

GlpG	86	FAALRRERAGPVTVMMIACVVVFIAM-----QILGDQE	VMLWLAWPF---DPTLKFEFWRYFTHALMHFSLMHILFNLLWWWYLGAV	165
RhoI	99	QHW-----PWFILVISIIEIAIFAYDRYT---MPAQNFGLPVP	SDSVLYVRP---DR---RLQVWRFFSYMFILHANFHLGFNIIVQLFGIPL	180
AnoI	128	MKLWPP-----PLMMIIFSIMEIIFFFVIDIVK---TQDQNGTSTSGP	MATLFIYNP---HL---RHEVWRFLTYMFVHIGFMIHLGNLLVQIFIGVAL	211
RHBDL2	65	---ANCFP---PPVFIISISLAELAVFIYYAVW---KPQKQWITLDTGI	LESPFIYSNP---EK---REEAWRFISYMLVHAGVGHILGNLCMQLRIGIPL	150
ToxI	56	HFSLSKS-----VLLAISVDWIFIVYTVCL---DTLPLIPAANI	LVHFGANYP---PLIKQGGVWRLLFVPLHANFHFVFNVFFQLRMGFTT	139
FallI	49	HFTWKS-----FMVVISI IQLVFIISVSI---KPADFLTSPDSL	LVLTGANVA---SRKQGGIHRPILIPILFIHANIFIHAFNIFPQLRMGFTL	132
aaRA	18	LGATAL-----TLTLVLLNIAVVFYQVIF---ASPLDSR	ESNLILFGANIYQLSLTGDWRRYLPISMMILHSGNTHLAFNLCMLVYIGC	98
ML1171	31	RRL-----RMMVGGVTILTFFVALLYVELI---DQLTRHS	LDNNGIRLL---K---TDVLWGISFAPVILHANWQHLVANTIPLLVIGFLI	106
MAV1554	16	-----STAVAGATTITFFVALLYVELI---DQLTRHA	LDVNGIRPQ---R---LDGLWGLIFAPVILHESWQHLMANTIPLLVIGFLM	90
Rv1337	33	-----PRWVVGTTILTFFVALLYVELI---DQLSGSR	LDVNGIRPL---K---TDGLWGVIFAPVILHANWHLMANTIPLLVIGFLM	107
MMAR4059	14	---RP---RMVTGGATITITFFVALLYVELI---DQLTRHS	LDLNGIRPL---Q---TDGLWGIIFAPVILHANWALMANTIPLLVIGFLM	89
MAB1481	21	---GRP---QWVTGGVLVASFVALLYVVEG---I---DSVTGHR	LDENGIRPL---E---TDGLDGLIFAPVILHANWGLHVANTVPALVIGF-L	96
MSMEG4904	39	---SP---AWKTGGTITLTFFVALLYVVELI---A---DQLSGGR	LDENGIRPL---E---TDGLWGLVFAPVILHANWEHVANTVPALVIGFLV	114
Mflv2355	17	---PVMVVGVTVVVSFVLLWLIEL---FDTLTGHR	LDNNGIRPL---E---TDGLTGLVIVAPVILHANWELHANTGPAVIGFLM	91
Mjls3833	19	-----PAWIVGGATTIVSFVLLYVIELV---DSLTGHR	LDENGIRPL---E---TDGLWGI VFSPLIHADWQHLANTGPAVIGFLM	93
Mvan4290	16	---RP---AAMVGGTLVLSFVLLWVIEL---F---DSLTGHR	LDENGIRPL---E---TDGLAGLIFAPVILHNSWEHLANTVPALVIGFLM	91
MAB0026	58	---VKPLQQRAW---ITWALIIVNNLVYTATV---SDGVGGDVTVGSQL	FRELVIYLP---WVA---QGELWRTVTTGFLHGLMILTAVNMLSLAMIGPL	144
Mflv1071	64	---LTP---VVTYIALIGNLLAFAL---QMASPGL	QRAFGLWSP---AVA---DGEMYRLLTSAFILHFLGLTLAFNMLALYFVGPPL	136
Mvan5753	74	---STTP---VVTYIALIGNLLMFAL---QMASPDL	DRAGLWLP---AAA---DGELYRLLTSAFILHFSVTHLAFNMLALYFVGPPL	147
MSMEG5036	80	---GAP---VLTYTTLIAVNVLMFVL---QIAGGDL	ESRLTLWPP---ALALHDEYYRLVTSMFILHYGAMHLFFNMWALYVVGPP	153
Mjls5529	73	---SKP---VVTYALIAVNVLVFLM---QTTSGQL	EREFVLWTP---GVA---DGEWYRLATSAFILHYGAMHLFFNMWALYVVGPP	145
Rv0110	34	---ATP---VVTYTLISNLAVFVM---QVTVMGL	ERQALWPP---AVA---SQGTLYRLVTSAFILHYGAMHLNMLWALYVVGPP	106
MMAR0300	69	---VTP---VVTFSLIAVSVLVFVL---QLVVAGL	GPHLALWPP---AVA---DGQLYRLVTSAFILHYGTLHLVFNMMWALYIVGPPL	141
MUL4822	34	---VTP---VVTFSLIAVSVLVFVL---QLVVGHR	GPHLALWPP---AVA---DGQLYRLVTSAFILHYGRLHLVFNMMWALYVVGPP	106
Consensus			..*.*.*.*	

GlpG	166	EKRLGSGKLIVITLISALLSGYVQ-----QKFSGPWF-----	GLISGVVYALMGYVWLGRGERD---PQ---SGIYLRQLRIIFALIWIIVAGWF	242
RhoI	181	EVMHGTARIGVIYAGVFAVAGSLGT---SVVDSEVFL	VGASGGVYALLAAHANITLNYAHMK---SASTQLGSVVFIVSCDLGYALY	261
AnoI	212	ELVHCWNRVALVYLAGVFAVAGSMGT---SLFTPRVFL	ACASGGVALITAHATITIMNWKQME---YAIQLGFVLVFCVTDLGVSIY	292
RHBDL2	151	EMVHGKLRVGLVLYAGVIAAGSLAS---SIFDPLRYL	VGASGGVYALMGGYFMNVLVNQPEMIPAFGIFRLLIILIIVLDMGFALY	223
ToxI	140	ERRYGLLKFTFGLFYASAYIENLLS---ATAFFCSNLSK	VGASTAGFGLIGQICEMALTWHMRM---HRDRMLTNMVSFVLMLVLMFT	231
FallI	133	EKNYGMIMKIILYFVTGMYGNILS---SSITYCPIK	VGASTSGMLVGI VTSSELILLWHIIR---HRERVVFNIIFFSLISFFYYFT	213
aaRA	99	ERAYGKFKLLATYIISGIGALFSAYWQYYEISNSDLWT---DSTVYITIG	VGASGAIMGIAAASVIYLIKVVINKP---NPHPVIQRRQKYQLYNIAMIYA	194
ML1171	107	ALA-GLSRFIVWTAMVWIFGGSAT---WLIGNMGSSF---GPTDH	IGVSLIFGWLAFLLVFGGLFV---RR---GWDI-IGCMVGLVGLVGLLVGM	188
MAV1554	91	TLA-GLARFVWATV I I W I V G G F G T---WLIGNVSGSS---GPTDH	IGASGLIFGWLAFLLVFGGFV---RR---VRDIIIGLAVMFAYGGVLLGAM	173
Rv1337	108	TLA-GLSRFVWATAIWIWLGGLGT---WLIGNVSGSS---GPTDH	IGASGLIFGWLAFLLVFGGLFV---RK---GWDIVIGLVVLFVYGGILLGAM	190
MMAR4059	90	TLA-GLARFVWATAIWIWLGGLGT---WLIGNVSGSS---GPTDH	IGASGLIFGWLAFLLVFGGLFV---RK---VWDIIGLAVLFFYGGILLGAL	172
MAB1481	97	AAAAGVGRFLLATAI I W I L L G G V G T---WLIGNIGLPY---ETNH	IGASGLIFGWLTVIIVVGFEN---RS---VQQLIGLAVLVLYGCVLLWGLV	179
MSMEG4904	115	TLA-GLARFVWATAIWIWLGGLGT---WLIGDVGGCP---LPTNH	IGASGLIFGWLTFLLVFGWFT---RN---AWQIVVGVILVLLVYGGILWGA	197
Mflv2355	92	TLA-GLSRFIFATAI I W I F A G G L G T---WLIGNVGAPT---YNGVIVETNH	IGASGLIFGWLTFLLVFGGFT---RT---VWEIVVGVVVFVYGGILLGLV	179
Mjls3833	94	TLA-GLSRFIFATAIWIWLGGLGT---WLIGNLGTHCPYGVGRCEVNH	IGASGLIFGWLAFLLVFGGFT---RK---AWEIVVGVVILVLFVYGGILLGLV	182
Mvan4290	92	TLA-GLSRFIFATAIWIWLGGLGT---WLIGNIGAHCPYGVGRCEVNH	IGASGLIFGWLAFLLVFGGFT---RK---VWEIVVGVVVLVYVSGVLLGLV	180
MAB0026	145	ERAFGGQRYAAIYGTALLGGSAAA---MWLSPNAVW	ACASGAIYGLLGAALVLSLRE-----RLNPQTIIVLLNIGLSL	218
Mflv1071	137	EALGRARFITLYLVLSALGGSVLV---YLLTLNALT	ACASCAVEGLFGATFVVGRKL-----NMDVRSVMAIIVLNLAFTFL	210
Mvan5753	148	EFALGRIRFVALYVLSALGGSVLV---YLLTFNALT	ACASCAVEGLFGATFVVGRKL-----NMDVRSVMIIIGNLAFTFL	221
MSMEG5036	154	EKMWGLTRFGVLYALSGLGGSVLV---YMLSPLNSAT	ACASCAIFGLFGAIFVVARHL-----NLDVRAIGIVIVINLVFTFV	228
Mjls5529	146	EMWLGRIRFGALYALSALGGSVLV---YLLSPINAT	ACASCAVEGLFGAMFVVARKL-----NLDIRGIAAIITILNVFTFV	220
Rv0110	107	EMWLGRIRFGALYAVSALGGSVLV---YLIAPLNTAT	ACASCAVEGLFGATFVMVARL-----HLDVRWVVALIVINLAFTFL	181
MMAR0300	142	EMWLGRIRFGGLYALSALGGSVLV---YLIAPLNTAT	ACASCAIEGLFGATFVVAKRL-----NLDIRWVVALIAINLAITFV	216
MUL4822	107	EMWLGRIRFGGLYALSALGGSVLV---YLIAPLNTAT	ACASCAIEGLFGATFVVAKRL-----NLDIRWVVALIAINLAITFV	181
Consensus			*.*	

GlpG	243	D-----LFGMSMANGA I T I A G L A V G L A M A F V D S L-----N	ARKRK-----	276
RhoI	262	QTYFDGSAFAKQPVSYIAHLLTALAGLTITGFLVLKNFG-----H	REYEQLIWWLALGVCAFTVFAIVFNLIINTVTAQLMEEQG-EVITQHLLH	350
AnoI	293	NSQIN-----DPFDKVGYIAHASCALAGLFGVIGVLRNLK	ESWERKLWCAVSIYFVIMTAGIMYHFLDPSHY-----	361
RHBDL2	234	RRFFVFP---EDGSPVSAFA I T I A G C F A G C S I G Y T V F S C F D---K	ALLKDPFRFWIAIAYLACVLFAVFFNIFLSPAN-----	303
ToxI	221	-----LNGSIDQMGLLGLLGGFSIGMLYNKE-----L	NDKPVMVYWSAAAIGILLALPAICPTVLYAYDRHCHRDLSYI-----	293
FallI	221	-----FNGSIDHVGHLGLLISIGSILGYNEH-----V	DNKPRWYNHKLIGSYISLVLAIPFTVLTITPTC-----	278
aaRA	195	LTLIN---GLQSGVDNAAH I G C A I I C A L I S I A Y I L-----V	PHKLRLVANLICITVIAASLLTMMYIYLSFSTNKHLLEREFIYQEVYTELA	277
ML1171	189	PVL---GRCCGVSWQCHLCCGAIAGVVAAYLLSA-----P	PERKTR---ALKEAGTDSPLRKT-----	238
MAV1554	174	PVL---GLCCGVSWQCHLCCGAIAGVLAAYLLSE-----P	ERKGR---SGRKTVGAVAPRPKT-----	223
Rv1337	191	PVL---GQCCGVSWQCHLCCGAVAGVVAAYLLSA-----P	ERKAR---ALKRAGARSHPKPL-----	240
MMAR4059	173	PRL---GVCGGVSWQCHLCCGALAGVVAAYFLSA-----P	ERKAR---ELKKAGERPSSPK-----	222
MAB1481	180	P---GQFGVSWQCHLCCGAVGVLAAYWL-----S	GREKVKQAARGPVPVPRILT-----	225
MSMEG4904	198	PVL---NGCCGVSWQCHLCCGAIAGVVAAYVLG-----P	ERKAR---D---SKRSRSPYLT-----	245
Mflv2355	180	P---GTFGVSWQCHLCCGALAGVLAAYLLSG-----P	ERKTR---ALRRPVRPPLSNT-----	225
Mjls3833	183	P---GTPGVSWQCHLCCGAVAGVVAAYVLLS-----P	ERKAR---ELRRSTAPPYLT-----	229
Mvan4290	181	P---GTPGVSWQCHLCCGAVAGVLAAYLLSG-----P	ERKAR---ERRKATNPYLT-----	225
MAB0026	219	L-----PGISLAGHMGGLLFGSAGALLYIREVCRGIGMPDLA	RAKST---PWLVAANAVALSVALIM-----AKVLAYAG-----	287
Mflv1071	211	IPL---FTSQNISWQCHLGLVLTGALVAAAFY-----A	PAQRQ---TLIQAGAVGAILVVFVGLVWRVTAELRTLMLGLG-----	279
Mvan5753	222	IPL---FTSQNISWQCHLGLVLTGAVVAAAFY-----A	PRQQR---NLVQAGAAVALVLVFLVWRTVELRTLMLGLG-----	290
MSMEG5036	229	GP---ALGTAIWQCHIGGLVLTGAVVAAAFY-----A	PRERR---TATAAGVTAFAMFLAALFVWTRDRLTLFLLGAG-----	296
Mjls5529	221	YPL---ISGQGISWQCHVGGVLVTCAGAIAGVYAY-----A	PAGRR---NLVQGGVTAAVLLLFVVLVWRTVEIFAMFGVR-----	289
Rv0110	182	A---PAISWQCHVGGVLVTCALVAAATYV-----A	PRERR---NLIQATVITVIVAFVVLVWRTVDLLALFGGRLNL-----	249
MMAR0300	217	APA---VGSQLISWQCHVGGVLVTCALVAAATYV-----A	PRERR---NFIQAGAVTLTVAVFVVLVWRTSELLAMFGGHLNLG-----	289
MUL4822	182	APA---VGSQLISWQCHVGGVLVTCALVAAATYV-----A	PRERR---NFIQAGAVTLTVAVFVVLVWRTSELLAMFGGHLNLG-----	254
Consensus				