.2	K	R	3.6	0.0	23.0	9.5
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	AVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA	3803.9	R	-	4.5	0.0	20.9	7.0
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	DLSDVTLGQFAGK	1350.7	K	R	4.7	0.9	91.8	12.3
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	DLSDVTLGQFAGKR	1506.8	K	K	3.8	0.7	79.9	11.5
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	FCGAEGLNNVITLSTFR	1898.9	R	N	4.6	0.9	75.2	11.1
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	KVLNIFPSIDTGVCAASVR	2047.1	R	K	4.5	0.6	62.2	8.5
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	NAEFLQAYGVAIADGPLK	1877.0	R	G	5.3	0.8	117.0	11.1
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	4.6	0.0	70.3	10.8
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	72.5	12.8
P0A862	17817.2	G	U	T	A	CID	LIT	11	83.3	VLNIFPSIDTGVCAASVR	1919.0	K	K	4.3	0.7	65.2	12.3
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	AQTFTLVAK	978.6	K	D	2.5	0.5	36.1	10.8
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	AVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA	3803.9	R	-	6.1	0.0	54.5	4.8
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	DLSDVTLGQFAGK	1350.7	K	R	4.9	0.8	92.0	10.4
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	DLSDVTLGQFAGKR	1506.8	K	K	4.0	0.8	84.6	11.5
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	FCGAEGLNNVITLSTFR	1898.9	R	N	5.6	0.8	63.5	12.0
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	3.6	0.0	24.7	10.4
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	KVLNIFPSIDTGVCAASVR	2047.1	R	K	5.0	0.5	62.0	9.0
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	NAEFLQAYGVAIADGPLK	1877.0	R	G	5.3	0.8	109.0	11.1
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	5.2	0.0	80.8	10.8
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	75.0	12.6
P0A862	17817.2	G	T	T	A	CID	LIT	11	99.4	VLNIFPSIDTGVCAASVR	1919.0	K	K	5.1	0.7	50.2	13.4
P0A862	17817.2	G	U	A	A	CID	LIT	3	26.2	DENDNVIFSQLV	1392.7	I	D	1.9	0.6	16.2	16.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A862	17817.2	G	U	A	A	CID	LIT	3	26.2	DNVIFSQLV	1034.6	N	D	2.6	0.5	27.1	15.7
P0A862	17817.2	G	U	A	A	CID	LIT	3	26.2	SQTVHFQGNPVTVANSIPQAGSKAQTFTLVAK	3326.7	M	D	0.0	0.0	47.0	10.8
P0A862	17817.2	G	T	A	A	CID	LIT	5	36.9	DENDNVIFSQLV	1392.7	I	D	2.3	0.5	35.8	16.9
P0A862	17817.2	G	T	A	A	CID	LIT	5	36.9	DGPLKGLAARAVVVI	1478.9	A	D	3.7	0.0	25.0	3.0
P0A862	17817.2	G	T	A	A	CID	LIT	5	36.9	DNVIFSQLV	1034.6	N	D	3.3	0.4	59.1	15.7
P0A862	17817.2	G	T	A	A	CID	LIT	5	36.9	SQTVHFQGNPVTVANSIPQAGSKAQTFTLVAK	3326.7	M	D	0.0	0.0	63.5	11.8
P0A862	17817.2	G	T	A	A	CID	LIT	5	36.9	SQTVHFQGNPVTVANSIPQAGSKAQTFTLVAKDLS	3641.9	M	D	0.0	0.0	21.5	13.6
P0A862	17817.2	G	T	T	B	CID	LIT	5	51.8	AQTFTLVAK	978.6	K	D	2.4	0.2	32.0	11.5
P0A862	17817.2	G	T	T	B	CID	LIT	5	51.8	DLSDVTLGQFAGKR	1506.8	K	K	2.2	0.6	7.2	12.3
P0A862	17817.2	G	T	T	B	CID	LIT	5	51.8	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	2.1	0.0	22.3	10.0
P0A862	17817.2	G	T	T	B	CID	LIT	5	51.8	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	76.1	12.6
P0A862	17817.2	G	T	T	B	CID	LIT	5	51.8	VLNIFPSIDTGVCAASVR	1919.0	K	K	3.1	0.4	22.3	12.8
P0A862	17817.2	G	T	A	B	CID	LIT	4	35.1	DENDNVIFSQLV	1392.7	I	D	2.1	0.1	17.6	16.9
P0A862	17817.2	G	T	A	B	CID	LIT	4	35.1	DGPLKGLAARAVVVI	1478.9	A	D	3.3	0.0	38.4	3.0
P0A862	17817.2	G	T	A	B	CID	LIT	4	35.1	DNVIFSQLV	1034.6	N	D	2.0	0.7	45.8	15.7
P0A862	17817.2	G	T	A	B	CID	LIT	4	35.1	SQTVHFQGNPVTVANSIPQAGSKAQTFTLVAK	3326.7	M	D	0.0	0.0	57.1	11.8
P0A862	17817.2	G	U	A	B	CID	LIT	2	24.4	DNVIFSQLV	1034.6	N	D	1.9	0.7	25.1	15.7
P0A862	17817.2	G	U	A	B	CID	LIT	2	24.4	SQTVHFQGNPVTVANSIPQAGSKAQTFTLVAK	3326.7	M	D	0.0	0.0	35.1	10.8
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	AQTFTLVAKDLSDVTLGQFAGKR	2466.3	K	K	2.9	0.6	58.4	13.0
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	AVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA	3803.9	R	-	5.2	0.0	39.8	18.5
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	DLSDVTLGQFAGK	1350.7	K	R	2.2	0.7	0.0	0.0
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	DLSDVTLGQFAGKR	1506.8	K	K	3.8	0.7	59.0	17.0
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	FCGAEGLNNVITLSTFR	1899.9	R	N	5.3	0.6	89.8	18.0
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	3.8	0.5	25.8	17.0
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	KVLNIFPSIDTGVCAASVR	2047.1	R	K	5.3	0.5	42.0	15.2
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	NAEFLQAYGVAIADGPLK	1877.0	R	G	5.4	0.6	66.0	16.9
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	4.8	0.7	42.2	16.1
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	72.4	19.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A862	17817.2	S	U	T	A	CID	LIT	11	99.4	VLNIFPSIDTGVCAASVR	1919.0	K	K	4.7	0.5	59.5	17.1
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	AQTFTLVAKDLSDVTLGQFAGKR	2466.3	K	K	2.3	0.0	31.8	12.6
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	AVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA	3803.9	R	-	4.6	0.0	46.0	18.5
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	DLSDVTLGQFAGK	1350.7	K	R	5.0	0.7	81.3	15.9
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	DLSDVTLGQFAGKR	1506.8	K	K	3.7	0.6	48.7	15.8
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	FCGAEGLNNVITLSTFR	1899.9	R	N	5.2	0.7	86.5	17.8
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	4.1	0.6	24.0	17.2
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	KVLNIFPSIDTGVCAASVR	2047.1	R	K	5.1	0.6	65.2	14.8
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	NAEFLQAYGVAIADGPLK	1877.0	R	G	4.7	0.5	72.9	16.9
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	78.9	18.9
P0A862	17817.2	S	U	T	B	CID	LIT	10	96.4	VLNIFPSIDTGVCAASVR	1919.0	K	K	3.9	0.5	30.4	16.4
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	AQTFTLVAKDLSDVTLGQFAGKR	2466.3	K	K	3.5	0.0	16.6	13.6
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	AVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA	3803.9	R	-	5.4	0.0	28.1	18.3
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	DLSDVTLGQFAGKR	1506.8	K	K	3.7	0.5	43.7	16.4
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	FCGAEGLNNVITLSTFR	1899.9	R	N	5.7	0.6	80.4	17.9
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	4.5	0.6	17.2	17.2
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	KVLNIFPSIDTGVCAASVR	2047.1	R	K	5.1	0.4	43.7	15.6
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	NAEFLQAYGVAIADGPLK	1877.0	R	G	6.7	0.7	73.6	17.0
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	72.7	18.5
P0A862	17817.2	S	U	T	C	CID	LIT	9	96.4	VLNIFPSIDTGVCAASVR	1919.0	K	K	4.8	0.5	49.5	17.2
P0A862	17817.2	S	U	T	A	ETD	LIT	7	58.9	AQTFTLVAK	978.6	K	D	1.2	0.4	18.1	14.0
P0A862	17817.2	S	U	T	A	ETD	LIT	7	58.9	AQTFTLVAKDLSDVTLGQFAGKR	2466.3	K	K	4.4	0.0	20.7	13.6
P0A862	17817.2	S	U	T	A	ETD	LIT	7	58.9	DLSDVTLGQFAGKR	1506.8	K	K	3.3	0.5	48.1	16.7
P0A862	17817.2	S	U	T	A	ETD	LIT	7	58.9	FCGAEGLNNVITLSTFR	1898.9	R	N	2.6	0.6	0.0	0.0
P0A862	17817.2	S	U	T	A	ETD	LIT	7	58.9	NAEFLQAYGVAIADGPLK	1877.0	R	G	4.2	0.5	41.5	16.9
P0A862	17817.2	S	U	T	A	ETD	LIT	7	58.9	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	56.9	19.1
P0A862	17817.2	S	U	T	A	ETD	LIT	7	58.9	VLNIFPSIDTGVCAASVR	1919.0	K	K	2.9	0.2	49.9	17.1
P0A862	17817.2	S	U	T	B	ETD	LIT	7	58.9	AQTFTLVAK	978.6	K	D	2.5	0.4	51.2	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A862	17817.2	S	U	T	B	ETD	LIT	7	58.9	DLSDVTLGQFAGK	1350.7	K	R	3.1	0.6	41.7	16.1
P0A862	17817.2	S	U	T	B	ETD	LIT	7	58.9	DLSDVTLGQFAGKR	1506.8	K	K	3.4	0.5	57.3	16.7
P0A862	17817.2	S	U	T	B	ETD	LIT	7	58.9	FCGAEGLNNVITLSTFR	1899.9	R	N	3.2	0.7	54.5	17.8
P0A862	17817.2	S	U	T	B	ETD	LIT	7	58.9	NAEFLQAYGVAIADGPLK	1877.0	R	G	3.0	0.7	55.9	17.3
P0A862	17817.2	S	U	T	B	ETD	LIT	7	58.9	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	50.3	18.6
P0A862	17817.2	S	U	T	B	ETD	LIT	7	58.9	VLNIFPSIDTGVCAASVR	1919.0	K	K	2.3	0.6	54.7	17.1
P0A862	17817.2	S	U	T	C	ETD	LIT	7	58.9	AQTFTLVAK	978.6	K	D	2.1	0.5	45.1	14.0
P0A862	17817.2	S	U	T	C	ETD	LIT	7	58.9	DLSDVTLGQFAGK	1350.7	K	R	3.1	0.4	52.4	16.0
P0A862	17817.2	S	U	T	C	ETD	LIT	7	58.9	DLSDVTLGQFAGKR	1506.8	K	K	3.2	0.6	55.5	16.7
P0A862	17817.2	S	U	T	C	ETD	LIT	7	58.9	FCGAEGLNNVITLSTFR	1899.9	R	N	3.8	0.5	72.3	17.6
P0A862	17817.2	S	U	T	C	ETD	LIT	7	58.9	NAEFLQAYGVAIADGPLK	1877.0	R	G	3.5	0.9	56.2	16.9
P0A862	17817.2	S	U	T	C	ETD	LIT	7	58.9	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	44.2	19.0
P0A862	17817.2	S	U	T	C	ETD	LIT	7	58.9	VLNIFPSIDTGVCAASVR	1919.0	K	K	3.1	0.5	76.6	17.1
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	DLSDVTLGQFAGKR	1506.8	K	K	0.0	0.0	59.7	15.9
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	FCGAEGLNNVITLSTFR	1898.9	R	N	0.0	0.0	86.4	16.8
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	0.0	0.0	43.6	16.9
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	KVLNIFPSIDTGVCAASVR	2047.1	R	K	0.0	0.0	68.8	15.6
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	NAEFLQAYGVAIADGPLK	1877.0	R	G	0.0	0.0	81.2	16.4
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	0.0	0.0	44.3	15.8
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	90.6	18.6
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	VLNIFPSIDTGVCAASVR	1919.0	K	K	0.0	0.0	62.0	17.1
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	AQTFTLVAKDLSDVTLGQFAGKR	2466.3	K	K	3.3	0.0	18.4	13.6
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	AVVVIDENDNVIFSQLVDEITTEPDYEAALAVLKA	3803.9	R	-	4.5	0.0	20.5	18.5
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	DLSDVTLGQFAGK	1350.7	K	R	5.0	0.7	85.8	16.1
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	DLSDVTLGQFAGKR	1506.8	K	K	4.3	0.6	84.5	16.7
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	EAAATAGEKEDAPR	1415.7	-	-	2.6	0.4	111.0	15.9
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	FCGAEGLNNVITLSTFR	1899.9	R	N	5.3	0.6	86.2	18.0
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	0.0	0.0	22.9	17.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	KVLNIFPSIDTGVCAASVR	2047.1	R	K	0.0	0.0	50.2	15.3
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	NAEFLQAYGVAIADGPLK	1877.0	R	G	3.6	0.7	0.0	0.0
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	3.4	0.7	46.3	16.1
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	80.2	18.9
P0A862	17817.2	S	U	T	A	ETD+CID	LIT	11	99.4	VLNIFPSIDTGVCAASVR	1919.0	K	K	0.0	0.0	65.5	17.1
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	DLSDVTLGQFAGKR	1506.8	K	K	3.8	0.6	59.7	15.9
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	FCGAEGLNNVITLSTFR	1898.9	R	N	0.0	0.0	86.4	16.8
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	0.0	0.0	43.6	16.9
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	KVLNIFPSIDTGVCAASVR	2047.1	R	K	4.6	0.5	68.8	15.6
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	NAEFLQAYGVAIADGPLK	1877.0	R	G	5.6	0.7	81.2	16.4
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	2.2	0.0	44.3	15.8
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	90.6	18.6
P0A862	17817.2	S	U	T	B	ETD+CID	LIT	8	73.2	VLNIFPSIDTGVCAASVR	1919.0	K	K	0.0	0.0	62.0	17.1
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	AQTFTLVAK	978.6	K	D	2.2	0.1	0.0	0.0
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	DLSDVTLGQFAGK	1350.7	K	R	2.5	0.7	9.1	16.1
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	DLSDVTLGQFAGKR	1506.8	K	K	3.5	0.6	0.0	0.0
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	FCGAEGLNNVITLSTFR	1899.9	R	N	5.6	0.6	86.2	18.0
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	0.0	0.0	22.0	17.2
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	KVLNIFPSIDTGVCAASVR	2047.1	R	K	4.7	0.6	47.1	14.9
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	NAEFLQAYGVAIADGPLK	1877.0	R	G	6.0	0.7	99.0	16.4
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	SQTVHFQGNPVTVANSIPQAGSK	2368.2	M	A	0.0	0.0	79.1	19.0
P0A862	17817.2	S	U	T	C	ETD+CID	LIT	9	75.6	VLNIFPSIDTGVCAASVR	1919.0	K	K	4.6	0.5	50.7	17.1
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	DLSDVTLGQFAGKR	1506.8	K	K	0.0	0.0	59.7	15.9
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	FCGAEGLNNVITLSTFR	1898.9	R	N	0.0	0.0	86.4	16.8
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	KFNQLATEIDNTVVLCISADLPFAQSR	3050.6	R	F	0.0	0.0	43.6	16.9
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	KVLNIFPSIDTGVCAASVR	2047.1	R	K	0.0	0.0	68.8	15.6
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	NAEFLQAYGVAIADGPLK	1877.0	R	G	0.0	0.0	81.2	16.4
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	NAEFLQAYGVAIADGPLKGLAAR	2345.3	R	A	0.0	0.0	44.3	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	SQTVHFQGNPVTVANSIPQAGSK	2367.2	M	A	0.0	0.0	90.6	18.6
P0A862	17817.2	S	U	T	B	HCD	FT	8	73.2	VLNIFPSIDTGVCAASVR	1919.0	K	K	0.0	0.0	62.0	17.1
P0A862	17817.2	S	U	T	A	HCD	FT	2	21.4	DLSDVTLGQFAGK	1350.7	K	R	3.7	0.8	67.0	15.8
P0A862	17817.2	S	U	T	A	HCD	FT	2	21.4	SQTVHFQGNPVTVANSIPQAGSK	2368.2	M	A	0.0	0.0	66.4	19.3
P0A862	17817.2	S	U	T	B	HCD	FT	3	22.0	DLSDVTLGQFAGK	1350.7	K	R	4.1	0.9	67.3	16.7
P0A862	17817.2	S	U	T	B	HCD	FT	3	22.0	DLSDVTLGQFAGKR	1506.8	K	K	4.3	0.0	81.0	16.7
P0A862	17817.2	S	U	T	B	HCD	FT	3	22.0	SQTVHFQGNPVTVANSIPQAGSK	2368.2	M	A	0.0	0.0	23.8	19.1
P64483	17832.8	G	U	T	A	CID	LIT	4	26.3	FDEIAFNAGMLDK	1470.7	R	S	3.6	0.7	74.9	10.0
P64483	17832.8	G	U	T	A	CID	LIT	4	26.3	LIALLSQEGADFR	1432.8	R	V	4.3	0.0	50.7	11.1
P64483	17832.8	G	U	T	A	CID	LIT	4	26.3	TADYLR	738.4	K	I	1.6	0.4	33.0	13.2
P64483	17832.8	G	U	T	A	CID	LIT	4	26.3	TEMAKGSVTHQR	1344.7	M	L	0.0	0.0	56.9	12.0
P64483	17832.8	G	U	A	A	CID	LIT	2	10.2	DKSVILKTA	974.6	L	D	2.1	0.6	17.7	8.5
P64483	17832.8	G	U	A	A	CID	LIT	2	10.2	DPLLFERF	1036.5	A	D	2.2	0.8	29.8	14.6
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	AAQSDEELYQIITDTEGTPDEA	2396.1	R	-	3.2	0.0	97.6	7.8
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	ALEIISELAAK	1157.7	R	Q	4.2	0.0	67.7	11.5
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	LADKTICR	976.5	R	R	2.9	0.3	60.5	15.1
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	LEEDTLR	875.4	K	A	2.2	0.8	25.8	12.0
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	QLSLPPQVVFEAILTR	1811.0	K	E	3.9	0.7	26.0	8.5
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	THLHTLSLVAK	1219.7	K	R	3.6	0.7	30.1	9.0
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	THLHTLSLVAKR	1375.8	K	L	3.5	0.0	52.7	9.0
P69829	17942.0	G	T	T	A	CID	LIT	8	55.8	TNNDTTLQLSSVLNR	1675.9	M	E	0.0	0.0	98.2	13.0
P33012	18063.0	G	T	T	A	CID	LIT	6	36.3	EWVAVYYDNPDETPAEK	2025.9	K	L	3.7	0.8	72.9	6.0
P33012	18063.0	G	T	T	A	CID	LIT	6	36.3	KGFEQLMMWVDSK	1598.8	K	N	3.5	0.9	39.1	11.1
P33012	18063.0	G	T	T	A	CID	LIT	6	36.3	MNYEIKQEEK	1311.6	-	R	2.1	0.7	0.0	0.0
P33012	18063.0	G	T	T	A	CID	LIT	6	36.3	RTVAGFHLVGPWEQTVK	1925.0	K	K	3.4	0.0	19.1	7.8
P33012	18063.0	G	T	T	A	CID	LIT	6	36.3	TVAGFHLVGPWEQTVK	1768.9	R	K	4.4	0.0	43.2	11.8
P33012	18063.0	G	T	T	A	CID	LIT	6	36.3	TVAGFHLVGPWEQTVKK	1897.0	R	G	2.7	0.6	20.7	9.5
P33012	18063.0	G	T	A	A	CID	LIT	2	18.5	DDFAKPWYQFFNSLLQ	2019.0	G	D	3.3	0.0	27.1	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P33012	18063.0	G	T	A	A	CID	LIT	2	18.5	DIEMYVAVQPKHH	1566.8	W	-	1.8	0.6	13.1	15.3
P33012	18063.0	G	T	A	B	CID	LIT	2	17.8	DIEMYVAVQPKHH	1566.8	W	-	3.6	0.5	34.6	15.6
P33012	18063.0	G	T	A	B	CID	LIT	2	17.8	DSKNIVPKEWVAVYY	1810.9	V	D	2.6	0.3	7.5	15.2
P33012	18063.0	S	U	T	B	CID	LIT	2	21.0	EWVAVYYDNPDETPAEK	2025.9	K	L	3.9	0.0	36.8	14.1
P33012	18063.0	S	U	T	B	CID	LIT	2	21.0	TVAGFHLVGPWEQTVK	1768.9	R	K	2.5	0.3	3.1	16.7
P33012	18063.0	S	U	T	C	CID	LIT	3	28.0	EWVAVYYDNPDETPAEK	2025.9	K	L	3.8	0.0	48.8	13.8
P33012	18063.0	S	U	T	C	CID	LIT	3	28.0	MNYEIKQEEKR	1467.7	-	T	3.1	0.3	21.6	16.0
P33012	18063.0	S	U	T	C	CID	LIT	3	28.0	TVAGFHLVGPWEQTVK	1768.9	R	K	2.3	0.3	6.2	16.5
P33012	18063.0	S	U	T	C	ETD+CID	LIT	2	21.0	EWVAVYYDNPDETPAEK	2025.9	K	L	4.1	0.0	49.1	13.8
P33012	18063.0	S	U	T	C	ETD+CID	LIT	2	21.0	TVAGFHLVGPWEQTVK	1768.9	R	K	2.8	0.5	0.0	0.0
P04128	18092.8	G	T	T	A	CID	LIT	3	45.1	AAVAFLGTAIDAGHTNVLALQSSAAGSATNVGVQILDR	3679.9	K	T	5.6	0.0	58.8	9.0
P04128	18092.8	G	T	T	A	CID	LIT	3	45.1	GEVVNAACAVDAGSVDQTVQLGQVR	2543.3	K	T	6.6	0.8	138.0	10.0
P04128	18092.8	G	T	T	A	CID	LIT	3	45.1	YFATGAATPGAANADATFK	1844.9	R	V	5.4	0.7	96.9	11.1
P04128	18092.8	G	T	A	A	CID	LIT	4	20.3	DATFKVQYQ	1099.5	A	-	1.8	0.4	2.1	14.5
P04128	18092.8	G	T	A	A	CID	LIT	4	20.3	DCDTNVASKAAVAFLGTAI	1923.9	N	D	2.8	0.0	36.9	15.1
P04128	18092.8	G	T	A	A	CID	LIT	4	20.3	DRTGAALTL	917.5	L	D	2.4	0.5	24.5	15.4
P04128	18092.8	G	T	A	A	CID	LIT	4	20.3	DTNVASKAAVAFLGTAI	1648.9	C	D	2.7	0.0	23.6	14.6
P04128	18092.8	G	T	T	B	CID	LIT	2	12.6	YFATGAATPGAANADATFK	1844.9	R	V	6.0	0.7	83.8	10.8
P04128	18092.8	G	T	T	B	CID	LIT	2	12.6	YFATGAATPGAANADATFKVQYQ	2363.1	R	-	6.1	0.7	77.6	10.8
P04128	18092.8	G	T	A	B	CID	LIT	5	34.6	DAGHTNVLALQSSAAGSATNVGVQIL	2494.3	I	D	3.9	0.6	19.1	15.8
P04128	18092.8	G	T	A	B	CID	LIT	5	34.6	DATFKVQYQ	1099.5	A	-	2.3	0.7	23.6	14.5
P04128	18092.8	G	T	A	B	CID	LIT	5	34.6	DCDTNVASKAAVAFLGTAI	1923.9	N	D	2.9	0.8	26.8	15.2
P04128	18092.8	G	T	A	B	CID	LIT	5	34.6	DRTGAALTL	917.5	L	D	2.3	0.6	28.3	15.3
P04128	18092.8	G	T	A	B	CID	LIT	5	34.6	DTNVASKAAVAFLGTAI	1648.9	C	D	3.8	0.8	35.2	13.6
P04128	18092.8	G	U	A	B	CID	LIT	4	33.5	DAGHTNVLALQSSAAGSATNVGVQIL	2494.3	I	D	4.4	0.0	81.4	15.1
P04128	18092.8	G	U	A	B	CID	LIT	4	33.5	DATFKVQYQ	1099.5	A	-	2.3	0.7	24.4	14.5
P04128	18092.8	G	U	A	B	CID	LIT	4	33.5	DRTGAALTL	917.5	L	D	2.0	0.7	17.9	15.3
P04128	18092.8	G	U	A	B	CID	LIT	4	33.5	DTNVASKAAVAFLGTAI	1648.9	C	D	3.8	0.0	44.3	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P04128	18092.8	S	U	T	B	CID	LIT	2	26.9	TGAALTLDGATFSSETTLNNGTNTIPFQAR	3070.5	R	Y	3.7	0.6	21.0	19.4
P04128	18092.8	S	U	T	B	CID	LIT	2	26.9	YFATGAATPGAANADATFK	1845.9	R	V	5.0	0.7	71.0	14.3
P04128	18092.8	S	U	T	C	CID	LIT	2	26.9	TGAALTLDGATFSSETTLNNGTNTIPFQAR	3069.5	R	Y	2.2	0.4	1.6	19.7
P04128	18092.8	S	U	T	C	CID	LIT	2	26.9	YFATGAATPGAANADATFK	1844.9	R	V	5.6	0.6	93.8	15.6
P04128	18092.8	S	U	T	B	ETD+CID	LIT	2	26.9	TGAALTLDGATFSSETTLNNGTNTIPFQAR	3069.5	R	Y	2.8	0.3	14.4	19.3
P04128	18092.8	S	U	T	B	ETD+CID	LIT	2	26.9	YFATGAATPGAANADATFK	1844.9	R	V	4.6	0.8	80.6	14.9
P04128	18092.8	S	U	T	C	ETD+CID	LIT	2	26.9	TGAALTLDGATFSSETTLNNGTNTIPFQAR	3070.5	R	Y	3.8	0.8	22.8	19.7
P04128	18092.8	S	U	T	C	ETD+CID	LIT	2	26.9	YFATGAATPGAANADATFK	1844.9	R	V	5.5	0.7	77.0	15.4
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	DFNALMAGETSFLATLANTSALLYER	2835.4	R	L	3.7	0.0	26.8	11.8
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	FTDEDEQGLR	1209.5	R	Q	3.1	0.0	41.3	7.8
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	GVCGTAVAR	890.5	R	N	3.3	0.4	42.2	12.3
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	IEDVHVFDGHIACDAASNSEIVLPLVVK	3047.6	R	N	7.3	0.0	56.3	10.4
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	MNKTEFYADLNR	1501.7	-	D	3.8	0.9	55.7	9.5
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	NQIIGVLDIDSTVFGR	1746.9	K	F	4.7	0.8	40.8	11.5
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	VLATTDYK	910.5	K	K	2.4	0.0	38.9	12.0
P76270	18103.8	G	T	T	A	CID	LIT	8	66.7	VLATTDYKK	1038.6	K	F	2.8	0.0	42.8	10.4
P76270	18103.8	G	T	A	A	CID	LIT	2	18.2	DAASNSEIVLPLVVKNQIIGVL	2292.3	C	D	4.4	0.0	39.2	10.4
P76270	18103.8	G	T	A	A	CID	LIT	2	18.2	MNKTEFYA	1003.5	-	D	2.6	0.0	21.1	13.0
P76270	18103.8	G	T	A	B	CID	LIT	4	26.7	DAASNSEIVLPLVVKNQIIGVL	2292.3	C	D	2.7	0.7	7.6	10.4
P76270	18103.8	G	T	A	B	CID	LIT	4	26.7	DGHIAC	672.3	F	D	1.9	0.2	9.0	11.5
P76270	18103.8	G	T	A	B	CID	LIT	4	26.7	DVHVF	616.3	E	D	1.6	0.4	18.4	10.4
P76270	18103.8	G	T	A	B	CID	LIT	4	26.7	DYKKFFASVAG	1232.6	T	-	2.0	0.5	7.6	16.0
P23869	18135.2	G	U	T	A	CID	LIT	5	39.0	EGFYNNTIFHR	1397.7	R	V	2.4	0.8	40.2	11.1
P23869	18135.2	G	U	T	A	CID	LIT	5	39.0	GTLAMAR	719.4	R	T	1.9	0.8	33.0	14.8
P23869	18135.2	G	U	T	A	CID	LIT	5	39.0	MVTFHTNHGDIVIK	1611.8	-	T	3.8	0.7	45.9	12.8
P23869	18135.2	G	U	T	A	CID	LIT	5	39.0	SGMHQDVPKEDVIIESVTVSE	2315.1	R	-	3.0	0.7	31.0	11.1
P23869	18135.2	G	U	T	A	CID	LIT	5	39.0	TFDDKAPETVK	1250.6	K	N	3.7	0.9	49.0	10.8
P23869	18135.2	G	T	T	A	CID	LIT	4	32.3	GTLAMAR	719.4	R	T	1.8	0.6	28.1	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P23869	18135.2	G	T	T	A	CID	LIT	4	32.3	MVTFHTNHGDIVIK	1611.8	-	T	3.2	0.4	14.1	12.6
P23869	18135.2	G	T	T	A	CID	LIT	4	32.3	SGMHQDVPKEDVIIESVTVSE	2299.1	R	-	2.8	0.0	50.0	10.4
P23869	18135.2	G	T	T	A	CID	LIT	4	32.3	TFDDKAPETVK	1250.6	K	N	3.7	0.8	42.7	12.3
P23869	18135.2	G	U	A	A	CID	LIT	6	28.0	DDKAPETVKNFL	1376.7	F	D	4.0	0.7	26.1	16.6
P23869	18135.2	G	U	A	A	CID	LIT	6	28.0	DIVIKTF	835.5	G	D	2.0	0.0	21.3	10.0
P23869	18135.2	G	U	A	A	CID	LIT	6	28.0	DKIKGVATGRSGMHQ	1584.8	V	D	4.4	0.7	50.5	13.8
P23869	18135.2	G	U	A	A	CID	LIT	6	28.0	DVVDKIKGVATGRSGMHQ	1898.0	M	D	4.3	0.6	47.1	16.2
P23869	18135.2	G	U	A	A	CID	LIT	6	28.0	MVTFHTNHG	1043.5	-	D	2.4	0.8	38.2	10.4
P23869	18135.2	G	U	A	A	CID	LIT	6	28.0	VTFHTNHG	912.4	M	D	0.0	0.0	38.0	13.8
P23869	18135.2	G	T	A	A	CID	LIT	5	26.2	DDKAPETVKNFL	1376.7	F	D	3.3	0.6	24.2	16.6
P23869	18135.2	G	T	A	A	CID	LIT	5	26.2	DIVIKTF	835.5	G	D	1.8	0.0	20.8	10.0
P23869	18135.2	G	T	A	A	CID	LIT	5	26.2	DIVIKTFD	950.5	G	D	2.3	0.7	14.9	14.1
P23869	18135.2	G	T	A	A	CID	LIT	5	26.2	DKIKGVATGRSGMHQ	1584.8	V	D	4.2	0.7	44.0	13.8
P23869	18135.2	G	T	A	A	CID	LIT	5	26.2	MVTFHTNHG	1043.5	-	D	2.1	0.0	37.3	10.4
P23869	18135.2	G	T	T	B	CID	LIT	4	44.5	GTLAMAR	719.4	R	T	1.8	0.4	30.2	15.3
P23869	18135.2	G	T	T	B	CID	LIT	4	44.5	MVTFHTNHGDIVIK	1611.8	-	T	2.1	0.1	13.1	12.8
P23869	18135.2	G	T	T	B	CID	LIT	4	44.5	NTRGTLAMAR	1090.6	K	T	2.2	0.7	16.0	12.8
P23869	18135.2	G	T	T	B	CID	LIT	4	44.5	SGMHQDVPKEDVIIESVTVSE	2299.1	R	-	4.4	0.0	63.2	11.1
P23869	18135.2	G	T	T	B	CID	LIT	4	44.5	TFDDKAPETVK	1250.6	K	N	3.4	0.6	23.3	12.0
P23869	18135.2	G	T	T	B	CID	LIT	4	44.5	VINGFMIQGGGFEPGMK	1781.9	R	Q	3.4	0.4	14.4	12.6
P23869	18135.2	G	T	A	B	CID	LIT	4	22.0	DDKAPETVKNFL	1376.7	F	D	2.5	0.6	17.4	16.6
P23869	18135.2	G	T	A	B	CID	LIT	4	22.0	DKIKGVATGRSGMHQ	1584.8	V	D	4.3	0.7	53.2	13.6
P23869	18135.2	G	T	A	B	CID	LIT	4	22.0	MVTFHTNHG	1043.5	-	D	2.5	0.0	43.1	11.8
P23869	18135.2	G	T	A	B	CID	LIT	4	22.0	VTFHTNHG	912.4	M	D	0.0	0.0	30.5	13.4
P23869	18135.2	G	U	A	B	CID	LIT	2	16.5	DDKAPETVKNFL	1376.7	F	D	2.5	0.7	4.5	16.2
P23869	18135.2	G	U	A	B	CID	LIT	2	16.5	DKIKGVATGRSGMHQ	1584.8	V	D	4.1	0.7	40.2	13.6
P23869	18135.2	S	U	T	A	CID	LIT	4	28.7	ATKEPIKNEANNGLK	1627.9	K	N	3.9	0.8	36.7	16.5
P23869	18135.2	S	U	T	A	CID	LIT	4	28.7	MVTFHTNHGDIVIK	1611.8	-	T	2.0	0.5	12.1	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P23869	18135.2	S	U	T	A	CID	LIT	4	28.7	NFLDYCR	987.4	K	E	2.0	0.0	20.0	9.0
P23869	18135.2	S	U	T	A	CID	LIT	4	28.7	TFDDKAPETVKNFLDYCR	2219.0	K	E	2.9	0.3	16.7	18.5
P23869	18135.2	S	U	T	B	CID	LIT	6	45.7	ATKEPIKNEANNGLK	1626.9	K	N	4.8	0.8	77.5	15.6
P23869	18135.2	S	U	T	B	CID	LIT	6	45.7	EGFYNNTIFHR	1397.7	R	V	2.8	0.6	45.5	13.6
P23869	18135.2	S	U	T	B	CID	LIT	6	45.7	MVTFHTNHGDIVIK	1611.8	-	T	2.6	0.6	27.0	16.6
P23869	18135.2	S	U	T	B	CID	LIT	6	45.7	NFLDYCR	987.4	K	E	1.9	0.5	12.3	10.8
P23869	18135.2	S	U	T	B	CID	LIT	6	45.7	TFDDKAPETVKNFLDYCR	2219.0	K	E	4.6	0.5	42.0	18.5
P23869	18135.2	S	U	T	B	CID	LIT	6	45.7	VINGFMIQGGGFEPGMK	1781.9	R	Q	3.5	0.5	18.4	17.1
P23869	18135.2	S	U	T	C	CID	LIT	7	58.5	ATKEPIKNEANNGLK	1627.9	K	N	5.1	0.7	68.4	16.5
P23869	18135.2	S	U	T	C	CID	LIT	7	58.5	EGFYNNTIFHR	1397.7	R	V	2.2	0.8	13.7	13.2
P23869	18135.2	S	U	T	C	CID	LIT	7	58.5	MVTFHTNHGDIVIK	1611.8	-	T	4.0	0.6	29.8	16.1
P23869	18135.2	S	U	T	C	CID	LIT	7	58.5	NFLDYCR	987.4	K	E	2.1	0.6	13.2	9.0
P23869	18135.2	S	U	T	C	CID	LIT	7	58.5	SGMHQDVPKEDVIIESVTVSE	2299.1	R	-	2.6	0.5	0.0	0.0
P23869	18135.2	S	U	T	C	CID	LIT	7	58.5	TFDDKAPETVKNFLDYCR	2219.0	K	E	4.5	0.5	30.5	18.5
P23869	18135.2	S	U	T	C	CID	LIT	7	58.5	VINGFMIQGGGFEPGMK	1782.9	R	Q	4.8	0.6	28.6	17.0
P23869	18135.2	S	U	T	C	CID	FT	2	17.7	ATKEPIKNEANNGLK	1627.9	K	N	4.4	0.0	60.8	14.9
P23869	18135.2	S	U	T	C	CID	FT	2	17.7	MVTFHTNHGDIVIK	1611.8	-	T	3.5	0.0	34.7	16.5
P23869	18135.2	S	U	T	A	ETD	LIT	2	20.1	ATKEPIKNEANNGLK	1627.9	K	N	6.7	0.5	73.8	17.1
P23869	18135.2	S	U	T	A	ETD	LIT	2	20.1	TFDDKAPETVKNFLDYCR	2219.0	K	E	2.7	0.0	32.5	18.4
P23869	18135.2	S	U	T	B	ETD	LIT	5	39.0	ATKEPIKNEANNGLK	1627.9	K	N	4.9	0.6	59.2	15.4
P23869	18135.2	S	U	T	B	ETD	LIT	5	39.0	MVTFHTNHGDIVIK	1611.8	-	T	4.8	0.8	37.0	15.7
P23869	18135.2	S	U	T	B	ETD	LIT	5	39.0	TFDDKAPETVK	1250.6	K	N	3.2	0.8	26.5	14.9
P23869	18135.2	S	U	T	B	ETD	LIT	5	39.0	TFDDKAPETVKNFLDYCR	2219.0	K	E	4.7	0.0	59.4	18.4
P23869	18135.2	S	U	T	B	ETD	LIT	5	39.0	VINGFMIQGGGFEPGMK	1782.9	R	Q	2.7	0.6	50.7	16.9
P23869	18135.2	S	U	T	C	ETD	LIT	5	39.0	ATKEPIKNEANNGLK	1627.9	K	N	6.7	0.6	76.8	15.1
P23869	18135.2	S	U	T	C	ETD	LIT	5	39.0	MVTFHTNHGDIVIK	1611.8	-	T	3.2	0.5	11.5	16.2
P23869	18135.2	S	U	T	C	ETD	LIT	5	39.0	TFDDKAPETVK	1250.6	K	N	3.2	0.0	26.6	15.2
P23869	18135.2	S	U	T	C	ETD	LIT	5	39.0	TFDDKAPETVKNFLDYCR	2219.0	K	E	3.8	0.0	35.3	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P23869	18135.2	S	U	T	C	ETD	LIT	5	39.0	VINGFMIQGGGFEPGMK	1782.9	R	Q	2.8	0.8	35.8	16.8
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	ATKEPIKNEANNGLK	1627.9	K	N	0.0	0.0	67.8	15.4
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	MVTFHTNHGDIVIK	1611.8	-	T	0.0	0.0	18.3	16.4
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	NFLDYCR	987.4	K	E	0.0	0.0	23.2	10.8
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	TFDDKAPETVKNFLDYCR	2219.0	K	E	0.0	0.0	22.6	18.4
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	VINGFMIQGGGFEPGMK	1782.9	R	Q	0.0	0.0	58.6	16.6
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	ATKEPIKNEANNGLK	1627.9	K	N	5.0	0.8	67.8	15.4
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	MVTFHTNHGDIVIK	1611.8	-	T	1.9	0.2	18.3	16.4
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	NFLDYCR	987.4	K	E	0.0	0.0	23.2	10.8
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	TFDDKAPETVKNFLDYCR	2219.0	K	E	3.6	0.6	22.6	18.4
P23869	18135.2	S	U	T	B	ETD+CID	LIT	5	39.0	VINGFMIQGGGFEPGMK	1782.9	R	Q	4.4	0.6	58.6	16.6
P23869	18135.2	S	U	T	C	ETD+CID	LIT	6	45.7	ATKEPIKNEANNGLK	1627.9	K	N	5.4	0.8	69.9	15.4
P23869	18135.2	S	U	T	C	ETD+CID	LIT	6	45.7	EGFYNNTIFHR	1397.7	R	V	2.1	0.0	28.0	13.6
P23869	18135.2	S	U	T	C	ETD+CID	LIT	6	45.7	MVTFHTNHGDIVIK	1611.8	-	T	2.8	0.3	16.6	16.6
P23869	18135.2	S	U	T	C	ETD+CID	LIT	6	45.7	NFLDYCR	987.4	K	E	0.0	0.0	25.9	7.8
P23869	18135.2	S	U	T	C	ETD+CID	LIT	6	45.7	TFDDKAPETVKNFLDYCR	2219.0	K	E	4.7	0.6	32.5	18.4
P23869	18135.2	S	U	T	C	ETD+CID	LIT	6	45.7	VINGFMIQGGGFEPGMK	1782.9	R	Q	4.6	0.4	42.4	16.6
P23869	18135.2	S	U	T	B	HCD	FT	5	39.0	ATKEPIKNEANNGLK	1627.9	K	N	0.0	0.0	67.8	15.4
P23869	18135.2	S	U	T	B	HCD	FT	5	39.0	MVTFHTNHGDIVIK	1611.8	-	T	0.0	0.0	18.3	16.4
P23869	18135.2	S	U	T	B	HCD	FT	5	39.0	NFLDYCR	987.4	K	E	0.0	0.0	23.2	10.8
P23869	18135.2	S	U	T	B	HCD	FT	5	39.0	TFDDKAPETVKNFLDYCR	2219.0	K	E	0.0	0.0	22.6	18.4
P23869	18135.2	S	U	T	B	HCD	FT	5	39.0	VINGFMIQGGGFEPGMK	1782.9	R	Q	0.0	0.0	58.6	16.6
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	AEEKIDNAVVR	1243.7	K	-	3.7	0.6	53.8	14.5
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	FVTAYLGDAGMLR	1413.7	K	Y	4.3	0.8	83.3	14.1
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	IAPYPQAEKGMK	1348.7	K	R	2.0	0.6	19.2	12.6
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	IDNAVVR	786.4	K	-	2.3	0.5	41.8	16.2
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	KFVTAYLGDAGMLR	1557.8	K	Y	4.7	0.5	50.4	13.2
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	LGGKLENK	858.5	R	T	2.8	0.1	37.2	16.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	LPIVVYTPDNVDVK	1571.9	K	Y	3.9	0.8	34.3	12.3
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	TLEGWGYDYYVFDK	1755.8	K	V	4.0	0.6	47.8	7.8
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	5.5	0.0	54.8	10.8
P23827	18174.2	G	U	T	A	CID	LIT	10	50.6	YRVWK	751.4	K	A	1.7	0.3	12.5	10.0
P23827	18174.2	G	T	T	A	CID	LIT	4	20.4	AEEKIDNAVVR	1243.7	K	-	2.0	0.5	5.1	14.8
P23827	18174.2	G	T	T	A	CID	LIT	4	20.4	IDNAVVR	786.4	K	-	2.2	0.5	41.7	16.2
P23827	18174.2	G	T	T	A	CID	LIT	4	20.4	LGGKLENK	858.5	R	T	2.7	0.2	46.2	16.8
P23827	18174.2	G	T	T	A	CID	LIT	4	20.4	LPIVVYTPDNVDVK	1571.9	K	Y	3.4	0.6	25.1	13.0
P23827	18174.2	G	U	A	A	CID	LIT	3	27.8	DAGMLRYNSKLPIVVYTPDNV	2365.2	G	D	4.1	0.4	31.8	15.8
P23827	18174.2	G	U	A	A	CID	LIT	3	27.8	DKVSSPVSTMMACP	1509.7	F	D	3.3	0.7	51.5	11.1
P23827	18174.2	G	U	A	A	CID	LIT	3	27.8	EEKIDNAVVR	1172.6	A	-	2.3	0.6	34.0	15.6
P23827	18174.2	G	T	T	B	CID	LIT	2	18.5	IAPYPQAEKGMK	1332.7	K	R	2.4	0.6	33.8	11.8
P23827	18174.2	G	T	T	B	CID	LIT	2	18.5	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	4.5	0.6	29.8	10.8
P23827	18174.2	G	T	A	B	CID	LIT	6	51.2	DAGMLRYNSKLPIVVYTPDNV	2365.2	G	D	4.5	0.6	41.8	15.8
P23827	18174.2	G	T	A	B	CID	LIT	6	51.2	DCNLHRLGGKLENKTLEGWGY	2460.2	V	D	2.3	0.7	0.0	0.0
P23827	18174.2	G	T	A	B	CID	LIT	6	51.2	DGKKEKKFVTAYLG	1583.9	P	D	3.5	0.8	27.0	13.6
P23827	18174.2	G	T	A	B	CID	LIT	6	51.2	DKVSSPVSTMMACP	1509.7	F	D	3.3	0.5	21.9	11.1
P23827	18174.2	G	T	A	B	CID	LIT	6	51.2	DKVSSPVSTMMACPDGKKEKKFVTAYLG	3074.5	F	D	3.3	0.0	15.5	14.9
P23827	18174.2	G	T	A	B	CID	LIT	6	51.2	DVKYRVWKAEEKI	1663.9	V	D	3.7	0.6	32.5	12.6
P23827	18174.2	G	U	A	B	CID	LIT	3	30.2	DAGMLRYNSKLPIVVYTPDNV	2365.2	G	D	3.5	0.5	37.7	16.0
P23827	18174.2	G	U	A	B	CID	LIT	3	30.2	DGKKEKKFVTAYLG	1583.9	P	D	3.6	0.5	5.1	13.6
P23827	18174.2	G	U	A	B	CID	LIT	3	30.2	DKVSSPVSTMMACP	1509.7	F	D	3.9	0.5	55.9	11.8
P23827	18174.2	S	U	T	A	CID	LIT	7	47.5	IAPYPQAEK	1016.5	K	G	1.4	0.6	11.5	18.0
P23827	18174.2	S	U	T	A	CID	LIT	7	47.5	KFVTAYLGDAGMLR	1541.8	K	Y	2.7	0.3	30.9	17.2
P23827	18174.2	S	U	T	A	CID	LIT	7	47.5	LGGKLENK	858.5	R	T	2.4	0.3	28.1	19.1
P23827	18174.2	S	U	T	A	CID	LIT	7	47.5	LPIVVYTPDNVDVK	1571.9	K	Y	4.4	0.8	37.3	16.6
P23827	18174.2	S	U	T	A	CID	LIT	7	47.5	TLEGWGYDYYVFDK	1755.8	K	V	3.4	0.5	25.0	12.6
P23827	18174.2	S	U	T	A	CID	LIT	7	47.5	VWKAEEKIDNAVVR	1656.9	R	-	4.4	0.6	71.6	16.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P23827	18174.2	S	U	T	A	CID	LIT	7	47.5	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	5.4	0.7	54.9	16.9
P23827	18174.2	S	U	T	B	CID	LIT	6	42.6	KFVTAYLGDAGMLR	1541.8	K	Y	2.8	0.3	29.6	17.9
P23827	18174.2	S	U	T	B	CID	LIT	6	42.6	LGGKLENK	858.5	R	T	2.2	0.2	33.3	19.1
P23827	18174.2	S	U	T	B	CID	LIT	6	42.6	LPIVVYTPDNVDVK	1571.9	K	Y	4.4	0.6	32.7	16.6
P23827	18174.2	S	U	T	B	CID	LIT	6	42.6	QVIQLTPQEDESTLK	1728.9	R	V	4.1	0.5	26.6	17.9
P23827	18174.2	S	U	T	B	CID	LIT	6	42.6	TLEGWGYDYYVFDK	1755.8	K	V	4.0	0.7	46.6	12.0
P23827	18174.2	S	U	T	B	CID	LIT	6	42.6	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	5.2	0.7	58.5	16.9
P23827	18174.2	S	U	T	C	CID	LIT	7	51.2	KFVTAYLGDAGMLR	1541.8	K	Y	2.8	0.7	20.9	17.6
P23827	18174.2	S	U	T	C	CID	LIT	7	51.2	LGGKLENK	858.5	R	T	2.4	0.2	18.0	19.1
P23827	18174.2	S	U	T	C	CID	LIT	7	51.2	LPIVVYTPDNVDVK	1571.9	K	Y	4.3	0.7	30.3	16.6
P23827	18174.2	S	U	T	C	CID	LIT	7	51.2	QVIQLTPQEDESTLK	1728.9	R	V	3.4	0.3	15.2	17.7
P23827	18174.2	S	U	T	C	CID	LIT	7	51.2	TLEGWGYDYYVFDK	1755.8	K	V	3.8	0.6	43.0	12.6
P23827	18174.2	S	U	T	C	CID	LIT	7	51.2	VWKAEEKIDNAVVR	1656.9	R	-	4.7	0.5	72.8	16.3
P23827	18174.2	S	U	T	C	CID	LIT	7	51.2	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	4.6	0.7	38.2	16.9
P23827	18174.2	S	U	T	A	ETD	LIT	4	24.7	LGGKLENK	858.5	R	T	0.0	0.0	22.0	19.1
P23827	18174.2	S	U	T	A	ETD	LIT	4	24.7	LPIVVYTPDNVDVK	1571.9	K	Y	3.1	0.7	35.1	16.6
P23827	18174.2	S	U	T	A	ETD	LIT	4	24.7	TLEGWGYDYYVFDK	1755.8	K	V	1.7	0.3	10.7	12.3
P23827	18174.2	S	U	T	A	ETD	LIT	4	24.7	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	6.0	0.5	52.1	17.0
P23827	18174.2	S	U	T	B	ETD	LIT	5	28.4	FVTAYLGDAGMLR	1413.7	K	Y	3.1	0.4	33.4	16.3
P23827	18174.2	S	U	T	B	ETD	LIT	5	28.4	KFVTAYLGDAGMLR	1541.8	K	Y	3.8	0.5	49.7	17.9
P23827	18174.2	S	U	T	B	ETD	LIT	5	28.4	LPIVVYTPDNVDVK	1571.9	K	Y	3.4	0.5	33.2	17.2
P23827	18174.2	S	U	T	B	ETD	LIT	5	28.4	TLEGWGYDYYVFDK	1755.8	K	V	0.0	0.0	23.8	12.6
P23827	18174.2	S	U	T	B	ETD	LIT	5	28.4	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	5.0	0.4	33.0	16.5
P23827	18174.2	S	U	T	C	ETD	LIT	6	37.7	FVTAYLGDAGMLR	1413.7	K	Y	1.8	0.2	22.1	17.1
P23827	18174.2	S	U	T	C	ETD	LIT	6	37.7	KFVTAYLGDAGMLR	1541.8	K	Y	1.9	0.0	34.6	17.4
P23827	18174.2	S	U	T	C	ETD	LIT	6	37.7	LPIVVYTPDNVDVK	1571.9	K	Y	3.0	0.5	27.6	16.6
P23827	18174.2	S	U	T	C	ETD	LIT	6	37.7	QVIQLTPQEDESTLK	1728.9	R	V	2.3	0.0	17.8	17.7
P23827	18174.2	S	U	T	C	ETD	LIT	6	37.7	TLEGWGYDYYVFDK	1755.8	K	V	2.1	0.7	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P23827	18174.2	S	U	T	C	ETD	LIT	6	37.7	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	4.6	0.4	28.5	16.5
P23827	18174.2	S	U	T	B	ETD+CID	LIT	5	34.0	LGGKLENK	858.5	R	T	0.0	0.0	23.8	19.1
P23827	18174.2	S	U	T	B	ETD+CID	LIT	5	34.0	LPIVVYTPDNVDVK	1571.9	K	Y	0.0	0.0	35.3	16.6
P23827	18174.2	S	U	T	B	ETD+CID	LIT	5	34.0	QVIQLTPQEDESTLK	1728.9	R	V	0.0	0.0	37.5	18.0
P23827	18174.2	S	U	T	B	ETD+CID	LIT	5	34.0	TLEGWGYDYYVFDK	1755.8	K	V	0.0	0.0	48.7	12.3
P23827	18174.2	S	U	T	B	ETD+CID	LIT	5	34.0	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	0.0	0.0	44.2	16.4
P23827	18174.2	S	U	T	A	ETD+CID	LIT	6	42.6	KFVTAYLGDAGMLR	1541.8	K	Y	2.4	0.2	7.7	17.9
P23827	18174.2	S	U	T	A	ETD+CID	LIT	6	42.6	KVSQALDILTYTNKK	1722.0	-	-	2.7	0.1	76.3	11.8
P23827	18174.2	S	U	T	A	ETD+CID	LIT	6	42.6	LGGKLENK	858.5	R	T	2.7	0.1	32.5	19.1
P23827	18174.2	S	U	T	A	ETD+CID	LIT	6	42.6	LPIVVYTPDNVDVK	1571.9	K	Y	3.9	0.8	32.0	16.6
P23827	18174.2	S	U	T	A	ETD+CID	LIT	6	42.6	QVIQLTPQEDESTLK	1728.9	R	V	4.3	0.5	29.8	17.1
P23827	18174.2	S	U	T	A	ETD+CID	LIT	6	42.6	TLEGWGYDYYVFDK	1755.8	K	V	3.9	0.6	33.3	12.0
P23827	18174.2	S	U	T	A	ETD+CID	LIT	6	42.6	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	5.7	0.7	100.0	16.9
P23827	18174.2	S	U	T	B	ETD+CID	LIT	6	42.6	KFVTAYLGDAGMLR	1541.8	K	Y	2.2	0.2	8.2	17.9
P23827	18174.2	S	U	T	B	ETD+CID	LIT	6	42.6	LGGKLENK	858.5	R	T	2.4	0.2	23.8	19.1
P23827	18174.2	S	U	T	B	ETD+CID	LIT	6	42.6	LPIVVYTPDNVDVK	1571.9	K	Y	4.2	0.7	35.3	16.6
P23827	18174.2	S	U	T	B	ETD+CID	LIT	6	42.6	QVIQLTPQEDESTLK	1728.9	R	V	4.9	0.5	37.5	18.0
P23827	18174.2	S	U	T	B	ETD+CID	LIT	6	42.6	TLEGWGYDYYVFDK	1755.8	K	V	4.2	0.5	48.7	12.3
P23827	18174.2	S	U	T	B	ETD+CID	LIT	6	42.6	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	5.1	0.7	44.2	16.4
P23827	18174.2	S	U	T	C	ETD+CID	LIT	7	42.0	FVTAYLGDAGMLR	1429.7	K	Y	1.7	0.6	2.7	16.3
P23827	18174.2	S	U	T	C	ETD+CID	LIT	7	42.0	KFVTAYLGDAGMLR	1541.8	K	Y	3.6	0.3	40.2	17.7
P23827	18174.2	S	U	T	C	ETD+CID	LIT	7	42.0	LGGKLENK	858.5	R	T	2.4	0.0	23.0	19.1
P23827	18174.2	S	U	T	C	ETD+CID	LIT	7	42.0	LPIVVYTPDNVDVK	1571.9	K	Y	4.2	0.7	31.7	16.6
P23827	18174.2	S	U	T	C	ETD+CID	LIT	7	42.0	TLEGWGYDYYVFDK	1755.8	K	V	3.6	0.7	46.8	12.6
P23827	18174.2	S	U	T	C	ETD+CID	LIT	7	42.0	VWKAEEKIDNAVVR	1656.9	R	-	4.8	0.5	58.1	16.1
P23827	18174.2	S	U	T	C	ETD+CID	LIT	7	42.0	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	5.6	0.7	44.2	16.3
P23827	18174.2	S	U	T	B	HCD	FT	5	34.0	LGGKLENK	858.5	R	T	0.0	0.0	23.8	19.1
P23827	18174.2	S	U	T	B	HCD	FT	5	34.0	LPIVVYTPDNVDVK	1571.9	K	Y	0.0	0.0	35.3	16.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P23827	18174.2	S	U	T	B	HCD	FT	5	34.0	QVIQLTPQEDESTLK	1728.9	R	V	0.0	0.0	37.5	18.0
P23827	18174.2	S	U	T	B	HCD	FT	5	34.0	TLEGWGYDYYVFDK	1755.8	K	V	0.0	0.0	48.7	12.3
P23827	18174.2	S	U	T	B	HCD	FT	5	34.0	YNSKLPIVVYTPDNVDVK	2064.1	R	Y	0.0	0.0	44.2	16.4
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	ANMLAHMETQNK	1419.6	K	I	3.9	0.0	28.9	7.8
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	DLNLTDAQK	1017.5	K	Q	1.9	0.5	14.4	12.6
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	IYNILTPEQK	1218.7	K	K	2.7	0.3	26.2	11.1
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	IYNILTPEQKK	1346.8	K	Q	3.1	0.5	22.0	10.4
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	KANMLAHMETQNK	1515.7	R	I	4.0	0.4	35.8	12.3
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	KQFNANFEK	1125.6	K	R	3.1	0.4	23.8	12.8
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	QFNANFEK	997.5	K	R	2.2	0.3	17.8	10.8
P77754	18181.8	G	T	T	A	CID	LIT	8	29.8	RPPLEER	896.5	K	R	2.7	0.5	31.1	11.1
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	5.0	0.0	91.0	11.8
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	IVGDGIAIKPTGNK	1382.8	K	M	4.0	0.6	39.4	10.0
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	LSGSVTVGETPVIR	1414.8	K	I	4.2	0.5	59.8	11.1
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	MVAPVDGTIGK	1087.6	K	I	3.1	0.7	40.5	13.6
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	STLTPVVISNMDEIK	1646.9	K	E	3.2	0.7	43.4	12.3
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	STLTPVVISNMDEIKELIK	2130.2	K	L	4.5	0.7	50.0	8.5
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	VGDTVIEFDLPLLEEK	1817.0	K	A	4.5	0.8	70.2	12.8
P69783	18233.5	G	U	T	A	CID	LIT	8	62.1	VKVGDTVIEFDLPLLEEK	2044.1	R	A	6.0	0.8	86.8	10.4
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	5.3	0.0	102.0	11.8
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	IVGDGIAIKPTGNK	1382.8	K	M	3.9	0.6	58.4	10.0
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	LSGSVTVGETPVIR	1414.8	K	I	3.9	0.5	64.5	11.5
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	MVAPVDGTIGK	1087.6	K	I	2.6	0.7	23.8	13.6
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	RIAEEGQR	958.5	K	V	2.1	0.6	22.5	15.2
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	SLVSDDKK	891.5	K	D	1.8	0.2	19.6	13.6
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	STLTPVVISNMDEIK	1646.9	K	E	3.7	0.6	41.7	12.3
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	VGDTVIEFDLPLLEEK	1817.0	K	A	4.9	0.8	64.9	12.3
P69783	18233.5	G	T	T	A	CID	LIT	9	69.2	VKVGDTVIEFDLPLLEEK	2044.1	R	A	4.7	0.7	27.1	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69783	18233.5	G	U	A	A	CID	LIT	5	27.2	DKLKSLVS	889.5	F	D	1.9	0.6	10.9	7.8
P69783	18233.5	G	U	A	A	CID	LIT	5	27.2	DKLKSLVSDDKK	1375.8	F	D	3.9	0.6	45.1	9.0
P69783	18233.5	G	U	A	A	CID	LIT	5	27.2	DLPLLEEKAKSTLTPVVISNM	2298.3	F	D	4.5	0.6	35.4	13.6
P69783	18233.5	G	U	A	A	CID	LIT	5	27.2	DVPDVVFAEKIVG	1387.7	E	D	2.1	0.7	21.5	13.8
P69783	18233.5	G	U	A	A	CID	LIT	5	27.2	DVVFAEKIVG	1076.6	P	D	2.9	0.7	36.6	12.3
P69783	18233.5	G	T	A	A	CID	LIT	4	32.5	DLPLLEEKAKSTLTPVVISNM	2298.3	F	D	4.1	0.0	18.4	13.4
P69783	18233.5	G	T	A	A	CID	LIT	4	32.5	DVPDVVFAEKIVG	1387.7	E	D	3.0	0.7	34.1	13.8
P69783	18233.5	G	T	A	A	CID	LIT	4	32.5	DVVFAEKIVG	1076.6	P	D	2.4	0.8	34.5	12.0
P69783	18233.5	G	T	A	A	CID	LIT	4	32.5	ELIKLSGSVTVGETPVIRIKK	2267.4	K	-	4.4	0.9	12.8	4.8
P69783	18233.5	G	T	T	B	CID	LIT	3	23.1	IVGDGIAIKPTGNK	1382.8	K	M	3.8	0.6	54.5	10.0
P69783	18233.5	G	T	T	B	CID	LIT	3	23.1	LSGSVTVGETPVIR	1414.8	K	I	3.2	0.4	24.3	12.0
P69783	18233.5	G	T	T	B	CID	LIT	3	23.1	MVAPVDGTIGK	1087.6	K	I	2.1	0.3	11.7	13.6
P69783	18233.5	G	T	A	B	CID	LIT	2	21.9	DGIAIKPTGNKMVAPV	1610.9	G	D	2.7	0.3	17.5	12.3
P69783	18233.5	G	T	A	B	CID	LIT	2	21.9	DLPLLEEKAKSTLTPVVISNM	2298.3	F	D	2.6	0.7	20.8	13.4
P69783	18233.5	G	U	A	B	CID	LIT	3	27.8	DLPLLEEKAKSTLTPVVISNM	2298.3	F	D	3.5	0.0	32.6	13.6
P69783	18233.5	G	U	A	B	CID	LIT	3	27.8	DVVFAEKIVG	1076.6	P	D	2.0	0.8	8.6	11.5
P69783	18233.5	G	U	A	B	CID	LIT	3	27.8	EGFKRIAEEGQRVKVG	1803.0	G	D	2.1	0.6	0.0	0.0
P69783	18233.5	S	U	T	A	CID	LIT	6	47.9	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	5.4	0.5	32.1	18.9
P69783	18233.5	S	U	T	A	CID	LIT	6	47.9	LSGSVTVGETPVIR	1414.8	K	I	2.8	0.4	28.5	14.8
P69783	18233.5	S	U	T	A	CID	LIT	6	47.9	MVAPVDGTIGK	1087.6	K	I	2.7	0.4	19.3	17.1
P69783	18233.5	S	U	T	A	CID	LIT	6	47.9	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	6.7	0.0	58.7	16.3
P69783	18233.5	S	U	T	A	CID	LIT	6	47.9	STLTPVVISNMDEIK	1646.9	K	E	3.7	0.7	51.2	17.9
P69783	18233.5	S	U	T	A	CID	LIT	6	47.9	STLTPVVISNMDEIKELIK	2130.2	K	L	3.4	0.7	48.9	14.0
P69783	18233.5	S	U	T	B	CID	LIT	7	58.6	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	5.1	0.8	41.0	18.8
P69783	18233.5	S	U	T	B	CID	LIT	7	58.6	LSGSVTVGETPVIR	1414.8	K	I	3.5	0.4	44.5	14.5
P69783	18233.5	S	U	T	B	CID	LIT	7	58.6	MVAPVDGTIGK	1087.6	K	I	3.3	0.6	43.9	17.2
P69783	18233.5	S	U	T	B	CID	LIT	7	58.6	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	6.5	0.0	63.8	16.4
P69783	18233.5	S	U	T	B	CID	LIT	7	58.6	STLTPVVISNMDEIK	1646.9	K	E	2.8	0.6	31.0	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69783	18233.5	S	U	T	B	CID	LIT	7	58.6	STLTPVVISNMDEIKELIK	2130.2	K	L	3.7	0.6	69.4	13.8
P69783	18233.5	S	U	T	B	CID	LIT	7	58.6	VKVGDTVIEFDLPLLEEK	2044.1	R	A	2.5	0.7	4.0	14.6
P69783	18233.5	S	U	T	C	CID	LIT	7	52.7	AKSTLTPVVISNMDEIKELIK	2329.3	K	L	2.3	0.3	0.0	0.0
P69783	18233.5	S	U	T	C	CID	LIT	7	52.7	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	6.5	0.7	44.0	18.8
P69783	18233.5	S	U	T	C	CID	LIT	7	52.7	IVGDGIAIKPTGNK	1382.8	K	M	4.3	0.6	59.6	13.4
P69783	18233.5	S	U	T	C	CID	LIT	7	52.7	LSGSVTVGETPVIR	1414.8	K	I	2.7	0.3	26.8	15.1
P69783	18233.5	S	U	T	C	CID	LIT	7	52.7	MVAPVDGTIGK	1087.6	K	I	2.4	0.5	0.0	0.0
P69783	18233.5	S	U	T	C	CID	LIT	7	52.7	STLTPVVISNMDEIK	1646.9	K	E	3.4	0.5	37.8	17.9
P69783	18233.5	S	U	T	C	CID	LIT	7	52.7	STLTPVVISNMDEIKELIK	2130.2	K	L	4.0	0.6	63.7	14.1
P69783	18233.5	S	U	T	A	ETD	LIT	4	47.3	IVGDGIAIKPTGNK	1382.8	K	M	5.9	0.6	56.0	12.8
P69783	18233.5	S	U	T	A	ETD	LIT	4	47.3	LSGSVTVGETPVIR	1414.8	K	I	0.0	0.0	27.0	15.2
P69783	18233.5	S	U	T	A	ETD	LIT	4	47.3	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	0.0	0.0	48.9	16.2
P69783	18233.5	S	U	T	A	ETD	LIT	4	47.3	STLTPVVISNMDEIK	1646.9	K	E	2.6	0.4	53.8	17.1
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	AKSTLTPVVISNMDEIKELIK	2329.3	K	L	4.5	0.5	33.9	14.5
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	IVGDGIAIKPTGNK	1382.8	K	M	4.8	0.5	45.9	15.1
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	LSGSVTVGETPVIR	1414.8	K	I	3.0	0.0	28.7	15.6
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	MVAPVDGTIGK	1087.6	K	I	2.1	0.3	5.1	17.2
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	0.0	0.0	36.5	16.4
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	STLTPVVISNMDEIK	1646.9	K	E	2.5	0.5	55.3	18.0
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	STLTPVVISNMDEIKELIK	2130.2	K	L	2.0	0.6	16.6	14.1
P69783	18233.5	S	U	T	B	ETD	LIT	7	68.0	VKVGDTVIEFDLPLLEEK	2044.1	R	A	5.3	0.4	0.0	0.0
P69783	18233.5	S	U	T	C	ETD	LIT	7	46.2	AKSTLTPVVISNMDEIKELIK	2329.3	K	L	5.8	0.5	52.4	14.1
P69783	18233.5	S	U	T	C	ETD	LIT	7	46.2	IVGDGIAIKPTGNK	1382.8	K	M	5.3	0.6	55.5	13.4
P69783	18233.5	S	U	T	C	ETD	LIT	7	46.2	LSGSVTVGETPVIR	1414.8	K	I	2.6	0.2	50.8	14.5
P69783	18233.5	S	U	T	C	ETD	LIT	7	46.2	MVAPVDGTIGK	1087.6	K	I	2.4	0.5	14.3	17.2
P69783	18233.5	S	U	T	C	ETD	LIT	7	46.2	STLTPVVISNMDEIK	1646.9	K	E	1.2	0.1	48.6	17.0
P69783	18233.5	S	U	T	C	ETD	LIT	7	46.2	STLTPVVISNMDEIKELIK	2130.2	K	L	4.4	0.6	0.0	0.0
P69783	18233.5	S	U	T	C	ETD	LIT	7	46.2	VKVGDTVIEFDLPLLEEK	2044.1	R	A	4.2	0.6	43.9	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69783	18233.5	S	U	T	C	ETD	FT	3	23.7	GLFDKLK	820.5	M	S	0.0	0.0	17.9	13.0
P69783	18233.5	S	U	T	C	ETD	FT	3	23.7	IVGDGIAIKPTGNK	1382.8	K	M	3.8	0.5	63.1	12.8
P69783	18233.5	S	U	T	C	ETD	FT	3	23.7	STLTPVVISNMDEIKELIK	2130.2	K	L	2.4	0.0	38.2	14.0
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	45.6	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	0.0	0.0	50.8	18.8
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	45.6	GLFDKLK	820.5	M	S	0.0	0.0	21.0	13.0
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	45.6	LSGSVTVGETPVIR	1414.8	K	I	0.0	0.0	46.8	14.5
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	45.6	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	0.0	0.0	51.2	16.0
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	45.6	STLTPVVISNMDEIK	1646.9	K	E	0.0	0.0	38.5	18.1
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	45.6	STLTPVVISNMDEIKELIK	2130.2	K	L	0.0	0.0	75.8	14.1
P69783	18233.5	S	U	T	A	ETD+CID	LIT	3	39.1	LSGSVTVGETPVIR	1414.8	K	I	3.4	0.4	0.0	0.0
P69783	18233.5	S	U	T	A	ETD+CID	LIT	3	39.1	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	3.4	0.5	10.3	16.2
P69783	18233.5	S	U	T	A	ETD+CID	LIT	3	39.1	STLTPVVISNMDEIK	1646.9	K	E	3.5	0.6	49.1	17.0
P69783	18233.5	S	U	T	B	ETD+CID	LIT	2	23.7	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	5.2	0.8	0.0	0.0
P69783	18233.5	S	U	T	B	ETD+CID	LIT	2	23.7	MVAPVDGTIGK	1087.6	K	I	2.2	0.3	0.0	0.0
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	47.9	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	5.2	0.8	50.8	18.8
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	47.9	LSGSVTVGETPVIR	1414.8	K	I	3.6	0.4	46.8	14.5
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	47.9	MVAPVDGTIGK	1087.6	K	I	2.2	0.3	7.8	17.2
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	47.9	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	5.8	0.0	51.2	16.0
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	47.9	STLTPVVISNMDEIK	1646.9	K	E	3.6	0.5	38.5	18.1
P69783	18233.5	S	U	T	B	ETD+CID	LIT	6	47.9	STLTPVVISNMDEIKELIK	2130.2	K	L	4.4	0.6	75.8	14.1
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	AKSTLTPVVISNMDEIK	1846.0	K	E	3.5	0.5	19.5	17.6
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	AKSTLTPVVISNMDEIKELIK	2329.3	K	L	3.4	0.0	22.6	14.0
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	6.7	0.8	38.4	18.8
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	IVGDGIAIKPTGNK	1382.8	K	M	5.8	0.7	54.3	13.4
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	LSGSVTVGETPVIR	1414.8	K	I	3.6	0.3	0.0	0.0
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	MVAPVDGTIGK	1087.6	K	I	1.9	0.4	2.6	17.2
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	4.8	0.0	45.8	16.2
P69783	18233.5	S	U	T	C	ETD+CID	LIT	8	57.4	STLTPVVISNMDEIK	1646.9	K	E	3.7	0.0	38.7	17.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69783	18233.5	S	U	T	B	HCD	FT	6	45.6	DTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3083.6	K	I	0.0	0.0	50.8	18.8
P69783	18233.5	S	U	T	B	HCD	FT	6	45.6	GLFDKLK	820.5	M	S	0.0	0.0	21.0	13.0
P69783	18233.5	S	U	T	B	HCD	FT	6	45.6	LSGSVTVGETPVIR	1414.8	K	I	0.0	0.0	46.8	14.5
P69783	18233.5	S	U	T	B	HCD	FT	6	45.6	SLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEK	3956.1	K	I	0.0	0.0	51.2	16.0
P69783	18233.5	S	U	T	B	HCD	FT	6	45.6	STLTPVVISNMDEIK	1646.9	K	E	0.0	0.0	38.5	18.1
P69783	18233.5	S	U	T	B	HCD	FT	6	45.6	STLTPVVISNMDEIKELIK	2130.2	K	L	0.0	0.0	75.8	14.1
P69783	18233.5	S	U	T	C	HCD	FT	2	10.7	GLFDKLK	820.5	M	S	0.0	0.0	25.1	13.0
P69783	18233.5	S	U	T	C	HCD	FT	2	10.7	MVAPVDGTIGK	1087.6	K	I	2.8	0.0	56.5	17.2
P0AFZ3	18244.4	G	T	T	A	CID	LIT	2	11.5	AVGNLELANDEVR	1399.7	R	F	3.7	0.6	44.7	12.8
P0AFZ3	18244.4	G	T	T	A	CID	LIT	2	11.5	FGGIPR	646.4	R	Q	1.6	0.5	16.6	11.1
P0A832	18251.5	G	U	T	A	CID	LIT	2	12.5	AHKPGSATIALNKR	1463.8	K	A	3.5	0.0	67.6	4.8
P0A832	18251.5	G	U	T	A	CID	LIT	2	12.5	EWQVDK	804.4	R	A	1.7	0.7	13.5	11.8
P0A832	18251.5	S	U	T	A	CID	LIT	2	9.4	AHKPGSATIALNKR	1463.8	K	A	1.8	0.0	33.0	7.8
P0A832	18251.5	S	U	T	A	CID	LIT	2	9.4	KAHKPGSATIALNKR	1591.9	K	A	2.7	0.0	31.1	6.0
P31131	18303.1	G	T	T	A	CID	LIT	4	27.3	ILSVSQQSLER	1259.7	K	Y	2.4	0.0	64.3	13.2
P31131	18303.1	G	T	T	A	CID	LIT	4	27.3	LASALCAAEDTPK	1346.7	K	F	4.0	0.6	58.4	12.0
P31131	18303.1	G	T	T	A	CID	LIT	4	27.3	LTTAESCTGGK	1124.5	R	L	2.9	0.0	41.6	9.0
P31131	18303.1	G	T	T	A	CID	LIT	4	27.3	VAAEMATGAIER	1218.6	K	A	3.8	0.7	72.5	14.1
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	GGDLGQPFQFK	1193.6	R	N	3.7	0.0	40.3	13.0
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	GIEGSSLDVPENIVHSGK	1837.9	R	T	4.6	0.6	74.6	13.4
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	LKQGIESATQK	1202.7	K	K	3.4	0.7	58.8	11.5
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	LKVQAQIQGDEIR	1497.8	K	V	4.5	0.7	84.7	12.0
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	NAVDNASREVESR	1446.7	R	F	2.7	0.4	19.5	10.4
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	NVEASFELNDASK	1423.7	R	T	4.4	0.0	90.3	10.8
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	PSFDIVSEVDLQEAR	1704.8	M	N	0.0	0.0	82.5	13.8
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	RGIEGSSLDVPENIVHSGK	1994.0	K	T	5.2	0.9	57.0	13.2
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	SRDDLQAVMAMVR	1491.7	K	G	5.0	0.7	53.3	13.4
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	TWFVEAK	880.5	K	L	2.1	0.8	31.6	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	VLSESDFQVNQLLDILR	1989.1	K	A	4.7	0.6	109.0	11.1
P0A8E7	18326.2	G	U	T	A	CID	LIT	12	81.0	VQAQIQGDEIR	1256.7	K	V	3.7	0.5	73.6	13.6
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	GGDLGQPFQFK	1193.6	R	N	2.7	0.6	11.2	12.6
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	GIEGSSLDVPENIVHSGK	1837.9	R	T	4.9	0.6	109.0	13.6
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	LKQGIESATQK	1202.7	K	K	3.2	0.9	47.4	12.0
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	LKVQAQIQGDEIR	1497.8	K	V	4.8	0.6	78.5	11.8
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	NAVDNASR	846.4	R	E	1.7	0.8	22.3	13.4
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	NVEASFELNDASK	1423.7	R	T	4.0	0.6	51.8	10.8
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	PSFDIVSEVDLQEAR	1704.8	M	N	0.0	0.0	42.2	13.8
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	RGIEGSSLDVPENIVHSGK	1994.0	K	T	3.5	0.5	12.2	13.6
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	TWFVEAK	880.5	K	L	2.0	0.6	10.0	14.9
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	VLSESDFQVNQLLDILR	1989.1	K	A	4.1	0.5	98.2	10.0
P0A8E7	18326.2	G	T	T	A	CID	LIT	11	69.9	VQAQIQGDEIR	1256.7	K	V	3.5	0.5	67.1	13.4
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DASKTIKVLSES	1277.7	N	D	3.4	0.8	43.4	10.0
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DASKTIKVLSESDFQVNQLL	2235.2	N	D	5.9	0.6	67.8	14.8
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DEIRVTGKSR	1160.6	G	D	2.4	0.7	33.4	13.2
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DEIRVTGKSRD	1275.7	G	D	2.2	0.6	20.6	15.1
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DFQVNQLL	976.5	S	D	2.1	0.4	29.3	16.1
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DFRNVEASFELN	1440.7	F	D	3.2	0.6	38.1	13.6
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DILRAKLLKRGIEGSSL	1869.1	L	D	2.2	0.8	9.9	7.0
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DLGQPFQFKNFRD	1611.8	G	-	3.1	0.0	33.2	14.6
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DLQEARNAV	1015.5	V	D	2.7	0.5	26.9	13.0
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DNASREVESRF	1309.6	V	D	1.9	0.7	0.0	0.0
P0A8E7	18326.2	G	U	A	A	CID	LIT	11	64.4	DSKLKVQAQIQG	1314.7	K	D	3.3	0.5	25.6	15.1
P0A8E7	18326.2	G	T	A	A	CID	LIT	5	28.2	DASKTIKVLSES	1277.7	N	D	3.1	0.7	20.1	7.8
P0A8E7	18326.2	G	T	A	A	CID	LIT	5	28.2	DEIRVTGKSR	1160.6	G	D	2.4	0.7	38.3	13.2
P0A8E7	18326.2	G	T	A	A	CID	LIT	5	28.2	DEIRVTGKSRD	1275.7	G	D	2.5	0.7	13.5	15.3
P0A8E7	18326.2	G	T	A	A	CID	LIT	5	28.2	DNASREVESRF	1309.6	V	D	1.9	0.7	19.8	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8E7	18326.2	G	T	A	A	CID	LIT	5	28.2	DSKLKVQAQIQG	1314.7	K	D	3.6	0.6	46.9	14.9
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	GGDLGQPFQFK	1193.6	R	N	3.7	0.9	30.1	12.6
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	GIEGSSLDVPENIVHSGK	1837.9	R	T	4.3	0.5	24.2	14.1
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	GIEGSSLDVPENIVHSGKTWFVEAK	2699.4	R	L	3.4	0.8	30.8	11.8
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	LKQGIESATQK	1202.7	K	K	3.5	0.4	42.9	12.6
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	LKVQAQIQGDEIR	1497.8	K	V	3.3	0.7	23.7	12.0
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	NAVDNASR	846.4	R	E	1.4	0.5	12.7	12.3
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	NAVDNASREVESR	1446.7	R	F	2.5	0.3	20.2	10.4
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	NVEASFELNDASK	1423.7	R	T	2.4	0.6	8.1	10.8
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	NVEASFELNDASKTIK	1765.9	R	V	4.5	0.6	75.3	10.4
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	PSFDIVSEVDLQEAR	1704.8	M	N	0.0	0.0	69.8	14.6
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	QGIESATQK	961.5	K	K	3.1	0.6	33.1	14.6
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	RGIEGSSLDVPENIVHSGK	1994.0	K	T	3.4	0.8	23.3	13.0
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	SRDDLQAVMAMVR	1491.7	K	G	4.8	0.7	69.0	12.6
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	TWFVEAK	880.5	K	L	1.4	0.4	20.4	14.9
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	VLSESDFQVNQLLDILR	1989.1	K	A	3.9	0.4	50.7	11.1
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	VQAQIQGDEIR	1256.7	K	V	3.5	0.4	47.8	14.1
P0A8E7	18326.2	G	T	T	B	CID	LIT	17	85.3	VQAQIQGDEIRVTGK	1641.9	K	S	4.6	0.7	53.7	10.0
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DASKTIKVLSES	1277.7	N	D	3.6	0.7	43.0	7.8
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DDLQAVMAMVRGG	1362.7	R	D	2.3	0.0	33.6	17.1
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DEIRVTGKSR	1160.6	G	D	3.0	0.6	31.9	13.2
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DFQVNQLL	976.5	S	D	1.8	0.5	9.2	16.1
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DFRNVEASFELN	1440.7	F	D	2.7	0.3	11.9	13.6
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DLGQPFQFKNFRD	1611.8	G	-	2.6	0.0	26.9	14.6
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DLQEARNAV	1015.5	V	D	2.7	0.0	32.6	11.8
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DNASREVESRF	1309.6	V	D	2.1	0.6	0.0	0.0
P0A8E7	18326.2	G	T	A	B	CID	LIT	9	61.3	DSKLKVQAQIQG	1314.7	K	D	3.4	0.6	20.3	15.4
P0A8E7	18326.2	G	U	A	B	CID	LIT	3	20.9	DEIRVTGKSR	1160.6	G	D	2.1	0.7	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8E7	18326.2	G	U	A	B	CID	LIT	3	20.9	DFRNVEASFELN	1440.7	F	D	3.2	0.6	41.8	13.6
P0A8E7	18326.2	G	U	A	B	CID	LIT	3	20.9	DSKLKVQAQIQG	1314.7	K	D	2.8	0.5	7.9	14.9
P0A8E7	18326.2	S	U	T	A	CID	LIT	5	36.8	GIEGSSLDVPENIVHSGK	1837.9	R	T	5.0	0.7	62.4	17.9
P0A8E7	18326.2	S	U	T	A	CID	LIT	5	36.8	LKQGIESATQK	1202.7	K	K	2.9	0.6	31.8	16.2
P0A8E7	18326.2	S	U	T	A	CID	LIT	5	36.8	NVEASFELNDASK	1423.7	R	T	3.7	0.4	9.9	15.7
P0A8E7	18326.2	S	U	T	A	CID	LIT	5	36.8	RGIEGSSLDVPENIVHSGK	1994.0	K	T	3.6	0.5	37.3	18.0
P0A8E7	18326.2	S	U	T	A	CID	LIT	5	36.8	VLSESDFQVNQLLDILR	1989.1	K	A	3.2	0.7	56.9	17.1
P0A8E7	18326.2	S	U	T	B	CID	LIT	4	31.3	GIEGSSLDVPENIVHSGK	1837.9	R	T	4.2	0.6	84.1	17.9
P0A8E7	18326.2	S	U	T	B	CID	LIT	4	31.3	PSFDIVSEVDLQEAR	1704.8	M	N	0.0	0.0	52.0	18.1
P0A8E7	18326.2	S	U	T	B	CID	LIT	4	31.3	RGIEGSSLDVPENIVHSGK	1994.0	K	T	4.4	0.0	47.9	17.9
P0A8E7	18326.2	S	U	T	B	CID	LIT	4	31.3	VLSESDFQVNQLLDILR	1989.1	K	A	3.9	0.0	22.2	17.3
P0A8E7	18326.2	S	U	T	C	CID	LIT	3	29.4	GIEGSSLDVPENIVHSGK	1837.9	R	T	5.7	0.6	75.1	17.9
P0A8E7	18326.2	S	U	T	C	CID	LIT	3	29.4	SRDDLQAVMAMVR	1491.7	K	G	3.0	0.5	24.7	16.6
P0A8E7	18326.2	S	U	T	C	CID	LIT	3	29.4	VLSESDFQVNQLLDILR	1989.1	K	A	3.9	0.5	26.1	17.0
P0A8E7	18326.2	S	U	T	A	ETD	LIT	4	36.2	GIEGSSLDVPENIVHSGK	1837.9	R	T	2.9	0.8	60.7	18.2
P0A8E7	18326.2	S	U	T	A	ETD	LIT	4	36.2	SRDDLQAVMAMVR	1491.7	K	G	2.6	0.2	25.3	16.9
P0A8E7	18326.2	S	U	T	A	ETD	LIT	4	36.2	VLSESDFQVNQLLDILR	1989.1	K	A	2.9	0.8	90.7	17.0
P0A8E7	18326.2	S	U	T	A	ETD	LIT	4	36.2	VQAQIQGDEIR	1256.7	K	V	2.1	0.0	45.7	16.4
P0A8E7	18326.2	S	U	T	B	ETD	LIT	4	36.2	GIEGSSLDVPENIVHSGK	1837.9	R	T	3.3	0.8	64.5	17.8
P0A8E7	18326.2	S	U	T	B	ETD	LIT	4	36.2	SRDDLQAVMAMVR	1491.7	K	G	3.4	0.3	16.4	16.6
P0A8E7	18326.2	S	U	T	B	ETD	LIT	4	36.2	VLSESDFQVNQLLDILR	1989.1	K	A	3.3	0.5	102.0	16.8
P0A8E7	18326.2	S	U	T	B	ETD	LIT	4	36.2	VQAQIQGDEIR	1256.7	K	V	1.8	0.0	37.7	16.4
P0A8E7	18326.2	S	U	T	C	ETD	LIT	2	21.5	GIEGSSLDVPENIVHSGK	1837.9	R	T	2.6	0.0	60.7	18.1
P0A8E7	18326.2	S	U	T	C	ETD	LIT	2	21.5	VLSESDFQVNQLLDILR	1989.1	K	A	4.4	0.4	43.2	17.1
P0A8E7	18326.2	S	U	T	B	ETD+CID	LIT	3	22.1	GIEGSSLDVPENIVHSGK	1837.9	R	T	0.0	0.0	73.9	17.9
P0A8E7	18326.2	S	U	T	B	ETD+CID	LIT	3	22.1	RGIEGSSLDVPENIVHSGK	1994.0	K	T	0.0	0.0	39.0	17.5
P0A8E7	18326.2	S	U	T	B	ETD+CID	LIT	3	22.1	VLSESDFQVNQLLDILR	1989.1	K	A	0.0	0.0	81.3	17.0
P0A8E7	18326.2	S	U	T	A	ETD+CID	LIT	2	21.5	GIEGSSLDVPENIVHSGK	1837.9	R	T	5.1	0.6	60.3	17.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8E7	18326.2	S	U	T	A	ETD+CID	LIT	2	21.5	VLSESDFQVNQLLDILR	1989.1	K	A	3.7	0.4	81.6	17.1
P0A8E7	18326.2	S	U	T	B	ETD+CID	LIT	3	22.1	GIEGSSLDVPENIVHSGK	1837.9	R	T	5.2	0.6	73.9	17.9
P0A8E7	18326.2	S	U	T	B	ETD+CID	LIT	3	22.1	RGIEGSSLDVPENIVHSGK	1994.0	K	T	3.8	0.0	39.0	17.5
P0A8E7	18326.2	S	U	T	B	ETD+CID	LIT	3	22.1	VLSESDFQVNQLLDILR	1989.1	K	A	4.4	0.7	81.3	17.0
P0A8E7	18326.2	S	U	T	C	ETD+CID	LIT	4	35.0	GIEGSSLDVPENIVHSGK	1837.9	R	T	5.6	0.6	65.7	17.9
P0A8E7	18326.2	S	U	T	C	ETD+CID	LIT	4	35.0	PSFDIVSEVDLQEAR	1704.8	M	N	0.0	0.0	54.8	17.8
P0A8E7	18326.2	S	U	T	C	ETD+CID	LIT	4	35.0	TWFVEAK	880.5	K	L	2.0	0.4	26.2	17.1
P0A8E7	18326.2	S	U	T	C	ETD+CID	LIT	4	35.0	VLSESDFQVNQLLDILR	1989.1	K	A	4.3	0.6	95.0	17.1
P0A8E7	18326.2	S	U	T	B	HCD	FT	3	22.1	GIEGSSLDVPENIVHSGK	1837.9	R	T	0.0	0.0	73.9	17.9
P0A8E7	18326.2	S	U	T	B	HCD	FT	3	22.1	RGIEGSSLDVPENIVHSGK	1994.0	K	T	0.0	0.0	39.0	17.5
P0A8E7	18326.2	S	U	T	B	HCD	FT	3	22.1	VLSESDFQVNQLLDILR	1989.1	K	A	0.0	0.0	81.3	17.0
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	EAIGYADSVHDYVSR	1681.8	R	D	3.8	0.5	52.4	11.5
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	HADRYIER	1059.5	K	I	3.0	0.7	18.8	12.8
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	ILFLEGLPNLQDLGK	1670.0	R	L	4.4	0.7	68.0	10.0
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	LNDVEYHESIDEMK	1721.8	R	H	2.5	0.0	32.1	9.5
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	LNIGEDVEEMLR	1417.7	K	S	3.5	0.8	58.2	14.1
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	MGLQNYLQAQIR	1434.8	K	E	2.9	0.4	20.0	14.0
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	MGLQNYLQAQIREEG	1749.9	K	-	4.1	0.0	38.7	8.5
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	SDLALELDGAK	1131.6	R	N	3.5	0.6	41.3	13.0
P0ABD3	18478.1	G	U	T	A	CID	LIT	9	61.4	VINYLNK	863.5	K	L	2.0	0.3	14.3	14.0
P0ABD3	18478.1	G	U	A	A	CID	LIT	3	25.9	DGAKNLREAIGYA	1377.7	L	D	2.8	0.6	29.3	14.6
P0ABD3	18478.1	G	U	A	A	CID	LIT	3	25.9	DLIQKMGLQNYLQAQIREEG	2347.2	L	-	4.7	0.7	53.9	15.9
P0ABD3	18478.1	G	U	A	A	CID	LIT	3	25.9	DMMIEILR	1052.5	R	D	2.1	0.8	7.2	14.9
P63417	18515.9	G	U	T	A	CID	LIT	5	40.1	FGFELAAHHDLR	1412.7	R	C	3.5	0.0	39.8	12.3
P63417	18515.9	G	U	T	A	CID	LIT	5	40.1	LADDALNGVTGLVEYHEHFNRF	2517.2	R	-	2.5	0.2	12.1	11.1
P63417	18515.9	G	U	T	A	CID	LIT	5	40.1	RSFESDAEAK	1139.5	R	L	2.9	0.0	30.9	9.5
P63417	18515.9	G	U	T	A	CID	LIT	5	40.1	VEIPIDAPGIDALLR	1591.9	R	R	3.3	0.0	41.0	7.0
P63417	18515.9	G	U	T	A	CID	LIT	5	40.1	YRGQGLAR	920.5	K	Q	2.7	0.3	20.1	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFD1	18571.9	G	U	T	A	CID	LIT	4	28.3	EAIEHEMHHYEDPR	1792.8	R	A	3.7	0.0	45.1	4.8
P0AFD1	18571.9	G	U	T	A	CID	LIT	4	28.3	KLNIKPGQTTFDGR	1574.9	K	F	3.7	0.8	44.0	12.3
P0AFD1	18571.9	G	U	T	A	CID	LIT	4	28.3	LNIKPGQTTFDGR	1446.8	K	F	3.2	0.0	22.6	11.1
P0AFD1	18571.9	G	U	T	A	CID	LIT	4	28.3	MHENQQPQTEAFELSAAER	2216.0	-	E	4.8	0.0	78.2	7.0
P0AFD1	18571.9	G	T	T	A	CID	LIT	2	13.3	AASIEALK	802.5	R	I	1.8	0.6	14.9	15.2
P0AFD1	18571.9	G	T	T	A	CID	LIT	2	13.3	KLNIKPGQTTFDGR	1574.9	K	F	3.5	0.8	22.1	12.6
P0AFD1	18571.9	G	T	T	B	CID	LIT	2	8.4	KLNIKPGQTTFDGR	1574.9	K	F	2.8	0.0	38.5	12.6
P0AFD1	18571.9	G	T	T	B	CID	LIT	2	8.4	LNIKPGQTTFDGR	1446.8	K	F	2.7	0.8	31.9	11.8
P0AFD1	18571.9	G	T	A	B	CID	LIT	2	12.0	DGAIHAIA	767.4	P	D	2.5	0.8	12.5	10.0
P0AFD1	18571.9	G	T	A	B	CID	LIT	2	12.0	MHENQQPQTEAF	1459.6	-	E	2.5	0.0	16.1	9.0
P0AFD1	18571.9	S	U	T	B	CID	LIT	3	31.9	LNIKPGQTTFDGR	1446.8	K	F	2.9	0.7	40.5	16.9
P0AFD1	18571.9	S	U	T	B	CID	LIT	3	31.9	MHENQQPQTEAFELSAAER	2216.0	-	E	5.1	0.6	60.1	14.8
P0AFD1	18571.9	S	U	T	B	CID	LIT	3	31.9	YCDSVVCHINGYQGIQAALEK	2426.1	R	K	3.1	0.6	32.5	16.7
P0AFD1	18571.9	S	U	T	C	CID	LIT	4	32.5	KLNIKPGQTTFDGR	1574.9	K	F	3.2	0.5	16.8	15.7
P0AFD1	18571.9	S	U	T	C	CID	LIT	4	32.5	MHENQQPQTEAFELSAAER	2216.0	-	E	4.0	0.6	31.2	14.5
P0AFD1	18571.9	S	U	T	C	CID	LIT	4	32.5	YCDSVVCHINGYQGIQAALEK	2426.1	R	K	4.7	0.7	47.3	16.0
P0AFD1	18571.9	S	U	T	C	CID	LIT	4	32.5	YCDSVVCHINGYQGIQAALEKK	2554.2	R	L	3.3	0.4	13.2	18.1
P0AFD1	18571.9	S	U	T	C	ETD	LIT	3	19.9	KLNIKPGQTTFDGR	1574.9	K	F	5.2	0.7	49.6	15.7
P0AFD1	18571.9	S	U	T	C	ETD	LIT	3	19.9	LNIKPGQTTFDGR	1446.8	K	F	4.0	0.5	50.2	15.9
P0AFD1	18571.9	S	U	T	C	ETD	LIT	3	19.9	MHENQQPQTEAFELSAAER	2216.0	-	E	4.1	0.0	46.2	14.6
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	3	24.7	MHENQQPQTEAFELSAAER	2216.0	-	E	0.0	0.0	61.1	14.1
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	3	24.7	YCDSVVCHINGYQGIQAALEK	2426.1	R	K	0.0	0.0	35.5	16.0
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	3	24.7	YCDSVVCHINGYQGIQAALEKK	2554.2	R	L	0.0	0.0	23.2	18.2
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	2	19.3	LNIKPGQTTFDGR	1446.8	K	F	2.3	0.5	0.0	0.0
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	2	19.3	MHENQQPQTEAFELSAAER	2216.0	-	E	4.6	0.5	0.0	0.0
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	4	32.5	LNIKPGQTTFDGR	1446.8	K	F	2.3	0.5	0.0	0.0
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	4	32.5	MHENQQPQTEAFELSAAER	2216.0	-	E	4.6	0.5	61.1	14.1
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	4	32.5	YCDSVVCHINGYQGIQAALEK	2426.1	R	K	0.0	0.0	35.5	16.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFD1	18571.9	S	U	T	B	ETD+CID	LIT	4	32.5	YCDSVVCHINGYQGIQAALEKK	2554.2	R	L	5.0	0.0	23.2	18.2
P0AFD1	18571.9	S	U	T	C	ETD+CID	LIT	2	21.1	KLNIKPGQTTFDGR	1574.9	K	F	3.3	0.8	38.5	17.3
P0AFD1	18571.9	S	U	T	C	ETD+CID	LIT	2	21.1	KVDVTGTSK	934.5	-	-	2.7	0.3	25.0	15.8
P0AFD1	18571.9	S	U	T	C	ETD+CID	LIT	2	21.1	YCDSVVCHINGYQGIQAALEK	2426.1	R	K	4.7	0.0	56.2	15.8
P0AFD1	18571.9	S	U	T	C	ETD+CID	LIT	2	21.1	YCDSVVCHINGYQGIQAALEKK	2554.2	R	L	0.7	-0.9	35.9	18.5
P0AFD1	18571.9	S	U	T	B	HCD	FT	2	24.1	MHENQQPQTEAFELSAAER	2216.0	-	E	0.0	0.0	61.1	14.1
P0AFD1	18571.9	S	U	T	B	HCD	FT	2	24.1	YCDSVVCHINGYQGIQAALEK	2426.1	R	K	0.0	0.0	35.5	16.0
P0A917	18585.0	S	U	T	C	CID	LIT	2	25.1	TASSGDYNKNQYYGITAGPAYR	2397.1	R	I	3.6	0.6	6.4	16.2
P0A917	18585.0	S	U	T	C	CID	LIT	2	25.1	YRYEEDNSPLGVIGSFTYTEK	2468.2	K	S	3.1	0.4	14.6	17.7
P0A917	18585.0	S	U	T	B	ETD+CID	LIT	2	25.1	TASSGDYNKNQYYGITAGPAYR	2397.1	R	I	2.2	0.5	7.1	16.0
P0A917	18585.0	S	U	T	B	ETD+CID	LIT	2	25.1	YRYEEDNSPLGVIGSFTYTEK	2468.2	K	S	3.3	0.3	12.1	17.6
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	DSAQEAGHHVVDK	1392.7	R	A	4.1	0.6	59.5	11.1
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	EVEGFGEVFR	1168.6	R	M	2.7	0.0	30.1	12.8
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	IAILTVSNR	986.6	R	R	3.2	0.8	55.3	13.2
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	MLSFEEIGTSTLQSR	1698.8	R	A	3.6	0.8	79.6	11.8
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	RGEEDDTSGHYLR	1534.7	R	D	4.9	0.7	53.5	4.8
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	SQVSTEFIPTR	1264.7	M	I	0.0	0.0	40.5	13.6
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	TAWENIIAPQLDAR	1597.8	R	T	4.3	0.0	81.4	10.0
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	TLIFAMPGSTK	1165.6	K	A	3.0	0.9	39.7	9.5
P0AEZ9	18647.1	G	U	T	A	CID	LIT	9	63.5	TRPCNFHPHLKK	1534.8	R	-	3.0	0.4	16.7	12.3
P0AEZ9	18647.1	G	U	A	A	CID	LIT	4	27.1	DARTRPCNFHPHLKK	1877.0	L	-	2.0	0.7	8.0	16.6
P0AEZ9	18647.1	G	U	A	A	CID	LIT	4	27.1	DDTSGHYLR	1063.5	E	D	2.9	0.6	57.0	13.4
P0AEZ9	18647.1	G	U	A	A	CID	LIT	4	27.1	DQAPEALLPLF	1213.6	G	D	1.8	0.6	17.0	12.0
P0AEZ9	18647.1	G	U	A	A	CID	LIT	4	27.1	DSAQEAGHHVV	1149.5	R	D	2.9	0.8	23.2	14.0
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	AIGEAKDDDTADILTAASR	1933.0	K	D	5.6	0.9	115.0	11.8
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	ATNLLYTR	951.5	K	N	2.9	0.6	54.7	9.5
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	ATVELLNR	915.5	K	Q	2.6	0.8	37.9	16.6
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	AVQLGGVALGTTQVINSK	1756.0	R	T	5.3	0.9	78.9	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	DLDKFLWFIESNIE	1768.9	R	-	3.8	0.0	42.1	12.6
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	ELADRYAIVANDVR	1604.8	K	K	4.0	0.6	39.8	12.8
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	FLWFIESNIE	1297.6	K	-	2.5	0.0	37.5	12.6
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	GANFIAVHEMLDGFR	1676.8	R	T	4.4	0.6	63.7	11.5
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	KATVELLNR	1043.6	K	Q	3.0	0.6	48.2	11.1
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	QAHWNMR	942.4	K	G	1.5	0.7	14.7	10.0
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	QVIQFIDLSLITK	1517.9	R	Q	4.0	0.0	71.6	3.0
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	SKATNLLYTR	1166.7	K	N	3.4	0.7	57.0	12.0
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	SYPLDIHNVQDHLK	1678.9	K	E	4.2	0.7	49.4	12.3
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	SYPLDIHNVQDHLKELADR	2263.1	K	Y	3.2	0.6	16.6	13.2
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	TALIDHLDTMAER	1501.7	R	A	3.4	0.7	51.5	11.8
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	TPLKSYPLDIHNVQDHLK	2118.1	K	E	2.8	0.7	13.4	11.1
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	YAIVANDVR	1020.5	R	K	3.2	0.5	41.1	14.5
P0ABT2	18678.1	G	U	T	A	CID	LIT	18	90.4	YAIVANDVRK	1148.6	R	A	1.2	0.6	11.7	12.8
P0ABT2	18678.1	G	T	T	A	CID	LIT	2	11.4	KATVELLNR	1043.6	K	Q	2.8	0.4	33.3	11.1
P0ABT2	18678.1	G	T	T	A	CID	LIT	2	11.4	SKATNLLYTR	1166.7	K	N	3.5	0.5	31.6	12.0
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DHLKELA	825.4	Q	D	1.9	0.6	23.1	12.6
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DIHNVQDHLKELA	1531.8	L	D	3.4	0.4	31.5	14.3
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DILTAASR	846.5	A	D	2.3	0.7	42.3	14.8
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DILTAASRDL	1074.6	A	D	3.6	0.5	59.4	16.8
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DKFLWFIESNIE	1540.8	L	-	3.9	0.6	29.4	14.6
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DLDKFLWFIESNIE	1768.9	R	-	4.1	0.5	0.0	0.0
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DRYAIVAN	921.5	A	D	2.2	0.6	28.9	14.5
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	DVRKAIGEAK	1086.6	N	D	2.8	0.6	21.7	12.6
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	STAKLVKSKATNLLYTRN	2008.2	M	D	0.0	0.0	67.0	10.8
P0ABT2	18678.1	G	U	A	A	CID	LIT	10	44.3	STAKLVKSKATNLLYTRNDVS	2309.3	M	D	0.0	0.0	32.3	12.0
P0ABT2	18678.1	G	T	A	A	CID	LIT	2	15.0	DHLKELA	825.4	Q	D	1.8	0.0	18.6	13.8
P0ABT2	18678.1	G	T	A	A	CID	LIT	2	15.0	STAKLVKSKATNLLYTRN	2008.2	M	D	0.0	0.0	31.0	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABT2	18678.1	G	U	T	B	CID	LIT	2	9.6	ATNLLYTR	951.5	K	N	3.0	0.0	54.3	10.8
P0ABT2	18678.1	G	U	T	B	CID	LIT	2	9.6	ATVELLNR	915.5	K	Q	2.7	0.3	35.8	16.0
P0ABT2	18678.1	G	T	A	B	CID	LIT	2	16.8	DVRKAIGEAK	1086.6	N	D	2.6	0.8	17.0	12.6
P0ABT2	18678.1	G	T	A	B	CID	LIT	2	16.8	STAKLVKSKATNLLYTRN	2008.2	M	D	0.0	0.0	32.7	11.5
P0ABT2	18678.1	S	U	T	A	CID	LIT	7	51.5	AIGEAKDDDTADILTAASR	1933.0	K	D	5.5	0.7	97.6	18.1
P0ABT2	18678.1	S	U	T	A	CID	LIT	7	51.5	AVQLGGVALGTTQVINSK	1756.0	R	T	5.2	0.6	53.4	14.1
P0ABT2	18678.1	S	U	T	A	CID	LIT	7	51.5	DLDKFLWFIESNIE	1768.9	R	-	3.6	0.0	57.7	16.5
P0ABT2	18678.1	S	U	T	A	CID	LIT	7	51.5	GANFIAVHEMLDGFR	1676.8	R	T	3.9	0.5	28.8	15.7
P0ABT2	18678.1	S	U	T	A	CID	LIT	7	51.5	KAIGEAKDDDTADILTAASR	2061.0	R	D	6.3	0.6	94.9	19.1
P0ABT2	18678.1	S	U	T	A	CID	LIT	7	51.5	SYPLDIHNVQDHLK	1678.9	K	E	2.9	0.4	21.6	16.5
P0ABT2	18678.1	S	U	T	A	CID	LIT	7	51.5	SYPLDIHNVQDHLKELADR	2263.1	K	Y	2.4	0.5	24.6	18.9
P0ABT2	18678.1	S	U	T	B	CID	LIT	4	39.5	AIGEAKDDDTADILTAASR	1933.0	K	D	5.0	0.5	102.0	18.2
P0ABT2	18678.1	S	U	T	B	CID	LIT	4	39.5	AVQLGGVALGTTQVINSK	1756.0	R	T	5.2	0.7	89.9	14.1
P0ABT2	18678.1	S	U	T	B	CID	LIT	4	39.5	DLDKFLWFIESNIE	1768.9	R	-	3.6	0.5	37.5	16.7
P0ABT2	18678.1	S	U	T	B	CID	LIT	4	39.5	GANFIAVHEMLDGFR	1676.8	R	T	3.4	0.5	37.6	15.3
P0ABT2	18678.1	S	U	T	C	CID	LIT	6	39.5	AIGEAKDDDTADILTAASR	1933.0	K	D	4.1	0.6	65.6	18.6
P0ABT2	18678.1	S	U	T	C	CID	LIT	6	39.5	AVQLGGVALGTTQVINSK	1756.0	R	T	5.2	0.6	57.7	14.1
P0ABT2	18678.1	S	U	T	C	CID	LIT	6	39.5	DLDKFLWFIESNIE	1768.9	R	-	3.3	0.4	28.6	17.2
P0ABT2	18678.1	S	U	T	C	CID	LIT	6	39.5	ELADRYAIVANDVR	1604.8	K	K	2.1	0.3	0.0	0.0
P0ABT2	18678.1	S	U	T	C	CID	LIT	6	39.5	KAIGEAKDDDTADILTAASR	2061.0	R	D	4.3	0.6	51.2	18.9
P0ABT2	18678.1	S	U	T	C	CID	LIT	6	39.5	YAIVANDVR	1020.5	R	K	1.9	0.3	13.6	17.0
P0ABT2	18678.1	S	U	T	A	CID	FT	2	12.0	AIGEAKDDDTADILTAASR	1933.0	K	D	3.2	0.0	80.4	18.6
P0ABT2	18678.1	S	U	T	A	CID	FT	2	12.0	KAIGEAKDDDTADILTAASR	2061.0	R	D	4.2	0.0	80.2	18.6
P0ABT2	18678.1	S	U	T	A	ETD	LIT	6	47.3	AIGEAKDDDTADILTAASR	1933.0	K	D	2.5	0.3	75.9	18.4
P0ABT2	18678.1	S	U	T	A	ETD	LIT	6	47.3	AVQLGGVALGTTQVINSK	1756.0	R	T	4.0	0.3	47.1	15.3
P0ABT2	18678.1	S	U	T	A	ETD	LIT	6	47.3	DLDKFLWFIESNIE	1768.9	R	-	2.8	0.6	0.0	0.0
P0ABT2	18678.1	S	U	T	A	ETD	LIT	6	47.3	ELADRYAIVANDVR	1604.8	K	K	2.8	0.4	52.6	17.7
P0ABT2	18678.1	S	U	T	A	ETD	LIT	6	47.3	SYPLDIHNVQDHLK	1678.9	K	E	2.3	0.7	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ABT2	18678.1	S	U	T	A	ETD	LIT	6	47.3	SYPLDIHNVQDHLKELADR	2263.1	K	Y	4.6	0.0	73.9	18.9
P0ABT2	18678.1	S	U	T	B	ETD	LIT	2	16.8	DLDKFLWFIESNIE	1768.9	R	-	1.3	0.5	16.8	17.2
P0ABT2	18678.1	S	U	T	B	ETD	LIT	2	16.8	SYPLDIHNVQDHLK	1678.9	K	E	3.9	0.4	38.4	16.3
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	5	47.3	AIGEAKDDDTADILTAASR	1933.0	K	D	0.0	0.0	76.5	18.3
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	5	47.3	AVQLGGVALGTTQVINSK	1756.0	R	T	0.0	0.0	68.1	14.1
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	5	47.3	DLDKFLWFIESNIE	1768.9	R	-	0.0	0.0	39.9	17.2
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	5	47.3	GANFIAVHEMLDGFR	1676.8	R	T	0.0	0.0	46.0	15.7
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	5	47.3	TALIDHLDTMAER	1485.7	R	A	0.0	0.0	22.9	16.0
P0ABT2	18678.1	S	U	T	A	ETD+CID	LIT	5	42.5	AIGEAKDDDTADILTAASR	1933.0	K	D	6.4	0.6	97.3	18.2
P0ABT2	18678.1	S	U	T	A	ETD+CID	LIT	5	42.5	AVQLGGVALGTTQVINSK	1756.0	R	T	5.5	0.8	81.9	13.8
P0ABT2	18678.1	S	U	T	A	ETD+CID	LIT	5	42.5	GANFIAVHEMLDGFR	1676.8	R	T	4.5	0.5	42.5	15.7
P0ABT2	18678.1	S	U	T	A	ETD+CID	LIT	5	42.5	SYPLDIHNVQDHLK	1678.9	K	E	3.5	0.6	24.2	16.5
P0ABT2	18678.1	S	U	T	A	ETD+CID	LIT	5	42.5	SYPLDIHNVQDHLKELADR	2263.1	K	Y	1.5	0.6	24.1	19.0
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	2	19.8	AIGEAKDDDTADILTAASR	1933.0	K	D	5.5	0.6	0.0	0.0
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	2	19.8	DLDKFLWFIESNIE	1768.9	R	-	3.6	0.3	0.0	0.0
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	6	55.7	AIGEAKDDDTADILTAASR	1933.0	K	D	5.5	0.6	76.5	18.3
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	6	55.7	AVQLGGVALGTTQVINSK	1756.0	R	T	5.1	0.6	68.1	14.1
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	6	55.7	DLDKFLWFIESNIE	1768.9	R	-	3.6	0.3	39.9	17.2
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	6	55.7	GANFIAVHEMLDGFR	1676.8	R	T	3.6	0.5	46.0	15.7
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	6	55.7	SYPLDIHNVQDHLK	1678.9	K	E	1.7	0.6	13.1	16.3
P0ABT2	18678.1	S	U	T	B	ETD+CID	LIT	6	55.7	TALIDHLDTMAER	1485.7	R	A	2.5	0.7	22.9	16.0
P0ABT2	18678.1	S	U	T	C	ETD+CID	LIT	2	19.8	AIGEAKDDDTADILTAASR	1933.0	K	D	5.3	0.6	77.7	18.2
P0ABT2	18678.1	S	U	T	C	ETD+CID	LIT	2	19.8	DLDKFLWFIESNIE	1768.9	R	-	3.4	0.3	12.4	17.2
P0ABT2	18678.1	S	U	T	B	HCD	FT	5	47.3	AIGEAKDDDTADILTAASR	1933.0	K	D	0.0	0.0	76.5	18.3
P0ABT2	18678.1	S	U	T	B	HCD	FT	5	47.3	AVQLGGVALGTTQVINSK	1756.0	R	T	0.0	0.0	68.1	14.1
P0ABT2	18678.1	S	U	T	B	HCD	FT	5	47.3	DLDKFLWFIESNIE	1768.9	R	-	0.0	0.0	39.9	17.2
P0ABT2	18678.1	S	U	T	B	HCD	FT	5	47.3	GANFIAVHEMLDGFR	1676.8	R	T	0.0	0.0	46.0	15.7
P0ABT2	18678.1	S	U	T	B	HCD	FT	5	47.3	TALIDHLDTMAER	1485.7	R	A	0.0	0.0	22.9	16.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	DIDALVEQAR	1129.6	R	E	4.2	0.5	57.2	12.8
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	DLEEFAMSYEESLKEESDSVFMR	2771.2	R	V	4.9	0.0	45.8	4.8
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	ELVASLSER	1003.5	R	L	2.7	0.7	44.7	14.6
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	ESLWQELADITDK	1547.8	K	T	3.5	0.0	39.3	12.3
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	ESLWQELADITDKTQLEWR	2361.2	K	E	2.9	0.7	19.0	11.5
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	3.5	0.0	24.8	10.8
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	TEVDELTR	962.5	R	A	2.7	0.7	42.6	13.6
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	TGELTRTEVDELTR	1619.8	K	A	4.4	0.7	46.2	11.8
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	VAQYYR	799.4	K	E	1.9	0.8	28.3	12.6
P0AAT9	18778.9	G	U	T	A	CID	LIT	10	69.4	VIKESLWQELADITDK	1888.0	R	T	4.7	0.5	47.1	13.4
P0AAT9	18778.9	G	U	A	A	CID	LIT	3	9.4	DITDKTQLEWR	1404.7	A	E	3.0	0.2	24.4	15.9
P0AAT9	18778.9	G	U	A	A	CID	LIT	3	9.4	DKTQLEWR	1075.6	T	E	2.0	0.5	14.1	15.9
P0AAT9	18778.9	G	U	A	A	CID	LIT	3	9.4	DKTQLEWREVFQ	1578.8	T	D	4.2	0.6	20.8	16.2
P0AAT9	18778.9	G	T	T	B	CID	LIT	2	13.8	CGHDQFQR	1047.4	K	R	3.1	0.0	48.3	3.0
P0AAT9	18778.9	G	T	T	B	CID	LIT	2	13.8	TGELTRTEVDELTR	1619.8	K	A	3.7	0.6	38.5	13.8
P0AAT9	18778.9	S	U	T	A	CID	LIT	3	36.9	CHFHLPIYTPEVLTLCPK	2225.1	K	C	3.7	0.6	28.6	18.5
P0AAT9	18778.9	S	U	T	A	CID	LIT	3	36.9	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	5.9	0.4	27.6	19.3
P0AAT9	18778.9	S	U	T	A	CID	LIT	3	36.9	TGELTRTEVDELTR	1619.8	K	A	2.7	0.2	5.7	17.5
P0AAT9	18778.9	S	U	T	B	CID	LIT	4	39.4	ESLWQELADITDKTQLEWR	2361.2	K	E	3.7	0.8	49.9	18.9
P0AAT9	18778.9	S	U	T	B	CID	LIT	4	39.4	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	4.3	0.5	20.4	19.3
P0AAT9	18778.9	S	U	T	B	CID	LIT	4	39.4	TGELTRTEVDELTR	1619.8	K	A	3.1	0.5	35.5	17.9
P0AAT9	18778.9	S	U	T	B	CID	LIT	4	39.4	VIKESLWQELADITDKTQLEWR	2701.4	R	E	1.9	0.0	30.3	17.4
P0AAT9	18778.9	S	U	T	C	CID	LIT	2	25.6	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	5.0	0.6	44.5	19.4
P0AAT9	18778.9	S	U	T	C	CID	LIT	2	25.6	TGELTRTEVDELTR	1619.8	K	A	3.1	0.2	19.2	17.5
P0AAT9	18778.9	S	U	T	B	ETD+CID	LIT	2	28.1	CHFHLPIYTPEVLTLCPK	2225.1	K	C	0.0	0.0	19.6	18.9
P0AAT9	18778.9	S	U	T	B	ETD+CID	LIT	2	28.1	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	0.0	0.0	40.3	19.5
P0AAT9	18778.9	S	U	T	A	ETD+CID	LIT	2	28.7	ESLWQELADITDKTQLEWR	2361.2	K	E	1.9	0.6	19.0	19.1
P0AAT9	18778.9	S	U	T	A	ETD+CID	LIT	2	28.7	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	5.7	0.5	41.7	19.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AAT9	18778.9	S	U	T	B	ETD+CID	LIT	3	36.9	CHFHLPIYTPEVLTLCPK	2225.1	K	C	2.1	0.6	19.6	18.9
P0AAT9	18778.9	S	U	T	B	ETD+CID	LIT	3	36.9	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	6.1	0.6	40.3	19.5
P0AAT9	18778.9	S	U	T	B	ETD+CID	LIT	3	36.9	NGERDIDALVEQAR	1585.8	R	E	3.3	0.4	0.6	15.3
P0AAT9	18778.9	S	U	T	B	HCD	FT	2	28.1	CHFHLPIYTPEVLTLCPK	2225.1	K	C	0.0	0.0	19.6	18.9
P0AAT9	18778.9	S	U	T	B	HCD	FT	2	28.1	EVFQDLNHHGVYHSGEVVGLGNLVCEK	3036.5	R	C	0.0	0.0	40.3	19.5
P0A912	18806.5	G	U	T	A	CID	LIT	4	26.0	EKPAVLGHDEAAYSK	1614.8	K	N	4.2	0.0	69.3	12.8
P0A912	18806.5	G	U	T	A	CID	LIT	4	26.0	GVSADQISIVSYGK	1423.7	K	E	4.8	0.0	82.1	11.5
P0A912	18806.5	G	U	T	A	CID	LIT	4	26.0	MYLQGK	739.4	K	G	2.1	0.4	28.2	13.2
P0A912	18806.5	G	U	T	A	CID	LIT	4	26.0	VTVEGHADER	1112.5	K	G	3.3	0.0	55.1	10.4
P0A912	18806.5	G	T	T	A	CID	LIT	4	24.9	EKPAVLGHDEAAYSK	1614.8	K	N	3.8	0.9	45.4	12.8
P0A912	18806.5	G	T	T	A	CID	LIT	4	24.9	GTPEYNISLGER	1335.7	R	R	2.5	0.5	2.4	12.3
P0A912	18806.5	G	T	T	A	CID	LIT	4	24.9	MYLQGK	739.4	K	G	1.6	0.5	16.4	10.8
P0A912	18806.5	G	T	T	A	CID	LIT	4	24.9	VTVEGHADER	1112.5	K	G	3.3	0.0	80.9	10.4
P0A912	18806.5	G	T	A	A	CID	LIT	2	22.5	DAHANFLRSNPSYKVTVEGHA	2313.1	L	D	3.7	0.5	17.2	12.8
P0A912	18806.5	G	T	A	A	CID	LIT	2	22.5	DQISIVSYGKEKPAVLGH	1941.0	A	D	3.0	0.4	26.5	14.6
P0A912	18806.5	S	U	T	C	CID	LIT	2	12.7	GTPEYNISLGER	1335.7	R	R	1.9	0.7	1.5	15.1
P0A912	18806.5	S	U	T	C	CID	LIT	2	12.7	VTVEGHADER	1112.5	K	G	2.5	0.5	14.7	13.2
P45470	18840.9	G	U	T	A	CID	LIT	2	11.6	AGHEVITIEK	1096.6	K	Q	2.1	0.8	16.9	10.8
P45470	18840.9	G	U	T	A	CID	LIT	2	11.6	TPDDLPAFNR	1145.6	R	E	3.4	0.0	44.1	10.8
P45470	18840.9	G	U	A	A	CID	LIT	2	14.0	DALLLPGGHSPDYLRG	1680.9	F	D	2.8	0.0	18.1	15.1
P45470	18840.9	G	U	A	A	CID	LIT	2	14.0	DQEVVVDK	931.5	Y	D	2.9	0.4	27.8	16.1
P0A8D6	18861.9	G	U	T	A	CID	LIT	3	16.9	AAAAEIAVK	843.5	R	T	1.9	0.2	10.4	14.8
P0A8D6	18861.9	G	U	T	A	CID	LIT	3	16.9	AVVHTVGPVWR	1220.7	K	G	2.4	0.7	30.2	8.5
P0A8D6	18861.9	G	U	T	A	CID	LIT	3	16.9	IHVVQGDITK	1109.6	R	L	2.5	0.5	27.4	10.4
P0A8D6	18861.9	G	U	A	A	CID	LIT	3	24.3	DACLKVRQQQG	1302.7	L	D	2.9	0.6	42.3	15.1
P0A8D6	18861.9	G	U	A	A	CID	LIT	3	24.3	DLPAKAVVHTVGPVWRGGEQNE	2359.2	G	D	3.2	0.6	20.1	15.3
P0A8D6	18861.9	G	U	A	A	CID	LIT	3	24.3	ERLLTQQGDE	1188.6	Y	-	3.3	0.0	50.0	15.7
P0A8D6	18861.9	G	T	A	A	CID	LIT	2	11.9	DACLKVRQQQG	1302.7	L	D	3.3	0.5	42.1	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8D6	18861.9	G	T	A	A	CID	LIT	2	11.9	MKTRIHVVQG	1184.7	-	D	0.0	0.0	22.4	14.1
P0A8D6	18861.9	G	T	A	B	CID	LIT	3	24.3	DACLKVRQQQG	1302.7	L	D	3.1	0.8	39.7	15.1
P0A8D6	18861.9	G	T	A	B	CID	LIT	3	24.3	DLPAKAVVHTVGPVWRGGEQNE	2359.2	G	D	3.1	0.5	5.9	15.3
P0A8D6	18861.9	G	T	A	B	CID	LIT	3	24.3	MKTRIHVVQG	1168.7	-	D	2.6	0.0	21.1	9.5
P0ACJ0	18869.3	G	U	T	A	CID	LIT	6	34.1	IDRNILNELQK	1355.8	R	D	3.4	0.5	24.2	10.4
P0ACJ0	18869.3	G	U	T	A	CID	LIT	6	34.1	ISNVELSKR	1045.6	R	V	3.2	0.7	55.8	13.2
P0ACJ0	18869.3	G	U	T	A	CID	LIT	6	34.1	LLGETLLR	914.6	K	L	2.9	0.4	38.6	11.5
P0ACJ0	18869.3	G	U	T	A	CID	LIT	6	34.1	LPGVNDTR	871.5	R	T	2.1	0.5	32.2	12.0
P0ACJ0	18869.3	G	U	T	A	CID	LIT	6	34.1	TYVVMEEVK	1097.6	R	Q	2.4	0.8	26.4	10.4
P0ACJ0	18869.3	G	U	T	A	CID	LIT	6	34.1	VGLSPTPCLER	1228.6	R	V	3.0	0.7	37.9	13.2
P0ACJ0	18869.3	G	U	A	A	CID	LIT	2	12.8	DRNILNELQK	1242.7	I	D	3.1	0.7	26.7	15.6
P0ACJ0	18869.3	G	U	A	A	CID	LIT	2	12.8	VDSKKRPGKDL	1242.7	M	D	0.0	0.0	30.9	12.6
P0ACJ0	18869.3	G	U	T	B	CID	LIT	3	17.1	LPGVNDTR	871.5	R	T	2.1	0.7	40.3	12.3
P0ACJ0	18869.3	G	U	T	B	CID	LIT	3	17.1	TYVVMEEVK	1097.6	R	Q	2.8	0.0	31.6	10.8
P0ACJ0	18869.3	G	U	T	B	CID	LIT	3	17.1	VGLSPTPCLER	1228.6	R	V	1.7	0.5	0.0	0.0
P0ACJ0	18869.3	S	U	T	C	CID	LIT	3	18.9	KLLGETLLR	1042.7	R	L	2.2	0.7	25.4	11.8
P0ACJ0	18869.3	S	U	T	C	CID	LIT	3	18.9	NILNELQKDGR	1299.7	R	I	3.3	0.3	35.8	16.2
P0ACJ0	18869.3	S	U	T	C	CID	LIT	3	18.9	VGLSPTPCLER	1228.6	R	V	2.7	0.2	2.1	15.9
P0ACJ0	18869.3	S	U	T	C	ETD+CID	LIT	2	17.1	KLLGETLLRLPGVNDTR	1895.1	R	T	4.2	0.0	39.2	9.0
P0ACJ0	18869.3	S	U	T	C	ETD+CID	LIT	2	17.1	NILNELQKDGR	1299.7	R	I	3.4	0.5	27.6	15.9
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	ALLNSMVIGVTEGFTK	1695.9	R	K	5.2	0.7	92.1	12.8
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	ALLNSMVIGVTEGFTKK	1808.0	R	L	4.0	0.0	59.5	10.0
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	APVVVPAGVDVK	1150.7	K	I	3.2	0.0	54.6	0.0
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	AYRRPEPYK	1179.6	R	G	1.8	0.7	9.5	13.0
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	DGYADGWAQAGTAR	1438.6	R	A	4.8	0.9	84.4	7.0
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	GADKQVIGQVAADLR	1540.8	K	A	4.3	0.8	75.3	11.5
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	4.2	0.0	20.6	9.5
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	HADNTLTFGPR	1228.6	K	D	3.9	0.8	66.7	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	INGQVITIK	985.6	K	G	2.5	0.7	55.2	11.8
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	KLQLVGVGYR	1132.7	K	A	3.6	0.8	39.1	8.5
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	LQLVGVGYR	1004.6	K	A	3.1	0.7	45.5	12.3
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	QVIGQVAADLR	1169.7	K	A	3.7	0.6	67.9	11.8
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	RPEPYKGK	974.5	R	G	2.3	0.6	19.9	13.4
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	TLNDAVEVK	988.5	R	H	3.1	0.6	49.1	13.6
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	TLNDAVEVKHADNTLTFGPR	2198.1	R	D	4.0	0.0	65.6	12.3
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	VAKAPVVVPAGVDVK	1448.9	R	I	4.1	0.0	47.4	0.0
P0AG55	18885.5	G	U	T	A	CID	LIT	17	85.9	YADEVVR	851.4	R	T	2.2	0.5	27.7	13.8
P0AG55	18885.5	G	T	T	A	CID	LIT	7	49.2	ALLNSMVIGVTEGFTK	1679.9	R	K	4.0	0.6	28.9	10.4
P0AG55	18885.5	G	T	T	A	CID	LIT	7	49.2	APVVVPAGVDVK	1150.7	K	I	2.2	0.0	53.8	0.0
P0AG55	18885.5	G	T	T	A	CID	LIT	7	49.2	DGYADGWAQAGTAR	1438.6	R	A	4.1	0.0	41.3	7.0
P0AG55	18885.5	G	T	T	A	CID	LIT	7	49.2	GADKQVIGQVAADLR	1540.8	K	A	4.1	0.6	60.8	10.8
P0AG55	18885.5	G	T	T	A	CID	LIT	7	49.2	HADNTLTFGPR	1228.6	K	D	3.6	0.8	49.5	11.8
P0AG55	18885.5	G	T	T	A	CID	LIT	7	49.2	KLQLVGVGYR	1132.7	K	A	3.5	0.8	29.2	8.5
P0AG55	18885.5	G	T	T	A	CID	LIT	7	49.2	TLNDAVEVK	988.5	R	H	2.8	0.5	42.0	13.6
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DAVEVKHA	868.5	N	D	2.1	0.6	26.6	13.0
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DAVEVKHADNTLTFGPR	1869.9	N	D	5.3	0.8	85.8	15.9
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DEVVRTKEAKKK	1430.8	A	-	3.1	0.7	42.4	7.8
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DHQLPAGITAECPTQTEIVLKGA	2449.2	V	D	3.8	0.0	24.1	15.6
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DKQVIGQVAA	1028.6	A	D	3.6	0.6	37.1	12.0
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DLRAYRRPEPYKGKGVRYA	2295.2	A	D	2.3	0.7	0.0	0.0
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DNTLTFGPR	1020.5	A	D	2.4	0.7	44.2	15.9
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	DNTLTFGPRDGYA	1426.7	A	D	3.9	0.7	50.4	14.5
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	SRVAKAPVVVPAGV	1349.8	M	D	0.0	0.0	33.7	4.8
P0AG55	18885.5	G	U	A	A	CID	LIT	10	68.9	SRVAKAPVVVPAGVDVKINGQVITIKGKNGELTRTLN	3842.2	M	D	0.0	0.0	28.2	0.0
P0AG55	18885.5	G	T	A	A	CID	LIT	7	32.2	DAVEVKHA	868.5	N	D	2.0	0.5	27.7	13.0
P0AG55	18885.5	G	T	A	A	CID	LIT	7	32.2	DAVEVKHADNTLTFGPR	1869.9	N	D	4.1	0.8	36.8	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	G	T	A	A	CID	LIT	7	32.2	DEVVRTKEAKKK	1430.8	A	-	2.7	0.0	41.5	7.8
P0AG55	18885.5	G	T	A	A	CID	LIT	7	32.2	DKQVIGQVAA	1028.6	A	D	3.4	0.6	39.1	12.0
P0AG55	18885.5	G	T	A	A	CID	LIT	7	32.2	DNTLTFGPR	1020.5	A	D	2.8	0.7	32.0	15.9
P0AG55	18885.5	G	T	A	A	CID	LIT	7	32.2	DNTLTFGPRDGYA	1426.7	A	D	3.9	0.7	42.5	14.5
P0AG55	18885.5	G	T	A	A	CID	LIT	7	32.2	SRVAKAPVVVPAGV	1349.8	M	D	0.0	0.0	40.6	4.8
P0AG55	18885.5	G	T	T	B	CID	LIT	5	32.2	APVVVPAGVDVK	1150.7	K	I	2.6	0.0	26.9	0.0
P0AG55	18885.5	G	T	T	B	CID	LIT	5	32.2	DGYADGWAQAGTAR	1438.6	R	A	4.3	0.7	87.1	8.5
P0AG55	18885.5	G	T	T	B	CID	LIT	5	32.2	GADKQVIGQVAADLR	1540.8	K	A	3.4	0.5	31.9	10.8
P0AG55	18885.5	G	T	T	B	CID	LIT	5	32.2	TLNDAVEVK	988.5	R	H	2.3	0.3	17.6	14.0
P0AG55	18885.5	G	T	T	B	CID	LIT	5	32.2	YADEVVR	851.4	R	T	2.4	0.3	18.8	13.6
P0AG55	18885.5	G	U	T	B	CID	LIT	5	32.2	ALLNSMVIGVTEGFTK	1679.9	R	K	3.9	0.8	75.0	10.0
P0AG55	18885.5	G	U	T	B	CID	LIT	5	32.2	DGYADGWAQAGTAR	1438.6	R	A	4.9	0.0	61.7	7.0
P0AG55	18885.5	G	U	T	B	CID	LIT	5	32.2	HADNTLTFGPR	1228.6	K	D	3.5	0.8	61.9	11.8
P0AG55	18885.5	G	U	T	B	CID	LIT	5	32.2	TLNDAVEVK	988.5	R	H	2.0	0.5	26.2	12.3
P0AG55	18885.5	G	U	T	B	CID	LIT	5	32.2	YADEVVR	851.4	R	T	1.8	0.0	19.2	13.8
P0AG55	18885.5	G	T	A	B	CID	LIT	7	40.7	DEVVRTKEAKKK	1430.8	A	-	2.2	0.0	25.1	7.8
P0AG55	18885.5	G	T	A	B	CID	LIT	7	40.7	DHQLPAGITAECPTQTEIVLKGA	2449.2	V	D	4.7	0.8	61.7	14.9
P0AG55	18885.5	G	T	A	B	CID	LIT	7	40.7	DKQVIGQVAA	1028.6	A	D	3.3	0.6	36.0	12.3
P0AG55	18885.5	G	T	A	B	CID	LIT	7	40.7	DNTLTFGPR	1020.5	A	D	2.9	0.7	39.5	15.7
P0AG55	18885.5	G	T	A	B	CID	LIT	7	40.7	DNTLTFGPRDGYA	1426.7	A	D	2.8	0.6	21.9	14.5
P0AG55	18885.5	G	T	A	B	CID	LIT	7	40.7	ECPTQTEIVLKGA	1445.7	A	D	2.2	0.0	18.8	17.3
P0AG55	18885.5	G	T	A	B	CID	LIT	7	40.7	SRVAKAPVVVPAGV	1349.8	M	D	0.0	0.0	25.9	4.8
P0AG55	18885.5	G	U	A	B	CID	LIT	6	38.4	DAVEVKHA	868.5	N	D	2.0	0.5	24.2	13.0
P0AG55	18885.5	G	U	A	B	CID	LIT	6	38.4	DHQLPAGITAECPTQTEIVLKGA	2449.2	V	D	5.2	0.0	28.2	15.3
P0AG55	18885.5	G	U	A	B	CID	LIT	6	38.4	DKQVIGQVAA	1028.6	A	D	3.7	0.7	35.3	12.6
P0AG55	18885.5	G	U	A	B	CID	LIT	6	38.4	DNTLTFGPR	1020.5	A	D	2.9	0.0	41.2	15.9
P0AG55	18885.5	G	U	A	B	CID	LIT	6	38.4	DNTLTFGPRDGYA	1426.7	A	D	3.9	0.7	62.4	14.5
P0AG55	18885.5	G	U	A	B	CID	LIT	6	38.4	SRVAKAPVVVPAGV	1349.8	M	D	0.0	0.0	45.2	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	ALLNSMVIGVTEGFTK	1695.9	R	K	4.0	0.5	46.9	16.3
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	ALLNSMVIGVTEGFTKK	1808.0	R	L	2.2	0.6	7.5	15.6
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	APVVVPAGVDVK	1150.7	K	I	3.2	0.0	50.9	3.0
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	DGYADGWAQAGTAR	1438.6	R	A	5.0	0.6	101.0	12.3
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	GADKQVIGQVAADLR	1540.8	K	A	4.4	0.8	66.6	14.9
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	6.6	0.0	52.5	16.9
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	LQLVGVGYR	1004.6	K	A	2.7	0.7	14.1	14.0
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	QVIGQVAADLR	1169.7	K	A	3.1	0.4	48.3	15.6
P0AG55	18885.5	S	U	T	A	CID	LIT	9	61.6	YADEVVR	851.4	R	T	1.9	0.0	23.0	16.3
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	ALLNSMVIGVTEGFTK	1679.9	R	K	5.4	0.6	107.0	14.0
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	ALLNSMVIGVTEGFTKK	1808.0	R	L	1.4	0.5	17.0	15.1
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	APVVVPAGVDVK	1150.7	K	I	2.9	0.0	34.9	3.0
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	DGYADGWAQAGTAR	1438.6	R	A	1.8	0.0	27.1	11.5
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	GADKQVIGQVAADLR	1540.8	K	A	4.1	0.8	59.3	14.5
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	6.8	0.0	54.5	16.6
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	INGQVITIK	986.6	K	G	3.2	0.5	45.6	15.6
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	LQLVGVGYR	1004.6	K	A	3.1	0.7	58.1	14.0
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	QVIGQVAADLR	1169.7	K	A	2.8	0.6	58.9	15.2
P0AG55	18885.5	S	U	T	B	CID	LIT	10	66.7	YADEVVR	851.4	R	T	2.7	0.6	35.0	16.3
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	ALLNSMVIGVTEGFTK	1679.9	R	K	4.9	0.7	93.8	14.1
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	ALLNSMVIGVTEGFTKK	1808.0	R	L	1.6	0.5	10.9	15.1
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	APVVVPAGVDVK	1150.7	K	I	3.0	0.0	50.9	3.0
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	AYRRPEPYKGK	1364.7	R	G	1.3	0.5	11.1	13.8
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	DGYADGWAQAGTAR	1438.6	R	A	5.0	0.6	90.5	11.8
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	GADKQVIGQVAADLR	1540.8	K	A	4.4	0.6	56.4	14.5
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	6.7	0.0	41.8	16.5
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	HADNTLTFGPR	1228.6	K	D	3.6	0.8	53.7	16.2
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	INGQVITIK	986.6	K	G	2.4	0.5	27.2	16.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	KLQLVGVGYR	1132.7	K	A	2.9	0.2	30.3	11.1
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	LQLVGVGYR	1004.6	K	A	3.1	0.6	48.0	14.0
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	NGELTR	690.3	K	T	0.0	0.0	35.8	18.3
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	TLNDAVEVK	988.5	R	H	2.0	0.5	5.8	15.6
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	VAKAPVVVPAGVDVK	1448.9	R	I	3.0	0.0	35.4	0.0
P0AG55	18885.5	S	U	T	C	CID	LIT	15	89.3	YADEVVR	851.4	R	T	2.6	0.6	32.8	16.6
P0AG55	18885.5	S	U	T	B	CID	FT	2	14.1	ALLNSMVIGVTEGFTK	1679.9	R	K	2.6	0.0	83.2	14.0
P0AG55	18885.5	S	U	T	B	CID	FT	2	14.1	INGQVITIK	986.6	K	G	1.1	0.0	20.9	15.6
P0AG55	18885.5	S	U	T	C	CID	FT	6	33.9	APVVVPAGVDVK	1150.7	K	I	3.2	0.0	31.3	3.0
P0AG55	18885.5	S	U	T	C	CID	FT	6	33.9	DGYADGWAQAGTAR	1438.6	R	A	3.7	0.0	97.7	11.8
P0AG55	18885.5	S	U	T	C	CID	FT	6	33.9	GADKQVIGQVAADLR	1540.8	K	A	3.3	0.0	44.1	14.5
P0AG55	18885.5	S	U	T	C	CID	FT	6	33.9	INGQVITIK	986.6	K	G	2.3	0.7	45.3	16.6
P0AG55	18885.5	S	U	T	C	CID	FT	6	33.9	KLQLVGVGYR	1132.7	K	A	3.0	0.0	20.5	11.1
P0AG55	18885.5	S	U	T	C	CID	FT	6	33.9	LQLVGVGYR	1004.6	K	A	2.8	0.0	38.1	14.0
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	ALLNSMVIGVTEGFTK	1679.9	R	K	2.9	0.7	0.0	0.0
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	APVVVPAGVDVK	1150.7	K	I	3.3	0.0	35.0	3.0
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	AYRRPEPYKGK	1364.7	R	G	2.5	0.3	11.6	14.5
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	DGYADGWAQAGTAR	1438.6	R	A	2.5	0.0	45.0	11.5
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	GADKQVIGQVAADLR	1540.8	K	A	7.2	0.6	81.1	15.8
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	0.0	0.0	23.9	16.5
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	HADNTLTFGPR	1228.6	K	D	2.2	0.8	0.0	0.0
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	INGQVITIK	985.6	K	G	1.9	0.4	18.1	14.3
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	KLQLVGVGYR	1132.7	K	A	4.3	0.7	59.1	11.1
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	LQLVGVGYR	1004.6	K	A	2.4	0.5	46.4	14.0
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	NGELTR	690.3	K	T	0.0	0.0	31.3	18.3
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	QVIGQVAADLR	1169.7	K	A	3.2	0.5	54.8	15.2
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	RPEPYKGK	974.5	R	G	2.5	0.0	24.4	16.7
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	VAKAPVVVPAGVDVK	1448.9	R	I	3.5	0.0	33.3	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	S	U	T	A	ETD	LIT	15	84.2	YADEVVR	851.4	R	T	2.0	0.0	43.6	16.3
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	ALLNSMVIGVTEGFTK	1680.9	R	K	2.5	0.6	11.4	16.4
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	ALLNSMVIGVTEGFTKK	1808.0	R	L	3.4	0.0	27.8	14.8
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	APVVVPAGVDVK	1150.7	K	I	3.2	0.0	35.3	3.0
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	DGYADGWAQAGTAR	1438.6	R	A	2.3	0.8	35.2	10.8
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	GADKQVIGQVAADLR	1540.8	K	A	6.1	0.6	50.4	15.6
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	HADNTLTFGPR	1228.6	K	D	2.1	0.8	0.0	0.0
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	INGQVITIK	985.6	K	G	2.2	0.4	0.0	0.0
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	KLQLVGVGYR	1132.7	K	A	2.4	0.0	26.5	11.5
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	LQLVGVGYR	1004.6	K	A	2.4	0.6	44.5	13.8
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	NGELTR	690.3	K	T	0.0	0.0	24.0	18.3
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	QVIGQVAADLR	1169.7	K	A	3.2	0.4	33.4	15.2
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	TLNDAVEVK	988.5	R	H	2.8	0.2	0.0	0.0
P0AG55	18885.5	S	U	T	B	ETD	LIT	13	61.6	YADEVVR	851.4	R	T	2.6	0.0	54.1	16.3
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	ALLNSMVIGVTEGFTK	1680.9	R	K	2.5	0.4	32.7	16.4
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	ALLNSMVIGVTEGFTKK	1808.0	R	L	3.9	0.0	40.5	14.8
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	APVVVPAGVDVK	1150.7	K	I	3.0	0.0	36.3	3.0
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	DGYADGWAQAGTAR	1438.6	R	A	0.0	0.0	37.7	11.5
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	GADKQVIGQVAADLR	1540.8	K	A	3.0	0.4	50.3	14.5
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	HADNTLTFGPR	1228.6	K	D	4.9	0.9	60.4	14.5
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	INGQVITIK	985.6	K	G	2.1	0.4	29.8	14.3
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	KLQLVGVGYR	1132.7	K	A	2.6	0.0	36.2	11.1
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	LQLVGVGYR	1004.6	K	A	2.0	0.5	37.2	14.0
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	NGELTR	690.3	K	T	0.0	0.0	28.7	18.3
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	QVIGQVAADLR	1169.7	K	A	3.1	0.4	31.9	15.1
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	TLNDAVEVK	988.5	R	H	2.0	0.2	17.2	15.9
P0AG55	18885.5	S	U	T	C	ETD	LIT	13	61.6	YADEVVR	851.4	R	T	2.0	0.0	45.6	16.3
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	2	18.1	ALLNSMVIGVTEGFTKK	1808.0	R	L	0.0	0.0	18.6	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	2	18.1	GADKQVIGQVAADLR	1540.8	K	A	0.0	0.0	73.4	14.5
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	ALLNSMVIGVTEGFTK	1679.9	R	K	0.0	0.0	106.0	15.1
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	ALLNSMVIGVTEGFTKK	1808.0	R	L	0.0	0.0	18.6	15.1
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	APVVVPAGVDVK	1150.7	K	I	0.0	0.0	42.3	3.0
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	DGYADGWAQAGTAR	1438.6	R	A	0.0	0.0	45.7	11.8
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	GADKQVIGQVAADLR	1540.8	K	A	0.0	0.0	73.4	14.5
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	0.0	0.0	46.9	17.5
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	HADNTLTFGPR	1228.6	K	D	0.0	0.0	67.6	15.2
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	LQLVGVGYR	1004.6	K	A	0.0	0.0	42.0	14.0
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	9	67.2	NGELTR	690.3	K	T	0.0	0.0	32.4	18.3
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	ALLNSMVIGVTEGFTK	1679.9	R	K	3.0	0.6	9.8	14.0
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	APVVVPAGVDVK	1150.7	K	I	3.1	0.0	27.1	3.0
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	DGYADGWAQAGTAR	1438.6	R	A	3.8	0.5	33.4	11.1
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	GADKQVIGQVAADLR	1540.8	K	A	2.9	0.6	24.7	14.5
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	0.0	0.0	47.1	16.8
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	INGQVITIK	985.6	K	G	2.9	0.4	40.5	14.3
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	LQLVGVGYR	1004.6	K	A	2.5	0.7	14.4	14.0
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	NGELTR	690.3	K	T	0.0	0.0	28.7	18.3
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	RPEPYK	789.4	R	G	1.9	0.2	18.3	17.3
P0AG55	18885.5	S	U	T	A	ETD+CID	LIT	10	70.1	RPEPYKGK	974.5	R	G	2.3	0.0	20.9	16.7
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	3	23.2	ALLNSMVIGVTEGFTK	1679.9	R	K	5.5	0.8	0.0	0.0
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	3	23.2	DGYADGWAQAGTAR	1438.6	R	A	3.9	0.7	0.0	0.0
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	3	23.2	HADNTLTFGPR	1228.6	K	D	3.8	0.8	0.0	0.0
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	ALLNSMVIGVTEGFTK	1679.9	R	K	5.5	0.8	106.0	15.1
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	ALLNSMVIGVTEGFTKK	1808.0	R	L	2.7	0.0	18.6	15.1
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	APVVVPAGVDVK	1150.7	K	I	3.1	0.0	42.3	3.0
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	DGYADGWAQAGTAR	1438.6	R	A	3.9	0.7	45.7	11.8
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	GADKQVIGQVAADLR	1540.8	K	A	6.5	0.5	73.4	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	0.0	0.0	46.9	17.5
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	HADNTLTFGPR	1228.6	K	D	3.8	0.8	67.6	15.2
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	INGQVITIK	985.6	K	G	2.2	0.4	7.5	13.8
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	LQLVGVGYR	1004.6	K	A	3.2	0.9	42.0	14.0
P0AG55	18885.5	S	U	T	B	ETD+CID	LIT	10	72.3	NGELTR	690.3	K	T	0.0	0.0	32.4	18.3
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	ALLNSMVIGVTEGFTK	1695.9	R	K	3.7	0.7	55.5	16.2
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	ALLNSMVIGVTEGFTKK	1808.0	R	L	3.3	0.0	23.5	14.8
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	APVVVPAGVDVK	1150.7	K	I	3.1	0.0	36.0	4.8
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	DGYADGWAQAGTAR	1438.6	R	A	4.8	0.6	87.7	11.5
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	GADKQVIGQVAADLR	1540.8	K	A	3.0	0.6	42.2	14.5
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	6.0	0.0	39.1	17.9
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	HADNTLTFGPR	1229.6	K	D	3.0	0.7	0.0	0.0
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	INGQVITIK	986.6	K	G	2.4	0.5	0.0	0.0
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	KLQLVGVGYR	1132.7	K	A	3.2	0.3	0.0	0.0
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	LQLVGVGYR	1004.6	K	A	3.0	0.7	47.5	14.0
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	NGELTR	690.3	K	T	0.0	0.0	26.4	18.3
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	VAKAPVVVPAGVDVK	1448.9	R	I	3.0	0.0	29.7	3.0
P0AG55	18885.5	S	U	T	C	ETD+CID	LIT	13	78.0	YADEVVR	851.4	R	T	2.4	0.7	28.9	16.5
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	ALLNSMVIGVTEGFTK	1679.9	R	K	0.0	0.0	106.0	15.1
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	APVVVPAGVDVK	1150.7	K	I	0.0	0.0	42.3	3.0
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	DGYADGWAQAGTAR	1438.6	R	A	0.0	0.0	45.7	11.8
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	GADKQVIGQVAADLR	1540.8	K	A	0.0	0.0	54.7	14.5
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	GNVINLSLGFSHPVDHQLPAGITAECPTQTEIVLK	3755.9	K	G	0.0	0.0	46.9	17.5
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	HADNTLTFGPR	1228.6	K	D	0.0	0.0	67.6	15.2
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	LQLVGVGYR	1004.6	K	A	0.0	0.0	42.0	14.0
P0AG55	18885.5	S	U	T	B	HCD	FT	8	66.7	NGELTR	690.3	K	T	0.0	0.0	32.4	18.3
P0AG55	18885.5	S	U	T	A	HCD	FT	2	11.9	APVVVPAGVDVK	1150.7	K	I	3.3	0.0	55.8	3.0
P0AG55	18885.5	S	U	T	A	HCD	FT	2	11.9	LQLVGVGYR	1004.6	K	A	2.0	0.0	27.1	14.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AG55	18885.5	S	U	T	B	HCD	FT	2	15.8	ALLNSMVIGVTEGFTK	1679.9	R	K	2.9	0.0	123.0	13.4
P0AG55	18885.5	S	U	T	B	HCD	FT	2	15.8	APVVVPAGVDVK	1150.7	K	I	3.3	0.0	54.6	6.0
P0AG55	18885.5	S	U	T	C	HCD	FT	2	7.9	NGELTR	689.4	K	T	1.3	0.0	25.3	18.3
P0AG55	18885.5	S	U	T	C	HCD	FT	2	7.9	RPEPYKGK	974.5	R	G	1.8	0.0	24.6	16.7
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	AQAEKMANEQIAR	1475.7	R	Q	3.2	0.7	45.1	10.0
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	DLMQQAR	861.4	R	H	1.9	0.3	22.2	12.8
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	HEQPPVNVSELETMHR	1918.9	R	L	4.9	0.7	65.0	10.8
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	LLTPEQQAVLNEK	1482.8	R	H	4.5	0.9	69.8	11.1
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	LVTAENFDENAVR	1477.7	R	A	4.0	0.6	92.0	12.6
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	MANEQIAR	932.5	K	Q	3.2	0.8	73.1	13.8
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	MEQLRDVTQWQK	1561.8	R	S	2.5	0.4	0.6	12.0
P0AE85	18946.5	G	T	T	A	CID	LIT	8	54.8	STQSHMFDGISLTEHQR	1973.9	R	Q	3.1	0.3	17.1	11.5
P0AE85	18946.5	G	T	A	A	CID	LIT	2	13.9	DENAVRAQA	973.5	F	E	3.0	0.6	37.2	15.3
P0AE85	18946.5	G	T	A	A	CID	LIT	2	13.9	DGISLTEHQRQQMR	1714.8	F	D	2.3	0.7	11.4	16.0
P0A6Q3	18951.6	G	U	A	A	CID	LIT	2	12.8	DGRLIYTAS	995.5	V	D	2.0	0.7	10.0	10.8
P0A6Q3	18951.6	G	U	A	A	CID	LIT	2	12.8	DLKVGLFQDTSAF	1440.7	S	-	3.6	0.5	40.4	14.9
P0A6Q3	18951.6	G	T	T	B	CID	LIT	2	12.2	ALGVGEVK	772.5	R	F	2.5	0.1	7.0	15.3
P0A6Q3	18951.6	G	T	T	B	CID	LIT	2	12.2	ESYTKEDLLASGR	1468.7	R	G	2.6	0.4	28.9	10.8
P0A6Q3	18951.6	G	T	A	B	CID	LIT	2	22.7	DLLASGRGELFGAKGPQLPAPNMLMM	2714.4	E	D	3.8	0.0	17.6	14.8
P0A6Q3	18951.6	G	T	A	B	CID	LIT	2	22.7	DRVVKMTETGGNF	1453.7	M	D	2.9	0.7	33.1	15.2
P0AGE0	18956.4	G	U	T	A	CID	LIT	5	28.1	GVNKVILVGNLGQDPEVR	1907.1	R	Y	3.7	0.8	12.2	9.0
P0AGE0	18956.4	G	U	T	A	CID	LIT	5	28.1	KGSQVYIEGQLR	1377.7	R	T	4.0	0.0	41.4	13.8
P0AGE0	18956.4	G	U	T	A	CID	LIT	5	28.1	KWTDQSGQDR	1220.6	R	Y	3.2	0.7	39.4	7.8
P0AGE0	18956.4	G	U	T	A	CID	LIT	5	28.1	LAEVASEYLR	1150.6	K	K	3.7	0.0	58.9	12.6
P0AGE0	18956.4	G	U	T	A	CID	LIT	5	28.1	VILVGNLGQDPEVR	1508.8	K	Y	4.3	0.8	51.8	11.1
P0AGE0	18956.4	S	U	T	A	CID	LIT	2	13.5	LAEVASEYLR	1150.6	K	K	3.2	0.7	48.4	16.4
P0AGE0	18956.4	S	U	T	A	CID	LIT	2	13.5	VILVGNLGQDPEVR	1508.8	K	Y	4.2	0.6	42.0	15.1
P0AGE0	18956.4	S	U	T	B	CID	LIT	2	13.5	LAEVASEYLR	1150.6	K	K	2.7	0.7	24.8	16.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AGE0	18956.4	S	U	T	B	CID	LIT	2	13.5	VILVGNLGQDPEVR	1508.8	K	Y	4.3	0.6	47.3	15.1
P0AGE0	18956.4	S	U	T	C	CID	LIT	2	13.5	LAEVASEYLR	1150.6	K	K	3.3	0.5	31.6	17.4
P0AGE0	18956.4	S	U	T	C	CID	LIT	2	13.5	VILVGNLGQDPEVR	1508.8	K	Y	4.2	0.7	40.9	14.3
P0AGE0	18956.4	S	U	T	A	ETD	LIT	2	13.5	LAEVASEYLR	1150.6	K	K	2.8	0.3	45.2	16.4
P0AGE0	18956.4	S	U	T	A	ETD	LIT	2	13.5	VILVGNLGQDPEVR	1508.8	K	Y	2.7	0.4	39.2	15.1
P0AGE0	18956.4	S	U	T	C	ETD	LIT	2	13.5	LAEVASEYLR	1150.6	K	K	1.5	0.0	24.8	16.4
P0AGE0	18956.4	S	U	T	C	ETD	LIT	2	13.5	VILVGNLGQDPEVR	1508.8	K	Y	3.8	0.5	78.2	15.1
P0AGE0	18956.4	S	U	T	A	ETD+CID	LIT	2	13.5	LAEVASEYLR	1150.6	K	K	2.8	0.5	47.5	16.4
P0AGE0	18956.4	S	U	T	A	ETD+CID	LIT	2	13.5	VILVGNLGQDPEVR	1508.8	K	Y	4.0	0.0	53.2	15.1
P75818	18973.8	G	U	A	A	CID	LIT	3	19.3	DARNIPLRV	1053.6	R	D	1.8	0.5	0.0	0.0
P75818	18973.8	G	U	A	A	CID	LIT	3	19.3	DPFSSRTTLPDSAHVASASTIPNR	2527.3	N	D	4.6	0.5	25.0	15.4
P75818	18973.8	G	U	A	A	CID	LIT	3	19.3	DSAHVASASTIPNR	1425.7	P	D	4.4	0.0	59.3	14.5
P0AC51	19235.7	G	U	T	A	CID	LIT	4	33.9	EAEPQAKPPTVYR	1485.8	R	A	2.2	0.6	12.8	13.0
P0AC51	19235.7	G	U	T	A	CID	LIT	4	33.9	HPEQCQHDHSVQVK	1728.8	R	K	3.4	0.8	27.2	9.0
P0AC51	19235.7	G	U	T	A	CID	LIT	4	33.9	LMSLQDGAISAYDLLDLLR	2107.1	R	E	5.7	0.7	86.9	11.8
P0AC51	19235.7	G	U	T	A	CID	LIT	4	33.9	TTTQELLAQAEK	1332.7	K	I	3.5	0.0	52.2	13.0
P0AC51	19235.7	S	U	T	B	ETD+CID	LIT	2	17.0	LMSLQDGAISAYDLLDLLR	2123.1	R	E	2.1	0.7	0.0	0.0
P0AC51	19235.7	S	U	T	B	ETD+CID	LIT	2	17.0	LTPQRLEVLR	1225.7	R	L	1.7	0.3	0.0	0.0
P0AB28	19296.3	G	U	A	B	CID	LIT	2	13.3	DEIILALPVVPVH	1414.8	E	D	3.0	0.0	27.1	11.5
P0AB28	19296.3	G	U	A	B	CID	LIT	2	13.3	DNQRLAVLNG	1099.6	I	D	2.7	0.6	1.9	12.6
P0AB28	19296.3	S	U	T	B	ETD+CID	LIT	2	8.7	LDYQGIYTPDQVER	1696.8	R	V	2.8	0.3	20.5	16.5
P0AB28	19296.3	S	U	T	B	ETD+CID	LIT	2	8.7	RLDYQGIYTPDQVER	1852.9	K	V	3.6	0.3	19.2	17.2
P0A6K3	19310.9	G	U	T	A	CID	LIT	6	36.1	IIVIDVSENRDER	1557.8	R	L	1.4	0.4	14.7	13.6
P0A6K3	19310.9	G	U	T	A	CID	LIT	6	36.1	KVAKPVEEVNAEIQR	1710.0	R	I	4.2	0.8	50.4	8.5
P0A6K3	19310.9	G	U	T	A	CID	LIT	6	36.1	LFMDYLSPLK	1226.6	K	Q	2.4	0.8	15.4	11.5
P0A6K3	19310.9	G	U	T	A	CID	LIT	6	36.1	LVLINPELLEK	1280.8	R	S	3.4	0.0	31.9	7.0
P0A6K3	19310.9	G	U	T	A	CID	LIT	6	36.1	SVLQVLHIPDER	1405.8	M	L	0.0	0.0	50.1	12.0
P0A6K3	19310.9	G	U	T	A	CID	LIT	6	36.1	VAKPVEEVNAEIQR	1581.9	K	I	3.7	0.8	66.0	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6K3	19310.9	S	U	T	C	CID	LIT	2	12.4	LFMDYLSPLK	1226.6	K	Q	3.0	0.5	28.8	14.8
P0A6K3	19310.9	S	U	T	C	CID	LIT	2	12.4	LVLINPELLEK	1280.8	R	S	2.9	0.0	30.5	7.0
P0A6K3	19310.9	S	U	T	C	ETD+CID	LIT	2	12.4	LFMDYLSPLK	1226.6	K	Q	1.9	0.6	16.4	14.8
P0A6K3	19310.9	S	U	T	C	ETD+CID	LIT	2	12.4	LVLINPELLEK	1280.8	R	S	3.3	0.0	30.3	7.0
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	AAFDFAVEHQSVER	1605.8	K	W	4.7	0.8	74.9	11.5
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	AGDMVIDGSVR	1119.5	R	G	3.6	0.5	46.8	14.0
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	AVSEATAEVDVISAAALSEQQLAK	2401.2	R	I	4.8	0.7	77.1	10.4
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	IDKSVMAGVIIR	1301.8	K	A	3.7	0.0	36.8	8.5
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	ISAAMEKR	905.5	K	L	1.8	0.5	17.2	16.1
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	LNALPDVLEQFIHLR	1778.0	R	A	2.6	0.6	15.0	10.0
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	LNCKIDK	890.5	K	S	2.6	0.3	20.5	16.2
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	SEFITVARPYAK	1381.7	M	A	0.0	0.0	65.5	10.4
P0ABA4	19314.3	G	U	T	A	CID	LIT	9	56.5	SVMAGVIIR	961.6	K	A	2.2	0.3	36.0	15.9
P0ABA4	19314.3	G	U	A	A	CID	LIT	2	15.8	DFAVEHQSVERWQ	1630.8	F	D	3.2	0.7	40.8	12.3
P0ABA4	19314.3	G	U	A	A	CID	LIT	2	15.8	SEFITVARPYAKAAF	1670.9	M	D	0.0	0.0	26.5	14.8
P0ABA4	19314.3	G	T	T	B	CID	LIT	3	19.8	AGDMVIDGSVR	1135.5	R	G	3.1	0.3	26.4	14.0
P0ABA4	19314.3	G	T	T	B	CID	LIT	3	19.8	LNALPDVLEQFIHLR	1778.0	R	A	2.2	0.5	0.0	0.0
P0ABA4	19314.3	G	T	T	B	CID	LIT	3	19.8	SVMAGVIIR	961.6	K	A	1.9	0.0	16.3	14.0
P0ABA4	19314.3	G	U	A	B	CID	LIT	2	14.1	DFAVEHQSVERWQ	1630.8	F	D	3.2	0.5	34.0	13.2
P0ABA4	19314.3	G	U	A	B	CID	LIT	2	14.1	ERWQDMLAFAAEVTKN	1924.9	V	E	2.0	0.5	0.0	0.0
P0ABA4	19314.3	S	U	T	C	ETD+CID	LIT	2	15.3	LNALPDVLEQFIHLR	1778.0	R	A	2.3	0.8	0.0	0.0
P0ABA4	19314.3	S	U	T	C	ETD+CID	LIT	2	15.3	SEFITVARPYAK	1381.7	M	A	0.0	0.0	37.4	14.6
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	AAMEDVLK	876.5	K	V	2.5	0.0	39.9	13.2
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	FCVPNKEVMPER	1505.7	R	G	4.1	0.8	32.2	12.0
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	GIHTLEHLFAGFMR	1628.8	R	N	2.6	0.5	19.5	14.3
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	INSNEELALPK	1227.7	R	E	3.5	0.5	61.3	11.5
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	PLLDSFTVDHTR	1400.7	M	M	0.0	0.0	49.8	13.4
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	TGFYMSLIGTPDEQR	1714.8	R	V	3.8	0.9	56.0	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	TMNTPHGDAITVFDLR	1787.9	K	F	4.2	0.7	107.0	10.8
P45578	19398.2	G	U	T	A	CID	LIT	8	69.6	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	4.9	0.0	51.9	4.8
P45578	19398.2	G	T	T	A	CID	LIT	3	11.7	INSNEELALPK	1227.7	R	E	3.4	0.7	70.0	10.0
P45578	19398.2	G	T	T	A	CID	LIT	3	11.7	INSNEELALPKEK	1484.8	R	L	4.5	0.6	46.3	10.8
P45578	19398.2	G	T	T	A	CID	LIT	3	11.7	MEAPAVR	773.4	R	V	1.5	0.6	21.3	10.0
P45578	19398.2	G	U	A	A	CID	LIT	6	39.8	DAWKAAME	921.4	A	D	2.1	0.2	8.2	16.4
P45578	19398.2	G	U	A	A	CID	LIT	6	39.8	DIARSILER	1072.6	Q	D	2.4	0.2	22.7	14.6
P45578	19398.2	G	U	A	A	CID	LIT	6	39.8	DQNQIPELNVYQCGTYQMHSLQEAQ	2994.3	Q	D	3.9	0.0	17.0	8.5
P45578	19398.2	G	U	A	A	CID	LIT	6	39.8	DSFTVDHTRM	1208.5	L	E	3.0	0.8	45.8	11.1
P45578	19398.2	G	U	A	A	CID	LIT	6	39.8	DSFTVDHTRMEAPAVRVAKTMNTPHG	2868.4	L	D	3.4	0.5	10.5	14.1
P45578	19398.2	G	U	A	A	CID	LIT	6	39.8	EAPAVRVAKTMNTPHG	1694.9	M	D	3.0	0.8	16.6	16.1
P45578	19398.2	G	T	T	B	CID	LIT	6	35.1	FCVPNKEVMPER	1505.7	R	G	3.7	0.6	24.7	13.4
P45578	19398.2	G	T	T	B	CID	LIT	6	35.1	INSNEELALPK	1227.7	R	E	3.3	0.0	43.7	10.0
P45578	19398.2	G	T	T	B	CID	LIT	6	35.1	INSNEELALPKEK	1484.8	R	L	3.1	0.4	33.1	11.5
P45578	19398.2	G	T	T	B	CID	LIT	6	35.1	PLLDSFTVDHTR	1400.7	M	M	0.0	0.0	65.1	12.8
P45578	19398.2	G	T	T	B	CID	LIT	6	35.1	PLLDSFTVDHTRMEAPAVR	2155.1	M	V	0.0	0.0	35.6	11.8
P45578	19398.2	G	T	T	B	CID	LIT	6	35.1	TMNTPHGDAITVFDLR	1787.9	K	F	3.7	0.0	29.1	10.8
P45578	19398.2	G	T	A	B	CID	LIT	2	15.2	DISPMGCRTGFYMSLIGTP	2103.0	I	D	1.8	0.4	14.5	14.3
P45578	19398.2	G	T	A	B	CID	LIT	2	15.2	EELALPK	799.5	N	E	2.0	0.2	0.0	0.0
P45578	19398.2	S	U	T	B	CID	LIT	3	34.5	PLLDSFTVDHTR	1400.7	M	M	0.0	0.0	52.8	16.5
P45578	19398.2	S	U	T	B	CID	LIT	3	34.5	TMNTPHGDAITVFDLR	1787.9	K	F	3.8	0.0	39.7	16.3
P45578	19398.2	S	U	T	B	CID	LIT	3	34.5	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	4.7	0.0	43.8	16.5
P45578	19398.2	S	U	T	C	CID	LIT	4	40.9	INSNEELALPK	1227.7	R	E	2.9	0.3	15.5	13.4
P45578	19398.2	S	U	T	C	CID	LIT	4	40.9	PLLDSFTVDHTR	1400.7	M	M	0.0	0.0	47.8	16.8
P45578	19398.2	S	U	T	C	CID	LIT	4	40.9	TMNTPHGDAITVFDLR	1787.9	K	F	3.5	0.0	19.9	15.9
P45578	19398.2	S	U	T	C	CID	LIT	4	40.9	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	4.3	0.0	32.1	16.7
P45578	19398.2	S	U	T	B	ETD	LIT	4	42.1	GIHTLEHLFAGFMR	1628.8	R	N	3.5	0.5	5.1	18.3
P45578	19398.2	S	U	T	B	ETD	LIT	4	42.1	INSNEELALPK	1227.7	R	E	2.3	0.3	24.8	14.3

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		digestion	lysis	protease	replicate												
P45578	19398.2	S	U	T	B	ETD	LIT	4	42.1	TMNTPHGDAITVFDLR	1787.9	K	F	2.8	0.0	31.4	15.9
P45578	19398.2	S	U	T	B	ETD	LIT	4	42.1	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	0.0	0.0	23.0	16.5
P45578	19398.2	S	U	T	B	ETD+CID	LIT	3	34.5	PLLDSFTVDHTR	1400.7	M	M	0.0	0.0	65.6	16.4
P45578	19398.2	S	U	T	B	ETD+CID	LIT	3	34.5	TMNTPHGDAITVFDLR	1787.9	K	F	0.0	0.0	25.4	16.3
P45578	19398.2	S	U	T	B	ETD+CID	LIT	3	34.5	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	0.0	0.0	39.5	16.7
P45578	19398.2	S	U	T	A	ETD+CID	LIT	2	27.5	TMNTPHGDAITVFDLR	1787.9	K	F	2.9	0.5	17.5	15.9
P45578	19398.2	S	U	T	A	ETD+CID	LIT	2	27.5	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	4.4	0.6	40.5	16.8
P45578	19398.2	S	U	T	B	ETD+CID	LIT	4	40.9	INSNEELALPK	1227.7	R	E	2.3	0.2	14.6	14.3
P45578	19398.2	S	U	T	B	ETD+CID	LIT	4	40.9	PLLDSFTVDHTR	1400.7	M	M	0.0	0.0	65.6	16.4
P45578	19398.2	S	U	T	B	ETD+CID	LIT	4	40.9	TMNTPHGDAITVFDLR	1787.9	K	F	3.7	0.8	25.4	16.3
P45578	19398.2	S	U	T	B	ETD+CID	LIT	4	40.9	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	3.7	0.0	39.5	16.7
P45578	19398.2	S	U	T	C	ETD+CID	LIT	4	42.1	INSNEELALPK	1227.7	R	E	3.3	0.3	53.7	13.4
P45578	19398.2	S	U	T	C	ETD+CID	LIT	4	42.1	TMNTPHGDAITVFDLR	1787.9	K	F	3.8	0.0	25.4	15.9
P45578	19398.2	S	U	T	C	ETD+CID	LIT	4	42.1	VADAWKAAMEDVLK	1562.8	R	V	2.0	0.6	0.0	0.0
P45578	19398.2	S	U	T	C	ETD+CID	LIT	4	42.1	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	4.3	0.0	35.0	16.7
P45578	19398.2	S	U	T	B	HCD	FT	3	34.5	PLLDSFTVDHTR	1400.7	M	M	0.0	0.0	65.6	16.4
P45578	19398.2	S	U	T	B	HCD	FT	3	34.5	TMNTPHGDAITVFDLR	1787.9	K	F	0.0	0.0	25.4	16.3
P45578	19398.2	S	U	T	B	HCD	FT	3	34.5	VQDQNQIPELNVYQCGTYQMHSLQEAQDIAR	3676.7	K	S	0.0	0.0	39.5	16.7
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	HAQEEMTHMQR	1397.6	R	L	3.9	0.9	54.8	6.0
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	INTVESPFAEYSSLDELFQETYKHEQLITQK	3687.8	R	I	4.6	0.0	52.8	9.5
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	LFDYLTDTGNLPR	1524.8	R	I	4.2	0.8	56.8	13.0
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	MLKPEMIEK	1118.6	-	L	2.2	0.6	0.0	0.0
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	RHAQEEMTHMQR	1553.7	R	L	3.7	0.9	29.0	11.5
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	SGEGLYFIDK	1128.6	K	E	3.3	0.0	36.6	8.5
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	SGEGLYFIDKELSTLDTQN	2130.0	K	-	4.1	0.0	50.9	12.0
P0A998	19406.6	G	U	T	A	CID	LIT	8	57.6	SIIDKLSLAGK	1144.7	K	S	3.4	0.5	42.8	9.0
P0A998	19406.6	S	U	T	A	CID	LIT	2	18.2	SGEGLYFIDKELSTLDTQN	2130.0	K	-	2.9	0.0	23.0	17.4
P0A998	19406.6	S	U	T	A	CID	LIT	2	18.2	SIIDKLSLAGK	1144.7	K	S	2.1	0.3	8.1	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A998	19406.6	S	U	T	A	ETD+CID	LIT	2	14.5	LFDYLTDTGNLPR	1524.8	R	I	1.9	0.3	0.0	0.0
P0A998	19406.6	S	U	T	A	ETD+CID	LIT	2	14.5	SIIDKLSLAGK	1144.7	K	S	2.7	0.6	26.5	10.8
P77368	19457.8	G	T	T	A	CID	LIT	2	14.2	DGTKLPTGAVQGR	1299.7	R	N	4.0	0.5	26.6	13.4
P77368	19457.8	G	T	T	A	CID	LIT	2	14.2	IATAEITPVYEIK	1447.8	K	-	3.4	0.0	45.9	9.5
P0A6D7	19520.1	G	U	T	A	CID	LIT	7	53.2	EVLEALANERNPLYEEIADVTIR	2657.4	R	T	4.6	0.0	19.2	11.8
P0A6D7	19520.1	G	U	T	A	CID	LIT	7	53.2	NIFLVGPMGAGK	1203.7	R	S	2.8	0.6	28.8	12.8
P0A6D7	19520.1	G	U	T	A	CID	LIT	7	53.2	NPLYEEIADVTIR	1532.8	R	T	2.4	0.5	14.6	12.6
P0A6D7	19520.1	G	U	T	A	CID	LIT	7	53.2	QGIVLATGGGSVK	1186.7	K	S	2.8	0.4	16.5	13.4
P0A6D7	19520.1	G	U	T	A	CID	LIT	7	53.2	QLAQQLNMEFYDSDQEIEKR	2485.2	R	T	4.2	0.0	35.4	12.6
P0A6D7	19520.1	G	U	T	A	CID	LIT	7	53.2	RPLLHVETPPR	1314.8	K	E	2.6	0.0	36.0	9.0
P0A6D7	19520.1	G	U	T	A	CID	LIT	7	53.2	VVANQIIHMLESN	1483.8	K	-	2.4	0.8	22.1	13.6
P0A6D7	19520.1	G	U	A	A	CID	LIT	2	16.8	DDQSAKVVANQIIHMLESN	2112.0	T	-	2.1	0.3	0.0	0.0
P0A6D7	19520.1	G	U	A	A	CID	LIT	2	16.8	DQEIEKRTGA	1146.6	S	D	2.5	0.5	26.6	15.7
P0A6D7	19520.1	G	T	A	B	CID	LIT	2	17.3	DDQSAKVVANQIIHMLESN	2112.0	T	-	2.3	0.5	16.1	14.0
P0A6D7	19520.1	G	T	A	B	CID	LIT	2	17.3	EALANERNPLY	1289.6	L	E	2.6	0.7	26.8	14.5
P0ABY4	19683.0	G	U	A	A	CID	LIT	2	13.9	DDSPKLMEQY	1241.5	K	D	2.1	0.7	0.0	0.0
P0ABY4	19683.0	G	U	A	A	CID	LIT	2	13.9	DIIGPELVTLHNLK	1561.9	R	D	3.4	0.0	20.5	7.8
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	AEIVASFER	1021.5	K	A	3.1	0.5	38.8	14.9
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	AQIAHFFEHYK	1390.7	K	D	4.6	0.8	43.7	13.2
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	AQIAHFFEHYKDLEK	1875.9	K	G	5.3	0.7	48.3	11.5
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	ESGALFVDR	993.5	K	F	1.7	0.3	22.2	14.5
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	EYDHIKDVNDLPELLK	1941.0	K	A	5.0	0.8	47.1	12.6
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	LSKEYDHIK	1132.6	K	D	2.9	0.3	25.3	14.1
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	LVAVPHSK	850.5	K	L	2.6	0.8	37.7	10.0
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	MTDEAGEDAKLVAVPHSK	1897.9	K	L	3.6	0.5	49.8	13.4
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	VEGWENAEAAK	1203.6	K	A	3.2	0.8	49.7	11.1
P0A7A9	19685.9	G	U	T	A	CID	LIT	10	46.0	VEGWENAEAAKAEIVASFER	2206.1	K	A	3.1	0.8	27.9	11.5
P0A7A9	19685.9	G	T	T	A	CID	LIT	2	11.4	AEIVASFER	1021.5	K	A	2.5	0.5	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7A9	19685.9	G	T	T	A	CID	LIT	2	11.4	VEGWENAEAAK	1203.6	K	A	2.7	0.5	15.5	10.8
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	DAKLVAVPHSKLSKEY	1785.0	E	D	4.3	0.8	41.8	14.8
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	DIYVVIEIPANA	1316.7	E	D	1.8	0.4	0.0	0.0
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	DLPELLKAQIAHFFEHYK	2199.2	N	D	2.2	0.6	10.8	15.1
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	DPIKYEI	877.5	A	D	1.9	0.1	19.5	14.8
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	EAAKAEIVASFERAKNK	1862.0	A	-	5.1	0.6	57.1	13.2
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	EIVASFERAKNK	1391.8	A	-	3.1	0.0	27.7	11.1
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	SLLNVPAGK	898.5	M	D	0.0	0.0	37.3	4.8
P0A7A9	19685.9	G	U	A	A	CID	LIT	8	47.2	SLLNVPAGKDLPE	1352.7	M	D	0.0	0.0	35.6	10.4
P0A7A9	19685.9	G	T	T	B	CID	LIT	4	14.8	CRPVGVLK	928.5	R	M	2.4	0.3	0.0	0.0
P0A7A9	19685.9	G	T	T	B	CID	LIT	4	14.8	LVAVPHSK	850.5	K	L	1.9	0.8	6.5	10.0
P0A7A9	19685.9	G	T	T	B	CID	LIT	4	14.8	MTDEAGEDAK	1066.4	K	L	2.3	0.0	44.8	3.0
P0A7A9	19685.9	G	T	T	B	CID	LIT	4	14.8	MTDEAGEDAKLVAVPHSK	1897.9	K	L	2.5	0.3	16.4	13.0
P0A7A9	19685.9	S	U	T	A	CID	LIT	2	10.8	EYDHIKDVNDLPELLK	1941.0	K	A	3.9	0.5	18.8	18.0
P0A7A9	19685.9	S	U	T	A	CID	LIT	2	10.8	LSKEYDHIKDVNDLPELLK	2269.2	K	A	2.0	0.2	18.7	16.5
P0A7A9	19685.9	S	U	T	A	ETD	LIT	2	10.8	EYDHIKDVNDLPELLK	1941.0	K	A	4.9	0.3	31.4	17.3
P0A7A9	19685.9	S	U	T	A	ETD	LIT	2	10.8	LSKEYDHIKDVNDLPELLK	2269.2	K	A	6.0	0.5	38.8	16.9
P0A7A9	19685.9	S	U	T	A	ETD+CID	LIT	3	19.3	AQIAHFFEHYKDLEK	1875.9	K	G	3.1	0.2	29.6	18.2
P0A7A9	19685.9	S	U	T	A	ETD+CID	LIT	3	19.3	EYDHIKDVNDLPELLK	1941.0	K	A	3.9	0.4	36.2	17.3
P0A7A9	19685.9	S	U	T	A	ETD+CID	LIT	3	19.3	LSKEYDHIKDVNDLPELLK	2269.2	K	A	3.9	0.6	31.3	16.3
P61949	19719.7	G	U	T	A	CID	LIT	6	51.7	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	94.3	12.0
P61949	19719.7	G	U	T	A	CID	LIT	6	51.7	DVADVHDIAK	1082.5	K	S	3.1	0.8	47.5	10.0
P61949	19719.7	G	U	T	A	CID	LIT	6	51.7	GATIVGHWPTAGYHFEASK	2029.0	R	G	6.1	0.7	54.5	10.4
P61949	19719.7	G	U	T	A	CID	LIT	6	51.7	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	4.2	0.4	51.1	11.8
P61949	19719.7	G	U	T	A	CID	LIT	6	51.7	QISEELHLDEILNA	1623.8	K	-	3.7	0.5	33.3	13.2
P61949	19719.7	G	U	T	A	CID	LIT	6	51.7	QLGKDVADVHDIAK	1508.8	K	S	2.7	0.8	41.9	10.4
P61949	19719.7	G	T	T	A	CID	LIT	5	43.8	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	83.8	12.0
P61949	19719.7	G	T	T	A	CID	LIT	5	43.8	DVADVHDIAK	1082.5	K	S	2.3	0.0	24.5	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61949	19719.7	G	T	T	A	CID	LIT	5	43.8	GATIVGHWPTAGYHFEASK	2029.0	R	G	5.7	0.7	58.3	10.8
P61949	19719.7	G	T	T	A	CID	LIT	5	43.8	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	3.6	0.5	62.9	11.8
P61949	19719.7	G	T	T	A	CID	LIT	5	43.8	QLGKDVADVHDIAK	1508.8	K	S	3.6	0.0	55.2	10.4
P61949	19719.7	G	U	A	A	CID	LIT	5	47.7	DALGTIR	745.4	C	D	1.5	0.2	21.6	19.3
P61949	19719.7	G	U	A	A	CID	LIT	5	47.7	DIIEPRGATIVGHWPTAGYHFEASKGLA	2993.5	R	D	5.5	0.0	21.4	14.8
P61949	19719.7	G	U	A	A	CID	LIT	5	47.7	DILLLGIPTWYYGEAQC	2012.0	Y	D	3.7	0.0	39.3	14.1
P61949	19719.7	G	U	A	A	CID	LIT	5	47.7	DTGNTENIAKMIQKQLGKDVA	2274.2	S	D	3.5	0.5	15.7	16.1
P61949	19719.7	G	U	A	A	CID	LIT	5	47.7	DVHDIAKSSKE	1228.6	A	D	3.0	0.8	27.9	13.6
P61949	19719.7	G	T	T	B	CID	LIT	3	29.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	93.0	11.5
P61949	19719.7	G	T	T	B	CID	LIT	3	29.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	2.5	0.0	20.2	11.5
P61949	19719.7	G	T	T	B	CID	LIT	3	29.5	QLGKDVADVHDIAK	1508.8	K	S	2.1	0.2	35.9	10.4
P61949	19719.7	S	U	T	A	CID	LIT	3	26.7	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	78.6	17.9
P61949	19719.7	S	U	T	A	CID	LIT	3	26.7	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	4.3	0.4	45.3	18.1
P61949	19719.7	S	U	T	A	CID	LIT	3	26.7	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	4.0	0.5	57.4	18.9
P61949	19719.7	S	U	T	B	CID	LIT	6	55.1	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	80.6	18.1
P61949	19719.7	S	U	T	B	CID	LIT	6	55.1	GATIVGHWPTAGYHFEASK	2029.0	R	G	4.3	0.7	40.8	17.9
P61949	19719.7	S	U	T	B	CID	LIT	6	55.1	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	4.7	0.8	40.1	18.5
P61949	19719.7	S	U	T	B	CID	LIT	6	55.1	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	5.0	0.7	51.4	19.1
P61949	19719.7	S	U	T	B	CID	LIT	6	55.1	LVALFGCGDQEDYAEYFCDALGTIR	2883.3	K	D	2.0	0.8	5.6	14.5
P61949	19719.7	S	U	T	B	CID	LIT	6	55.1	LVALFGCGDQEDYAEYFCDALGTIRDIIEPR	3606.7	K	G	3.4	0.0	30.1	18.5
P61949	19719.7	S	U	T	C	CID	LIT	5	45.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	55.9	17.4
P61949	19719.7	S	U	T	C	CID	LIT	5	45.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	5.2	0.8	54.2	18.1
P61949	19719.7	S	U	T	C	CID	LIT	5	45.5	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	4.0	0.4	34.0	17.5
P61949	19719.7	S	U	T	C	CID	LIT	5	45.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	3.4	0.4	43.0	19.1
P61949	19719.7	S	U	T	C	CID	LIT	5	45.5	QLGKDVADVHDIAK	1508.8	K	S	2.7	0.7	22.6	14.8
P61949	19719.7	S	U	T	A	ETD	LIT	3	34.7	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	73.1	17.4
P61949	19719.7	S	U	T	A	ETD	LIT	3	34.7	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	6.8	0.0	48.1	19.1
P61949	19719.7	S	U	T	A	ETD	LIT	3	34.7	QLGKDVADVHDIAK	1508.8	K	S	2.0	0.0	17.3	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61949	19719.7	S	U	T	B	ETD	LIT	6	45.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	104.0	17.3
P61949	19719.7	S	U	T	B	ETD	LIT	6	45.5	DVADVHDIAK	1082.5	K	S	2.1	0.2	0.0	0.0
P61949	19719.7	S	U	T	B	ETD	LIT	6	45.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	2.7	0.6	26.7	17.9
P61949	19719.7	S	U	T	B	ETD	LIT	6	45.5	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	2.3	0.0	24.0	17.9
P61949	19719.7	S	U	T	B	ETD	LIT	6	45.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	5.4	0.0	47.0	19.0
P61949	19719.7	S	U	T	B	ETD	LIT	6	45.5	QLGKDVADVHDIAK	1508.8	K	S	4.7	0.6	67.1	14.9
P61949	19719.7	S	U	T	C	ETD	LIT	3	37.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	72.0	17.3
P61949	19719.7	S	U	T	C	ETD	LIT	3	37.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	4.0	0.0	46.4	18.2
P61949	19719.7	S	U	T	C	ETD	LIT	3	37.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	0.0	0.0	43.8	19.1
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	89.3	17.9
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	0.0	0.0	65.6	18.3
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	0.0	0.0	49.0	18.6
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	0.0	0.0	47.8	19.1
P61949	19719.7	S	U	T	A	ETD+CID	LIT	2	37.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	77.8	17.9
P61949	19719.7	S	U	T	A	ETD+CID	LIT	2	37.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	4.2	0.6	43.2	17.6
P61949	19719.7	S	U	T	A	ETD+CID	LIT	2	37.5	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	4.4	0.7	31.6	18.6
P61949	19719.7	S	U	T	A	ETD+CID	LIT	2	37.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	1.0	-0.9	67.1	19.0
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	89.3	17.9
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	4.6	0.8	65.6	18.3
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	4.8	0.6	49.0	18.6
P61949	19719.7	S	U	T	B	ETD+CID	LIT	2	37.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	3.8	0.8	41.6	19.2
P61949	19719.7	S	U	T	C	ETD+CID	LIT	3	45.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	80.7	17.9
P61949	19719.7	S	U	T	C	ETD+CID	LIT	3	45.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	5.2	0.8	57.1	17.9
P61949	19719.7	S	U	T	C	ETD+CID	LIT	3	45.5	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	2.8	0.3	63.5	18.8
P61949	19719.7	S	U	T	C	ETD+CID	LIT	3	45.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	4.2	0.6	15.8	18.9
P61949	19719.7	S	U	T	C	ETD+CID	LIT	3	45.5	QLGKDVADVHDIAK	1508.8	K	S	3.4	0.7	47.5	14.6
P61949	19719.7	S	U	T	B	HCD	FT	2	37.5	AITGIFFGSDTGNTENIAK	1956.0	M	M	0.0	0.0	89.3	17.9
P61949	19719.7	S	U	T	B	HCD	FT	2	37.5	GATIVGHWPTAGYHFEASK	2029.0	R	G	0.0	0.0	65.6	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61949	19719.7	S	U	T	B	HCD	FT	2	37.5	GLADDDHFVGLAIDEDRQPELTAER	2782.3	K	V	0.0	0.0	49.0	18.6
P61949	19719.7	S	U	T	B	HCD	FT	2	37.5	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	K	W	0.0	0.0	41.6	19.2
P0AEE1	19769.7	G	T	T	A	CID	LIT	3	24.3	LGTQANNMHVWSDATGQK	1957.9	K	A	2.5	0.6	14.3	9.5
P0AEE1	19769.7	G	T	T	A	CID	LIT	3	24.3	LSFSLPADMTDQSGK	1596.8	K	L	3.8	0.0	41.7	10.4
P0AEE1	19769.7	G	T	T	A	CID	LIT	3	24.3	SRDPQLQVVTNK	1384.8	R	A	4.0	0.6	61.8	12.3
P45771	19852.6	S	U	T	B	CID	LIT	2	20.6	HGPFLGCSQYPACDYVRPLK	2365.1	K	S	2.9	0.4	27.2	17.5
P45771	19852.6	S	U	T	B	CID	LIT	2	20.6	VLEGQVCPACGANLVLR	1856.0	K	Q	4.8	0.6	37.8	17.8
P45771	19852.6	S	U	T	C	CID	LIT	2	20.6	HGPFLGCSQYPACDYVRPLK	2365.1	K	S	5.5	0.7	32.3	17.7
P45771	19852.6	S	U	T	C	CID	LIT	2	20.6	VLEGQVCPACGANLVLR	1856.0	K	Q	3.3	0.6	57.7	18.1
P45771	19852.6	S	U	T	B	ETD+CID	LIT	2	20.6	HGPFLGCSQYPACDYVRPLK	2365.1	K	S	0.0	0.0	31.6	17.5
P45771	19852.6	S	U	T	B	ETD+CID	LIT	2	20.6	VLEGQVCPACGANLVLR	1856.0	K	Q	0.0	0.0	65.2	18.3
P45771	19852.6	S	U	T	A	ETD+CID	LIT	2	29.4	FGMFIGCINYPECEHTELIDKPDETAITCPQCR	4001.8	R	T	4.7	0.0	26.4	12.3
P45771	19852.6	S	U	T	A	ETD+CID	LIT	2	29.4	HGPFLGCSQYPACDYVRPLK	2365.1	K	S	5.1	0.5	20.3	17.6
P45771	19852.6	S	U	T	B	ETD+CID	LIT	2	20.6	HGPFLGCSQYPACDYVRPLK	2365.1	K	S	5.0	0.5	31.6	17.5
P45771	19852.6	S	U	T	B	ETD+CID	LIT	2	20.6	VLEGQVCPACGANLVLR	1856.0	K	Q	4.8	0.7	65.2	18.3
P45771	19852.6	S	U	T	C	ETD+CID	LIT	2	27.8	FGMFIGCINYPECEHTELIDKPDETAITCPQCR	4001.8	R	T	5.1	0.0	29.0	13.0
P45771	19852.6	S	U	T	C	ETD+CID	LIT	2	27.8	VLEGQVCPACGANLVLR	1856.0	K	Q	4.5	0.6	64.2	18.3
P45771	19852.6	S	U	T	B	HCD	FT	2	20.6	HGPFLGCSQYPACDYVRPLK	2365.1	K	S	0.0	0.0	31.6	17.5
P45771	19852.6	S	U	T	B	HCD	FT	2	20.6	VLEGQVCPACGANLVLR	1856.0	K	Q	0.0	0.0	65.2	18.3
P51024	19905.5	G	T	T	B	CID	LIT	2	14.0	LLVDNNSEGEYAIIPASVADK	2218.1	R	I	5.8	0.9	69.3	12.6
P51024	19905.5	G	T	T	B	CID	LIT	2	14.0	LLVDNNSEGEYAIIPASVADKIAQR	2686.4	R	D	4.0	0.4	54.6	12.8
P51024	19905.5	G	T	A	B	CID	LIT	6	26.8	DASSIVLHSALSAEEQ	1656.8	R	D	3.7	0.0	57.6	14.9
P51024	19905.5	G	T	A	B	CID	LIT	6	26.8	DFKVP	605.3	A	D	1.3	0.0	23.9	7.0
P51024	19905.5	G	T	A	B	CID	LIT	6	26.8	DFKVPD	720.4	A	D	2.2	0.2	21.1	18.7
P51024	19905.5	G	T	A	B	CID	LIT	6	26.8	DGNLIKKIFV	1146.7	T	D	2.2	0.0	16.0	7.8
P51024	19905.5	G	T	A	B	CID	LIT	6	26.8	DKIAQR	730.4	A	D	1.9	0.5	23.3	12.8
P51024	19905.5	G	T	A	B	CID	LIT	6	26.8	EENKKAQLER	1244.7	V	D	2.7	0.8	36.9	13.6
P51024	19905.5	S	U	T	A	ETD+CID	LIT	2	14.0	LLVDNNSEGEYAIIPASVADK	2218.1	R	I	5.2	0.4	61.5	17.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P51024	19905.5	S	U	T	A	ETD+CID	LIT	2	14.0	LLVDNNSEGEYAIIPASVADKIAQR	2686.4	R	D	4.3	0.5	69.8	18.1
P0ABZ4	19979.9	G	U	A	A	CID	LIT	2	13.8	DAHPLLIPRA	1102.6	A	D	2.1	0.0	22.7	10.0
P0ABZ4	19979.9	G	U	A	A	CID	LIT	2	13.8	SKAGASLATCYGPVSA	1539.7	M	D	0.0	0.0	40.5	14.9
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	FGSELLAK	864.5	K	F	2.9	0.3	51.6	14.3
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	FVNILMVDGK	1135.6	K	K	3.7	0.8	51.3	12.3
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	FVNILMVDGKK	1263.7	K	S	3.4	0.5	42.9	10.0
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	KILPDPK	810.5	R	F	2.4	0.0	40.5	0.0
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	KSTAESIVYSALETLAQR	1967.0	K	S	5.2	0.6	90.1	11.1
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	LANELSDAAENK	1274.6	R	G	4.6	0.8	67.4	12.0
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	LANELSDAAENKGTAVK	1730.9	R	K	4.9	0.5	70.1	12.6
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	MAEANKAFAHYR	1408.7	R	W	4.1	0.7	51.6	12.8
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	NALAMR	675.4	R	W	1.8	0.7	30.6	10.8
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	RNALAMR	831.5	R	W	2.8	0.4	24.1	11.8
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	RVGGSTYQVPVEVRPVR	1899.1	R	R	3.1	0.3	12.8	9.0
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	SELEAFEVALENVRPTVEVK	2259.2	K	S	5.7	0.7	70.4	11.5
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	SFSHQAGASSK	1106.5	R	Q	3.2	0.7	77.9	10.4
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	SFSHQAGASSKQPALGYLN	1963.0	R	-	3.0	0.7	36.5	10.4
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	6.6	0.0	64.6	9.5
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	STAESIVYSALETLAQR	1839.0	K	S	3.2	0.9	80.0	11.1
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	VGGSTYQVPVEVRPVR	1743.0	R	R	2.5	0.7	34.7	11.8
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	VGGSTYQVPVEVRPVRR	1899.1	R	N	1.6	0.5	37.5	10.0
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	WIVEAAR	844.5	R	K	2.2	0.7	27.5	12.8
P02359	20001.3	G	U	T	A	CID	LIT	20	81.6	WIVEAARK	972.6	R	R	2.1	0.6	20.5	14.0
P02359	20001.3	G	T	T	A	CID	LIT	7	45.8	AFAHYR	764.4	K	W	1.8	0.7	19.4	12.0
P02359	20001.3	G	T	T	A	CID	LIT	7	45.8	FGSELLAK	864.5	K	F	2.0	0.2	16.6	14.3
P02359	20001.3	G	T	T	A	CID	LIT	7	45.8	LANELSDAAENK	1274.6	R	G	4.1	0.7	57.5	12.3
P02359	20001.3	G	T	T	A	CID	LIT	7	45.8	LANELSDAAENKGTAVK	1730.9	R	K	5.2	0.5	62.4	13.0
P02359	20001.3	G	T	T	A	CID	LIT	7	45.8	SFSHQAGASSK	1106.5	R	Q	3.5	0.7	51.0	10.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02359	20001.3	G	T	T	A	CID	LIT	7	45.8	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	2.2	0.7	12.3	7.8
P02359	20001.3	G	T	T	A	CID	LIT	7	45.8	STAESIVYSALETLAQR	1839.0	K	S	3.2	0.8	50.1	12.0
P02359	20001.3	G	U	A	A	CID	LIT	2	15.1	DAAENKGTAVKKRE	1516.8	S	D	4.6	0.6	74.0	16.0
P02359	20001.3	G	U	A	A	CID	LIT	2	15.1	DKSMALRLANELS	1463.8	G	D	2.8	0.3	32.8	15.2
P02359	20001.3	G	T	T	B	CID	LIT	2	17.3	LANELSDAAENK	1274.6	R	G	4.1	0.4	43.4	12.3
P02359	20001.3	G	T	T	B	CID	LIT	2	17.3	SFSHQAGASSKQPALGYLN	1963.0	R	-	2.8	0.6	11.8	10.4
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	FGSELLAK	864.5	K	F	2.3	0.3	40.2	14.3
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	FVNILMVDGK	1135.6	K	K	3.1	0.0	37.3	12.3
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	FVNILMVDGKK	1263.7	K	S	2.5	0.0	28.0	12.6
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	KILPDPK	810.5	R	F	1.7	0.0	30.0	0.0
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	KSTAESIVYSALETLAQR	1967.0	K	S	4.0	0.6	22.6	11.1
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	LANELSDAAENKGTAVK	1730.9	R	K	3.1	0.5	19.0	14.1
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	SFSHQAGASSK	1106.5	R	Q	3.2	0.0	53.7	10.4
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	5.7	0.0	40.6	6.0
P02359	20001.3	G	U	T	B	CID	LIT	9	52.5	STAESIVYSALETLAQR	1839.0	K	S	4.2	0.9	30.8	11.8
P02359	20001.3	G	T	A	B	CID	LIT	2	15.1	DAAENKGTAVKKRE	1516.8	S	D	2.6	0.4	47.3	17.3
P02359	20001.3	G	T	A	B	CID	LIT	2	15.1	DKSMALRLANELS	1447.8	G	D	2.1	0.2	0.8	15.3
P02359	20001.3	G	U	A	B	CID	LIT	4	21.2	DAAENKGTAVKKRE	1516.8	S	D	3.7	0.6	67.1	16.0
P02359	20001.3	G	U	A	B	CID	LIT	4	21.2	DKSMALRLANELS	1447.8	G	D	3.1	0.6	35.7	15.3
P02359	20001.3	G	U	A	B	CID	LIT	4	21.2	ENKGTAVKKRE	1259.7	A	D	1.8	0.6	12.4	12.8
P02359	20001.3	G	U	A	B	CID	LIT	4	21.2	EVALENVRPTV	1226.7	F	E	2.8	0.4	30.8	12.0
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	FVNILMVDGK	1135.6	K	K	3.9	0.6	40.4	14.6
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	FVNILMVDGKK	1263.7	K	S	3.4	0.5	27.8	13.0
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	SELEAFEVALENVRPTVEVK	2259.2	K	S	5.6	0.7	74.3	18.0
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	SFSHQAGASSKQPALGYLN	1963.0	R	-	4.8	0.5	38.5	19.0
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	6.4	0.6	53.9	16.1
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	STAESIVYSALETLAQR	1839.0	K	S	4.9	0.8	49.8	16.4
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	VGGSTYQVPVEVRPVR	1743.0	R	R	2.6	0.8	34.9	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	VGGSTYQVPVEVRPVRR	1899.1	R	N	1.8	0.0	28.4	13.4
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	WIVEAAR	844.5	R	K	2.0	0.0	24.3	13.0
P02359	20001.3	S	U	T	A	CID	LIT	10	55.3	WLSLR	674.4	R	S	1.3	0.4	11.2	9.0
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	FGSELLAK	864.5	K	F	2.7	0.2	48.4	15.9
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	FVNILMVDGKK	1263.7	K	S	2.4	0.0	20.1	13.2
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	KSTAESIVYSALETLAQR	1967.0	K	S	5.0	0.6	36.4	15.7
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	LANELSDAAENKGTAVK	1730.9	R	K	3.4	0.5	31.0	18.2
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	SELEAFEVALENVRPTVEVK	2259.2	K	S	5.5	0.7	73.3	18.1
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	SFSHQAGASSKQPALGYLN	1963.0	R	-	5.1	0.6	47.6	17.6
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	6.4	0.7	77.2	15.3
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	STAESIVYSALETLAQR	1839.0	K	S	4.3	0.8	63.5	16.0
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	VGGSTYQVPVEVRPVR	1743.0	R	R	2.6	0.7	39.5	16.0
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	VGGSTYQVPVEVRPVRR	1899.1	R	N	3.1	0.7	32.7	14.1
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	WIVEAAR	844.5	R	K	2.2	0.8	27.2	13.0
P02359	20001.3	S	U	T	B	CID	LIT	12	69.3	WLSLR	674.4	R	S	1.4	0.4	12.3	18.0
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	FGSELLAK	864.5	K	F	2.1	0.2	39.2	16.0
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	FVNILMVDGKK	1263.7	K	S	3.4	0.7	39.6	13.0
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	LANELSDAAENK	1274.6	R	G	4.0	0.5	45.8	16.0
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	LANELSDAAENKGTAVK	1730.9	R	K	3.1	0.4	22.0	18.6
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	RVGGSTYQVPVEVRPVR	1899.1	R	R	3.9	0.4	13.9	13.8
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	RVGGSTYQVPVEVRPVRR	2055.2	R	N	1.9	0.6	24.5	11.8
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	SELEAFEVALENVRPTVEVK	2259.2	K	S	2.5	0.3	35.4	18.0
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	SFSHQAGASSKQPALGYLN	1963.0	R	-	4.9	0.5	38.3	18.7
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	5.6	0.7	41.5	15.3
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	STAESIVYSALETLAQR	1839.0	K	S	4.3	0.8	52.2	16.0
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	VGGSTYQVPVEVRPVR	1743.0	R	R	3.9	0.5	23.4	14.8
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	VGGSTYQVPVEVRPVRR	1899.1	R	N	2.7	0.5	23.6	14.0
P02359	20001.3	S	U	T	C	CID	LIT	13	67.0	WIVEAAR	844.5	R	K	2.1	0.6	19.4	18.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02359	20001.3	S	U	T	A	CID	FT	2	19.6	SFSHQAGASSKQPALGYLN	1963.0	R	-	3.5	0.0	38.8	18.6
P02359	20001.3	S	U	T	A	CID	FT	2	19.6	VGGSTYQVPVEVRPVR	1743.0	R	R	2.6	0.0	34.6	15.8
P02359	20001.3	S	U	T	B	CID	FT	2	12.3	FVNILMVDGK	1135.6	K	K	3.5	0.0	48.1	15.3
P02359	20001.3	S	U	T	B	CID	FT	2	12.3	LANELSDAAENK	1274.6	R	G	3.9	0.0	65.1	17.5
P02359	20001.3	S	U	T	C	CID	FT	2	19.6	SFSHQAGASSKQPALGYLN	1963.0	R	-	4.1	0.0	51.1	19.0
P02359	20001.3	S	U	T	C	CID	FT	2	19.6	VGGSTYQVPVEVRPVR	1743.0	R	R	1.7	0.0	52.0	14.6
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	FGSELLAK	864.5	K	F	1.8	0.0	33.4	16.0
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	FVNILMVDGKK	1263.7	K	S	5.1	0.6	53.1	13.2
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	KSTAESIVYSALETLAQR	1967.0	K	S	0.0	0.0	94.6	16.9
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	LANELSDAAENK	1274.6	R	G	2.2	0.6	26.1	16.4
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	LANELSDAAENKGTAVK	1730.9	R	K	6.9	0.5	69.0	18.5
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	RVGGSTYQVPVEVRPVRR	2055.2	R	N	7.2	0.0	94.9	12.3
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	SELEAFEVALENVRPTVEVK	2259.2	K	S	4.7	0.0	33.0	18.0
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	SFSHQAGASSK	1106.5	R	Q	3.0	0.0	37.5	12.8
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	SFSHQAGASSKQPALGYLN	1963.0	R	-	6.5	0.6	69.4	17.7
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	7.1	0.0	61.1	15.7
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	STAESIVYSALETLAQR	1839.0	K	S	1.8	0.6	45.4	18.3
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	VGGSTYQVPVEVRPVR	1743.0	R	R	5.4	0.6	80.6	14.8
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	VGGSTYQVPVEVRPVRR	1899.1	R	N	2.6	0.5	62.5	11.8
P02359	20001.3	S	U	T	A	ETD	LIT	14	67.0	WIVEAAR	844.5	R	K	2.4	0.3	53.6	18.2
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	FGSELLAK	864.5	K	F	2.2	0.7	0.0	0.0
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	FVNILMVDGKK	1263.7	K	S	4.5	0.6	48.3	13.8
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	KSTAESIVYSALETLAQR	1967.0	K	S	7.0	0.0	91.8	15.8
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	LANELSDAAENK	1274.6	R	G	3.3	0.4	0.0	0.0
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	LANELSDAAENKGTAVK	1730.9	R	K	7.1	0.5	92.4	18.6
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	RVGGSTYQVPVEVRPVR	1899.1	R	R	2.9	0.8	0.0	0.0
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	RVGGSTYQVPVEVRPVRR	2055.2	R	N	0.0	0.0	103.0	11.5
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	SELEAFEVALENVRPTVEVK	2259.2	K	S	4.4	0.6	40.6	18.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	SFSHQAGASSKQPALGYLN	1963.0	R	-	5.1	0.6	45.7	17.6
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	5.0	0.6	35.5	15.7
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	STAESIVYSALETLAQR	1839.0	K	S	3.4	0.6	117.0	16.0
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	VGGSTYQVPVEVRPVR	1743.0	R	R	5.5	0.7	92.7	16.0
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	VGGSTYQVPVEVRPVRR	1899.1	R	N	4.7	0.0	64.8	14.9
P02359	20001.3	S	U	T	B	ETD	LIT	14	67.0	WIVEAAR	844.5	R	K	1.9	0.4	26.5	18.2
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	FGSELLAK	864.5	K	F	2.2	0.7	24.8	15.2
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	FVNILMVDGK	1135.6	K	K	1.4	0.7	12.1	15.1
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	FVNILMVDGKK	1263.7	K	S	4.4	0.6	46.4	13.4
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	LANELSDAAENK	1274.6	R	G	3.5	0.4	16.6	15.9
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	LANELSDAAENKGTAVK	1730.9	R	K	7.2	0.5	109.0	18.5
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	RVGGSTYQVPVEVRPVRR	2055.2	R	N	5.3	0.0	74.3	12.3
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	SELEAFEVALENVRPTVEVK	2259.2	K	S	5.4	0.6	0.0	0.0
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	SFSHQAGASSKQPALGYLN	1963.0	R	-	5.9	0.5	62.2	18.7
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	5.3	0.6	64.5	15.7
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	STAESIVYSALETLAQR	1839.0	K	S	6.1	0.6	86.3	16.0
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	VGGSTYQVPVEVRPVR	1743.0	R	R	3.7	0.5	69.1	16.0
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	VGGSTYQVPVEVRPVRR	1899.1	R	N	2.4	0.5	48.2	13.6
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	WIVEAAR	844.5	R	K	2.1	0.3	34.2	18.2
P02359	20001.3	S	U	T	C	ETD	LIT	14	69.8	WLSLR	674.4	R	S	1.7	0.0	33.0	18.0
P02359	20001.3	S	U	T	C	ETD	FT	4	17.3	FGSELLAK	864.5	K	F	0.0	0.0	30.2	15.8
P02359	20001.3	S	U	T	C	ETD	FT	4	17.3	RVGGSTYQVPVEVRPVRR	2055.2	R	N	1.6	0.0	68.5	11.5
P02359	20001.3	S	U	T	C	ETD	FT	4	17.3	VGGSTYQVPVEVRPVR	1743.0	R	R	2.7	0.0	71.1	14.8
P02359	20001.3	S	U	T	C	ETD	FT	4	17.3	WLSLR	674.4	R	S	1.0	0.3	24.2	18.0
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	FVNILMVDGKK	1263.7	K	S	0.0	0.0	29.3	13.2
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	LANELSDAAENKGTAVK	1731.9	R	K	0.0	0.0	23.0	18.1
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	RVGGSTYQVPVEVRPVRR	2055.2	R	N	0.0	0.0	18.3	11.8
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	SELEAFEVALENVRPTVEVK	2259.2	K	S	0.0	0.0	74.7	18.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	SFSHQAGASSK	1106.5	R	Q	0.0	0.0	38.4	12.8
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	0.0	0.0	67.1	15.6
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	STAESIVYSALETLAQR	1839.0	K	S	0.0	0.0	63.7	17.2
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	VGGSTYQVPVEVRPVR	1743.0	R	R	0.0	0.0	32.3	14.9
P02359	20001.3	S	U	T	B	ETD+CID	LIT	9	58.1	WIVEAAR	844.5	R	K	0.0	0.0	23.1	16.0
P02359	20001.3	S	U	T	A	ETD+CID	LIT	7	43.6	FVNILMVDGK	1135.6	K	K	3.8	0.5	46.4	14.6
P02359	20001.3	S	U	T	A	ETD+CID	LIT	7	43.6	FVNILMVDGKK	1263.7	K	S	3.4	0.5	35.3	13.0
P02359	20001.3	S	U	T	A	ETD+CID	LIT	7	43.6	SELEAFEVALENVRPTVEVK	2259.2	K	S	5.8	0.6	66.6	18.1
P02359	20001.3	S	U	T	A	ETD+CID	LIT	7	43.6	SFSHQAGASSK	1106.5	R	Q	3.2	0.6	60.9	12.8
P02359	20001.3	S	U	T	A	ETD+CID	LIT	7	43.6	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	0.0	0.0	63.7	15.1
P02359	20001.3	S	U	T	A	ETD+CID	LIT	7	43.6	STAESIVYSALETLAQR	1839.0	K	S	4.8	0.8	53.5	16.0
P02359	20001.3	S	U	T	A	ETD+CID	LIT	7	43.6	VGGSTYQVPVEVRPVR	1743.0	R	R	2.4	0.7	36.5	15.8
P02359	20001.3	S	U	T	B	ETD+CID	LIT	2	16.2	FVNILMVDGKK	1263.7	K	S	2.5	0.7	0.0	0.0
P02359	20001.3	S	U	T	B	ETD+CID	LIT	2	16.2	RVGGSTYQVPVEVRPVRR	2055.2	R	N	2.6	0.8	0.0	0.0
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	FVNILMVDGKK	1263.7	K	S	2.5	0.7	29.3	13.2
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	LANELSDAAENKGTAVK	1731.9	R	K	3.3	0.3	23.0	18.1
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	RVGGSTYQVPVEVRPVRR	2055.2	R	N	2.6	0.8	19.9	12.0
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	SELEAFEVALENVRPTVEVK	2259.2	K	S	5.8	0.7	74.7	18.1
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	SFSHQAGASSK	1106.5	R	Q	1.6	-0.4	38.4	12.8
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	6.8	0.0	67.1	15.6
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	STAESIVYSALETLAQR	1839.0	K	S	5.1	0.6	63.7	17.2
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	VGGSTYQVPVEVRPVR	1743.0	R	R	4.0	0.5	21.4	14.9
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	WIVEAAR	844.5	R	K	2.1	0.0	23.1	16.0
P02359	20001.3	S	U	T	B	ETD+CID	LIT	10	60.9	WLSLR	674.4	R	S	1.4	0.4	17.7	9.0
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	FGSELLAK	864.5	K	F	0.0	0.0	37.7	16.0
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	FVNILMVDGKK	1263.7	K	S	3.0	0.7	0.0	0.0
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	LANELSDAAENK	1274.6	R	G	4.4	0.6	61.0	16.0
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	RVGGSTYQVPVEVRPVRR	2055.2	R	N	2.0	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	SELEAFEVALENVRPTVEVK	2259.2	K	S	2.1	0.4	9.3	17.6
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	SFSHQAGASSK	1106.5	R	Q	1.5	0.3	33.6	12.8
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	6.2	0.7	61.3	15.3
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	STAESIVYSALETLAQR	1839.0	K	S	5.2	0.7	70.3	17.4
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	VGGSTYQVPVEVRPVR	1743.0	R	R	3.2	0.7	41.2	15.4
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	VGGSTYQVPVEVRPVRR	1899.1	R	N	4.1	0.0	60.1	14.0
P02359	20001.3	S	U	T	C	ETD+CID	LIT	11	59.8	WIVEAAR	844.5	R	K	2.5	0.3	16.0	18.2
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	FVNILMVDGKK	1263.7	K	S	0.0	0.0	29.3	13.2
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	LANELSDAAENKGTAVK	1731.9	R	K	0.0	0.0	23.0	18.1
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	RVGGSTYQVPVEVRPVRR	2055.2	R	N	0.0	0.0	18.3	11.8
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	SELEAFEVALENVRPTVEVK	2259.2	K	S	0.0	0.0	74.7	18.1
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	SFSHQAGASSK	1106.5	R	Q	0.0	0.0	38.4	12.8
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	SGKSELEAFEVALENVRPTVEVK	2531.3	R	S	0.0	0.0	61.9	15.2
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	STAESIVYSALETLAQR	1839.0	K	S	0.0	0.0	63.7	17.2
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	VGGSTYQVPVEVRPVR	1743.0	R	R	0.0	0.0	32.3	14.9
P02359	20001.3	S	U	T	B	HCD	FT	9	58.1	WIVEAAR	844.5	R	K	0.0	0.0	23.1	16.0
P02359	20001.3	S	U	T	B	HCD	FT	2	11.7	VGGSTYQVPVEVRPVR	1743.0	R	R	2.8	0.0	37.8	14.8
P02359	20001.3	S	U	T	B	HCD	FT	2	11.7	WLSLR	674.4	R	S	1.4	0.5	18.0	18.0
P64596	20009.7	G	U	T	A	CID	LIT	2	12.6	SQLLTSDLVK	1103.6	R	S	2.8	0.0	27.2	11.8
P64596	20009.7	G	U	T	A	CID	LIT	2	12.6	SVGTQVDDGTLEVR	1475.7	R	V	3.6	0.0	47.8	13.4
P64596	20009.7	G	T	T	A	CID	LIT	5	29.8	INVTAYQGK	993.5	R	V	2.1	0.7	29.6	14.8
P64596	20009.7	G	T	T	A	CID	LIT	5	29.8	SQLLTSDLVK	1103.6	R	S	2.1	0.4	7.3	11.8
P64596	20009.7	G	T	T	A	CID	LIT	5	29.8	SVGTQVDDGTLEVR	1475.7	R	V	4.0	0.6	63.0	12.8
P64596	20009.7	G	T	T	A	CID	LIT	5	29.8	VLLVGQSPNAELSAR	1553.9	K	A	3.9	0.0	57.4	8.5
P64596	20009.7	G	T	T	A	CID	LIT	5	29.8	VTTAFTFIK	1027.6	R	-	2.0	0.6	12.8	10.8
P64596	20009.7	G	U	A	B	CID	LIT	2	15.7	DTWITTKVRSQLLTS	1749.0	N	D	2.8	0.0	24.4	13.6
P64596	20009.7	G	U	A	B	CID	LIT	2	15.7	EIRQGQPIGLGEASN	1568.8	N	D	4.6	0.8	54.0	13.8
P64596	20009.7	S	U	T	A	CID	LIT	2	17.8	QGQPIGLGEASNDTWITTK	2016.0	R	V	4.3	0.8	58.2	18.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P64596	20009.7	S	U	T	A	CID	LIT	2	17.8	VLLVGQSPNAELSAR	1553.9	K	A	3.4	0.5	29.1	13.6
P64596	20009.7	S	U	T	C	CID	LIT	2	17.8	QGQPIGLGEASNDTWITTK	2016.0	R	V	4.7	0.6	65.4	18.1
P64596	20009.7	S	U	T	C	CID	LIT	2	17.8	VLLVGQSPNAELSAR	1553.9	K	A	3.2	0.8	43.7	14.1
P64596	20009.7	S	U	T	C	ETD	LIT	2	13.1	SQLLTSDLVK	1103.6	R	S	1.4	0.4	13.6	13.6
P64596	20009.7	S	U	T	C	ETD	LIT	2	13.1	VLLVGQSPNAELSAR	1553.9	K	A	2.3	0.0	46.4	13.6
P64596	20009.7	S	U	T	A	ETD+CID	LIT	2	17.8	QGQPIGLGEASNDTWITTK	2016.0	R	V	4.6	0.7	83.1	17.9
P64596	20009.7	S	U	T	A	ETD+CID	LIT	2	17.8	VLLVGQSPNAELSAR	1553.9	K	A	2.3	0.7	0.0	0.0
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	APLIITVVAK	1024.7	R	C	2.9	0.0	34.3	0.0
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	ASTSINVPDPTPFVTYF	1855.9	K	-	3.1	0.6	15.4	12.8
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	FSAVLEQGAIAAGSDDK	1678.8	R	A	5.2	0.0	72.1	13.2
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	FSAVLEQGAIAAGSDDKAIDK	2106.1	R	A	5.4	0.6	45.9	14.3
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	IVGFLYLGTPQLK	1448.9	K	A	3.5	0.0	25.5	7.0
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	LAEPAPTGEQLQNILR	1750.0	R	A	4.4	0.7	75.1	9.5
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	MDALELLINR	1187.6	-	R	3.6	0.0	66.8	12.6
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	SGALTESPVVR	1115.6	R	E	3.4	0.6	38.8	12.0
P0ACY1	20041.1	G	U	T	A	CID	LIT	9	61.7	SMQPWHFFVIEGEGR	1819.9	K	E	3.3	0.7	41.7	9.5
P0ACY1	20041.1	S	U	T	B	CID	LIT	3	22.4	LAEPAPTGEQLQNILR	1750.0	R	A	4.2	0.0	75.0	14.9
P0ACY1	20041.1	S	U	T	B	CID	LIT	3	22.4	MDALELLINR	1187.6	-	R	2.5	0.4	25.9	17.5
P0ACY1	20041.1	S	U	T	B	CID	LIT	3	22.4	SMQPWHFFVIEGEGR	1819.9	K	E	4.2	0.4	17.5	15.8
P0ACY1	20041.1	S	U	T	C	CID	LIT	3	23.0	LAEPAPTGEQLQNILR	1750.0	R	A	4.0	0.7	58.8	14.9
P0ACY1	20041.1	S	U	T	C	CID	LIT	3	23.0	MDALELLINRR	1343.7	-	S	2.4	0.1	19.7	17.5
P0ACY1	20041.1	S	U	T	C	CID	LIT	3	23.0	SMQPWHFFVIEGEGR	1819.9	K	E	2.7	0.1	25.8	15.7
P0ACY1	20041.1	S	U	T	A	ETD	LIT	2	14.8	LAEPAPTGEQLQNILR	1750.0	R	A	2.8	0.7	0.0	0.0
P0ACY1	20041.1	S	U	T	A	ETD	LIT	2	14.8	MDALELLINRR	1343.7	-	S	3.3	0.0	18.8	17.5
P0ACY1	20041.1	S	U	T	B	ETD	LIT	3	20.8	LAEPAPTGEQLQNILR	1750.0	R	A	0.0	0.0	44.6	14.8
P0ACY1	20041.1	S	U	T	B	ETD	LIT	3	20.8	MDALELLINRR	1343.7	-	S	3.0	0.4	16.0	16.4
P0ACY1	20041.1	S	U	T	B	ETD	LIT	3	20.8	SGALTESPVVR	1115.6	R	E	2.4	0.0	29.5	16.4
P0ACY1	20041.1	S	U	T	C	ETD	LIT	2	12.0	MDALELLINRR	1343.7	-	S	3.8	0.5	35.7	16.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACY1	20041.1	S	U	T	C	ETD	LIT	2	12.0	SGALTESPVVR	1115.6	R	E	2.3	0.3	17.9	16.4
P0ACY1	20041.1	S	U	T	B	ETD+CID	LIT	3	22.4	LAEPAPTGEQLQNILR	1750.0	R	A	0.0	0.0	78.7	14.9
P0ACY1	20041.1	S	U	T	B	ETD+CID	LIT	3	22.4	MDALELLINR	1187.6	-	R	0.0	0.0	34.4	16.1
P0ACY1	20041.1	S	U	T	B	ETD+CID	LIT	3	22.4	SMQPWHFFVIEGEGR	1819.9	K	E	0.0	0.0	25.4	15.8
P0ACY1	20041.1	S	U	T	B	ETD+CID	LIT	3	22.4	LAEPAPTGEQLQNILR	1750.0	R	A	4.0	0.8	78.7	14.9
P0ACY1	20041.1	S	U	T	B	ETD+CID	LIT	3	22.4	MDALELLINR	1187.6	-	R	2.9	0.5	34.4	16.1
P0ACY1	20041.1	S	U	T	B	ETD+CID	LIT	3	22.4	SMQPWHFFVIEGEGR	1819.9	K	E	3.5	0.4	25.4	15.8
P0ACY1	20041.1	S	U	T	C	ETD+CID	LIT	4	29.0	LAEPAPTGEQLQNILR	1750.0	R	A	3.7	0.7	66.9	14.9
P0ACY1	20041.1	S	U	T	C	ETD+CID	LIT	4	29.0	MDALELLINRR	1343.7	-	S	1.6	0.4	27.9	17.5
P0ACY1	20041.1	S	U	T	C	ETD+CID	LIT	4	29.0	SGALTESPVVR	1115.6	R	E	2.5	0.4	11.1	16.8
P0ACY1	20041.1	S	U	T	C	ETD+CID	LIT	4	29.0	SMQPWHFFVIEGEGR	1819.9	K	E	2.5	0.2	18.5	15.7
P0ACY1	20041.1	S	U	T	B	HCD	FT	3	22.4	LAEPAPTGEQLQNILR	1750.0	R	A	0.0	0.0	78.7	14.9
P0ACY1	20041.1	S	U	T	B	HCD	FT	3	22.4	MDALELLINR	1187.6	-	R	0.0	0.0	34.4	16.1
P0ACY1	20041.1	S	U	T	B	HCD	FT	3	22.4	SMQPWHFFVIEGEGR	1819.9	K	E	0.0	0.0	25.4	15.8
P77791	20078.0	G	U	T	A	CID	LIT	3	26.8	AVINPGVTIGDNVVVASGAVVTK	2180.2	R	D	6.0	0.0	112.0	4.8
P77791	20078.0	G	U	T	A	CID	LIT	3	26.8	DVPDNVVVGGNPAR	1408.7	K	I	3.6	0.0	41.6	12.8
P77791	20078.0	G	U	T	A	CID	LIT	3	26.8	YNHSLAEEHTLR	1469.7	R	Q	3.8	0.8	46.8	13.0
P0A9M2	20097.9	G	U	T	A	CID	LIT	7	43.3	EILSLREPK	1084.6	R	S	2.5	0.7	22.5	11.1
P0A9M2	20097.9	G	U	T	A	CID	LIT	7	43.3	GKDVLIVEDIIDSGNTLSK	2016.1	R	V	3.7	0.8	26.5	13.2
P0A9M2	20097.9	G	U	T	A	CID	LIT	7	43.3	HLPYIGK	827.5	R	V	2.1	0.6	11.3	11.5
P0A9M2	20097.9	G	U	T	A	CID	LIT	7	43.3	ILKDLDEDIR	1229.7	K	G	2.4	0.7	14.1	12.0
P0A9M2	20097.9	G	U	T	A	CID	LIT	7	43.3	MKHTVEVMIPEAEIK	1770.9	-	A	3.2	0.5	8.8	12.0
P0A9M2	20097.9	G	U	T	A	CID	LIT	7	43.3	YKDSGSDMVLVGLLR	1652.9	R	G	2.2	0.5	13.1	12.8
P0A9M2	20097.9	G	U	T	A	CID	LIT	7	43.3	YRHLPYIGK	1146.6	R	V	3.2	0.7	18.9	12.0
P67095	20104.0	G	U	A	A	CID	LIT	3	15.8	DQSIIAQVAINP	1268.7	N	-	2.4	0.2	18.1	14.0
P67095	20104.0	G	U	A	A	CID	LIT	3	15.8	DVLVYGHTHLPVA	1420.8	N	E	3.1	0.0	44.7	14.3
P67095	20104.0	G	U	A	A	CID	LIT	3	15.8	DVLVYGHTHLPVAEQRG	1891.0	N	E	3.1	0.3	9.5	13.2
P0ADV1	20108.7	G	U	T	A	CID	LIT	3	17.8	INADKVVVTRPGGEQGK	1768.0	K	E	3.9	0.0	30.3	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADV1	20108.7	G	U	T	A	CID	LIT	3	17.8	VTTVLVPSQLQDK	1427.8	R	N	3.1	0.0	31.6	9.5
P0ADV1	20108.7	G	U	T	A	CID	LIT	3	17.8	VTTVLVPSQLQDKNNK	1784.0	R	G	3.8	0.0	35.3	11.5
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	DFVVLTGNAYLQQVDSNIK	2124.1	K	G	5.1	0.0	87.9	12.3
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	DFVVLTGNAYLQQVDSNIKGDK	2424.2	K	I	5.9	0.5	72.8	12.3
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	GDKITYLVK	1036.6	K	E	2.5	0.7	12.4	9.5
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	INADKVVVTRPGGEQGK	1768.0	K	E	4.9	0.7	63.7	10.0
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	ITYLVKEQK	1121.7	K	M	2.9	0.8	43.2	7.8
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	MQAFSDK	826.4	K	G	1.9	0.3	10.1	11.1
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	MQAFSDKGK	1011.5	K	R	3.0	0.5	38.9	13.6
P0ADV1	20108.7	G	T	T	A	CID	LIT	8	30.8	VVVTRPGGEQGK	1226.7	K	E	3.5	0.4	41.3	11.1
P0ADV1	20108.7	G	U	A	A	CID	LIT	7	49.2	DGYGKPATFYQMQ	1521.7	I	D	3.6	0.7	52.7	9.0
P0ADV1	20108.7	G	U	A	A	CID	LIT	7	49.2	DKGKRVTTVLVPSQLQ	1769.0	S	D	2.4	0.5	16.4	8.5
P0ADV1	20108.7	G	U	A	A	CID	LIT	7	49.2	DKITYLVKEQKMQAFS	1929.0	G	D	3.5	0.9	0.0	0.0
P0ADV1	20108.7	G	U	A	A	CID	LIT	7	49.2	DKVVVTRPGGEQGKEVI	1811.0	A	D	4.3	0.5	40.1	13.6
P0ADV1	20108.7	G	U	A	A	CID	LIT	7	49.2	DNGKPVEGHASQMHY	1669.7	Q	E	2.8	0.8	44.1	11.1
P0ADV1	20108.7	G	U	A	A	CID	LIT	7	49.2	DNGKPVEGHASQMHYELAK	2111.0	Q	D	4.7	0.0	31.0	14.3
P0ADV1	20108.7	G	U	A	A	CID	LIT	7	49.2	DTDQPIHIES	1154.5	G	D	3.0	0.5	39.8	12.3
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DFVVLTGNAYLQQV	1566.8	K	D	4.3	0.6	43.4	13.0
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DFVVLTGNAYLQQVDSNIKG	2181.1	K	D	4.4	0.5	83.0	15.3
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DGYGKPATFYQMQ	1521.7	I	D	3.8	0.7	70.5	9.0
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DKITYLVKEQKMQAFS	1929.0	G	D	3.8	0.4	29.8	15.2
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DKVVVTRPGGEQGK	1469.8	A	E	4.2	0.6	52.4	14.3
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DKVVVTRPGGEQGKEVI	1811.0	A	D	4.0	0.4	30.7	13.6
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DNGKPVEGHASQMHY	1669.7	Q	E	2.7	0.6	31.9	9.5
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DQPIHIES	938.5	T	D	2.2	0.4	3.8	16.2
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DQPIHIESDQQSL	1509.7	T	D	3.4	0.4	13.7	15.7
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	DTDQPIHIES	1154.5	G	D	3.5	0.6	51.5	12.3
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	ELAKDFVVLTGNAYLQQV	2008.1	Y	D	3.9	0.8	27.8	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADV1	20108.7	G	T	A	A	CID	LIT	12	54.1	ELAKDFVVLTGNAYLQQVDSNIKG	2622.4	Y	D	3.5	0.0	20.3	15.4
P0ADV1	20108.7	G	T	T	B	CID	LIT	2	14.1	INADKVVVTRPGGEQGK	1768.0	K	E	3.4	0.2	20.8	8.5
P0ADV1	20108.7	G	T	T	B	CID	LIT	2	14.1	MQAFSDKGK	1011.5	K	R	3.0	0.5	40.2	13.6
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DFVVLTGNAYLQQV	1566.8	K	D	4.9	0.7	73.3	13.0
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DGYGKPATFYQMQ	1505.7	I	D	4.3	0.6	64.4	10.8
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DKITYLVKEQKMQAFS	1929.0	G	D	3.4	0.5	58.6	15.6
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DKVVVTRPGGEQGKEVI	1811.0	A	D	4.5	0.5	36.6	13.4
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DMQGNVVTFTGNVIVTQGTIKINA	2520.3	L	D	3.8	0.8	4.9	14.1
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DNGKPVEGHASQMHY	1669.7	Q	E	3.7	0.8	50.4	9.5
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DQPIHIES	938.5	T	D	1.5	0.4	11.6	15.6
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	DTDQPIHIES	1154.5	G	D	3.5	0.5	43.5	12.6
P0ADV1	20108.7	G	T	A	B	CID	LIT	9	61.1	ELAKDFVVLTGNAYLQQV	2008.1	Y	D	3.3	0.0	16.9	12.6
P0ADV1	20108.7	S	U	T	A	ETD	LIT	2	13.0	RVTTVLVPSQLQDKNNK	1940.1	K	G	3.9	0.2	32.5	13.2
P0ADV1	20108.7	S	U	T	A	ETD	LIT	2	13.0	VTTVLVPSQLQDKNNKGQTPAQK	2494.4	R	K	2.5	0.2	30.9	14.8
P0A6L9	20120.4	G	U	T	A	CID	LIT	2	11.7	SSAEQLEEK	1020.5	R	L	3.1	0.0	28.3	9.5
P0A6L9	20120.4	G	U	T	A	CID	LIT	2	11.7	YQLDTQALSLR	1307.7	R	F	3.3	0.5	45.9	13.0
_sp|P2	20193.8	G	T	T	B	CID	LIT	2	13.6	IMLPALLPQERR	1436.8	R	G	1.9	0.5	0.0	0.0
_sp|P2	20193.8	G	T	T	B	CID	LIT	2	13.6	LRYSHYDLLAR	1406.8	K	G	1.7	0.7	0.0	0.0
P0A9W9	20227.0	G	U	T	A	CID	LIT	2	15.2	LADDVGIWPLVVIR	1565.9	R	G	3.6	0.5	39.8	9.5
P0A9W9	20227.0	G	U	T	A	CID	LIT	2	15.2	TNIQDGSMLHVTHK	1580.8	R	S	4.3	0.7	51.7	10.0
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	ALLAAFDFPFRK	1395.8	R	-	3.0	0.8	24.5	9.5
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	EQIIFPEIDYDK	1509.7	R	V	2.7	0.0	22.8	11.1
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	EQIIFPEIDYDKVDR	1879.9	R	V	3.8	0.6	38.3	11.1
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	GLDITITTTAK	1133.6	R	S	3.9	0.0	71.9	12.3
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	GNYSMGVR	883.4	R	E	2.3	0.0	39.8	8.5
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	IRQGYPIGCK	1191.6	K	V	2.7	0.6	29.3	10.4
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	ITLNMGVGEAIADK	1431.8	K	K	4.1	0.6	57.0	11.8
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	ITLNMGVGEAIADKK	1559.8	K	L	4.0	0.6	88.7	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	KLLDNAAADLAAISGQKPLITK	2251.3	K	A	6.5	0.6	63.5	7.0
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	KLMTEFNYNSVMQVPR	1973.0	K	V	3.3	0.9	13.1	10.0
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	LHDYYKDEVVK	1408.7	K	K	3.7	0.8	38.6	12.0
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	LITIAVPR	882.6	R	I	2.7	0.2	33.0	9.5
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	LLDNAAADLAAISGQKPLITK	2123.2	K	A	5.5	0.0	72.6	4.8
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	LMTEFNYNSVMQVPR	1828.9	K	V	3.6	0.0	92.3	10.4
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	MWEFFER	1044.5	R	L	2.1	0.0	26.3	6.0
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	QGYPIGCK	922.4	R	V	2.2	0.7	26.4	12.6
P62399	20284.6	G	U	T	A	CID	LIT	17	77.7	SFDGRGNYSMGVR	1445.7	K	E	2.2	0.6	0.0	0.0
P62399	20284.6	G	U	T	B	CID	LIT	3	22.3	GLDITITTTAK	1133.6	R	S	3.4	0.8	34.6	13.8
P62399	20284.6	G	U	T	B	CID	LIT	3	22.3	GNYSMGVR	883.4	R	E	2.0	0.0	21.3	8.5
P62399	20284.6	G	U	T	B	CID	LIT	3	22.3	LLDNAAADLAAISGQKPLITK	2123.2	K	A	3.3	0.0	37.6	7.0
P62399	20284.6	G	U	A	B	CID	LIT	3	14.5	DEEGRALLAAF	1191.6	S	D	2.0	0.5	7.9	16.7
P62399	20284.6	G	U	A	B	CID	LIT	3	14.5	DITITTTAKS	1050.6	L	D	2.6	0.7	28.8	13.0
P62399	20284.6	G	U	A	B	CID	LIT	3	14.5	DKKLL	616.4	A	D	1.3	0.3	14.8	13.8
P62399	20284.6	S	U	T	A	CID	LIT	5	41.9	ALLAAFDFPFRK	1395.8	R	-	2.1	0.5	20.4	13.2
P62399	20284.6	S	U	T	A	CID	LIT	5	41.9	EQIIFPEIDYDKVDR	1879.9	R	V	3.5	0.5	28.6	16.8
P62399	20284.6	S	U	T	A	CID	LIT	5	41.9	LHDYYKDEVVKK	1536.8	K	L	3.0	0.4	22.0	14.0
P62399	20284.6	S	U	T	A	CID	LIT	5	41.9	LLDNAAADLAAISGQKPLITK	2123.2	K	A	5.3	0.0	81.3	9.5
P62399	20284.6	S	U	T	A	CID	LIT	5	41.9	LMTEFNYNSVMQVPR	1828.9	K	V	3.0	0.4	9.9	16.6
P62399	20284.6	S	U	T	B	CID	LIT	7	46.9	ALLAAFDFPFR	1267.7	R	-	1.8	0.8	0.0	0.0
P62399	20284.6	S	U	T	B	CID	LIT	7	46.9	EQIIFPEIDYDKVDR	1879.9	R	V	4.0	0.6	52.1	16.8
P62399	20284.6	S	U	T	B	CID	LIT	7	46.9	ITLNMGVGEAIADKK	1559.8	K	L	2.6	0.4	0.0	0.0
P62399	20284.6	S	U	T	B	CID	LIT	7	46.9	KLLDNAAADLAAISGQKPLITK	2251.3	K	A	2.4	0.0	25.4	4.8
P62399	20284.6	S	U	T	B	CID	LIT	7	46.9	LLDNAAADLAAISGQKPLITK	2123.2	K	A	5.3	0.6	62.3	10.0
P62399	20284.6	S	U	T	B	CID	LIT	7	46.9	LMTEFNYNSVMQVPR	1828.9	K	V	3.7	0.5	44.5	16.5
P62399	20284.6	S	U	T	B	CID	LIT	7	46.9	MWEFFER	1044.5	R	L	2.4	0.8	25.6	9.5
P62399	20284.6	S	U	T	C	CID	LIT	3	28.5	EQIIFPEIDYDKVDR	1879.9	R	V	3.2	0.5	18.2	16.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62399	20284.6	S	U	T	C	CID	LIT	3	28.5	LLDNAAADLAAISGQKPLITK	2123.2	K	A	5.0	0.6	76.7	10.0
P62399	20284.6	S	U	T	C	CID	LIT	3	28.5	LMTEFNYNSVMQVPR	1828.9	K	V	3.5	0.5	44.0	16.6
P62399	20284.6	S	U	T	B	CID	FT	2	12.3	EQIIFPEIDYDKVDR	1879.9	R	V	2.9	0.0	50.0	16.8
P62399	20284.6	S	U	T	B	CID	FT	2	12.3	MWEFFER	1044.5	R	L	2.1	0.0	41.4	9.5
P62399	20284.6	S	U	T	A	ETD	LIT	3	26.8	ALLAAFDFPFRK	1395.8	R	-	1.4	0.7	16.2	13.2
P62399	20284.6	S	U	T	A	ETD	LIT	3	26.8	EQIIFPEIDYDKVDR	1879.9	R	V	5.8	0.5	60.8	17.2
P62399	20284.6	S	U	T	A	ETD	LIT	3	26.8	LLDNAAADLAAISGQKPLITK	2123.2	K	A	3.4	0.0	23.9	10.4
P62399	20284.6	S	U	T	B	ETD	LIT	6	38.0	ALLAAFDFPFRK	1395.8	R	-	1.0	0.4	12.4	13.2
P62399	20284.6	S	U	T	B	ETD	LIT	6	38.0	EQIIFPEIDYDKVDR	1879.9	R	V	4.1	0.6	38.9	17.2
P62399	20284.6	S	U	T	B	ETD	LIT	6	38.0	EQIIFPEIDYDKVDRVR	2135.1	R	G	3.5	0.5	19.7	19.1
P62399	20284.6	S	U	T	B	ETD	LIT	6	38.0	KSVAGFK	736.4	R	I	1.2	0.5	22.0	12.8
P62399	20284.6	S	U	T	B	ETD	LIT	6	38.0	LHDYYKDEVVK	1408.7	K	K	2.6	0.3	25.8	15.9
P62399	20284.6	S	U	T	B	ETD	LIT	6	38.0	LLDNAAADLAAISGQKPLITK	2123.2	K	A	3.0	0.0	30.4	10.4
P62399	20284.6	S	U	T	C	ETD	LIT	4	31.3	ALLAAFDFPFRK	1395.8	R	-	3.7	0.0	38.7	12.3
P62399	20284.6	S	U	T	C	ETD	LIT	4	31.3	EQIIFPEIDYDKVDR	1879.9	R	V	4.7	0.5	57.8	17.2
P62399	20284.6	S	U	T	C	ETD	LIT	4	31.3	LITIAVPR	882.6	R	I	2.4	0.0	39.1	9.5
P62399	20284.6	S	U	T	C	ETD	LIT	4	31.3	LLDNAAADLAAISGQKPLITK	2123.2	K	A	5.7	0.0	58.0	12.3
P62399	20284.6	S	U	T	B	ETD+CID	LIT	3	28.5	EQIIFPEIDYDKVDR	1879.9	R	V	0.0	0.0	35.1	16.8
P62399	20284.6	S	U	T	B	ETD+CID	LIT	3	28.5	LLDNAAADLAAISGQKPLITK	2123.2	K	A	0.0	0.0	65.4	9.5
P62399	20284.6	S	U	T	B	ETD+CID	LIT	3	28.5	LMTEFNYNSVMQVPR	1828.9	K	V	0.0	0.0	53.8	16.6
P62399	20284.6	S	U	T	A	ETD+CID	LIT	4	31.3	ALLAAFDFPFRK	1395.8	R	-	3.1	0.8	34.8	13.2
P62399	20284.6	S	U	T	A	ETD+CID	LIT	4	31.3	EQIIFPEIDYDKVDR	1879.9	R	V	3.9	0.6	53.8	16.8
P62399	20284.6	S	U	T	A	ETD+CID	LIT	4	31.3	LITIAVPR	882.6	R	I	2.3	0.3	34.9	9.5
P62399	20284.6	S	U	T	A	ETD+CID	LIT	4	31.3	LLDNAAADLAAISGQKPLITK	2123.2	K	A	5.4	0.0	89.6	10.0
P62399	20284.6	S	U	T	B	ETD+CID	LIT	3	28.5	EQIIFPEIDYDKVDR	1879.9	R	V	3.5	0.4	35.1	16.8
P62399	20284.6	S	U	T	B	ETD+CID	LIT	3	28.5	LLDNAAADLAAISGQKPLITK	2123.2	K	A	4.1	0.5	65.4	9.5
P62399	20284.6	S	U	T	B	ETD+CID	LIT	3	28.5	LMTEFNYNSVMQVPR	1828.9	K	V	3.8	0.5	53.8	16.6
P62399	20284.6	S	U	T	C	ETD+CID	LIT	4	35.2	ALLAAFDFPFRK	1395.8	R	-	2.6	0.8	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P62399	20284.6	S	U	T	C	ETD+CID	LIT	4	35.2	EQIIFPEIDYDKVDR	1879.9	R	V	3.6	0.5	53.9	16.8
P62399	20284.6	S	U	T	C	ETD+CID	LIT	4	35.2	LLDNAAADLAAISGQKPLITK	2123.2	K	A	5.2	0.7	54.6	9.5
P62399	20284.6	S	U	T	C	ETD+CID	LIT	4	35.2	LMTEFNYNSVMQVPR	1828.9	K	V	3.4	0.4	36.9	16.5
P62399	20284.6	S	U	T	B	HCD	FT	3	28.5	EQIIFPEIDYDKVDR	1879.9	R	V	0.0	0.0	35.1	16.8
P62399	20284.6	S	U	T	B	HCD	FT	3	28.5	LLDNAAADLAAISGQKPLITK	2123.2	K	A	0.0	0.0	65.4	9.5
P62399	20284.6	S	U	T	B	HCD	FT	3	28.5	LMTEFNYNSVMQVPR	1828.9	K	V	0.0	0.0	53.8	16.6
P0AFY8	20297.8	G	U	T	A	CID	LIT	4	28.2	ELLLSDEYAEQKR	1593.8	R	A	2.6	0.6	16.9	11.5
P0AFY8	20297.8	G	U	T	A	CID	LIT	4	28.2	FSAASQPAAPVTK	1274.7	K	E	3.2	0.0	59.8	15.2
P0AFY8	20297.8	G	U	T	A	CID	LIT	4	28.2	HIGESASDILRR	1353.7	K	M	2.6	0.7	12.6	11.5
P0AFY8	20297.8	G	U	T	A	CID	LIT	4	28.2	VASPAIVEAKPVK	1308.8	R	T	3.2	0.0	49.5	3.0
P65556	20357.3	G	U	T	A	CID	LIT	4	30.0	ALALWMK	832.5	K	R	2.3	0.0	21.5	15.9
P65556	20357.3	G	U	T	A	CID	LIT	4	30.0	ATYIVVHDGMGK	1290.7	R	I	3.2	0.0	33.7	13.4
P65556	20357.3	G	U	T	A	CID	LIT	4	30.0	LASTEWVDIVNEENEVIAQASR	2473.2	R	E	4.7	0.7	79.6	11.5
P65556	20357.3	G	U	T	A	CID	LIT	4	30.0	NAKNEAVETETAE	1405.6	R	-	3.5	0.0	45.0	7.0
P39187	20402.9	G	U	T	A	CID	LIT	2	15.2	DGALTPEEVQQVMDLLQK	2014.0	K	L	3.4	0.5	34.8	14.8
P39187	20402.9	G	U	T	A	CID	LIT	2	15.2	TWNSAQLVGK	1103.6	K	V	3.0	0.6	22.3	13.2
P39187	20402.9	G	T	T	A	CID	LIT	7	48.4	DGALTPEEVQQVMDLLQK	2014.0	K	L	4.2	0.9	58.2	14.8
P39187	20402.9	G	T	T	A	CID	LIT	7	48.4	EKNATLIEAIK	1229.7	K	S	2.6	0.6	11.8	12.3
P39187	20402.9	G	T	T	A	CID	LIT	7	48.4	GELVLDKDQFSYK	1541.8	R	T	4.1	0.5	53.8	12.8
P39187	20402.9	G	T	T	A	CID	LIT	7	48.4	SAKLPHDR	923.5	K	Y	1.4	0.5	18.4	11.1
P39187	20402.9	G	T	T	A	CID	LIT	7	48.4	TWNSAQLVGK	1103.6	K	V	3.2	0.7	54.0	13.2
P39187	20402.9	G	T	T	A	CID	LIT	7	48.4	VLQHIAGR	893.5	R	T	2.8	0.8	55.6	8.5
P39187	20402.9	G	T	T	A	CID	LIT	7	48.4	YQTTTIVNTDDAIPGSGMFVR	2286.1	R	S	3.8	0.0	64.5	13.2
P39187	20402.9	G	T	A	A	CID	LIT	2	13.0	DRYQTTTIVNTD	1426.7	H	D	2.9	0.4	25.6	15.6
P39187	20402.9	G	T	A	A	CID	LIT	2	13.0	DSNGVALGAWQL	1230.6	V	D	2.0	0.5	6.9	15.8
P39187	20402.9	G	T	T	B	CID	LIT	2	9.2	NATLIEAIK	972.6	K	S	2.3	0.7	30.5	13.6
P39187	20402.9	G	T	T	B	CID	LIT	2	9.2	VLQHIAGR	893.5	R	T	3.0	0.8	52.2	9.0
P39187	20402.9	G	T	A	B	CID	LIT	3	15.2	DGRVQWAK	959.5	K	D	2.0	0.5	15.2	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P39187	20402.9	G	T	A	B	CID	LIT	3	15.2	DLLQKLLK	970.6	M	-	2.5	0.0	42.4	0.0
P39187	20402.9	G	T	A	B	CID	LIT	3	15.2	DRYQTTTIVNTD	1426.7	H	D	3.1	0.7	31.9	15.6
P39187	20402.9	S	U	T	B	CID	LIT	4	31.5	LPHDRYQTTTIVNTDDAIPGSGMFVR	2904.4	K	S	2.8	0.0	25.4	19.6
P39187	20402.9	S	U	T	B	CID	LIT	4	31.5	TWNSAQLVGK	1103.6	K	V	2.7	0.4	36.2	17.2
P39187	20402.9	S	U	T	B	CID	LIT	4	31.5	VPPIGITDRGELVLDKDQFSYK	2490.3	R	T	3.6	0.4	11.3	17.2
P39187	20402.9	S	U	T	B	CID	LIT	4	31.5	YQTTTIVNTDDAIPGSGMFVR	2286.1	R	S	4.1	0.7	49.8	18.4
P39187	20402.9	S	U	T	C	CID	LIT	4	33.2	LPHDRYQTTTIVNTDDAIPGSGMFVR	2904.4	K	S	3.9	0.6	12.6	20.1
P39187	20402.9	S	U	T	C	CID	LIT	4	33.2	SAKLPHDRYQTTTIVNTDDAIPGSGMFVR	3190.6	K	S	3.3	0.7	20.6	18.6
P39187	20402.9	S	U	T	C	CID	LIT	4	33.2	TWNSAQLVGK	1103.6	K	V	2.8	0.5	29.9	17.4
P39187	20402.9	S	U	T	C	CID	LIT	4	33.2	VPPIGITDRGELVLDKDQFSYK	2490.3	R	T	3.7	0.6	27.3	17.2
P39187	20402.9	S	U	T	B	ETD	LIT	2	15.8	DGALTPEEVQQVMDLLQK	2014.0	K	L	3.3	0.4	12.9	18.6
P39187	20402.9	S	U	T	B	ETD	LIT	2	15.8	EKNATLIEAIK	1229.7	K	S	2.6	0.1	10.0	15.1
P39187	20402.9	S	U	T	B	ETD+CID	LIT	2	14.1	LPHDRYQTTTIVNTDDAIPGSGMFVR	2904.4	K	S	0.0	0.0	19.5	19.7
P39187	20402.9	S	U	T	B	ETD+CID	LIT	2	14.1	YQTTTIVNTDDAIPGSGMFVR	2286.1	R	S	0.0	0.0	27.6	18.4
P39187	20402.9	S	U	T	B	ETD+CID	LIT	3	19.0	LPHDRYQTTTIVNTDDAIPGSGMFVR	2904.4	K	S	4.6	0.0	19.5	19.7
P39187	20402.9	S	U	T	B	ETD+CID	LIT	3	19.0	NATLIEAIK	972.6	K	S	2.6	0.5	17.4	17.2
P39187	20402.9	S	U	T	B	ETD+CID	LIT	3	19.0	YQTTTIVNTDDAIPGSGMFVR	2286.1	R	S	4.0	0.6	27.6	18.4
P39187	20402.9	S	U	T	C	ETD+CID	LIT	6	38.0	LPHDRYQTTTIVNTDDAIPGSGMFVR	2904.4	K	S	4.6	0.9	19.8	20.0
P39187	20402.9	S	U	T	C	ETD+CID	LIT	6	38.0	NATLIEAIK	972.6	K	S	2.6	0.4	17.1	17.2
P39187	20402.9	S	U	T	C	ETD+CID	LIT	6	38.0	SAKLPHDRYQTTTIVNTDDAIPGSGMFVR	3190.6	K	S	5.0	0.8	47.5	18.8
P39187	20402.9	S	U	T	C	ETD+CID	LIT	6	38.0	TWNSAQLVGK	1103.6	K	V	2.9	0.6	0.0	0.0
P39187	20402.9	S	U	T	C	ETD+CID	LIT	6	38.0	VPPIGITDRGELVLDKDQFSYK	2490.3	R	T	3.6	0.5	32.0	17.2
P39187	20402.9	S	U	T	C	ETD+CID	LIT	6	38.0	YQTTTIVNTDDAIPGSGMFVR	2286.1	R	S	4.0	0.0	57.1	19.0
P39187	20402.9	S	U	T	B	HCD	FT	2	14.1	LPHDRYQTTTIVNTDDAIPGSGMFVR	2904.4	K	S	0.0	0.0	19.5	19.7
P39187	20402.9	S	U	T	B	HCD	FT	2	14.1	YQTTTIVNTDDAIPGSGMFVR	2286.1	R	S	0.0	0.0	27.6	18.4
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	APVSVQNFVDYVNSGFYNNTTFHR	2776.3	K	V	6.5	0.0	88.1	10.8
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	DFGYAVFGK	1003.5	R	V	2.9	0.7	27.5	9.0
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	4.4	0.0	40.0	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	GTIAMAR	719.4	R	T	1.9	0.8	33.0	14.8
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	4.6	0.0	23.9	7.0
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	KPNPPIKNEADNGLR	1662.9	K	N	4.3	0.9	43.7	11.1
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	6.5	0.8	60.9	10.8
P0AFL3	20413.3	G	U	T	A	CID	LIT	8	70.0	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	3.3	0.7	17.4	14.1
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	APVSVQNFVDYVNSGFYNNTTFHR	2776.3	K	V	5.1	0.0	50.0	10.8
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	DFGYAVFGK	1003.5	R	V	3.0	0.8	27.6	9.0
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	4.9	0.0	24.1	8.5
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	5.6	0.0	46.8	7.0
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	KPNPPIK	793.5	K	N	1.9	0.7	16.1	7.8
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	KPNPPIKNEADNGLR	1662.9	K	N	4.5	0.7	66.8	10.8
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	5.7	0.0	34.4	10.8
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	5.3	0.9	75.1	13.6
P0AFL3	20413.3	G	T	T	A	CID	LIT	9	67.9	VVKGMDVADK	1077.6	K	I	2.1	0.7	3.7	14.6
P0AFL3	20413.3	G	U	A	A	CID	LIT	5	37.4	DFGYAVFGKVVKGMDVA	1802.9	R	D	4.1	0.0	37.0	16.7
P0AFL3	20413.3	G	U	A	A	CID	LIT	5	37.4	DKISQVPTH	1024.5	A	D	3.2	0.8	38.0	11.8
P0AFL3	20413.3	G	U	A	A	CID	LIT	5	37.4	DKQKAPVSVQNFV	1459.8	L	D	4.4	0.5	38.5	14.8
P0AFL3	20413.3	G	U	A	A	CID	LIT	5	37.4	DNAFLDHGQR	1172.5	A	D	3.3	0.8	35.0	11.5
P0AFL3	20413.3	G	U	A	A	CID	LIT	5	37.4	DVGPYQNVPSKPVVILSAKVLP	2320.3	H	-	2.4	0.5	0.0	0.0
P0AFL3	20413.3	G	T	A	A	CID	LIT	4	30.5	DFGYAVFGKVVKGMDVA	1802.9	R	D	3.3	0.0	17.6	16.9
P0AFL3	20413.3	G	T	A	A	CID	LIT	4	30.5	DKISQVPTH	1024.5	A	D	3.3	0.8	44.0	11.8
P0AFL3	20413.3	G	T	A	A	CID	LIT	4	30.5	DNAFLDHGQR	1172.5	A	D	2.8	0.0	36.8	12.0
P0AFL3	20413.3	G	T	A	A	CID	LIT	4	30.5	DVGPYQNVPSKPVVILSAKVLP	2320.3	H	-	2.1	0.6	10.9	11.1
P0AFL3	20413.3	G	T	T	B	CID	LIT	5	36.8	GTIAMAR	719.4	R	T	1.8	0.4	30.2	15.3
P0AFL3	20413.3	G	T	T	B	CID	LIT	5	36.8	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	6.2	0.0	31.4	7.0
P0AFL3	20413.3	G	T	T	B	CID	LIT	5	36.8	KPNPPIKNEADNGLR	1662.9	K	N	5.0	0.8	61.7	12.0
P0AFL3	20413.3	G	T	T	B	CID	LIT	5	36.8	NTRGTIAMAR	1090.6	R	T	2.2	0.7	16.0	12.8
P0AFL3	20413.3	G	T	T	B	CID	LIT	5	36.8	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	5.5	0.0	77.0	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFL3	20413.3	G	T	A	B	CID	LIT	6	41.1	DFGYAVFGKVVKGM	1517.8	R	D	2.9	0.8	12.0	15.1
P0AFL3	20413.3	G	T	A	B	CID	LIT	6	41.1	DFGYAVFGKVVKGMDVA	1802.9	R	D	2.7	0.6	1.8	16.9
P0AFL3	20413.3	G	T	A	B	CID	LIT	6	41.1	DKISQVPTH	1024.5	A	D	3.2	0.8	37.8	11.8
P0AFL3	20413.3	G	T	A	B	CID	LIT	6	41.1	DKQKAPVSVQNFV	1459.8	L	D	3.3	0.0	43.1	14.8
P0AFL3	20413.3	G	T	A	B	CID	LIT	6	41.1	DNGLRNTRGTIAMARTA	1817.9	A	D	2.0	0.8	11.4	15.8
P0AFL3	20413.3	G	T	A	B	CID	LIT	6	41.1	DVGPYQNVPSKPVVILSAKVLP	2320.3	H	-	2.4	0.7	0.0	0.0
P0AFL3	20413.3	G	U	A	B	CID	LIT	4	29.5	DKISQVPTH	1024.5	A	D	2.4	0.6	14.7	11.8
P0AFL3	20413.3	G	U	A	B	CID	LIT	4	29.5	DKQKAPVSVQNFV	1459.8	L	D	3.1	0.4	17.2	14.8
P0AFL3	20413.3	G	U	A	B	CID	LIT	4	29.5	DSATSQFFINVA	1299.6	K	D	1.9	0.7	16.5	13.4
P0AFL3	20413.3	G	U	A	B	CID	LIT	4	29.5	DVGPYQNVPSKPVVILSAKVLP	2320.3	H	-	2.6	0.6	4.1	11.1
P0AFL3	20413.3	S	U	T	A	CID	LIT	7	66.3	APVSVQNFVDYVNSGFYNNTTFHR	2777.3	K	V	4.7	0.5	37.1	17.2
P0AFL3	20413.3	S	U	T	A	CID	LIT	7	66.3	DFGYAVFGK	1003.5	R	V	2.7	0.7	23.7	14.3
P0AFL3	20413.3	S	U	T	A	CID	LIT	7	66.3	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	5.0	0.6	23.0	16.3
P0AFL3	20413.3	S	U	T	A	CID	LIT	7	66.3	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	4.2	0.6	24.8	13.6
P0AFL3	20413.3	S	U	T	A	CID	LIT	7	66.3	KPNPPIKNEADNGLR	1662.9	K	N	3.8	0.0	67.8	15.6
P0AFL3	20413.3	S	U	T	A	CID	LIT	7	66.3	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	4.0	0.3	5.4	19.0
P0AFL3	20413.3	S	U	T	A	CID	LIT	7	66.3	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	4.4	0.7	49.6	18.2
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	APVSVQNFVDYVNSGFYNNTTFHR	2777.3	K	V	5.7	0.6	85.0	16.6
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	DFGYAVFGK	1003.5	R	V	2.7	0.6	29.4	14.3
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	4.7	0.0	39.7	15.8
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	5.4	0.0	38.2	13.4
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	KPNPPIKNEADNGLR	1662.9	K	N	4.7	0.6	70.8	14.5
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	QKAPVSVQNFVDYVNSGFYNNTTFHR	3032.5	K	V	3.6	0.0	30.7	18.6
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	5.9	0.6	55.8	19.0
P0AFL3	20413.3	S	U	T	B	CID	LIT	8	67.4	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	4.8	0.7	56.1	18.1
P0AFL3	20413.3	S	U	T	C	CID	LIT	7	66.3	APVSVQNFVDYVNSGFYNNTTFHR	2776.3	K	V	6.0	0.6	75.3	17.9
P0AFL3	20413.3	S	U	T	C	CID	LIT	7	66.3	DFGYAVFGK	1003.5	R	V	2.4	0.6	17.5	14.3
P0AFL3	20413.3	S	U	T	C	CID	LIT	7	66.3	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	6.2	0.0	35.9	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFL3	20413.3	S	U	T	C	CID	LIT	7	66.3	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	3.8	0.0	34.8	12.8
P0AFL3	20413.3	S	U	T	C	CID	LIT	7	66.3	KPNPPIKNEADNGLR	1662.9	K	N	4.2	0.6	57.0	15.6
P0AFL3	20413.3	S	U	T	C	CID	LIT	7	66.3	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	5.3	0.5	23.7	19.0
P0AFL3	20413.3	S	U	T	C	CID	LIT	7	66.3	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	4.8	0.7	59.3	18.3
P0AFL3	20413.3	S	U	T	A	ETD	LIT	4	30.0	DFGYAVFGK	1003.5	R	V	2.3	0.0	24.2	14.3
P0AFL3	20413.3	S	U	T	A	ETD	LIT	4	30.0	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	0.0	0.0	38.8	16.2
P0AFL3	20413.3	S	U	T	A	ETD	LIT	4	30.0	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	4.2	0.0	33.7	13.8
P0AFL3	20413.3	S	U	T	A	ETD	LIT	4	30.0	KPNPPIKNEADNGLR	1662.9	K	N	5.6	0.0	46.9	15.6
P0AFL3	20413.3	S	U	T	B	ETD	LIT	5	42.6	APVSVQNFVDYVNSGFYNNTTFHR	2776.3	K	V	0.0	0.0	57.8	17.8
P0AFL3	20413.3	S	U	T	B	ETD	LIT	5	42.6	DFGYAVFGK	1003.5	R	V	3.1	0.7	32.1	14.3
P0AFL3	20413.3	S	U	T	B	ETD	LIT	5	42.6	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	0.0	0.0	46.0	15.9
P0AFL3	20413.3	S	U	T	B	ETD	LIT	5	42.6	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	4.4	0.0	48.9	13.8
P0AFL3	20413.3	S	U	T	B	ETD	LIT	5	42.6	KPNPPIKNEADNGLR	1662.9	K	N	5.6	0.6	53.4	16.7
P0AFL3	20413.3	S	U	T	C	ETD	LIT	4	38.9	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	0.0	0.0	49.9	16.2
P0AFL3	20413.3	S	U	T	C	ETD	LIT	4	38.9	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	3.8	0.0	17.5	13.8
P0AFL3	20413.3	S	U	T	C	ETD	LIT	4	38.9	KPNPPIKNEADNGLR	1662.9	K	N	5.6	0.6	47.7	16.8
P0AFL3	20413.3	S	U	T	C	ETD	LIT	4	38.9	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	6.1	0.0	67.1	18.9
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	4	38.9	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	0.0	0.0	36.6	15.8
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	4	38.9	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	0.0	0.0	62.1	14.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	4	38.9	KPNPPIKNEADNGLR	1662.9	K	N	0.0	0.0	56.1	15.3
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	4	38.9	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	0.0	0.0	77.9	19.1
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	APVSVQNFVDYVNSGFYNNTTFHR	2777.3	K	V	0.0	0.0	74.8	17.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	DFGYAVFGK	1003.5	R	V	0.0	0.0	30.0	14.3
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	0.0	0.0	36.6	15.8
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	0.0	0.0	62.1	14.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	KPNPPIKNEADNGLR	1662.9	K	N	0.0	0.0	94.1	16.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	QKAPVSVQNFVDYVNSGFYNNTTFHR	3032.5	K	V	0.0	0.0	20.4	18.5
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	0.0	0.0	77.9	19.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	0.0	0.0	57.9	18.3
P0AFL3	20413.3	S	U	T	A	ETD+CID	LIT	5	45.8	DFGYAVFGK	1003.5	R	V	1.8	0.4	6.0	14.3
P0AFL3	20413.3	S	U	T	A	ETD+CID	LIT	5	45.8	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	5.4	0.0	36.8	15.9
P0AFL3	20413.3	S	U	T	A	ETD+CID	LIT	5	45.8	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	4.3	0.6	24.7	14.1
P0AFL3	20413.3	S	U	T	A	ETD+CID	LIT	5	45.8	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	6.0	0.6	40.6	18.9
P0AFL3	20413.3	S	U	T	A	ETD+CID	LIT	5	45.8	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	4.3	0.6	65.8	18.2
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	5	52.6	APVSVQNFVDYVNSGFYNNTTFHR	2777.3	K	V	5.7	0.7	0.0	0.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	5	52.6	DFGYAVFGK	1003.5	R	V	2.9	0.6	0.0	0.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	5	52.6	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	5.9	0.9	0.0	0.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	5	52.6	KPNPPIKNEADNGLR	1663.9	K	N	4.8	0.7	0.0	0.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	5	52.6	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	4.9	0.9	0.0	0.0
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	APVSVQNFVDYVNSGFYNNTTFHR	2777.3	K	V	6.6	0.6	70.3	16.8
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	DFGYAVFGK	1003.5	R	V	2.9	0.6	30.0	14.3
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	2.7	0.4	23.2	16.5
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	5.9	0.9	27.6	14.1
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	KPNPPIKNEADNGLR	1663.9	K	N	4.8	0.7	49.7	16.6
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	QKAPVSVQNFVDYVNSGFYNNTTFHR	3032.5	K	V	4.0	0.0	20.4	18.5
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	0.9	-0.9	77.9	19.1
P0AFL3	20413.3	S	U	T	B	ETD+CID	LIT	8	67.4	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	5.4	0.7	57.9	18.3
P0AFL3	20413.3	S	U	T	C	ETD+CID	LIT	6	53.7	DFGYAVFGK	1003.5	R	V	3.0	0.6	20.8	14.3
P0AFL3	20413.3	S	U	T	C	ETD+CID	LIT	6	53.7	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	6.0	0.7	0.0	0.0
P0AFL3	20413.3	S	U	T	C	ETD+CID	LIT	6	53.7	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	3.1	0.0	25.3	14.3
P0AFL3	20413.3	S	U	T	C	ETD+CID	LIT	6	53.7	KPNPPIKNEADNGLR	1662.9	K	N	4.4	0.6	56.8	16.0
P0AFL3	20413.3	S	U	T	C	ETD+CID	LIT	6	53.7	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	5.2	0.6	26.6	19.3
P0AFL3	20413.3	S	U	T	C	ETD+CID	LIT	6	53.7	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	4.1	0.5	0.0	0.0
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	APVSVQNFVDYVNSGFYNNTTFHR	2777.3	K	V	0.0	0.0	74.8	17.0
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	DFGYAVFGK	1003.5	R	V	0.0	0.0	30.0	14.3
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	GMDVADKISQVPTHDVGPYQNVPSKPVVILSAK	3489.8	K	V	0.0	0.0	43.9	16.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	ISQVPTHDVGPYQNVPSKPVVILSAK	2773.5	K	V	0.0	0.0	27.6	14.1
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	KPNPPIKNEADNGLR	1662.9	K	N	0.0	0.0	94.1	16.0
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	QKAPVSVQNFVDYVNSGFYNNTTFHR	3032.5	K	V	0.0	0.0	20.4	18.5
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	TADKDSATSQFFINVADNAFLDHGQR	2868.4	R	D	0.0	0.0	66.6	18.9
P0AFL3	20413.3	S	U	T	B	HCD	FT	8	67.4	VIPGFMIQGGGFTEQMQQK	2096.0	R	K	0.0	0.0	57.9	18.3
P0ADI7	20434.5	G	U	T	A	CID	LIT	2	17.0	ASGQPVFLVR	1073.6	R	V	3.2	0.7	32.8	14.0
P0ADI7	20434.5	G	U	T	A	CID	LIT	2	17.0	VGWSADYAEALKQPVDAPSPAK	2300.2	R	V	4.3	0.0	48.4	12.0
P0ADI7	20434.5	G	T	T	A	CID	LIT	3	21.8	ASGQPVFLVR	1073.6	R	V	3.4	0.6	43.1	13.8
P0ADI7	20434.5	G	T	T	A	CID	LIT	3	21.8	SVEEILNAL	987.5	R	-	2.1	0.3	25.7	14.3
P0ADI7	20434.5	G	T	T	A	CID	LIT	3	21.8	VGWSADYAEALKQPVDAPSPAK	2300.2	R	V	5.1	0.6	56.5	11.1
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	ATPVELDFSQVEK	1462.7	R	-	3.6	0.0	60.0	12.8
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	ATPVELDFSQVEKA	1533.8	R	-	4.7	0.9	87.3	12.3
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	LHNMEDLFGEVMVPTEEVVEIR	2586.3	K	G	4.1	0.5	32.2	11.1
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	LQQVGDKPRPK	1265.7	R	T	3.3	0.0	40.2	9.5
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	TLFEPGEMVR	1178.6	K	V	2.5	0.8	17.0	13.0
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	VATSLREHIK	1153.7	R	L	1.9	0.5	24.4	9.5
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	2.5	0.7	15.6	13.2
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	4.2	0.0	50.0	7.8
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	VSVSIFGR	864.5	K	A	2.0	0.0	35.8	15.6
P0AFG0	20513.0	G	U	T	A	CID	LIT	10	74.0	WYVVQAFSGFEGR	1545.7	R	V	3.5	0.0	55.4	12.8
P0AFG0	20513.0	G	U	A	A	CID	LIT	2	12.2	DAIMNRLQQVG	1244.6	V	D	2.2	0.7	23.2	13.8
P0AFG0	20513.0	G	U	A	A	CID	LIT	2	12.2	DRPAPISDKEV	1226.6	S	D	2.3	0.5	21.4	13.8
P0AFG0	20513.0	G	T	T	B	CID	LIT	6	45.9	ATPVELDFSQVEKA	1533.8	R	-	4.4	0.8	69.9	12.3
P0AFG0	20513.0	G	T	T	B	CID	LIT	6	45.9	LQQVGDKPRPK	1265.7	R	T	3.3	0.6	35.8	9.5
P0AFG0	20513.0	G	T	T	B	CID	LIT	6	45.9	TLFEPGEMVR	1178.6	K	V	2.6	0.7	20.9	13.2
P0AFG0	20513.0	G	T	T	B	CID	LIT	6	45.9	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	4.9	0.7	59.0	13.2
P0AFG0	20513.0	G	T	T	B	CID	LIT	6	45.9	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	5.0	0.0	117.0	8.5
P0AFG0	20513.0	G	T	T	B	CID	LIT	6	45.9	VNDGPFADFNGVVEEVDYEKSR	2486.1	R	L	4.1	0.0	33.7	10.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFG0	20513.0	G	T	A	B	CID	LIT	5	26.5	DAIMNRLQQVG	1244.6	V	D	2.4	0.7	36.0	14.8
P0AFG0	20513.0	G	T	A	B	CID	LIT	5	26.5	DFSQVEKA	923.4	L	-	2.3	0.6	21.4	15.8
P0AFG0	20513.0	G	T	A	B	CID	LIT	5	26.5	DKPRPKTLFEPGEMVRVN	2113.1	G	D	2.9	0.5	34.9	15.2
P0AFG0	20513.0	G	T	A	B	CID	LIT	5	26.5	DRPAPIS	755.4	S	D	1.4	0.5	18.1	9.5
P0AFG0	20513.0	G	T	A	B	CID	LIT	5	26.5	DRPAPISDKEV	1226.6	S	D	3.0	0.6	61.6	13.6
P0AFG0	20513.0	G	U	A	B	CID	LIT	2	12.2	DAIMNRLQQVG	1244.6	V	D	2.7	0.0	36.6	15.4
P0AFG0	20513.0	G	U	A	B	CID	LIT	2	12.2	DRPAPISDKEV	1226.6	S	D	2.0	0.0	18.4	13.6
P0AFG0	20513.0	S	U	T	A	CID	LIT	3	31.5	LQQVGDKPRPK	1265.7	R	T	1.9	0.7	0.0	0.0
P0AFG0	20513.0	S	U	T	A	CID	LIT	3	31.5	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	3.8	0.8	25.0	19.5
P0AFG0	20513.0	S	U	T	A	CID	LIT	3	31.5	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	5.0	0.0	80.1	14.9
P0AFG0	20513.0	S	U	T	B	CID	LIT	3	31.5	LQQVGDKPRPK	1265.7	R	T	2.0	0.7	6.4	11.5
P0AFG0	20513.0	S	U	T	B	CID	LIT	3	31.5	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	3.9	0.7	23.9	19.4
P0AFG0	20513.0	S	U	T	B	CID	LIT	3	31.5	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	4.9	0.0	80.0	14.8
P0AFG0	20513.0	S	U	T	C	CID	LIT	4	40.3	ATPVELDFSQVEKA	1533.8	R	-	2.0	0.3	7.0	17.7
P0AFG0	20513.0	S	U	T	C	CID	LIT	4	40.3	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	4.8	0.5	40.9	19.3
P0AFG0	20513.0	S	U	T	C	CID	LIT	4	40.3	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	5.3	0.7	96.5	15.3
P0AFG0	20513.0	S	U	T	C	CID	LIT	4	40.3	WYVVQAFSGFEGR	1545.7	R	V	3.3	0.5	53.1	16.6
P0AFG0	20513.0	S	U	T	C	ETD	LIT	2	14.9	ATPVELDFSQVEKA	1533.8	R	-	3.3	0.6	38.3	17.0
P0AFG0	20513.0	S	U	T	C	ETD	LIT	2	14.9	WYVVQAFSGFEGR	1545.7	R	V	1.4	0.7	33.6	16.6
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	2	25.4	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	0.0	0.0	36.8	19.3
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	2	25.4	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	0.0	0.0	60.7	14.5
P0AFG0	20513.0	S	U	T	A	ETD+CID	LIT	2	25.4	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	4.6	0.5	28.0	19.3
P0AFG0	20513.0	S	U	T	A	ETD+CID	LIT	2	25.4	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	5.1	0.7	96.6	14.8
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	5	51.9	ATPVELDFSQVEKA	1533.8	R	-	2.0	0.6	0.0	0.0
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	5	51.9	GLADDDHFVGLAIDEDRQPELTAERVEK	3138.5	-	-	1.4	-0.8	47.8	19.1
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	5	51.9	LQQVGDKPRPK	1265.7	R	T	2.7	0.4	11.0	11.5
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	5	51.9	TLFEPGEMVR	1178.6	K	V	2.1	0.3	16.9	16.5
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	5	51.9	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	4.1	0.5	36.8	19.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	5	51.9	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	4.7	0.0	60.7	14.5
P0AFG0	20513.0	S	U	T	B	ETD+CID	LIT	5	51.9	WYVVQAFSGFEGR	1545.7	R	V	2.6	0.5	0.0	0.0
P0AFG0	20513.0	S	U	T	C	ETD+CID	LIT	3	33.1	ATPVELDFSQVEKA	1533.8	R	-	2.4	0.6	7.2	17.0
P0AFG0	20513.0	S	U	T	C	ETD+CID	LIT	3	33.1	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	4.4	0.4	30.7	19.4
P0AFG0	20513.0	S	U	T	C	ETD+CID	LIT	3	33.1	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	4.3	0.0	92.5	14.8
P0AFG0	20513.0	S	U	T	B	HCD	FT	2	25.4	VMGFIGGTSDRPAPISDKEVDAIMNR	2776.4	R	L	0.0	0.0	36.8	19.3
P0AFG0	20513.0	S	U	T	B	HCD	FT	2	25.4	VNDGPFADFNGVVEEVDYEK	2243.0	R	S	0.0	0.0	60.7	14.5
P0ACR9	20546.1	G	U	T	A	CID	LIT	4	21.0	ASRHEDFPYQEILLTR	1975.0	R	L	6.0	0.8	48.5	13.4
P0ACR9	20546.1	G	U	T	A	CID	LIT	4	21.0	HEDFPYQEILLTR	1660.8	R	L	3.8	0.8	50.8	10.0
P0ACR9	20546.1	G	U	T	A	CID	LIT	4	21.0	IADELEKR	973.5	R	G	2.7	0.6	50.4	15.1
P0ACR9	20546.1	G	U	T	A	CID	LIT	4	21.0	MDSSFTPIEQMLK	1526.7	-	F	2.6	0.0	33.8	9.5
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	4.7	0.6	44.4	12.6
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	6.0	0.7	41.2	13.2
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	EIKFRPGTDEGDYQVK	1881.9	K	L	3.0	0.8	8.5	13.8
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	EMAHQQIGMEVLNR	1671.8	R	V	4.6	0.6	35.2	10.8
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	FLEEGDK	837.4	R	A	1.8	0.7	25.0	10.0
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	FLEEGDKAK	1036.5	R	I	2.1	0.6	34.1	14.3
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	FLYEK	699.4	K	S	1.4	0.7	13.4	7.8
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	FRPGTDEGDYQVK	1511.7	K	L	4.4	0.0	37.3	9.5
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	GREMAHQQIGMEVLNR	1868.9	R	V	5.5	0.6	70.2	12.8
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	IMDYGK	726.3	R	F	1.3	0.6	17.3	10.0
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	LTGLEGEQLGIVSLR	1584.9	R	E	4.6	0.7	64.7	10.8
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	QKVIQVK	842.5	K	E	2.5	0.4	20.6	14.0
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	QMIMVLAPK	1030.6	R	K	2.7	0.5	46.4	15.2
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	VKDDLQELAVVESFPTK	1918.0	R	I	5.0	0.0	80.5	10.4
P0A707	20546.4	G	U	T	A	CID	LIT	15	74.4	VQTARPNR	941.5	R	I	2.1	0.3	13.9	12.3
P0A707	20546.4	G	T	T	A	CID	LIT	3	10.0	FLEEGDK	837.4	R	A	2.1	0.4	6.7	10.8
P0A707	20546.4	G	T	T	A	CID	LIT	3	10.0	FLEEGDKAK	1036.5	R	I	2.1	0.3	14.0	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A707	20546.4	G	T	T	A	CID	LIT	3	10.0	RVQTARPNR	1097.6	K	I	2.2	0.6	6.5	11.1
P0A707	20546.4	G	T	T	B	CID	LIT	2	13.9	GREMAHQQIGMEVLNR	1868.9	R	V	2.5	0.3	0.0	0.0
P0A707	20546.4	G	T	T	B	CID	LIT	2	13.9	RVQTARPNR	1097.6	K	I	2.4	0.3	24.3	11.1
P0A707	20546.4	S	U	T	A	CID	LIT	5	34.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	4.5	0.4	58.6	17.6
P0A707	20546.4	S	U	T	A	CID	LIT	5	34.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	5.2	0.6	53.5	18.9
P0A707	20546.4	S	U	T	A	CID	LIT	5	34.4	LTGLEGEQLGIVSLR	1584.9	R	E	5.3	0.5	63.5	15.9
P0A707	20546.4	S	U	T	A	CID	LIT	5	34.4	VKDDLQELAVVESFPTK	1918.0	R	I	4.3	0.6	54.7	16.3
P0A707	20546.4	S	U	T	A	CID	LIT	5	34.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	5.4	0.6	81.4	16.9
P0A707	20546.4	S	U	T	B	CID	LIT	5	34.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	4.5	0.6	62.4	17.5
P0A707	20546.4	S	U	T	B	CID	LIT	5	34.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	6.3	0.6	76.8	19.1
P0A707	20546.4	S	U	T	B	CID	LIT	5	34.4	LTGLEGEQLGIVSLR	1584.9	R	E	5.3	0.6	60.7	14.9
P0A707	20546.4	S	U	T	B	CID	LIT	5	34.4	VKDDLQELAVVESFPTK	1918.0	R	I	5.5	0.5	74.2	16.9
P0A707	20546.4	S	U	T	B	CID	LIT	5	34.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	5.9	0.6	64.0	17.2
P0A707	20546.4	S	U	T	C	CID	LIT	5	34.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	4.1	0.5	35.0	17.5
P0A707	20546.4	S	U	T	C	CID	LIT	5	34.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	5.6	0.7	34.8	18.9
P0A707	20546.4	S	U	T	C	CID	LIT	5	34.4	LTGLEGEQLGIVSLR	1584.9	R	E	5.3	0.6	63.5	16.0
P0A707	20546.4	S	U	T	C	CID	LIT	5	34.4	VKDDLQELAVVESFPTK	1918.0	R	I	5.5	0.6	54.0	16.9
P0A707	20546.4	S	U	T	C	CID	LIT	5	34.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	6.3	0.5	70.1	17.2
P0A707	20546.4	S	U	T	A	ETD	LIT	5	39.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	4.6	0.6	40.0	19.0
P0A707	20546.4	S	U	T	A	ETD	LIT	5	39.4	FLEEGDKAK	1036.5	R	I	4.4	0.4	44.8	16.2
P0A707	20546.4	S	U	T	A	ETD	LIT	5	39.4	LTGLEGEQLGIVSLR	1584.9	R	E	3.2	0.5	76.2	15.9
P0A707	20546.4	S	U	T	A	ETD	LIT	5	39.4	VKDDLQELAVVESFPTK	1918.0	R	I	6.6	0.6	80.2	16.9
P0A707	20546.4	S	U	T	A	ETD	LIT	5	39.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	6.7	0.6	62.0	17.2
P0A707	20546.4	S	U	T	B	ETD	LIT	4	27.2	FRPGTDEGDYQVK	1511.7	K	L	3.1	0.8	47.6	14.9
P0A707	20546.4	S	U	T	B	ETD	LIT	4	27.2	LTGLEGEQLGIVSLR	1584.9	R	E	3.5	0.4	60.6	15.4
P0A707	20546.4	S	U	T	B	ETD	LIT	4	27.2	VKDDLQELAVVESFPTK	1918.0	R	I	6.3	0.6	75.1	16.2
P0A707	20546.4	S	U	T	B	ETD	LIT	4	27.2	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	5.4	0.5	46.9	17.2
P0A707	20546.4	S	U	T	C	ETD	LIT	4	27.2	FRPGTDEGDYQVK	1511.7	K	L	2.7	0.7	35.4	14.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A707	20546.4	S	U	T	C	ETD	LIT	4	27.2	LTGLEGEQLGIVSLR	1584.9	R	E	3.4	0.3	58.3	14.9
P0A707	20546.4	S	U	T	C	ETD	LIT	4	27.2	VKDDLQELAVVESFPTK	1918.0	R	I	4.3	0.5	55.0	16.2
P0A707	20546.4	S	U	T	C	ETD	LIT	4	27.2	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	5.9	0.6	40.4	17.3
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	0.0	0.0	59.1	17.6
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	0.0	0.0	30.8	19.0
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	LTGLEGEQLGIVSLR	1584.9	R	E	0.0	0.0	63.5	14.9
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	VKDDLQELAVVESFPTK	1918.0	R	I	0.0	0.0	94.7	16.7
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	0.0	0.0	73.8	17.2
P0A707	20546.4	S	U	T	A	ETD+CID	LIT	5	39.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	5.5	0.7	71.7	18.9
P0A707	20546.4	S	U	T	A	ETD+CID	LIT	5	39.4	FLEEGDKAK	1036.5	R	I	2.0	0.4	18.1	15.8
P0A707	20546.4	S	U	T	A	ETD+CID	LIT	5	39.4	LTGLEGEQLGIVSLR	1584.9	R	E	5.3	0.5	57.9	15.9
P0A707	20546.4	S	U	T	A	ETD+CID	LIT	5	39.4	VKDDLQELAVVESFPTK	1918.0	R	I	5.9	0.6	87.0	16.3
P0A707	20546.4	S	U	T	A	ETD+CID	LIT	5	39.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	5.7	0.7	70.9	17.2
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	4.8	0.6	59.1	17.6
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	5.5	0.7	30.8	19.0
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	LTGLEGEQLGIVSLR	1584.9	R	E	5.2	0.6	63.5	14.9
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	VKDDLQELAVVESFPTK	1918.0	R	I	5.5	0.6	94.7	16.7
P0A707	20546.4	S	U	T	B	ETD+CID	LIT	5	34.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	5.5	0.7	73.8	17.2
P0A707	20546.4	S	U	T	C	ETD+CID	LIT	5	34.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	4.5	0.5	60.6	17.9
P0A707	20546.4	S	U	T	C	ETD+CID	LIT	5	34.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	5.8	0.6	51.6	19.0
P0A707	20546.4	S	U	T	C	ETD+CID	LIT	5	34.4	LTGLEGEQLGIVSLR	1584.9	R	E	5.3	0.5	63.3	15.9
P0A707	20546.4	S	U	T	C	ETD+CID	LIT	5	34.4	VKDDLQELAVVESFPTK	1918.0	R	I	6.3	0.6	79.1	16.1
P0A707	20546.4	S	U	T	C	ETD+CID	LIT	5	34.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	4.2	0.6	68.1	17.2
P0A707	20546.4	S	U	T	B	HCD	FT	5	34.4	AEEAGVDLVEISPNAEPPVCR	2252.1	K	I	0.0	0.0	59.1	17.6
P0A707	20546.4	S	U	T	B	HCD	FT	5	34.4	EALEKAEEAGVDLVEISPNAEPPVCR	2822.4	R	I	0.0	0.0	30.8	19.0
P0A707	20546.4	S	U	T	B	HCD	FT	5	34.4	LTGLEGEQLGIVSLR	1584.9	R	E	0.0	0.0	63.5	14.9
P0A707	20546.4	S	U	T	B	HCD	FT	5	34.4	VKDDLQELAVVESFPTK	1918.0	R	I	0.0	0.0	94.7	16.7
P0A707	20546.4	S	U	T	B	HCD	FT	5	34.4	VKDDLQELAVVESFPTKIEGR	2373.3	R	Q	0.0	0.0	73.8	17.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6N4	20573.5	G	U	T	A	CID	LIT	5	25.5	ATYYSNDFR	1136.5	M	A	0.0	0.0	47.0	9.0
P0A6N4	20573.5	G	U	T	A	CID	LIT	5	25.5	GDTAGTGGKPATLSTGAVVK	1788.0	K	V	4.6	0.0	43.7	12.3
P0A6N4	20573.5	G	U	T	A	CID	LIT	5	25.5	LLTGTR	660.4	R	V	1.3	0.6	21.7	13.8
P0A6N4	20573.5	G	U	T	A	CID	LIT	5	25.5	RLLTGTR	816.5	R	V	2.4	0.3	14.6	10.8
P0A6N4	20573.5	G	U	T	A	CID	LIT	5	25.5	VPLFVQIGEVIK	1341.8	K	V	2.5	0.6	28.9	4.8
P0A6N4	20573.5	G	T	T	B	CID	LIT	3	15.4	GDTAGTGGKPATLSTGAVVK	1788.0	K	V	5.4	0.6	43.9	12.0
P0A6N4	20573.5	G	T	T	B	CID	LIT	3	15.4	SGEYVSR	797.4	R	V	2.1	0.0	36.6	6.0
P0A6N4	20573.5	G	T	T	B	CID	LIT	3	15.4	SGEYVSRVK	1024.5	R	-	2.7	0.7	29.1	10.8
P0A6N4	20573.5	G	T	A	B	CID	LIT	5	38.8	DGEFWHFMNNETF	1673.7	N	E	2.8	0.0	34.5	3.0
P0A6N4	20573.5	G	T	A	B	CID	LIT	5	38.8	DMNLTYLYN	1146.5	V	D	1.4	0.0	22.6	12.0
P0A6N4	20573.5	G	T	A	B	CID	LIT	5	38.8	DNAKWLL	859.5	G	D	2.6	0.0	20.6	9.0
P0A6N4	20573.5	G	T	A	B	CID	LIT	5	38.8	DTAGTGGKPATLSTGAVVKVPLFVQIGEVIKV	3152.8	G	D	6.2	0.0	30.1	4.8
P0A6N4	20573.5	G	T	A	B	CID	LIT	5	38.8	DTRSGEYVSRVK	1396.7	V	-	2.3	0.8	24.1	15.2
P0A7X6	20587.5	G	U	T	A	CID	LIT	2	13.2	KVDLTTR	832.5	K	S	2.1	0.7	40.1	11.8
P0A7X6	20587.5	G	U	T	A	CID	LIT	2	13.2	SKQLTAQAPVDPIVLGK	1765.0	M	M	0.0	0.0	72.3	7.0
P0A7X6	20587.5	G	U	A	A	CID	LIT	3	19.2	DAFGIKERLVPFL	1504.9	K	D	2.1	0.6	1.3	11.8
P0A7X6	20587.5	G	U	A	A	CID	LIT	3	19.2	DMIIKLKGVDDR	1402.8	Q	D	2.2	0.7	25.0	13.8
P0A7X6	20587.5	G	U	A	A	CID	LIT	3	19.2	DVLVIKANLK	1112.7	N	D	3.0	0.0	22.4	0.0
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	AIMASDLGLNPNSAGSDIR	1917.9	K	V	4.6	0.7	67.2	11.8
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	4.1	0.0	82.0	11.1
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	ASPSLLDGIVVEYYGTPTPLR	2248.2	R	Q	5.7	0.0	112.0	12.3
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	DANDKVK	789.4	R	A	2.2	0.3	15.4	14.1
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	IEAALADKEAELMQF	1678.8	K	-	2.6	0.0	43.2	13.4
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	INVFDR	763.4	K	S	2.4	0.7	37.4	16.4
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	IVRGEAEQAR	1128.6	K	V	3.6	0.5	39.4	11.5
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	LTDAAIK	731.4	K	K	2.4	0.0	31.0	15.2
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	MISDIRK	862.5	-	D	2.1	0.5	17.5	16.1
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	QLASVTVEDSR	1204.6	R	T	3.0	0.0	45.8	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	SMSPAVEK	848.4	R	A	1.9	0.6	31.9	11.5
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	SQDDVQKLTDAAIK	1531.8	R	K	4.1	0.6	70.4	13.8
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	TLKINVFDR	1105.6	R	S	3.3	0.0	35.7	10.8
P0A805	20621.3	G	U	T	A	CID	LIT	14	70.8	VPLPPLTEER	1150.6	R	R	2.9	0.0	26.1	11.5
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	AIMASDLGLNPNSAGSDIR	1917.9	K	V	4.2	0.8	90.4	12.3
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3049.6	K	R	5.2	0.7	38.4	10.0
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	ASPSLLDGIVVEYYGTPTPLR	2248.2	R	Q	3.5	0.0	54.7	12.3
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	DKEISEDDDR	1221.5	K	R	3.3	0.0	27.9	4.8
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	EISEDDDRR	1134.5	K	S	2.3	0.0	25.1	4.8
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	IEAALADKEAELMQF	1694.8	K	-	3.0	0.6	22.5	12.0
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	INVFDR	763.4	K	S	1.9	0.6	31.2	16.5
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	IVRGEAEQAR	1128.6	K	V	2.8	0.6	22.2	11.5
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	KIEAALADK	958.6	K	E	2.4	0.0	45.3	13.2
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	LTDAAIKK	859.5	K	I	2.9	0.8	45.5	13.2
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	QLASVTVEDSR	1204.6	R	T	2.5	0.5	24.5	11.5
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	SMSPAVEK	848.4	R	A	1.8	0.7	26.4	12.8
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	SQDDVQK	819.4	R	L	1.9	0.3	0.0	0.0
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	SQDDVQKLTDAAIK	1531.8	R	K	4.6	0.7	87.8	13.8
P0A805	20621.3	G	T	T	A	CID	LIT	15	68.1	VPLPPLTEER	1150.6	R	R	1.8	0.5	0.0	0.0
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DAAIKKIEAALA	1213.7	T	D	2.8	0.4	50.9	10.0
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DAEVRM	720.3	K	D	1.7	0.6	20.5	12.6
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DANDKVKALLK	1214.7	R	D	3.2	0.5	17.9	13.6
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DDVQKLT	818.4	Q	D	2.1	0.5	25.0	16.7
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DGIVVEYYGTPTPLRQLASVTVE	2507.3	L	D	4.5	0.0	29.7	15.9
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DIRKDAEVRM	1232.6	S	D	2.7	0.4	22.8	15.2
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DIRVPLPPLTEERRK	1819.1	S	D	2.2	0.7	15.8	7.0
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DKEAELMQF	1126.5	A	-	3.0	0.6	38.3	13.6
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DKVKALLK	914.6	N	D	2.9	0.0	23.0	3.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DLGLNPNSAGS	1044.5	S	D	1.9	0.6	0.0	0.0
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DRRSQDDVQKLT	1460.7	D	D	3.0	0.5	19.3	18.0
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DRSMSPAVEKAIMAS	1592.8	F	D	3.4	0.6	24.4	16.8
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DRSMSPAVEKAIMASDLGLNPNSAGS	2618.3	F	D	3.3	0.7	16.4	12.0
P0A805	20621.3	G	U	A	A	CID	LIT	14	69.2	DSRTLKINVF	1192.7	E	D	2.3	0.3	13.6	11.5
P0A805	20621.3	G	T	A	A	CID	LIT	7	41.6	DAAIKKIEAALA	1213.7	T	D	2.7	0.0	47.2	10.0
P0A805	20621.3	G	T	A	A	CID	LIT	7	41.6	DDVQKLT	818.4	Q	D	2.3	0.2	18.4	16.7
P0A805	20621.3	G	T	A	A	CID	LIT	7	41.6	DIRVPLPPLTEERRK	1819.1	S	D	1.4	0.0	18.0	7.0
P0A805	20621.3	G	T	A	A	CID	LIT	7	41.6	DKEAELMQF	1110.5	A	-	3.0	0.8	42.3	16.4
P0A805	20621.3	G	T	A	A	CID	LIT	7	41.6	DLGLNPNSAGS	1044.5	S	D	3.3	0.7	47.7	14.1
P0A805	20621.3	G	T	A	A	CID	LIT	7	41.6	DRRSQDDVQKLT	1460.7	D	D	2.6	0.4	13.8	18.0
P0A805	20621.3	G	T	A	A	CID	LIT	7	41.6	EYYGTPTPLRQLASVTVE	2024.0	V	D	2.7	0.5	12.8	14.0
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	AIMASDLGLNPNSAGSDIR	1901.9	K	V	4.8	0.0	28.7	12.6
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3049.6	K	R	4.7	0.0	72.1	9.5
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	DANDKVK	789.4	R	A	2.5	0.3	24.8	14.1
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	GEAEQAR	760.4	R	V	2.3	0.7	20.0	8.5
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	GEAEQARVAVR	1185.6	R	N	2.7	0.2	20.3	12.6
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	INVFDR	763.4	K	S	1.7	0.5	16.4	12.8
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	INVFDRSMSPAVEK	1592.8	K	A	4.0	0.6	30.4	13.8
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	IVRGEAEQAR	1128.6	K	V	3.5	0.5	41.8	11.5
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	KDAEVR	717.4	R	M	2.3	0.1	21.0	17.7
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	LTDAAIK	731.4	K	K	1.9	0.1	10.8	15.4
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	MISDIR	734.4	-	K	1.9	0.6	6.3	16.1
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	QLASVTVEDSR	1204.6	R	T	2.9	0.4	39.8	11.5
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	QLASVTVEDSRTLK	1546.8	R	I	3.6	0.6	28.4	7.8
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	RSQDDVQK	975.5	R	L	2.1	0.5	10.0	12.6
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	SMSPAVEK	848.4	R	A	2.0	0.5	26.4	11.5
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	SQDDVQK	819.4	R	L	2.4	0.6	20.8	12.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	SQDDVQKLTDAAIK	1531.8	R	K	4.4	0.6	75.7	13.6
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	TLKINVFDR	1105.6	R	S	2.6	0.0	32.3	10.0
P0A805	20621.3	G	T	T	B	CID	LIT	19	56.8	VPLPPLTEER	1150.6	R	R	2.5	0.0	36.5	11.8
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DAAIKKIEAALA	1213.7	T	D	2.6	0.5	37.9	10.0
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DAEVRM	736.3	K	D	0.0	0.0	22.8	13.4
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DDVQKLT	818.4	Q	D	2.5	0.4	30.3	18.1
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DGIVVEYYGTPTPLRQLASVTVE	2507.3	L	D	3.1	0.7	14.4	15.9
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DIRVPLPPLTEERRK	1819.1	S	D	1.8	0.0	17.8	7.0
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DKCVEAFKTQISKIRTGRASPSLL	2705.5	M	D	2.7	0.3	6.0	13.6
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DKEAELMQF	1110.5	A	-	2.4	0.8	23.8	16.6
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DKVKALLK	914.6	N	D	2.2	0.0	31.1	3.0
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DLGLNPNSAGS	1044.5	S	D	2.4	0.7	32.8	13.8
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DLTKIVRGEA	1101.6	K	E	1.8	0.7	17.3	14.3
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DRSMSPAVEKAIMAS	1592.8	F	D	2.9	0.6	45.9	16.5
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	DSRTLKINVF	1192.7	E	D	1.7	0.5	7.3	11.5
P0A805	20621.3	G	T	A	B	CID	LIT	13	87.6	EQARVAVRNVRR	1453.8	A	D	2.2	0.8	0.0	0.0
P0A805	20621.3	G	U	A	B	CID	LIT	4	24.9	DAAIKKIEAALA	1213.7	T	D	2.0	0.7	22.5	10.0
P0A805	20621.3	G	U	A	B	CID	LIT	4	24.9	DKEAELMQF	1110.5	A	-	3.0	0.7	43.2	16.6
P0A805	20621.3	G	U	A	B	CID	LIT	4	24.9	DLTKIVRGEA	1101.6	K	E	2.0	0.0	14.6	14.3
P0A805	20621.3	G	U	A	B	CID	LIT	4	24.9	DRSMSPAVEKAIMAS	1592.8	F	D	2.6	0.0	22.6	16.9
P0A805	20621.3	S	U	T	A	CID	LIT	4	31.9	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	4.3	0.0	56.7	18.6
P0A805	20621.3	S	U	T	A	CID	LIT	4	31.9	INVFDR	763.4	K	S	1.9	0.6	29.8	17.7
P0A805	20621.3	S	U	T	A	CID	LIT	4	31.9	IVRGEAEQAR	1128.6	K	V	3.0	0.5	21.6	14.3
P0A805	20621.3	S	U	T	A	CID	LIT	4	31.9	SQDDVQKLTDAAIK	1531.8	R	K	3.5	0.3	22.8	18.1
P0A805	20621.3	S	U	T	B	CID	LIT	6	34.1	AIMASDLGLNPNSAGSDIR	1901.9	K	V	5.7	0.7	93.0	17.8
P0A805	20621.3	S	U	T	B	CID	LIT	6	34.1	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	4.8	0.7	43.4	18.7
P0A805	20621.3	S	U	T	B	CID	LIT	6	34.1	INVFDR	763.4	K	S	1.4	0.5	10.0	17.7
P0A805	20621.3	S	U	T	B	CID	LIT	6	34.1	MDKCVEAFKTQISK	1684.8	R	I	2.6	0.6	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A805	20621.3	S	U	T	B	CID	LIT	6	34.1	SQDDVQKLTDAAIK	1531.8	R	K	3.7	0.5	27.5	18.1
P0A805	20621.3	S	U	T	B	CID	LIT	6	34.1	VPLPPLTEER	1150.6	R	R	2.7	0.0	23.6	15.2
P0A805	20621.3	S	U	T	C	CID	LIT	5	42.2	AIMASDLGLNPNSAGSDIR	1901.9	K	V	5.7	0.7	102.0	17.9
P0A805	20621.3	S	U	T	C	CID	LIT	5	42.2	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	5.3	0.0	81.2	18.2
P0A805	20621.3	S	U	T	C	CID	LIT	5	42.2	ASPSLLDGIVVEYYGTPTPLR	2248.2	R	Q	2.2	0.5	0.0	0.0
P0A805	20621.3	S	U	T	C	CID	LIT	5	42.2	MDKCVEAFKTQISK	1684.8	R	I	3.7	0.5	26.4	17.2
P0A805	20621.3	S	U	T	C	CID	LIT	5	42.2	SQDDVQKLTDAAIK	1531.8	R	K	4.7	0.5	68.0	17.6
P0A805	20621.3	S	U	T	A	ETD	LIT	3	28.6	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	4.3	0.0	33.1	18.7
P0A805	20621.3	S	U	T	A	ETD	LIT	3	28.6	IVRGEAEQAR	1128.6	K	V	2.6	0.3	20.6	14.3
P0A805	20621.3	S	U	T	A	ETD	LIT	3	28.6	SQDDVQKLTDAAIK	1531.8	R	K	3.6	0.6	36.8	17.9
P0A805	20621.3	S	U	T	B	ETD	LIT	5	37.8	AIMASDLGLNPNSAGSDIR	1901.9	K	V	2.9	0.7	0.0	0.0
P0A805	20621.3	S	U	T	B	ETD	LIT	5	37.8	ASPSLLDGIVVEYYGTPTPLR	2248.2	R	Q	3.0	0.0	25.5	17.1
P0A805	20621.3	S	U	T	B	ETD	LIT	5	37.8	INVFDR	763.4	K	S	0.0	0.0	43.2	17.9
P0A805	20621.3	S	U	T	B	ETD	LIT	5	37.8	IVRGEAEQAR	1128.6	K	V	2.7	0.4	37.3	14.5
P0A805	20621.3	S	U	T	B	ETD	LIT	5	37.8	SQDDVQKLTDAAIK	1531.8	R	K	1.8	0.4	25.0	17.5
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	AIMASDLGLNPNSAGSDIR	1901.9	K	V	0.0	0.0	100.0	17.6
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	0.0	0.0	60.6	18.6
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	DKEISEDDDRR	1377.6	K	S	0.0	0.0	43.5	14.3
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	IVRGEAEQAR	1128.6	K	V	0.0	0.0	22.5	14.3
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	SQDDVQKLTDAAIK	1531.8	R	K	0.0	0.0	75.0	17.7
P0A805	20621.3	S	U	T	A	ETD+CID	LIT	4	28.6	AIMASDLGLNPNSAGSDIR	1901.9	K	V	5.1	0.7	80.1	17.9
P0A805	20621.3	S	U	T	A	ETD+CID	LIT	4	28.6	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	5.2	0.7	53.4	18.6
P0A805	20621.3	S	U	T	A	ETD+CID	LIT	4	28.6	IVRGEAEQAR	1128.6	K	V	3.7	0.2	49.4	14.3
P0A805	20621.3	S	U	T	A	ETD+CID	LIT	4	28.6	SQDDVQKLTDAAIK	1531.8	R	K	4.5	0.5	80.3	17.9
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	2	16.2	AIMASDLGLNPNSAGSDIR	1901.9	K	V	5.6	0.6	0.0	0.0
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	2	16.2	DKEISEDDDRR	1377.6	K	S	2.9	0.4	0.0	0.0
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	AIMASDLGLNPNSAGSDIR	1901.9	K	V	5.6	0.6	0.0	0.0
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	5.0	0.0	60.6	18.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	DKEISEDDDRR	1377.6	K	S	2.9	0.4	43.5	14.3
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	IVRGEAEQAR	1128.6	K	V	2.9	0.0	22.5	14.3
P0A805	20621.3	S	U	T	B	ETD+CID	LIT	5	34.6	SQDDVQKLTDAAIK	1531.8	R	K	4.1	0.5	75.0	17.7
P0A805	20621.3	S	U	T	C	ETD+CID	LIT	5	31.9	AIMASDLGLNPNSAGSDIR	1901.9	K	V	5.6	0.7	85.2	17.9
P0A805	20621.3	S	U	T	C	ETD+CID	LIT	5	31.9	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	4.9	0.0	59.3	18.7
P0A805	20621.3	S	U	T	C	ETD+CID	LIT	5	31.9	INVFDR	763.4	K	S	1.6	0.0	28.7	17.7
P0A805	20621.3	S	U	T	C	ETD+CID	LIT	5	31.9	IVRGEAEQAR	1128.6	K	V	3.1	0.0	30.2	14.3
P0A805	20621.3	S	U	T	C	ETD+CID	LIT	5	31.9	SQDDVQKLTDAAIK	1531.8	R	K	4.5	0.5	83.5	17.6
P0A805	20621.3	S	U	T	B	HCD	FT	4	28.6	AIMASDLGLNPNSAGSDIR	1901.9	K	V	0.0	0.0	100.0	17.6
P0A805	20621.3	S	U	T	B	HCD	FT	4	28.6	AIMASDLGLNPNSAGSDIRVPLPPLTEER	3033.6	K	R	0.0	0.0	60.6	18.6
P0A805	20621.3	S	U	T	B	HCD	FT	4	28.6	IVRGEAEQAR	1128.6	K	V	0.0	0.0	22.5	14.3
P0A805	20621.3	S	U	T	B	HCD	FT	4	28.6	SQDDVQKLTDAAIK	1531.8	R	K	0.0	0.0	75.0	17.7
P0A805	20621.3	S	U	T	B	HCD	FT	2	17.8	AIMASDLGLNPNSAGSDIR	1901.9	K	V	3.0	0.0	76.3	18.1
P0A805	20621.3	S	U	T	B	HCD	FT	2	17.8	SQDDVQKLTDAAIK	1531.8	R	K	4.3	0.0	75.1	17.7
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	AAQYVASHPGEVCPAK	1684.8	K	W	4.6	0.7	68.3	12.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	AAQYVASHPGEVCPAKWK	1999.0	K	E	5.2	0.7	48.2	13.2
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	5.5	0.8	69.7	12.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	AWHSSSETIAK	1216.6	K	I	3.9	0.6	53.7	10.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	DASDLLR	789.4	R	K	2.1	0.6	30.8	14.1
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	DASDLLRK	917.5	R	I	2.5	0.7	33.5	14.1
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	EDEGLADR	904.4	R	A	2.3	0.6	38.5	7.8
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	EGEATLAPSLDLVGK	1499.8	K	-	2.4	0.8	4.8	11.8
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	EGEATLAPSLDLVGKI	1612.9	K	-	3.7	0.9	68.9	10.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	IKAAQYVASHPGEVCPAK	1926.0	K	W	5.4	0.7	71.1	12.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	IKYAMIGDPTGALTR	1606.9	K	N	5.0	0.8	60.8	12.3
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	LGVDVYAVSTDTHFTHK	1889.9	K	A	5.0	0.7	71.3	13.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	NFDNMREDEGLADR	1681.7	R	A	4.4	0.0	45.9	6.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	NGEFIEITEK	1179.6	K	D	3.6	0.8	46.2	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	NGEFIEITEKDTEGR	1737.8	K	W	4.0	0.6	86.8	13.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	WKEGEATLAPSLDLVGK	1814.0	K	-	4.7	0.7	62.4	12.6
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	3.3	0.0	23.6	6.0
P0AE08	20743.9	G	U	T	A	CID	LIT	18	90.9	YAMIGDPTGALTR	1365.7	K	N	3.8	0.8	54.0	11.1
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	AAQYVASHPGEVCPAK	1684.8	K	W	5.0	0.7	64.6	11.1
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	5.3	0.9	93.4	11.5
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	AWHSSSETIAK	1216.6	K	I	3.0	0.7	15.1	10.0
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	DASDLLR	789.4	R	K	1.7	0.5	13.6	14.1
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	EGEATLAPSLDLVGK	1499.8	K	-	2.3	0.7	11.5	13.2
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	EGEATLAPSLDLVGKI	1612.9	K	-	3.6	0.0	40.2	9.0
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	NFDNMREDEGLADR	1681.7	R	A	2.7	0.0	19.4	7.0
P0AE08	20743.9	G	T	T	A	CID	LIT	8	53.5	YAMIGDPTGALTR	1381.7	K	N	2.7	0.5	30.3	13.2
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DFTFVCPTELG	1285.6	A	D	2.3	0.0	19.9	13.4
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DHYEELQKLGV	1330.7	A	D	2.9	0.7	45.5	14.3
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DLVGKI	644.4	L	-	1.3	0.4	19.3	15.7
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DPQGIIQAIEVTAEGIGR	1867.0	V	D	3.0	0.7	14.2	14.3
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DPTGALTRNF	1091.5	G	D	3.9	0.7	42.3	13.2
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DRATFVV	807.4	A	D	1.7	0.7	15.0	14.3
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DTHFTHKAWHSSSETIAKIKYAMIG	2875.4	T	D	4.1	0.0	27.5	14.6
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	DTHFTHKAWHSSSETIAKIKYAMIGDPTGALTRNF	3948.0	T	D	2.7	0.5	8.3	12.6
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	EELQKLGVDVYAVST	1650.9	Y	D	3.9	0.0	60.6	13.0
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	EGEATLAPSLDLVGKI	1612.9	K	-	2.5	0.0	20.5	12.3
P0AE08	20743.9	G	U	A	A	CID	LIT	11	60.4	EVCPAKWKEGEATLAPSL	1986.0	G	D	2.5	0.6	25.8	15.7
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	AAQYVASHPGEVCPAK	1684.8	K	W	4.4	0.6	48.9	12.0
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	AAQYVASHPGEVCPAKWK	1999.0	K	E	6.0	0.7	61.7	13.2
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	AWHSSSETIAK	1216.6	K	I	3.6	0.0	38.8	10.0
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	DASDLLR	789.4	R	K	1.9	0.6	25.7	14.1
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	EGEATLAPSLDLVGKI	1612.9	K	-	3.9	0.9	47.2	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	IKYAMIGDPTGALTR	1622.9	K	N	3.0	0.8	22.6	10.4
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	NFDNMREDEGLADR	1681.7	R	A	4.0	0.6	40.4	6.0
P0AE08	20743.9	G	T	T	B	CID	LIT	8	43.3	YAMIGDPTGALTR	1365.7	K	N	2.7	0.6	30.7	10.4
P0AE08	20743.9	G	U	T	B	CID	LIT	6	33.7	AAQYVASHPGEVCPAK	1684.8	K	W	2.2	0.6	18.4	11.8
P0AE08	20743.9	G	U	T	B	CID	LIT	6	33.7	AWHSSSETIAK	1216.6	K	I	2.3	0.0	21.2	10.0
P0AE08	20743.9	G	U	T	B	CID	LIT	6	33.7	DASDLLR	789.4	R	K	1.9	0.5	27.9	14.6
P0AE08	20743.9	G	U	T	B	CID	LIT	6	33.7	DASDLLRK	917.5	R	I	1.9	0.2	14.3	14.1
P0AE08	20743.9	G	U	T	B	CID	LIT	6	33.7	NGEFIEITEKDTEGR	1737.8	K	W	2.1	0.7	11.9	13.0
P0AE08	20743.9	G	U	T	B	CID	LIT	6	33.7	YAMIGDPTGALTR	1365.7	K	N	3.7	0.0	35.0	11.1
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	DHYEELQKLGV	1330.7	A	D	2.8	0.4	22.4	13.4
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	DLVGKI	644.4	L	-	1.5	0.2	11.1	15.7
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	DPQGIIQAI	954.5	V	E	1.7	0.3	11.4	13.0
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	DPQGIIQAIEVTAEGIGR	1867.0	V	D	5.3	0.7	83.9	14.3
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	DPTGALTRNF	1091.5	G	D	3.6	0.6	43.8	13.2
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	DRATFVVDPQGIIQAIEVTA	2143.1	A	E	2.8	0.0	18.3	13.2
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	EELQKLGV	915.5	Y	D	1.8	0.5	9.4	15.8
P0AE08	20743.9	G	T	A	B	CID	LIT	8	37.4	EVCPAKWKEGEATLAPSL	1986.0	G	D	2.9	0.0	26.1	14.8
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DFTFVCPTELG	1285.6	A	D	2.2	0.0	59.1	13.4
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DHYEELQKLGV	1330.7	A	D	3.2	0.6	46.3	13.8
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DLVGKI	644.4	L	-	1.3	0.0	25.4	15.7
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DPQGIIQAIEVTA	1354.7	V	E	2.1	0.0	15.3	10.4
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DPQGIIQAIEVTAEGIGR	1867.0	V	D	5.5	0.9	63.8	14.3
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DPTGALTRNF	1091.5	G	D	3.8	0.7	48.2	13.2
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DRATFVV	807.4	A	D	2.1	0.0	21.3	14.3
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	DRATFVVDPQGIIQAIEVTA	2143.1	A	E	4.2	0.0	64.8	13.2
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	EELQKLGV	915.5	Y	D	2.0	0.5	14.7	15.8
P0AE08	20743.9	G	U	A	B	CID	LIT	10	37.4	EELQKLGVDVYAVST	1650.9	Y	D	3.5	0.0	51.8	13.0
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.3	0.7	99.3	16.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	AWHSSSETIAK	1216.6	K	I	2.1	0.6	27.1	14.8
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	EGEATLAPSLDLVGK	1499.8	K	-	2.9	0.3	0.0	0.0
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	EGEATLAPSLDLVGKI	1612.9	K	-	3.8	0.6	45.4	14.0
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	IKPFKNQAFK	1220.7	K	N	1.7	0.7	14.4	9.0
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	IKYAMIGDPTGALTR	1606.9	K	N	3.2	0.4	12.4	16.6
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	LGVDVYAVSTDTHFTHK	1889.9	K	A	4.7	0.6	48.0	18.4
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	NGEFIEITEKDTEGR	1737.8	K	W	3.9	0.7	87.4	18.0
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	WKEGEATLAPSLDLVGK	1814.0	K	-	2.3	0.3	4.6	16.8
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	WKEGEATLAPSLDLVGKI	1927.1	K	-	5.2	0.7	37.4	16.1
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	3.3	0.0	46.3	16.1
P0AE08	20743.9	S	U	T	A	CID	LIT	12	74.9	YAMIGDPTGALTR	1365.7	K	N	3.2	0.7	39.9	16.0
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.8	0.8	89.4	16.3
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	AWHSSSETIAK	1216.6	K	I	3.2	0.6	29.2	15.2
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	EGEATLAPSLDLVGK	1499.8	K	-	3.6	0.6	31.7	17.6
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	EGEATLAPSLDLVGKI	1612.9	K	-	3.9	0.5	37.0	15.6
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	IKYAMIGDPTGALTR	1606.9	K	N	4.4	0.6	56.4	16.7
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	LGVDVYAVSTDTHFTHK	1889.9	K	A	4.5	0.5	52.0	18.4
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	NGEFIEITEKDTEGR	1737.8	K	W	4.0	0.4	47.5	17.5
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	NQAFKNGEFIEITEKDTEGR	2327.1	K	W	5.3	0.6	69.6	18.4
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	WKEGEATLAPSLDLVGK	1814.0	K	-	4.5	0.6	36.0	16.6
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	WKEGEATLAPSLDLVGKI	1927.1	K	-	5.3	0.6	55.2	15.9
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	4.8	0.0	62.8	15.6
P0AE08	20743.9	S	U	T	B	CID	LIT	12	72.2	YAMIGDPTGALTR	1365.7	K	N	3.7	0.7	59.3	15.1
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	AAQYVASHPGEVCPAKWK	1999.0	K	E	4.9	0.5	42.8	18.3
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.5	0.8	108.0	15.9
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	AWHSSSETIAK	1216.6	K	I	2.7	0.6	27.2	14.1
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	EGEATLAPSLDLVGKI	1612.9	K	-	3.5	0.5	42.5	16.5
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	IKPFKNQAFK	1220.7	K	N	1.8	0.7	9.0	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	IKYAMIGDPTGALTR	1606.9	K	N	3.1	0.6	33.1	16.3
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	LGVDVYAVSTDTHFTHK	1889.9	K	A	4.5	0.5	44.9	18.3
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	NFDNMREDEGLADR	1681.7	R	A	1.8	0.8	11.3	10.8
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	NGEFIEITEKDTEGR	1737.8	K	W	4.1	0.5	31.3	17.2
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	WKEGEATLAPSLDLVGKI	1927.1	K	-	5.4	0.6	60.9	16.1
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	3.6	0.0	46.8	16.3
P0AE08	20743.9	S	U	T	C	CID	LIT	12	90.9	YAMIGDPTGALTR	1365.7	K	N	3.3	0.7	41.8	15.9
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	AAQYVASHPGEVCPAKWK	1999.0	K	E	6.1	0.6	49.5	18.0
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	4.5	0.0	13.9	16.8
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	DASDLLR	789.4	R	K	2.2	0.2	33.6	19.1
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	EGEATLAPSLDLVGKI	1612.9	K	-	4.0	0.6	46.8	13.8
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	IKYAMIGDPTGALTR	1606.9	K	N	4.8	0.6	47.2	16.8
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	LGVDVYAVSTDTHFTHK	1889.9	K	A	4.1	0.4	45.3	17.5
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	NFDNMREDEGLADR	1681.7	R	A	3.0	0.0	36.5	11.1
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	NGEFIEITEKDTEGR	1737.8	K	W	3.9	0.5	61.8	17.9
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	WKEGEATLAPSLDLVGKI	1927.1	K	-	6.5	0.5	71.9	16.1
P0AE08	20743.9	S	U	T	A	ETD	LIT	10	83.4	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	3.2	0.0	16.8	16.3
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	AAQYVASHPGEVCPAK	1684.8	K	W	3.8	0.5	39.2	16.9
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	AAQYVASHPGEVCPAKWK	1999.0	K	E	5.6	0.0	45.3	18.0
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.3	0.7	60.1	16.3
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	DASDLLR	789.4	R	K	0.0	0.0	33.2	19.2
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	EGEATLAPSLDLVGK	1499.8	K	-	2.8	0.0	19.8	16.6
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	EGEATLAPSLDLVGKI	1612.9	K	-	4.4	0.6	49.8	14.0
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	IKYAMIGDPTGALTR	1606.9	K	N	6.1	0.6	80.7	16.0
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	LGVDVYAVSTDTHFTHK	1889.9	K	A	0.0	0.0	73.8	17.9
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	NFDNMREDEGLADR	1681.7	R	A	3.2	0.0	36.0	11.1
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	NGEFIEITEKDTEGR	1737.8	K	W	3.3	0.4	0.0	0.0
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	NQAFKNGEFIEITEKDTEGR	2327.1	K	W	4.9	0.5	25.9	18.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	WKEGEATLAPSLDLVGK	1814.0	K	-	6.3	0.7	76.4	16.0
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	WKEGEATLAPSLDLVGKI	1927.1	K	-	3.6	0.5	46.0	16.1
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	4.7	0.0	23.7	16.3
P0AE08	20743.9	S	U	T	B	ETD	LIT	15	86.1	YAMIGDPTGALTR	1365.7	K	N	1.9	0.7	0.0	0.0
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	AAQYVASHPGEVCPAK	1684.8	K	W	2.6	0.7	40.2	17.2
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	AAQYVASHPGEVCPAKWK	1999.0	K	E	3.8	0.4	24.0	17.9
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	5.4	0.7	39.6	17.2
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	AWHSSSETIAK	1216.6	K	I	5.0	0.6	67.1	14.1
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	EGEATLAPSLDLVGKI	1612.9	K	-	3.7	0.6	42.5	14.0
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	IKAAQYVASHPGEVCPAK	1926.0	K	W	4.5	0.5	48.0	18.1
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	IKYAMIGDPTGALTR	1606.9	K	N	3.6	0.0	54.9	16.1
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	LGVDVYAVSTDTHFTHK	1889.9	K	A	4.9	0.5	63.7	17.8
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	NFDNMREDEGLADR	1681.7	R	A	3.4	0.8	29.8	12.0
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	NGEFIEITEKDTEGR	1737.8	K	W	2.7	0.5	52.4	17.5
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	WKEGEATLAPSLDLVGKI	1927.1	K	-	4.8	0.5	46.5	16.1
P0AE08	20743.9	S	U	T	C	ETD	LIT	12	70.1	YAMIGDPTGALTR	1365.7	K	N	2.7	0.7	48.2	15.7
P0AE08	20743.9	S	U	T	C	ETD	FT	2	17.1	AAQYVASHPGEVCPAKWK	1999.0	K	E	2.1	0.0	30.6	17.9
P0AE08	20743.9	S	U	T	C	ETD	FT	2	17.1	NFDNMREDEGLADR	1681.7	R	A	2.1	0.0	35.0	11.5
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	2	15.0	AWHSSSETIAK	1216.6	K	I	0.0	0.0	53.2	14.1
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	2	15.0	LGVDVYAVSTDTHFTHK	1889.9	K	A	0.0	0.0	62.6	18.3
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	AAQYVASHPGEVCPAKWK	1999.0	K	E	0.0	0.0	45.0	18.3
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	0.0	0.0	102.0	16.1
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	AWHSSSETIAK	1216.6	K	I	0.0	0.0	53.2	14.1
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	EGEATLAPSLDLVGK	1499.8	K	-	0.0	0.0	33.1	17.7
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	EGEATLAPSLDLVGKI	1612.9	K	-	0.0	0.0	43.5	14.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	IKYAMIGDPTGALTR	1606.9	K	N	0.0	0.0	37.7	16.2
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	LGVDVYAVSTDTHFTHK	1889.9	K	A	0.0	0.0	62.6	18.3
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	NGEFIEITEKDTEGR	1737.8	K	W	0.0	0.0	49.3	17.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	NQAFKNGEFIEITEKDTEGR	2327.1	K	W	0.0	0.0	82.9	18.1
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	WKEGEATLAPSLDLVGK	1814.0	K	-	0.0	0.0	48.1	17.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	WKEGEATLAPSLDLVGKI	1927.1	K	-	0.0	0.0	46.3	16.3
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	0.0	0.0	69.1	16.6
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	13	80.7	YAMIGDPTGALTR	1365.7	K	N	0.0	0.0	57.8	16.0
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.8	0.8	99.8	16.1
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	AWHSSSETIAK	1216.6	K	I	3.1	0.7	29.0	13.8
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	EGEATLAPSLDLVGK	1499.8	K	-	3.2	0.5	29.3	17.3
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	EGEATLAPSLDLVGKI	1612.9	K	-	3.6	0.5	47.9	14.0
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	IKYAMIGDPTGALTR	1606.9	K	N	3.1	0.5	18.8	16.2
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	LGVDVYAVSTDTHFTHK	1889.9	K	A	4.6	0.6	49.0	18.3
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	NGEFIEITEKDTEGR	1737.8	K	W	3.4	0.5	48.5	16.1
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	WKEGEATLAPSLDLVGK	1814.0	K	-	2.2	0.2	0.0	0.0
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	WKEGEATLAPSLDLVGKI	1927.1	K	-	4.9	0.8	50.1	15.6
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	4.5	0.0	61.2	16.4
P0AE08	20743.9	S	U	T	A	ETD+CID	LIT	11	69.5	YAMIGDPTGALTR	1365.7	K	N	2.5	0.6	0.0	0.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	2	20.9	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.1	0.7	0.0	0.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	2	20.9	EGEATLAPSLDLVGKI	1612.9	K	-	3.5	0.5	0.0	0.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	AAQYVASHPGEVCPAKWK	1999.0	K	E	6.0	0.6	45.0	18.3
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.8	0.8	102.0	16.1
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	AWHSSSETIAK	1216.6	K	I	5.3	0.5	53.2	14.1
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	EGEATLAPSLDLVGK	1499.8	K	-	3.1	0.6	33.1	17.7
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	EGEATLAPSLDLVGKI	1612.9	K	-	3.5	0.5	43.5	14.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	IKYAMIGDPTGALTR	1606.9	K	N	3.1	0.5	0.0	0.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	LGVDVYAVSTDTHFTHK	1889.9	K	A	6.6	0.7	62.6	18.3
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	NFDNMREDEGLADRATFVVDPQGIIQAIEVTAEGIGR	4047.0	R	D	3.1	0.0	13.7	17.9
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	NGEFIEITEKDTEGR	1737.8	K	W	4.2	0.5	49.3	17.4
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	NQAFKNGEFIEITEKDTEGR	2327.1	K	W	6.1	0.7	82.9	18.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	WKEGEATLAPSLDLVGK	1814.0	K	-	5.2	0.6	48.1	17.0
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	WKEGEATLAPSLDLVGKI	1927.1	K	-	5.5	0.6	46.3	16.3
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	0.0	0.0	69.1	16.6
P0AE08	20743.9	S	U	T	B	ETD+CID	LIT	14	88.2	YAMIGDPTGALTR	1365.7	K	N	4.0	0.8	57.8	16.0
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	AAQYVASHPGEVCPAKWK	1999.0	K	E	4.3	0.5	42.4	18.5
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	6.7	0.7	121.0	16.3
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	AWHSSSETIAK	1216.6	K	I	2.8	0.6	36.9	14.5
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	EGEATLAPSLDLVGK	1499.8	K	-	2.7	0.3	24.0	16.5
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	EGEATLAPSLDLVGKI	1612.9	K	-	3.9	0.8	53.8	14.0
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	IKYAMIGDPTGALTR	1606.9	K	N	3.0	0.8	51.6	16.5
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	LGVDVYAVSTDTHFTHK	1889.9	K	A	5.3	0.6	68.5	17.6
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	NGEFIEITEKDTEGR	1738.8	K	W	0.0	0.0	56.7	16.0
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	WKEGEATLAPSLDLVGK	1814.0	K	-	2.3	0.2	3.3	17.0
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	WKEGEATLAPSLDLVGKI	1927.1	K	-	5.3	0.5	42.2	15.9
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	4.0	0.0	54.8	16.1
P0AE08	20743.9	S	U	T	C	ETD+CID	LIT	12	78.1	YAMIGDPTGALTR	1381.7	K	N	2.5	0.2	0.0	0.0
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	AAQYVASHPGEVCPAKWK	1999.0	K	E	0.0	0.0	45.0	18.3
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	ATFVVDPQGIIQAIEVTAEGIGR	2384.3	R	D	0.0	0.0	102.0	16.1
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	AWHSSSETIAK	1216.6	K	I	0.0	0.0	36.4	14.1
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	EGEATLAPSLDLVGK	1499.8	K	-	0.0	0.0	33.1	17.7
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	EGEATLAPSLDLVGKI	1612.9	K	-	0.0	0.0	43.5	14.0
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	IKYAMIGDPTGALTR	1606.9	K	N	0.0	0.0	37.7	16.2
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	LGVDVYAVSTDTHFTHK	1889.9	K	A	0.0	0.0	48.4	18.3
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	NGEFIEITEKDTEGR	1737.8	K	W	0.0	0.0	49.3	17.4
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	NQAFKNGEFIEITEKDTEGR	2327.1	K	W	0.0	0.0	82.9	18.1
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	WKEGEATLAPSLDLVGK	1814.0	K	-	0.0	0.0	48.1	17.0
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	WKEGEATLAPSLDLVGKI	1927.1	K	-	0.0	0.0	46.3	16.3
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	WSVFFFYPADFTFVCPTELGDVADHYEELQK	3757.7	R	L	0.0	0.0	69.1	16.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AE08	20743.9	S	U	T	B	HCD	FT	13	80.7	YAMIGDPTGALTR	1365.7	K	N	0.0	0.0	57.8	16.0
P0AE08	20743.9	S	U	T	C	HCD	FT	2	16.0	IKYAMIGDPTGALTR	1606.9	K	N	3.1	0.0	37.9	16.8
P0AE08	20743.9	S	U	T	C	HCD	FT	2	16.0	NGEFIEITEKDTEGR	1737.8	K	W	3.5	0.0	45.3	17.5
P63224	20797.4	G	T	T	A	CID	LIT	3	18.8	AAVLLADSFK	1034.6	R	A	2.0	0.5	19.2	12.6
P63224	20797.4	G	T	T	A	CID	LIT	3	18.8	EGDVLLGISTSGNSANVIK	1874.0	R	A	5.3	0.7	75.7	9.5
P63224	20797.4	G	T	T	A	CID	LIT	3	18.8	YVEAVGR	793.4	R	E	2.2	0.7	30.3	16.4
P63224	20797.4	G	U	A	A	CID	LIT	2	13.5	DDANIHAIQRAAVLLA	1690.9	K	D	3.0	0.0	29.9	13.8
P63224	20797.4	G	U	A	A	CID	LIT	2	13.5	DVSHISCVGN	1087.5	S	D	1.8	0.5	3.0	12.8
P63224	20797.4	G	T	A	B	CID	LIT	2	5.7	EAAETLANFLK	1206.6	N	D	2.0	0.6	0.0	0.0
P63224	20797.4	G	T	A	B	CID	LIT	2	5.7	ETLANFLK	935.5	A	D	2.2	0.6	25.6	13.0
P0A784	20798.4	G	U	T	A	CID	LIT	2	11.0	ESVAELAYYR	1200.6	R	E	3.6	0.4	40.2	11.5
P0A784	20798.4	G	U	T	A	CID	LIT	2	11.0	THTASGLVER	1070.6	R	V	3.0	0.0	36.2	12.0
P0A784	20798.4	G	U	A	A	CID	LIT	3	22.7	DANLNILAEGPTIAVHQS	1863.0	T	D	4.5	0.6	58.2	15.6
P0A784	20798.4	G	U	A	A	CID	LIT	3	22.7	DGFTKQGTHQAM	1320.6	L	D	2.3	0.0	18.4	12.6
P0A784	20798.4	G	U	A	A	CID	LIT	3	22.7	DRIIEIATLVT	1243.7	R	D	2.1	0.4	30.1	11.1
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	AGGKTQTAPVATPQELADYDAIIFGTPTR	2989.5	K	F	5.9	0.0	54.1	11.5
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	AVAEGASKVDGAEVVVK	1628.9	R	R	5.1	0.7	67.1	13.6
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	FGNMSGQMR	1027.4	R	T	2.9	0.0	46.4	3.0
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	GGTPYGATTIAGGDGSR	1537.7	R	Q	4.3	0.9	76.6	10.8
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	GGTPYGATTIAGGDGSRQPSQEELSIAR	2776.4	R	Y	3.0	0.0	38.5	12.6
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	QPSQEELSIAR	1257.6	R	Y	2.7	0.0	38.4	11.1
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	TQTAPVATPQELADYDAIIFGTPTR	2676.4	K	F	4.5	0.0	69.9	11.1
P0A8G6	20827.4	G	U	T	A	CID	LIT	8	48.0	YQGEYVAGLAVK	1297.7	R	L	2.9	0.7	39.3	12.3
P0A8G6	20827.4	S	U	T	A	CID	LIT	2	23.7	AGGKTQTAPVATPQELADYDAIIFGTPTR	2989.5	K	F	3.4	0.5	12.1	19.7
P0A8G6	20827.4	S	U	T	A	CID	LIT	2	23.7	TFLDQTGGLWASGALYGK	1884.9	R	L	4.6	0.6	23.3	18.3
P0A8G6	20827.4	S	U	T	B	CID	LIT	2	23.2	GGTPYGATTIAGGDGSRQPSQEELSIAR	2776.4	R	Y	1.9	0.0	23.9	19.0
P0A8G6	20827.4	S	U	T	B	CID	LIT	2	23.2	TFLDQTGGLWASGALYGK	1884.9	R	L	3.8	0.4	30.6	18.5
P0A9K9	20833.0	G	U	T	A	CID	LIT	2	23.0	FLAETDQGPVPVEITAVEDDHVVVDGNHMLAGQNLK	3857.9	R	F	3.4	0.0	26.5	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9K9	20833.0	G	U	T	A	CID	LIT	2	23.0	FNVEVVAIR	1046.6	K	E	3.1	0.5	63.6	13.4
P0A9K9	20833.0	G	U	A	B	CID	LIT	3	18.4	DENLVQRVPK	1197.7	Y	D	2.4	0.5	16.3	12.6
P0A9K9	20833.0	G	U	A	B	CID	LIT	3	18.4	DLVVSLAYQVRTE	1492.8	K	D	2.7	0.0	23.1	14.1
P0A9K9	20833.0	G	U	A	B	CID	LIT	3	18.4	DQGPVPVEITAVE	1353.7	T	D	3.5	0.5	50.5	14.0
P0A9K9	20833.0	S	U	T	A	CID	LIT	2	23.0	FLAETDQGPVPVEITAVEDDHVVVDGNHMLAGQNLK	3857.9	R	F	3.5	0.0	38.1	18.5
P0A9K9	20833.0	S	U	T	A	CID	LIT	2	23.0	FNVEVVAIR	1046.6	K	E	3.3	0.4	48.7	15.9
P0A9K9	20833.0	S	U	T	B	CID	LIT	2	23.0	FLAETDQGPVPVEITAVEDDHVVVDGNHMLAGQNLK	3857.9	R	F	4.8	0.0	28.4	18.5
P0A9K9	20833.0	S	U	T	B	CID	LIT	2	23.0	FNVEVVAIR	1046.6	K	E	2.3	0.0	46.8	15.3
P0A9K9	20833.0	S	U	T	C	CID	LIT	2	23.0	FLAETDQGPVPVEITAVEDDHVVVDGNHMLAGQNLK	3857.9	R	F	4.2	0.0	19.9	18.5
P0A9K9	20833.0	S	U	T	C	CID	LIT	2	23.0	FNVEVVAIR	1046.6	K	E	3.4	0.4	57.2	15.9
P0A9K9	20833.0	S	U	T	B	ETD+CID	LIT	2	10.2	DLVVSLAYQVR	1262.7	K	T	2.0	0.6	0.0	0.0
P0A9K9	20833.0	S	U	T	B	ETD+CID	LIT	2	10.2	FNVEVVAIR	1046.6	K	E	3.1	0.5	64.7	15.3
P0A9K9	20833.0	S	U	T	C	ETD+CID	LIT	3	28.6	DLVVSLAYQVR	1262.7	K	T	1.9	0.5	0.0	0.0
P0A9K9	20833.0	S	U	T	C	ETD+CID	LIT	3	28.6	FLAETDQGPVPVEITAVEDDHVVVDGNHMLAGQNLK	3857.9	R	F	3.9	0.5	36.0	18.3
P0A9K9	20833.0	S	U	T	C	ETD+CID	LIT	3	28.6	FNVEVVAIR	1046.6	K	E	2.9	0.4	28.9	15.3
P0A8X2	20895.3	G	U	T	A	CID	LIT	5	35.1	NPAADKVNVTINTTSVDTNHAER	2467.2	K	D	6.7	0.9	66.3	11.1
P0A8X2	20895.3	G	U	T	A	CID	LIT	5	35.1	SADFLNTAK	966.5	R	Y	2.8	0.7	26.2	14.3
P0A8X2	20895.3	G	U	T	A	CID	LIT	5	35.1	TDLGPASQEVDLIISVEGVQQK	2326.2	K	-	4.4	0.6	42.6	13.8
P0A8X2	20895.3	G	U	T	A	CID	LIT	5	35.1	YPQATFTSTSVK	1329.7	K	K	2.8	0.0	38.4	12.8
P0A8X2	20895.3	G	U	T	A	CID	LIT	5	35.1	YPQATFTSTSVKK	1457.8	K	D	3.6	0.0	42.6	12.3
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	AGFEAEGK	808.4	R	I	2.1	0.4	18.8	13.0
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	IDKEGQHAFVNFR	1560.8	K	I	3.5	0.0	35.0	12.3
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	LIGQGDDPWGGKR	1398.7	K	A	3.3	0.7	28.7	10.8
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	LKDFNIK	877.5	K	T	2.4	0.4	24.8	12.8
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	NPAADKVNVTINTTSVDTNHAER	2467.2	K	D	6.6	0.0	66.8	11.5
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	SADFLNTAK	966.5	R	Y	3.1	0.5	47.3	13.8
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	YPQATFTSTSVK	1329.7	K	K	3.7	0.6	42.7	14.3
P0A8X2	20895.3	G	T	T	A	CID	LIT	8	45.0	YPQATFTSTSVKK	1457.8	K	D	3.7	0.4	20.2	13.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8X2	20895.3	G	U	A	A	CID	LIT	4	31.4	DFLNTAKYPQATFTSTSVKKDG	2419.2	A	D	3.9	0.0	30.0	14.0
P0A8X2	20895.3	G	U	A	A	CID	LIT	4	31.4	DKHLRSA	826.5	R	D	1.1	0.5	13.1	7.0
P0A8X2	20895.3	G	U	A	A	CID	LIT	4	31.4	DKVNVTINTTSVDTNHAER	2114.0	A	D	5.5	0.7	85.4	15.7
P0A8X2	20895.3	G	U	A	A	CID	LIT	4	31.4	DLIISVEGVQQK	1328.7	V	-	4.4	0.6	59.2	14.0
P0A8X2	20895.3	G	T	A	A	CID	LIT	3	16.2	DKVNVTINTTSV	1290.7	A	D	2.8	0.2	2.7	14.5
P0A8X2	20895.3	G	T	A	A	CID	LIT	3	16.2	DKVNVTINTTSVDTNHAER	2114.0	A	D	4.9	0.0	53.7	15.7
P0A8X2	20895.3	G	T	A	A	CID	LIT	3	16.2	DLIISVEGVQQK	1328.7	V	-	3.1	0.8	36.9	13.8
P0A8X2	20895.3	G	T	T	B	CID	LIT	2	11.5	LIGQGDDPWGGKR	1398.7	K	A	3.2	0.4	7.8	11.1
P0A8X2	20895.3	G	T	T	B	CID	LIT	2	11.5	SADFLNTAK	966.5	R	Y	2.4	0.4	13.5	14.1
P0A8X2	20895.3	G	T	A	B	CID	LIT	4	28.8	DFLNTAKYPQATFTSTSVKK	2247.2	A	D	4.0	0.0	19.3	13.8
P0A8X2	20895.3	G	T	A	B	CID	LIT	4	28.8	DFLNTAKYPQATFTSTSVKKDG	2419.2	A	D	4.8	0.0	43.0	14.6
P0A8X2	20895.3	G	T	A	B	CID	LIT	4	28.8	DKVNVTINTTSV	1290.7	A	D	3.7	0.0	18.6	14.1
P0A8X2	20895.3	G	T	A	B	CID	LIT	4	28.8	DLTLNGVTKPVTLEAKLIGQG	2167.2	G	D	3.3	0.5	8.3	9.0
P0A8X2	20895.3	G	U	A	B	CID	LIT	2	9.4	DFNIKT	737.4	K	D	2.0	0.8	14.8	13.4
P0A8X2	20895.3	G	U	A	B	CID	LIT	2	9.4	DLIISVEGVQQK	1328.7	V	-	3.8	0.5	50.2	13.4
P0A8X2	20895.3	S	U	T	C	CID	LIT	3	17.8	IDKEGQHAFVNFR	1560.8	K	I	3.5	0.7	52.5	16.9
P0A8X2	20895.3	S	U	T	C	CID	LIT	3	17.8	SADFLNTAK	966.5	R	Y	2.1	0.3	31.9	17.2
P0A8X2	20895.3	S	U	T	C	CID	LIT	3	17.8	SADFLNTAKYPQATFTSTSVK	2277.1	R	K	3.0	0.6	8.9	18.3
P0A8X2	20895.3	S	U	T	B	ETD	LIT	5	28.8	AGFEAEGK	808.4	R	I	1.8	0.5	20.2	15.3
P0A8X2	20895.3	S	U	T	B	ETD	LIT	5	28.8	IDKEGQHAFVNFR	1560.8	K	I	5.4	0.6	62.1	16.8
P0A8X2	20895.3	S	U	T	B	ETD	LIT	5	28.8	LIGQGDDPWGGK	1242.6	K	R	2.4	0.3	16.2	12.6
P0A8X2	20895.3	S	U	T	B	ETD	LIT	5	28.8	SADFLNTAKYPQATFTSTSVK	2277.1	R	K	4.1	0.4	44.1	18.6
P0A8X2	20895.3	S	U	T	B	ETD	LIT	5	28.8	YPQATFTSTSVKK	1457.8	K	D	2.0	0.7	6.6	16.7
P0A8X2	20895.3	S	U	T	C	ETD	LIT	6	25.1	IDKEGQHAFVNFR	1560.8	K	I	2.9	0.5	19.0	16.8
P0A8X2	20895.3	S	U	T	C	ETD	LIT	6	25.1	LIGQGDDPWGGK	1242.6	K	R	2.8	0.4	30.8	12.3
P0A8X2	20895.3	S	U	T	C	ETD	LIT	6	25.1	LIGQGDDPWGGKR	1398.7	K	A	2.5	0.0	50.2	14.0
P0A8X2	20895.3	S	U	T	C	ETD	LIT	6	25.1	SADFLNTAKYPQATFTSTSVK	2277.1	R	K	5.3	0.7	55.2	18.1
P0A8X2	20895.3	S	U	T	C	ETD	LIT	6	25.1	SADFLNTAKYPQATFTSTSVKK	2405.2	R	D	2.9	0.0	30.1	18.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A8X2	20895.3	S	U	T	C	ETD	LIT	6	25.1	YPQATFTSTSVK	1329.7	K	K	1.7	0.0	25.8	15.9
P0A8X2	20895.3	S	U	T	C	ETD+CID	LIT	3	18.3	IDKEGQHAFVNFR	1560.8	K	I	3.9	0.5	62.1	16.8
P0A8X2	20895.3	S	U	T	C	ETD+CID	LIT	3	18.3	LIGQGDDPWGGKR	1398.7	K	A	2.3	0.3	10.9	14.5
P0A8X2	20895.3	S	U	T	C	ETD+CID	LIT	3	18.3	SADFLNTAK	966.5	R	Y	2.6	0.4	41.6	16.8
P0ADA5	20932.4	G	T	T	A	CID	LIT	5	22.4	ASYNVEGAFQASNK	1485.7	R	N	4.0	0.0	74.1	11.1
P0ADA5	20932.4	G	T	T	A	CID	LIT	5	22.4	DNQIVTLTASR	1217.6	R	D	3.0	0.6	27.3	14.0
P0ADA5	20932.4	G	T	T	A	CID	LIT	5	22.4	FLLQEVLEK	1118.6	R	Q	2.7	0.8	30.0	9.5
P0ADA5	20932.4	G	T	T	A	CID	LIT	5	22.4	VTRDNQIVTLTASR	1573.9	K	D	3.2	0.8	21.8	11.5
P0ADA5	20932.4	G	T	T	A	CID	LIT	5	22.4	YNIATK	709.4	R	A	2.3	0.3	31.5	12.6
P0ADA5	20932.4	G	U	A	A	CID	LIT	2	11.5	DQALAKVTR	1001.6	T	D	2.7	0.3	28.9	13.2
P0ADA5	20932.4	G	U	A	A	CID	LIT	2	11.5	DTSIHEFIKQNAR	1558.8	Q	-	3.5	0.6	26.4	14.5
P0ADA5	20932.4	G	T	A	A	CID	LIT	2	11.5	DQALAKVTR	1001.6	T	D	2.5	0.4	30.2	14.3
P0ADA5	20932.4	G	T	A	A	CID	LIT	2	11.5	DTSIHEFIKQNAR	1558.8	Q	-	2.5	0.4	16.7	13.6
P0ADA5	20932.4	G	T	A	B	CID	LIT	2	11.5	DQALAKVTR	1001.6	T	D	2.6	0.7	42.0	13.6
P0ADA5	20932.4	G	T	A	B	CID	LIT	2	11.5	DTSIHEFIKQNAR	1558.8	Q	-	2.2	0.7	3.4	14.0
P63020	20979.9	G	U	T	A	CID	LIT	6	33.0	ISDAAQAHFAK	1158.6	R	L	2.5	0.5	16.1	12.8
P63020	20979.9	G	U	T	A	CID	LIT	6	33.0	KVADDAPLMER	1244.6	R	V	2.5	0.7	15.4	11.1
P63020	20979.9	G	U	T	A	CID	LIT	6	33.0	LLANQEEGTQIR	1371.7	K	V	4.2	0.9	72.8	12.0
P63020	20979.9	G	U	T	A	CID	LIT	6	33.0	QLLNEFPELK	1230.7	K	G	2.7	0.5	40.4	14.5
P63020	20979.9	G	U	T	A	CID	LIT	6	33.0	VADDAPLMER	1116.5	K	V	3.4	0.0	38.8	8.5
P63020	20979.9	G	U	T	A	CID	LIT	6	33.0	VEYMLQSQINPQLAGHGGR	2098.1	R	V	3.5	0.0	60.5	13.4
P63020	20979.9	G	U	A	A	CID	LIT	3	20.4	DLTEHQRGEHSYY	1634.7	R	-	2.5	0.4	0.0	0.0
P63020	20979.9	G	U	A	A	CID	LIT	3	20.4	DQLGSQLTLKAPNAKMRKVA	2169.2	T	D	3.4	0.8	27.8	12.3
P63020	20979.9	G	U	A	A	CID	LIT	3	20.4	DTALKF	694.4	T	D	2.0	0.0	18.5	14.8
P63020	20979.9	G	T	T	B	CID	LIT	3	12.0	ISDAAQAHFAK	1158.6	R	L	3.5	0.8	52.9	13.0
P63020	20979.9	G	T	T	B	CID	LIT	3	12.0	ISDAAQAHFAKLLANQEEGTQIR	2511.3	R	V	4.9	0.7	62.9	12.3
P63020	20979.9	G	T	T	B	CID	LIT	3	12.0	LLANQEEGTQIR	1371.7	K	V	3.8	0.6	64.5	13.2
P63020	20979.9	S	U	T	B	CID	LIT	2	22.0	ISDAAQAHFAK	1158.6	R	L	2.9	0.6	27.1	14.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P63020	20979.9	S	U	T	B	CID	LIT	2	22.0	VFVINPGTPNAECGVSYCPPDAVEATDTALK	3292.6	R	F	5.6	0.0	40.5	17.8
P63020	20979.9	S	U	T	B	ETD+CID	LIT	2	21.5	QLLNEFPELK	1230.7	K	G	1.8	0.3	0.8	17.5
P63020	20979.9	S	U	T	B	ETD+CID	LIT	2	21.5	VFVINPGTPNAECGVSYCPPDAVEATDTALK	3292.6	R	F	0.0	0.0	47.5	17.7
P52061	21021.2	G	U	T	A	CID	LIT	5	38.6	EPAGTGGFGYDPIFFVPSEGK	2172.0	R	T	3.5	0.0	55.8	12.6
P52061	21021.2	G	U	T	A	CID	LIT	5	38.6	LLLDALR	813.5	K	N	2.7	0.4	28.8	10.0
P52061	21021.2	G	U	T	A	CID	LIT	5	38.6	VTALPAIADDSGLAVDVLGGAPGIYSAR	2669.4	K	Y	3.6	0.0	37.9	10.0
P52061	21021.2	G	U	T	A	CID	LIT	5	38.6	VVLATGNVGK	957.6	K	V	2.9	0.6	37.7	15.4
P52061	21021.2	G	U	T	A	CID	LIT	5	38.6	YSGEDATDQK	1113.5	R	N	3.3	0.0	42.3	4.8
P0AFH8	21055.1	G	U	T	A	CID	LIT	6	24.9	AALVDHDNIK	1095.6	K	S	1.8	0.6	25.7	11.1
P0AFH8	21055.1	G	U	T	A	CID	LIT	6	24.9	GVEGVTSVSDK	1077.5	K	L	3.0	0.0	39.6	12.6
P0AFH8	21055.1	G	U	T	A	CID	LIT	6	24.9	GVEGVTSVSDKLHVR	1582.9	K	D	2.0	0.6	23.7	10.8
P0AFH8	21055.1	G	U	T	A	CID	LIT	6	24.9	GYAGDTATTSEIK	1313.6	K	A	4.3	0.8	76.7	10.0
P0AFH8	21055.1	G	U	T	A	CID	LIT	6	24.9	LLADDIVPSR	1098.6	K	H	3.0	0.0	57.1	10.0
P0AFH8	21055.1	G	U	T	A	CID	LIT	6	24.9	VKAALVDHDNIK	1322.7	K	S	4.6	0.0	61.6	7.0
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	AALVDHDNIK	1095.6	K	S	3.1	0.8	50.2	11.1
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	AALVDHDNIKSTDISVK	1826.0	K	T	2.2	0.6	20.8	11.5
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	EGSVKGYAGDTATTSEIK	1813.9	K	A	4.5	0.7	72.9	12.8
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	GVEGVTSVSDK	1077.5	K	L	3.0	0.8	48.8	13.0
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	GVEGVTSVSDKLHVR	1582.9	K	D	4.3	0.6	73.9	10.4
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	GYAGDTATTSEIK	1313.6	K	A	3.8	0.8	80.4	10.0
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	GYAGDTATTSEIKAK	1512.8	K	L	5.0	0.7	85.7	10.4
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	HVKVETTDGVVQLSGTVDSQAQSDR	2656.3	R	A	6.4	0.8	76.9	13.0
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	LLADDIVPSR	1098.6	K	H	3.4	0.8	52.8	10.0
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	STDISVKTDQK	1221.6	K	V	3.4	0.6	48.5	15.7
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	TDQKVVTLSGFVESQAQAEEAVK	2464.3	K	V	5.3	0.8	54.2	12.6
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	VETTDGVVQLSGTVDSQAQSDR	2292.1	K	A	6.1	0.0	123.0	11.1
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	VETTDGVVQLSGTVDSQAQSDRAESIAK	2891.4	K	A	4.0	0.0	74.9	12.3
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	VGNFMDDSAITAK	1368.6	K	V	4.8	0.7	74.5	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	VKAALVDHDNIK	1322.7	K	S	4.8	0.7	69.5	7.0
P0AFH8	21055.1	G	T	T	A	CID	LIT	16	65.2	VVTLSGFVESQAQAEEAVK	1992.0	K	V	6.0	0.7	89.1	12.8
P0AFH8	21055.1	G	U	A	A	CID	LIT	6	43.3	DAKEGSVKGYAG	1181.6	R	D	3.3	0.8	35.8	13.2
P0AFH8	21055.1	G	U	A	A	CID	LIT	6	43.3	DDIVPSRHVKVETT	1595.8	A	D	2.5	0.0	23.1	11.1
P0AFH8	21055.1	G	U	A	A	CID	LIT	6	43.3	DDSAITAKVKAALVDH	1653.9	M	D	2.7	0.4	12.3	13.4
P0AFH8	21055.1	G	U	A	A	CID	LIT	6	43.3	DNIKSTDISVKT	1320.7	H	D	4.0	0.9	47.3	14.6
P0AFH8	21055.1	G	U	A	A	CID	LIT	6	43.3	DRAESIAKAVDGVKSVKN	1887.0	S	D	4.5	0.7	57.3	14.0
P0AFH8	21055.1	G	U	A	A	CID	LIT	6	43.3	ENNAQTTNESAGQKV	1590.7	A	D	3.2	0.8	64.5	8.5
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DAKEGSVKGYAG	1181.6	R	D	3.5	0.7	39.2	13.2
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DDIVPSRHVKVETT	1595.8	A	D	2.8	0.6	32.3	10.8
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DDSAITAKVKAALV	1401.8	M	D	3.4	0.7	28.9	11.5
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DDSAITAKVKAALVDH	1653.9	M	D	4.4	0.8	53.1	13.8
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DGVVQLSGTVDSQAQS	1590.8	T	D	2.8	0.5	30.4	12.8
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DHDNIKSTDISVKT	1572.8	V	D	2.8	0.5	8.4	14.6
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DISVKT	662.4	T	D	1.8	0.0	22.2	10.8
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DKLHVR	767.5	S	D	1.8	0.0	25.8	0.0
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DNIKSTDISVKT	1320.7	H	D	4.2	0.8	49.5	13.0
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DRAESIAKAV	1059.6	S	D	1.9	0.6	13.9	17.0
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DRAESIAKAVDGVKSVKN	1887.0	S	D	3.3	0.5	14.2	13.0
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DSAITAKVKAALVDH	1538.9	D	D	2.2	0.2	21.6	12.0
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DSSMNKVGNFM	1245.5	V	D	2.4	0.8	6.9	11.1
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	DTATTSEIKAKLLA	1461.8	G	D	3.4	0.7	23.3	11.5
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	ENNAQTTNESAGQKV	1590.7	A	D	4.0	0.8	78.1	8.5
P0AFH8	21055.1	G	T	A	A	CID	LIT	16	66.7	ENNAQTTNESAGQKVDSSMNKVGNFM	2801.2	A	D	4.4	0.0	50.2	6.0
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	AALVDHDNIKSTDISVK	1826.0	K	T	4.4	0.9	47.4	10.4
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	DAKEGSVK	833.4	R	G	1.9	0.4	14.2	12.6
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	EGSVKGYAGDTATTSEIK	1813.9	K	A	5.4	0.7	54.7	12.8
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	GVEGVTSVSDK	1077.5	K	L	2.6	0.6	13.9	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	GVEGVTSVSDKLHVR	1582.9	K	D	4.1	0.6	55.0	10.4
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	GYAGDTATTSEIK	1313.6	K	A	4.1	0.9	61.7	10.0
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	GYAGDTATTSEIKAK	1512.8	K	L	4.9	0.6	87.5	12.3
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	LLADDIVPSR	1098.6	K	H	3.3	0.7	49.2	10.0
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	STDISVKTDQK	1221.6	K	V	2.9	0.6	38.9	14.6
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	VGNFMDDSAITAK	1368.6	K	V	4.1	0.6	52.8	12.6
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	VGNFMDDSAITAKVK	1595.8	K	A	4.4	0.5	55.2	12.3
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	VKAALVDHDNIK	1322.7	K	S	3.0	0.4	6.6	9.5
P0AFH8	21055.1	G	T	T	B	CID	LIT	13	51.2	VVTLSGFVESQAQAEEAVK	1992.0	K	V	5.8	0.6	89.3	12.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DAKEGSVKGYAG	1181.6	R	D	2.7	0.4	36.1	14.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DDIVPSRHVKVETT	1595.8	A	D	3.0	0.7	26.4	11.5
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DDSAITAKVKAALV	1401.8	M	D	3.7	0.6	48.3	12.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DDSAITAKVKAALVDH	1653.9	M	D	5.2	0.7	63.5	13.6
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DGVKSVKN	846.5	V	D	2.2	0.4	15.3	14.9
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DGVVQLSGTVDSQAQS	1590.8	T	D	4.0	0.6	51.7	12.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DISVKT	662.4	T	D	1.6	0.0	26.2	10.8
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DLKTK	604.4	N	-	1.0	0.4	24.0	12.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DNIKSTDISVKT	1320.7	H	D	2.6	0.7	17.9	13.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DQKVVTLSGFVESQAQA	1806.9	T	E	3.2	0.9	28.4	15.6
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DRAESIAKAV	1059.6	S	D	2.2	0.7	19.6	17.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DRAESIAKAVDGVKSVKN	1887.0	S	D	4.0	0.5	50.0	14.1
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DSSMNKVGNFM	1229.5	V	D	3.7	0.8	31.4	12.3
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DSSMNKVGNFMD	1344.6	V	D	3.0	0.0	28.8	10.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	DTATTSEIKAKLLA	1461.8	G	D	2.6	0.8	28.9	11.5
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	EEAVKVAKGVEGVTSVS	1688.9	A	D	4.4	0.0	41.5	13.8
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	ENNAQTTNESAGQKV	1590.7	A	D	4.1	0.8	69.3	9.0
P0AFH8	21055.1	G	T	A	B	CID	LIT	18	83.1	ENNAQTTNESAGQKVDSSMNKVGNFM	2801.2	A	D	3.3	0.0	34.0	6.0
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DAKEGSVKGYAG	1181.6	R	D	2.5	0.8	19.0	13.4

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DDIVPSRHVKVETT	1595.8	A	D	1.9	0.7	15.5	11.5
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DDSAITAKVKAALV	1401.8	M	D	3.0	0.8	19.2	11.5
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DGVVQLSGTV	974.5	T	D	2.6	0.4	40.9	17.5
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DGVVQLSGTVDSQAQS	1590.8	T	D	4.8	0.6	86.8	13.0
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DRAESIAKAV	1059.6	S	D	2.2	0.3	18.1	17.0
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DRAESIAKAVDGVKSVKN	1887.0	S	D	2.8	0.4	16.7	14.0
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	DSSMNKVGNFM	1229.5	V	D	2.8	0.7	29.5	13.4
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	EEAVKVAKGVEGVTSVS	1688.9	A	D	3.0	0.0	23.0	14.8
P0AFH8	21055.1	G	U	A	B	CID	LIT	10	58.2	ENNAQTTNESAGQKV	1590.7	A	D	3.6	0.0	68.4	9.0
P0AFH8	21055.1	S	U	T	B	CID	LIT	4	31.8	AALVDHDNIK	1095.6	K	S	3.2	0.8	39.4	15.7
P0AFH8	21055.1	S	U	T	B	CID	LIT	4	31.8	HVKVETTDGVVQLSGTVDSQAQSDRAESIAK	3255.6	R	A	2.4	0.0	20.4	18.1
P0AFH8	21055.1	S	U	T	B	CID	LIT	4	31.8	LLADDIVPSR	1098.6	K	H	3.1	0.4	58.2	13.4
P0AFH8	21055.1	S	U	T	B	CID	LIT	4	31.8	VGNFMDDSAITAK	1368.6	K	V	2.5	0.8	24.1	15.2
P0AFH8	21055.1	S	U	T	C	CID	LIT	4	32.8	AALVDHDNIK	1095.6	K	S	3.1	0.0	44.8	15.6
P0AFH8	21055.1	S	U	T	C	CID	LIT	4	32.8	GVEGVTSVSDKLHVR	1582.9	K	D	3.1	0.5	21.3	13.6
P0AFH8	21055.1	S	U	T	C	CID	LIT	4	32.8	HVKVETTDGVVQLSGTVDSQAQSDRAESIAK	3255.6	R	A	3.1	0.0	30.5	18.4
P0AFH8	21055.1	S	U	T	C	CID	LIT	4	32.8	LLADDIVPSR	1098.6	K	H	3.0	0.5	35.7	13.4
P0AFH8	21055.1	S	U	T	B	ETD	LIT	3	18.9	GVEGVTSVSDKLHVR	1582.9	K	D	4.8	0.0	34.0	15.1
P0AFH8	21055.1	S	U	T	B	ETD	LIT	3	18.9	LLADDIVPSR	1098.6	K	H	2.6	0.3	43.1	13.0
P0AFH8	21055.1	S	U	T	B	ETD	LIT	3	18.9	VGNFMDDSAITAK	1368.6	K	V	2.5	0.8	36.8	15.2
P0AFH8	21055.1	S	U	T	C	ETD	LIT	3	16.4	AALVDHDNIK	1095.6	K	S	3.3	0.4	42.1	14.9
P0AFH8	21055.1	S	U	T	C	ETD	LIT	3	16.4	LLADDIVPSR	1098.6	K	H	2.1	0.4	33.8	13.4
P0AFH8	21055.1	S	U	T	C	ETD	LIT	3	16.4	VGNFMDDSAITAK	1368.6	K	V	2.4	0.7	18.8	15.2
P0AFH8	21055.1	S	U	T	B	ETD+CID	LIT	3	25.4	AALVDHDNIK	1095.6	K	S	0.0	0.0	40.9	15.7
P0AFH8	21055.1	S	U	T	B	ETD+CID	LIT	3	25.4	HVKVETTDGVVQLSGTVDSQAQSDRAESIAK	3255.6	R	A	0.0	0.0	24.3	18.7
P0AFH8	21055.1	S	U	T	B	ETD+CID	LIT	3	25.4	LLADDIVPSR	1098.6	K	H	0.0	0.0	58.1	13.4
P0AFH8	21055.1	S	U	T	B	ETD+CID	LIT	4	31.8	AALVDHDNIK	1095.6	K	S	3.1	0.0	40.9	15.7
P0AFH8	21055.1	S	U	T	B	ETD+CID	LIT	4	31.8	HVKVETTDGVVQLSGTVDSQAQSDRAESIAK	3255.6	R	A	4.3	0.6	24.3	18.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFH8	21055.1	S	U	T	B	ETD+CID	LIT	4	31.8	LLADDIVPSR	1098.6	K	H	3.2	0.4	58.1	13.4
P0AFH8	21055.1	S	U	T	B	ETD+CID	LIT	4	31.8	VGNFMDDSAITAK	1368.6	K	V	2.8	0.4	17.3	15.2
P0AFH8	21055.1	S	U	T	C	ETD+CID	LIT	4	32.8	AALVDHDNIK	1095.6	K	S	0.0	0.0	34.6	15.6
P0AFH8	21055.1	S	U	T	C	ETD+CID	LIT	4	32.8	GVEGVTSVSDKLHVR	1582.9	K	D	3.3	0.5	40.5	14.6
P0AFH8	21055.1	S	U	T	C	ETD+CID	LIT	4	32.8	HVKVETTDGVVQLSGTVDSQAQSDRAESIAK	3255.6	R	A	0.0	0.0	42.0	18.3
P0AFH8	21055.1	S	U	T	C	ETD+CID	LIT	4	32.8	LLADDIVPSR	1098.6	K	H	3.2	0.4	58.0	13.4
P0AFH8	21055.1	S	U	T	B	HCD	FT	3	25.4	AALVDHDNIK	1095.6	K	S	0.0	0.0	40.9	15.7
P0AFH8	21055.1	S	U	T	B	HCD	FT	3	25.4	HVKVETTDGVVQLSGTVDSQAQSDRAESIAK	3255.6	R	A	0.0	0.0	24.3	18.7
P0AFH8	21055.1	S	U	T	B	HCD	FT	3	25.4	LLADDIVPSR	1098.6	K	H	0.0	0.0	58.1	13.4
P0A7D1	21065.1	G	U	T	A	CID	LIT	2	13.9	LIDEAIDEAAR	1215.6	K	C	3.7	0.6	44.7	11.8
P0A7D1	21065.1	G	U	T	A	CID	LIT	2	13.9	LIVGLANPGAEYAATR	1615.9	K	H	3.9	0.0	61.1	12.8
P0A7D1	21065.1	G	T	T	B	CID	LIT	2	9.3	LGNNPNFHR	1068.5	K	L	1.8	0.4	1.1	9.5
P0A7D1	21065.1	G	T	T	B	CID	LIT	2	9.3	VTLGGEDVR	945.5	R	L	2.2	0.1	0.0	0.0
P0AF03	21204.4	G	U	T	A	CID	LIT	5	35.9	DVTPDATLAVADR	1343.7	R	E	3.9	0.0	61.6	12.6
P0AF03	21204.4	G	U	T	A	CID	LIT	5	35.9	GIPALEEWLTSALTTPFELETR	2474.3	K	L	4.8	0.0	61.1	12.6
P0AF03	21204.4	G	U	T	A	CID	LIT	5	35.9	IGLVSISDR	959.6	R	A	2.5	0.0	62.8	14.9
P0AF03	21204.4	G	U	T	A	CID	LIT	5	35.9	QALILNLPGQPK	1291.8	K	S	3.1	0.0	31.3	3.0
P0AF03	21204.4	G	U	T	A	CID	LIT	5	35.9	QISLHFVPTAILSR	1581.9	R	Q	3.0	0.0	40.3	7.0
P0AF03	21204.4	G	U	A	A	CID	LIT	2	14.4	DEMSCHLVLTTGGTGPARR	2058.0	V	D	2.2	0.5	19.4	14.1
P0AF03	21204.4	G	U	A	A	CID	LIT	2	14.4	DRASSGVYQ	982.5	S	D	2.5	0.0	22.3	13.8
P0A8E1	21208.8	G	U	T	A	CID	LIT	6	35.0	FKNISPHLQR	1239.7	K	I	2.3	0.8	22.2	9.0
P0A8E1	21208.8	G	U	T	A	CID	LIT	6	35.0	HDMQHLLK	1021.5	K	E	2.6	0.7	18.3	12.0
P0A8E1	21208.8	G	U	T	A	CID	LIT	6	35.0	IDRPEEYADIATK	1520.8	K	C	3.8	0.7	37.3	11.5
P0A8E1	21208.8	G	U	T	A	CID	LIT	6	35.0	NISPHLQR	964.5	K	I	2.2	0.6	22.3	10.4
P0A8E1	21208.8	G	U	T	A	CID	LIT	6	35.0	TSEELHHYYEIVWDEEQTHK	2573.2	R	F	5.8	0.0	49.8	8.5
P0A8E1	21208.8	G	U	T	A	CID	LIT	6	35.0	VLQLQFIDPDVR	1442.8	K	L	4.0	0.6	46.8	13.0
P0AGD3	21248.2	G	U	T	A	CID	LIT	6	38.9	AQFTDAAIK	964.5	K	N	2.7	0.8	17.8	14.3
P0AGD3	21248.2	G	U	T	A	CID	LIT	6	38.9	DALAPHISAETIEYHYGK	2015.0	K	H	4.3	0.7	77.2	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AGD3	21248.2	G	U	T	A	CID	LIT	6	38.9	HHQTYVTNLNNLIK	1694.9	K	G	3.7	0.0	48.4	8.5
P0AGD3	21248.2	G	U	T	A	CID	LIT	6	38.9	SFELPALPYAK	1235.7	M	D	0.0	0.0	35.7	14.8
P0AGD3	21248.2	G	U	T	A	CID	LIT	6	38.9	SLEEIIR	859.5	K	S	2.4	0.7	23.5	14.6
P0AGD3	21248.2	G	U	T	A	CID	LIT	6	38.9	VAEAIAASFGSFADFK	1630.8	K	A	3.7	0.6	91.1	12.8
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	AQFTDAAIK	964.5	K	N	3.0	0.7	35.1	14.3
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	AQFTDAAIKNFGSGWTWLVK	2240.2	K	N	5.3	0.0	61.8	10.8
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	DALAPHISAETIEYHYGK	2015.0	K	H	4.6	0.6	61.3	12.3
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	DALAPHISAETIEYHYGKHHQTYVTNLNNLIK	3690.9	K	G	4.6	0.0	41.6	9.0
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	GTAFEGK	709.4	K	S	1.6	0.4	14.9	10.0
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	GTAFEGKSLEEIIR	1549.8	K	S	3.6	0.5	59.5	13.0
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	HHQTYVTNLNNLIK	1694.9	K	G	5.3	0.8	49.0	7.8
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	LAIVSTSNAGTPLTTDATPLLTVDVWEHAYYIDYR	3866.9	K	N	5.5	0.0	45.1	10.0
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	NARPGYLEHFWALVNWEFVAK	2547.3	R	N	4.4	0.0	25.3	12.8
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	NFGSGWTWLVK	1294.7	K	N	2.6	0.7	12.5	12.6
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	SFELPALPYAK	1235.7	M	D	0.0	0.0	46.2	12.3
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	SLEEIIR	859.5	K	S	2.6	0.5	43.0	14.8
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	SSEGGVFNNAAQVWNHTFYWNCLAPNAGGEPTGK	3680.7	R	V	6.1	0.0	51.7	6.0
P0AGD3	21248.2	G	T	T	A	CID	LIT	14	94.8	VAEAIAASFGSFADFK	1630.8	K	A	5.2	0.9	114.0	13.0
P0AGD3	21248.2	G	T	A	A	CID	LIT	5	28.0	DALAPHISA	894.5	K	E	1.9	0.0	15.8	15.3
P0AGD3	21248.2	G	T	A	A	CID	LIT	5	28.0	DFKAQFT	856.4	A	D	1.9	0.6	17.2	12.0
P0AGD3	21248.2	G	T	A	A	CID	LIT	5	28.0	DGKLAIVSTSNAGTPLTT	1745.9	S	D	3.9	0.0	50.5	14.3
P0AGD3	21248.2	G	T	A	A	CID	LIT	5	28.0	EFVAKNLAA	962.5	W	-	2.1	0.8	0.0	0.0
P0AGD3	21248.2	G	T	A	A	CID	LIT	5	28.0	SFELPALPYAK	1235.7	M	D	0.0	0.0	51.7	15.1
P0AGD3	21248.2	G	T	A	B	CID	LIT	4	28.0	DAAIKNFGSGWTWLVKNS	1994.0	T	D	2.5	0.0	14.6	16.1
P0AGD3	21248.2	G	T	A	B	CID	LIT	4	28.0	DFKAQFT	856.4	A	D	2.0	0.0	17.4	8.5
P0AGD3	21248.2	G	T	A	B	CID	LIT	4	28.0	DGKLAIVSTSNAGTPLTT	1745.9	S	D	3.4	0.7	42.1	15.6
P0AGD3	21248.2	G	T	A	B	CID	LIT	4	28.0	SFELPALPYAK	1235.7	M	D	0.0	0.0	38.5	15.1
P0AGD3	21248.2	S	U	T	B	CID	LIT	2	13.0	DALAPHISAETIEYHYGK	2015.0	K	H	4.5	0.6	48.7	18.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AGD3	21248.2	S	U	T	B	CID	LIT	2	13.0	SLEEIIR	859.5	K	S	2.2	0.1	14.4	18.0
P63228	21276.2	G	U	A	A	CID	LIT	2	14.7	DCRKPHPGMLLSAR	1637.8	C	D	2.1	0.7	20.1	12.8
P63228	21276.2	G	U	A	A	CID	LIT	2	14.7	DLPQAIKKQQKPAQ	1592.9	A	-	3.5	0.0	32.7	9.0
P63228	21276.2	G	T	A	B	CID	LIT	2	12.0	AKSVPAIFL	945.6	M	D	0.0	0.0	31.1	3.0
P63228	21276.2	G	T	A	B	CID	LIT	2	12.0	DLPQAIKKQQKPAQ	1592.9	A	-	3.7	0.0	36.7	11.5
P0ADC1	21339.2	G	T	T	A	CID	LIT	2	8.3	AAEQLIR	800.5	R	K	2.4	0.4	41.6	15.2
P0ADC1	21339.2	G	T	T	A	CID	LIT	2	8.3	DNEQDMIVK	1091.5	K	E	1.7	0.5	18.1	6.0
P0ADC1	21339.2	G	U	A	A	CID	LIT	4	27.5	DMIVKEMY	1028.5	Q	D	2.2	0.8	16.0	13.6
P0ADC1	21339.2	G	U	A	A	CID	LIT	4	27.5	DNPQMALAKDNEQ	1473.7	F	D	4.2	0.0	38.5	15.1
P0ADC1	21339.2	G	U	A	A	CID	LIT	4	27.5	DRAAEQLIRKLPSIRAA	1908.1	Y	D	3.0	0.0	33.1	7.0
P0ADC1	21339.2	G	U	A	A	CID	LIT	4	27.5	DTPATPARVSTTLGN	1500.8	T	-	4.8	0.4	41.7	15.4
P0ADC1	21339.2	G	T	A	A	CID	LIT	3	23.3	DNPQMALAKDNEQ	1473.7	F	D	4.1	0.6	52.5	15.1
P0ADC1	21339.2	G	T	A	A	CID	LIT	3	23.3	DRAAEQLIRKLPSIRAA	1908.1	Y	D	1.6	0.0	19.9	6.0
P0ADC1	21339.2	G	T	A	A	CID	LIT	3	23.3	DTPATPARVSTTLGN	1500.8	T	-	3.7	0.5	35.4	15.4
P0ADC1	21339.2	G	T	A	B	CID	LIT	2	16.6	DRAAEQLIRKLPSIRAA	1908.1	Y	D	2.5	0.0	20.9	6.0
P0ADC1	21339.2	G	T	A	B	CID	LIT	2	16.6	DTPATPARVSTTLGN	1500.8	T	-	3.0	0.5	22.5	14.9
P0A8X0	21342.5	G	U	T	A	CID	LIT	2	11.5	AAIELAQR	871.5	R	I	2.9	0.6	42.9	14.1
P0A8X0	21342.5	G	U	T	A	CID	LIT	2	11.5	NALDKIPLDADLR	1453.8	K	A	3.0	0.4	21.9	12.0
P25536	21497.4	G	U	T	A	CID	LIT	2	15.7	DAEHAAQMLR	1141.5	R	K	2.2	0.4	18.7	10.0
P25536	21497.4	G	U	T	A	CID	LIT	2	15.7	IVTGIEEQRQPQESAQQYVVR	2458.3	R	L	4.7	0.0	43.9	12.0
P0A6N8	21515.4	G	U	T	A	CID	LIT	6	35.8	DIDIQSPTAR	1115.6	K	G	3.0	0.0	39.4	12.6
P0A6N8	21515.4	G	U	T	A	CID	LIT	6	35.8	FKGDDIVDTVTLTR	1579.8	R	R	4.1	0.9	47.9	9.0
P0A6N8	21515.4	G	U	T	A	CID	LIT	6	35.8	GAATLYK	723.4	R	M	2.5	0.4	29.0	13.4
P0A6N8	21515.4	G	U	T	A	CID	LIT	6	35.8	IHIEER	796.4	R	R	1.8	0.6	32.6	11.5
P0A6N8	21515.4	G	U	T	A	CID	LIT	6	35.8	NKPATLSTGLVIQVPEYLSPGEK	2441.3	R	I	5.8	0.0	71.4	7.0
P0A6N8	21515.4	G	U	T	A	CID	LIT	6	35.8	TGLKVEER	931.5	R	F	3.1	0.6	46.4	15.2
P0A6N8	21515.4	G	U	A	A	CID	LIT	2	13.7	DKEDYTPYTFTK	1507.7	M	D	3.2	0.5	24.5	14.3
P0A6N8	21515.4	G	U	A	A	CID	LIT	2	13.7	DVRTGLKVEERFKG	1633.9	S	D	1.7	0.5	10.1	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A6N8	21515.4	G	T	T	B	CID	LIT	2	9.5	DIDIQSPTAR	1115.6	K	G	2.5	0.6	12.9	12.6
P0A6N8	21515.4	G	T	T	B	CID	LIT	2	9.5	TGLKVEER	931.5	R	F	2.1	0.7	25.0	15.9
P0A6N8	21515.4	S	U	T	C	CID	LIT	2	19.5	FKGDDIVDTVTLTR	1579.8	R	R	3.8	0.4	53.0	15.9
P0A6N8	21515.4	S	U	T	C	CID	LIT	2	19.5	NKPATLSTGLVIQVPEYLSPGEK	2441.3	R	I	3.6	0.6	6.4	14.6
P0A6N8	21515.4	S	U	T	B	ETD+CID	LIT	2	19.5	FKGDDIVDTVTLTR	1579.8	R	R	4.0	0.5	0.0	0.0
P0A6N8	21515.4	S	U	T	B	ETD+CID	LIT	2	19.5	NKPATLSTGLVIQVPEYLSPGEK	2441.3	R	I	2.9	0.4	0.0	0.0
P0A6N8	21515.4	S	U	T	B	ETD+CID	LIT	2	19.5	FKGDDIVDTVTLTR	1579.8	R	R	4.0	0.5	57.3	15.9
P0A6N8	21515.4	S	U	T	B	ETD+CID	LIT	2	19.5	NKPATLSTGLVIQVPEYLSPGEK	2441.3	R	I	2.9	0.4	3.0	14.6
P41407	21640.4	G	U	A	A	CID	LIT	2	13.4	DAKAAIDSIVSA	1160.6	S	-	2.6	0.7	27.2	14.9
P41407	21640.4	G	U	A	A	CID	LIT	2	13.4	DAPLTPRQQEALALS	1609.9	S	D	2.9	0.6	16.4	14.0
P41407	21640.4	G	T	A	B	CID	LIT	2	11.9	DAPLTPRQQEALALS	1609.9	S	D	2.1	0.0	19.0	14.3
P41407	21640.4	G	T	A	B	CID	LIT	2	11.9	ELVGALRPSDAPLTPRQQ	1948.1	G	E	2.0	0.5	0.0	0.0
P0A729	21673.5	G	U	T	A	CID	LIT	3	11.9	HLSEAEIDNYVR	1445.7	R	K	3.0	0.5	8.0	11.8
P0A729	21673.5	G	U	T	A	CID	LIT	3	11.9	HLSEAEIDNYVRK	1573.8	R	E	4.0	0.7	17.8	11.8
P0A729	21673.5	G	U	T	A	CID	LIT	3	11.9	LILASTSPWR	1143.7	K	R	3.1	0.7	51.2	13.4
P0AGB6	21678.1	G	U	T	A	CID	LIT	2	14.1	EAIDNKVQPLIR	1395.8	R	-	3.3	0.0	35.6	9.0
P0AGB6	21678.1	G	U	T	A	CID	LIT	2	14.1	EISNPENLMLSEELR	1773.9	K	Q	3.2	0.0	61.8	11.8
P32160	21746.1	G	U	T	A	CID	LIT	2	10.6	LALSESLEGLNK	1273.7	K	-	2.8	0.7	44.9	12.3
P32160	21746.1	G	U	T	A	CID	LIT	2	10.6	LQSLLTAGK	930.6	K	N	2.0	0.4	26.7	11.8
P09372	21779.8	G	T	T	A	CID	LIT	4	16.8	DEKVANLEAQLAEAQTR	1886.0	R	E	4.9	0.6	61.6	12.6
P09372	21779.8	G	T	T	A	CID	LIT	4	16.8	ERDGILR	858.5	R	V	2.2	0.1	23.3	16.5
P09372	21779.8	G	T	T	A	CID	LIT	4	16.8	VANLEAQLAEAQTR	1513.8	K	E	4.1	0.6	78.8	15.1
P09372	21779.8	G	T	T	A	CID	LIT	4	16.8	VKAEMENLR	1089.6	R	R	2.5	0.6	45.3	14.9
P09372	21779.8	G	T	A	A	CID	LIT	2	7.6	DGILRVKA	871.5	R	E	1.7	0.5	0.0	0.0
P09372	21779.8	G	T	A	A	CID	LIT	2	7.6	DSLDRAL	789.4	I	E	2.1	0.2	21.3	18.5
P09372	21779.8	S	U	T	B	CID	LIT	3	28.4	TPEGQAPEEIIMDQHEEIEAVEPEASAEQVDPR	3673.7	K	D	5.0	0.0	20.1	14.9
P09372	21779.8	S	U	T	B	CID	LIT	3	28.4	VANLEAQLAEAQTR	1513.8	K	E	2.9	0.5	17.6	17.0
P09372	21779.8	S	U	T	B	CID	LIT	3	28.4	VKAEMENLR	1089.6	R	R	2.6	0.3	14.8	17.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7I7	21818.4	G	U	T	A	CID	LIT	2	9.2	NPNNEHYLDTK	1344.6	R	A	4.0	0.0	45.3	10.4
P0A7I7	21818.4	G	U	T	A	CID	LIT	2	9.2	VPLIVGR	753.5	R	N	1.9	0.0	37.5	6.0
P0A7I7	21818.4	G	U	A	A	CID	LIT	2	13.3	DTKAEKMGHLLNK	1484.8	L	-	4.3	0.5	49.1	13.0
P0A7I7	21818.4	G	U	A	A	CID	LIT	2	13.3	DTVEANHQLGFAA	1372.6	Y	D	1.9	0.6	0.0	0.0
P0AEY5	21873.2	G	U	T	A	CID	LIT	2	8.8	YGSGGLVQGK	965.5	K	K	2.5	0.0	26.7	14.6
P0AEY5	21873.2	G	U	T	A	CID	LIT	2	8.8	YTEEYRK	988.5	R	H	2.1	0.5	28.8	8.5
P0AEY5	21873.2	G	T	T	A	CID	LIT	3	12.4	DLGHDVR	811.4	R	I	1.8	0.7	27.2	13.0
P0AEY5	21873.2	G	T	T	A	CID	LIT	3	12.4	YGSGGLVQGK	965.5	K	K	3.7	0.3	69.0	14.6
P0AEY5	21873.2	G	T	T	A	CID	LIT	3	12.4	YTEEYRK	988.5	R	H	2.5	0.0	32.8	8.5
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	ALFDQVLPAER	1258.7	K	Y	3.4	0.0	29.8	13.4
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	AVVNAVK	700.4	R	R	2.0	0.7	35.0	15.7
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	AVVNAVKR	856.5	R	A	2.3	0.6	52.8	15.3
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	ISGADDAHWAVK	1269.6	K	K	3.7	0.7	42.5	11.8
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	KISGADDAHWAVK	1397.7	K	K	4.8	0.6	34.3	12.6
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	TTIAEQASLQQK	1317.7	K	A	4.3	0.3	63.7	13.0
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	VTEHHETPGLGDK	1419.7	R	I	3.4	0.6	53.7	12.8
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	VTEHHETPGLGDKIELR	1931.0	R	L	5.1	0.6	52.8	11.5
P77285	21894.3	G	T	T	A	CID	LIT	9	40.8	YNNALAQSCYLVTAPELGKGEHR	2591.3	R	V	3.3	0.0	21.6	11.5
P77285	21894.3	G	T	T	B	CID	LIT	2	13.6	AGLYAQTLPAQLSQLPACGE	2088.0	R	-	4.3	0.0	62.6	10.4
P77285	21894.3	G	T	T	B	CID	LIT	2	13.6	AVVNAVKR	856.5	R	A	2.4	0.0	57.9	15.2
P0A9H5	21980.4	G	U	T	A	CID	LIT	2	12.2	DILELADTVSELRPVK	1798.0	R	H	4.2	0.5	57.9	9.0
P0A9H5	21980.4	G	U	T	A	CID	LIT	2	12.2	HAFDAGVK	844.4	K	A	2.2	0.7	19.8	11.1
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	AEVTGSGKKPWR	1315.7	R	Q	3.4	0.8	60.0	13.6
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	DAQSALTVSETTFGR	1582.8	K	D	4.0	0.8	51.3	12.0
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	DATGIDPVSLIAFDK	1561.8	R	V	4.4	0.8	63.4	13.4
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	5.2	0.0	85.1	11.5
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	4.9	0.6	39.6	10.0
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	FSVEAPK	777.4	K	T	2.4	0.7	30.7	15.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	LIVVEK	700.5	R	F	1.6	0.7	19.0	9.0
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	LKDMALEDVLIITGELDENLFLAAR	2802.5	K	N	4.4	0.8	43.7	10.0
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	MELVLK	732.4	-	D	1.8	0.7	22.5	9.0
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	NLHKVDVR	980.6	R	D	2.1	0.6	20.9	12.6
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	QDRLIVVEK	1099.6	R	F	2.7	0.3	18.8	13.8
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	SGGVTFAARPQDHSQK	1685.8	R	V	3.7	0.5	47.5	10.8
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	SGGVTFAARPQDHSQKVNK	2027.0	R	K	2.1	0.7	21.9	13.0
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	SGSIKSPIWR	1130.6	R	S	3.6	0.7	47.3	13.2
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	SILSELVR	916.5	K	Q	2.4	0.7	33.5	13.4
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	SPIWR	658.4	K	S	1.5	0.7	25.8	4.8
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	TRAEVTGSGK	1005.5	K	K	4.0	0.5	47.1	11.5
P60723	22068.6	G	U	T	A	CID	LIT	18	81.6	VVMTADAVK	949.5	K	Q	2.6	0.7	40.6	13.8
P60723	22068.6	G	U	A	A	CID	LIT	7	34.3	DAQSALTVSETTFGR	1582.8	K	D	3.8	0.5	73.8	15.9
P60723	22068.6	G	U	A	A	CID	LIT	7	34.3	DATGIDPVSLIAF	1318.7	R	D	1.9	0.5	2.5	16.7
P60723	22068.6	G	U	A	A	CID	LIT	7	34.3	DAVKQVEEMLA	1248.6	A	-	2.8	0.7	19.6	13.8
P60723	22068.6	G	U	A	A	CID	LIT	7	34.3	DENLFLAARNLHKV	1639.9	L	D	4.2	0.0	46.4	13.0
P60723	22068.6	G	U	A	A	CID	LIT	7	34.3	DKVVMTA	763.4	F	D	1.9	0.2	28.8	16.5
P60723	22068.6	G	U	A	A	CID	LIT	7	34.3	DVRDATGIDPVSLIAF	1688.9	V	D	3.1	0.0	26.1	15.2
P60723	22068.6	G	U	A	A	CID	LIT	7	34.3	MELVLK	732.4	-	D	1.8	0.1	24.0	10.4
P60723	22068.6	G	U	T	B	CID	LIT	4	28.9	DAQSALTVSETTFGR	1582.8	K	D	4.4	0.9	89.9	12.3
P60723	22068.6	G	U	T	B	CID	LIT	4	28.9	DATGIDPVSLIAFDK	1561.8	R	V	4.2	0.9	54.3	13.6
P60723	22068.6	G	U	T	B	CID	LIT	4	28.9	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	4.5	0.7	51.9	10.0
P60723	22068.6	G	U	T	B	CID	LIT	4	28.9	VVMTADAVK	933.5	K	Q	2.7	0.0	24.2	14.3
P60723	22068.6	G	T	A	B	CID	LIT	3	16.9	DAQSALTVSETTFGR	1582.8	K	D	4.2	0.5	66.2	16.3
P60723	22068.6	G	T	A	B	CID	LIT	3	16.9	DATGIDPVSLIAF	1318.7	R	D	2.3	0.4	10.8	16.7
P60723	22068.6	G	T	A	B	CID	LIT	3	16.9	MELVLK	732.4	-	D	1.5	0.6	11.1	10.4
P60723	22068.6	G	U	A	B	CID	LIT	5	25.9	DAQSALTVSETTFGR	1582.8	K	D	4.2	0.5	85.7	16.0
P60723	22068.6	G	U	A	B	CID	LIT	5	25.9	DATGIDPVSLIAF	1318.7	R	D	2.9	0.4	29.7	16.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60723	22068.6	G	U	A	B	CID	LIT	5	25.9	DAVKQVEEMLA	1232.6	A	-	2.4	0.2	26.6	14.3
P60723	22068.6	G	U	A	B	CID	LIT	5	25.9	DKVVMTA	763.4	F	D	2.1	0.2	21.4	16.5
P60723	22068.6	G	U	A	B	CID	LIT	5	25.9	MELVLK	732.4	-	D	2.0	0.2	22.3	10.4
P60723	22068.6	S	U	T	A	CID	LIT	7	45.8	DAQSALTVSETTFGR	1582.8	K	D	3.3	0.5	28.5	17.1
P60723	22068.6	S	U	T	A	CID	LIT	7	45.8	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	2.3	0.3	30.5	18.1
P60723	22068.6	S	U	T	A	CID	LIT	7	45.8	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	5.9	0.7	76.8	17.6
P60723	22068.6	S	U	T	A	CID	LIT	7	45.8	SGGVTFAARPQDHSQK	1685.8	R	V	2.2	0.7	20.2	14.8
P60723	22068.6	S	U	T	A	CID	LIT	7	45.8	SGGVTFAARPQDHSQKVNK	2027.0	R	K	1.7	0.3	27.3	17.9
P60723	22068.6	S	U	T	A	CID	LIT	7	45.8	SGGVTFAARPQDHSQKVNKK	2155.1	R	M	2.3	0.6	11.3	17.6
P60723	22068.6	S	U	T	A	CID	LIT	7	45.8	TRAEVTGSGKKPWR	1572.9	K	Q	3.3	0.2	27.2	15.9
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	DAQSALTVSETTFGR	1582.8	K	D	3.0	0.6	39.7	17.1
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	DATGIDPVSLIAFDK	1561.8	R	V	2.9	0.5	13.4	18.0
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	2.3	0.0	32.4	18.3
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	4.9	0.6	39.0	18.1
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	NLHKVDVR	980.6	R	D	1.6	0.6	12.1	14.0
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	SGGVTFAARPQDHSQK	1685.8	R	V	4.3	0.6	47.6	15.3
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	SGGVTFAARPQDHSQKVNK	2027.0	R	K	3.1	0.4	24.4	18.1
P60723	22068.6	S	U	T	B	CID	LIT	8	46.3	SILSELVR	916.5	K	Q	2.7	0.7	39.3	15.2
P60723	22068.6	S	U	T	C	CID	LIT	6	34.3	DAQSALTVSETTFGR	1582.8	K	D	3.9	0.8	52.4	15.8
P60723	22068.6	S	U	T	C	CID	LIT	6	34.3	DATGIDPVSLIAFDK	1561.8	R	V	3.2	0.6	18.5	18.2
P60723	22068.6	S	U	T	C	CID	LIT	6	34.3	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	5.4	0.6	66.7	18.1
P60723	22068.6	S	U	T	C	CID	LIT	6	34.3	SGGVTFAARPQDHSQK	1685.8	R	V	1.7	0.5	31.0	16.6
P60723	22068.6	S	U	T	C	CID	LIT	6	34.3	SGGVTFAARPQDHSQKVNK	2027.0	R	K	2.3	0.3	0.0	0.0
P60723	22068.6	S	U	T	C	CID	LIT	6	34.3	SGGVTFAARPQDHSQKVNKK	2155.1	R	M	1.8	0.5	15.5	18.0
P60723	22068.6	S	U	T	A	ETD	LIT	7	44.3	AEVTGSGKKPWR	1315.7	R	Q	5.3	0.6	50.9	16.8
P60723	22068.6	S	U	T	A	ETD	LIT	7	44.3	DAQSALTVSETTFGR	1582.8	K	D	2.2	0.3	47.7	15.8
P60723	22068.6	S	U	T	A	ETD	LIT	7	44.3	DATGIDPVSLIAFDK	1561.8	R	V	2.3	0.5	11.0	17.3
P60723	22068.6	S	U	T	A	ETD	LIT	7	44.3	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	4.9	0.6	32.9	18.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60723	22068.6	S	U	T	A	ETD	LIT	7	44.3	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	4.3	0.6	0.0	0.0
P60723	22068.6	S	U	T	A	ETD	LIT	7	44.3	SGGVTFAARPQDHSQK	1685.8	R	V	5.9	0.7	49.6	16.0
P60723	22068.6	S	U	T	A	ETD	LIT	7	44.3	SGGVTFAARPQDHSQKVNK	2027.0	R	K	6.1	0.5	70.7	17.7
P60723	22068.6	S	U	T	B	ETD	LIT	4	27.4	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	4.6	0.0	21.4	18.5
P60723	22068.6	S	U	T	B	ETD	LIT	4	27.4	FSVEAPK	777.4	K	T	1.7	0.7	20.3	14.1
P60723	22068.6	S	U	T	B	ETD	LIT	4	27.4	NLHKVDVR	980.6	R	D	2.2	0.7	26.9	14.0
P60723	22068.6	S	U	T	B	ETD	LIT	4	27.4	SGGVTFAARPQDHSQK	1685.8	R	V	5.9	0.6	47.4	16.8
P60723	22068.6	S	U	T	C	ETD	LIT	2	11.9	SGGVTFAARPQDHSQK	1685.8	R	V	6.1	0.7	47.8	16.6
P60723	22068.6	S	U	T	C	ETD	LIT	2	11.9	SILSELVR	916.5	K	Q	1.7	0.3	20.5	15.1
P60723	22068.6	S	U	T	C	ETD	FT	2	11.4	FSVEAPK	777.4	K	T	1.0	0.0	20.9	14.1
P60723	22068.6	S	U	T	C	ETD	FT	2	11.4	SGGVTFAARPQDHSQK	1685.8	R	V	3.0	0.0	40.9	15.8
P60723	22068.6	S	U	T	B	ETD+CID	LIT	5	31.3	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	0.0	0.0	28.8	18.3
P60723	22068.6	S	U	T	B	ETD+CID	LIT	5	31.3	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	0.0	0.0	28.4	18.1
P60723	22068.6	S	U	T	B	ETD+CID	LIT	5	31.3	SGGVTFAARPQDHSQK	1685.8	R	V	0.0	0.0	40.0	16.0
P60723	22068.6	S	U	T	B	ETD+CID	LIT	5	31.3	SGGVTFAARPQDHSQKVNK	2027.0	R	K	0.0	0.0	31.6	17.8
P60723	22068.6	S	U	T	B	ETD+CID	LIT	5	31.3	SGGVTFAARPQDHSQKVNKK	2155.1	R	M	0.0	0.0	17.4	17.7
P60723	22068.6	S	U	T	A	ETD+CID	LIT	5	31.3	DATGIDPVSLIAFDK	1561.8	R	V	3.6	0.6	17.4	17.6
P60723	22068.6	S	U	T	A	ETD+CID	LIT	5	31.3	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	3.5	0.8	28.4	17.5
P60723	22068.6	S	U	T	A	ETD+CID	LIT	5	31.3	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	6.1	0.6	63.3	18.1
P60723	22068.6	S	U	T	A	ETD+CID	LIT	5	31.3	SGGVTFAARPQDHSQK	1685.8	R	V	1.5	0.7	23.7	16.0
P60723	22068.6	S	U	T	A	ETD+CID	LIT	5	31.3	SGGVTFAARPQDHSQKVNKK	2155.1	R	M	3.4	0.6	26.8	17.8
P60723	22068.6	S	U	T	B	ETD+CID	LIT	2	21.4	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	2.4	0.5	0.0	0.0
P60723	22068.6	S	U	T	B	ETD+CID	LIT	2	21.4	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	5.0	0.7	0.0	0.0
P60723	22068.6	S	U	T	B	ETD+CID	LIT	6	38.8	DAQSALTVSETTFGR	1582.8	K	D	2.2	0.6	0.0	0.0
P60723	22068.6	S	U	T	B	ETD+CID	LIT	6	38.8	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	2.4	0.5	0.0	0.0
P60723	22068.6	S	U	T	B	ETD+CID	LIT	6	38.8	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	4.5	0.6	30.0	18.1
P60723	22068.6	S	U	T	B	ETD+CID	LIT	6	38.8	SGGVTFAARPQDHSQK	1685.8	R	V	4.2	0.5	40.0	16.0
P60723	22068.6	S	U	T	B	ETD+CID	LIT	6	38.8	SGGVTFAARPQDHSQKVNK	2027.0	R	K	0.0	0.0	31.6	17.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60723	22068.6	S	U	T	B	ETD+CID	LIT	6	38.8	SGGVTFAARPQDHSQKVNKK	2155.1	R	M	3.2	0.8	17.4	17.7
P60723	22068.6	S	U	T	C	ETD+CID	LIT	3	26.9	DAQSALTVSETTFGR	1582.8	K	D	3.7	0.4	0.0	0.0
P60723	22068.6	S	U	T	C	ETD+CID	LIT	3	26.9	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	3.6	0.5	37.6	18.1
P60723	22068.6	S	U	T	C	ETD+CID	LIT	3	26.9	SGGVTFAARPQDHSQKVNKK	2155.1	R	M	2.7	0.4	15.7	17.9
P60723	22068.6	S	U	T	B	HCD	FT	4	31.3	DATGIDPVSLIAFDKVVMTADAVK	2476.3	R	Q	0.0	0.0	28.8	18.3
P60723	22068.6	S	U	T	B	HCD	FT	4	31.3	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	0.0	0.0	28.4	18.1
P60723	22068.6	S	U	T	B	HCD	FT	4	31.3	SGGVTFAARPQDHSQK	1685.8	R	V	0.0	0.0	40.0	16.0
P60723	22068.6	S	U	T	B	HCD	FT	4	31.3	SGGVTFAARPQDHSQKVNKK	2155.1	R	M	0.0	0.0	17.4	17.7
P60723	22068.6	S	U	T	A	HCD	FT	2	11.4	DAQSALTVSETTFGR	1582.8	K	D	2.9	0.0	67.9	17.1
P60723	22068.6	S	U	T	A	HCD	FT	2	11.4	SILSELVR	916.5	K	Q	1.3	0.0	23.6	15.1
P60723	22068.6	S	U	T	B	HCD	FT	2	13.4	DFNEALVHQVVVAYAAGAR	2030.0	R	Q	4.2	0.0	42.2	17.7
P60723	22068.6	S	U	T	B	HCD	FT	2	13.4	SILSELVR	916.5	K	Q	1.3	0.0	24.0	15.2
P76576	22158.4	G	U	A	A	CID	LIT	2	12.6	DKQGARSAWEAGVKS	1589.8	G	D	2.5	0.6	28.9	15.3
P76576	22158.4	G	U	A	A	CID	LIT	2	12.6	DLRGEALLSKG	1158.6	A	D	2.4	0.3	7.1	15.1
P37665	22179.6	G	T	T	A	CID	LIT	4	26.5	ADSVASALITQGVDASR	1660.9	R	I	3.6	0.6	43.5	14.6
P37665	22179.6	G	T	T	A	CID	LIT	4	26.5	IRTQGLGPANPIASNSTAEGK	2082.1	R	A	6.9	0.0	89.9	11.1
P37665	22179.6	G	T	T	A	CID	LIT	4	26.5	TAVNVIGYTDSTGGHDLNMR	2121.0	K	L	5.1	0.0	106.0	9.0
P37665	22179.6	G	T	T	A	CID	LIT	4	26.5	TQGLGPANPIASNSTAEGK	1812.9	R	A	4.5	0.9	48.7	10.0
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	ALREIHER	1023.6	R	A	3.0	0.7	26.2	10.8
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	EGVNSTESGLQFR	1423.7	K	V	3.1	0.0	42.0	10.0
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	FQAMAAEGVK	1051.5	R	Y	2.2	0.3	12.8	14.1
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	KEGVNSTESGLQFR	1551.8	K	V	4.3	0.6	37.3	12.8
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	LIDGTVFDSSVAR	1379.7	K	G	3.9	0.0	81.7	12.6
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	VINQGEGAIPAR	1224.7	R	T	3.4	0.7	55.8	13.2
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	VINQGEGAIPARTDR	1596.8	R	V	2.4	0.7	20.0	12.3
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	WELTIPQELAYGER	1704.9	K	G	3.1	0.8	17.9	13.0
P0A9L3	22198.1	G	U	T	A	CID	LIT	9	39.3	YLEENAKK	994.5	K	E	2.2	0.6	22.6	11.8
P0A9L3	22198.1	G	U	A	A	CID	LIT	2	9.7	DALEGKHPAVPV	1232.7	A	D	2.5	0.4	14.7	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A9L3	22198.1	G	U	A	A	CID	LIT	2	9.7	DALEGKHPAVPVDVVHRALR	2179.2	A	E	2.7	0.0	35.6	11.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	AIQVTTGAK	888.5	R	K	2.0	0.3	28.4	13.4
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	ANRVTKPEAGHFAK	1525.8	K	A	3.3	0.0	27.9	10.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	DLANDGYR	923.4	K	A	2.3	0.7	17.6	7.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.3	0.6	25.2	6.0
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	GAVPGATGSDLIVKPAVKA	1751.0	K	-	4.6	0.0	66.8	6.0
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	GFAGTVKR	835.5	K	W	1.9	0.6	26.4	13.2
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	GLWEFR	807.4	R	L	1.6	0.7	19.0	15.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	4.4	0.7	55.9	12.0
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	KMAGQMGNER	1121.5	K	V	3.4	0.8	64.5	9.5
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	MAGQMGNER	993.4	K	V	3.1	0.0	64.9	4.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	MIGLVGK	717.4	-	K	1.9	0.6	18.0	10.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	MIGLVGKK	845.5	-	V	2.7	0.0	30.0	6.0
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	NLLLVK	699.5	R	G	1.5	0.5	27.0	9.5
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	TQDATHGNSLSHR	1423.7	R	V	3.1	0.7	59.7	11.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	VDAERNLLLVK	1269.8	R	G	2.5	0.4	12.3	10.0
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	VTKPEAGHFAK	1184.6	R	A	3.1	0.8	34.1	13.8
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	VTQVKDLANDGYR	1478.8	R	A	3.9	0.8	51.8	14.0
P60438	22224.8	G	U	T	A	CID	LIT	18	67.5	VTVQSLDVVR	1115.6	R	V	3.8	0.6	64.4	14.0
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	AIQVTTGAK	888.5	R	K	2.5	0.4	27.5	13.2
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	DLANDGYR	923.4	K	A	2.3	0.8	18.6	7.0
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	GAVPGATGSDLIVKPAVK	1680.0	K	-	5.1	0.7	50.6	7.8
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	GAVPGATGSDLIVKPAVKA	1751.0	K	-	4.8	0.0	43.5	6.0
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	4.6	0.9	67.5	11.8
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	KMAGQMGNER	1121.5	K	V	3.8	0.8	59.1	9.5
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	MAGQMGNER	993.4	K	V	2.6	0.0	39.1	4.8
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	NLLLVK	699.5	R	G	1.5	0.4	22.5	9.5
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	TQDATHGNSLSHR	1423.7	R	V	3.2	0.5	43.5	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	VTQVKDLANDGYR	1478.8	R	A	3.5	0.8	47.0	13.6
P60438	22224.8	G	T	T	A	CID	LIT	11	47.8	VTVQSLDVVR	1115.6	R	V	3.9	0.5	70.7	13.0
P60438	22224.8	G	T	A	A	CID	LIT	6	26.3	DAERNLLLVKGAVPGATGSDLIVKPAVKA	2902.7	V	-	4.0	0.0	25.1	8.5
P60438	22224.8	G	T	A	A	CID	LIT	6	26.3	DGVSIPVTVIEVEANRVTQVK	2253.2	E	D	3.4	0.0	39.9	12.3
P60438	22224.8	G	T	A	A	CID	LIT	6	26.3	DLIVKPAVKA	1053.7	S	-	2.4	0.0	19.1	0.0
P60438	22224.8	G	T	A	A	CID	LIT	6	26.3	DVVRVDAERNLLLVKGAVPGATGS	2436.4	L	D	2.4	0.2	9.5	10.4
P60438	22224.8	G	T	A	A	CID	LIT	6	26.3	ERNLLLVKGAVPGATGS	1682.0	A	D	2.0	0.7	0.0	0.0
P60438	22224.8	G	T	A	A	CID	LIT	6	26.3	ERNLLLVKGAVPGATGSDLIVKPAVKA	2716.6	A	-	3.2	0.0	22.0	3.0
P60438	22224.8	G	T	T	B	CID	LIT	6	35.9	AIQVTTGAK	888.5	R	K	2.3	0.2	20.8	13.2
P60438	22224.8	G	T	T	B	CID	LIT	6	35.9	GAVPGATGSDLIVKPAVKA	1751.0	K	-	3.9	0.0	42.4	6.0
P60438	22224.8	G	T	T	B	CID	LIT	6	35.9	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	3.7	0.0	42.8	11.5
P60438	22224.8	G	T	T	B	CID	LIT	6	35.9	KMAGQMGNER	1121.5	K	V	4.0	0.5	58.7	11.1
P60438	22224.8	G	T	T	B	CID	LIT	6	35.9	KVGMTR	691.4	K	I	2.5	0.1	23.1	17.2
P60438	22224.8	G	T	T	B	CID	LIT	6	35.9	VTKPEAGHFAK	1184.6	R	A	2.3	0.7	2.2	13.8
P60438	22224.8	G	U	T	B	CID	LIT	4	23.0	AIQVTTGAK	888.5	R	K	2.7	0.3	32.9	13.4
P60438	22224.8	G	U	T	B	CID	LIT	4	23.0	DLANDGYR	923.4	K	A	2.7	0.0	20.7	7.8
P60438	22224.8	G	U	T	B	CID	LIT	4	23.0	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	4.1	0.5	25.8	11.8
P60438	22224.8	G	U	T	B	CID	LIT	4	23.0	VTKPEAGHFAK	1184.6	R	A	3.0	0.0	38.0	13.8
P60438	22224.8	G	T	A	B	CID	LIT	5	25.4	DAERNLLLVKGAVPGATGS	1868.0	V	D	2.2	0.2	5.9	13.4
P60438	22224.8	G	T	A	B	CID	LIT	5	25.4	DGVSIPVTVIEVEANRVTQVK	2253.2	E	D	4.5	0.6	48.3	12.3
P60438	22224.8	G	T	A	B	CID	LIT	5	25.4	DVVRVDA	773.4	L	E	2.1	0.6	34.5	19.2
P60438	22224.8	G	T	A	B	CID	LIT	5	25.4	ERNLLLVKGAVPGATGS	1682.0	A	D	3.8	0.9	36.6	8.5
P60438	22224.8	G	T	A	B	CID	LIT	5	25.4	ERVTVQSL	931.5	N	D	2.0	0.5	12.9	14.9
P60438	22224.8	G	U	A	B	CID	LIT	5	34.4	DAERNLLLVKGAVPGATGS	1868.0	V	D	2.0	0.7	13.7	13.4
P60438	22224.8	G	U	A	B	CID	LIT	5	34.4	DGVSIPVTVIEVEANRVTQVK	2253.2	E	D	2.9	0.0	20.0	12.0
P60438	22224.8	G	U	A	B	CID	LIT	5	34.4	DLIVKPAVKA	1053.7	S	-	2.6	0.0	24.7	0.0
P60438	22224.8	G	U	A	B	CID	LIT	5	34.4	DVVRVDA	773.4	L	E	1.8	0.3	16.4	18.8
P60438	22224.8	G	U	A	B	CID	LIT	5	34.4	MIGLVGKKVGMTRIFTE	1880.1	-	D	2.8	0.4	14.2	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	ANRVTKPEAGHFAK	1525.8	K	A	3.8	0.5	26.0	15.1
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	DLANDGYR	923.4	K	A	2.9	0.0	31.2	11.5
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.0	0.6	66.4	11.1
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	GAVPGATGSDLIVKPAVKA	1751.0	K	-	4.5	0.0	42.4	11.8
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	GKGFAGTVK	864.5	K	R	2.0	0.4	6.3	16.4
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	5.1	0.7	70.8	17.1
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	KANRVTKPEAGHFAK	1653.9	K	A	2.8	0.5	17.4	14.6
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	KVDVTGTSK	934.5	K	G	2.3	0.7	14.8	14.9
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	4.3	0.6	46.5	19.2
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	VTKPEAGHFAK	1184.6	R	A	3.1	0.7	16.2	15.9
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	VTVQSLDVVR	1115.6	R	V	2.7	0.4	31.9	16.7
P60438	22224.8	S	U	T	A	CID	LIT	12	56.0	VTVQSLDVVRVDAER	1685.9	R	N	2.7	0.4	0.0	0.0
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	ANRVTKPEAGHFAK	1525.8	K	A	3.7	0.5	38.4	14.6
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.6	0.6	80.3	10.8
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	GAVPGATGSDLIVKPAVKA	1751.0	K	-	4.6	0.0	63.0	11.5
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	4.4	0.6	46.6	17.2
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	KANRVTKPEAGHFAK	1653.9	K	A	3.2	0.5	34.2	15.9
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	4.0	0.7	79.2	19.0
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	VTKPEAGHFAK	1184.6	R	A	2.9	0.0	23.7	14.5
P60438	22224.8	S	U	T	B	CID	LIT	8	41.1	VTVQSLDVVR	1115.6	R	V	3.3	0.5	52.0	16.7
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	ANRVTKPEAGHFAK	1525.8	K	A	3.8	0.5	31.2	16.2
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.4	0.6	41.3	11.5
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	GAVPGATGSDLIVKPAVKA	1751.0	K	-	3.8	0.0	32.7	12.6
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	4.6	0.7	67.6	17.1
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	KANRVTKPEAGHFAK	1653.9	K	A	3.0	0.3	18.3	14.6
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	KVDVTGTSK	934.5	K	G	2.1	0.6	23.4	14.9
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	4.1	0.6	40.2	18.8
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	MIGLVGK	717.4	-	K	1.9	0.6	11.6	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	TQDATHGNSLSHR	1423.7	R	V	2.8	0.0	24.6	15.7
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	VTKPEAGHFAK	1184.6	R	A	2.2	0.4	8.9	15.1
P60438	22224.8	S	U	T	C	CID	LIT	11	55.0	VTVQSLDVVR	1115.6	R	V	2.9	0.4	36.7	16.9
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	ANRVTKPEAGHFAK	1525.8	K	A	5.3	0.6	53.3	15.1
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.9	0.7	0.0	0.0
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	GAVPGATGSDLIVKPAVKA	1751.0	K	-	4.6	0.6	56.7	11.5
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	3.8	0.9	28.6	17.2
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	KVDVTGTSK	934.5	K	G	2.3	0.7	22.7	14.9
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	3.9	0.4	0.0	0.0
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	MIGLVGK	717.4	-	K	1.9	0.5	10.5	11.1
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	TQDATHGNSLSHR	1423.7	R	V	2.3	0.2	19.2	15.7
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	VTKPEAGHFAK	1184.6	R	A	3.5	0.4	14.8	15.1
P60438	22224.8	S	U	T	A	ETD	LIT	10	54.5	VTVQSLDVVR	1115.6	R	V	2.5	0.3	34.8	16.7
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	GAVPGATGSDLIVKPAVK	1680.0	K	-	5.1	0.7	0.0	0.0
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	GAVPGATGSDLIVKPAVKA	1751.0	K	-	4.9	0.6	51.0	10.4
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	GKGFAGTVK	864.5	K	R	2.2	0.0	24.7	16.4
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	GLWEFR	807.4	R	L	1.3	0.3	19.5	17.1
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	4.2	0.8	52.2	17.3
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	KVDVTGTSK	934.5	K	G	2.0	0.7	31.5	14.9
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	VTKPEAGHFAK	1184.6	R	A	3.6	0.6	34.1	15.2
P60438	22224.8	S	U	T	B	ETD	LIT	8	40.2	VTVQSLDVVR	1115.6	R	V	2.4	0.3	32.5	16.8
P60438	22224.8	S	U	T	C	ETD	LIT	7	37.8	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.6	0.7	61.2	10.8
P60438	22224.8	S	U	T	C	ETD	LIT	7	37.8	GAVPGATGSDLIVKPAVKA	1751.0	K	-	3.8	0.6	48.7	11.8
P60438	22224.8	S	U	T	C	ETD	LIT	7	37.8	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	2.9	0.7	37.3	17.3
P60438	22224.8	S	U	T	C	ETD	LIT	7	37.8	KVDVTGTSK	934.5	K	G	2.2	0.0	30.0	15.8
P60438	22224.8	S	U	T	C	ETD	LIT	7	37.8	MIGLVGK	717.4	-	K	2.1	0.8	26.8	10.0
P60438	22224.8	S	U	T	C	ETD	LIT	7	37.8	TQDATHGNSLSHR	1423.7	R	V	2.9	0.4	26.3	15.7
P60438	22224.8	S	U	T	C	ETD	LIT	7	37.8	VTKPEAGHFAK	1184.6	R	A	4.0	0.5	30.9	15.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P60438	22224.8	S	U	T	B	ETD	FT	2	12.4	GAVPGATGSDLIVKPAVKA	1751.0	K	-	0.0	0.0	18.7	11.5
P60438	22224.8	S	U	T	B	ETD	FT	2	12.4	MIGLVGK	717.4	-	K	0.0	0.0	23.7	11.1
P60438	22224.8	S	U	T	C	ETD	FT	2	6.2	MIGLVGK	717.4	-	K	0.0	0.0	23.8	11.1
P60438	22224.8	S	U	T	C	ETD	FT	2	6.2	NLLLVK	699.5	R	G	0.0	0.0	19.5	9.5
P60438	22224.8	S	U	T	B	ETD+CID	LIT	7	45.9	ANRVTKPEAGHFAK	1525.8	K	A	0.0	0.0	38.3	16.2
P60438	22224.8	S	U	T	B	ETD+CID	LIT	7	45.9	GAVPGATGSDLIVKPAVK	1680.0	K	-	0.0	0.0	71.6	11.8
P60438	22224.8	S	U	T	B	ETD+CID	LIT	7	45.9	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	0.0	0.0	96.0	16.8
P60438	22224.8	S	U	T	B	ETD+CID	LIT	7	45.9	KVDVTGTSK	934.5	K	G	0.0	0.0	28.3	14.9
P60438	22224.8	S	U	T	B	ETD+CID	LIT	7	45.9	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	0.0	0.0	60.0	18.8
P60438	22224.8	S	U	T	B	ETD+CID	LIT	7	45.9	TQDATHGNSLSHR	1423.7	R	V	0.0	0.0	21.5	15.6
P60438	22224.8	S	U	T	B	ETD+CID	LIT	7	45.9	VTKPEAGHFAK	1184.6	R	A	0.0	0.0	20.7	15.1
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	ANRVTKPEAGHFAK	1525.8	K	A	4.4	0.4	51.2	15.8
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.8	0.6	46.2	11.1
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	4.8	0.6	47.5	16.8
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	KANRVTKPEAGHFAK	1653.9	K	A	3.7	0.4	15.3	15.9
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	KVDVTGTSK	934.5	K	G	2.2	0.5	18.1	14.9
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	4.7	0.7	70.7	19.0
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	TQDATHGNSLSHR	1423.7	R	V	1.1	0.2	16.9	15.9
P60438	22224.8	S	U	T	A	ETD+CID	LIT	8	46.4	VTKPEAGHFAK	1184.6	R	A	3.1	0.5	18.3	15.1
P60438	22224.8	S	U	T	B	ETD+CID	LIT	5	30.6	ANRVTKPEAGHFAK	1525.8	K	A	4.4	0.4	0.0	0.0
P60438	22224.8	S	U	T	B	ETD+CID	LIT	5	30.6	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.6	0.6	0.0	0.0
P60438	22224.8	S	U	T	B	ETD+CID	LIT	5	30.6	KANRVTKPEAGHFAK	1653.9	K	A	3.1	0.4	0.0	0.0
P60438	22224.8	S	U	T	B	ETD+CID	LIT	5	30.6	KVDVTGTSK	934.5	K	G	2.6	0.6	0.0	0.0
P60438	22224.8	S	U	T	B	ETD+CID	LIT	5	30.6	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	4.2	0.7	0.0	0.0
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	ANRVTKPEAGHFAK	1525.8	K	A	4.4	0.4	38.3	16.2
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.6	0.6	71.6	11.8
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	GKGFAGTVK	864.5	K	R	1.9	0.7	4.4	16.4
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	5.3	0.7	96.0	16.8

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		digestion	lysis	protease	replicate												
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	KANRVTKPEAGHFAK	1653.9	K	A	3.1	0.4	11.6	15.9
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	KVDVTGTSK	934.5	K	G	2.6	0.6	28.3	14.9
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	4.5	0.8	0.0	0.0
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	TQDATHGNSLSHR	1423.7	R	V	1.0	0.2	21.5	15.6
P60438	22224.8	S	U	T	B	ETD+CID	LIT	9	50.7	VTKPEAGHFAK	1184.6	R	A	3.1	0.6	20.7	15.1
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	ANRVTKPEAGHFAK	1525.8	K	A	1.1	-0.3	35.4	16.0
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	GAVPGATGSDLIVKPAVK	1680.0	K	-	4.8	0.6	60.6	10.0
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	3.9	0.5	13.4	17.2
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	KANRVTKPEAGHFAK	1653.9	K	A	2.2	0.8	10.4	15.1
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	KLNIKPGQTTFDGR	1574.9	-	-	2.7	0.3	39.2	16.1
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	KVDVTGTSK	934.5	K	G	2.7	0.3	25.0	15.8
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	5.4	0.6	71.2	18.8
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	MIGLVGK	717.4	-	K	1.7	0.6	1.9	11.1
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	TQDATHGNSLSHR	1423.7	R	V	3.2	0.0	33.3	15.6
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	VTKPEAGHFAK	1184.6	R	A	1.1	-0.3	32.8	15.1
P60438	22224.8	S	U	T	C	ETD+CID	LIT	11	54.5	VTVQSLDVVR	1115.6	R	V	2.8	0.3	28.3	16.7
P60438	22224.8	S	U	T	B	HCD	FT	7	45.9	ANRVTKPEAGHFAK	1525.8	K	A	0.0	0.0	29.2	14.3
P60438	22224.8	S	U	T	B	HCD	FT	7	45.9	GAVPGATGSDLIVKPAVK	1680.0	K	-	0.0	0.0	71.6	11.8
P60438	22224.8	S	U	T	B	HCD	FT	7	45.9	IFTEDGVSIPVTVIEVEANR	2188.2	R	V	0.0	0.0	96.0	16.8
P60438	22224.8	S	U	T	B	HCD	FT	7	45.9	KVDVTGTSK	934.5	K	G	0.0	0.0	28.3	14.9
P60438	22224.8	S	U	T	B	HCD	FT	7	45.9	LAEGEEFTVGQSISVELFADVK	2368.2	R	K	0.0	0.0	60.0	18.8
P60438	22224.8	S	U	T	B	HCD	FT	7	45.9	TQDATHGNSLSHR	1423.7	R	V	0.0	0.0	21.5	15.6
P60438	22224.8	S	U	T	B	HCD	FT	7	45.9	VTKPEAGHFAK	1184.6	R	A	0.0	0.0	20.7	15.1
P0A955	22266.3	G	U	T	A	CID	LIT	5	37.1	AATEGTIPLIPGISTVSELMLGMDYGLK	2877.5	K	E	3.2	0.0	52.0	10.4
P0A955	22266.3	G	U	T	A	CID	LIT	5	37.1	ALQAIAGPFSQVR	1357.8	K	F	3.7	0.8	36.8	11.8
P0A955	22266.3	G	U	T	A	CID	LIT	5	37.1	KLEHAVPMAK	1123.6	K	A	3.5	0.8	51.3	8.5
P0A955	22266.3	G	U	T	A	CID	LIT	5	37.1	TECAVDAIR	1034.5	R	A	2.6	0.0	45.5	11.5
P0A955	22266.3	G	U	T	A	CID	LIT	5	37.1	TSAESILTTGPVVPVIVVK	1910.1	K	K	3.8	0.0	33.7	3.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A955	22266.3	G	T	T	A	CID	LIT	2	6.6	ALVAGGVR	742.5	K	V	1.5	0.4	10.5	12.3
P0A955	22266.3	G	T	T	A	CID	LIT	2	6.6	DYLALK	722.4	R	S	1.5	0.4	16.5	12.6
P0A7C2	22339.8	G	U	T	A	CID	LIT	3	15.3	IDDEVTVKR	1074.6	R	L	2.7	0.6	57.2	13.8
P0A7C2	22339.8	G	U	T	A	CID	LIT	3	15.3	KGVIEIVSGASR	1215.7	R	G	2.1	0.8	14.9	10.4
P0A7C2	22339.8	G	U	T	A	CID	LIT	3	15.3	SPNAAEEHLK	1095.5	R	A	3.8	0.7	43.1	13.0
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	DATGNTPFMLIAR	1406.7	K	N	3.8	0.7	60.8	12.6
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	DGTIHQFSAVEQDDQR	1845.8	R	S	5.0	0.0	72.8	10.4
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	FTFTPPQGVTVDDQR	1707.8	K	-	4.2	0.0	61.0	14.0
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	NQSSDWQQYNIK	1510.7	R	Q	3.9	0.0	57.8	8.5
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	QFTINVGR	934.5	K	D	2.5	0.6	18.6	13.0
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	TLWFYNPFVEQATATWLK	2215.1	K	D	4.8	0.0	72.0	12.3
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	VSSFHASFTQK	1238.6	K	V	3.1	0.0	28.7	12.0
P61316	22479.1	G	U	T	A	CID	LIT	8	55.2	VTDGSGAAVQEGQGDLWVK	1916.9	K	R	5.3	0.0	68.0	11.8
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	DATGNTPFMLIAR	1422.7	K	N	4.0	0.6	86.2	12.6
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	DGTIHQFSAVEQDDQR	1845.8	R	S	4.6	0.8	73.8	10.8
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	FTFTPPQGVTVDDQR	1707.8	K	-	3.9	0.8	44.4	13.8
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	FTFTPPQGVTVDDQRK	1835.9	K	-	3.8	0.8	65.8	13.4
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	LDKVSSFHASFTQK	1594.8	R	V	2.9	0.5	26.2	10.4
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	NQSSDWQQYNIK	1510.7	R	Q	4.7	0.7	71.5	8.5
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	QFTINVGR	934.5	K	D	2.6	0.6	36.5	13.2
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	QNGDDFVLTPK	1233.6	K	A	2.9	0.6	38.9	13.0
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	TLWFYNPFVEQATATWLK	2215.1	K	D	5.3	0.8	60.1	12.3
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	VSSFHASFTQK	1238.6	K	V	3.4	0.6	36.1	12.6
P61316	22479.1	G	T	T	A	CID	LIT	11	62.6	VTDGSGAAVQEGQGDLWVK	1916.9	K	R	5.0	0.0	72.2	11.8
P61316	22479.1	G	U	A	A	CID	LIT	2	14.8	DAAKFTFTPPQGVTVDDQRK	2221.1	V	-	3.9	0.7	49.6	15.6
P61316	22479.1	G	U	A	A	CID	LIT	2	14.8	DAASDLKSRL	1075.6	A	D	2.0	0.6	20.7	14.8
P61316	22479.1	G	T	A	A	CID	LIT	7	32.5	DAAKFTFTPPQGVTV	1578.8	V	D	3.1	0.8	14.0	15.9
P61316	22479.1	G	T	A	A	CID	LIT	7	32.5	DAAKFTFTPPQGVTVD	1693.8	V	D	3.5	0.0	25.5	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61316	22479.1	G	T	A	A	CID	LIT	7	32.5	DAASDLKSRL	1075.6	A	D	2.5	0.0	33.2	14.8
P61316	22479.1	G	T	A	A	CID	LIT	7	32.5	DATGNTPFMLIARNQSS	1822.9	K	D	4.2	0.6	38.3	14.1
P61316	22479.1	G	T	A	A	CID	LIT	7	32.5	DGTIHQFSAVEQ	1331.6	R	D	3.0	0.4	25.9	13.2
P61316	22479.1	G	T	A	A	CID	LIT	7	32.5	DLKSRL	731.4	S	D	0.9	0.3	16.2	12.8
P61316	22479.1	G	T	A	A	CID	LIT	7	32.5	DWQQYNIKQNG	1393.7	S	D	2.1	0.3	8.7	13.2
P61316	22479.1	G	T	T	B	CID	LIT	4	19.2	FTFTPPQGVTVDDQR	1707.8	K	-	2.9	0.0	23.6	14.1
P61316	22479.1	G	T	T	B	CID	LIT	4	19.2	FTFTPPQGVTVDDQRK	1835.9	K	-	3.6	0.7	43.7	14.1
P61316	22479.1	G	T	T	B	CID	LIT	4	19.2	NQSSDWQQYNIK	1510.7	R	Q	3.6	0.7	37.4	8.5
P61316	22479.1	G	T	T	B	CID	LIT	4	19.2	VSSFHASFTQK	1238.6	K	V	3.3	0.4	20.7	12.0
P61316	22479.1	G	T	A	B	CID	LIT	5	34.5	DAAKFTFTPPQGVTV	1578.8	V	D	2.6	0.8	16.4	16.1
P61316	22479.1	G	T	A	B	CID	LIT	5	34.5	DATGNTPFMLIARNQSS	1822.9	K	D	2.5	0.0	15.3	14.3
P61316	22479.1	G	T	A	B	CID	LIT	5	34.5	DGTIHQFSAVEQ	1331.6	R	D	2.3	0.0	20.6	13.2
P61316	22479.1	G	T	A	B	CID	LIT	5	34.5	DKVSSFHASFTQKVT	1681.9	L	D	3.4	0.4	12.8	14.5
P61316	22479.1	G	T	A	B	CID	LIT	5	34.5	DWQQYNIKQNG	1393.7	S	D	2.4	0.8	17.6	13.2
P61316	22479.1	S	U	T	A	CID	LIT	3	27.6	FTFTPPQGVTVDDQR	1707.8	K	-	4.5	0.6	62.9	18.1
P61316	22479.1	S	U	T	A	CID	LIT	3	27.6	NQSSDWQQYNIKQNGDDFVLTPK	2726.3	R	A	4.2	0.6	27.9	17.2
P61316	22479.1	S	U	T	A	CID	LIT	3	27.6	TLWFYNPFVEQATATWLK	2215.1	K	D	4.0	0.7	39.9	17.5
P61316	22479.1	S	U	T	B	CID	LIT	3	29.6	NQSSDWQQYNIKQNGDDFVLTPK	2726.3	R	A	4.6	0.7	30.5	17.3
P61316	22479.1	S	U	T	B	CID	LIT	3	29.6	TLWFYNPFVEQATATWLK	2215.1	K	D	4.0	0.0	65.8	17.6
P61316	22479.1	S	U	T	B	CID	LIT	3	29.6	VTDGSGAAVQEGQGDLWVK	1916.9	K	R	5.7	0.6	61.9	17.9
P61316	22479.1	S	U	T	C	CID	LIT	2	16.3	FTFTPPQGVTVDDQR	1707.8	K	-	3.5	0.6	32.1	18.1
P61316	22479.1	S	U	T	C	CID	LIT	2	16.3	TLWFYNPFVEQATATWLK	2215.1	K	D	3.4	0.6	35.9	17.5
P61316	22479.1	S	U	T	B	ETD+CID	LIT	3	29.6	NQSSDWQQYNIKQNGDDFVLTPK	2726.3	R	A	0.0	0.0	38.5	17.1
P61316	22479.1	S	U	T	B	ETD+CID	LIT	3	29.6	TLWFYNPFVEQATATWLK	2215.1	K	D	0.0	0.0	50.8	17.6
P61316	22479.1	S	U	T	B	ETD+CID	LIT	3	29.6	VTDGSGAAVQEGQGDLWVK	1916.9	K	R	0.0	0.0	61.2	18.1
P61316	22479.1	S	U	T	A	ETD+CID	LIT	3	28.1	FTFTPPQGVTVDDQR	1707.8	K	-	3.8	0.6	55.2	17.9
P61316	22479.1	S	U	T	A	ETD+CID	LIT	3	28.1	NQSSDWQQYNIKQNGDDFVLTPK	2726.3	R	A	3.3	0.0	25.3	17.3
P61316	22479.1	S	U	T	A	ETD+CID	LIT	3	28.1	VTDGSGAAVQEGQGDLWVK	1916.9	K	R	4.7	0.4	50.6	18.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P61316	22479.1	S	U	T	B	ETD+CID	LIT	3	29.6	NQSSDWQQYNIKQNGDDFVLTPK	2726.3	R	A	4.2	0.5	38.5	17.1
P61316	22479.1	S	U	T	B	ETD+CID	LIT	3	29.6	TLWFYNPFVEQATATWLK	2215.1	K	D	4.4	0.7	0.0	0.0
P61316	22479.1	S	U	T	B	ETD+CID	LIT	3	29.6	VTDGSGAAVQEGQGDLWVK	1916.9	K	R	5.6	0.5	61.2	18.1
P61316	22479.1	S	U	T	B	HCD	FT	3	29.6	NQSSDWQQYNIKQNGDDFVLTPK	2726.3	R	A	0.0	0.0	38.5	17.1
P61316	22479.1	S	U	T	B	HCD	FT	3	29.6	TLWFYNPFVEQATATWLK	2215.1	K	D	0.0	0.0	50.8	17.6
P61316	22479.1	S	U	T	B	HCD	FT	3	29.6	VTDGSGAAVQEGQGDLWVK	1916.9	K	R	0.0	0.0	61.2	18.1
P0AB38	22497.2	G	T	T	A	CID	LIT	4	29.6	FTLVSAQQLSMAK	1423.8	K	Q	3.8	0.6	43.1	13.0
P0AB38	22497.2	G	T	T	A	CID	LIT	4	29.6	MLGADGVTAGSVLLVDSVNNR	2088.1	K	T	2.7	0.5	0.0	0.0
P0AB38	22497.2	G	T	T	A	CID	LIT	4	29.6	QQLGLSPQDSLGTR	1499.8	K	S	2.9	0.8	42.2	13.0
P0AB38	22497.2	G	T	T	A	CID	LIT	4	29.6	TNGSLNAAEATETLR	1547.8	R	N	4.0	0.5	46.8	13.0
P0AB38	22497.2	G	T	T	B	CID	LIT	2	16.4	MLGADGVTAGSVLLVDSVNNR	2088.1	K	T	2.3	0.2	0.0	0.0
P0AB38	22497.2	G	T	T	B	CID	LIT	2	16.4	QQLGLSPQDSLGTR	1499.8	K	S	2.7	0.7	7.0	12.6
P0A8F0	22515.8	G	U	T	A	CID	LIT	6	34.1	ITVVPILR	910.6	K	A	2.4	0.0	21.3	0.0
P0A8F0	22515.8	G	U	T	A	CID	LIT	6	34.1	IVEVKHPLVK	1161.7	K	H	2.5	0.0	39.6	3.0
P0A8F0	22515.8	G	U	T	A	CID	LIT	6	34.1	LVSNIDER	945.5	K	M	2.5	0.3	12.5	16.5
P0A8F0	22515.8	G	U	T	A	CID	LIT	6	34.1	NEETLEPVPYFQK	1593.8	R	L	4.6	0.0	65.2	12.0
P0A8F0	22515.8	G	U	T	A	CID	LIT	6	34.1	VLVLVAAPEGIAALEK	1593.0	K	A	3.8	0.0	29.7	0.0
P0A8F0	22515.8	G	U	T	A	CID	LIT	6	34.1	VTIEGWNGPVEIDQIK	1797.9	K	G	4.2	0.0	60.7	11.5
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	EKIIASVAEK	1087.6	R	F	2.3	0.7	1.3	11.5
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	FICIADASK	1024.5	K	Q	2.3	0.7	34.5	11.5
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	FPLPVEVIPMAR	1384.8	K	S	2.7	0.6	33.5	12.8
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	GADVALIGTPDGVK	1312.7	R	T	3.8	0.9	62.3	8.5
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	GQIEGAVSSSDASTEK	1565.7	K	L	4.9	0.8	81.2	7.8
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	GQIEGAVSSSDASTEKLK	1806.9	K	S	4.8	0.7	62.8	13.6
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	LGGRPEYR	947.5	K	Q	2.5	0.6	22.7	14.6
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	MTQDELKK	992.5	-	A	1.8	0.5	19.9	14.3
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	QVDILGK	772.5	K	F	2.1	0.5	27.5	15.3
P0A7Z0	22842.5	G	U	T	A	CID	LIT	10	39.3	QVDILGKFPLPVEVIPMAR	2122.2	K	S	4.7	0.0	19.1	4.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7Z0	22842.5	G	T	T	A	CID	LIT	3	14.2	FICIADASK	1024.5	K	Q	1.8	0.6	8.6	10.8
P0A7Z0	22842.5	G	T	T	A	CID	LIT	3	14.2	GADVALIGTPDGVK	1312.7	R	T	2.9	0.4	8.9	12.0
P0A7Z0	22842.5	G	T	T	A	CID	LIT	3	14.2	LGGRPEYR	947.5	K	Q	2.4	0.4	14.9	14.6
P0A7Z0	22842.5	G	U	A	A	CID	LIT	6	37.4	DALGTMKGQIEGAVSSS	1650.8	I	D	3.6	0.8	54.1	15.6
P0A7Z0	22842.5	G	U	A	A	CID	LIT	6	37.4	DASTEKLKSLGIHVF	1644.9	S	D	3.7	0.7	32.0	12.8
P0A7Z0	22842.5	G	U	A	A	CID	LIT	6	37.4	DGVKTIVK	859.5	P	-	2.0	0.0	18.2	9.5
P0A7Z0	22842.5	G	U	A	A	CID	LIT	6	37.4	DPIAMENAINAIPGVVTVGLFANRGA	2610.4	L	D	5.4	0.0	79.2	15.1
P0A7Z0	22842.5	G	U	A	A	CID	LIT	6	37.4	DVALIGTPDGVKTIVK	1625.9	A	-	4.6	0.5	51.9	7.0
P0A7Z0	22842.5	G	U	A	A	CID	LIT	6	37.4	DVHGMEIL	913.4	L	D	1.9	0.4	0.0	0.0
P0A7Z0	22842.5	G	T	T	B	CID	LIT	6	27.9	GADVALIGTPDGVK	1312.7	R	T	2.4	0.0	16.8	8.5
P0A7Z0	22842.5	G	T	T	B	CID	LIT	6	27.9	GADVALIGTPDGVKTIVK	1754.0	R	-	4.8	0.5	38.6	10.4
P0A7Z0	22842.5	G	T	T	B	CID	LIT	6	27.9	GQIEGAVSSSDASTEKLK	1806.9	K	S	2.6	0.2	6.2	14.1
P0A7Z0	22842.5	G	T	T	B	CID	LIT	6	27.9	LGGRPEYR	947.5	K	Q	2.1	0.2	14.7	14.6
P0A7Z0	22842.5	G	T	T	B	CID	LIT	6	27.9	MTQDELKK	992.5	-	A	2.1	0.6	35.8	14.8
P0A7Z0	22842.5	G	T	T	B	CID	LIT	6	27.9	SAVARQLVK	971.6	R	L	2.3	0.5	10.1	10.0
P0A7Z0	22842.5	G	U	A	B	CID	LIT	5	33.8	DALGTMKGQIEGAVSSS	1650.8	I	D	3.8	0.6	46.7	15.6
P0A7Z0	22842.5	G	U	A	B	CID	LIT	5	33.8	DASTEKLKSLGIHVF	1644.9	S	D	2.4	0.3	0.0	0.0
P0A7Z0	22842.5	G	U	A	B	CID	LIT	5	33.8	DGVKTIVK	859.5	P	-	2.2	0.2	1.5	9.5
P0A7Z0	22842.5	G	U	A	B	CID	LIT	5	33.8	DPIAMENAINAIPGVVTVGLFANRGA	2610.4	L	D	4.7	0.7	34.0	15.1
P0A7Z0	22842.5	G	U	A	B	CID	LIT	5	33.8	DVALIGTPDGVKTIVK	1625.9	A	-	3.2	0.0	21.9	7.0
P0A7Z0	22842.5	S	U	T	A	CID	LIT	2	19.6	AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	3487.8	K	G	5.9	0.0	75.0	17.6
P0A7Z0	22842.5	S	U	T	A	CID	LIT	2	19.6	GGGAALTR	702.4	K	E	2.5	0.0	20.6	18.4
P0A7Z0	22842.5	S	U	T	C	CID	LIT	2	22.4	AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	3487.8	K	G	3.9	0.8	15.1	17.3
P0A7Z0	22842.5	S	U	T	C	CID	LIT	2	22.4	GADVALIGTPDGVK	1312.7	R	T	2.3	0.5	7.0	13.0
P0A7Z0	22842.5	S	U	T	B	ETD	LIT	2	12.3	LGGRPEYR	947.5	K	Q	2.5	0.2	5.4	17.2
P0A7Z0	22842.5	S	U	T	B	ETD	LIT	2	12.3	QVDILGKFPLPVEVIPMAR	2122.2	K	S	2.9	0.1	18.3	13.6
P0A7Z0	22842.5	S	U	T	B	ETD+CID	LIT	2	22.4	AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	3487.8	K	G	0.0	0.0	62.3	17.4
P0A7Z0	22842.5	S	U	T	B	ETD+CID	LIT	2	22.4	GADVALIGTPDGVK	1312.7	R	T	0.0	0.0	52.7	12.3

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7Z0	22842.5	S	U	T	B	ETD+CID	LIT	2	22.4	AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	3487.8	K	G	2.9	0.6	12.9	17.5
P0A7Z0	22842.5	S	U	T	B	ETD+CID	LIT	2	22.4	GADVALIGTPDGVK	1312.7	R	T	3.7	0.8	52.7	12.3
P0A7Z0	22842.5	S	U	T	B	HCD	FT	2	22.4	AVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMK	3487.8	K	G	0.0	0.0	62.3	17.4
P0A7Z0	22842.5	S	U	T	B	HCD	FT	2	22.4	GADVALIGTPDGVK	1312.7	R	T	0.0	0.0	52.7	12.3
P18776	22850.6	G	U	T	A	CID	LIT	2	11.2	ALDFGPIDELR	1245.6	R	K	2.9	0.0	25.8	14.8
P18776	22850.6	G	U	T	A	CID	LIT	2	11.2	HGDLAAVAPLPR	1216.7	K	A	2.5	0.8	15.8	12.8
P43340	23018.2	G	T	T	A	CID	LIT	2	12.2	HDSLTAHIADAIHQR	1684.9	R	A	3.2	0.0	43.0	14.0
P43340	23018.2	G	T	T	A	CID	LIT	2	12.2	IYLVWAHPR	1154.6	R	H	1.6	0.0	28.0	7.8
P0ADT8	23058.8	G	T	T	A	CID	LIT	2	17.0	LVGTVNAGEEVTLLQTDANTNYAQVK	2748.4	R	D	3.4	0.5	0.0	0.0
P0ADT8	23058.8	G	T	T	A	CID	LIT	2	17.0	QLSTEPSLR	1030.6	K	S	2.3	0.6	24.4	16.4
P00448	23079.8	G	U	T	A	CID	LIT	5	22.8	DFGSVDNFKAEFEK	1632.8	R	A	3.4	0.0	54.5	8.5
P00448	23079.8	G	U	T	A	CID	LIT	5	22.8	GTTLQGDLK	932.5	K	A	2.3	0.3	26.0	15.2
P00448	23079.8	G	U	T	A	CID	LIT	5	22.8	KGTTLQGDLK	1060.6	K	A	3.6	0.6	33.1	10.0
P00448	23079.8	G	U	T	A	CID	LIT	5	22.8	LDQLPADKK	1027.6	K	T	2.8	0.8	33.9	12.6
P00448	23079.8	G	U	T	A	CID	LIT	5	22.8	NNAGGHANHSLFWK	1552.7	R	G	2.4	0.7	12.0	10.4
P00448	23079.8	G	T	T	A	CID	LIT	7	25.7	DFGSVDNFK	1028.5	R	A	2.3	0.0	26.0	10.0
P00448	23079.8	G	T	T	A	CID	LIT	7	25.7	DFGSVDNFKAEFEK	1632.8	R	A	4.2	0.0	56.2	8.5
P00448	23079.8	G	T	T	A	CID	LIT	7	25.7	GTTLQGDLK	932.5	K	A	2.6	0.2	25.6	15.2
P00448	23079.8	G	T	T	A	CID	LIT	7	25.7	KGTTLQGDLK	1060.6	K	A	3.2	0.7	30.6	10.0
P00448	23079.8	G	T	T	A	CID	LIT	7	25.7	LDQLPADKK	1027.6	K	T	2.8	0.6	39.1	12.6
P00448	23079.8	G	T	T	A	CID	LIT	7	25.7	NNAGGHANHSLFWK	1552.7	R	G	5.2	0.0	60.5	11.1
P00448	23079.8	G	T	T	A	CID	LIT	7	25.7	RPDYIK	791.4	R	E	2.3	0.4	19.3	13.4
P00448	23079.8	G	U	A	A	CID	LIT	2	8.7	DALEPHF	828.4	Y	D	1.7	0.3	5.2	11.1
P00448	23079.8	G	U	A	A	CID	LIT	2	8.7	DEAAARFAAKK	1177.6	W	-	2.2	0.6	40.2	13.6
P00448	23079.8	G	T	T	B	CID	LIT	2	11.7	KGTTLQGDLK	1060.6	K	A	3.7	0.7	19.5	10.0
P00448	23079.8	G	T	T	B	CID	LIT	2	11.7	NNAGGHANHSLFWK	1552.7	R	G	2.3	0.8	22.4	10.4
P00448	23079.8	G	T	A	B	CID	LIT	4	24.3	DEAAARFAAKK	1177.6	W	-	0.0	0.0	20.7	13.6
P00448	23079.8	G	T	A	B	CID	LIT	4	24.3	DKLAVVSTANQ	1145.6	G	D	3.4	0.5	60.4	15.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P00448	23079.8	G	T	A	B	CID	LIT	4	24.3	DLKAAIER	915.5	G	D	2.7	0.4	35.5	16.5
P00448	23079.8	G	T	A	B	CID	LIT	4	24.3	DSPLMGEAISGASGFPIMGL	1949.9	Q	D	2.7	0.6	18.3	16.1
P00448	23079.8	G	U	A	B	CID	LIT	3	18.4	DALEPHF	828.4	Y	D	1.7	0.6	11.9	11.1
P00448	23079.8	G	U	A	B	CID	LIT	3	18.4	DKLAVVSTANQ	1145.6	G	D	3.1	0.6	21.2	16.6
P00448	23079.8	G	U	A	B	CID	LIT	3	18.4	DSPLMGEAISGASGFPIMGL	1949.9	Q	D	3.0	0.7	45.7	16.9
P00448	23079.8	S	U	T	B	CID	LIT	2	13.6	DFGSVDNFKAEFEK	1632.8	R	A	3.4	0.6	21.6	14.0
P00448	23079.8	S	U	T	B	CID	LIT	2	13.6	FGSGWAWLVLKGDK	1563.8	R	L	2.2	0.2	0.1	17.2
P00448	23079.8	S	U	T	C	CID	LIT	3	16.0	AAIERDFGSVDNFK	1568.8	K	A	2.3	0.3	0.1	15.6
P00448	23079.8	S	U	T	C	CID	LIT	3	16.0	DFGSVDNFKAEFEK	1632.8	R	A	3.2	0.5	11.8	14.8
P00448	23079.8	S	U	T	C	CID	LIT	3	16.0	FGSGWAWLVLKGDK	1563.8	R	L	2.5	0.7	6.2	16.9
P00448	23079.8	S	U	T	B	ETD+CID	LIT	3	32.5	DFGSVDNFKAEFEK	1632.8	R	A	0.0	0.0	33.1	14.9
P00448	23079.8	S	U	T	B	ETD+CID	LIT	3	32.5	FGSGWAWLVLKGDK	1563.8	R	L	0.0	0.0	27.2	17.2
P00448	23079.8	S	U	T	B	ETD+CID	LIT	3	32.5	HHQTYVNNANAALESLPEFANLPVEELITKLDQLPADKK	4371.3	K	T	0.0	0.0	14.0	16.7
P00448	23079.8	S	U	T	B	ETD+CID	LIT	3	32.5	DFGSVDNFKAEFEK	1632.8	R	A	3.7	0.5	33.1	14.9
P00448	23079.8	S	U	T	B	ETD+CID	LIT	3	32.5	FGSGWAWLVLKGDK	1563.8	R	L	2.9	0.0	27.2	17.2
P00448	23079.8	S	U	T	B	ETD+CID	LIT	3	32.5	HHQTYVNNANAALESLPEFANLPVEELITKLDQLPADKK	4371.3	K	T	2.3	0.0	14.0	16.7
P00448	23079.8	S	U	T	C	ETD+CID	LIT	4	43.7	AAIERDFGSVDNFKAEFEK	2173.1	K	A	4.1	0.0	18.3	18.8
P00448	23079.8	S	U	T	C	ETD+CID	LIT	4	43.7	FGSGWAWLVLKGDK	1563.8	R	L	3.8	0.8	34.5	17.2
P00448	23079.8	S	U	T	C	ETD+CID	LIT	4	43.7	HHQTYVNNANAALESLPEFANLPVEELITKLDQLPADKK	4371.3	K	T	2.4	0.0	24.4	17.1
P00448	23079.8	S	U	T	C	ETD+CID	LIT	4	43.7	KTVLRNNAGGHANHSLFWK	2153.1	K	G	1.8	0.8	0.0	0.0
P00448	23079.8	S	U	T	B	HCD	FT	2	13.6	DFGSVDNFKAEFEK	1632.8	R	A	0.0	0.0	33.1	14.9
P00448	23079.8	S	U	T	B	HCD	FT	2	13.6	FGSGWAWLVLKGDK	1563.8	R	L	0.0	0.0	27.2	17.2
P21367	23082.9	G	T	T	A	CID	LIT	5	37.0	DIEPDKFK	991.5	R	N	1.8	0.5	8.0	13.6
P21367	23082.9	G	T	T	A	CID	LIT	5	37.0	LDKNDAAVLLVDHQAGLLSLVR	2360.3	R	D	4.7	0.0	33.5	9.0
P21367	23082.9	G	T	T	A	CID	LIT	5	37.0	NLMTSYDTLTK	1302.6	R	Q	3.3	0.8	44.8	11.5
P21367	23082.9	G	T	T	A	CID	LIT	5	37.0	NNVLALGDLAK	1127.6	K	Y	3.5	0.0	47.6	12.3
P21367	23082.9	G	T	T	A	CID	LIT	5	37.0	YFNLPTILTTSFETGPNGPLVPELK	2748.5	K	A	4.1	0.0	46.3	11.8
P0AEG4	23086.3	G	U	T	A	CID	LIT	6	36.1	AAADVQLR	843.5	K	G	2.9	0.0	51.1	14.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AEG4	23086.3	G	U	T	A	CID	LIT	6	36.1	KLPEGVK	770.5	K	M	1.9	0.7	14.3	6.0
P0AEG4	23086.3	G	U	T	A	CID	LIT	6	36.1	SASDIRDVFINAGIK	1605.9	R	G	3.3	0.4	16.8	12.8
P0AEG4	23086.3	G	U	T	A	CID	LIT	6	36.1	SLVAQQEK	902.5	K	A	2.3	0.1	28.1	16.1
P0AEG4	23086.3	G	U	T	A	CID	LIT	6	36.1	YHVNFMGGDLGK	1337.6	K	D	3.0	0.8	23.0	9.5
P0AEG4	23086.3	G	U	T	A	CID	LIT	6	36.1	YQLNPQGMDTSNMDVFVQQYADTVK	2892.3	K	Y	3.2	0.0	68.9	9.0
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	AAADVQLR	843.5	K	G	2.5	0.6	48.9	14.8
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	DLTQAWAVAMALGVEDK	1817.9	K	V	5.3	0.0	92.5	12.3
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	DLTQAWAVAMALGVEDKVTVPLFEGVQK	3031.6	K	T	4.8	0.0	56.6	7.8
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	DVFINAGIK	976.5	R	G	1.9	0.4	0.0	0.0
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	DVFINAGIKGEEYDAAWNSFVVK	2572.3	R	S	3.3	0.0	25.1	11.5
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	GEEYDAAWNSFVVK	1614.7	K	S	4.3	0.8	52.9	7.8
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	GVPAMFVNGK	1019.5	R	Y	2.1	0.8	31.0	14.0
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	KLPEGVK	770.5	K	M	2.3	0.0	36.1	6.0
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	MTKYHVNFMGGDLGK	1713.8	K	D	3.7	0.7	40.2	11.1
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	SASDIRDVFINAGIK	1605.9	R	G	3.4	0.8	35.8	12.8
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	SLVAQQEK	902.5	K	A	2.6	0.0	34.7	15.9
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	SLVAQQEKAAADVQLR	1726.9	K	G	4.5	0.6	73.2	13.2
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	TQTIR	618.4	K	S	1.3	0.5	13.8	17.0
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	VTVPLFEGVQK	1216.7	K	T	2.5	0.8	44.3	11.1
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	YHVNFMGGDLGK	1353.6	K	D	3.0	0.8	32.0	8.5
P0AEG4	23086.3	G	T	T	A	CID	LIT	16	64.9	YQLNPQGMDTSNMDVFVQQYADTVK	2892.3	K	Y	5.3	0.7	84.6	9.0
P0AEG4	23086.3	G	U	A	A	CID	LIT	3	21.2	DAAWNSFVVKSLVAQQEKAAA	2233.2	Y	D	5.4	0.6	48.5	12.6
P0AEG4	23086.3	G	U	A	A	CID	LIT	3	21.2	DTVKYLSEKK	1210.7	A	-	3.0	0.0	27.6	10.4
P0AEG4	23086.3	G	U	A	A	CID	LIT	3	21.2	DVFINAGIKGEEY	1454.7	R	D	3.5	0.6	30.1	15.2
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DAAWNSFVVKSLVAQQEKAAA	2233.2	Y	D	4.5	0.6	41.0	12.6
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DGKQYTTL	925.5	E	E	2.7	0.0	26.2	12.8
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DKVTVPLFEGVQKTQTIRSAS	2304.3	E	D	2.5	0.4	6.7	13.8
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DTVKYLSEKK	1210.7	A	-	2.9	0.8	30.4	11.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DVFINAGIKGEEY	1454.7	R	D	4.3	0.7	44.1	15.2
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DVFVQQYA	969.5	M	D	2.6	0.0	51.2	10.8
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DVFVQQYADTVKYLSEKK	2161.1	M	-	2.5	0.6	3.7	15.8
P0AEG4	23086.3	G	T	A	A	CID	LIT	8	52.4	DVQLRGVPAMFVNGKYQLNPQGMDTSNM	3158.5	A	D	0.0	0.0	33.9	9.5
P0AEG4	23086.3	G	T	T	B	CID	LIT	2	7.7	AAADVQLR	843.5	K	G	2.1	0.5	21.4	14.5
P0AEG4	23086.3	G	T	T	B	CID	LIT	2	7.7	SLVAQQEKAAADVQLR	1726.9	K	G	5.0	0.6	75.7	12.0
P0AEG4	23086.3	G	T	A	B	CID	LIT	7	55.3	DAAWNSFVVKSLVAQQEKAAA	2233.2	Y	D	4.5	0.0	36.8	13.0
P0AEG4	23086.3	G	T	A	B	CID	LIT	7	55.3	DGKQYTTLEKPVAGAPQVL	2015.1	E	E	4.3	0.0	37.1	14.9
P0AEG4	23086.3	G	T	A	B	CID	LIT	7	55.3	DKVTVPLFEGVQKTQTIRSAS	2304.3	E	D	2.4	0.6	11.9	14.5
P0AEG4	23086.3	G	T	A	B	CID	LIT	7	55.3	DTVKYLSEKK	1210.7	A	-	2.8	0.8	12.8	11.1
P0AEG4	23086.3	G	T	A	B	CID	LIT	7	55.3	DVFINAGIKGEEY	1454.7	R	D	3.3	0.5	34.5	15.2
P0AEG4	23086.3	G	T	A	B	CID	LIT	7	55.3	DVFVQQYA	969.5	M	D	2.4	0.7	44.2	13.4
P0AEG4	23086.3	G	T	A	B	CID	LIT	7	55.3	DVQLRGVPAMFVNGKYQLNPQGM	2562.3	A	D	4.0	0.0	38.3	15.6
P0AEG4	23086.3	G	U	A	B	CID	LIT	4	22.1	DLTQAWAVAMALGVE	1574.8	K	D	2.8	0.0	22.9	15.6
P0AEG4	23086.3	G	U	A	B	CID	LIT	4	22.1	DTVKYLSEKK	1210.7	A	-	2.6	0.0	16.3	10.4
P0AEG4	23086.3	G	U	A	B	CID	LIT	4	22.1	DVFINAGIKGEEY	1454.7	R	D	3.6	0.5	43.2	15.1
P0AEG4	23086.3	G	U	A	B	CID	LIT	4	22.1	DVFVQQYA	969.5	M	D	2.9	0.0	50.4	13.4
P0AEG4	23086.3	S	U	T	B	ETD	LIT	2	9.1	SLVAQQEK	902.5	K	A	1.6	0.1	21.2	19.7
P0AEG4	23086.3	S	U	T	B	ETD	LIT	2	9.1	VTVPLFEGVQK	1216.7	K	T	2.7	0.4	16.6	16.0
P0AEG4	23086.3	S	U	T	C	ETD+CID	LIT	2	17.3	VTVPLFEGVQK	1216.7	K	T	2.6	0.6	12.6	13.0
P0AEG4	23086.3	S	U	T	C	ETD+CID	LIT	2	17.3	YQLNPQGMDTSNMDVFVQQYADTVK	2892.3	K	Y	4.9	0.6	61.5	16.5
P0A6G7	23169.3	G	U	T	A	CID	LIT	3	29.5	FLSAPEAVEYGLVDSILTHRN	2331.2	R	-	4.6	0.9	78.8	11.8
P0A6G7	23169.3	G	U	T	A	CID	LIT	3	29.5	MNELMALHTGQSLEQIER	2100.0	R	D	5.1	0.7	53.0	10.4
P0A6G7	23169.3	G	U	T	A	CID	LIT	3	29.5	VMIHQPLGGYQGQATDIEIHAR	2434.2	R	E	5.6	0.6	45.4	13.2
P0A6G7	23169.3	G	U	A	A	CID	LIT	2	11.1	DRFLSAPEAVEYGLV	1665.8	R	D	3.6	0.8	55.5	17.4
P0A6G7	23169.3	G	U	A	A	CID	LIT	2	11.1	DSILTHRN	955.5	V	-	2.1	0.7	20.1	9.0
P0A6G7	23169.3	G	T	A	A	CID	LIT	2	11.1	DRFLSAPEAVEYGLV	1665.8	R	D	2.5	0.5	26.2	17.3
P0A6G7	23169.3	G	T	A	A	CID	LIT	2	11.1	DSILTHRN	955.5	V	-	2.2	0.0	24.0	9.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AFR4	23194.4	G	U	T	A	CID	LIT	6	35.0	DLSELSTYSFVDNVAFR	1962.9	R	L	4.1	0.0	47.4	10.8
P0AFR4	23194.4	G	U	T	A	CID	LIT	6	35.0	EGVGDVKPFL	1060.6	R	-	3.1	0.8	46.5	15.6
P0AFR4	23194.4	G	U	T	A	CID	LIT	6	35.0	IEDKNAMER	1105.5	K	I	3.1	0.8	52.0	11.1
P0AFR4	23194.4	G	U	T	A	CID	LIT	6	35.0	LINQAVEIVR	1154.7	R	K	3.6	0.6	43.0	8.5
P0AFR4	23194.4	G	U	T	A	CID	LIT	6	35.0	NNTPGNYTFILK	1381.7	K	G	2.3	0.7	13.8	11.8
P0AFR4	23194.4	G	U	T	A	CID	LIT	6	35.0	SQFFYIHPDNPQQR	1776.8	M	L	0.0	0.0	63.0	13.0
P0AFR4	23194.4	G	U	A	A	CID	LIT	2	15.5	DDTPVVVREGVG	1242.6	T	D	2.8	0.8	27.0	14.1
P0AFR4	23194.4	G	U	A	A	CID	LIT	2	15.5	DLIIHGGYLGQKPTTVIDLT	2154.2	V	D	4.5	0.0	50.3	11.8
P0AFR4	23194.4	G	T	A	B	CID	LIT	3	17.0	DDTPVVVREGVG	1242.6	T	D	3.0	0.7	32.0	14.8
P0AFR4	23194.4	G	T	A	B	CID	LIT	3	17.0	DLIIHGGYLGQKPTTVI	1825.0	V	D	2.9	0.3	1.7	10.4
P0AFR4	23194.4	G	T	A	B	CID	LIT	3	17.0	DVKPFL	718.4	G	-	1.7	0.5	8.7	14.9
P0AFR4	23194.4	S	U	T	A	CID	LIT	2	9.7	EGVGDVKPFL	1060.6	R	-	2.4	0.2	20.6	18.3
P0AFR4	23194.4	S	U	T	A	CID	LIT	2	9.7	LINQAVEIVR	1154.7	R	K	3.1	0.8	32.8	11.1
P0AFR4	23194.4	S	U	T	B	CID	LIT	2	11.7	EGVGDVKPFL	1060.6	R	-	2.7	0.4	5.7	18.3
P0AFR4	23194.4	S	U	T	B	CID	LIT	2	11.7	SQFFYIHPDNPQQR	1776.8	M	L	0.0	0.0	38.4	17.5
P0A7A5	23239.6	G	U	T	A	CID	LIT	4	18.3	AQGIQDEQVLNALAAVPR	1893.0	R	E	4.4	0.7	86.4	11.8
P0A7A5	23239.6	G	U	T	A	CID	LIT	4	18.3	NLDLHNVSTR	1168.6	K	H	2.6	0.0	24.7	10.4
P0A7A5	23239.6	G	U	T	A	CID	LIT	4	18.3	RVQALLDQLR	1211.7	R	A	3.6	0.5	31.2	11.5
P0A7A5	23239.6	G	U	T	A	CID	LIT	4	18.3	VQALLDQLR	1055.6	R	A	2.5	0.7	30.4	8.5
P0A7A5	23239.6	G	U	A	A	CID	LIT	2	9.1	DLHNVSTRHG	1135.6	L	D	2.3	0.7	20.2	16.0
P0A7A5	23239.6	G	U	A	A	CID	LIT	2	9.1	DQLRAQGIQ	1028.5	L	D	2.4	0.2	20.1	11.8
P0A744	23296.9	G	U	T	A	CID	LIT	2	12.7	HLVSPADALPGR	1232.7	K	N	3.3	0.0	36.8	12.8
P0A744	23296.9	G	U	T	A	CID	LIT	2	12.7	SAIYPLTPEQDAAAR	1602.8	R	A	3.2	0.7	40.4	15.1
P0A744	23296.9	G	T	T	B	CID	LIT	2	13.7	EVCSGDTGHAEAVR	1487.7	R	I	4.2	0.0	75.2	3.0
P0A744	23296.9	G	T	T	B	CID	LIT	2	13.7	SAIYPLTPEQDAAAR	1602.8	R	A	3.6	0.0	48.5	14.6
P0A744	23296.9	S	U	T	C	CID	LIT	2	12.3	EVCSGDTGHAEAVR	1487.7	R	I	4.2	0.8	74.5	11.1
P0A744	23296.9	S	U	T	C	CID	LIT	2	12.3	HLVSPADALPGR	1232.7	K	N	2.7	0.7	23.9	16.4
P0A744	23296.9	S	U	T	C	ETD	LIT	2	13.7	EVCSGDTGHAEAVR	1487.7	R	I	5.6	0.8	71.2	11.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A744	23296.9	S	U	T	C	ETD	LIT	2	13.7	SAIYPLTPEQDAAAR	1602.8	R	A	0.0	0.0	33.6	18.0
P21369	23343.7	G	T	T	A	CID	LIT	3	13.6	FTVLDALQLGYK	1367.8	K	V	3.2	0.8	28.2	12.0
P21369	23343.7	G	T	T	A	CID	LIT	3	13.6	LIDWCQSR	1077.5	R	G	2.6	0.7	40.2	11.8
P21369	23343.7	G	T	T	A	CID	LIT	3	13.6	VNVITDGCR	1033.5	K	G	2.9	0.6	41.2	12.0
P21369	23343.7	G	U	A	B	CID	LIT	3	16.0	DALQLGYKVNVIT	1433.8	L	D	3.1	0.0	30.1	10.8
P21369	23343.7	G	U	A	B	CID	LIT	3	16.0	DVANRLI	800.5	V	D	2.0	0.2	7.6	16.4
P21369	23343.7	G	U	A	B	CID	LIT	3	16.0	DWCQSRGEAVIASQ	1606.7	I	D	2.9	0.0	19.2	12.6
P0AFU8	23426.8	G	U	T	A	CID	LIT	2	9.4	LVSIDEKPNFR	1317.7	K	T	2.9	0.0	33.7	11.1
P0AFU8	23426.8	G	U	T	A	CID	LIT	2	9.4	VGDWVNVER	1073.5	K	A	3.1	0.5	20.3	12.3
P0AFU8	23426.8	S	U	T	C	ETD+CID	LIT	2	8.5	VNIEIDPQTQAVVDTVER	2026.0	R	V	4.3	0.6	38.7	17.4
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	AALELAEQR	1000.5	K	E	3.0	0.2	43.8	13.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	CKIEQAPGQHGAR	1451.7	K	K	4.2	0.8	60.1	12.6
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	EGTDLFLK	922.5	R	S	1.8	0.6	12.9	13.2
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	EKPTWLEVDAGK	1372.7	R	M	2.9	0.7	48.7	12.0
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	EKPTWLEVDAGKMEGTFK	2082.0	R	R	3.1	0.8	43.2	12.0
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	GNTGENLLALLEGR	1456.8	K	L	4.3	0.0	73.1	10.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	IEQAPGQHGAR	1163.6	K	K	3.4	0.5	39.9	13.2
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	IYGVLER	849.5	R	Q	1.7	0.7	22.9	14.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	LDNVVYR	878.5	R	M	2.3	0.6	39.0	17.2
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	LKGNTGENLLALLEGR	1698.0	R	L	4.9	0.6	97.5	10.0
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	LSDYGVQLR	1050.6	R	E	3.3	0.8	57.5	13.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	LSDYGVQLREK	1307.7	R	Q	3.0	0.4	38.4	12.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	MEGTFKR	868.4	K	K	1.9	0.7	26.4	9.5
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	MGFGATR	739.4	R	A	1.9	0.7	15.3	10.0
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	NYYKEAAR	1014.5	R	L	2.1	0.8	17.8	10.4
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	REGTDLFLK	1078.6	R	S	3.1	0.5	29.9	14.5
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	RIYGVLER	1005.6	R	Q	3.3	0.4	34.0	11.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	SDLSADINEHLIVELYSK	2046.0	R	-	5.2	0.7	69.6	10.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	VKAALELAEQR	1227.7	R	E	4.3	0.4	72.7	11.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	VVNIASYQVSPNDVVSIR	1960.1	R	E	5.5	0.7	56.4	10.8
P0A7V8	23451.7	G	U	T	A	CID	LIT	21	71.4	VVNIASYQVSPNDVVSIREK	2217.2	R	A	3.7	0.0	22.3	10.4
P0A7V8	23451.7	G	T	T	A	CID	LIT	2	9.7	IEQAPGQHGAR	1163.6	K	K	3.2	0.4	30.0	13.4
P0A7V8	23451.7	G	T	T	A	CID	LIT	2	9.7	LSDYGVQLR	1050.6	R	E	3.0	0.7	41.5	13.8
P0A7V8	23451.7	G	U	A	A	CID	LIT	2	11.7	DINEHLIVELYSK	1572.8	A	-	3.6	0.9	28.9	13.0
P0A7V8	23451.7	G	U	A	A	CID	LIT	2	11.7	EGTFKRKPERS	1334.7	M	D	2.2	0.4	2.7	14.3
P0A7V8	23451.7	G	U	T	B	CID	LIT	3	14.6	CKIEQAPGQHGAR	1451.7	K	K	3.4	0.0	26.5	12.6
P0A7V8	23451.7	G	U	T	B	CID	LIT	3	14.6	LSDYGVQLR	1050.6	R	E	2.6	0.7	39.3	13.8
P0A7V8	23451.7	G	U	T	B	CID	LIT	3	14.6	RIYGVLER	1005.6	R	Q	2.9	0.3	13.3	11.8
P0A7V8	23451.7	G	T	A	B	CID	LIT	2	14.1	DAGKMEGTFKRKPERS	1836.9	V	D	2.9	0.3	33.8	15.4
P0A7V8	23451.7	G	T	A	B	CID	LIT	2	14.1	DINEHLIVELYSK	1572.8	A	-	4.1	0.6	37.4	13.0
P0A7V8	23451.7	G	U	A	B	CID	LIT	3	21.8	DINEHLIVELYSK	1572.8	A	-	4.1	0.0	43.7	13.0
P0A7V8	23451.7	G	U	A	B	CID	LIT	3	21.8	DLFLKSGVRAI	1218.7	T	D	2.4	0.7	17.3	9.5
P0A7V8	23451.7	G	U	A	B	CID	LIT	3	21.8	DTKCKIEQAPGQHGARKPRLS	2377.3	I	D	3.7	0.0	23.1	12.6
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	CKIEQAPGQHGAR	1451.7	K	K	2.9	0.6	33.9	17.4
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	EKPTWLEVDAGKMEGTFK	2066.0	R	R	2.2	0.7	7.0	17.2
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	1.6	0.0	26.6	18.3
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	LKGNTGENLLALLEGR	1698.0	R	L	4.8	0.5	62.9	13.6
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	REGTDLFLK	1078.6	R	S	2.1	0.2	36.7	16.2
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	SDLSADINEHLIVELYSK	2046.0	R	-	4.8	0.6	19.7	18.1
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	VVNIASYQVSPNDVVSIR	1960.1	R	E	5.1	0.6	41.5	16.3
P0A7V8	23451.7	S	U	T	A	CID	LIT	8	46.1	VVNIASYQVSPNDVVSIREK	2217.2	R	A	4.4	0.6	56.7	17.2
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	CKIEQAPGQHGAR	1451.7	K	K	4.6	0.6	58.4	17.2
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	EGTDLFLK	922.5	R	S	1.4	0.4	18.5	15.6
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	EKPTWLEVDAGK	1372.7	R	M	2.5	0.5	36.5	17.5
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	EKPTWLEVDAGKMEGTFK	2066.0	R	R	2.3	0.4	6.1	18.2
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	LKGNTGENLLALLEGR	1698.0	R	L	5.4	0.5	97.2	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	NYYKEAAR	1014.5	R	L	2.0	0.7	13.4	14.0
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	REGTDLFLK	1078.6	R	S	2.3	0.5	25.0	16.3
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	SDLSADINEHLIVELYSK	2046.0	R	-	3.7	0.7	12.6	18.6
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	VVNIASYQVSPNDVVSIR	1960.1	R	E	5.3	0.5	52.1	16.3
P0A7V8	23451.7	S	U	T	B	CID	LIT	10	49.5	VVNIASYQVSPNDVVSIREK	2217.2	R	A	3.6	0.0	29.1	17.6
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	AALELAEQR	1000.5	K	E	3.0	0.1	37.1	17.0
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	CKIEQAPGQHGAR	1451.7	K	K	3.7	0.6	36.6	16.6
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	EGTDLFLK	922.5	R	S	1.6	0.4	16.7	14.9
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	EKPTWLEVDAGK	1372.7	R	M	2.3	0.5	0.0	0.0
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	EKPTWLEVDAGKMEGTFK	2066.0	R	R	3.6	0.5	27.2	17.9
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	2.7	0.4	26.8	18.3
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	LKGNTGENLLALLEGR	1698.0	R	L	4.7	0.5	97.7	13.8
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	LSDYGVQLR	1050.6	R	E	3.3	0.5	44.2	16.2
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	REGTDLFLK	1078.6	R	S	2.6	0.3	19.1	16.2
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	RIYGVLER	1005.6	R	Q	2.3	0.3	8.0	12.8
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	SDLSADINEHLIVELYSK	2046.0	R	-	2.5	0.7	0.0	0.0
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	VVNIASYQVSPNDVVSIR	1960.1	R	E	5.5	0.7	65.0	16.4
P0A7V8	23451.7	S	U	T	C	CID	LIT	13	58.7	VVNIASYQVSPNDVVSIREK	2217.2	R	A	1.8	0.6	28.7	17.2
P0A7V8	23451.7	S	U	T	B	CID	FT	2	15.0	CKIEQAPGQHGAR	1451.7	K	K	2.6	0.8	32.7	17.5
P0A7V8	23451.7	S	U	T	B	CID	FT	2	15.0	VVNIASYQVSPNDVVSIR	1961.0	R	E	3.7	0.0	30.6	17.9
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	AALELAEQR	1000.5	K	E	2.0	0.2	32.3	17.1
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	CKIEQAPGQHGAR	1451.7	K	K	5.4	0.5	0.0	0.0
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	EGTDLFLK	922.5	R	S	1.9	0.0	26.1	16.2
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	5.2	0.0	51.0	18.8
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	IEQAPGQHGAR	1163.6	K	K	2.7	0.7	12.9	16.1
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	LKGNTGENLLALLEGR	1698.0	R	L	4.3	0.5	68.7	14.8
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	LSDYGVQLR	1050.6	R	E	1.5	0.3	18.2	16.3
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	REGTDLFLK	1078.6	R	S	3.1	0.5	38.6	16.2

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	VKAALELAEQR	1227.7	R	E	2.0	0.1	22.1	13.6
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	VVNIASYQVSPNDVVSIR	1960.1	R	E	6.3	0.0	89.1	16.3
P0A7V8	23451.7	S	U	T	A	ETD	LIT	11	47.1	VVNIASYQVSPNDVVSIREK	2217.2	R	A	2.7	0.3	34.9	17.9
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	AALELAEQR	1000.5	K	E	2.3	0.1	43.8	17.1
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	CKIEQAPGQHGAR	1451.7	K	K	3.5	0.5	0.0	0.0
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	EGTDLFLK	922.5	R	S	2.2	0.6	29.2	14.9
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	EKPTWLEVDAGKMEGTFK	2066.0	R	R	4.1	0.0	28.3	17.4
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	5.1	0.6	23.4	18.8
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	LKGNTGENLLALLEGR	1698.0	R	L	4.8	0.5	77.5	13.8
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	REGTDLFLK	1078.6	R	S	3.4	0.5	0.0	0.0
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	RIYGVLER	1005.6	R	Q	2.1	0.5	14.8	13.4
P0A7V8	23451.7	S	U	T	B	ETD	LIT	9	44.7	VVNIASYQVSPNDVVSIR	1960.1	R	E	7.4	0.7	88.5	16.3
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	AALELAEQR	1000.5	K	E	2.2	0.3	0.0	0.0
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	CKIEQAPGQHGAR	1451.7	K	K	4.8	0.6	0.0	0.0
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	EGTDLFLK	922.5	R	S	2.1	0.6	19.4	15.6
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	EKPTWLEVDAGK	1372.7	R	M	2.6	0.3	20.1	17.6
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	EKPTWLEVDAGKMEGTFK	2066.0	R	R	7.5	0.7	86.6	17.3
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	5.2	0.0	35.2	18.7
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	IEQAPGQHGAR	1163.6	K	K	1.9	0.4	12.6	16.2
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	LKGNTGENLLALLEGR	1698.0	R	L	3.4	0.5	63.3	13.8
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	REGTDLFLK	1078.6	R	S	3.0	0.5	0.0	0.0
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	RIYGVLER	1005.6	R	Q	2.0	0.0	18.0	12.6
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	VVNIASYQVSPNDVVSIR	1960.1	R	E	5.5	0.6	64.0	16.2
P0A7V8	23451.7	S	U	T	C	ETD	LIT	12	45.6	VVNIASYQVSPNDVVSIREK	2217.2	R	A	4.3	0.5	42.6	17.7
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	7	41.7	CKIEQAPGQHGAR	1451.7	K	K	0.0	0.0	50.1	17.5
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	7	41.7	EKPTWLEVDAGK	1372.7	R	M	0.0	0.0	27.5	17.6
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	7	41.7	IEQAPGQHGAR	1163.6	K	K	0.0	0.0	26.2	17.7
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	7	41.7	LKGNTGENLLALLEGR	1698.0	R	L	0.0	0.0	80.2	13.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	7	41.7	REGTDLFLK	1078.6	R	S	0.0	0.0	24.2	16.2
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	7	41.7	SDLSADINEHLIVELYSK	2046.0	R	-	0.0	0.0	29.1	18.4
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	7	41.7	VVNIASYQVSPNDVVSIR	1961.0	R	E	0.0	0.0	55.8	17.5
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	CKIEQAPGQHGAR	1451.7	K	K	2.2	0.3	46.2	17.5
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	EKPTWLEVDAGK	1372.7	R	M	2.1	0.5	8.2	15.8
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	EKPTWLEVDAGKMEGTFK	2066.0	R	R	0.0	0.0	50.8	18.3
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	3.1	0.0	14.7	18.5
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	IEQAPGQHGAR	1163.6	K	K	1.8	0.3	33.0	17.7
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	LKGNTGENLLALLEGR	1698.0	R	L	4.8	0.6	94.7	13.8
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	SDLSADINEHLIVELYSK	2046.0	R	-	4.7	0.7	0.0	0.0
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	VVNIASYQVSPNDVVSIR	1961.0	R	E	5.0	0.5	42.0	17.5
P0A7V8	23451.7	S	U	T	A	ETD+CID	LIT	9	41.7	VVNIASYQVSPNDVVSIREK	2217.2	R	A	3.2	0.0	25.4	17.6
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	2	14.6	EKPTWLEVDAGK	1372.7	R	M	2.9	0.5	0.0	0.0
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	2	14.6	SDLSADINEHLIVELYSK	2046.0	R	-	4.3	0.6	0.0	0.0
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	CKIEQAPGQHGAR	1451.7	K	K	3.4	0.7	50.1	17.5
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	EKPTWLEVDAGK	1372.7	R	M	2.9	0.5	27.5	17.6
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	2.0	0.7	13.6	18.2
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	GNTGENLLALLEGR	1456.8	K	L	2.0	0.1	20.4	16.3
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	IEQAPGQHGAR	1163.6	K	K	2.0	0.2	26.2	17.7
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	LKGNTGENLLALLEGR	1698.0	R	L	4.7	0.6	80.2	13.8
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	MQAASGQLQQSHLLK	1639.9	-	-	2.0	0.1	73.1	17.7
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	REGTDLFLK	1078.6	R	S	2.5	0.4	24.2	16.2
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	SDLSADINEHLIVELYSK	2046.0	R	-	4.1	0.6	0.0	0.0
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	VVNIASYQVSPNDVVSIR	1960.1	R	E	5.3	0.5	45.0	16.1
P0A7V8	23451.7	S	U	T	B	ETD+CID	LIT	11	46.1	VVNIASYQVSPNDVVSIREK	2217.2	R	A	2.4	0.6	0.3	17.6
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	CKIEQAPGQHGAR	1451.7	K	K	0.0	0.0	61.0	17.2
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	EKPTWLEVDAGKMEGTFK	2066.0	R	R	2.6	0.5	0.0	0.0
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	EKPTWLEVDAGKMEGTFKR	2222.1	R	K	1.8	0.2	17.7	18.7

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	LKGNTGENLLALLEGR	1698.0	R	L	5.1	0.5	97.9	13.6
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	LSDYGVQLR	1050.6	R	E	3.2	0.5	31.6	16.3
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	REGTDLFLK	1078.6	R	S	2.0	0.4	18.5	16.2
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	RIYGVLER	1005.6	R	Q	2.0	0.4	0.0	0.0
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	SDLSADINEHLIVELYSK	2046.0	R	-	4.1	0.6	0.0	0.0
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	VKAALELAEQR	1227.7	R	E	3.5	0.4	29.6	14.0
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	VVNIASYQVSPNDVVSIR	1960.1	R	E	5.4	0.6	47.2	16.3
P0A7V8	23451.7	S	U	T	C	ETD+CID	LIT	11	59.7	VVNIASYQVSPNDVVSIREK	2217.2	R	A	2.1	0.7	28.4	17.2
P0A7V8	23451.7	S	U	T	B	HCD	FT	7	41.7	CKIEQAPGQHGAR	1451.7	K	K	0.0	0.0	50.1	17.5
P0A7V8	23451.7	S	U	T	B	HCD	FT	7	41.7	EKPTWLEVDAGK	1372.7	R	M	0.0	0.0	27.5	17.6
P0A7V8	23451.7	S	U	T	B	HCD	FT	7	41.7	IEQAPGQHGAR	1163.6	K	K	0.0	0.0	26.2	17.7
P0A7V8	23451.7	S	U	T	B	HCD	FT	7	41.7	LKGNTGENLLALLEGR	1698.0	R	L	0.0	0.0	80.2	13.8
P0A7V8	23451.7	S	U	T	B	HCD	FT	7	41.7	REGTDLFLK	1078.6	R	S	0.0	0.0	24.2	16.2
P0A7V8	23451.7	S	U	T	B	HCD	FT	7	41.7	SDLSADINEHLIVELYSK	2046.0	R	-	0.0	0.0	29.1	18.4
P0A7V8	23451.7	S	U	T	B	HCD	FT	7	41.7	VVNIASYQVSPNDVVSIR	1961.0	R	E	0.0	0.0	55.8	17.5
P0A7V8	23451.7	S	U	T	B	HCD	FT	2	12.6	EGTDLFLK	922.5	R	S	2.2	0.7	56.3	15.6
P0A7V8	23451.7	S	U	T	B	HCD	FT	2	12.6	EKPTWLEVDAGKMEGTFK	2066.0	R	R	2.5	0.0	32.2	17.4
P39310	23487.1	G	T	T	A	CID	LIT	2	12.7	EAQLDIQSQSQPPTEEQLR	2197.1	R	A	4.1	0.0	66.1	11.5
P39310	23487.1	G	T	T	A	CID	LIT	2	12.7	SYRVEPGK	935.5	R	T	2.8	0.6	22.5	16.2
P61320	23533.6	G	T	T	A	CID	LIT	2	9.2	GAFAYISDQQK	1227.6	R	V	2.3	0.6	16.8	11.8
P61320	23533.6	G	T	T	A	CID	LIT	2	9.2	NLNQYQTR	1036.5	R	G	2.7	0.7	18.4	11.5
P0A6P7	23543.2	G	U	T	A	CID	LIT	2	11.9	SSALNTLTNQK	1176.6	K	S	3.6	0.5	56.5	13.4
P0A6P7	23543.2	G	U	T	A	CID	LIT	2	11.9	TQLINLFEVADGKR	1603.9	R	L	3.2	0.7	32.8	12.6
P69441	23568.4	G	U	T	A	CID	LIT	6	34.6	GTQAQFIMEK	1152.6	K	Y	2.8	0.0	35.3	12.8
P69441	23568.4	G	U	T	A	CID	LIT	6	34.6	IILLGAPGAGK	1009.6	R	G	2.5	0.7	24.1	3.0
P69441	23568.4	G	U	T	A	CID	LIT	6	34.6	LVEYHQMTAPLIGYYSK	2013.0	R	E	4.2	0.0	35.5	13.2
P69441	23568.4	G	U	T	A	CID	LIT	6	34.6	LVTDELVIALVK	1312.8	K	E	4.4	0.0	74.5	3.0
P69441	23568.4	G	U	T	A	CID	LIT	6	34.6	VDGTKPVAEVR	1170.6	K	A	3.5	0.6	32.8	14.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69441	23568.4	G	U	T	A	CID	LIT	6	34.6	YGIPQISTGDMLR	1450.7	K	A	3.5	0.7	27.6	13.2
P69441	23568.4	G	T	T	A	CID	LIT	3	15.9	GTQAQFIMEK	1168.6	K	Y	3.7	0.5	36.7	13.8
P69441	23568.4	G	T	T	A	CID	LIT	3	15.9	VDGTKPVAEVR	1170.6	K	A	2.9	0.7	54.0	14.3
P69441	23568.4	G	T	T	A	CID	LIT	3	15.9	YGIPQISTGDMLR	1466.7	K	A	2.7	0.8	28.5	11.8
P69441	23568.4	G	U	A	A	CID	LIT	4	21.5	DGFPRTIPQA	1101.6	L	D	2.2	0.7	13.4	13.2
P69441	23568.4	G	U	A	A	CID	LIT	4	21.5	DGTKPVAEVRA	1142.6	V	D	2.4	0.6	24.0	15.1
P69441	23568.4	G	U	A	A	CID	LIT	4	21.5	DLEKILG	787.5	A	-	1.9	0.3	32.4	17.3
P69441	23568.4	G	U	A	A	CID	LIT	4	21.5	DMLRAAVKSGSELGKQAK	1889.0	G	D	5.1	0.5	37.4	14.6
P69441	23568.4	G	T	A	A	CID	LIT	4	14.0	DGTKPVAEVRA	1142.6	V	D	2.5	0.7	37.1	15.4
P69441	23568.4	G	T	A	A	CID	LIT	4	14.0	DLEKILG	787.5	A	-	2.0	0.4	24.0	17.3
P69441	23568.4	G	T	A	A	CID	LIT	4	14.0	EAEAGNTKYAKV	1280.6	K	D	3.7	0.5	62.4	14.3
P69441	23568.4	G	T	A	A	CID	LIT	4	14.0	EAEAGNTKYAKVDGTKPVA	1949.0	K	E	3.6	0.0	51.4	14.8
P69441	23568.4	G	T	T	B	CID	LIT	6	25.2	IAQEDCR	891.4	R	N	2.1	0.6	27.5	10.0
P69441	23568.4	G	T	T	B	CID	LIT	6	25.2	IILLGAPGAGK	1009.6	R	G	2.1	0.0	17.1	3.0
P69441	23568.4	G	T	T	B	CID	LIT	6	25.2	LVTDELVIALVK	1312.8	K	E	3.1	0.0	13.3	3.0
P69441	23568.4	G	T	T	B	CID	LIT	6	25.2	SGSELGKQAK	1004.5	K	D	1.9	0.1	0.0	0.0
P69441	23568.4	G	T	T	B	CID	LIT	6	25.2	VDGTKPVAEVR	1170.6	K	A	2.8	0.8	49.4	14.3
P69441	23568.4	G	T	T	B	CID	LIT	6	25.2	YAKVDGTKPVAEVR	1532.8	K	A	2.2	0.0	22.0	10.4
P69441	23568.4	G	T	A	B	CID	LIT	5	26.2	DAMKEAGINV	1047.5	A	D	2.7	0.7	33.0	14.6
P69441	23568.4	G	T	A	B	CID	LIT	5	26.2	DGFPRTIPQA	1101.6	L	D	2.0	0.0	15.9	14.0
P69441	23568.4	G	T	A	B	CID	LIT	5	26.2	DGTKPVAEVRA	1142.6	V	D	2.6	0.5	42.3	14.3
P69441	23568.4	G	T	A	B	CID	LIT	5	26.2	DLEKILG	787.5	A	-	1.3	0.5	21.0	17.4
P69441	23568.4	G	T	A	B	CID	LIT	5	26.2	DMLRAAVKSGSELGKQAK	1889.0	G	D	4.6	0.6	35.2	14.5
P69441	23568.4	S	U	T	A	CID	LIT	5	32.7	FNPPKVEGKDDVTGEELTTR	2232.1	K	K	4.5	0.0	78.6	18.9
P69441	23568.4	S	U	T	A	CID	LIT	5	32.7	GTQAQFIMEK	1152.6	K	Y	2.6	0.4	31.3	15.8
P69441	23568.4	S	U	T	A	CID	LIT	5	32.7	IILLGAPGAGK	1009.6	R	G	2.5	0.6	28.0	7.0
P69441	23568.4	S	U	T	A	CID	LIT	5	32.7	LVEYHQMTAPLIGYYSK	2013.0	R	E	5.2	0.6	47.1	17.9
P69441	23568.4	S	U	T	A	CID	LIT	5	32.7	LVTDELVIALVK	1312.8	K	E	3.0	0.8	37.7	8.5

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69441	23568.4	S	U	T	B	CID	LIT	5	32.2	FNPPKVEGKDDVTGEELTTR	2232.1	K	K	2.0	0.0	26.5	19.1
P69441	23568.4	S	U	T	B	CID	LIT	5	32.2	GTQAQFIMEK	1152.6	K	Y	2.3	0.3	23.0	15.8
P69441	23568.4	S	U	T	B	CID	LIT	5	32.2	IILLGAPGAGK	1009.6	R	G	2.6	0.6	19.7	7.0
P69441	23568.4	S	U	T	B	CID	LIT	5	32.2	LVEYHQMTAPLIGYYSK	2013.0	R	E	5.1	0.6	44.0	17.9
P69441	23568.4	S	U	T	B	CID	LIT	5	32.2	VDGTKPVAEVR	1170.6	K	A	2.2	0.6	23.7	16.8
P69441	23568.4	S	U	T	C	CID	LIT	5	32.7	FNPPKVEGKDDVTGEELTTR	2232.1	K	K	4.7	0.9	83.8	19.1
P69441	23568.4	S	U	T	C	CID	LIT	5	32.7	IILLGAPGAGK	1009.6	R	G	2.3	0.6	8.5	7.0
P69441	23568.4	S	U	T	C	CID	LIT	5	32.7	LVEYHQMTAPLIGYYSK	2013.0	R	E	5.4	0.6	45.4	18.7
P69441	23568.4	S	U	T	C	CID	LIT	5	32.7	LVTDELVIALVK	1312.8	K	E	3.1	0.6	32.5	8.5
P69441	23568.4	S	U	T	C	CID	LIT	5	32.7	NGFLLDGFPR	1135.6	R	T	2.4	0.0	28.9	14.8
P69441	23568.4	S	U	T	A	ETD	LIT	4	23.4	IILLGAPGAGK	1009.6	R	G	2.9	0.7	33.0	7.0
P69441	23568.4	S	U	T	A	ETD	LIT	4	23.4	LVEYHQMTAPLIGYYSK	2013.0	R	E	1.7	0.7	15.8	18.5
P69441	23568.4	S	U	T	A	ETD	LIT	4	23.4	LVTDELVIALVK	1312.8	K	E	1.8	0.7	22.0	8.5
P69441	23568.4	S	U	T	A	ETD	LIT	4	23.4	NGFLLDGFPR	1135.6	R	T	1.4	0.6	12.9	14.8
P69441	23568.4	S	U	T	C	ETD	LIT	4	25.2	FNPPKVEGKDDVTGEELTTR	2232.1	K	K	4.4	0.5	35.4	19.0
P69441	23568.4	S	U	T	C	ETD	LIT	4	25.2	IILLGAPGAGK	1009.6	R	G	2.3	0.0	17.2	7.0
P69441	23568.4	S	U	T	C	ETD	LIT	4	25.2	NGFLLDGFPR	1135.6	R	T	1.8	0.6	13.0	16.1
P69441	23568.4	S	U	T	C	ETD	LIT	4	25.2	YGIPQISTGDMLR	1450.7	K	A	2.7	0.3	35.9	17.5
P69441	23568.4	S	U	T	C	ETD	FT	2	14.5	FNPPKVEGKDDVTGEELTTR	2232.1	K	K	1.5	0.0	20.4	19.0
P69441	23568.4	S	U	T	C	ETD	FT	2	14.5	VDGTKPVAEVR	1170.6	K	A	1.2	0.0	22.1	16.8
P69441	23568.4	S	U	T	B	ETD+CID	LIT	4	23.4	LVEYHQMTAPLIGYYSK	2013.0	R	E	0.0	0.0	57.4	18.5
P69441	23568.4	S	U	T	B	ETD+CID	LIT	4	23.4	LVTDELVIALVK	1312.8	K	E	0.0	0.0	21.8	8.5
P69441	23568.4	S	U	T	B	ETD+CID	LIT	4	23.4	NGFLLDGFPR	1135.6	R	T	0.0	0.0	39.7	14.8
P69441	23568.4	S	U	T	B	ETD+CID	LIT	4	23.4	VDGTKPVAEVR	1170.6	K	A	0.0	0.0	23.1	17.1
P69441	23568.4	S	U	T	A	ETD+CID	LIT	4	28.0	FNPPKVEGKDDVTGEELTTR	2232.1	K	K	2.7	0.7	26.4	19.0
P69441	23568.4	S	U	T	A	ETD+CID	LIT	4	28.0	LVEYHQMTAPLIGYYSK	2013.0	R	E	5.8	0.6	54.7	18.0
P69441	23568.4	S	U	T	A	ETD+CID	LIT	4	28.0	LVTDELVIALVK	1312.8	K	E	3.2	0.8	43.1	8.5
P69441	23568.4	S	U	T	A	ETD+CID	LIT	4	28.0	VDGTKPVAEVR	1170.6	K	A	2.9	0.4	23.5	17.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P69441	23568.4	S	U	T	B	ETD+CID	LIT	5	28.5	IILLGAPGAGK	1009.6	R	G	1.8	0.7	8.0	7.0
P69441	23568.4	S	U	T	B	ETD+CID	LIT	5	28.5	LVEYHQMTAPLIGYYSK	2013.0	R	E	5.5	0.6	57.4	18.5
P69441	23568.4	S	U	T	B	ETD+CID	LIT	5	28.5	LVTDELVIALVK	1312.8	K	E	3.3	0.4	21.8	8.5
P69441	23568.4	S	U	T	B	ETD+CID	LIT	5	28.5	NGFLLDGFPR	1135.6	R	T	2.5	0.6	39.7	14.8
P69441	23568.4	S	U	T	B	ETD+CID	LIT	5	28.5	VDGTKPVAEVR	1170.6	K	A	3.0	0.5	23.1	17.1
P69441	23568.4	S	U	T	C	ETD+CID	LIT	4	23.4	IILLGAPGAGK	1009.6	R	G	2.4	0.6	29.4	7.0
P69441	23568.4	S	U	T	C	ETD+CID	LIT	4	23.4	LVEYHQMTAPLIGYYSK	2013.0	R	E	5.3	0.6	69.0	18.7
P69441	23568.4	S	U	T	C	ETD+CID	LIT	4	23.4	LVTDELVIALVK	1312.8	K	E	3.0	0.0	37.2	9.0
P69441	23568.4	S	U	T	C	ETD+CID	LIT	4	23.4	NGFLLDGFPR	1135.6	R	T	2.3	0.6	14.1	14.8
P69441	23568.4	S	U	T	B	HCD	FT	4	23.4	LVEYHQMTAPLIGYYSK	2013.0	R	E	0.0	0.0	57.4	18.5
P69441	23568.4	S	U	T	B	HCD	FT	4	23.4	LVTDELVIALVK	1312.8	K	E	0.0	0.0	21.8	8.5
P69441	23568.4	S	U	T	B	HCD	FT	4	23.4	NGFLLDGFPR	1135.6	R	T	0.0	0.0	39.7	14.8
P69441	23568.4	S	U	T	B	HCD	FT	4	23.4	VDGTKPVAEVR	1170.6	K	A	0.0	0.0	23.1	17.1
P60546	23575.2	G	U	T	A	CID	LIT	4	30.0	AQGTLYIVSAPSGAGK	1519.8	M	S	0.0	0.0	83.8	13.2
P60546	23575.2	G	U	T	A	CID	LIT	4	30.0	DAFLEHAEVFGNYYGTSR	2075.9	R	E	5.0	0.8	63.2	9.0
P60546	23575.2	G	U	T	A	CID	LIT	4	30.0	GRGQDSEEVIAK	1288.6	R	R	3.2	0.2	19.9	11.1
P60546	23575.2	G	U	T	A	CID	LIT	4	30.0	TQPLYDTQVSVSHTTR	1832.9	K	Q	4.2	0.0	93.4	12.6
P60546	23575.2	G	U	A	A	CID	LIT	2	9.2	DALISKLLAD	1058.6	H	-	3.0	0.8	25.8	13.2
P60546	23575.2	G	U	A	A	CID	LIT	2	9.2	DEFKEMISR	1154.6	H	D	2.4	0.4	20.2	15.4
P0ADA1	23605.0	G	U	T	A	CID	LIT	2	11.5	AANAEPLLMQIR	1326.7	K	L	2.8	0.7	25.3	13.6
P0ADA1	23605.0	G	U	T	A	CID	LIT	2	11.5	GFQPQQTEQTLR	1432.7	R	Q	4.0	0.8	50.2	12.0
P0ADA1	23605.0	G	T	T	A	CID	LIT	5	26.4	AANAEPLLMQIR	1326.7	K	L	2.8	0.7	28.8	13.6
P0ADA1	23605.0	G	T	T	A	CID	LIT	5	26.4	GFQPQQTEQTLR	1432.7	R	Q	3.0	0.8	42.8	12.6
P0ADA1	23605.0	G	T	T	A	CID	LIT	5	26.4	RYNEAFSAIYPK	1458.7	R	L	2.6	0.4	7.1	12.6
P0ADA1	23605.0	G	T	T	A	CID	LIT	5	26.4	TSVVNASISGDTSQQGLAR	1891.0	K	L	4.8	0.0	80.0	12.6
P0ADA1	23605.0	G	T	T	A	CID	LIT	5	26.4	YNEAFSAIYPK	1302.6	R	L	2.4	0.0	38.6	11.1
P0ADA1	23605.0	G	T	T	B	CID	LIT	3	10.6	QLQPLVNHDS	1150.6	K	-	2.6	0.7	10.5	12.3
P0ADA1	23605.0	G	T	T	B	CID	LIT	3	10.6	RYNEAFSAIYPK	1458.7	R	L	2.0	0.2	0.0	0.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADA1	23605.0	G	T	T	B	CID	LIT	3	10.6	YNEAFSAIYPK	1302.6	R	L	2.3	0.6	14.4	11.1
P0ADA1	23605.0	G	T	A	B	CID	LIT	2	13.9	DKWQSKTSVVNASISG	1706.9	N	D	2.4	0.7	13.9	15.2
P0ADA1	23605.0	G	T	A	B	CID	LIT	2	13.9	DWMAKQLQPLVNH	1579.8	A	D	4.1	0.8	50.8	14.8
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	AETLYYIVK	1099.6	K	G	3.0	0.0	29.8	7.8
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	IAQTLLNLAK	1084.7	R	Q	4.0	0.8	67.8	12.8
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	ITRQEIGQIVGCSR	1616.9	K	E	4.5	0.6	55.1	13.4
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	LQVTSEK	804.4	R	V	2.0	0.4	18.0	13.2
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	LSAQMAR	776.4	R	R	2.3	0.5	31.8	15.1
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	MLEDQNLISAHGK	1455.7	K	T	4.3	0.8	60.0	13.2
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	QEIGQIVGCSR	1246.6	R	E	3.1	0.8	48.4	11.8
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	QLIQVNPDILMR	1439.8	R	L	3.7	0.7	66.1	6.0
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	RLQVTSEK	960.5	R	V	2.5	0.4	24.1	14.5
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	TIVVYGTR	908.5	K	-	2.7	0.0	30.9	10.8
P0ACJ8	23622.9	G	U	T	A	CID	LIT	11	44.3	VGNLAFLDVTGR	1261.7	K	I	4.4	0.9	52.4	12.6
P0ACJ8	23622.9	G	T	T	A	CID	LIT	3	13.3	LSAQMAR	776.4	R	R	2.3	0.6	27.8	15.1
P0ACJ8	23622.9	G	T	T	A	CID	LIT	3	13.3	MLEDQNLISAHGK	1455.7	K	T	4.0	0.8	52.2	13.2
P0ACJ8	23622.9	G	T	T	A	CID	LIT	3	13.3	TIVVYGTR	908.5	K	-	2.2	0.6	11.0	10.8
P0ACJ8	23622.9	G	T	T	B	CID	LIT	4	17.1	AETLYYIVK	1099.6	K	G	1.9	0.5	0.0	0.0
P0ACJ8	23622.9	G	T	T	B	CID	LIT	4	17.1	LQVTSEK	804.4	R	V	2.0	0.1	9.1	13.2
P0ACJ8	23622.9	G	T	T	B	CID	LIT	4	17.1	QEIGQIVGCSR	1246.6	R	E	2.8	0.8	34.6	13.0
P0ACJ8	23622.9	G	T	T	B	CID	LIT	4	17.1	RLQVTSEK	960.5	R	V	2.3	0.1	5.7	14.8
P0ACJ8	23622.9	G	T	T	B	CID	LIT	4	17.1	TIVVYGTR	908.5	K	-	2.1	0.5	14.2	10.8
P0ACJ8	23622.9	G	U	T	B	CID	LIT	5	25.7	IAQTLLNLAK	1084.7	R	Q	2.6	0.5	45.4	12.8
P0ACJ8	23622.9	G	U	T	B	CID	LIT	5	25.7	MLEDQNLISAHGK	1455.7	K	T	3.4	0.8	22.3	13.2
P0ACJ8	23622.9	G	U	T	B	CID	LIT	5	25.7	QEIGQIVGCSR	1246.6	R	E	3.5	0.7	46.2	13.0
P0ACJ8	23622.9	G	U	T	B	CID	LIT	5	25.7	TIVVYGTR	908.5	K	-	2.3	0.6	23.2	10.8
P0ACJ8	23622.9	G	U	T	B	CID	LIT	5	25.7	VGNLAFLDVTGR	1261.7	K	I	3.9	0.0	62.8	12.6
P0ACJ8	23622.9	S	U	T	B	CID	LIT	2	11.0	QEIGQIVGCSR	1246.6	R	E	2.7	0.4	31.8	17.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ACJ8	23622.9	S	U	T	B	CID	LIT	2	11.0	VGNLAFLDVTGR	1261.7	K	I	3.3	0.6	39.0	16.5
P0ACJ8	23622.9	S	U	T	C	CID	LIT	3	17.1	MLEDQNLISAHGK	1455.7	K	T	2.5	0.8	20.2	16.5
P0ACJ8	23622.9	S	U	T	C	CID	LIT	3	17.1	QEIGQIVGCSR	1246.6	R	E	2.9	0.4	23.2	17.9
P0ACJ8	23622.9	S	U	T	C	CID	LIT	3	17.1	VGNLAFLDVTGR	1261.7	K	I	3.6	0.5	34.2	16.2
P0ACJ8	23622.9	S	U	T	C	ETD+CID	LIT	2	11.9	MLEDQNLISAHGK	1455.7	K	T	2.7	0.7	9.8	15.4
P0ACJ8	23622.9	S	U	T	C	ETD+CID	LIT	2	11.9	VGNLAFLDVTGR	1261.7	K	I	3.6	0.5	41.3	16.1
P69407	23654.2	G	U	T	A	CID	LIT	2	15.7	ISAGGYGDKR	1023.5	K	L	3.0	0.5	63.3	12.6
P69407	23654.2	G	U	T	A	CID	LIT	2	15.7	LGVENDIALLNYLSSVTLSPADKD	2547.3	K	-	3.5	0.0	29.4	10.0
P69407	23654.2	G	T	T	B	CID	LIT	4	14.4	ALAALQKGK	899.6	K	K	1.7	0.3	21.5	14.5
P69407	23654.2	G	T	T	B	CID	LIT	4	14.4	ISAGGYGDK	867.4	K	R	2.8	0.6	10.4	11.1
P69407	23654.2	G	T	T	B	CID	LIT	4	14.4	KFTPESVSR	1050.6	K	L	2.6	0.0	45.3	13.8
P69407	23654.2	G	T	T	B	CID	LIT	4	14.4	LLEKISAGGYGDK	1350.7	R	R	3.7	0.6	41.9	10.0
P69407	23654.2	G	T	A	B	CID	LIT	3	12.5	DIEGIVLKQGAPT	1340.7	L	D	2.9	0.7	27.9	10.8
P69407	23654.2	G	T	A	B	CID	LIT	3	12.5	DLDIEGIVLKQGAPT	1568.9	L	D	3.3	0.7	33.6	12.6
P69407	23654.2	G	T	A	B	CID	LIT	3	12.5	DSTALINNLPKL	1298.7	E	D	3.3	0.5	59.4	13.2
P33218	23669.7	G	T	A	B	CID	LIT	3	13.7	DALKIPQ	784.5	G	D	2.7	0.7	28.1	10.8
P33218	23669.7	G	T	A	B	CID	LIT	3	13.7	DGHIDAKERAAI	1295.7	S	D	1.9	0.7	0.0	0.0
P33218	23669.7	G	T	A	B	CID	LIT	3	13.7	DLEQQKRTLAE	1330.7	R	-	2.8	0.4	39.8	16.5
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	DQAAIDASCK	1078.5	R	E	3.5	0.9	41.7	10.0
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	DQAAIDASCKECDALFALLDAELAK	2738.3	R	V	4.9	0.6	23.9	13.0
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	GILMGLVR	874.5	R	T	2.0	0.6	43.4	13.4
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	KVVMIPVS	872.5	R	-	1.6	0.7	13.6	15.7
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	LWIDSPAR	957.5	R	R	1.9	0.7	23.9	13.2
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	RLWIDSPAR	1113.6	K	R	3.0	0.2	24.5	10.4
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	VLLTLEELELPYEQILAGR	2199.2	K	E	4.8	0.0	64.5	7.8
P0ACA7	23696.0	G	T	T	A	CID	LIT	8	37.5	YLAAQYGQK	1041.5	R	R	3.1	0.0	37.5	12.0
P0A720	23765.5	G	U	T	A	CID	LIT	2	13.1	SIHTIDATQPLEAVMDAIR	2081.1	K	T	2.6	0.7	6.1	11.1
P0A720	23765.5	G	U	T	A	CID	LIT	2	13.1	YLELAAQDK	1050.5	R	S	2.0	0.6	21.3	14.9

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P75849	23766.4	G	U	T	A	CID	LIT	4	22.8	GDHNQLISSIKDK	1454.8	R	L	2.7	0.5	20.9	12.6
P75849	23766.4	G	U	T	A	CID	LIT	4	22.8	LAALVDPGGDAEK	1255.7	R	I	3.5	0.0	33.9	9.5
P75849	23766.4	G	U	T	A	CID	LIT	4	22.8	LHNPFLQDEMPVW	1625.8	R	-	3.4	0.9	40.4	11.1
P75849	23766.4	G	U	T	A	CID	LIT	4	22.8	LLISGDVIFK	1104.7	K	G	1.8	0.6	10.1	4.8
P75849	23766.4	G	U	A	B	CID	LIT	2	9.3	DDRAKLLISG	1087.6	F	D	2.1	0.2	8.7	14.9
P75849	23766.4	G	U	A	B	CID	LIT	2	9.3	DHNQLISSIK	1154.6	G	D	2.7	0.7	18.5	13.4
P75849	23766.4	S	U	T	C	CID	LIT	2	15.3	IIPVTAFSQNCSLIWCEQTR	2423.2	R	L	2.6	0.0	25.5	19.4
P75849	23766.4	S	U	T	C	CID	LIT	2	15.3	LAALVDPGGDAEK	1255.7	R	I	2.8	0.6	17.4	11.8
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	DLHDDAEWMAK	1330.6	K	Q	3.4	0.0	31.8	3.0
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	FATPEAK	763.4	R	A	2.2	0.8	38.0	14.9
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	FFADMHRK	1051.5	K	D	2.7	0.4	16.7	7.8
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	3.6	0.0	20.8	9.0
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	KLTPEQAEQIK	1284.7	K	T	4.1	0.8	58.7	11.1
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	KMLDASHVVVFCAK	1604.8	R	T	3.9	0.9	42.3	13.0
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	LVVDQEDADGR	1216.6	K	F	3.8	0.8	77.7	8.5
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	LVVDQEDADGRFATPEAK	1961.0	K	A	4.2	0.6	42.6	13.0
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	MDIISVALKR	1145.7	-	H	2.8	0.7	61.1	11.8
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	MLDASHVVVFCAK	1476.7	K	T	1.9	0.5	12.4	13.8
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	SAAGNYVFNER	1227.6	K	K	3.8	0.7	41.1	7.8
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	SRLPQNITLTEV	1370.8	K	-	3.3	0.7	38.8	11.1
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	TAMDDVWLK	1094.5	K	L	2.3	0.7	34.1	10.0
P38489	23887.3	G	U	T	A	CID	LIT	14	71.0	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	3.3	0.0	27.4	10.8
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	FATPEAK	763.4	R	A	2.3	0.7	25.2	13.0
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	KLTPEQAEQIK	1284.7	K	T	3.3	0.5	56.4	11.5
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	KMLDASHVVVFCAK	1604.8	R	T	4.2	0.8	29.5	13.8
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	LVVDQEDADGR	1216.6	K	F	3.1	0.7	45.7	8.5
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	MDIISVALKR	1161.7	-	H	0.0	0.0	57.1	12.0
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	SAAGNYVFNER	1227.6	K	K	3.9	0.8	41.5	7.0

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	SRLPQNITLTEV	1370.8	K	-	2.7	0.4	18.9	11.1
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	TAMDDVWLK	1094.5	K	L	2.1	0.0	27.0	10.0
P38489	23887.3	G	T	T	A	CID	LIT	9	51.2	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	3.5	0.0	24.4	10.4
P38489	23887.3	G	U	A	A	CID	LIT	2	15.2	DFNATLPKSRLPQNITLTEV	2257.2	E	-	2.8	0.6	22.2	13.6
P38489	23887.3	G	U	A	A	CID	LIT	2	15.2	DGRFATPEAKAAN	1347.7	A	D	2.4	0.3	11.8	14.0
P38489	23887.3	G	T	A	A	CID	LIT	4	29.0	DASHVVVFCAKTAM	1535.7	L	D	4.0	0.9	36.5	12.8
P38489	23887.3	G	T	A	A	CID	LIT	4	29.0	DFNATLPKSRLPQNITLTEV	2257.2	E	-	2.8	0.7	19.3	13.6
P38489	23887.3	G	T	A	A	CID	LIT	4	29.0	DGRFATPEAKAAN	1347.7	A	D	2.5	0.3	6.5	15.3
P38489	23887.3	G	T	A	A	CID	LIT	4	29.0	MDIISVALKRHSTKAF	1817.0	-	D	2.2	0.7	6.2	13.0
P38489	23887.3	G	T	A	B	CID	LIT	2	11.1	DASKKLTPEQA	1187.6	F	E	2.2	0.6	8.9	15.6
P38489	23887.3	G	T	A	B	CID	LIT	2	11.1	DGRFATPEAKAAN	1347.7	A	D	3.2	0.5	29.8	14.3
P38489	23887.3	S	U	T	A	CID	LIT	3	28.1	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	3.3	0.0	14.3	18.0
P38489	23887.3	S	U	T	A	CID	LIT	3	28.1	SAAGNYVFNER	1227.6	K	K	3.0	0.5	18.1	12.0
P38489	23887.3	S	U	T	A	CID	LIT	3	28.1	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	4.9	0.6	36.0	19.4
P38489	23887.3	S	U	T	B	CID	LIT	3	28.1	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	2.6	0.6	25.4	18.0
P38489	23887.3	S	U	T	B	CID	LIT	3	28.1	SAAGNYVFNER	1227.6	K	K	3.1	0.6	24.3	11.1
P38489	23887.3	S	U	T	B	CID	LIT	3	28.1	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	3.1	0.5	17.9	19.9
P38489	23887.3	S	U	T	A	ETD	LIT	3	28.1	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	6.4	0.0	47.3	17.7
P38489	23887.3	S	U	T	A	ETD	LIT	3	28.1	SAAGNYVFNER	1227.6	K	K	2.1	0.6	11.8	10.0
P38489	23887.3	S	U	T	A	ETD	LIT	3	28.1	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	1.9	0.2	10.1	19.7
P38489	23887.3	S	U	T	B	ETD	LIT	2	16.1	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	5.0	0.0	38.3	17.9
P38489	23887.3	S	U	T	B	ETD	LIT	2	16.1	KLTPEQAEQIK	1284.7	K	T	2.4	0.3	31.9	15.1
P38489	23887.3	S	U	T	B	ETD+CID	LIT	2	17.1	SAAGNYVFNER	1227.6	K	K	0.0	0.0	37.2	12.6
P38489	23887.3	S	U	T	B	ETD+CID	LIT	2	17.1	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	0.0	0.0	22.8	19.7
P38489	23887.3	S	U	T	A	ETD+CID	LIT	2	23.0	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	3.5	0.6	11.7	17.7
P38489	23887.3	S	U	T	A	ETD+CID	LIT	2	23.0	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	3.6	0.5	0.0	0.0
P38489	23887.3	S	U	T	B	ETD+CID	LIT	3	28.1	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	3.6	0.0	15.7	17.8
P38489	23887.3	S	U	T	B	ETD+CID	LIT	3	28.1	SAAGNYVFNER	1227.6	K	K	3.3	0.5	37.2	12.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P38489	23887.3	S	U	T	B	ETD+CID	LIT	3	28.1	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	2.9	0.5	22.8	19.7
P38489	23887.3	S	U	T	C	ETD+CID	LIT	2	23.0	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	3.1	0.0	22.0	18.0
P38489	23887.3	S	U	T	C	ETD+CID	LIT	2	23.0	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	4.1	0.5	0.0	0.0
P38489	23887.3	S	U	T	B	HCD	FT	2	17.1	SAAGNYVFNER	1227.6	K	K	0.0	0.0	37.2	12.6
P38489	23887.3	S	U	T	B	HCD	FT	2	17.1	TLLQYSPSSTNSQPWHFIVASTEEGK	2907.4	K	A	0.0	0.0	22.8	19.7
P38489	23887.3	S	U	T	B	HCD	FT	2	15.7	GYTSLVVVPVGHHSVEDFNATLPK	2566.3	K	S	4.0	0.0	21.4	17.9
P38489	23887.3	S	U	T	B	HCD	FT	2	15.7	MDIISVALKR	1145.7	-	H	3.5	0.0	42.0	12.8
P0AF28	23909.5	G	U	T	A	CID	LIT	3	20.4	ALHQAAAGEMVLSEALTPVLAASLR	2519.4	K	A	3.9	0.0	17.1	10.0
P0AF28	23909.5	G	U	T	A	CID	LIT	3	20.4	LIAQGLPNK	953.6	K	M	2.5	0.7	35.1	7.0
P0AF28	23909.5	G	U	T	A	CID	LIT	3	20.4	RLDITESTVK	1161.6	R	V	2.5	0.3	7.5	10.4
P0AF28	23909.5	S	U	T	A	CID	LIT	2	16.7	GADGYLLKDMEPEDLLK	1906.9	R	A	2.5	0.4	0.0	0.0
P0AF28	23909.5	S	U	T	A	CID	LIT	2	16.7	IVVFSVSNHEEDVVTALKR	2142.2	R	G	1.2	0.0	21.5	16.9
P0AF28	23909.5	S	U	T	B	CID	LIT	2	16.2	GADGYLLKDMEPEDLLK	1906.9	R	A	2.5	0.2	0.0	0.0
P0AF28	23909.5	S	U	T	B	CID	LIT	2	16.2	SNQEPATILLIDDHPMLR	2063.1	M	T	0.0	0.0	30.3	18.3
P0AF28	23909.5	S	U	T	B	ETD+CID	LIT	2	16.2	GADGYLLKDMEPEDLLK	1906.9	R	A	2.6	0.4	0.0	0.0
P0AF28	23909.5	S	U	T	B	ETD+CID	LIT	2	16.2	SNQEPATILLIDDHPMLR	2063.1	M	T	0.0	0.0	26.7	18.3
P0AF28	23909.5	S	U	T	C	ETD+CID	LIT	3	20.4	GADGYLLKDMEPEDLLK	1906.9	R	A	3.9	0.5	9.0	18.6
P0AF28	23909.5	S	U	T	C	ETD+CID	LIT	3	20.4	LIAQGLPNK	953.6	K	M	1.8	0.6	12.9	8.5
P0AF28	23909.5	S	U	T	C	ETD+CID	LIT	3	20.4	SNQEPATILLIDDHPMLR	2063.1	M	T	0.0	0.0	46.1	18.1
P0AAV4	23928.4	G	T	A	B	CID	LIT	2	10.1	DEPILLRPG	1009.6	R	D	2.6	0.7	18.2	10.0
P0AAV4	23928.4	G	T	A	B	CID	LIT	2	10.1	DSVRFVPQKEGVC	1520.8	G	-	3.3	0.5	44.3	14.6
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	ANPDYLR	848.4	R	T	1.9	0.6	29.1	16.0
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	GIDGLTAQLK	1015.6	K	S	4.0	0.6	67.6	13.4
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	ITLEEKK	860.5	K	-	2.6	0.3	31.1	7.8
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	LDFQWR	864.4	R	K	2.2	0.7	25.3	12.6
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	LKNEQPQIR	1125.6	R	A	2.7	0.4	33.4	10.0
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	LMDEAAQK	905.4	K	T	2.2	0.4	9.4	12.6
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	QNEWGTLLR	1116.6	K	T	2.9	0.4	27.8	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	TIVDQELLPYVQVK	1644.9	R	Y	4.4	0.7	50.9	10.4
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	TIVPIR	698.5	K	V	1.6	0.6	14.7	10.4
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	TKGIDGLTAQLK	1244.7	R	S	3.8	0.0	41.8	10.8
P0ADV7	23945.5	G	U	T	A	CID	LIT	11	42.7	YAGALVLGQYYK	1345.7	K	S	4.2	0.8	69.2	15.3
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	ANPDYLR	848.4	R	T	1.4	0.5	25.7	15.7
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	EAYFAAFR	974.5	R	E	2.2	0.6	31.0	11.1
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	GIDGLTAQLK	1015.6	K	S	4.1	0.6	67.6	13.4
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	ITLEEK	732.4	K	-	2.0	0.7	24.0	10.4
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	ITLEEKK	860.5	K	-	2.6	0.3	30.6	7.8
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	KNSQTGNWQAYDMIAEGVSMITTK	2673.3	R	Q	5.1	0.0	69.3	10.8
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	LDFQWR	864.4	R	K	1.9	0.8	26.7	12.6
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	LKNEQPQIR	1125.6	R	A	2.9	0.9	32.2	10.0
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	LMDEAAQK	905.4	K	T	2.8	0.7	30.0	12.6
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	LMDEAAQKTFDR	1424.7	K	L	3.4	0.5	41.2	13.2
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	NSQTGNWQAYDMIAEGVSMITTK	2545.2	K	Q	4.4	0.0	52.5	10.4
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	QAYGQALAMYHGQTYQIAPEQPLGDK	2878.4	K	T	5.4	0.0	49.6	11.5
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	QNEWGTLLR	1116.6	K	T	3.0	0.4	27.5	14.1
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	SATPAQR	730.4	K	E	1.5	0.4	18.0	14.9
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	SISQQK	690.4	K	I	1.1	0.4	18.2	15.1
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	TFDRLK	779.4	K	N	2.1	0.5	16.8	15.3
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	TIVDQELLPYVQVK	1644.9	R	Y	4.6	0.7	58.8	10.8
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	TIVPIR	698.5	K	V	1.6	0.6	20.5	10.4
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	TKGIDGLTAQLK	1244.7	R	S	4.0	0.9	58.4	10.8
P0ADV7	23945.5	G	T	T	A	CID	LIT	20	78.2	YAGALVLGQYYK	1345.7	K	S	4.2	0.8	64.8	15.3
P0ADV7	23945.5	G	U	A	A	CID	LIT	4	22.3	DEAAQKTF	909.4	M	D	2.7	0.8	44.4	15.1
P0ADV7	23945.5	G	U	A	A	CID	LIT	4	22.3	DFQWRKNSQTGNWQAY	2028.9	L	D	2.4	0.8	18.1	11.8
P0ADV7	23945.5	G	U	A	A	CID	LIT	4	22.3	DQTNPYKLM	1125.5	A	D	0.0	0.0	24.1	13.2
P0ADV7	23945.5	G	U	A	A	CID	LIT	4	22.3	DRLKNEQPQIRANP	1678.9	F	D	3.3	0.5	15.6	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADV7	23945.5	G	T	A	A	CID	LIT	2	8.1	DEAAQKTF	909.4	M	D	3.0	0.9	34.8	16.3
P0ADV7	23945.5	G	T	A	A	CID	LIT	2	8.1	DQTNPYKLM	1109.5	A	D	2.3	0.0	22.0	15.2
P0ADV7	23945.5	G	T	T	B	CID	LIT	2	9.0	GIDGLTAQLK	1015.6	K	S	3.1	0.4	39.0	13.4
P0ADV7	23945.5	G	T	T	B	CID	LIT	2	9.0	QNEWGTLLR	1116.6	K	T	2.0	0.2	11.1	14.1
P0ADV7	23945.5	G	T	A	B	CID	LIT	2	10.4	DEAAQKTF	909.4	M	D	2.5	0.7	36.6	16.3
P0ADV7	23945.5	G	T	A	B	CID	LIT	2	10.4	DRLKNEQPQIRANP	1678.9	F	D	2.4	0.0	16.1	14.3
P0ADV7	23945.5	G	U	A	B	CID	LIT	2	9.5	DEAAQKTF	909.4	M	D	2.0	0.4	26.2	16.3
P0ADV7	23945.5	G	U	A	B	CID	LIT	2	9.5	DKTIVPIRVTII	1367.9	G	D	2.8	0.0	15.9	4.8
P0ADV7	23945.5	S	U	T	A	CID	LIT	2	11.4	GIDGLTAQLK	1015.6	K	S	3.3	0.3	51.0	17.2
P0ADV7	23945.5	S	U	T	A	CID	LIT	2	11.4	TIVDQELLPYVQVK	1644.9	R	Y	4.1	0.6	56.6	14.1
P0ADV7	23945.5	S	U	T	B	CID	LIT	5	32.2	GIDGLTAQLK	1015.6	K	S	3.6	0.6	48.3	17.2
P0ADV7	23945.5	S	U	T	B	CID	LIT	5	32.2	LKNEQPQIR	1126.6	R	A	2.9	0.3	12.1	13.2
P0ADV7	23945.5	S	U	T	B	CID	LIT	5	32.2	QAYGQALAMYHGQTYQIAPEQPLGDK	2878.4	K	T	3.6	0.7	21.3	19.4
P0ADV7	23945.5	S	U	T	B	CID	LIT	5	32.2	QNEWGTLLR	1116.6	K	T	2.4	0.3	39.9	16.7
P0ADV7	23945.5	S	U	T	B	CID	LIT	5	32.2	TIVDQELLPYVQVK	1644.9	R	Y	2.2	0.7	0.0	0.0
P0ADV7	23945.5	S	U	T	C	CID	LIT	4	24.6	GIDGLTAQLK	1015.6	K	S	3.5	0.5	46.3	17.8
P0ADV7	23945.5	S	U	T	C	CID	LIT	4	24.6	QAYGQALAMYHGQTYQIAPEQPLGDK	2878.4	K	T	2.9	0.3	7.5	19.4
P0ADV7	23945.5	S	U	T	C	CID	LIT	4	24.6	TIVDQELLPYVQVK	1644.9	R	Y	3.6	0.6	29.3	14.8
P0ADV7	23945.5	S	U	T	C	CID	LIT	4	24.6	TKGIDGLTAQLK	1244.7	R	S	3.9	0.4	30.5	13.6
P0ADV7	23945.5	S	U	T	A	ETD	LIT	2	12.3	TIVDQELLPYVQVK	1644.9	R	Y	2.1	0.6	12.3	14.3
P0ADV7	23945.5	S	U	T	A	ETD	LIT	2	12.3	TKGIDGLTAQLK	1244.7	R	S	3.6	0.4	31.8	13.6
P0ADV7	23945.5	S	U	T	B	ETD	LIT	3	17.5	GIDGLTAQLK	1015.6	K	S	2.7	0.2	31.8	17.0
P0ADV7	23945.5	S	U	T	B	ETD	LIT	3	17.5	TFDRLKNEQPQIR	1644.9	K	A	2.3	0.2	43.6	16.5
P0ADV7	23945.5	S	U	T	B	ETD	LIT	3	17.5	TIVDQELLPYVQVK	1644.9	R	Y	3.9	0.4	56.9	14.8
P0ADV7	23945.5	S	U	T	C	ETD	LIT	3	16.6	QNEWGTLLR	1116.6	K	T	1.5	0.4	24.9	16.7
P0ADV7	23945.5	S	U	T	C	ETD	LIT	3	16.6	TIVDQELLPYVQVK	1644.9	R	Y	1.4	0.6	19.4	14.8
P0ADV7	23945.5	S	U	T	C	ETD	LIT	3	16.6	TKGIDGLTAQLK	1244.7	R	S	3.7	0.5	48.8	13.6
P0ADV7	23945.5	S	U	T	B	ETD+CID	LIT	2	16.6	QAYGQALAMYHGQTYQIAPEQPLGDK	2878.4	K	T	0.0	0.0	53.2	19.6

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0ADV7	23945.5	S	U	T	B	ETD+CID	LIT	2	16.6	QNEWGTLLR	1116.6	K	T	0.0	0.0	25.7	16.7
P0ADV7	23945.5	S	U	T	B	ETD+CID	LIT	2	16.6	QAYGQALAMYHGQTYQIAPEQPLGDK	2878.4	K	T	5.7	0.7	53.2	19.6
P0ADV7	23945.5	S	U	T	B	ETD+CID	LIT	2	16.6	QNEWGTLLR	1116.6	K	T	2.2	0.2	25.7	16.7
P0ADV7	23945.5	S	U	T	C	ETD+CID	LIT	3	24.6	QAYGQALAMYHGQTYQIAPEQPLGDK	2878.4	K	T	4.0	0.5	25.4	19.5
P0ADV7	23945.5	S	U	T	C	ETD+CID	LIT	3	24.6	TIVDQELLPYVQVK	1644.9	R	Y	3.5	0.4	20.6	14.3
P0ADV7	23945.5	S	U	T	C	ETD+CID	LIT	3	24.6	TKGIDGLTAQLK	1244.7	R	S	4.2	0.5	43.5	13.6
P0ADV7	23945.5	S	U	T	B	HCD	FT	2	16.6	QAYGQALAMYHGQTYQIAPEQPLGDK	2878.4	K	T	0.0	0.0	53.2	19.6
P0ADV7	23945.5	S	U	T	B	HCD	FT	2	16.6	QNEWGTLLR	1116.6	K	T	0.0	0.0	25.7	16.7
P77247	24312.9	G	T	T	A	CID	LIT	2	9.5	FVLADVK	791.5	R	L	2.3	0.2	26.0	10.0
P77247	24312.9	G	T	T	A	CID	LIT	2	9.5	SIVVPAPEAQNDPR	1492.8	R	F	2.7	0.5	16.4	13.4
P0AC59	24333.7	G	T	T	A	CID	LIT	7	26.0	LLLPR	611.4	K	F	1.5	0.4	19.2	8.5
P0AC59	24333.7	G	T	T	A	CID	LIT	7	26.0	NISDDLR	832.4	K	A	2.1	0.5	7.0	14.6
P0AC59	24333.7	G	T	T	A	CID	LIT	7	26.0	QTQINLLSSMAI	1334.7	K	-	2.6	0.7	24.2	13.2
P0AC59	24333.7	G	T	T	A	CID	LIT	7	26.0	RSPAIEEWLR	1256.7	K	K	2.0	0.7	17.9	10.4
P0AC59	24333.7	G	T	T	A	CID	LIT	7	26.0	SAFDEFSTPAAR	1298.6	K	K	2.9	0.0	28.0	10.8
P0AC59	24333.7	G	T	T	A	CID	LIT	7	26.0	SPAIEEWLR	1100.6	R	K	2.9	0.4	21.3	10.4
P0AC59	24333.7	G	T	T	A	CID	LIT	7	26.0	VADYRDNMAK	1182.6	R	Q	3.2	0.8	55.7	10.8
P0AC59	24333.7	G	T	A	A	CID	LIT	7	36.7	DDAETPTRMVGQKQVPILQK	2270.2	N	D	3.1	0.6	25.8	15.8
P0AC59	24333.7	G	T	A	A	CID	LIT	7	36.7	DDLRAL	702.4	S	D	2.1	0.2	27.3	18.8
P0AC59	24333.7	G	T	A	A	CID	LIT	7	36.7	DIVHYV	745.4	M	D	1.7	0.6	8.3	14.9
P0AC59	24333.7	G	T	A	A	CID	LIT	7	36.7	DKKEASAGNFA	1137.6	V	D	2.6	0.6	23.6	16.2
P0AC59	24333.7	G	T	A	A	CID	LIT	7	36.7	DKLIVKPNAVNG	1267.7	L	E	2.9	0.3	21.4	10.4
P0AC59	24333.7	G	T	A	A	CID	LIT	7	36.7	DNMAKQTQINLLSSMAI	1877.9	R	-	3.0	0.6	42.0	17.1
P0AC59	24333.7	G	T	A	A	CID	LIT	7	36.7	ELHVLLN	837.5	V	D	1.9	0.1	17.3	8.5
P0AC59	24333.7	G	T	T	B	CID	LIT	6	27.0	FAKSAFDEFSTPAAR	1644.8	R	K	1.9	0.5	10.6	10.8
P0AC59	24333.7	G	T	T	B	CID	LIT	6	27.0	KVNGYANK	893.5	R	L	3.0	0.5	18.7	14.0
P0AC59	24333.7	G	T	T	B	CID	LIT	6	27.0	MKLYIYDHCPYCLK	1903.9	-	A	2.6	0.0	18.0	10.0
P0AC59	24333.7	G	T	T	B	CID	LIT	6	27.0	QVPILQKDDSR	1298.7	K	Y	2.3	0.4	28.5	11.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0AC59	24333.7	G	T	T	B	CID	LIT	6	27.0	SAFDEFSTPAAR	1298.6	K	K	4.0	0.5	46.7	9.5
P0AC59	24333.7	G	T	T	B	CID	LIT	6	27.0	VADYRDNMAK	1182.6	R	Q	2.9	0.0	39.3	10.8
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DDAETPTRMVGQKQVPILQK	2254.2	N	D	2.3	0.7	0.0	0.0
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DDLRAL	702.4	S	D	1.9	0.2	1.4	18.8
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DEFSTPAARKYFV	1530.8	F	D	2.8	0.0	10.8	15.4
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DGLIKNIS	859.5	S	D	1.7	0.3	12.9	16.8
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DKKEASAGNFA	1137.6	V	D	2.9	0.7	36.1	16.3
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DKLIVKPNAVNGELSE	1725.9	L	D	3.9	0.0	21.3	12.3
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DLLAHS	655.3	A	D	1.3	0.6	12.7	14.8
P0AC59	24333.7	G	T	A	B	CID	LIT	8	45.1	DNMAKQTQINLLSSMAI	1877.9	R	-	3.3	0.8	16.4	17.1
P0AF12	24336.1	G	U	T	A	CID	LIT	3	16.4	IGIIGAMEEEVTLLR	1643.9	K	D	4.3	0.2	41.0	10.8
P0AF12	24336.1	G	U	T	A	CID	LIT	3	16.4	QSSLMVESLVQK	1348.7	K	L	3.4	0.7	53.6	15.3
P0AF12	24336.1	G	U	T	A	CID	LIT	3	16.4	VGDIVVSDEAR	1159.6	K	Y	3.8	0.8	44.1	11.1
P0AF12	24336.1	G	U	A	A	CID	LIT	2	14.2	DEFLAVAAKQSSLMVESLVQKLAHG	2671.4	F	-	2.8	0.0	23.7	13.6
P0AF12	24336.1	G	U	A	A	CID	LIT	2	14.2	DQQSHLSF	961.4	A	D	2.5	0.0	27.9	14.5
P0AF12	24336.1	G	U	A	B	CID	LIT	2	11.6	DQQSHLSF	961.4	A	D	2.6	0.0	25.0	14.5
P0AF12	24336.1	G	U	A	B	CID	LIT	2	11.6	DVIINTGSAGGLAPTLKVG	1783.0	P	D	3.4	0.0	31.0	11.1
P64451	24409.3	S	U	T	C	CID	LIT	2	19.4	EGLQFYEVVPVALVVAGTQMATGHR	2672.4	K	T	3.4	0.7	35.5	19.0
P64451	24409.3	S	U	T	C	CID	LIT	2	19.4	LYFEGELIDAATNKPVIK	2021.1	R	V	3.5	0.5	31.0	16.0
P0A9R7	24422.0	G	T	T	A	CID	LIT	3	12.2	NFPIQLSGGEQQR	1473.7	K	V	2.2	0.7	29.0	12.3
P0A9R7	24422.0	G	T	T	A	CID	LIT	3	12.2	RVSAALDK	859.5	R	V	2.1	0.1	22.9	15.4
P0A9R7	24422.0	G	T	T	A	CID	LIT	3	12.2	VGLLDK	644.4	K	A	1.8	0.4	23.9	13.8
P0AG07	24536.9	G	U	A	A	CID	LIT	3	17.3	DEMRSELAKVSHE	1530.7	I	-	3.3	0.8	0.0	0.0
P0AG07	24536.9	G	U	A	A	CID	LIT	3	17.3	DFARLGEDTAKALAAGA	1676.9	A	D	2.5	0.3	28.8	16.5
P0AG07	24536.9	G	U	A	A	CID	LIT	3	17.3	DQPDYKKVI	1105.6	F	D	2.0	0.6	22.1	14.9
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	AAGAELVGMEDLADQIK	1730.9	K	K	4.3	0.8	98.6	13.6
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	GATVLPHGTGR	1065.6	R	S	2.5	0.7	31.1	11.1
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	KGEMNFDVVIASPDAMR	1879.9	K	V	3.6	0.7	22.8	12.3

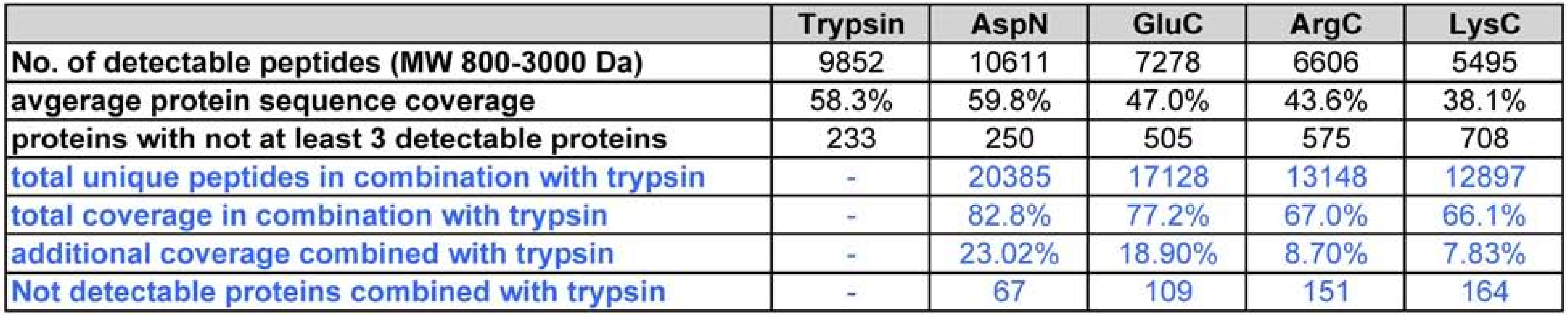
SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	KSDQNVR	846.4	R	G	1.4	0.6	11.1	14.5
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	QYDINEAIALLK	1390.8	K	E	2.7	0.8	71.2	11.8
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	VAVFTQGANAEAAK	1376.7	R	A	4.5	0.6	61.4	14.0
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	VGTVTPNVAEAVK	1284.7	K	N	2.6	0.7	43.4	11.5
P0A7L0	24711.4	G	U	T	A	CID	LIT	8	44.0	VVGQLGQVLGPR	1222.7	R	G	3.3	0.8	71.1	7.0
P0A7L0	24711.4	G	T	T	A	CID	LIT	6	31.6	AAGAELVGMEDLADQIK	1746.9	K	K	4.7	0.5	51.4	13.2
P0A7L0	24711.4	G	T	T	A	CID	LIT	6	31.6	GATVLPHGTGR	1065.6	R	S	1.9	0.8	0.0	0.0
P0A7L0	24711.4	G	T	T	A	CID	LIT	6	31.6	KSDQNVR	846.4	R	G	1.8	0.3	10.2	14.5
P0A7L0	24711.4	G	T	T	A	CID	LIT	6	31.6	VAVFTQGANAEAAK	1376.7	R	A	4.2	0.5	52.5	13.8
P0A7L0	24711.4	G	T	T	A	CID	LIT	6	31.6	VGTVTPNVAEAVK	1284.7	K	N	2.1	0.7	7.9	11.5
P0A7L0	24711.4	G	T	T	A	CID	LIT	6	31.6	VVGQLGQVLGPR	1222.7	R	G	3.7	0.8	56.9	7.0
P0A7L0	24711.4	G	U	A	A	CID	LIT	3	11.1	DQIKKGEMNF	1209.6	A	D	2.7	0.7	22.3	16.9
P0A7L0	24711.4	G	U	A	A	CID	LIT	3	11.1	DVAVNLGIDARKS	1357.7	V	D	3.6	0.5	19.5	14.0
P0A7L0	24711.4	G	U	A	A	CID	LIT	3	11.1	ESVDVAVNLGI	1115.6	V	D	2.0	0.2	11.6	16.9
P0A7L0	24711.4	G	T	A	A	CID	LIT	3	13.7	DQIKKGEMNF	1209.6	A	D	2.6	0.4	17.4	15.1
P0A7L0	24711.4	G	T	A	A	CID	LIT	3	13.7	DVAVNLGIDARKS	1357.7	V	D	3.8	0.5	34.3	14.3
P0A7L0	24711.4	G	T	A	A	CID	LIT	3	13.7	EKVDATKQY	1081.6	R	D	2.7	0.0	22.2	16.1
P0A7L0	24711.4	G	T	T	B	CID	LIT	7	35.0	AAGAELVGMEDLADQIK	1730.9	K	K	3.9	0.7	64.9	13.6
P0A7L0	24711.4	G	T	T	B	CID	LIT	7	35.0	GATVLPHGTGR	1065.6	R	S	2.1	0.0	30.4	11.1
P0A7L0	24711.4	G	T	T	B	CID	LIT	7	35.0	QYDINEAIALLK	1390.8	K	E	3.0	0.6	24.8	11.8
P0A7L0	24711.4	G	T	T	B	CID	LIT	7	35.0	VAVFTQGANAEAAK	1376.7	R	A	3.8	0.5	45.8	14.0
P0A7L0	24711.4	G	T	T	B	CID	LIT	7	35.0	VGTVTPNVAEAVK	1284.7	K	N	2.8	0.4	18.5	11.5
P0A7L0	24711.4	G	T	T	B	CID	LIT	7	35.0	VGTVTPNVAEAVKNAK	1597.9	K	A	4.0	0.0	24.3	12.0
P0A7L0	24711.4	G	T	T	B	CID	LIT	7	35.0	VVGQLGQVLGPR	1222.7	R	G	3.2	0.5	33.3	7.0
P0A7L0	24711.4	G	T	A	B	CID	LIT	5	22.6	DATKQY	725.3	V	D	1.5	0.7	13.6	10.4
P0A7L0	24711.4	G	T	A	B	CID	LIT	5	22.6	DINEAIALLK	1099.6	Y	E	3.0	0.4	35.9	10.4
P0A7L0	24711.4	G	T	A	B	CID	LIT	5	22.6	DQIKKGEMNF	1209.6	A	D	2.9	0.7	18.5	15.1
P0A7L0	24711.4	G	T	A	B	CID	LIT	5	22.6	DVAVNLGIDARKS	1357.7	V	D	3.6	0.7	26.3	15.8

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7L0	24711.4	G	T	A	B	CID	LIT	5	22.6	EAAKAAGAELVGME	1346.7	A	D	4.3	0.6	35.8	16.0
P0A7L0	24711.4	G	U	A	B	CID	LIT	3	14.5	DINEAIALLK	1099.6	Y	E	2.5	0.6	11.4	10.4
P0A7L0	24711.4	G	U	A	B	CID	LIT	3	14.5	DQAGLSASVN	961.5	V	-	2.4	0.4	6.9	14.6
P0A7L0	24711.4	G	U	A	B	CID	LIT	3	14.5	EAAKAAGAELVGME	1346.7	A	D	2.4	0.6	1.7	15.6
P0A7L0	24711.4	S	U	T	A	CID	LIT	4	26.9	AAGAELVGMEDLADQIK	1730.9	K	K	4.2	0.7	63.1	18.4
P0A7L0	24711.4	S	U	T	A	CID	LIT	4	26.9	FVESVDVAVNLGIDAR	1703.9	K	K	4.6	0.4	47.7	18.0
P0A7L0	24711.4	S	U	T	A	CID	LIT	4	26.9	QYDINEAIALLKELATAK	2004.1	K	F	4.1	0.0	33.9	14.0
P0A7L0	24711.4	S	U	T	A	CID	LIT	4	26.9	VVGQLGQVLGPR	1222.7	R	G	3.3	0.0	35.4	9.0
P0A7L0	24711.4	S	U	T	B	CID	LIT	6	37.2	AAGAELVGMEDLADQIK	1730.9	K	K	4.6	0.6	52.6	18.4
P0A7L0	24711.4	S	U	T	B	CID	LIT	6	37.2	ENLEALLVALK	1212.7	K	K	2.3	0.3	35.3	14.0
P0A7L0	24711.4	S	U	T	B	CID	LIT	6	37.2	FVESVDVAVNLGIDAR	1703.9	K	K	4.3	0.5	36.7	17.9
P0A7L0	24711.4	S	U	T	B	CID	LIT	6	37.2	QYDINEAIALLKELATAK	2004.1	K	F	3.5	0.4	34.0	14.0
P0A7L0	24711.4	S	U	T	B	CID	LIT	6	37.2	VGTVTPNVAEAVK	1284.7	K	N	1.7	0.7	15.8	14.9
P0A7L0	24711.4	S	U	T	B	CID	LIT	6	37.2	VVGQLGQVLGPR	1222.7	R	G	3.8	0.8	74.4	9.0
P0A7L0	24711.4	S	U	T	C	CID	LIT	6	38.5	AAGAELVGMEDLADQIK	1730.9	K	K	4.3	0.4	54.0	18.0
P0A7L0	24711.4	S	U	T	C	CID	LIT	6	38.5	FVESVDVAVNLGIDAR	1703.9	K	K	3.5	0.3	13.1	18.2
P0A7L0	24711.4	S	U	T	C	CID	LIT	6	38.5	GATVLPHGTGR	1065.6	R	S	1.9	0.6	22.4	14.1
P0A7L0	24711.4	S	U	T	C	CID	LIT	6	38.5	VAVFTQGANAEAAK	1376.7	R	A	4.4	0.5	54.6	17.2
P0A7L0	24711.4	S	U	T	C	CID	LIT	6	38.5	VDFDADKLKENLEALLVALK	2244.2	K	K	3.5	0.8	13.7	13.6
P0A7L0	24711.4	S	U	T	C	CID	LIT	6	38.5	VVGQLGQVLGPR	1222.7	R	G	3.7	0.0	63.3	9.0
P0A7L0	24711.4	S	U	T	A	ETD	LIT	7	43.2	AAGAELVGMEDLADQIK	1730.9	K	K	2.6	0.5	53.1	18.4
P0A7L0	24711.4	S	U	T	A	ETD	LIT	7	43.2	FVESVDVAVNLGIDAR	1703.9	K	K	2.3	0.5	11.3	17.6
P0A7L0	24711.4	S	U	T	A	ETD	LIT	7	43.2	GATVLPHGTGR	1065.6	R	S	3.1	0.0	25.5	14.1
P0A7L0	24711.4	S	U	T	A	ETD	LIT	7	43.2	QYDINEAIALLKELATAK	2004.1	K	F	0.0	0.0	51.3	14.0
P0A7L0	24711.4	S	U	T	A	ETD	LIT	7	43.2	VAVFTQGANAEAAK	1377.7	R	A	3.0	0.4	26.9	16.2
P0A7L0	24711.4	S	U	T	A	ETD	LIT	7	43.2	VGTVTPNVAEAVK	1284.7	K	N	3.3	0.5	27.4	15.6
P0A7L0	24711.4	S	U	T	A	ETD	LIT	7	43.2	VVGQLGQVLGPR	1222.7	R	G	1.7	0.0	33.6	9.0
P0A7L0	24711.4	S	U	T	B	ETD	LIT	7	40.6	AAGAELVGMEDLADQIK	1730.9	K	K	3.9	0.4	62.5	18.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. $[M+H]^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7L0	24711.4	S	U	T	B	ETD	LIT	7	40.6	ENLEALLVALKK	1340.8	K	A	3.3	0.5	12.5	12.3
P0A7L0	24711.4	S	U	T	B	ETD	LIT	7	40.6	QYDINEAIALLKELATAK	2004.1	K	F	4.6	0.0	31.3	14.6
P0A7L0	24711.4	S	U	T	B	ETD	LIT	7	40.6	VAVFTQGANAEAAK	1376.7	R	A	3.0	0.3	29.0	17.6
P0A7L0	24711.4	S	U	T	B	ETD	LIT	7	40.6	VDFDADKLKENLEALLVALK	2244.2	K	K	5.3	0.0	61.7	12.3
P0A7L0	24711.4	S	U	T	B	ETD	LIT	7	40.6	VGTVTPNVAEAVK	1284.7	K	N	3.5	0.5	33.7	15.6
P0A7L0	24711.4	S	U	T	B	ETD	LIT	7	40.6	VVGQLGQVLGPR	1222.7	R	G	0.0	0.0	47.4	9.0
P0A7L0	24711.4	S	U	T	C	ETD	LIT	6	37.6	AAGAELVGMEDLADQIK	1730.9	K	K	3.0	0.4	50.9	18.4
P0A7L0	24711.4	S	U	T	C	ETD	LIT	6	37.6	QYDINEAIALLK	1390.8	K	E	2.8	0.7	21.3	15.3
P0A7L0	24711.4	S	U	T	C	ETD	LIT	6	37.6	VAVFTQGANAEAAK	1376.7	R	A	3.4	0.4	0.0	0.0
P0A7L0	24711.4	S	U	T	C	ETD	LIT	6	37.6	VDFDADKLKENLEALLVALK	2244.2	K	K	5.1	0.0	57.2	12.3
P0A7L0	24711.4	S	U	T	C	ETD	LIT	6	37.6	VGTVTPNVAEAVK	1284.7	K	N	3.2	0.5	39.4	15.6
P0A7L0	24711.4	S	U	T	C	ETD	LIT	6	37.6	VVGQLGQVLGPR	1222.7	R	G	2.7	0.4	40.7	9.0
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	5	32.5	AAGAELVGMEDLADQIK	1730.9	K	K	0.0	0.0	57.0	18.4
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	5	32.5	FVESVDVAVNLGIDAR	1703.9	K	K	0.0	0.0	48.4	18.5
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	5	32.5	GATVLPHGTGR	1065.6	R	S	0.0	0.0	32.1	14.1
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	5	32.5	VDFDADKLKENLEALLVALK	2244.2	K	K	0.0	0.0	18.1	13.2
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	5	32.5	VVGQLGQVLGPR	1222.7	R	G	0.0	0.0	63.2	9.0
P0A7L0	24711.4	S	U	T	A	ETD+CID	LIT	6	39.3	AAGAELVGMEDLADQIK	1730.9	K	K	3.0	0.6	32.4	18.0
P0A7L0	24711.4	S	U	T	A	ETD+CID	LIT	6	39.3	FVESVDVAVNLGIDAR	1703.9	K	K	4.1	0.4	44.6	17.9
P0A7L0	24711.4	S	U	T	A	ETD+CID	LIT	6	39.3	VAVFTQGANAEAAK	1377.7	R	A	3.0	0.3	9.9	16.6
P0A7L0	24711.4	S	U	T	A	ETD+CID	LIT	6	39.3	VDFDADKLKENLEALLVALK	2244.2	K	K	3.2	0.0	27.3	13.2
P0A7L0	24711.4	S	U	T	A	ETD+CID	LIT	6	39.3	VGTVTPNVAEAVK	1284.7	K	N	2.4	0.2	0.0	0.0
P0A7L0	24711.4	S	U	T	A	ETD+CID	LIT	6	39.3	VVGQLGQVLGPR	1222.7	R	G	3.3	0.0	45.9	9.0
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	2	14.1	AAGAELVGMEDLADQIK	1730.9	K	K	4.0	0.3	0.0	0.0
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	2	14.1	FVESVDVAVNLGIDAR	1703.9	K	K	4.3	0.4	0.0	0.0
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	6	38.0	AAGAELVGMEDLADQIK	1730.9	K	K	4.0	0.3	0.0	0.0
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	6	38.0	FVESVDVAVNLGIDAR	1703.9	K	K	4.3	0.4	48.4	18.5
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	6	38.0	GATVLPHGTGR	1065.6	R	S	2.4	0.0	32.1	14.1

SwissProt Accession No	molecular weight [Da]	Sample				fragmentation type	MS/MS mass analyzer	number of unique peptides	sequence coverage [%]	peptide sequence	calc. [M+H]$^+$	previous amino acid	next amino acid	best SEQUEST XCorr score	best SEQUEST DCn score	best Mascot Ion score	best Mascot Identity score
		digestion	lysis	protease	replicate												
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	6	38.0	VDFDADKLKENLEALLVALK	2244.2	K	K	2.1	0.0	18.1	13.2
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	6	38.0	VGTVTPNVAEAVK	1284.7	K	N	1.9	0.7	0.0	0.0
P0A7L0	24711.4	S	U	T	B	ETD+CID	LIT	6	38.0	VVGQLGQVLGPR	1222.7	R	G	3.8	0.0	63.2	9.0
P0A7L0	24711.4	S	U	T	C	ETD+CID	LIT	5	29.5	AAGAELVGMEDLADQIK	1730.9	K	K	4.6	0.5	0.0	0.0
P0A7L0	24711.4	S	U	T	C	ETD+CID	LIT	5	29.5	FVESVDVAVNLGIDAR	1703.9	K	K	4.1	0.2	21.6	18.2
P0A7L0	24711.4	S	U	T	C	ETD+CID	LIT	5	29.5	GATVLPHGTGR	1065.6	R	S	2.4	0.3	23.1	14.1
P0A7L0	24711.4	S	U	T	C	ETD+CID	LIT	5	29.5	VGTVTPNVAEAVK	1284.7	K	N	1.2	0.0	33.5	14.6
P0A7L0	24711.4	S	U	T	C	ETD+CID	LIT	5	29.5	VVGQLGQVLGPR	1222.7	R	G	3.6	0.0	41.0	9.0
P0A7L0	24711.4	S	U	T	B	HCD	FT	4	23.9	AAGAELVGMEDLADQIK	1730.9	K	K	0.0	0.0	57.0	18.4
P0A7L0	24711.4	S	U	T	B	HCD	FT	4	23.9	FVESVDVAVNLGIDAR	1703.9	K	K	0.0	0.0	48.4	18.5
P0A7L0	24711.4	S	U	T	B	HCD	FT	4	23.9	GATVLPHGTGR	1065.6	R	S	0.0	0.0	32.1	14.1
P0A7L0	24711.4	S	U	T	B	HCD	FT	4	23.9	VVGQLGQVLGPR	1222.7	R	G	0.0	0.0	63.2	9.0
P0A6I0	24728.6	G	T	T	A	CID	LIT	4	22.5	ALQYAR	721.4	K	Q	1.6	0.0	28.2	13.2
P0A6I0	24728.6	G	T	T	A	CID	LIT	4	22.5	AVAPLVPAADALVLDSTTLSIEQVIEK	2763.5	R	A	3.7	0.0	21.8	6.0
P0A6I0	24728.6	G	T	T	A	CID	LIT	4	22.5	IFLDASSEER	1166.6	K	A	2.1	0.6	16.0	12.3
P0A6I0	24728.6	G	T	T	A	CID	LIT	4	22.5	RMLQLQEK	1061.6	R	G	1.9	0.1	20.9	15.2
P0A6I0	24728.6	G	T	T	B	CID	LIT	4	19.4	AFRELPGLIADGR	1414.8	R	D	2.1	0.2	0.0	0.0
P0A6I0	24728.6	G	T	T	B	CID	LIT	4	19.4	DMGTVVFPDAPVK	1375.7	R	I	3.1	0.8	20.3	13.2
P0A6I0	24728.6	G	T	T	B	CID	LIT	4	19.4	TQEVANAASQVAAFPR	1659.8	R	V	3.7	0.0	33.2	10.8
P0A6I0	24728.6	G	T	T	B	CID	LIT	4	19.4	TQEVANAASQVAAFPRVR	1915.0	R	E	2.3	0.3	9.1	12.8
P0A6I0	24728.6	G	T	A	B	CID	LIT	3	13.7	DALVPLASHL	1035.6	E	D	2.6	0.0	31.4	12.6
P0A6I0	24728.6	G	T	A	B	CID	LIT	3	13.7	DAPVKIFL	902.5	P	D	1.9	0.8	17.9	10.0
P0A6I0	24728.6	G	T	A	B	CID	LIT	3	13.7	DRNRAVAPLVPAA	1349.8	R	D	1.8	0.6	15.5	10.0
P0A6T5	24813.0	G	U	T	A	CID	LIT	2	7.7	EAALVHEALVAR	1278.7	K	G	3.2	0.7	40.3	11.1
P0A6T5	24813.0	G	U	T	A	CID	LIT	2	7.7	HEFLR	701.4	R	A	1.9	0.5	12.4	12.3

Table S4: Comparison of *in-silico* digestions with different proteases.



	Trypsin	AspN	GluC	ArgC	LysC
No. of detectable peptides (MW 800-3000 Da)	9852	10611	7278	6606	5495
avgerage protein sequence coverage	58.3%	59.8%	47.0%	43.6%	38.1%
proteins with not at least 3 detectable proteins	233	250	505	575	708
total unique peptides in combination with trypsin	-	20385	17128	13148	12897
total coverage in combination with trypsin	-	82.8%	77.2%	67.0%	66.1%
additional coverage combined with trypsin	-	23.02%	18.90%	8.70%	7.83%
Not detectable proteins combined with trypsin	-	67	109	151	164

Table S5: Detected proteins in this and previous studies.

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P0AD92	LPW_ECOLI	1723.0	11.7	-	-	-	-	-	-	-
P0AD74	LPF2_ECOLI	1761.8	11.1	-	-	-	-	-	-	-
C1P619	ILVX_ECOLI	1909.9	11.4	-	-	-	-	-	-	-
P0AD72	LPF_ECOLI	1924.0	10.1	-	-	-	-	-	-	-
C1P621	YJEV_ECOLI	2056.0	7.0	-	-	-	-	-	-	-
C1P608	IBSB_ECOLI	2063.2	10.1	-	-	-	-	-	-	-
P60995	LPHI_ECOLI	2081.0	10.0	-	-	-	-	-	-	-
P0AD86	LPT_ECOLI	2138.1	11.5	-	-	-	-	-	-	-
C1P616	IBSD_ECOLI	2150.3	10.1	-	-	-	-	-	-	-
C1P617	IBSE_ECOLI	2206.3	10.1	-	-	-	-	-	-	-
C1P615	IBSC_ECOLI	2208.3	11.1	-	-	-	-	-	-	-
C1P607	IBSA_ECOLI	2231.3	10.1	-	-	-	-	-	-	-
C1P606	YOEI_ECOLI	2241.1	5.2	-	-	-	-	-	-	-
A5A621	YPFM_ECOLI	2407.3	7.2	-	-	-	-	-	-	-
P56980	REPL1_ECOLI	2587.3	5.9	-	-	-	-	-	-	-
C1P600	YNBG_ECOLI	2656.4	10.5	-	-	-	-	-	-	-
C1P604	YOBI_ECOLI	2664.5	7.8	-	-	-	-	-	-	-
C1P603	YOAJ_ECOLI	2690.5	9.8	-	-	-	-	-	-	-
C1P610	YPDK_ECOLI	2703.4	10.1	-	-	-	-	-	-	-
P0AD89	LPTN_ECOLI	2893.5	8.9	-	-	1	-	-	-	-
C1P618	YRBN_ECOLI	2978.5	5.8	-	-	-	-	-	-	-
A5A618	YNHF_ECOLI	2996.7	7.8	-	-	-	-	-	-	-
P36937	KDPF_ECOLI	3070.7	3.3	-	-	-	-	-	-	-
C1P609	YOHP_ECOLI	3090.9	10.6	-	-	-	-	-	-	-
C1P611	SHOB_ECOLI	3101.9	10.6	-	-	-	-	-	-	-
A8DYP9	LPFUR_ECOLI	3107.6	10.8	-	-	-	-	-	-	-
P0AD79	LPL_ECOLI	3144.8	13.0	-	-	-	-	-	-	-
C1P613	YQEL_ECOLI	3201.6	4.0	-	-	-	-	-	-	-
P03061	LPIV_ECOLI	3204.8	11.5	-	-	-	-	-	-	-
A5A627	TISB_ECOLI	3221.0	9.7	-	-	-	-	-	-	-
P62522	LPID_ECOLI	3230.0	11.4	-	-	-	-	-	-	-
A5A617	YDGU_ECOLI	3234.8	10.8	-	-	-	-	-	-	-
P0ADF0	LPFS_ECOLI	3289.6	12.2	-	-	-	-	-	-	-
C1P605	AZUC_ECOLI	3406.8	11.1	-	-	-	-	-	-	-
P02338	PRTL_ECOLI	3445.7	12.4	-	-	1	-	-	-	-
C1P602	YOAK_ECOLI	3456.9	11.1	-	-	-	-	-	-	-
A5A616	YNEM_ECOLI	3507.7	5.1	-	-	-	-	-	-	-
A5A615	YNCL_ECOLI	3536.9	12.5	-	-	-	-	-	-	-
P24244	YCCB_ECOLI	3596.0	8.9	-	-	-	-	-	-	-
C1P620	YSHB_ECOLI	3616.8	4.1	-	-	-	-	-	-	-
Q2EES6	YOHO_ECOLI	3641.1	12.5	-	-	-	-	-	-	-
Q47268	YLCH_ECOLI	3642.7	6.9	-	-	-	-	-	-	-
P0ADF3	LPRH_ECOLI	3748.8	11.9	-	-	-	-	-	-	-
P76239	YOAI_ECOLI	3770.1	3.9	-	-	-	-	-	-	-
Q6BF25	LDRD_ECOLI	3915.1	9.8	-	-	-	-	-	-	-
Q6BF87	LDRB_ECOLI	3970.1	11.4	-	-	-	-	-	-	-
C1P5Z8	YKGR_ECOLI	3997.2	9.7	-	-	-	-	-	-	-
Q6BF86	LDRA_ECOLI	4012.2	11.4	-	-	-	-	-	-	-
P56100	YBGT_ECOLI	4040.0	4.2	-	-	-	-	-	-	-
Q2EES1	YNID_ECOLI	4113.2	11.0	-	-	-	-	-	-	-

SwissProt Accession No	**SwissProt entry name**	**molecular weight [Da]**	***pI***	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
C1P5Z9	YMIB_ECOLI	4120.2	11.8	-	-	-	-	-	-	-
P0ADB4	ECNA_ECOLI	4357.4	10.6	-	-	1	-	-	-	-
P0A7Q6	RL36_ECOLI	4362.5	11.2	1	-	1	-	-	-	-
P56976	BLR_ECOLI	4554.5	6.0	-	-	-	-	-	-	-
P29009	YDFB_ECOLI	4686.1	3.8	-	-	-	-	-	-	-
A8DYQ1	YTHA_ECOLI	4776.6	9.8	-	-	-	-	-	-	-
C1P614	YQFG_ECOLI	4788.5	8.9	-	-	-	-	-	-	-
P0ADB7	ECNB_ECOLI	4807.5	8.9	1	-	1	-	-	-	-
P64567	YQGB_ECOLI	4856.6	9.7	-	-	-	-	-	-	-
A5A624	DINQ_ECOLI	4879.9	12.1	-	-	-	-	-	-	-
P0ADD9	YJJY_ECOLI	4883.7	8.9	-	-	-	-	-	-	-
P68191	SRA_ECOLI	5093.8	11.5	1	1	1	1	-	-	-
P0AD83	LPPY_ECOLI	5095.7	11.9	-	-	-	-	-	-	-
P76061	YDAG_ECOLI	5191.4	4.7	-	-	-	-	-	-	-
A5A609	YBHU_ECOLI	5199.6	9.9	-	-	-	-	-	-	-
P64508	YOBF_ECOLI	5209.6	8.5	-	-	-	-	-	-	-
A5A622	YGDT_ECOLI	5228.5	4.1	-	-	-	-	-	-	-
P0AAW9	YBHT_ECOLI	5297.9	7.7	-	-	-	-	-	-	-
Q2EET0	YPDJ_ECOLI	5312.6	4.4	-	-	-	-	-	-	-
A5A620	YPAB_ECOLI	5322.7	11.1	-	-	-	-	-	-	-
C1P5Z7	SGRT_ECOLI	5335.6	8.9	-	-	-	-	-	-	-
P0A7P5	RL34_ECOLI	5378.1	13.5	1	1	-	1	-	-	-
C1P612	YQCG_ECOLI	5380.8	4.9	-	-	-	-	-	-	-
Q2EEQ2	RL362_ECOLI	5464.1	12.2	-	-	-	-	-	-	-
Q47272	YLCG_ECOLI	5490.9	12.2	-	-	-	-	1	-	-
P0ACG4	HOKC_ECOLI	5498.9	7.2	-	-	-	-	-	-	-
Q2M5U1	YTJA_ECOLI	5533.2	12.8	-	-	-	-	-	-	-
P64512	MGRB_ECOLI	5548.8	8.0	-	-	-	-	-	-	-
P77091	HOKE_ECOLI	5561.1	8.3	-	-	1	-	-	-	-
P77494	HOKB_ECOLI	5623.0	8.5	-	-	-	-	1	-	-
P76157	YNFN_ECOLI	5636.9	5.8	-	-	-	-	-	-	-
P0ACG6	HOKD_ECOLI	5734.1	6.5	-	-	-	-	-	-	-
P39221	YABQ_ECOLI	5734.2	7.2	-	-	-	-	-	-	-
P0ACW0	YDAF_ECOLI	5765.9	9.6	-	-	-	-	-	-	-
P52136	YFJU_ECOLI	5782.8	4.8	-	-	-	-	-	-	-
P0ACW8	YDFA_ECOLI	5789.8	4.9	-	-	-	-	-	-	-
P64627	YHFL_ECOLI	5816.0	8.5	-	-	-	-	-	-	-
P0ACW4	YDCA_ECOLI	5856.9	9.9	-	-	1	-	-	-	-
P0AE42	YQAE_ECOLI	5862.4	11.4	-	-	-	-	-	-	-
P56614	YMDF_ECOLI	5880.8	10.4	-	-	1	-	-	-	-
P76096	MOKB_ECOLI	5890.9	6.3	-	-	-	-	-	-	-
P64442	YCEO_ECOLI	5894.2	10.7	-	-	-	-	-	-	-
P42625	YHAL_ECOLI	5958.1	7.3	-	-	-	-	-	-	-
P37305	HOKA_ECOLI	5995.2	8.0	-	-	-	-	-	-	-
P21361	YCIG_ECOLI	5999.8	10.4	-	-	1	-	-	-	-
P45807	YBAM_ECOLI	6022.2	4.3	-	-	1	-	-	-	-
P58037	YRHD_ECOLI	6024.0	4.7	-	-	-	-	-	-	-
P62670	FLMA_ECOLI	6105.2	9.8	-	-	-	-	-	-	-
A5A619	YOJO_ECOLI	6215.3	10.1	-	-	-	-	-	-	-
P58094	YCIX_ECOLI	6334.9	3.8	-	-	-	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
P0A7N9	RL33_ECOLI	6368.6	11.0	1	1	1	1	-	-	-
P75979	YMFR_ECOLI	6377.5	10.1	-	-	-	-	-	-	-
A5A614	YCIZ_ECOLI	6438.4	4.4	1	-	-	-	-	-	-
P0A7N4	RL32_ECOLI	6443.4	12.1	1	1	1	1	-	-	-
Q47270	NINE_ECOLI	6490.7	12.5	-	-	-	-	-	-	-
P0AFW2	RMF_ECOLI	6504.3	12.0	1	-	1	-	-	-	-
A5A611	YMGI_ECOLI	6514.6	5.5	-	-	-	-	-	-	-
P0AG51	RL30_ECOLI	6538.7	11.5	1	1	1	1	1	-	-
P77695	GNSB_ECOLI	6544.6	9.7	1	1	1	1	1	1	-
P67338	YOAH_ECOLI	6551.2	4.5	-	-	1	-	-	-	-
P64646	YJDO_ECOLI	6551.7	10.6	-	-	-	-	-	-	-
P0AC92	GNSA_ECOLI	6572.4	5.2	1	1	1	-	-	-	-
P38394	YDAE_ECOLI	6580.2	7.8	-	-	-	-	-	-	-
P0ADX5	YHFG_ECOLI	6595.5	10.9	-	-	1	-	-	-	-
P64496	YOAG_ECOLI	6605.1	4.0	-	-	-	-	-	-	-
P64453	YDCX_ECOLI	6642.5	11.5	-	-	-	-	-	-	-
P64517	YODC_ECOLI	6675.1	4.5	-	-	1	-	-	-	-
P58041	RZOD_ECOLI	6686.4	10.2	-	-	-	-	-	-	-
P39390	YJIS_ECOLI	6705.5	11.6	-	-	1	-	-	-	-
Q2EER5	YMJC_ECOLI	6721.8	11.7	-	-	-	-	-	-	-
P58042	RZOR_ECOLI	6757.4	9.1	-	-	-	-	-	-	-
P76106	YNCN_ECOLI	6778.6	11.0	-	-	-	-	-	-	-
P64448	YNBE_ECOLI	6836.7	4.8	-	-	1	-	-	-	-
P29010	YDFD_ECOLI	6838.4	4.5	-	-	-	-	-	-	-
P0AAZ7	YCAR_ECOLI	6851.5	4.8	1	1	1	1	-	1	-
P69913	CSRA_ECOLI	6852.7	9.7	1	1	1	-	-	-	-
P76138	YNEL_ECOLI	6876.5	8.9	-	-	-	-	-	-	-
P0AEG8	DSRB_ECOLI	6942.5	4.4	1	-	-	-	-	-	-
P0ADA7	OSMB_ECOLI	6944.6	10.5	-	-	1	-	-	-	-
Q2EEP9	YAFF_ECOLI	6949.7	11.4	-	-	-	-	-	-	-
P64526	YEEW_ECOLI	6955.4	4.0	-	-	-	-	-	-	-
P09557	DICB_ECOLI	6960.7	9.1	-	-	-	-	-	-	-
P0ADJ3	YHJR_ECOLI	7014.6	4.1	-	-	-	-	-	-	-
P33229	LAR_ECOLI	7015.3	9.2	-	-	-	-	-	-	-
P0A843	TATE_ECOLI	7020.9	9.7	-	-	-	-	-	-	-
P41070	TRBD_ECOLI	7049.5	5.5	-	-	-	-	-	-	-
P77087	YLCE_ECOLI	7084.4	3.7	-	-	-	-	-	-	-
A5A613	YCIY_ECOLI	7098.9	12.9	-	-	-	-	-	-	-
P0ACX9	YDIE_ECOLI	7113.8	10.5	-	-	-	-	-	-	-
P0AF73	YJET_ECOLI	7162.0	11.6	-	-	-	-	-	-	-
P0ADN6	YIFL_ECOLI	7173.7	9.5	-	-	1	-	-	-	1
P64619	YHDU_ECOLI	7199.6	4.9	-	-	-	-	-	-	-
P0A8K5	YAEP_ECOLI	7210.6	4.3	1	-	1	-	-	-	-
P76136	YNEN_ECOLI	7268.0	9.7	-	-	-	-	-	-	-
P0A7M6	RL29_ECOLI	7270.0	10.5	1	1	1	1	-	1	-
P64463	YDFZ_ECOLI	7272.8	8.9	1	1	1	1	-	-	-
P0AAN5	YAIA_ECOLI	7277.6	6.1	1	-	1	1	-	-	-
P0A7Q1	RL35_ECOLI	7285.3	12.5	1	1	1	-	-	-	-
P0A8H8	YACG_ECOLI	7302.4	4.3	1	-	1	1	-	-	-
O32583	THIS_ECOLI	7307.7	4.2	-	-	-	-	-	-	-

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P76275	YEBW_ECOLI	7311.3	3.6	-	-	-	-	-	-	-
A5A612	YMGJ_ECOLI	7358.0	12.2	-	-	-	-	-	-	-
P0AE56	BFD_ECOLI	7358.7	8.7	-	-	-	-	-	-	-
P0ADJ5	YHJT_ECOLI	7360.2	12.2	-	-	-	-	-	-	-
P0AF45	YJBE_ECOLI	7382.7	7.0	-	-	-	-	-	-	-
P0AAS7	YBCJ_ECOLI	7385.9	8.3	1	1	1	1	-	1	-
P0A9Y6	CSPC_ECOLI	7398.8	7.7	1	1	1	1	-	1	1
P75975	YMFT_ECOLI	7398.9	10.2	-	-	-	-	-	-	-
P0A9X9	CSPA_ECOLI	7399.6	5.5	1	1	1	-	-	-	-
P64622	YHDV_ECOLI	7447.8	7.1	-	-	1	-	-	-	-
P64545	YFGG_ECOLI	7457.9	12.6	-	-	-	-	-	-	-
P0A972	CSPE_ECOLI	7459.8	9.5	1	1	1	1	-	1	1
P0AAS9	YBDD_ECOLI	7463.5	7.2	-	-	-	-	-	-	-
P45505	YFAH_ECOLI	7513.1	6.5	-	-	-	-	-	-	-
A5A607	YLCI_ECOLI	7516.9	11.3	-	-	-	-	-	-	-
P31121	MARB_ECOLI	7532.7	5.2	-	-	-	-	-	-	-
P0A976	CSPF_ECOLI	7559.0	10.1	-	-	-	-	-	-	-
P0ADW8	YHEV_ECOLI	7594.7	7.1	1	-	1	-	-	-	-
P64435	YBCW_ECOLI	7619.8	4.7	-	-	1	-	-	-	-
Q2EES9	TORI_ECOLI	7674.0	10.2	-	-	-	-	-	-	-
P0A986	CSPI_ECOLI	7679.9	6.1	-	1	-	-	-	-	-
P52134	YPJK_ECOLI	7699.6	11.0	-	-	-	-	-	-	-
P36995	CSPB_ECOLI	7712.9	7.7	1	1	-	-	-	-	-
P0A982	CSPH_ECOLI	7716.1	11.0	-	-	-	-	-	-	-
P0ADC8	YJIX_ECOLI	7724.6	9.0	-	-	-	-	-	-	-
P0C0L9	ISCX_ECOLI	7727.6	3.7	1	1	1	1	-	-	-
P77237	ESSQ_ECOLI	7737.1	10.5	-	-	-	-	-	-	-
P33236	MOKC_ECOLI	7738.2	9.6	-	-	-	-	-	-	-
P0ABM5	CCMD_ECOLI	7741.1	12.2	-	-	-	-	-	-	-
P0A9R2	ESSD_ECOLI	7774.1	10.4	-	-	-	-	-	-	-
P0A978	CSPG_ECOLI	7776.9	5.6	-	1	1	-	-	1	-
P13970	SRNB_ECOLI	7788.1	9.2	-	-	-	-	-	-	-
P39901	YBFI_ECOLI	7826.0	11.7	-	-	-	-	-	-	-
P46478	AAEX_ECOLI	7842.3	8.3	-	-	-	-	-	-	-
P75688	Y309_ECOLI	7849.9	6.3	-	-	-	-	-	-	-
P58033	YPJJ_ECOLI	7857.0	11.9	-	-	-	-	-	-	-
P33230	YDAC_ECOLI	7859.1	10.3	-	-	-	-	-	-	-
P0A7M9	RL31_ECOLI	7866.9	9.8	1	1	1	1	1	1	-
P65294	YGDR_ECOLI	7872.8	4.4	1	-	1	-	-	-	-
P58036	YJBS_ECOLI	7884.2	7.7	-	-	-	-	-	-	-
P75620	YAAY_ECOLI	7886.1	10.6	-	-	-	-	-	-	-
P26649	GLGS_ECOLI	7887.6	5.3	1	-	1	1	-	-	-
P11519	FLMC1_ECOLI	7890.1	8.3	-	-	-	-	-	-	-
P0ACX5	YDHZ_ECOLI	7903.3	9.9	1	-	1	-	-	-	-
P0A968	CSPD_ECOLI	7964.9	5.8	1	1	1	-	-	-	-
P76127	BDM_ECOLI	7982.9	3.9	-	-	-	-	-	-	-
P76575	YFGJ_ECOLI	7989.8	6.6	1	-	1	-	-	-	-
Q2M7R5	YIBT_ECOLI	7991.3	10.4	1	-	1	-	-	-	-
P0AFV8	PSPD_ECOLI	8037.7	12.9	-	-	-	-	-	-	-
Q46789	YGEI_ECOLI	8050.8	3.7	-	-	-	-	-	-	-

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Q2EET2	YPFN_ECOLI	8067.3	9.3	-	-	1	-	-	-	-
P0ADE2	YTFK_ECOLI	8067.5	11.0	-	-	1	-	-	-	-
P0AAQ0	YAIZ_ECOLI	8093.3	9.8	-	-	-	-	-	-	-
P64570	YQGC_ECOLI	8110.4	12.2	-	-	-	-	-	-	-
P33997	ALPA_ECOLI	8128.4	11.1	-	-	-	-	-	-	-
P33014	YEED_ECOLI	8144.1	4.0	1	-	1	-	-	-	-
Q9JMS8	YUAL_ECOLI	8146.1	11.5	-	-	-	-	-	-	-
P36675	YHDL_ECOLI	8167.3	11.1	-	-	-	-	-	-	-
Q9JMR9	YUAV_ECOLI	8168.2	10.0	-	-	-	-	-	-	-
P65292	YGDI_ECOLI	8169.9	5.5	-	-	1	1	1	-	-
P0ADQ5	YIIE_ECOLI	8201.4	10.5	-	-	-	-	-	-	-
P0A8R4	SLYX_ECOLI	8210.2	4.7	1	-	1	-	-	-	-
P0AD07	YECF_ECOLI	8234.1	5.1	1	-	1	1	-	-	-
P69222	IF1_ECOLI	8245.3	10.0	1	1	1	1	-	1	-
P58034	YMGF_ECOLI	8250.6	10.0	-	-	-	-	-	-	-
P68699	ATPL_ECOLI	8251.4	4.2	-	1	1	-	-	-	-
P76118	YNCH_ECOLI	8265.3	9.7	-	-	-	-	-	-	-
P18393	YBDZ_ECOLI	8266.9	4.2	-	1	-	-	-	-	-
P0AAU2	YBFA_ECOLI	8270.2	10.5	-	-	-	-	-	-	-
P0AD24	YEJL_ECOLI	8284.3	5.4	1	1	1	1	-	-	-
P41065	TRAR_ECOLI	8309.1	7.0	-	-	-	-	-	-	-
P69776	LPP_ECOLI	8319.3	9.9	1	1	1	1	1	-	1
P68206	YJBJ_ECOLI	8321.1	5.3	1	1	1	1	1	-	-
P21418	YDFC_ECOLI	8346.3	4.9	1	-	-	-	-	-	-
P0AEL3	FEOA_ECOLI	8366.5	10.1	-	-	-	-	-	-	-
P64562	YQFE_ECOLI	8367.5	12.1	-	-	-	-	-	-	-
P62552	CCDA_ECOLI	8368.1	4.9	-	-	-	-	-	-	-
P64521	YEET_ECOLI	8406.3	11.3	-	-	-	-	-	-	-
P0AD40	YPEB_ECOLI	8410.6	9.5	-	-	1	-	-	-	-
P64467	CNU_ECOLI	8412.3	6.3	1	-	1	-	1	-	-
P37057	OGRK_ECOLI	8425.1	8.7	-	-	-	-	-	-	-
P38393	KIL_ECOLI	8429.5	10.5	-	-	-	-	-	-	-
P0AFU6	YIIF_ECOLI	8438.3	4.4	-	-	-	-	-	-	-
P0AB31	YCEK_ECOLI	8438.4	5.8	-	-	-	-	-	-	-
P76057	YDAQ_ECOLI	8451.3	10.0	-	-	-	-	-	-	-
P67624	YHEU_ECOLI	8465.2	4.5	1	-	1	-	-	-	-
P75687	YKGI_ECOLI	8467.4	10.2	-	-	-	-	-	-	-
P77528	YBCD_ECOLI	8488.6	10.8	-	-	-	-	-	-	-
P68679	RS21_ECOLI	8495.7	12.0	1	1	1	1	-	1	-
P18355	YPFU_ECOLI	8508.2	4.7	-	-	-	-	-	-	-
Q2MB16	YOBH_ECOLI	8509.6	10.3	-	-	1	-	-	-	-
P0AB14	YCCJ_ECOLI	8520.2	4.5	1	1	1	1	-	1	-
P0AF59	YJDI_ECOLI	8545.3	8.7	1	-	1	-	-	-	-
P0AAX3	YBIJ_ECOLI	8563.4	9.5	-	-	-	-	-	-	-
Q9JMR8	YUAW_ECOLI	8571.2	4.7	-	-	-	-	-	-	-
P06965	DICC_ECOLI	8573.4	10.4	-	-	-	-	-	-	-
P64519	YODD_ECOLI	8575.1	4.4	1	-	1	1	-	-	-
Q9XB42	YKFH_ECOLI	8576.3	11.2	-	-	-	-	-	-	-
P11866	TDCR_ECOLI	8603.2	8.3	-	-	-	-	-	-	-
Q9S4X1	YUBE_ECOLI	8623.2	6.1	-	-	-	-	-	-	-

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P0ACE3	HHA_ECOLI	8623.5	9.5	1	1	1	-	1	-	-
P46887	YECH_ECOLI	8624.2	6.2	-	-	-	-	-	-	-
P0AA31	YEDF_ECOLI	8634.4	4.7	1	-	1	1	-	-	-
P0A6A8	ACP_ECOLI	8635.2	3.8	1	1	1	1	-	1	1
P64638	FEOC_ECOLI	8655.3	7.8	-	-	-	-	-	-	-
P64485	YEAQ_ECOLI	8665.8	10.7	-	-	-	-	-	-	-
P31992	PPTA_ECOLI	8668.4	4.7	1	-	1	-	-	-	-
Q7DFV3	YMGG_ECOLI	8680.8	11.0	-	-	-	-	-	-	-
P0ACW2	YDBJ_ECOLI	8691.1	7.6	-	-	-	-	-	-	-
P55914	YJJZ_ECOLI	8691.7	10.1	-	-	-	-	-	-	-
P64459	YNCJ_ECOLI	8704.4	6.6	-	-	-	-	-	-	-
P39355	YJHE_ECOLI	8709.7	4.7	-	-	-	-	-	-	-
P76164	YDFW_ECOLI	8721.8	10.9	-	-	-	-	-	-	-
P0AAA5	SFA_ECOLI	8722.4	6.4	-	-	-	-	-	-	-
P64503	YEBV_ECOLI	8748.2	4.3	1	-	1	1	-	-	-
P30748	MOAD_ECOLI	8753.4	4.2	1	1	1	-	-	-	-
P0AFM9	PSPB_ECOLI	8758.6	7.9	-	-	1	1	-	-	-
P56257	YKGL_ECOLI	8762.5	9.7	-	-	-	-	-	-	-
P75991	YCGZ_ECOLI	8764.5	6.5	-	-	1	-	-	-	-
P76011	YMGE_ECOLI	8769.9	10.1	-	-	-	-	-	-	-
P64455	YDCY_ECOLI	8795.5	5.6	1	1	1	1	-	-	-
P0AAM7	HYBG_ECOLI	8803.4	4.0	-	-	-	-	-	-	-
P0AB40	BHSA_ECOLI	8810.5	9.5	-	-	1	-	-	-	-
P39354	YJHD_ECOLI	8816.4	6.9	-	-	-	-	-	-	-
P0ABS8	HOLE_ECOLI	8841.7	9.9	1	1	1	-	1	-	-
P76521	YFDY_ECOLI	8868.5	8.5	-	-	-	-	-	-	-
P0ACW6	YDCH_ECOLI	8873.6	10.0	1	-	1	1	-	-	-
P64471	YDHI_ECOLI	8885.8	8.3	-	-	-	-	-	-	-
P75692	YAHM_ECOLI	8885.8	11.2	-	-	-	-	-	-	-
P0AAX6	MCBA_ECOLI	8891.5	8.8	-	-	-	-	-	-	-
P76611	PINH_ECOLI	8897.8	10.3	-	-	-	-	-	-	-
P64493	YOAF_ECOLI	8937.5	7.8	-	-	1	-	-	-	-
P0AE63	CHAB_ECOLI	8940.4	6.6	-	-	1	-	-	-	-
P0ABR1	DINI_ECOLI	8944.5	4.5	1	-	-	-	-	-	-
P0A8G9	EX7S_ECOLI	8947.5	4.2	1	1	1	1	-	1	-
P0AFT8	YEIW_ECOLI	8949.2	6.2	-	-	-	-	-	-	-
P0A7T7	RS18_ECOLI	8981.9	12.2	1	1	1	1	-	1	-
P0A7M2	RL28_ECOLI	9001.9	12.1	1	1	1	1	-	1	-
P75677	YKFF_ECOLI	9009.5	10.5	-	-	-	-	-	-	-
P32696	YJBO_ECOLI	9018.2	11.6	-	-	-	-	-	-	-
Q2EES0	YNFO_ECOLI	9018.7	11.0	-	-	1	-	-	-	-
P0C079	RELB_ECOLI	9066.8	4.6	1	-	1	1	-	-	-
P0A890	TUSA_ECOLI	9089.5	5.1	1	-	1	-	-	-	-
P45566	YHDT_ECOLI	9092.7	4.9	-	-	-	-	-	-	-
P0AA04	PTHP_ECOLI	9114.7	5.5	1	1	1	1	-	-	-
P0AD10	YECJ_ECOLI	9117.8	4.7	1	-	1	-	-	-	-
P0A7L8	RL27_ECOLI	9119.9	11.1	1	1	1	1	-	-	-
P41072	TRBG_ECOLI	9121.6	6.5	-	-	-	-	-	-	-
P0AC62	GLRX3_ECOLI	9132.6	7.1	1	1	1	1	-	1	-
P0AC65	NRDH_ECOLI	9134.5	8.3	-	-	-	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P0A7T3	RS16_ECOLI	9186.0	11.3	1	1	1	1	-	1	-
P64614	YHCN_ECOLI	9191.6	5.7	-	-	1	-	-	-	-
P76544	YFFM_ECOLI	9200.7	6.9	-	-	-	-	-	-	-
P0ACF4	DBHB_ECOLI	9221.0	10.2	1	1	1	1	-	1	-
P07010	REM_ECOLI	9229.7	5.2	-	-	-	-	-	-	-
P64536	YEIS_ECOLI	9258.9	10.9	-	-	-	-	-	-	-
Q9JMT2	YUAG_ECOLI	9259.7	11.3	-	-	-	-	-	-	-
Q9JMS6	YUAN_ECOLI	9266.6	5.9	-	-	-	-	-	-	-
P08365	CHPS_ECOLI	9266.7	4.5	-	-	-	-	-	-	-
P75970	VXIS_ECOLI	9281.9	10.4	-	-	-	-	-	-	-
P0ABW3	YFAE_ECOLI	9287.5	4.8	-	-	-	-	-	-	-
P69346	YEFM_ECOLI	9302.6	4.9	-	-	-	-	-	-	-
P0ACV8	YMJA_ECOLI	9316.4	4.0	1	1	1	-	-	-	-
P64445	YNAJ_ECOLI	9334.1	10.0	-	-	-	-	-	-	-
P0AE72	CHPR_ECOLI	9350.9	4.6	-	-	1	-	-	-	-
P64474	YDHL_ECOLI	9353.5	8.4	-	-	-	-	-	-	-
Q9JMR3	YUBL1_ECOLI	9371.6	8.0	-	-	-	-	-	-	-
P0AE60	CEDA_ECOLI	9371.8	10.5	1	-	1	-	-	-	-
P0A8C8	YIDD_ECOLI	9376.0	10.8	-	-	-	-	-	-	-
P0AB61	YCIN_ECOLI	9380.8	5.4	1	1	1	1	1	-	-
P77506	YBDJ_ECOLI	9398.1	8.3	-	-	-	-	-	-	-
Q47150	DINJ_ECOLI	9401.0	5.1	1	-	1	1	-	-	-
P0A9W6	YRBA_ECOLI	9446.7	5.8	1	1	1	1	-	-	-
C1P601	RZOQ_ECOLI	9458.1	10.1	-	-	-	-	-	-	-
P0A9I5	NAPD_ECOLI	9463.7	4.0	-	-	-	-	-	-	-
P0AFW8	ROF_ECOLI	9474.7	4.5	1	-	1	1	-	-	-
P46121	YBFK_ECOLI	9493.8	5.3	-	-	-	-	-	-	-
P75885	GFCA_ECOLI	9502.7	6.0	-	-	-	-	-	-	-
P65298	YQHH_ECOLI	9507.9	8.7	-	-	-	-	-	-	-
P46879	YQGD_ECOLI	9514.1	10.3	-	-	-	-	-	-	-
P0ACF0	DBHA_ECOLI	9530.2	10.1	1	1	1	1	-	1	-
Q2EEQ8	YBFQ_ECOLI	9549.9	4.8	-	-	-	-	-	-	-
P13959	COPB1_ECOLI	9599.1	11.4	-	-	-	-	-	-	-
P76023	YCHS_ECOLI	9601.9	9.2	-	-	1	-	-	-	-
P0AC07	FLIQ_ECOLI	9626.4	4.7	-	-	-	-	-	-	-
P0AF36	ZAPB_ECOLI	9629.8	4.5	1	1	1	1	-	1	1
Q46905	YGCO_ECOLI	9656.8	6.8	-	-	-	-	-	-	-
P0AB33	BSSS_ECOLI	9658.8	4.7	-	-	-	-	-	-	-
P69428	TATA_ECOLI	9659.0	5.7	-	1	1	1	-	-	1
P0A7U7	RS20_ECOLI	9679.3	11.9	1	1	1	1	1	1	-
P68688	GLRX1_ECOLI	9679.8	4.7	1	-	1	-	-	-	-
P75993	ARIR_ECOLI	9689.0	4.4	-	-	1	-	-	-	-
P75994	YMGC_ECOLI	9696.0	5.1	-	-	-	-	-	-	-
P0ADG1	ILVM_ECOLI	9698.0	9.1	-	-	-	-	-	-	-
P0AG63	RS17_ECOLI	9699.3	10.2	1	1	1	1	-	-	-
P0AAM3	HYPC_ECOLI	9726.8	4.0	-	-	-	-	-	-	-
Q2EEU2	YJHX_ECOLI	9729.3	11.2	-	-	-	-	-	-	-
P32693	YJBL_ECOLI	9744.2	10.5	-	-	-	-	-	-	-
P41039	YBII_ECOLI	9750.7	5.0	-	-	1	-	-	-	-
P08868	YUAZ_ECOLI	9757.8	11.5	-	-	-	-	-	-	-

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P76068	YNAK_ECOLI	9782.1	6.4	-	-	-	-	-	-	-
P52102	YFHL_ECOLI	9785.5	4.7	1	-	1	-	-	-	-
P58035	SGCB_ECOLI	9797.9	5.5	-	-	1	-	-	-	-
P0A9N0	PTSO_ECOLI	9804.9	4.1	1	-	1	-	-	-	-
P75675	YKFJ_ECOLI	9815.0	11.7	-	-	-	-	-	-	-
P0A8J4	YBED_ECOLI	9822.1	5.4	1	1	1	1	-	-	-
P0ABF4	EUTM_ECOLI	9860.2	6.1	1	-	-	-	-	-	-
P0C650	INSA1_ECOLI	9862.9	11.3	-	-	-	-	-	-	-
P37590	PMRD_ECOLI	9865.0	8.4	1	-	1	-	-	1	-
P75694	YAHO_ECOLI	9890.2	5.7	1	-	1	1	1	-	-
P0C651	INSA2_ECOLI	9896.9	11.3	-	-	-	-	-	-	-
Q05807	TRBE_ECOLI	9905.2	4.4	-	-	-	-	-	-	-
Q79CP2	YGIA_ECOLI	9911.1	10.5	-	-	-	-	-	-	-
P0A7N1	RL31B_ECOLI	9915.1	10.2	-	-	-	-	-	-	-
P19767	INSA7_ECOLI	9919.0	11.7	-	-	1	-	-	-	-
P0AAN9	IRAP_ECOLI	9932.2	4.7	1	-	1	1	-	-	-
P76227	YNJH_ECOLI	9942.0	6.9	1	-	1	-	-	-	-
P0AF82	YJFN_ECOLI	9943.9	4.0	-	-	-	-	-	-	-
P0AEJ8	EUTN_ECOLI	9951.1	5.6	-	-	-	-	-	-	-
P52128	YFJM_ECOLI	9961.9	6.5	-	-	-	-	-	-	-
P0AAY4	YBJH_ECOLI	9965.1	6.3	-	-	-	-	-	-	-
P64540	YFCL_ECOLI	9994.9	4.1	1	1	1	1	-	-	-
P45795	YRDB_ECOLI	10001.6	4.0	-	-	1	-	-	-	-
P15033	RACC_ECOLI	10010.3	5.6	-	-	-	-	-	-	-
P23873	HIPB_ECOLI	10011.0	6.7	-	-	-	-	1	-	-
A5A628	YJBT_ECOLI	10043.2	10.2	-	-	-	-	-	-	-
P33669	YBBD_ECOLI	10046.2	4.1	-	-	-	-	-	-	-
P75786	YLIL_ECOLI	10057.4	12.3	-	-	-	-	-	-	-
P58095	YPJI_ECOLI	10084.8	4.8	-	-	-	-	-	-	-
P76073	YNAE_ECOLI	10103.5	10.3	-	-	-	-	-	-	-
P76692	YZGL_ECOLI	10123.5	8.3	-	-	-	-	-	-	-
P64530	RCNR_ECOLI	10128.5	9.4	1	-	1	-	-	-	-
P76154	YDFK_ECOLI	10130.6	10.4	-	-	-	-	-	-	-
P33344	YEHE_ECOLI	10131.1	9.8	-	-	-	-	-	-	-
P0AF86	YJFY_ECOLI	10144.0	5.0	-	-	-	-	-	-	-
O32528	YPDI_ECOLI	10156.2	9.5	-	-	-	-	-	-	-
P69348	YOEB_ECOLI	10210.2	8.8	-	-	-	-	-	-	-
P37188	PTKB_ECOLI	10216.3	5.8	1	1	1	-	-	1	-
P0A9L5	PPIC_ECOLI	10226.5	9.8	1	-	1	1	1	1	-
P0C037	YAIE_ECOLI	10228.9	4.3	1	1	1	-	-	-	-
P0A734	MINE_ECOLI	10229.5	5.0	1	1	1	1	1	1	1
P0A800	RPOZ_ECOLI	10231.4	4.7	1	1	1	1	-	1	1
Q9JMS2	YUAS_ECOLI	10243.2	9.7	-	-	-	-	-	-	-
P37614	YHHL_ECOLI	10245.8	11.0	-	-	1	-	-	-	-
A5A630	YTCA_ECOLI	10250.5	12.1	-	-	-	-	-	-	-
Q9JMS9	YUAK_ECOLI	10254.3	7.8	-	-	-	-	-	-	-
P13960	REA1_ECOLI	10255.3	9.9	-	-	-	-	-	-	-
P0ADZ4	RS15_ECOLI	10263.5	11.4	1	1	1	1	-	1	-
P0ADP9	YIHD_ECOLI	10267.4	5.0	1	1	1	1	-	1	-
P0AB65	ACYP_ECOLI	10294.3	9.0	1	-	1	-	-	-	-

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P32700	YJCB_ECOLI	10297.3	5.5	-	-	-	-	-	-	-
P0AD33	YFCZ_ECOLI	10311.7	4.1	1	1	1	1	-	1	-
P0AAP3	FRMR_ECOLI	10312.3	5.8	1	-	1	1	-	-	-
P76509	YFDM_ECOLI	10330.0	4.6	-	-	-	-	-	-	-
P76231	YEAC_ECOLI	10332.1	5.1	-	-	1	-	-	-	-
P0AEM4	FLGM_ECOLI	10335.3	5.1	1	-	1	-	-	-	-
P75992	YMGA_ECOLI	10339.4	10.5	-	-	1	-	-	-	-
P68661	YBCO_ECOLI	10342.3	8.0	-	-	-	-	-	-	-
P08321	TRAL1_ECOLI	10373.6	10.7	-	-	-	-	-	-	-
P0A6F9	CH10_ECOLI	10381.6	5.0	1	1	1	1	-	1	1
P67699	YDDM_ECOLI	10395.5	9.6	-	-	1	-	-	-	-
P0A7U3	RS19_ECOLI	10424.7	11.2	1	1	1	1	1	-	-
P77330	BORD_ECOLI	10441.5	9.8	-	-	-	-	-	-	-
P64476	YDIH_ECOLI	10448.4	6.5	1	-	1	-	-	-	-
Q9JMS4	YUAP_ECOLI	10448.5	10.8	-	-	-	-	-	-	-
P52060	YGGU_ECOLI	10450.8	10.1	1	-	1	-	-	-	-
P39274	YJDJ_ECOLI	10462.5	8.7	1	-	1	-	-	-	-
P76172	YNFD_ECOLI	10471.1	4.6	1	-	1	1	-	-	-
P68646	FIXX_ECOLI	10473.2	5.1	-	-	-	-	-	-	-
P0AB49	YCHH_ECOLI	10480.4	12.0	-	-	1	-	-	-	-
P0ACH1	SFSB_ECOLI	10489.4	10.6	-	-	-	-	-	-	-
P75717	YBCC_ECOLI	10503.1	5.3	-	-	-	-	-	-	-
P45956	YGBF_ECOLI	10512.5	4.9	-	-	-	-	-	-	-
P46119	YBJC_ECOLI	10514.8	10.1	-	-	-	-	-	-	-
P32685	YJBD_ECOLI	10526.6	10.9	-	-	1	-	-	-	-
P64559	YGFY_ECOLI	10541.2	5.2	1	-	1	1	-	-	-
P08339	Y4223_ECOLI	10579.4	12.3	-	-	-	-	-	-	-
P36560	ASR_ECOLI	10585.8	11.1	-	-	-	-	-	-	-
P77295	YGAV_ECOLI	10590.5	9.0	-	-	-	-	-	-	-
P0AB55	YCII_ECOLI	10596.4	5.1	1	-	1	1	-	-	1
P46857	YRHB_ECOLI	10607.2	4.6	-	-	-	-	-	-	-
P75704	YKIA_ECOLI	10612.8	10.0	-	-	-	-	-	-	-
Q2EEQ3	YAHH_ECOLI	10628.6	8.0	-	-	-	-	-	-	-
P0A6Y1	IHFB_ECOLI	10645.5	10.1	1	1	1	1	1	-	-
P64602	MLAB_ECOLI	10674.6	4.6	1	1	1	-	-	-	-
P69330	CITD_ECOLI	10683.6	4.4	-	-	1	-	-	-	-
P68919	RL25_ECOLI	10687.7	10.3	1	1	1	1	1	1	-
P0ACY9	YEBG_ECOLI	10711.3	4.2	-	1	-	1	-	-	-
P45530	TUSB_ECOLI	10712.7	5.0	-	-	1	-	-	-	-
P77714	YDIT_ECOLI	10718.1	5.3	-	-	-	-	-	-	-
P76323	INTG_ECOLI	10726.4	11.0	-	-	-	-	-	-	-
P77519	YDDL_ECOLI	10730.4	7.8	-	-	-	-	-	-	-
Q9JMR7	YUAX_ECOLI	10742.2	4.3	-	-	-	-	-	-	-
P0AFX0	RP5M_ECOLI	10744.6	6.6	1	1	1	-	-	1	-
P32162	YIIS_ECOLI	10770.2	4.4	1	-	1	-	-	-	-
P0AGK4	YHBY_ECOLI	10778.1	10.0	1	1	1	1	-	-	-
P52119	YFJF_ECOLI	10783.8	9.8	1	-	1	-	-	-	-
P64499	YEBO_ECOLI	10786.8	4.8	-	-	-	1	-	-	-
P64616	YHCO_ECOLI	10790.4	4.3	-	-	1	-	-	-	-
P75711	YBBV_ECOLI	10838.1	12.2	-	-	1	-	-	-	-

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P0AFE4	NUOK_ECOLI	10839.0	10.6	-	-	1	-	-	-	-
Q47149	YAFQ_ECOLI	10840.7	10.3	-	-	-	-	-	-	-
P64479	YDIZ_ECOLI	10859.3	4.1	1	-	1	-	-	-	-
P18033	TRAQ_ECOLI	10859.7	9.8	-	-	-	-	-	-	-
P69822	ULAB_ECOLI	10889.5	6.3	1	-	1	-	-	-	-
P69937	SUGE_ECOLI	10894.1	10.8	-	-	-	-	-	-	-
P0AAV0	YBGE_ECOLI	10925.9	9.1	-	-	-	-	-	-	-
P76078	PAAB_ECOLI	10936.3	5.9	-	-	1	-	-	-	-
P64574	YGHW_ECOLI	10939.3	10.0	-	-	1	-	-	-	-
P0A8P3	FETP_ECOLI	10946.4	5.9	1	1	1	1	-	1	-
P75971	Y1142_ECOLI	10956.8	9.8	-	-	-	-	-	-	-
P76063	YDAS_ECOLI	10969.4	8.8	-	-	-	-	-	-	-
P76165	YDFX_ECOLI	10969.7	8.8	-	-	-	-	-	-	-
Q02885	YUBO_ECOLI	11001.7	10.4	-	-	-	-	-	-	-
P0A9V5	YIAG_ECOLI	11026.8	8.7	-	-	1	-	-	-	-
P64581	YQJD_ECOLI	11045.9	9.8	1	1	1	1	-	1	1
Q2M7X4	YICS_ECOLI	11063.5	4.9	1	-	1	-	-	-	-
P0ADF8	ILVN_ECOLI	11099.6	5.7	1	-	1	-	-	-	-
P0A8T5	FLIE_ECOLI	11120.6	5.0	-	-	-	-	-	-	-
P75718	REND_ECOLI	11154.8	10.9	-	-	-	-	-	-	-
P0A6X3	HFQ_ECOLI	11160.6	8.1	-	1	1	-	-	-	-
P75917	YMDA_ECOLI	11187.7	9.5	-	-	-	-	-	-	-
P0ADZ0	RL23_ECOLI	11193.2	10.5	1	1	1	1	-	-	-
P0C077	RELE_ECOLI	11219.2	10.4	-	-	1	-	-	-	-
Q46865	MQSR_ECOLI	11225.9	9.5	-	-	-	-	-	-	-
Q47156	YAFN_ECOLI	11227.7	5.3	-	-	1	1	-	-	-
P0A6R3	FIS_ECOLI	11233.8	10.2	1	1	1	-	1	-	1
P69816	PTFB2_ECOLI	11241.8	5.2	-	-	-	-	-	-	-
P64461	LSRG_ECOLI	11248.6	5.6	1	-	1	-	-	-	-
P45472	YHBQ_ECOLI	11264.0	10.7	-	-	-	-	-	-	-
Q46868	YQIC_ECOLI	11270.1	5.8	1	1	1	-	1	-	1
P0AAU7	YBFE_ECOLI	11274.0	10.6	-	-	1	1	-	-	-
P0ACX3	YDHR_ECOLI	11281.8	5.0	1	1	1	-	-	-	1
Q46796	YGEP_ECOLI	11285.0	6.1	-	-	-	-	-	-	-
P0AEH5	ELAB_ECOLI	11299.8	5.2	1	1	1	1	-	1	-
P76163	YDFV_ECOLI	11301.8	11.3	-	-	-	-	-	-	-
P60624	RL24_ECOLI	11310.3	10.7	1	1	1	1	-	1	-
P0ABW0	HCAC_ECOLI	11322.4	4.1	-	-	-	-	-	-	-
Q2M7M3	YSAB_ECOLI	11329.5	8.5	-	-	-	-	-	-	-
P0ACV4	YCIS_ECOLI	11345.3	10.5	-	-	1	-	-	-	-
P0A6X7	IHFA_ECOLI	11348.0	10.0	1	1	1	1	1	1	-
P75616	YAAX_ECOLI	11348.8	11.2	-	-	-	-	-	-	-
P0AG99	SECG_ECOLI	11358.9	7.2	-	-	1	1	-	-	-
Q9JMR2	YUBN_ECOLI	11382.7	11.8	-	-	-	-	-	-	-
P08245	YCIH_ECOLI	11390.1	9.8	1	-	1	-	-	-	-
P0AAP7	YAIY_ECOLI	11418.1	11.2	-	-	-	-	-	-	-
P69795	PTQB_ECOLI	11420.2	8.7	-	-	1	-	-	-	-
Q9S4X3	YUBC_ECOLI	11423.0	12.6	-	-	-	-	-	-	-
P0A8C1	YBJQ_ECOLI	11430.8	4.7	-	-	1	1	-	-	-
P07013	PRIB_ECOLI	11435.8	8.3	-	-	1	-	-	-	-

SwissProt Accession No	**SwissProt entry name**	**molecular weight [Da]**	**p*I***	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
P75973	YMFJ_ECOLI	11452.0	9.5	-	-	-	-	-	-	-
P76406	YEGR_ECOLI	11458.9	9.4	-	-	-	-	-	-	-
P0AF61	YJDK_ECOLI	11461.6	4.2	1	-	1	-	1	-	-
P23857	PSPE_ECOLI	11469.0	8.7	1	-	1	1	1	-	-
P63264	CBPM_ECOLI	11506.0	5.1	-	-	1	-	-	-	-
P0ADU2	YGIN_ECOLI	11525.8	5.8	1	1	1	1	1	-	-
P0AAC8	ISCA_ECOLI	11549.7	4.6	1	1	1	1	-	1	1
P39212	INSN2_ECOLI	11552.2	10.6	-	-	-	-	-	-	-
P0AG48	RL21_ECOLI	11558.2	10.5	1	1	1	1	1	1	-
P0AG59	RS14_ECOLI	11574.3	11.8	1	1	1	1	-	1	-
P0AAT6	YBEB_ECOLI	11575.8	4.4	1	1	1	1	-	-	-
P0A6S5	FTSB_ECOLI	11616.0	7.7	-	-	-	-	-	-	-
P63746	EUTS_ECOLI	11643.1	5.1	-	-	-	-	-	-	-
P0AF54	YJCH_ECOLI	11665.3	7.9	-	-	1	-	-	-	-
P0AFM4	PSIF_ECOLI	11679.9	10.3	-	-	1	-	-	-	-
P62554	CCDB_ECOLI	11700.0	6.1	-	-	-	-	-	-	-
P69210	MDTI_ECOLI	11713.6	11.0	-	-	-	-	-	-	-
P69808	PTFB1_ECOLI	11728.9	4.2	-	-	1	-	-	-	-
P0A7R5	RS10_ECOLI	11729.4	10.3	1	1	1	1	-	1	-
P52141	YFJZ_ECOLI	11730.7	6.0	-	-	-	-	-	-	-
P76308	YECR_ECOLI	11734.9	6.7	-	-	-	-	-	-	-
P0AB20	HSPQ_ECOLI	11772.9	4.4	1	-	1	-	-	-	-
P0AAL9	YKGJ_ECOLI	11791.5	8.3	-	-	-	-	-	-	-
P46126	YFIM_ECOLI	11798.6	6.5	-	-	-	-	-	-	-
P0AA25	THIO_ECOLI	11800.1	4.5	1	1	1	1	-	1	1
Q47710	YQJK_ECOLI	11804.3	12.6	-	-	1	-	-	-	-
P39283	YJEN_ECOLI	11812.0	5.2	-	-	-	-	-	-	-
P0ADM4	YIDQ_ECOLI	11818.8	5.6	-	-	1	-	-	-	-
P0AB46	YMGD_ECOLI	11845.1	5.2	1	-	1	-	-	-	-
P0AES9	HDEA_ECOLI	11851.2	4.9	1	-	1	1	-	1	1
P76076	YDBL_ECOLI	11871.4	10.1	1	-	1	-	-	-	-
P0ADZ7	YAJC_ECOLI	11880.4	10.2	1	1	1	1	1	1	-
P67603	YQFB_ECOLI	11898.9	4.5	1	1	1	-	-	-	-
P0ADH3	INSE_ECOLI	11906.3	10.7	-	-	-	-	-	-	-
P76169	YNFA_ECOLI	11912.5	9.2	-	-	-	-	-	-	-
Q47684	YAFW_ECOLI	11932.9	6.3	-	-	-	-	-	-	-
P23895	EMRE_ECOLI	11951.3	8.0	-	-	-	-	-	-	-
P0AF70	YJEI_ECOLI	11951.8	5.4	-	-	1	1	1	-	-
P52107	CSGC_ECOLI	11960.3	7.0	-	-	-	-	-	-	-
P0ABE2	BOLA_ECOLI	11987.1	6.2	1	1	1	1	-	1	-
P75734	YBFN_ECOLI	11992.0	7.7	1	-	-	-	-	-	-
P08372	PPDC_ECOLI	11997.0	12.0	-	-	-	-	-	-	-
Q7DFV4	YMDE_ECOLI	12001.0	5.7	-	-	-	-	-	-	-
P0A8B5	YBAB_ECOLI	12007.9	4.9	1	1	1	1	1	-	-
P46141	YGBE_ECOLI	12010.2	4.8	-	-	-	-	-	-	-
P0ADB1	OSME_ECOLI	12013.9	8.0	1	-	1	1	-	-	1
P43667	YGAH_ECOLI	12016.7	11.7	-	-	-	-	-	-	-
P76402	YEGP_ECOLI	12018.0	10.2	1	-	1	-	1	1	-
P0ABJ6	CYOD_ECOLI	12022.1	6.7	-	-	-	-	-	-	-
P39297	YJFO_ECOLI	12031.3	10.4	-	-	1	-	-	-	-

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P0AET2	HDEB_ECOLI	12036.0	5.7	1	-	1	1	1	-	1
P0A6V5	GLPE_ECOLI	12075.6	4.3	1	-	1	-	-	-	-
P76160	YDFR_ECOLI	12084.1	5.5	-	-	-	-	-	-	-
P0AE70	CHPA_ECOLI	12091.2	8.5	1	-	1	-	-	-	-
P62066	YCEQ_ECOLI	12092.7	8.7	-	-	-	-	1	-	-
P0ACC3	ERPA_ECOLI	12093.8	3.9	1	1	1	1	-	1	1
P64578	YGJN_ECOLI	12096.3	10.2	-	-	-	-	-	-	-
P18032	ARTA_ECOLI	12123.7	8.9	-	-	-	-	-	-	-
P76516	YFDT_ECOLI	12126.1	4.8	-	-	1	-	-	-	-
P75987	IRAM_ECOLI	12126.3	9.1	-	-	-	-	-	-	-
P77354	YAFU_ECOLI	12129.3	5.7	-	-	-	-	-	-	-
P0A8U6	METJ_ECOLI	12134.2	5.3	1	1	1	1	1	-	-
P75977	YMFM_ECOLI	12149.1	9.8	-	-	1	-	-	-	-
P39351	YJGZ_ECOLI	12154.3	9.1	-	-	-	-	-	-	-
P0A8Q6	CLPS_ECOLI	12172.1	4.8	-	-	-	-	-	-	-
Q47377	ARNE_ECOLI	12184.8	10.2	-	-	-	-	-	-	-
P39394	SYME_ECOLI	12196.3	8.9	-	-	-	-	-	-	-
P77609	FLXA_ECOLI	12201.3	4.9	-	-	-	-	-	-	-
P61175	RL22_ECOLI	12219.8	10.8	1	1	1	1	1	1	-
P27838	CYAY_ECOLI	12224.8	4.1	1	1	1	1	-	1	-
P39309	YTFA_ECOLI	12240.4	6.9	-	-	-	-	-	-	-
P77214	CUSF_ECOLI	12244.3	8.0	-	-	-	-	-	-	-
P0AC55	GLNK_ECOLI	12252.7	5.8	-	-	1	-	-	1	1
P32156	RHAM_ECOLI	12258.0	5.2	1	-	-	-	-	-	-
P0A9I8	NIRD_ECOLI	12277.2	4.9	1	-	1	1	-	-	-
P0ADQ7	YGAM_ECOLI	12281.1	8.3	-	-	1	1	-	-	-
P0A7K2	RL7_ECOLI	12288.5	4.4	1	1	1	1	-	1	1
P0A937	SMPA_ECOLI	12295.2	9.0	-	1	1	-	-	-	-
Q46953	YPJF_ECOLI	12301.5	7.4	-	-	-	-	-	-	-
P42589	YGJH_ECOLI	12308.2	4.9	-	-	-	-	-	-	-
P0ACX0	YDGC_ECOLI	12315.8	10.5	-	-	-	-	-	-	-
P0A9R4	FER_ECOLI	12323.8	4.3	1	1	1	1	-	1	-
P69488	CUTA_ECOLI	12324.2	4.7	1	-	1	-	-	-	-
A5A625	YIBV_ECOLI	12333.4	9.6	-	-	-	-	-	-	-
P0AFJ1	PHNA_ECOLI	12338.0	4.8	1	1	1	1	-	-	1
P0A881	TRPR_ECOLI	12348.4	5.3	1	-	1	-	-	-	-
P15373	SOHA_ECOLI	12352.2	4.9	-	-	1	1	-	-	-
Q9JMT1	YUAH_ECOLI	12364.3	10.1	-	-	-	-	-	-	-
P64506	YEBY_ECOLI	12371.5	8.2	1	1	1	1	1	-	-
P0ADK4	YIAW_ECOLI	12401.6	8.1	-	-	-	-	-	-	-
P0AB18	TUSE_ECOLI	12403.4	7.2	1	-	1	1	1	-	-
P0AB43	YCGL_ECOLI	12407.5	9.8	1	-	1	1	1	-	-
P0A9Z1	GLNB_ECOLI	12418.6	5.0	1	1	1	1	1	-	1
P64534	YOHN_ECOLI	12459.3	7.9	1	1	1	-	-	1	-
P64631	YHFU_ECOLI	12471.5	9.0	-	-	1	-	-	-	-
P33647	CHPB_ECOLI	12485.5	5.4	-	-	-	-	-	-	-
P0AEB7	YOAB_ECOLI	12486.4	4.8	1	1	1	-	-	-	-
P0AD21	YEJG_ECOLI	12518.1	4.6	-	-	-	-	-	-	-
P75681	FBPB_ECOLI	12529.0	10.3	-	-	-	-	-	-	-
P11286	YIAB_ECOLI	12547.8	9.6	-	-	-	-	-	-	-

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P0AAU5	YBFB_ECOLI	12549.9	10.5	-	-	-	-	-	-	-
P28224	MLIC_ECOLI	12560.5	8.5	-	-	1	-	-	-	-
P18353	TRBJ_ECOLI	12579.7	9.0	-	-	-	-	-	-	-
P0ADS2	ZAPA_ECOLI	12587.4	5.0	1	1	1	1	-	-	-
P33347	YEHK_ECOLI	12596.4	4.6	-	-	-	-	-	-	-
P32676	PTFB3_ECOLI	12629.5	5.5	-	-	-	-	-	-	-
P39284	YJEO_ECOLI	12630.3	6.4	-	-	-	-	-	-	-
P77326	TFAS_ECOLI	12651.4	4.5	-	-	-	-	-	-	-
P22586	FLIO_ECOLI	12663.1	11.1	-	-	1	-	-	-	-
P0A8L7	YCIU_ECOLI	12680.0	3.8	-	-	1	-	-	-	-
P0AB52	YCHN_ECOLI	12685.7	4.9	1	1	1	1	1	-	-
P0A703	HYBF_ECOLI	12690.2	4.9	1	-	-	-	-	-	-
P0AAR8	YBAV_ECOLI	12696.7	9.4	-	-	1	-	-	-	-
P0AD37	YFEC_ECOLI	12712.8	10.2	-	-	-	-	-	-	-
P69791	PTQA_ECOLI	12740.5	4.7	-	-	-	-	-	-	-
P04737	PIL1_ECOLI	12760.9	11.3	-	-	-	-	-	-	-
P0C018	RL18_ECOLI	12762.9	11.4	1	1	1	1	-	1	-
P0A8M6	YEEX_ECOLI	12770.8	9.9	1	1	1	1	-	1	-
P0ADM0	YIDH_ECOLI	12772.0	9.7	-	-	-	-	-	-	-
P0AD49	RAIA_ECOLI	12777.6	6.2	1	1	1	1	1	1	-
Q46919	YQCC_ECOLI	12779.4	4.7	-	-	1	-	-	-	-
P0AA95	YACC_ECOLI	12846.4	5.1	-	-	-	-	-	-	-
Q79E92	YKGN_ECOLI	12849.6	8.6	-	-	-	-	-	-	-
P0AE48	YTFP_ECOLI	12859.4	6.5	1	1	1	1	-	1	-
P0AC44	DHSD_ECOLI	12860.1	9.8	-	-	1	-	-	-	-
P76122	YDDJ_ECOLI	12864.3	4.7	-	-	-	-	-	-	-
P0AAV6	YBGS_ECOLI	12865.0	4.5	-	-	1	1	-	-	-
P0AC69	GLRX4_ECOLI	12871.5	4.5	1	1	1	1	1	1	1
P38521	YGGL_ECOLI	12873.4	4.7	1	1	1	1	-	1	-
P75972	YMFI_ECOLI	12875.3	4.7	-	-	-	-	-	-	-
P77692	YKFI_ECOLI	12897.9	10.0	-	-	-	-	-	-	-
P76170	YNFB_ECOLI	12901.6	9.5	1	-	1	1	-	-	1
P0A9E2	SOXS_ECOLI	12903.8	11.2	-	-	-	-	-	-	-
P18034	TRBA_ECOLI	12936.8	8.5	-	-	-	-	-	-	-
P15081	GUTM_ECOLI	12946.0	11.0	-	-	-	-	-	-	-
P33219	YEBF_ECOLI	12954.6	9.0	1	-	1	-	-	1	-
Q2EES3	YOEF_ECOLI	12961.5	6.5	-	-	-	-	-	-	-
P0AF40	YIJD_ECOLI	13016.0	10.3	-	-	-	-	-	-	-
P0A8S5	USPB_ECOLI	13019.8	9.3	-	-	-	-	-	-	-
P45531	TUSC_ECOLI	13037.8	4.5	-	-	-	-	-	-	-
P0AD53	YGAC_ECOLI	13058.6	8.8	-	-	-	-	-	-	-
Q9Z3A0	YJGW_ECOLI	13077.7	11.7	-	-	-	-	-	-	-
P0A7S9	RS13_ECOLI	13092.3	11.6	1	1	1	1	1	1	-
P76512	YFDP_ECOLI	13094.8	5.7	-	-	-	-	-	-	-
P0A8Q3	FRDD_ECOLI	13099.1	9.8	-	-	1	-	-	-	-
P69212	MDTJ_ECOLI	13107.3	9.9	-	-	-	-	-	-	-
P0A7K6	RL19_ECOLI	13126.2	11.5	1	1	1	1	-	1	-
P0ADN2	YIFE_ECOLI	13126.5	6.1	1	1	1	1	-	-	1
P0A700	HYPA_ECOLI	13160.4	5.2	-	-	-	-	-	-	-
P0A9T6	YBAQ_ECOLI	13163.9	5.7	-	-	-	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P37008	YAGB_ECOLI	13176.7	7.4	-	-	-	-	-	-	-
Q46867	YGIZ_ECOLI	13192.8	7.8	-	-	-	-	-	-	-
P11289	YFIL_ECOLI	13196.3	4.7	-	-	1	-	-	-	-
P77682	GTRA_ECOLI	13217.9	10.5	-	-	-	-	-	-	-
P64490	YOAC_ECOLI	13223.6	5.0	-	-	1	-	-	-	-
P0ACE7	HINT_ECOLI	13233.9	5.7	1	1	1	1	-	1	-
P0ABN1	KDGL_ECOLI	13237.1	6.1	-	-	1	-	-	-	-
P37309	ARSR_ECOLI	13245.0	8.0	-	-	-	-	-	-	-
P64542	YPEC_ECOLI	13255.5	11.7	-	-	-	-	-	-	-
P77667	SUFA_ECOLI	13292.5	4.7	1	-	1	-	-	-	-
P05706	PTHA_ECOLI	13296.7	4.8	-	-	-	-	-	-	-
P0A8S9	FLHD_ECOLI	13309.0	6.6	-	-	-	-	-	-	-
P0AAQ6	YBAA_ECOLI	13310.5	4.6	1	-	1	-	-	-	-
P0AAQ2	YAJD_ECOLI	13356.4	6.2	1	-	1	-	-	-	1
P76243	YEAO_ECOLI	13379.0	6.4	1	-	1	1	-	-	-
P76322	YEDM_ECOLI	13388.7	4.6	-	-	-	-	-	-	-
P76569	YFGD_ECOLI	13391.1	5.8	1	1	1	1	-	-	-
P0AA57	YOBA_ECOLI	13403.0	10.2	1	-	1	-	-	-	-
P76001	YCGJ_ECOLI	13406.3	5.2	1	-	1	-	-	-	-
P0C5W2	INSC_ECOLI	13444.2	10.2	-	-	-	-	-	-	-
P64592	YHAI_ECOLI	13448.2	10.8	-	-	-	-	-	-	-
Q6BEX5	YJDP_ECOLI	13461.6	4.6	-	-	-	-	-	-	-
P76069	YDAY_ECOLI	13466.0	5.3	-	-	-	-	-	-	-
P37615	YHHM_ECOLI	13489.0	10.9	-	-	-	-	-	-	-
P0A7L3	RL20_ECOLI	13489.7	12.6	1	1	1	1	-	1	-
P0AFN2	PSPC_ECOLI	13509.1	6.8	-	-	1	-	-	-	-
P0AF50	YJBR_ECOLI	13512.0	6.1	1	-	1	1	1	1	-
P45551	YHFY_ECOLI	13519.6	4.5	-	-	-	-	-	-	-
P0ADY3	RL14_ECOLI	13533.5	11.1	1	1	1	1	1	1	-
P76148	YNEG_ECOLI	13536.0	10.5	-	-	-	-	-	-	-
P24178	YFFB_ECOLI	13592.9	6.1	1	1	1	1	-	-	-
P64488	YEAR_ECOLI	13603.8	6.1	1	-	-	-	-	-	-
P0AF93	YJGF_ECOLI	13604.2	5.2	1	1	1	1	-	1	1
P0AC16	FOLB_ECOLI	13612.1	4.5	-	-	-	1	-	-	-
P0AEN4	FTSL_ECOLI	13619.3	6.3	-	-	1	-	-	-	-
P0ABC0	ATPZ_ECOLI	13623.9	12.1	-	-	-	-	-	-	-
P45532	TUSD_ECOLI	13633.8	4.8	-	-	1	-	-	-	-
P0AG96	SECE_ECOLI	13635.7	11.7	-	-	1	-	-	-	-
P52130	YFJO_ECOLI	13656.9	4.3	-	-	-	-	-	-	-
P76515	YFDS_ECOLI	13663.8	4.7	-	-	-	-	-	-	-
P76364	YEEU_ECOLI	13675.7	5.6	1	-	-	-	-	-	-
P0ADK8	YIBL_ECOLI	13688.3	10.1	1	1	1	1	1	-	-
P42905	PTPC2_ECOLI	13713.4	6.3	-	-	-	-	-	-	-
Q47702	YFEK_ECOLI	13724.3	8.9	-	-	-	-	-	-	-
P0AEQ1	GLCG_ECOLI	13729.2	5.7	1	-	1	-	-	-	-
P0A7S3	RS12_ECOLI	13729.5	12.0	1	1	1	1	-	1	-
P0AFQ5	RUTC_ECOLI	13755.1	5.4	-	-	-	-	-	-	-
P0ADL6	YIDG_ECOLI	13760.4	11.7	-	-	-	-	-	-	-
P65870	QUED_ECOLI	13764.9	6.0	-	-	-	-	-	-	-
P37002	CRCB_ECOLI	13769.3	10.1	-	-	-	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P76545	YFFN_ECOLI	13770.0	4.6	-	-	-	-	-	-	-
P09996	YIDB_ECOLI	13779.1	4.2	1	-	1	-	-	-	-
P0A7Y8	RNPA_ECOLI	13781.7	12.3	-	-	1	-	1	-	-
P0A6T9	GCSH_ECOLI	13803.7	3.8	1	1	1	-	-	-	-
P76548	YFFQ_ECOLI	13811.4	4.7	-	-	-	-	-	-	-
P0ABY2	FLIT_ECOLI	13821.0	4.5	-	-	-	-	-	-	-
P0A790	PAND_ECOLI	13826.0	5.7	-	1	-	-	-	-	-
P76334	YEDR_ECOLI	13830.0	10.4	-	-	-	-	-	-	-
P0A7R9	RS11_ECOLI	13837.4	12.0	1	1	1	1	1	1	-
P0AG74	RUSA_ECOLI	13838.1	10.5	-	-	-	-	-	-	-
P0ACD4	NIFU_ECOLI	13840.9	4.7	1	1	1	1	-	1	1
P32108	YIBI_ECOLI	13858.3	6.4	-	-	-	-	-	-	-
P62672	APAG_ECOLI	13859.0	4.6	-	-	1	-	-	-	-
P64524	YEEV_ECOLI	13891.3	8.3	-	-	-	-	-	-	-
P45760	GSPI_ECOLI	13893.8	4.5	-	-	-	-	-	-	-
P42616	YQJC_ECOLI	13898.2	9.3	1	-	1	-	-	-	-
Q9JMR4	YUBK_ECOLI	13907.7	11.4	-	-	-	-	-	-	-
P77688	YLBG_ECOLI	13908.3	10.6	-	-	-	-	-	-	-
P76196	YDIL_ECOLI	13920.9	6.5	-	-	-	-	-	-	-
P25728	YGBA_ECOLI	13932.2	10.1	-	-	-	-	-	-	-
P0A8E5	YACL_ECOLI	13933.5	4.3	1	-	1	-	1	-	-
P36677	YHDN_ECOLI	13937.2	4.8	-	-	-	-	-	-	-
P0ABX2	FLGC_ECOLI	13960.1	5.1	-	-	-	-	-	-	-
P75946	YCFL_ECOLI	13973.2	7.4	-	-	-	-	-	-	-
P27238	YFED_ECOLI	13975.1	5.1	-	-	1	-	-	-	-
P45736	YCJD_ECOLI	13981.1	9.7	-	-	-	-	-	-	-
P0AGL2	TDCF_ECOLI	13999.3	4.9	1	-	1	1	-	-	-
P0ADU5	YGIW_ECOLI	14003.1	4.9	1	1	1	1	-	1	1
P0AAT2	YBDF_ECOLI	14042.4	9.3	-	-	1	-	-	-	-
P24224	ACPS_ECOLI	14044.5	9.9	-	-	1	-	-	-	-
P76297	FLHE_ECOLI	14051.5	11.5	-	-	-	-	-	-	-
P0ACN2	YTFH_ECOLI	14067.5	5.9	-	-	1	-	-	-	-
P0AC19	FOLX_ECOLI	14074.4	6.6	-	1	1	-	1	1	-
P76474	ARNF_ECOLI	14076.6	10.0	-	-	-	-	-	-	-
P0AE67	CHEY_ECOLI	14089.3	4.7	-	-	1	-	-	-	1
P42619	YQJF_ECOLI	14093.6	10.3	-	-	-	-	-	-	-
P31130	YDEI_ECOLI	14113.2	6.5	1	-	1	-	-	-	-
P0A7W7	RS8_ECOLI	14118.5	10.1	1	1	1	1	1	1	-
P18006	TRBI_ECOLI	14124.3	10.0	-	-	-	-	1	-	-
P33668	YBBC_ECOLI	14144.2	5.6	-	-	-	-	-	-	-
P69411	RCSF_ECOLI	14155.2	9.6	-	1	1	1	-	-	-
P42615	YQJB_ECOLI	14164.3	10.3	-	-	-	-	-	-	-
Q47274	REQ1_ECOLI	14167.9	5.8	-	-	-	-	-	-	-
P64439	YBJM_ECOLI	14194.5	10.5	-	-	-	-	-	-	-
P0AF80	YJFL_ECOLI	14215.4	7.4	-	-	-	-	-	-	-
P0A8Z0	YCIA_ECOLI	14222.3	8.0	-	-	1	-	-	-	-
P25738	MSYB_ECOLI	14251.3	3.4	1	1	1	1	1	1	-
P64590	YHAH_ECOLI	14272.6	10.7	-	-	-	-	-	-	-
P68066	GRCA_ECOLI	14276.4	4.9	1	1	1	1	1	1	1
P69054	DHSC_ECOLI	14290.8	10.7	-	-	1	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
P0ADR2	YGDD_ECOLI	14324.6	11.9	-	-	-	-	-	-	-
P0AG44	RL17_ECOLI	14356.7	11.9	1	1	1	1	1	1	-
P0AD35	YFDO_ECOLI	14393.0	7.7	-	-	-	-	-	-	-
P27843	YIGG_ECOLI	14399.5	9.1	-	-	-	-	-	-	-
P09162	YJAA_ECOLI	14438.6	9.9	-	-	-	-	-	-	-
P0AFP2	YBAZ_ECOLI	14441.4	10.0	-	-	1	-	-	-	-
P15068	TRBF_ECOLI	14471.4	8.8	-	-	-	-	-	-	-
P28696	YAAI_ECOLI	14473.4	7.8	-	-	-	-	-	-	-
P37613	YHHK_ECOLI	14497.4	7.0	-	-	1	1	-	-	-
P10026	TRAM1_ECOLI	14499.3	5.2	-	-	-	-	-	-	-
P0ADX1	YHFA_ECOLI	14508.4	5.4	1	-	1	-	-	-	-
P32711	NRFF_ECOLI	14514.6	9.1	-	-	-	-	-	-	-
P28911	YHHH_ECOLI	14522.5	8.0	-	-	-	-	-	-	-
P0AAY1	BSSR_ECOLI	14527.4	6.5	-	-	-	-	-	-	-
P27842	YIGF_ECOLI	14540.7	10.4	-	-	-	-	-	-	-
P76549	YFFR_ECOLI	14545.4	6.1	1	-	-	-	-	-	-
P0AAR0	YBAJ_ECOLI	14549.0	4.8	-	-	-	-	-	-	-
P60632	YOHJ_ECOLI	14570.0	9.7	-	-	-	-	-	-	-
P39332	YJGH_ECOLI	14582.2	4.4	1	-	1	-	-	-	-
Q46755	SIRB2_ECOLI	14630.4	12.4	-	-	-	-	-	-	-
Q46835	YGHG_ECOLI	14661.6	10.1	-	-	-	-	-	-	-
P75874	YCCU_ECOLI	14692.8	7.3	1	1	1	1	1	1	1
Q46864	YGIT_ECOLI	14694.6	9.4	1	-	1	-	-	-	-
P52096	YAER_ECOLI	14728.4	5.0	-	-	1	-	-	-	-
P39375	IRAD_ECOLI	14738.4	6.0	-	-	-	-	-	-	-
P0AAR5	YBAN_ECOLI	14761.2	12.2	-	-	-	-	-	-	-
P45465	YRAN_ECOLI	14789.6	10.6	-	-	-	-	-	-	-
P76084	PAAI_ECOLI	14842.2	6.3	-	-	-	-	-	-	-
P15070	FLIN_ECOLI	14846.6	4.3	-	-	-	-	-	-	-
P0A7X3	RS9_ECOLI	14848.0	12.1	1	1	1	1	1	1	-
P0A7J7	RL11_ECOLI	14866.9	10.2	1	1	1	1	1	1	-
P0AE95	CSGE_ECOLI	14870.6	5.2	-	-	-	-	-	-	-
P19931	HYAE_ECOLI	14881.4	4.3	-	-	1	-	-	-	-
P76002	YCGK_ECOLI	14897.7	10.3	1	1	1	1	-	-	-
P0AC81	LGUL_ECOLI	14911.5	4.8	1	1	1	-	-	-	-
P0AFW4	RNK_ECOLI	14918.6	4.3	1	-	1	-	1	-	-
P08337	MUTT_ECOLI	14918.6	4.9	-	-	1	-	-	-	-
P0AF76	YJFI_ECOLI	14926.5	3.8	-	-	-	-	-	-	-
P77781	YDII_ECOLI	14936.7	7.2	-	-	1	1	-	-	-
P26608	FLIS_ECOLI	14941.7	4.5	-	-	-	-	-	-	-
P0A742	MSCL_ECOLI	14948.2	7.7	-	-	1	1	-	-	-
P0ADW3	YHCB_ECOLI	14952.5	5.6	1	-	1	1	1	1	-
P0A8Y8	YBDB_ECOLI	14961.4	6.2	-	1	-	-	-	-	-
P08370	YGDB_ECOLI	14964.6	6.8	-	-	-	-	-	-	-
P02413	RL15_ECOLI	14972.3	11.9	1	1	1	1	1	1	1
P31063	YEDD_ECOLI	14974.7	4.7	1	-	1	1	1	-	1
P67701	YGJM_ECOLI	14986.8	4.6	-	-	-	-	-	-	-
P0A8Q0	FRDC_ECOLI	15006.2	10.5	-	-	1	-	-	-	-
P77788	NUDG_ECOLI	15037.7	5.0	-	-	-	-	-	-	-
P28307	CSGA_ECOLI	15041.2	4.9	-	-	-	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
P0AE98	CSGF_ECOLI	15047.5	5.5	-	-	-	-	-	-	-
P0AG11	UMUD_ECOLI	15054.8	4.4	-	-	-	-	-	-	-
Q47719	Y4286_ECOLI	15058.5	8.0	-	-	-	-	-	-	-
P0A6E6	ATPE_ECOLI	15059.8	5.4	1	1	1	1	-	-	1
P0C0L2	OSMC_ECOLI	15079.7	5.5	1	1	1	1	-	1	1
P77712	TESC_ECOLI	15079.9	5.2	-	-	1	-	-	-	-
P0A6Z6	NIKR_ECOLI	15085.5	5.8	1	-	1	1	-	-	-
P62768	YAEH_ECOLI	15087.9	7.2	1	1	1	1	-	1	1
P45750	YRFA_ECOLI	15089.7	9.0	-	-	-	-	-	-	-
P64585	YQJE_ECOLI	15138.2	8.0	-	-	1	1	1	-	-
P0A7G2	RBFA_ECOLI	15145.8	5.9	1	1	1	1	1	1	-
P52644	HSLJ_ECOLI	15156.6	7.1	-	-	1	-	-	-	-
P28632	HOLD_ECOLI	15165.8	5.4	-	-	1	-	-	-	-
P06627	TRAY1_ECOLI	15174.9	10.1	-	-	-	-	-	-	-
P0ACH5	MARA_ECOLI	15175.6	10.2	-	-	-	-	-	-	-
P0A8I1	RUVX_ECOLI	15178.0	7.8	1	-	1	-	-	1	-
P0AAA9	ZRAP_ECOLI	15190.3	9.9	1	-	-	-	-	-	-
P0AD47	YPHA_ECOLI	15202.2	10.5	-	-	-	-	-	-	-
P64515	YECN_ECOLI	15216.8	11.0	-	-	1	-	-	-	-
P20343	CYSX_ECOLI	15224.8	11.7	-	-	-	-	-	-	-
P0A9G4	CUER_ECOLI	15226.6	5.7	-	-	1	-	-	-	-
P0ABW9	FLGB_ECOLI	15231.6	4.9	-	-	1	-	1	-	-
P67697	YDCQ_ECOLI	15238.0	4.8	-	-	-	-	-	-	-
P75679	INSN1_ECOLI	15240.8	10.1	-	-	-	-	-	-	-
P0ACY6	YEAL_ECOLI	15246.8	11.5	-	-	-	-	-	-	-
P0ADY7	RL16_ECOLI	15272.5	12.0	1	1	1	1	1	1	-
P04982	RBSD_ECOLI	15283.8	5.9	1	1	1	1	-	-	-
P0A772	NRDI_ECOLI	15331.9	10.5	-	-	-	-	-	-	-
P0ACG1	STPA_ECOLI	15339.0	9.3	1	1	1	1	1	1	-
P0ABV6	TOLR_ECOLI	15374.4	5.3	1	-	1	-	-	-	-
P75684	YAGP_ECOLI	15402.1	9.0	-	-	-	-	-	-	-
P09154	YMFS_ECOLI	15425.6	4.3	-	-	-	-	-	-	-
P0AE58	CAIF_ECOLI	15427.0	9.1	-	-	-	-	-	-	-
P0A746	MSRB_ECOLI	15442.2	5.5	1	1	1	1	-	1	-
P76341	HIUH_ECOLI	15451.1	9.9	1	-	1	-	-	-	-
P0A763	NDK_ECOLI	15454.8	5.5	1	1	1	1	-	1	1
P0AAW5	YBHQ_ECOLI	15455.5	10.8	-	-	-	-	-	-	-
P0AEV7	HYCH_ECOLI	15455.7	5.0	-	-	-	-	-	-	-
P0AEN8	FUCM_ECOLI	15464.2	5.5	1	-	1	-	-	-	-
Q47157	YAFO_ECOLI	15479.0	7.5	-	-	-	-	-	-	-
P0ACG8	HSLR_ECOLI	15487.3	10.6	1	1	1	-	-	-	-
P0ABV2	EXBD_ECOLI	15517.9	4.5	1	-	1	-	-	-	-
P0ACF8	HNS_ECOLI	15531.0	5.3	1	1	1	1	-	1	1
P0AGG4	THIO2_ECOLI	15545.7	4.9	1	1	1	1	-	1	1
Q46795	YGEO_ECOLI	15552.0	8.3	-	-	-	-	-	-	-
P0A8Z3	YBGC_ECOLI	15552.9	7.5	-	-	1	-	-	-	-
P77453	HYFJ_ECOLI	15567.8	4.8	-	-	-	-	-	-	-
P0ADR0	YQAA_ECOLI	15580.3	10.9	-	-	-	-	-	-	-
P0AF63	NSRR_ECOLI	15584.1	8.0	-	-	1	-	-	-	-
P0AG27	YIBN_ECOLI	15587.5	9.9	-	1	1	1	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P0A7C8	PSIE_ECOLI	15587.7	9.0	-	-	-	-	-	-	-
P0A905	SLYB_ECOLI	15593.1	10.0	1	1	1	1	-	-	1
P0AF90	YJGD_ECOLI	15594.1	3.5	-	1	1	1	-	-	-
P36647	PPDD_ECOLI	15612.7	4.5	-	-	-	-	-	-	-
P40711	YAEJ_ECOLI	15614.6	11.8	-	-	-	-	-	-	-
P46888	USPC_ECOLI	15623.9	5.5	-	-	1	1	-	-	-
P39363	SGCA_ECOLI	15629.0	5.1	-	-	1	-	-	-	-
P24251	CRL_ECOLI	15646.0	6.4	-	1	1	1	-	1	-
P0AF48	YJBQ_ECOLI	15646.9	6.6	-	-	1	-	1	-	-
P06966	DICA_ECOLI	15647.4	10.3	-	-	1	1	-	-	-
P0A780	NUSB_ECOLI	15680.3	7.2	1	1	1	1	-	1	1
P0C243	YUBJ_ECOLI	15685.6	4.2	-	-	-	-	-	-	-
P02358	RS6_ECOLI	15694.6	4.8	1	1	1	1	1	1	1
P31446	YIDI_ECOLI	15719.6	9.4	-	-	-	-	-	-	-
P76546	YFFO_ECOLI	15720.0	7.4	-	-	-	-	-	-	-
P76064	YDAT_ECOLI	15734.3	7.6	-	-	-	-	-	-	-
P75988	YCGX_ECOLI	15760.2	9.7	-	-	-	-	-	-	-
P0A7R1	RL9_ECOLI	15760.5	6.2	1	1	1	1	1	1	1
P0C054	IBPA_ECOLI	15765.1	5.5	1	1	1	1	-	-	-
P76194	SUFE_ECOLI	15791.2	5.8	-	-	1	-	-	-	-
P03817	MIOC_ECOLI	15798.9	4.1	1	1	1	1	-	1	-
P71297	YAGN_ECOLI	15806.0	9.7	-	-	-	-	-	-	-
P75680	INSO1_ECOLI	15840.9	10.4	-	-	-	-	-	-	-
P10031	PSIB1_ECOLI	15843.8	4.6	-	-	-	-	-	-	-
P0AB96	ARSC_ECOLI	15844.3	5.3	1	-	1	1	-	-	-
Q9JMT5	YUAE_ECOLI	15844.9	9.9	-	-	-	-	-	-	-
P76111	YDCZ_ECOLI	15845.8	12.2	-	-	-	-	-	-	-
P43533	FLGN_ECOLI	15858.0	6.5	-	-	-	-	-	-	-
P03825	PIOO_ECOLI	15867.0	4.6	-	-	-	-	-	-	-
P0ABK7	CSGB_ECOLI	15873.1	10.5	-	-	-	-	-	-	-
P41442	GSPG_ECOLI	15896.2	5.0	-	-	-	-	-	-	-
P39177	USPG_ECOLI	15926.3	6.0	1	1	1	1	1	-	1
P0AGF2	YGDK_ECOLI	15931.3	6.1	-	-	1	-	-	-	-
P0A6M4	DTD_ECOLI	15941.0	4.6	-	-	1	-	-	-	-
P46856	YRHA_ECOLI	15941.0	4.3	-	-	-	-	-	-	-
Q9S4X0	YUBF_ECOLI	16004.1	4.5	-	-	-	-	-	-	-
P37903	USPF_ECOLI	16007.5	5.6	1	-	1	1	-	1	-
P0AA10	RL13_ECOLI	16009.5	10.7	1	1	1	1	1	1	-
P69824	PTMA_ECOLI	16037.1	4.3	-	1	-	-	1	-	-
P0ADE6	YGAU_ECOLI	16054.3	5.6	1	1	1	1	-	-	1
Q46824	YGFX_ECOLI	16054.5	11.7	-	-	1	-	-	-	-
P27245	MARR_ECOLI	16055.6	8.3	-	-	-	-	-	-	-
P0AED0	USPA_ECOLI	16057.2	5.0	1	1	1	1	1	-	1
P37351	RPIB_ECOLI	16064.3	6.7	-	-	-	-	-	-	-
P0AEM0	FKBX_ECOLI	16071.9	4.1	1	1	1	1	-	1	-
P69432	PGAD_ECOLI	16072.5	10.7	-	-	-	-	-	-	-
P0C058	IBPB_ECOLI	16084.2	5.1	-	1	-	-	-	-	-
P32155	PTFA_ECOLI	16084.3	6.6	-	-	-	-	-	-	-
P0ADJ8	YIAA_ECOLI	16113.3	4.9	-	-	-	-	-	-	-
Q9JMT7	YUAC_ECOLI	16131.1	5.6	-	-	-	-	-	-	-

SwissProt Accession No	**SwissProt entry name**	**molecular weight [Da]**	***pI***	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
P06968	DUT_ECOLI	16146.3	4.9	1	1	1	1	-	-	1
P61714	RISB_ECOLI	16147.6	5.0	1	1	1	1	-	1	1
P16681	PHNB_ECOLI	16161.7	4.9	1	-	1	-	-	-	-
P0ACS5	ZNTR_ECOLI	16170.0	6.0	-	-	1	-	-	-	-
P0AEH8	YJIG_ECOLI	16183.5	7.2	-	-	-	-	-	-	-
P77136	YQEK_ECOLI	16262.3	9.4	-	-	-	-	-	-	-
P65367	YQCA_ECOLI	16265.0	3.8	1	-	1	-	-	-	-
P0AB12	YCCF_ECOLI	16265.9	9.8	-	-	1	1	-	-	-
P0AAB8	USPD_ECOLI	16283.5	6.4	1	-	1	1	1	-	-
P0ABL3	NAPB_ECOLI	16286.9	8.1	1	-	1	-	-	-	-
P76539	YPEA_ECOLI	16302.1	4.7	-	-	1	1	-	-	-
P76180	YDGK_ECOLI	16309.2	12.4	-	-	-	-	-	-	-
P0A8W2	SLYA_ECOLI	16343.9	6.7	1	-	1	1	-	-	-
P52006	NUDI_ECOLI	16361.4	4.8	-	-	1	-	-	-	-
Q9S4W7	YUBI_ECOLI	16369.9	4.7	-	-	-	-	-	-	-
P0ACZ2	ETP_ECOLI	16376.6	10.0	-	-	-	-	-	-	-
P77656	YFDK_ECOLI	16399.0	4.2	-	-	-	-	-	-	-
P77598	YBCV_ECOLI	16404.5	10.0	-	-	-	-	-	-	-
P09163	YJAB_ECOLI	16437.3	4.7	-	-	-	-	-	-	-
P0AFC3	NUOA_ECOLI	16447.6	11.1	-	1	1	1	-	-	-
Q9JMT9	YUAA_ECOLI	16453.4	9.1	-	-	-	-	-	-	-
P77551	RZPR_ECOLI	16476.4	7.8	-	-	-	-	-	-	-
P76156	YDFO_ECOLI	16487.7	10.7	-	-	-	-	-	-	-
Q9S4X4	YUBB_ECOLI	16497.7	4.0	-	-	-	-	-	-	-
P36881	YADI_ECOLI	16530.2	5.9	-	-	-	-	-	-	-
P16685	PHNG_ECOLI	16530.3	6.6	-	-	-	-	-	-	-
P0AF34	YIIR_ECOLI	16531.7	10.5	-	-	-	-	-	-	-
P76000	YCGI_ECOLI	16532.2	10.4	-	-	-	-	-	-	-
P0ADU7	YQIB_ECOLI	16538.2	9.6	-	-	-	-	-	-	-
P76362	YEES_ECOLI	16547.8	8.2	-	-	-	-	-	-	-
P16691	PHNO_ECOLI	16560.3	6.0	-	-	1	-	-	-	-
P33354	YEHR_ECOLI	16584.6	8.6	-	-	-	-	-	-	-
P0A944	RIMI_ECOLI	16600.4	4.7	-	-	1	-	-	-	-
P0ADX7	YHHA_ECOLI	16614.4	11.8	1	-	1	-	1	-	-
P28905	HOLC_ECOLI	16623.5	5.9	-	-	1	-	-	-	-
P46187	RSEC_ECOLI	16629.7	6.8	-	-	-	-	-	-	-
P31468	CBRB_ECOLI	16673.3	8.3	-	-	-	-	-	-	-
P0ABD8	BCCP_ECOLI	16677.4	4.5	1	1	1	1	-	-	1
P76012	YCGY_ECOLI	16685.5	5.3	-	-	-	-	-	-	-
P0AAB2	WZB_ECOLI	16699.4	7.7	-	-	-	-	-	-	-
O52982	YFJS_ECOLI	16725.3	4.7	-	-	-	-	-	-	-
P67762	YHBP_ECOLI	16766.7	9.4	-	1	1	-	1	-	-
P0A9A9	FUR_ECOLI	16785.4	5.7	1	1	1	1	1	1	1
P77365	YAFY_ECOLI	16805.3	4.4	-	-	-	-	-	-	-
P0A8A8	RIMP_ECOLI	16811.6	4.4	-	1	1	-	1	-	-
P45751	YRFB_ECOLI	16836.6	5.6	-	-	-	-	-	-	-
P0AF67	YJEE_ECOLI	16843.4	4.3	1	-	1	1	-	-	-
P0AF96	YJGK_ECOLI	16855.6	5.2	1	1	1	1	-	-	-
P0AD59	IVY_ECOLI	16862.3	6.3	1	-	1	1	1	-	1
P56259	YIFN_ECOLI	16863.8	10.2	-	-	-	-	-	-	-

SwissProt Accession No	**SwissProt entry name**	**molecular weight [Da]**	***pI***	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
Q46786	YGEF_ECOLI	16868.9	9.5	-	-	-	-	-	-	-
P0ACI6	ASNC_ECOLI	16877.9	6.4	-	-	1	-	-	-	-
P62617	ISPF_ECOLI	16887.8	6.1	-	-	1	1	-	-	-
P69828	PTKA_ECOLI	16897.8	5.0	1	1	1	1	-	1	-
P0A731	MGSA_ECOLI	16908.8	6.2	1	1	1	-	1	-	1
Q46801	XDHC_ECOLI	16911.4	6.9	-	-	-	-	-	-	-
P0AAS3	YBBJ_ECOLI	16928.9	8.2	-	-	1	-	-	-	-
P64550	YGAW_ECOLI	16938.7	10.5	-	-	-	-	-	-	-
P0A8D3	YAII_ECOLI	16959.8	5.4	1	-	1	-	1	-	-
P0A9M5	XGPT_ECOLI	16960.8	5.5	1	1	1	1	-	-	-
P30749	MOAE_ECOLI	16971.5	5.1	1	-	1	1	1	1	-
P37052	YCHJ_ECOLI	16980.0	7.0	-	-	1	-	-	-	-
P0A6D0	ARGR_ECOLI	16984.9	4.8	-	-	1	-	-	-	-
P77162	YKFB_ECOLI	17016.0	4.3	-	-	1	-	-	-	-
P0A6Q6	FABZ_ECOLI	17022.9	7.3	-	1	1	1	1	-	1
P45424	YHCH_ECOLI	17027.5	4.8	-	-	1	-	-	-	-
P0ADD2	YJJB_ECOLI	17036.1	11.8	-	-	-	-	-	-	-
P00816	CYNS_ECOLI	17039.1	4.8	-	-	-	-	-	-	-
P0AEV9	HYCI_ECOLI	17046.4	3.9	-	-	1	1	-	-	-
P75916	YCDZ_ECOLI	17064.2	9.6	-	-	-	-	-	-	-
P12994	YBHB_ECOLI	17075.3	5.2	1	-	1	1	1	-	-
P42904	PTPB2_ECOLI	17076.0	5.5	-	-	1	-	-	-	-
P0AAR3	YBAK_ECOLI	17083.2	9.7	1	1	1	1	-	-	-
P52135	YFJT_ECOLI	17089.3	6.3	-	-	-	-	-	-	-
P37664	YIAC_ECOLI	17093.7	6.5	-	-	-	-	1	-	-
P0AE91	CREA_ECOLI	17098.0	9.6	1	1	1	1	-	-	-
P0A7F3	PYRI_ECOLI	17110.9	7.2	-	1	1	-	-	1	1
P0ACS2	SOXR_ECOLI	17140.1	9.5	-	-	-	-	-	-	-
P0ADP2	YIGI_ECOLI	17152.8	6.5	-	-	1	1	-	-	-
P76538	YFEZ_ECOLI	17158.4	10.5	-	-	-	-	-	-	-
P76502	SIXA_ECOLI	17197.6	4.3	-	-	1	1	1	-	-
P0A8D9	YFBV_ECOLI	17203.2	10.8	-	-	-	-	-	-	-
P0ADL3	YICN_ECOLI	17209.1	6.6	-	-	-	-	-	-	-
P0ABX8	FLIL_ECOLI	17211.2	9.8	-	-	-	-	-	-	-
P75719	RZPD_ECOLI	17215.9	9.8	-	-	-	-	-	-	-
P0A8D0	NRDR_ECOLI	17218.8	7.8	1	-	1	1	1	-	-
P36678	GSPM_ECOLI	17224.1	6.1	-	-	-	-	-	-	-
P69820	ULAC_ECOLI	17227.8	4.4	-	-	-	-	-	-	-
P07021	YFIB_ECOLI	17234.7	9.4	-	-	-	-	-	-	-
P0ABA0	ATPF_ECOLI	17254.3	5.9	1	1	1	1	-	-	1
P0AG86	SECB_ECOLI	17267.3	4.1	1	1	1	1	-	1	-
P23898	NLPC_ECOLI	17272.8	10.0	-	-	-	-	-	-	-
P52139	YFJX_ECOLI	17292.9	4.3	-	-	-	-	-	-	-
P0AFC0	NUDB_ECOLI	17295.9	5.8	-	-	1	-	-	-	-
P52613	FLIJ_ECOLI	17296.7	8.7	-	-	1	-	-	-	-
P77219	YAHC_ECOLI	17300.8	8.5	-	-	-	-	-	-	-
P08190	FIMG_ECOLI	17307.6	5.4	-	-	-	-	-	-	-
P0AGK8	ISCR_ECOLI	17326.9	7.2	1	1	1	1	-	1	-
P0A8I8	RLMH_ECOLI	17331.2	9.3	-	-	-	-	-	-	-
P11291	Y3808_ECOLI	17331.7	7.6	-	-	-	-	-	-	-

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P18390	YJJA_ECOLI	17342.8	5.6	1	1	1	1	-	-	-
P0A8R0	RRAA_ECOLI	17350.6	3.9	1	1	1	1	-	-	-
P22186	MRAZ_ECOLI	17375.9	5.3	-	-	1	-	-	-	-
P75962	YMFA_ECOLI	17406.0	10.2	-	-	-	-	-	-	-
P75676	YAFX_ECOLI	17409.1	4.5	-	-	-	-	-	-	-
P0AEH3	ELAA_ECOLI	17409.7	4.6	-	-	1	1	-	-	-
P76394	YEGJ_ECOLI	17417.8	5.3	-	-	-	-	1	-	-
P0AEI6	NUDJ_ECOLI	17422.7	4.9	-	-	1	1	-	-	-
Q47269	YBCN_ECOLI	17422.8	7.2	-	-	-	-	-	-	-
P0ACJ5	YBAO_ECOLI	17427.0	5.6	-	-	1	-	-	-	-
P0A9N8	NRDG_ECOLI	17435.8	7.2	-	-	1	-	-	-	-
P0AC73	EBGC_ECOLI	17446.7	5.4	-	-	-	-	-	-	-
P56256	YSAA_ECOLI	17448.3	7.4	-	-	-	-	-	-	-
P0A738	MOAC_ECOLI	17457.0	6.7	-	-	1	1	1	-	-
Q46819	YGFS_ECOLI	17502.5	5.3	-	-	-	-	-	-	-
P37674	YIAM_ECOLI	17505.5	8.5	-	-	-	-	-	-	-
P42906	AGAA_ECOLI	17508.7	6.6	-	-	-	-	1	-	-
P0A898	YBEY_ECOLI	17515.5	4.1	-	-	1	-	-	-	-
P0ABS1	DKSA_ECOLI	17517.8	4.9	1	1	1	1	-	-	1
P37673	YIAL_ECOLI	17539.1	5.2	-	-	-	-	-	-	-
Q47158	YAFP_ECOLI	17544.9	10.1	-	-	-	-	-	-	-
P0A6G3	YGAD_ECOLI	17571.7	4.9	1	-	1	1	1	1	-
P0A7Y4	RNH_ECOLI	17586.9	8.5	-	-	1	-	-	-	-
P0A7W1	RS5_ECOLI	17593.3	10.8	1	1	1	1	1	1	-
P75980	YMFO_ECOLI	17598.8	8.4	-	-	-	-	-	-	-
P67601	YOBD_ECOLI	17604.9	11.4	-	-	-	-	-	-	-
P0ACC9	WCAB_ECOLI	17605.2	8.8	-	-	-	-	-	-	-
P42909	PTPB1_ECOLI	17612.3	6.4	-	-	1	-	-	-	-
P69789	PTXB_ECOLI	17616.0	5.9	-	-	-	-	-	-	-
P0AEV4	HYCA_ECOLI	17616.9	5.7	-	-	1	-	-	-	-
P0AE52	BCP_ECOLI	17623.7	4.9	1	1	1	1	-	1	1
P0A9F1	MNTR_ECOLI	17630.2	6.4	1	-	1	1	-	-	-
P0A6W5	GREA_ECOLI	17631.1	4.6	1	1	1	1	1	1	1
P76556	EUTP_ECOLI	17648.9	5.0	-	-	-	-	-	-	-
P76062	RACR_ECOLI	17653.2	9.2	-	-	1	-	-	-	-
P0AAY6	YBJN_ECOLI	17655.6	4.0	-	-	-	-	-	-	-
P0AGD1	SODC_ECOLI	17671.0	6.0	1	-	1	-	-	-	1
P0AEU7	SKP_ECOLI	17678.3	10.3	1	1	1	1	1	-	-
P37147	FXSA_ECOLI	17681.5	9.5	-	-	1	-	-	-	-
P0A8N0	YCBG_ECOLI	17683.4	10.2	1	-	1	1	-	-	-
P69490	CCME_ECOLI	17688.2	6.4	-	-	1	-	-	-	-
P65290	YFGH_ECOLI	17694.9	8.6	-	-	-	-	-	-	-
P0A7J3	RL10_ECOLI	17701.4	9.7	1	1	1	1	1	1	1
P0AGJ7	YIBK_ECOLI	17716.0	6.2	-	-	1	-	-	-	-
P0AGL5	YFJG_ECOLI	17716.1	8.9	-	-	1	-	1	-	-
P77184	LOMR_ECOLI	17719.4	4.9	-	-	-	-	-	-	-
P75893	RUTF_ECOLI	17738.6	6.2	-	-	-	-	-	-	-
P37182	HYBD_ECOLI	17740.5	4.5	1	-	1	-	-	-	-
P0AG18	PUR6_ECOLI	17770.2	6.1	-	1	1	-	-	-	1
P33227	STFE_ECOLI	17778.9	5.0	-	-	-	-	-	-	-

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Q46866	YGIV_ECOLI	17817.0	5.2	-	-	-	-	-	-	-
P0A862	TPX_ECOLI	17825.2	4.6	1	1	1	1	-	1	1
P64594	YHAV_ECOLI	17826.1	10.0	-	-	1	-	-	-	-
P0A6I6	COAD_ECOLI	17826.1	6.6	-	-	1	-	-	-	-
P64483	YEAK_ECOLI	17840.4	6.6	1	-	1	1	-	-	-
P33554	PPDA_ECOLI	17854.9	7.8	-	-	-	-	-	-	-
P76500	YFCQ_ECOLI	17879.8	4.5	-	-	-	-	-	-	-
P76501	YFCR_ECOLI	17879.9	4.8	-	-	-	-	-	-	-
P76319	YEDL_ECOLI	17881.1	6.5	-	-	-	-	-	-	-
P76540	EUTK_ECOLI	17882.4	7.3	-	-	-	-	-	-	-
P08550	CVPA_ECOLI	17896.5	5.7	-	-	1	-	-	-	-
P0A8L5	YCGN_ECOLI	17899.4	4.8	-	-	1	1	-	-	-
P69829	PTSN_ECOLI	17949.4	5.5	1	1	1	1	-	-	-
P0AAN1	HYBE_ECOLI	17952.9	5.2	-	-	1	-	-	-	-
P52140	YFJY_ECOLI	17953.5	9.6	-	-	-	-	-	-	-
P78285	LYSD_ECOLI	17961.4	10.2	-	-	-	-	-	-	-
P33355	YEHS_ECOLI	17962.5	9.7	-	-	1	-	-	-	-
P00894	ILVH_ECOLI	17966.7	9.4	-	1	1	-	-	1	-
P76356	YOEA_ECOLI	17970.3	4.7	-	-	-	-	-	-	-
P0ABQ4	DYR_ECOLI	17988.9	4.7	-	-	1	-	-	1	1
P09184	VSR_ECOLI	18005.2	7.2	-	-	1	-	-	-	-
P76613	YPJC_ECOLI	18014.0	6.5	-	-	1	-	-	-	-
P0AAL0	NAPF_ECOLI	18036.4	7.5	-	-	-	-	-	-	-
P32106	YIBG_ECOLI	18068.0	10.1	-	-	-	-	-	-	-
P26281	HPPK_ECOLI	18068.4	5.2	-	-	1	-	-	-	-
P33012	GYRI_ECOLI	18070.8	4.5	1	-	1	1	-	-	-
P0A964	CHEW_ECOLI	18073.6	4.2	-	-	-	-	-	-	-
Q47685	YKFG_ECOLI	18088.6	9.7	-	-	-	-	-	-	-
P04128	FIMA1_ECOLI	18101.2	5.0	1	-	-	-	-	-	-
A5A605	YKFM_ECOLI	18106.7	10.2	-	-	-	-	-	-	-
P76270	YEBR_ECOLI	18111.3	4.5	1	1	1	1	-	1	1
Q9JMS1	YUAT_ECOLI	18121.9	9.0	-	-	-	-	-	-	-
P77294	YDER_ECOLI	18134.3	6.1	-	-	-	-	-	-	-
P23869	PPIB_ECOLI	18142.9	5.4	1	1	1	1	1	1	1
P00804	LSPA_ECOLI	18145.5	9.0	-	-	-	-	-	-	-
P77731	ALLA_ECOLI	18159.1	4.7	-	-	-	-	-	-	-
P23827	ECOT_ECOLI	18181.4	7.0	1	1	1	-	-	-	1
P77754	SPY_ECOLI	18188.3	10.2	1	-	1	-	-	-	-
P39411	YJJX_ECOLI	18202.4	5.7	-	-	1	1	-	-	-
P38052	SFMF_ECOLI	18212.1	4.4	-	-	-	-	-	-	-
P76485	YFBO_ECOLI	18224.8	4.0	-	-	-	-	-	-	-
P0AFX4	RSD_ECOLI	18232.5	5.6	-	-	1	1	-	-	-
P69783	PTGA_ECOLI	18240.7	4.6	1	1	1	1	1	1	1
P76508	YFDL_ECOLI	18241.3	6.9	-	-	-	-	-	-	-
P0AFZ3	SSPB_ECOLI	18252.1	4.2	1	1	1	1	-	-	1
P0AAS0	YLAC_ECOLI	18256.5	7.3	-	-	1	1	-	-	-
P0A832	SSRP_ECOLI	18258.7	10.6	1	1	1	1	-	-	-
P32056	NUDD_ECOLI	18263.2	4.9	-	-	-	-	-	-	-
Q46790	PBL_ECOLI	18266.4	10.2	-	-	-	-	-	-	-
P75737	YBFP_ECOLI	18271.1	8.4	-	-	-	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P76158	RZPQ_ECOLI	18299.4	8.7	-	-	-	-	-	-	-
P31131	YDEJ_ECOLI	18310.3	4.6	1	-	1	-	-	-	-
P0AFW0	RFAH_ECOLI	18329.6	8.9	-	-	1	-	-	-	-
P0A8E7	YAJQ_ECOLI	18333.6	5.9	1	1	1	1	-	1	1
P69425	TATB_ECOLI	18410.6	5.0	-	1	1	-	-	-	1
P0ABW5	SFMA_ECOLI	18464.1	4.2	-	-	-	-	-	-	-
P0ABD3	BFR_ECOLI	18484.3	4.5	1	1	1	1	1	1	-
P0A828	SMG_ECOLI	18499.0	3.9	-	-	-	-	-	-	-
P76080	PAAD_ECOLI	18501.1	5.6	-	-	-	-	-	-	-
P75860	YCBV_ECOLI	18501.4	5.1	-	-	-	-	-	-	-
P0AAZ0	YBJO_ECOLI	18507.0	10.7	-	-	-	-	-	-	-
P30128	GREB_ECOLI	18516.6	8.7	-	-	1	-	1	-	-
P63417	YHBS_ECOLI	18523.3	4.4	1	-	1	1	-	1	1
P41443	GSPH_ECOLI	18554.4	4.4	-	-	-	-	-	-	-
P41069	TRAV_ECOLI	18577.6	9.8	-	-	-	-	-	-	-
P0AFD1	NUOE_ECOLI	18579.2	5.3	1	1	1	1	-	-	1
P21362	YCIF_ECOLI	18586.7	5.4	1	-	1	1	-	1	1
P0A917	OMPX_ECOLI	18591.9	7.2	1	1	-	1	1	-	1
P76471	YFAZ_ECOLI	18599.1	4.6	-	-	-	-	-	-	-
P39337	YJGM_ECOLI	18611.3	5.1	-	-	1	-	-	-	-
P55734	YGAP_ECOLI	18627.9	6.5	-	-	1	-	-	-	-
P67244	YQHA_ECOLI	18629.9	6.6	-	-	-	-	-	-	-
P0AEZ9	MOAB_ECOLI	18654.5	5.7	1	1	1	1	1	1	1
P30176	YBIA_ECOLI	18658.5	10.2	-	-	1	-	-	-	-
P0A9H1	MUG_ECOLI	18662.8	9.8	-	-	1	-	-	1	-
P75855	YCBQ_ECOLI	18669.2	4.1	-	-	-	-	-	-	-
P0ABT2	DPS_ECOLI	18684.7	5.7	1	1	1	1	1	1	1
P76632	YGCK_ECOLI	18690.7	10.3	-	-	-	-	-	-	-
P08189	FIMF_ECOLI	18704.5	7.2	-	-	-	-	-	-	-
P68398	TADA_ECOLI	18706.4	7.4	-	-	1	-	-	-	-
Q46943	YQEJ_ECOLI	18708.5	9.6	-	-	1	-	-	-	-
P0A814	RUVC_ECOLI	18736.0	10.4	-	-	-	-	-	-	-
P76510	YFDN_ECOLI	18755.4	10.8	-	-	1	-	-	-	-
P26602	UBIC_ECOLI	18766.1	8.2	-	-	1	-	-	-	-
P0ABH4	MRED_ECOLI	18776.5	12.2	-	-	-	-	-	-	-
P46854	YHHY_ECOLI	18782.5	7.3	-	-	1	-	1	-	-
P0AAT9	YBEL_ECOLI	18786.4	5.0	1	-	1	1	-	1	-
P0AFZ5	SULA_ECOLI	18790.5	6.7	-	-	-	-	-	-	-
P0A912	PAL_ECOLI	18813.2	6.4	1	1	1	1	-	-	1
P28369	RFH_ECOLI	18823.4	10.2	-	-	-	-	1	-	-
P45470	YHBO_ECOLI	18847.9	5.1	1	-	1	1	-	-	-
P62395	SECM_ECOLI	18868.8	11.3	1	-	1	-	-	-	-
P0A8D6	YMDB_ECOLI	18869.6	5.3	1	-	1	-	-	1	-
P76296	YECT_ECOLI	18874.3	4.5	-	-	-	-	-	-	-
P0ACJ0	LRP_ECOLI	18876.0	9.4	1	1	1	1	1	1	-
P0A9A2	FTNB_ECOLI	18883.3	5.0	-	-	-	-	-	-	-
P0AG55	RL6_ECOLI	18893.2	10.4	1	1	1	1	1	1	-
P31991	YDCD_ECOLI	18895.7	9.3	-	-	-	-	-	-	-
P75859	YCBU_ECOLI	18902.6	4.8	-	-	-	-	-	-	-
P0AB35	YCFJ_ECOLI	18909.7	10.0	-	-	-	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P77789	YDES_ECOLI	18937.7	5.7	-	-	-	-	-	-	-
P76499	YFCP_ECOLI	18940.5	5.2	-	-	1	-	-	-	-
P21363	YCIE_ECOLI	18950.5	4.8	-	-	1	-	1	-	-
P0AE85	CPXP_ECOLI	18954.3	6.4	1	-	1	-	1	-	-
P0A6Q3	FABA_ECOLI	18957.7	6.2	1	1	1	1	1	1	-
P0AGE0	SSB_ECOLI	18964.3	5.3	1	1	1	1	-	1	-
P64548	YFIR_ECOLI	18966.8	7.8	-	-	-	-	-	-	-
P75818	YBJP_ECOLI	18980.5	6.1	1	-	1	1	-	-	1
P76483	YFBM_ECOLI	19007.6	4.7	-	-	-	-	-	-	-
P0AAK4	HYDN_ECOLI	19014.2	7.8	-	-	-	-	-	-	-
P0A8H6	YIHI_ECOLI	19048.7	6.4	-	1	1	1	1	-	-
P33343	YEHD_ECOLI	19049.5	4.6	-	-	1	-	-	-	-
Q9S4X5	YUBA_ECOLI	19055.4	4.9	-	-	-	-	-	-	-
P0A7B8	HSLV_ECOLI	19082.0	6.0	1	1	1	1	-	-	-
Q46787	YGEG_ECOLI	19082.0	4.6	-	-	-	-	-	-	-
P0A6E1	AROL_ECOLI	19139.8	4.6	-	-	1	-	-	-	-
P28247	BICB_ECOLI	19142.1	11.1	-	-	-	-	-	-	-
P0AFH0	OGT_ECOLI	19167.9	8.5	-	-	1	1	-	-	-
P31443	YIDF_ECOLI	19176.3	5.8	-	-	-	-	-	-	-
P45421	YHCE_ECOLI	19181.5	4.7	-	-	-	-	-	-	-
P38392	SIEB_ECOLI	19232.3	10.7	-	-	-	-	-	-	-
P76112	YNCA_ECOLI	19236.6	5.9	-	-	1	-	-	-	-
P0AC51	ZUR_ECOLI	19242.6	6.0	1	-	1	1	-	-	-
P11663	YGGD_ECOLI	19260.6	4.2	-	-	-	-	-	-	-
P47737	X19F_ECOLI	19273.8	10.1	-	-	-	-	-	-	-
P0AB28	YCED_ECOLI	19303.6	4.3	1	1	1	1	-	1	1
P0A6K3	DEF_ECOLI	19317.3	5.1	1	1	1	1	-	-	-
P0ABA4	ATPD_ECOLI	19321.0	4.8	1	1	1	1	1	1	1
P39902	SPRT_ECOLI	19337.2	10.9	-	-	1	-	-	-	-
P32125	MOBB_ECOLI	19352.1	5.2	-	-	1	-	-	-	-
P39264	FIMI_ECOLI	19362.0	10.2	-	-	-	-	-	-	-
P45578	LUXS_ECOLI	19404.6	5.1	1	1	1	1	1	1	1
P18200	PGPA_ECOLI	19406.0	7.5	-	-	-	-	-	-	-
P0A998	FTNA_ECOLI	19412.4	4.6	1	1	1	1	-	1	-
P33596	RECX_ECOLI	19412.9	9.0	-	-	-	-	-	-	-
P77717	YBAY_ECOLI	19420.3	8.8	-	-	1	1	-	-	-
P0A8J2	DNAT_ECOLI	19444.0	5.0	1	-	1	-	-	-	-
P77368	YBCL_ECOLI	19464.8	7.3	1	-	1	-	-	-	-
P23484	FECI_ECOLI	19469.0	5.8	-	-	-	-	-	-	-
P42597	YGJP_ECOLI	19471.2	10.2	-	-	-	-	-	-	-
P39834	YGIL_ECOLI	19482.8	4.9	-	-	-	-	-	-	-
Q9JMR5	YUBH_ECOLI	19498.2	12.1	-	-	-	-	-	-	-
P09129	TRAS1_ECOLI	19505.8	10.6	-	-	-	-	-	-	-
P45570	YBCI_ECOLI	19518.5	11.6	-	-	-	-	-	-	-
P0A8W8	YFBU_ECOLI	19524.5	6.1	-	1	1	1	-	1	1
P0A6D7	AROK_ECOLI	19527.1	5.1	1	1	1	1	1	1	1
P46859	GNTK_ECOLI	19532.0	6.3	-	-	1	-	-	-	-
P46122	YAJI_ECOLI	19549.1	5.2	-	-	1	-	1	-	-
P03830	INSB1_ECOLI	19553.2	11.4	-	-	-	-	-	-	-
P64604	MLAD_ECOLI	19565.2	4.6	-	1	1	1	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P18310	SSBF_ECOLI	19625.0	8.7	-	-	-	-	-	-	-
P76159	LYSQ_ECOLI	19650.9	8.9	-	-	1	-	-	-	-
P64599	YHBT_ECOLI	19660.3	4.9	-	-	-	-	-	-	-
P57998	INSB4_ECOLI	19688.3	11.6	-	-	-	-	-	-	-
P0ABY4	FLAW_ECOLI	19688.5	3.9	1	-	1	-	-	-	-
P0A7A9	IPYR_ECOLI	19692.0	4.9	1	1	1	1	-	1	1
P18035	TRBB_ECOLI	19707.1	8.9	-	-	-	-	1	-	-
P19768	INSJ_ECOLI	19713.8	10.8	-	-	-	-	-	-	-
P77626	YDCN_ECOLI	19719.8	5.7	-	-	-	-	-	-	-
P61949	FLAV_ECOLI	19725.5	4.1	1	1	1	1	-	1	1
Q47302	INSB2_ECOLI	19746.3	11.8	-	-	-	-	-	-	-
P0AEE1	DCRB_ECOLI	19776.1	4.9	1	1	1	1	1	-	1
P37909	YBGD_ECOLI	19826.8	4.3	-	-	-	-	-	-	-
P39404	BGLJ_ECOLI	19837.3	10.0	-	-	-	-	-	-	-
P77288	YFCV_ECOLI	19839.7	4.9	-	-	-	-	-	-	-
P0A901	BLC_ECOLI	19840.1	9.5	-	-	1	-	-	-	-
P69503	APT_ECOLI	19847.7	5.1	-	1	1	1	-	1	1
P45771	YRDD_ECOLI	19858.7	8.1	1	-	1	-	-	-	-
P0AFE0	NUOJ_ECOLI	19862.8	5.4	-	-	1	-	-	-	-
P51024	YAIL_ECOLI	19911.6	9.1	1	1	1	1	1	1	-
P37025	LIGT_ECOLI	19922.5	11.6	-	-	1	-	-	-	-
P39368	YJHQ_ECOLI	19944.9	5.9	-	-	-	-	-	-	-
P0ACD2	WCAF_ECOLI	19950.5	10.0	-	-	-	-	-	-	-
P76321	YEDN_ECOLI	19952.1	5.7	-	-	-	-	-	-	-
P0ABZ4	KDSC_ECOLI	19985.5	4.8	1	1	1	1	-	-	-
P02359	RS7_ECOLI	20007.7	11.3	1	1	1	1	-	1	-
P64596	YRAP_ECOLI	20016.7	9.6	1	1	1	1	1	-	1
Q47152	YAFM_ECOLI	20030.1	10.4	-	-	-	-	-	-	-
P0ACY1	YDJA_ECOLI	20047.1	6.4	1	1	1	1	-	1	1
P0AC98	YAAH_ECOLI	20058.7	8.8	-	-	-	-	-	-	-
P0A9U6	PUUR_ECOLI	20080.2	5.2	-	-	1	-	-	-	-
P77791	MAA_ECOLI	20084.3	6.2	1	-	-	-	-	-	-
P0AAA3	MATB_ECOLI	20100.1	4.5	-	-	-	-	-	-	-
P0A9M2	HPRT_ECOLI	20103.4	4.9	1	1	1	1	-	-	1
P76264	YEBN_ECOLI	20104.7	7.5	-	-	-	-	-	-	-
P37050	YADN_ECOLI	20106.0	5.1	-	-	-	-	-	-	-
P67095	YFCE_ECOLI	20110.4	5.6	1	1	1	1	-	-	1
P0ADV1	LPTA_ECOLI	20115.4	9.7	1	-	1	-	-	-	1
P0A6L9	HSCB_ECOLI	20126.2	4.9	1	1	1	1	-	-	1
P0A6M2	DSBB_ECOLI	20129.6	8.6	-	-	1	-	-	-	-
P77423	HYFH_ECOLI	20147.0	7.9	-	-	-	-	-	-	-
P0AE76	COBU_ECOLI	20152.2	5.2	-	-	1	-	-	-	-
P0A754	KEFF_ECOLI	20158.0	6.1	-	-	1	-	-	-	-
P24252	YBGA_ECOLI	20199.5	11.2	-	-	1	-	-	-	-
P75976	YMFL_ECOLI	20200.2	4.7	-	-	-	-	-	-	-
P76573	YFGI_ECOLI	20219.2	6.2	-	-	1	-	-	-	-
P0A9W9	YRDA_ECOLI	20233.3	5.2	1	-	1	1	-	1	1
P76514	YFDR_ECOLI	20243.1	5.4	-	-	1	-	-	-	-
P03961	ATKC_ECOLI	20255.7	7.7	-	-	-	-	-	-	-
P0A6G5	CITX_ECOLI	20258.7	6.9	-	-	-	-	-	-	-

SwissProt Accession No	**SwissProt entry name**	**molecular weight [Da]**	***pI***	**Mueller *et al.***	**Ishihama *et al.* [9]**	**Iwasaki *et al.* [10]**	**Taoka *et al.* [8]**	**Geveart *et al.* [6]**	**Corbin *et al.* [7]**	**Lopez-Campistrous *et al.* [4]**
P0ABE5	C561_ECOLI	20273.8	11.4	-	-	-	-	-	-	-
P62399	RL5_ECOLI	20289.7	10.2	1	1	1	1	1	1	-
P37018	YADM_ECOLI	20295.2	8.2	-	-	-	-	-	-	-
P75811	YBJK_ECOLI	20295.3	6.4	-	-	-	-	-	-	-
P16432	HYCF_ECOLI	20297.0	6.9	-	-	-	-	-	-	-
P0AFY8	SEQA_ECOLI	20303.5	9.3	1	1	1	1	-	1	-
P76345	C56H_ECOLI	20324.7	11.8	-	-	-	-	-	-	-
P0AB06	YCBK_ECOLI	20342.8	11.6	-	-	-	-	-	-	-
P03012	TNR1_ECOLI	20350.7	10.4	-	-	-	-	-	-	-
P76208	YNIB_ECOLI	20354.8	8.8	-	-	1	-	-	-	-
P0AGE6	YIEF_ECOLI	20363.6	4.9	-	1	1	1	-	-	-
P23862	PRIC_ECOLI	20363.8	10.6	-	-	1	-	-	-	-
P65556	YFCD_ECOLI	20363.9	4.5	1	1	1	1	-	-	1
Q46832	YGHD_ECOLI	20382.8	10.6	-	-	-	-	-	-	-
P37195	DCTR_ECOLI	20395.8	9.1	-	-	1	-	-	-	-
P39187	YTFJ_ECOLI	20408.7	8.7	1	-	1	-	-	-	1
P31062	NOHB_ECOLI	20416.5	4.7	-	-	-	-	-	-	-
P0AFL3	PPIA_ECOLI	20419.4	9.6	1	1	1	1	-	1	-
P0ADI7	YECD_ECOLI	20440.6	5.3	1	1	1	1	-	-	-
P06610	BTUE_ECOLI	20457.4	4.7	-	-	1	1	1	1	1
P71311	YAIS_ECOLI	20474.5	6.3	-	-	-	-	-	-	-
P0AB26	YCEB_ECOLI	20487.7	6.2	-	-	1	-	-	-	-
Q46822	IDI_ECOLI	20496.2	5.9	-	-	1	-	-	-	-
P42603	YGJV_ECOLI	20499.8	10.6	-	-	-	-	-	-	-
P08371	PPDB_ECOLI	20507.6	5.3	-	-	1	-	1	-	-
P39380	KPTA_ECOLI	20517.8	10.0	-	-	1	-	-	-	-
P0AFG0	NUSG_ECOLI	20519.5	6.4	1	1	1	1	1	1	1
P76222	YNJA_ECOLI	20520.8	8.7	-	-	1	-	-	-	-
P13016	AMPD_ECOLI	20524.2	5.2	-	-	1	-	-	-	-
P0AFD6	NUOI_ECOLI	20525.1	5.3	-	-	1	1	-	1	-
P77223	RNFB_ECOLI	20531.0	4.5	-	-	-	-	-	-	-
P0ACR9	MPRA_ECOLI	20551.3	5.8	1	1	1	1	1	1	-
P0A707	IF3_ECOLI	20552.1	10.1	1	1	1	1	1	1	-
P03014	PINE_ECOLI	20560.9	10.6	-	-	-	-	-	-	-
P11865	YHAB_ECOLI	20564.3	6.5	-	-	-	-	-	-	-
Q47140	HCAF_ECOLI	20567.5	6.2	-	-	-	-	-	-	-
P56579	PTHC_ECOLI	20567.7	8.7	-	-	-	-	-	-	-
P75862	YCBW_ECOLI	20576.1	5.1	-	-	-	-	-	-	-
P0A6N4	EFP_ECOLI	20579.4	4.7	1	1	1	1	-	1	1
P63204	GADE_ECOLI	20587.2	10.4	-	-	1	-	-	-	-
P0A7X6	RIMM_ECOLI	20593.3	4.5	1	1	1	1	1	1	1
P0AB10	YMBA_ECOLI	20622.7	5.8	-	-	1	-	1	-	-
P0A805	RRF_ECOLI	20626.9	6.9	1	1	1	1	1	1	1
P13857	RIML_ECOLI	20668.5	5.8	-	-	1	-	-	-	-
P0A8W5	YQGE_ECOLI	20673.8	5.2	-	1	1	1	1	-	1
P0AG03	UBIX_ECOLI	20683.0	6.3	-	-	-	-	-	-	-
P0ABF8	PGSA_ECOLI	20688.1	9.7	-	-	1	-	-	-	-
P0A8U0	SYDP_ECOLI	20696.4	4.8	-	-	1	-	-	-	-
P0ABL1	NRFB_ECOLI	20702.0	6.9	-	-	1	-	-	-	-
P75915	YCDY_ECOLI	20712.1	4.0	-	1	1	1	-	1	-

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P16690	PHNN_ECOLI	20717.7	8.5	-	-	-	-	-	-	-
P75925	C56I_ECOLI	20723.8	9.9	-	-	-	-	-	-	-
P42913	YRAH_ECOLI	20732.4	4.3	-	-	-	-	-	-	-
P0AE08	AHPC_ECOLI	20749.4	4.9	1	1	1	1	1	1	1
P45748	RIMN_ECOLI	20755.7	4.8	1	1	1	1	-	1	1
P0A9I3	GCVR_ECOLI	20756.5	5.3	-	1	1	-	-	-	-
P00903	PABA_ECOLI	20759.6	6.1	-	-	1	-	-	-	-
Q46948	THIJ_ECOLI	20764.9	5.1	-	1	1	1	-	-	1
P77475	YQAB_ECOLI	20767.6	5.5	-	-	1	1	-	-	-
Q46906	YGCP_ECOLI	20774.1	7.6	-	-	-	-	-	-	-
P0A710	ISPZ_ECOLI	20777.4	10.5	-	-	-	-	-	-	-
P0A776	RPPH_ECOLI	20782.6	11.2	-	-	1	-	-	-	-
P64634	YRFC_ECOLI	20784.1	11.6	-	-	1	-	-	-	-
P0AA86	DSBE_ECOLI	20796.9	5.7	-	-	1	-	-	-	-
P63224	GMHA_ECOLI	20802.6	6.0	1	1	1	1	1	1	1
P0A784	ORN_ECOLI	20803.5	4.8	1	1	1	1	-	1	1
P0A8G6	WRBA_ECOLI	20833.4	5.5	1	1	1	1	-	1	1
P0A9K9	SLYD_ECOLI	20840.7	4.7	1	1	1	1	1	-	1
P0AA97	YAEQ_ECOLI	20864.5	4.8	-	-	1	-	-	-	-
P0AGA6	UHPA_ECOLI	20876.9	5.7	-	-	1	-	-	-	-
P0A766	RNFA_ECOLI	20884.5	10.0	-	-	-	-	-	-	-
P76537	YFEY_ECOLI	20885.1	5.1	1	-	1	1	1	-	-
P0AET5	HDED_ECOLI	20890.6	10.3	-	-	1	-	-	-	-
P0A8X2	YCEI_ECOLI	20900.6	5.5	1	1	1	-	-	-	-
P77296	YBET_ECOLI	20902.7	10.3	-	-	-	-	-	-	-
P0AA91	YEAY_ECOLI	20908.8	10.5	-	-	1	-	1	-	-
P0ADA5	YAJG_ECOLI	20937.8	9.4	1	1	1	1	-	-	1
P0A756	KEFG_ECOLI	20945.6	8.3	-	-	1	-	-	-	-
P37194	SLP_ECOLI	20951.7	7.4	-	1	1	1	-	-	1
Q9JMT6	YUAD_ECOLI	20953.6	5.6	-	-	-	-	-	-	-
P76121	YDDH_ECOLI	20954.6	5.6	-	-	-	-	-	-	-
P63020	NFUA_ECOLI	20985.3	4.4	1	1	1	1	-	1	1
P39208	IDNK_ECOLI	20991.7	6.6	-	-	-	-	-	-	-
P0A8B2	YFCN_ECOLI	21001.0	8.5	1	-	1	1	-	-	-
P16686	PHNH_ECOLI	21015.0	5.2	-	-	-	-	-	-	-
P52061	RDGB_ECOLI	21026.9	5.1	1	1	1	1	-	1	-
P0AFV4	SPR_ECOLI	21027.8	11.1	-	-	-	-	-	-	-
P37017	YADL_ECOLI	21034.7	8.6	-	-	1	-	-	-	-
P0AFH8	OSMY_ECOLI	21061.9	6.4	1	1	1	1	1	1	1
P0A7D1	PTH_ECOLI	21070.1	9.6	1	1	1	1	1	1	-
P05100	3MG1_ECOLI	21087.3	6.2	-	-	1	-	-	-	-
P0AC28	YGFA_ECOLI	21092.9	6.3	-	-	-	-	-	-	-
P66817	DIAA_ECOLI	21093.7	5.2	-	-	1	1	-	-	-
P37016	YADK_ECOLI	21099.5	5.8	-	-	-	-	-	-	-
P77460	YBCY_ECOLI	21108.6	6.7	-	-	-	-	-	-	-
P27375	HTRC_ECOLI	21118.8	10.0	-	-	-	-	-	-	-
P76938	YFCM_ECOLI	21133.1	4.6	-	-	1	-	-	-	-
P45799	NUDE_ECOLI	21140.8	4.7	-	1	1	1	-	-	1
P64564	YGGT_ECOLI	21153.9	10.5	-	-	1	-	-	-	-
P52007	YECM_ECOLI	21192.8	5.2	-	-	1	-	-	1	1

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P77790	DDPX_ECOLI	21200.5	4.9	-	-	-	-	-	-	-
P22707	FINO_ECOLI	21209.5	10.3	-	-	-	-	-	-	-
P0AF03	MOG_ECOLI	21210.0	4.8	1	1	1	1	1	-	-
P08322	TRAE1_ECOLI	21212.0	10.0	-	-	-	-	-	-	-
P28697	HTGA_ECOLI	21212.3	9.1	-	-	-	-	-	-	-
P0A8E1	YCFP_ECOLI	21213.7	6.1	1	1	1	1	-	1	1
P0ACB4	HEMG_ECOLI	21213.9	10.6	-	-	1	-	-	-	-
P0A8C4	YGFB_ECOLI	21217.1	4.0	1	1	1	1	-	-	-
P39206	CAIE_ECOLI	21231.8	6.3	-	-	-	-	-	-	-
P38101	EAMB_ECOLI	21235.4	10.9	-	-	-	-	-	-	-
P28248	DCD_ECOLI	21237.0	5.5	-	1	1	1	-	-	-
P80644	SSUE_ECOLI	21241.3	6.4	-	-	-	-	-	-	-
P0AGD3	SODF_ECOLI	21253.5	5.5	1	1	1	1	-	1	1
P37745	RFBC_ECOLI	21257.8	5.4	-	1	1	1	-	1	1
P63228	GMHB_ECOLI	21281.5	4.8	1	1	1	1	-	-	-
P77181	PAAY_ECOLI	21312.1	6.2	-	-	1	1	-	-	-
P77163	TFAR_ECOLI	21324.7	4.3	-	-	-	-	-	-	-
P76155	TFAQ_ECOLI	21325.6	4.3	-	-	-	-	-	-	-
P0ADC1	LPTE_ECOLI	21344.1	9.4	1	-	1	1	-	-	-
P0A8X0	YJGA_ECOLI	21347.3	5.2	1	1	1	1	-	1	-
Q6BF16	DGOA_ECOLI	21378.1	4.8	-	-	-	-	-	-	-
P31061	NOHA_ECOLI	21392.0	5.1	-	-	-	-	-	-	-
P43337	NUDL_ECOLI	21423.3	5.8	-	-	1	-	-	-	-
P33366	YOHD_ECOLI	21431.9	11.7	-	-	-	-	-	-	-
P67143	YHGN_ECOLI	21477.0	10.2	-	-	-	-	-	-	-
P39334	YJGJ_ECOLI	21488.8	6.7	-	-	1	-	-	-	-
P76053	YDAL_ECOLI	21500.1	9.8	-	-	1	-	-	-	-
Q46810	YGFJ_ECOLI	21500.9	5.7	-	-	-	-	-	-	-
P25536	YHDE_ECOLI	21503.2	5.5	1	-	1	-	-	-	1
P10442	RNH2_ECOLI	21513.4	7.6	-	-	1	-	-	-	-
P0A6N8	EFPL_ECOLI	21520.0	4.7	1	-	1	1	-	1	1
P19930	HYAD_ECOLI	21533.8	4.7	-	-	1	-	-	-	-
P0ABY7	FLHC_ECOLI	21553.0	8.1	-	-	-	-	-	-	-
P75894	RUTE_ECOLI	21557.8	5.9	-	-	-	-	-	-	-
P76214	VES_ECOLI	21563.9	8.5	-	-	1	-	-	-	-
P0A8Z7	YQIA_ECOLI	21628.8	4.5	-	-	1	-	-	-	-
P32173	MOBA_ECOLI	21630.0	5.9	-	-	1	-	-	-	-
P75982	YMFQ_ECOLI	21630.6	4.9	-	-	-	-	-	-	-
P60595	HIS5_ECOLI	21639.8	5.2	-	-	1	-	-	1	-
P52627	FLIZ_ECOLI	21645.1	9.5	-	-	-	-	-	-	-
P41407	AZOR_ECOLI	21645.3	4.9	1	1	1	1	-	1	-
P09153	TFAE_ECOLI	21649.6	4.4	-	-	-	-	1	-	-
P37750	WBBJ_ECOLI	21662.5	10.2	-	-	1	-	-	-	-
P0ADX9	RSMD_ECOLI	21665.2	5.9	-	-	1	-	-	-	-
P77736	YAHD_ECOLI	21674.4	5.4	-	-	-	-	-	-	-
P0AD17	YOHC_ECOLI	21677.4	7.3	-	-	-	-	-	-	-
P0A729	YCEF_ECOLI	21678.2	5.9	1	-	1	1	-	1	-
P0AGB6	RPOE_ECOLI	21683.3	5.2	1	1	1	1	1	-	1
P0ADV9	LPTC_ECOLI	21690.2	6.4	-	-	1	-	-	-	-
P37128	NUDK_ECOLI	21736.1	4.7	-	-	1	-	-	-	-

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P27862	YIGZ_ECOLI	21744.2	5.3	-	-	-	-	-	-	-
P32160	YIIQ_ECOLI	21750.3	9.6	1	-	1	-	-	-	-
P37623	ACPT_ECOLI	21755.0	5.4	-	-	-	-	-	-	-
P37001	CRCA_ECOLI	21756.6	6.1	-	-	-	-	-	-	-
P09372	GRPE_ECOLI	21785.2	4.5	1	1	1	1	1	1	1
P0ACT6	UIDR_ECOLI	21786.0	5.6	-	-	1	-	1	-	-
P17446	BETI_ECOLI	21802.4	11.2	-	-	-	-	-	-	-
P0A7I7	RIBA_ECOLI	21823.2	5.5	1	-	1	1	-	-	-
P77170	PINQ_ECOLI	21839.6	10.2	-	-	-	-	-	-	-
P0AAK1	HYCB_ECOLI	21859.7	6.6	-	-	-	-	-	-	-
P0A951	ATDA_ECOLI	21874.1	6.2	-	1	1	-	1	-	-
P0AEY5	MDAB_ECOLI	21878.0	5.8	1	1	1	1	-	-	-
P75685	YKGB_ECOLI	21886.4	5.9	-	-	-	-	-	-	-
P0ADI0	PINR_ECOLI	21895.7	10.4	-	-	-	-	-	-	-
P77285	RNFG_ECOLI	21899.4	6.7	1	-	1	-	-	-	1
P0ACU7	YJDC_ECOLI	21918.0	4.8	-	-	1	1	-	1	-
P41068	TRAP_ECOLI	21948.2	9.5	-	-	-	-	-	-	-
P28915	YBFC_ECOLI	21948.3	9.3	-	-	-	-	-	-	-
P0A7H6	RECR_ECOLI	21949.9	5.0	-	-	1	-	-	-	-
P0AF10	MTLR_ECOLI	21977.3	4.6	-	-	1	-	-	-	-
P0A9H5	BTUR_ECOLI	21986.2	6.1	1	-	1	-	-	-	-
P45581	YCFK_ECOLI	22007.0	5.2	-	-	-	-	-	-	-
P0AGM2	YICG_ECOLI	22035.1	10.4	-	-	-	-	-	-	-
P0A809	RUVA_ECOLI	22072.7	5.7	-	-	1	1	1	-	-
P60723	RL4_ECOLI	22073.9	10.3	1	1	1	1	1	1	-
P76066	YDAW_ECOLI	22108.3	5.9	-	-	-	-	-	-	-
P0AFP0	YADS_ECOLI	22114.0	9.0	-	-	-	-	-	-	-
P0ADP7	YIGP_ECOLI	22139.8	5.8	-	-	1	1	-	-	-
P23481	HYFA_ECOLI	22140.8	6.1	-	-	-	-	-	-	-
P76576	YFGM_ECOLI	22163.4	4.9	1	1	1	1	-	-	1
P60782	PLSY_ECOLI	22179.9	10.3	-	-	1	-	-	-	-
P37665	YIAD_ECOLI	22184.5	10.6	1	1	1	1	-	-	-
P0A9L3	FKBB_ECOLI	22203.5	4.7	1	1	1	-	1	1	1
P0C960	EMTA_ECOLI	22213.5	9.9	-	-	1	1	-	-	-
P45761	GSPJ_ECOLI	22218.4	5.8	-	-	-	-	-	-	-
P60438	RL3_ECOLI	22230.9	10.5	1	1	1	1	-	1	-
P45565	AIS_ECOLI	22243.6	9.6	-	-	-	-	-	-	-
Q47718	INSO2_ECOLI	22251.4	11.5	-	-	-	-	-	-	-
P67430	NEMR_ECOLI	22262.1	6.5	-	-	-	-	-	-	-
P0A955	ALKH_ECOLI	22270.9	5.4	1	1	1	1	-	1	1
Q46897	YGCH_ECOLI	22279.9	10.2	-	-	-	-	-	-	-
P0A6J1	CYSC_ECOLI	22308.5	5.9	-	-	-	-	-	1	-
P0A7C2	LEXA_ECOLI	22344.9	6.3	1	1	1	1	1	-	1
P0AAL6	YDHY_ECOLI	22352.9	7.8	-	-	-	-	-	-	-
P75806	YBJG_ECOLI	22384.9	8.5	-	-	-	-	-	-	-
P0AG34	RHTB_ECOLI	22413.3	12.3	-	-	-	-	-	-	-
P0AG38	RHTC_ECOLI	22460.0	10.9	-	-	-	-	-	-	-
P31469	CBRC_ECOLI	22471.2	4.3	-	-	-	-	-	-	-
P30126	LEUD_ECOLI	22474.3	5.0	-	1	1	-	-	1	1
P61316	LOLA_ECOLI	22484.2	6.4	1	1	1	1	1	1	1

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P0AB38	YCFM_ECOLI	22502.4	6.5	1	1	1	-	-	-	-
P76090	YNBA_ECOLI	22510.2	8.3	-	-	-	-	-	-	-
P25397	TEHB_ECOLI	22517.4	7.2	-	1	1	-	1	1	1
P0A8F0	UPP_ECOLI	22520.0	5.2	1	1	1	1	1	1	1
P0ACA1	YIBF_ECOLI	22531.8	5.0	1	1	1	1	-	-	-
P36662	TORD_ECOLI	22560.4	4.6	-	-	-	-	-	-	-
P37640	YHJB_ECOLI	22590.6	6.4	-	-	-	-	-	-	-
P32680	YJAG_ECOLI	22599.1	4.3	-	1	1	1	-	-	-
P0ABJ3	CYOC_ECOLI	22608.5	6.6	-	-	1	-	-	-	-
P0A6I9	COAE_ECOLI	22608.9	5.8	-	-	1	-	-	-	1
P76014	DHAL_ECOLI	22618.3	5.1	-	1	1	-	-	1	1
P0AC35	TTDB_ECOLI	22665.8	6.2	-	-	-	-	-	-	-
P0A948	RIMJ_ECOLI	22674.4	10.0	-	1	1	-	-	-	-
P0ACZ4	EVGA_ECOLI	22676.8	7.2	-	1	1	-	1	-	1
P24238	YEBB_ECOLI	22690.7	7.9	-	-	-	-	-	-	-
P76491	YFBR_ECOLI	22694.6	5.4	-	-	1	1	-	-	-
P0A8Y3	YIHX_ECOLI	22718.4	5.1	1	-	1	1	-	1	-
P0AAJ1	YNFG_ECOLI	22737.6	5.8	-	-	1	-	-	-	-
P76226	YNJF_ECOLI	22738.2	8.0	-	-	-	-	-	-	-
P06989	HIS2_ECOLI	22742.5	5.1	-	-	1	-	-	1	1
P32712	NRFG_ECOLI	22770.7	9.4	-	-	-	-	-	-	-
P76541	EUTL_ECOLI	22774.5	4.6	-	-	1	-	-	-	-
P07464	THGA_ECOLI	22785.5	6.3	-	-	-	-	-	-	-
P64481	YDJM_ECOLI	22815.0	9.6	-	-	-	-	-	-	-
P0C093	SLMA_ECOLI	22823.1	9.4	-	-	1	1	-	-	-
P0A7Z0	RPIA_ECOLI	22847.0	5.1	1	1	1	1	1	1	1
P18776	DMSB_ECOLI	22854.7	6.2	1	-	1	1	-	-	-
P0A9D2	GST_ECOLI	22854.8	5.8	1	-	1	1	1	1	-
P76547	YFFP_ECOLI	22893.2	5.3	-	-	-	-	-	-	-
P0A915	OMPW_ECOLI	22914.3	6.1	-	-	1	1	-	-	1
P09549	DEDD_ECOLI	22925.3	9.1	-	-	1	1	-	-	-
P25746	HFLD_ECOLI	22934.2	10.0	-	-	1	-	-	-	-
P32668	YIJF_ECOLI	22941.8	9.7	-	-	-	-	-	-	-
P76459	ATOA_ECOLI	22945.7	5.6	-	-	-	-	-	-	-
P20605	FIC_ECOLI	22946.5	5.0	-	-	1	-	1	-	-
P21515	ACPH_ECOLI	22947.4	5.9	-	-	-	-	-	-	-
P0AAA1	YAGU_ECOLI	22953.0	6.6	-	-	1	-	-	-	-
P76520	YFDX_ECOLI	22963.8	5.2	-	-	1	-	-	-	-
P0ABU5	ELBB_ECOLI	22967.8	4.5	-	1	1	1	-	1	-
P30866	YAFE_ECOLI	22977.7	5.7	-	-	-	-	1	-	-
P0ADH5	FIMB_ECOLI	22980.0	11.2	-	-	-	-	-	-	-
P78055	FSAA_ECOLI	22983.2	5.9	-	-	-	-	-	-	-
P77625	YFBT_ECOLI	22994.1	5.7	-	-	1	1	-	-	-
P30137	THIE_ECOLI	23002.1	5.4	-	1	1	-	-	1	1
P43340	YCAK_ECOLI	23022.3	5.1	1	-	1	-	-	-	-
P33931	CCMA_ECOLI	23040.0	6.8	-	-	1	-	-	-	-
P0ADT8	YGIM_ECOLI	23063.2	9.8	1	1	1	1	-	-	-
P76657	YQIJ_ECOLI	23073.1	5.7	-	-	-	-	-	-	-
P00448	SODM_ECOLI	23083.7	6.5	1	1	1	1	-	1	1
P0ABL5	NAPC_ECOLI	23086.3	8.7	-	-	1	-	-	-	-

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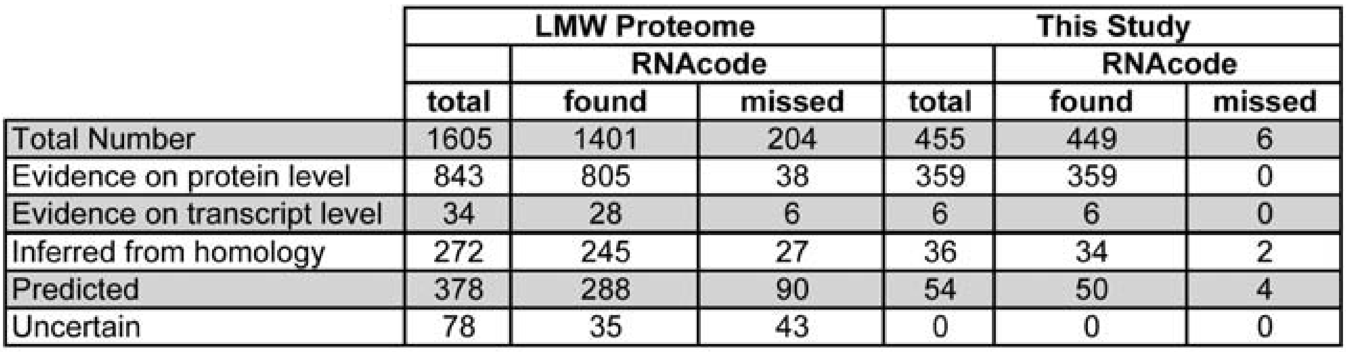
P21367	YCAC_ECOLI	23086.8	5.1	1	-	1	1	-	-	-
P0AEG4	DSBA_ECOLI	23090.7	5.9	1	1	1	1	1	1	1
P0ADH7	FIME_ECOLI	23102.9	11.1	-	-	-	-	-	-	-
P32167	YIIX_ECOLI	23126.1	10.3	-	-	-	-	-	-	-
P11667	ARGO_ECOLI	23161.3	10.4	-	-	-	-	-	-	-
P0A6G7	CLPP_ECOLI	23172.6	5.5	1	1	1	1	1	-	1
P45469	YRAR_ECOLI	23184.0	8.9	-	-	1	-	-	-	1
P76249	LEUE_ECOLI	23186.6	10.6	-	-	-	-	-	-	-
P0AFR4	YCIO_ECOLI	23198.0	5.9	1	1	1	1	-	1	1
P0AFV2	YHID_ECOLI	23199.3	6.7	-	-	1	-	-	-	-
P39362	SGCE_ECOLI	23200.7	5.9	-	-	-	-	-	-	-
Q46890	YGBL_ECOLI	23208.8	5.5	-	-	-	-	-	-	-
P08179	PUR3_ECOLI	23224.8	5.5	-	1	1	1	-	-	-
P31547	METI_ECOLI	23241.9	12.1	-	-	1	-	-	-	-
P0A7A5	PIMT_ECOLI	23244.3	6.6	1	-	1	1	-	-	-
P71301	MATA_ECOLI	23260.1	10.2	-	-	1	-	-	-	-
P52086	COBC_ECOLI	23294.7	5.8	-	-	-	-	-	-	-
P0A744	MSRA_ECOLI	23301.1	4.9	1	-	1	-	-	1	1
P76117	YNCG_ECOLI	23306.9	4.6	-	-	-	-	-	-	-
P0C0R7	RLME_ECOLI	23321.1	10.1	-	1	1	1	1	-	-
P69853	DMSD_ECOLI	23330.8	4.8	-	-	1	-	-	-	-
P39295	YJFM_ECOLI	23338.1	10.2	-	-	1	-	-	-	-
P0A7J0	RIBB_ECOLI	23339.5	4.8	-	1	1	-	-	1	1
P0AEW1	HYFE_ECOLI	23346.8	9.6	-	-	-	-	-	-	-
P75952	YCFQ_ECOLI	23347.6	6.6	-	-	1	-	-	-	-
P21369	PNCA_ECOLI	23348.3	4.5	1	-	1	-	-	-	-
P0AAC6	YCCA_ECOLI	23348.4	9.7	-	-	-	-	-	-	-
P64588	YQJI_ECOLI	23387.6	6.3	-	1	1	-	-	1	-
Q46791	YGEK_ECOLI	23412.2	8.9	-	-	-	-	-	-	-
P0A6U5	RSMG_ECOLI	23417.4	6.1	-	1	1	1	1	-	-
P18473	TRBC_ECOLI	23419.1	9.3	-	-	-	-	-	-	-
P39270	YJDF_ECOLI	23427.5	9.2	-	-	-	-	-	-	-
P0AFU8	RISA_ECOLI	23431.0	5.6	1	1	1	1	1	1	1
P37678	SGBH_ECOLI	23431.1	5.2	-	-	1	-	-	-	-
P23331	KITH_ECOLI	23442.7	6.0	-	1	1	-	-	-	-
P0A7V8	RS4_ECOLI	23455.6	10.9	1	1	1	1	-	1	-
P0ADT2	YGIB_ECOLI	23465.2	10.0	-	-	1	-	-	-	-
P39310	YTFB_ECOLI	23491.9	4.9	1	-	1	-	-	-	-
P69405	RCSA_ECOLI	23502.3	9.8	-	-	-	-	-	-	-
P75933	FLGA_ECOLI	23505.5	11.0	-	-	-	-	-	-	-
P25743	YCHE_ECOLI	23506.8	10.4	-	-	-	-	1	-	-
P30014	RNT_ECOLI	23508.6	5.1	-	-	1	1	-	-	1
P76458	ATOD_ECOLI	23512.4	5.0	-	-	-	-	-	-	-
P61320	LOLB_ECOLI	23537.0	9.7	1	1	1	1	1	-	1
P32669	FSAB_ECOLI	23541.4	4.9	-	-	-	-	-	-	-
P0A6P7	ENGB_ECOLI	23547.2	7.8	1	1	1	1	1	-	-
P0AB83	END3_ECOLI	23548.4	8.2	-	-	1	-	-	-	-
P77366	PGMB_ECOLI	23551.3	5.2	-	-	-	-	-	-	-
P0A7E3	PYRE_ECOLI	23553.2	5.2	-	1	1	1	-	-	-
P31802	NARP_ECOLI	23561.4	4.7	-	-	1	1	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P75936	FLGD_ECOLI	23561.8	4.0	-	-	-	-	-	-	1
P39304	ULAD_ECOLI	23564.1	4.9	-	-	1	-	1	-	-
P69441	KAD_ECOLI	23572.3	5.4	1	1	1	1	1	1	1
P60546	KGUA_ECOLI	23579.0	6.1	1	1	1	1	-	-	-
P19925	ENTD_ECOLI	23590.0	5.8	-	-	-	-	-	-	-
P0AEY1	MARC_ECOLI	23602.6	8.8	-	-	1	-	-	-	-
P0ABL8	CCMB_ECOLI	23604.3	8.0	-	-	-	-	-	-	-
P0ADA1	TESA_ECOLI	23608.2	8.0	1	1	1	-	-	1	-
P18472	TRAW_ECOLI	23616.3	9.4	-	-	-	-	1	-	-
P0ACJ8	CRP_ECOLI	23626.4	8.5	1	1	1	1	1	1	-
Q9JMS0	YUAU_ECOLI	23642.7	5.0	-	-	-	-	-	-	-
P0AEL8	FIMZ_ECOLI	23649.5	9.3	-	-	-	-	-	-	-
Q93K97	ADPP_ECOLI	23653.1	4.8	-	1	1	-	-	-	-
P69407	RCSB_ECOLI	23656.8	7.8	1	1	1	1	-	1	-
P33218	YEBE_ECOLI	23673.4	5.2	1	-	1	1	-	-	-
P0ACU2	RUTR_ECOLI	23673.6	9.6	-	-	1	-	-	-	-
P60844	AQPZ_ECOLI	23688.6	7.4	-	-	-	-	-	-	-
P76004	YCGM_ECOLI	23697.1	5.9	-	-	1	1	1	-	-
P0ACA7	YLIJ_ECOLI	23699.2	4.9	1	1	1	1	1	1	-
P31450	GLVG_ECOLI	23709.1	9.7	-	-	-	-	-	-	-
P32687	YJBF_ECOLI	23741.0	4.8	-	-	-	-	-	-	-
P0ABE9	CYNT_ECOLI	23750.1	7.2	-	-	-	-	-	-	-
P76466	YFAT_ECOLI	23752.8	8.7	-	-	-	-	-	-	-
P0AB87	FUCA_ECOLI	23761.3	6.1	-	-	1	-	-	-	-
Q47154	MBHA_ECOLI	23765.2	7.8	-	-	-	-	-	-	-
P0A720	KTHY_ECOLI	23769.5	5.2	1	1	1	1	-	-	-
P75849	YCBL_ECOLI	23770.0	4.8	1	1	1	1	1	1	1
P0ADI9	YHHN_ECOLI	23775.7	10.9	-	-	1	-	-	-	-
P39379	YJIH_ECOLI	23779.5	5.0	-	-	1	-	-	-	-
P67153	YQFA_ECOLI	23832.1	10.2	-	-	-	-	-	-	-
P60720	LIPB_ECOLI	23868.3	5.8	-	-	1	1	-	-	-
P0AED5	UVRY_ECOLI	23878.4	6.6	1	-	1	1	-	-	-
P38489	NFNB_ECOLI	23891.2	5.8	1	1	1	1	1	1	1
P0AF28	NARL_ECOLI	23912.7	5.7	1	1	1	1	1	1	-
P77174	YBDM_ECOLI	23929.3	8.2	-	-	-	-	-	-	-
P0AAV4	YBGJ_ECOLI	23932.5	5.0	1	-	1	-	-	-	-
P0ADV7	MLAC_ECOLI	23948.5	10.2	1	-	1	-	-	-	1
P0A9H9	CHEZ_ECOLI	23962.0	4.3	-	-	-	-	-	-	-
P76909	YNJD_ECOLI	24002.6	5.7	-	-	1	-	-	-	-
P0A7A2	GPMB_ECOLI	24051.3	5.4	-	-	1	1	1	1	-
P76343	YEDZ_ECOLI	24053.8	12.4	-	-	1	-	-	-	-
P0A761	NANE_ECOLI	24059.5	4.7	-	1	1	-	-	-	-
P05050	ALKB_ECOLI	24061.2	7.9	-	-	1	-	-	-	-
Q9JMT4	YUAF_ECOLI	24066.6	9.8	-	-	-	-	-	-	-
P0AGC7	SMP_ECOLI	24068.9	9.4	-	-	-	-	-	-	-
P76220	YDJY_ECOLI	24111.0	6.2	-	-	1	-	-	-	-
P0AA60	YGHB_ECOLI	24119.0	10.2	-	-	-	-	-	-	-
P13000	BIOD_ECOLI	24125.4	5.5	-	1	-	-	-	1	1
P75869	SXY_ECOLI	24132.6	9.6	-	-	-	-	-	-	-
P0ADM6	YIDX_ECOLI	24155.2	8.9	-	-	1	-	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	*pI*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P29217	YCEH_ECOLI	24163.2	4.9	-	1	1	1	1	1	-
P76396	YEGL_ECOLI	24203.4	5.0	-	-	1	-	-	-	-
P27832	RFFC_ECOLI	24206.4	7.2	-	-	-	-	-	-	-
P75884	GFCB_ECOLI	24253.3	6.4	-	-	-	-	-	-	-
Q46941	YQEH_ECOLI	24271.8	7.1	-	-	-	-	-	-	-
P0ACA3	SSPA_ECOLI	24290.4	5.1	-	1	1	1	1	1	1
P0AFX7	RSEA_ECOLI	24307.0	5.0	-	-	1	-	1	-	-
P77544	YFCF_ECOLI	24311.5	5.2	-	-	1	-	-	-	-
P77247	YNIC_ECOLI	24315.7	4.6	1	1	1	-	1	-	-
P77165	YAGT_ECOLI	24328.1	5.5	-	-	1	-	-	-	-
P64610	YRBL_ECOLI	24330.6	8.9	-	-	1	-	-	-	-
P0AC59	GLRX2_ECOLI	24335.7	8.2	1	1	1	1	1	1	-
P0A8F4	URK_ECOLI	24338.6	6.4	-	1	1	1	1	-	1
P0AF12	MTNN_ECOLI	24339.6	5.0	1	1	1	1	-	1	1
P0AEQ6	GLNP_ECOLI	24349.6	11.5	-	-	1	-	-	-	-
P76280	YOBB_ECOLI	24380.4	8.9	-	-	-	-	-	-	-
P0ACU5	FABR_ECOLI	24389.6	10.2	-	-	-	1	-	-	-
P77564	YDHW_ECOLI	24405.8	4.4	-	-	-	-	-	-	-
P64451	YDCL_ECOLI	24412.5	8.8	1	-	1	1	1	-	-
P0AD42	YFHB_ECOLI	24424.8	9.8	-	-	1	-	-	-	-
P0A9R7	FTSE_ECOLI	24424.9	10.0	1	-	1	1	-	-	-
P77179	RNFE_ECOLI	24444.2	8.5	-	-	-	-	-	-	-
P0AD19	YOHK_ECOLI	24454.3	10.0	-	-	-	-	-	-	-
P77657	YAGK_ECOLI	24456.2	7.5	-	-	-	-	-	-	-
P0ABP6	DEDA_ECOLI	24495.3	9.4	-	-	1	-	-	-	-
P77526	YFCG_ECOLI	24501.6	6.5	-	-	1	-	1	-	-
P77188	MATC_ECOLI	24502.7	10.1	-	-	-	-	-	-	-
P0A752	NADD_ECOLI	24513.6	5.4	-	-	1	-	-	-	-
P0A9T8	YBBA_ECOLI	24518.8	5.4	-	-	1	-	-	-	-
P0AG07	RPE_ECOLI	24539.7	5.0	1	1	1	1	-	1	1
P52125	YFJJ_ECOLI	24546.3	10.1	-	-	-	-	-	-	-
P0AAK7	NRFC_ECOLI	24552.2	8.5	-	-	1	-	-	-	-
P0A7C6	PEPE_ECOLI	24556.0	5.6	-	-	1	1	1	-	-
P0AA63	YQJA_ECOLI	24570.3	10.6	-	-	-	-	-	-	-
P0A8X4	YCCT_ECOLI	24579.9	5.2	-	-	-	-	-	-	-
P39333	YJGI_ECOLI	24583.6	6.6	-	-	-	-	-	-	-
P0AEL0	FDOI_ECOLI	24591.1	11.4	-	1	1	-	-	-	-
P37003	YBFG_ECOLI	24598.1	4.3	-	-	-	-	-	-	-
Q46831	YQGA_ECOLI	24598.5	9.2	-	-	-	-	-	-	-
P0A6S0	FLGH_ECOLI	24601.4	8.8	-	-	-	-	-	-	-
P52094	HISQ_ECOLI	24634.3	9.9	-	-	-	-	-	-	-
P31467	YIEH_ECOLI	24649.2	5.0	-	-	-	-	-	-	-
P68739	NFI_ECOLI	24657.9	8.5	1	-	1	-	1	-	-
P52076	QSEB_ECOLI	24663.1	6.6	-	-	1	-	-	-	-
P16679	PHNL_ECOLI	24691.2	9.5	-	-	-	-	-	-	-
P0A7L0	RL1_ECOLI	24715.3	10.2	1	1	1	1	1	1	1
P0A6I0	KCY_ECOLI	24732.1	5.5	1	1	1	1	1	1	1
P76344	YODA_ECOLI	24747.1	5.9	-	1	-	-	-	1	-
P0ACS9	ACRR_ECOLI	24751.7	5.6	-	-	1	-	1	-	-
P18196	MINC_ECOLI	24760.9	6.4	-	1	1	1	-	-	-

SwissProt Accession No	SwissProt entry name	molecular weight [Da]	p*I*	Mueller *et al.*	Ishihama *et al.* [9]	Iwasaki *et al.* [10]	Taoka *et al.* [8]	Geveart *et al.* [6]	Corbin *et al.* [7]	Lopez-Campistrous *et al.* [4]
P39220	YABP_ECOLI	24775.8	10.0	-	-	-	-	-	-	-
P0AFT2	YECS_ECOLI	24786.2	10.5	-	-	1	-	-	-	-
P75693	YAHN_ECOLI	24796.2	12.0	-	-	-	-	-	-	-
P0A6T5	GCH1_ECOLI	24815.9	6.9	1	1	1	1	-	1	-
P76561	YPFH_ECOLI	24840.5	4.6	-	-	1	1	1	-	-
P0AA37	RLUA_ECOLI	24845.7	8.3	-	-	1	-	-	-	-
P75966	RLUE_ECOLI	24866.0	11.1	-	-	1	-	-	-	-
P69506	RCMNS_ECOLI	24867.6	5.1	-	-	1	-	-	-	-
P45422	YHCF_ECOLI	24885.7	8.9	-	-	-	-	-	-	-
P0AE30	ARTM_ECOLI	24898.5	9.9	-	-	-	-	-	-	-
P0AER5	GLTK_ECOLI	24899.4	10.7	-	-	1	-	-	-	-
P0AE28	AROM_ECOLI	24902.2	4.7	-	-	1	-	-	-	-
P0AAL3	NAPG_ECOLI	24909.4	7.8	-	-	1	-	-	-	-
P75697	YAIX_ECOLI	24917.3	8.1	-	-	-	-	-	-	-
P52106	CSGD_ECOLI	24921.0	10.0	-	-	1	-	-	-	-
P0AF01	MODB_ECOLI	24923.7	11.4	-	-	-	-	-	-	-
P25960	LEP4_ECOLI	24941.3	7.6	-	-	-	-	-	-	-
P76318	YEDK_ECOLI	24964.5	5.1	-	-	1	-	-	-	-
P0A6E9	BIOD2_ECOLI	24966.4	6.1	-	-	1	-	-	-	-
P37338	YGAE_ECOLI	24975.9	6.2	-	-	1	-	-	-	-
P31548	THIQ_ECOLI	24984.1	9.6	-	-	1	-	-	-	-
P39293	YJFK_ECOLI	24994.3	4.4	-	-	-	-	-	-	-

Table S6: Protein evaluation by RNAcode Summary of protein evidence according to SwissProt database and RNAcode support for all LMW proteins listed in the SwissProt database as well as the proteins identified in this study.



	LMW Proteome			This Study		
		RNAcode			RNAcode	
	total	**found**	**missed**	**total**	**found**	**missed**
Total Number	1605	1401	204	455	449	6
Evidence on protein level	843	805	38	359	359	0
Evidence on transcript level	34	28	6	6	6	0
Inferred from homology	272	245	27	36	34	2
Predicted	378	288	90	54	50	4
Uncertain	78	35	43	0	0	0