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SRDB

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Search Protein list Cart (0) Tools

Search Result

Symbol	Name	Internal Standard	Peptides	Species
AOFKE6	Chloroplast threonine deaminase 1		1	Tomato
AOFKE6	Chloroplast threonine deaminase 1	QconCAT(SOLR02)	2	Tomato
AORZC9	Constitutive plastid-lipid associated protein		1	Tomato
B1Q3F1	Glutamate decarboxylase isoform2	QconCAT(SOLR02)	2	Tomato
B1Q3F8	Succinic semialdehyde dehydrogenase		1	Tomato
B5M9E4	Beta-gluc		1	Tomato
B5M9E4	Beta-gluc	QconCAT(SOLR01)	2	Tomato
C6K8M2	Plastid isopentenyl diph		3	Tomato
D0VNY3	ISPH protein		1	Tomato
D0VNY3	ISPH protein	QconCAT(SOLR01)	2	Tomato
E0YCS8	Methylketone synthase Ila		3	Tomato
E0Z1D0	Sucr		3	Tomato
K4AQJ2	Uncharacterized protein		1	Tomato
K4AS92	Uncharacterized protein	QconCAT(SOLR02)	1	Tomato
K4ASC2	Isocitrate dehydrogenase [NADP]	QconCAT(SOLR02)	1	Tomato
K4ASL8	Uncharacterized protein		1	Tomato
K4ASM0	Lipoxygenase		1	Tomato
K4ASM0	Lipoxygenase	QconCAT(SOLR01)	2	Tomato
K4AS06	Uncharacterized protein		2	Tomato
K4ASU4	ATP synthase subunit beta		3	Tomato

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 ALL

Select	Sequence	Position	SRM/MSM Assay	Redundancy	Protease	Com
☐	VVOLLAPVR	155-163	P_S_00102	Arabi/Tomato/Tobacco/Artemisia_annua	Trypsin	
☐	INPTTSGSGVSTLEK	3-17	P_S_00100	0 / 0 / 2 / 0	Trypsin	
☐	IVGEHYETAQR	379-390	P_S_00101	0 / - / ATPB / ATPB,ATPB NITACP030 / -		

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- Protein Information (From UniprotKB)

Sequence Information

>tr|K4ASU4|K4ASU4_SOLIC Uncharacterized protein OS=Solanum lycopersicum OX=4081 PE=3 SV=1

MRINPTTSGS GVSITLKKNP GRVQIIGPV LDVAFPPGKM PNIYNALVVQ GRDSVGQPIN 60

VACEVQQLG NNRVRVAMS ATEGLTRGMA VIDTGAPISV PVGGATIGRI FNVLGEFVDN 120

LGFVDTSTTS PIHRSAPAFI QLDTLSIFE TGIRVVDLLA PYRNGGKIGL FGGAGVGKTV 180

LIMELINNIA KAHGGVSVFG VGERTREGN DLYHEMKESG VINKENIAES KVALVTGQMH 240

EPGARMRVG LTALTMAEYF RDVNEQVLL FIDNIFRFVQ AGEVSALLG RHPSAVGYQP 300

TLSTEMGSLQ ERITSTKEGS ITSIQAVYVP ADDLTPAPA TTFAMLDATT VLSKGLAAG 360

IYPADVPLDS TSTMLQPRIV GEHYETAQR VKQTLQRYKE LQDIIAILGL DELSEEDRL 420

VARARKIERF LSQPPFVAEV FTGSPGKYVG LAETIRGFQL ILSGELDGLP EQAFYLVGTI 480

DEATAKAMHL EMEKVETIVL STNSQIGIL PHAPIATAV DIGILIRLRL DQMLTHALMG 540

GPARIGHNEI TVLVNDAERG SDINFQEAQQ TLEIAEANKV KAEGRHQKIE ANLALRRART 600

RVEASNPIS 609

Sequence Annotation

Start	Stop	Type	Remarks
164	356	DOMAIN	AAA. [ECO:0000259] SMART:SM00382).
572	592	COILED	[ECO:0000256] [SAM:Colls].

Redundancy	Protease
Arabi/Tomato/Tobacco/Artemisia_annua	
2 / 1 / 2 / 2	Trypsin
0 / 0 / 2 / 0	Trypsin
0 / - / ATPB / ATPB,ATPB NITACP030 / -	