

MATRIX SCIENCE **MASCOT Search Results**

Protein View: LONP2_MAIZE

Lon protease homolog 2, peroxisomal OS=Zea mays OX=4577 GN=LON1 PE=2 SV=1

Database: SwissProt
Score: 79
Expect: 0.0065
Monoisotopic mass (M_r): 97900
Calculated pI: 7.70
Taxonomy: Zea mays

Sequence similarity is available as [an NCBI BLAST search of LONP2_MAIZE against nr.](#)

Search parameters

MS data file: sal.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Mass values searched: 13
Mass values matched: 10

Protein sequence coverage: 15%

Matched peptides shown in **bold red**.

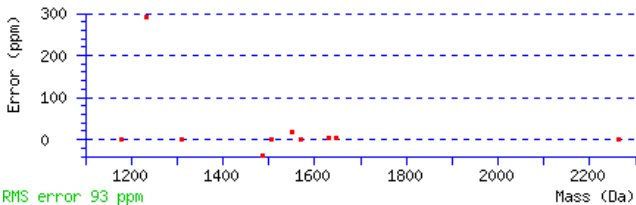
1 **MSDSPVELPS** RLAVLPFR**NK** **VLLPGAIVRI** RCTNPSSVKL VEQELWQ**KEE**
51 **KGLIGVLPVR** DSEATAVGS**L** LSPGVGSDSG **EGGSK**VGGSA VESSKQDTKN
101 G**K**EP**I**H**W**HSK **GVAARALHLS** RGVEKPSGRV TYIVVLEGLC RFSVQEL**SAR**
151 GPYHVARVSR LD**M**TKTELEQ AEQDPDLIAL SRQFKATAME LISVLEQ**KQK**
201 TVGR**T**KVLLD TVPVYRLADI FVASFEISFE EQLSMLDSVH LK**VRLSKATE**
251 LVDRHLQ**SIL** VAEKITQKVE GQLSKSQKEF LLRQQMRAIK EELGDND**DDE**
301 DDVAALERKM QNAGMPANIW KHAQREMRRL RKM**Q**PQPGY SSSRAYLELL
351 ADLPWQKVSE ERELDLRVAK **ESLDQDHYGL** **TKVKQRIEY** LAVRKLKPDA
401 RGPVLCFVGP PGVGK**T**SLAS SI**A**KALNRKF IRISLGGVKD EADIRGHRRT
451 YIGSMPGRLI DGLKRVSVSN PVMLLDEIDK TGS**D**VRGDPA SALLEVL**DPE**
501 QNKA**F**NDHYL NVPFDLSKVI FVATANRMQP IPPPLLD**RME** **I**IELPGYT**P**E
551 **E**K**L**KIAMKHL IPRVLEQHGL STTNLQIPEA MVKLVIERYT REAGVRNLER
601 NLAAALAAAA VKVAEQVKTL RLGKEIQPIT TTLDSRLAD GGEVEMEVIP
651 MEHDISNTYE NPSPMIVDEA MLEKVLGPPR FDDREAADRV ASPGVS**VGLV**
701 WTSVGGEVQF VEATAMVGKG DLHLTGQLGD VIKESAQLAL TWVRARAADL
751 NLSPTSDINL LESRDIHIHF PAGAVPKDGP SAGVTLVTAL VSLFSNR**KVR**
801 **ADTAMTGEMT** **LR**GLVLPVGG VKDKVLAHR YGIKRVILPE RNLKDLSEVP
851 LPILSDMEIL LVK**R**IEEVLD **HAFEGRCPLR** SRSKL

Unformatted sequence string: **885 residues** (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass
Show ☒ matched peptides only ☐ predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	M	Peptide
1 - 11	1233.9388	1232.9316	1232.5707	293.0	0	-.MSDSPVELPSR.L + Oxidation (M)
19 - 29	1179.7573	1178.7500	1178.7499	0.091	1	R.NKVLLPGAIVR.I
49 - 60	1309.7839	1308.7766	1308.7765	0.073	1	K.EEKGLIGVLPVR.D
61 - 85	2264.0525	2263.0452	2263.0452	-0.010	0	R.DSEATAVGSLLSPGVGSDSGEGGSK.V
103 - 115	1487.7278	1486.7205	1486.7793	-39.5	1	K.EPIHWHSKGVAAR.A
116 - 129	1506.8497	1505.8424	1505.8426	-0.13	1	R.ALHLSRGVEKPSGR.V
371 - 384	1632.8273	1631.8200	1631.8155	2.76	1	K.ESLDQDHYGLTKVK.Q
539 - 552	1648.8183	1647.8110	1647.8065	2.70	0	R.MEIIELPGYTPEEK.L
799 - 812	1551.7908	1550.7835	1550.7545	18.7	1	K.VRADTAMTGEMTLR.G
864 - 876	1570.7965	1569.7893	1569.7899	-0.42	1	K.RIEEVLDHAFEGR.C

No match to: 842.7330, 2211.6135, 2705.7922



ID LONP2_MAIZE Reviewed; 885 AA.
AC P93647;
DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-MAY-1997, sequence version 1.
DT 12-OCT-2022, entry version 144.
DE RecName: Full=Lon protease homolog 2, peroxisomal {ECO:0000255|HAMAP-Rule:MF_03121};
DE EC=3.4.21.53 {ECO:0000255|HAMAP-Rule:MF_03121};
GN Name=LON1;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACMAD clade;
OC Panicoideae; Andropogonodae; Andropogoneae; Tripsacinae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=cv. B73;
RX PubMed=9620272; DOI=10.1023/a:1005912831051;
RA Barakat S., Pearce D.A., Sherman F., Rapp W.D.;
RT "Maize contains a Lon protease gene that can partially complement a yeast
RT pim1-deletion mutant.";
RL Plant Mol. Biol. 37:141-154(1998).
CC -!- FUNCTION: ATP-dependent serine protease that mediates the selective
CC degradation of misfolded and unassembled polypeptides in the
CC peroxisomal matrix. Necessary for type 2 peroxisome targeting signal
CC (PTS2)-containing protein processing and facilitates peroxisome matrix
CC protein import. {ECO:0000255|HAMAP-Rule:MF_03121}.
CC -!- CATALYTIC ACTIVITY:
CC Reaction=Hydrolysis of proteins in presence of ATP.; EC=3.4.21.53;
CC Evidence={ECO:0000255|HAMAP-Rule:MF_03121};
CC -!- SUBCELLULAR LOCATION: Peroxisome matrix {ECO:0000255|HAMAP-
CC Rule:MF_03121}.
CC -!- SIMILARITY: Belongs to the peptidase S16 family. {ECO:0000255|HAMAP-
CC Rule:MF_03121}.
CC -----
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CC Distributed under the Creative Commons Attribution (CC BY 4.0) License
CC -----
DR EMBL; U85494; AAC50011.1; -; mRNA.
DR PIR; T04321; T04321.
DR RefSeq; NP_001105903.1; NM_001112433.1.
DR AlphaFoldDB; P93647; -.
DR SMR; P93647; -.
DR STRING; 4577.GRMZM2G109560_P01; -.
DR MEROPS; S16.003; -.
DR PaxDb; P93647; -.
DR EnsemblPlants; Zm00001eb319680_T001; Zm00001eb319680_P001; Zm00001eb319680.
DR GeneID; 732820; -.
DR Gramene; Zm00001eb319680_T001; Zm00001eb319680_P001; Zm00001eb319680.
DR KEGG; zma:732820; -.
DR eggNOG; KOG2004; Eukaryota.
DR HOGENOM; CLU_004109_4_0_1; -.
DR OrthoDB; 528132at2759; -.
DR BRENDA; 3.6.4.7; 6752.
DR Proteomes; UP000007305; Chromosome 7.
DR ExpressionAtlas; P93647; baseline and differential.
DR Genevisible; P93647; ZM.
DR GO; GO:0005739; C:mitochondrion; IEA:GOC.
DR GO; GO:0005782; C:peroxisomal matrix; IBA:GO_Central.
DR GO; GO:0005524; F:ATP binding; IEA:UniProtKB-UniRule.
DR GO; GO:0016887; F:ATP hydrolysis activity; IEA:UniProtKB-UniRule.
DR GO; GO:0004176; F:ATP-dependent peptidase activity; IEA:UniProtKB-UniRule.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA:UniProtKB-UniRule.
DR GO; GO:0032042; P:mitochondrial DNA metabolic process; IDA:AgBase.
DR GO; GO:0016558; P:protein import into peroxisome matrix; IEA:UniProtKB-UniRule.
DR GO; GO:0016485; P:protein processing; IBA:GO_Central.
DR GO; GO:0006515; P:protein quality control for misfolded or incompletely synthesized proteins; IEA:UniProtKB-UniRule.
DR GO; GO:0006625; P:protein targeting to peroxisome; IBA:GO_Central.
DR GO; GO:0009408; P:response to heat; IDA:AgBase.
DR Gene3D; 2.30.130.40; -; 1.
DR Gene3D; 3.30.230.10; -; 1.
DR Gene3D; 3.40.50.300; -; 1.
DR HAMAP; MF_03121; lonp2_euk; 1.
DR InterPro; IPR003593; AAA+ ATPase.
DR InterPro; IPR003959; ATPase_AAA_core.
DR InterPro; IPR004815; Lon_bac/euk-typ.
DR InterPro; IPR008269; Lon_proteolytic.
DR InterPro; IPR027065; Lon_Prtase.
DR InterPro; IPR003111; Lon_prtase_N.
DR InterPro; IPR046336; Lon_prtase_N_sf.
DR InterPro; IPR027501; Lonp2_euk.
DR InterPro; IPR027417; P-loop_NTPase.
DR InterPro; IPR008268; Peptidase_S16_AS.
DR InterPro; IPR015947; PUA-like_sf.
DR InterPro; IPR020568; Ribosomal_S5_D2-typ_fold.
DR InterPro; IPR014721; Ribosomal_S5_D2-typ_fold_subgr.
DR PANTHER; PTHR10046; PTHR10046; 1.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF05362; Lon_C; 1.
DR Pfam; PF02190; LON_substr_bdg; 1.
DR PIRSF; PIRSF001174; Lon_proteas; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00464; LON; 1.
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DR SUPFAM; SSF54211; SSF54211; 1.

DR SUPFAM; SSF88697; SSF88697; 1.
DR TIGRFAMs; TIGR00763; lon; 1.
DR PROSITE; PS51787; LON_N; 1.
DR PROSITE; PS51786; LON_PROTEOLYTIC; 1.
DR PROSITE; PS01046; LON_SER; 1.
PE 2: Evidence at transcript level;
KW ATP-binding; Hydrolase; Nucleotide-binding; Peroxisome; Protease;
KW Reference proteome; Serine protease.
FT CHAIN 1..885
FT /note="Lon protease homolog 2, peroxisomal"
FT /id="PRO_0000026737"
FT DOMAIN 12..254
FT /note="Lon N-terminal"
FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01123"
FT DOMAIN 690..875
FT /note="Lon proteolytic"
FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01122"
FT REGION 70..104
FT /note="Disordered"
FT /evidence="ECO:0000256|SAM:MobiDB-lite"
FT MOTIF 883..885
FT /note="Microbody targeting signal"
FT /evidence="ECO:0000255|HAMAP-Rule:MF_03121"
FT ACT_SITE 781
FT /evidence="ECO:0000255|HAMAP-Rule:MF_03121"
FT ACT_SITE 824
FT /evidence="ECO:0000255|HAMAP-Rule:MF_03121"
FT BINDING 409..416
FT /ligand="ATP"
FT /ligand_id="ChEBI:CHEBI:30616"
FT /evidence="ECO:0000255|HAMAP-Rule:MF_03121"
SQ SEQUENCE 885 AA; 97733 MW; 331A321B56C75407 CRC64;
MSDSPVELPS RLAVLPFRNK VLLPGAIVRI RCTNPSSVKL VEQELWQKEE KGLIGVLPVR
DSEATAVGSL LSPGVGSDSG EGGSKVGGS VESSKQDTKN GKEPIHWHSK GVAARALHLS
RGVEKPSGRV TYIVVLEGLC RFSVQELSAR GPYHVARVSR LDMTKTELEQ AEQDPDLIAL
SRQFKATAME LISVLEQKQK TVGRTKVLLD TVPVYRLADI FVASFEISFE EQLSMLDSVH
LKVRLSKATE LVDRHLQSI LVAEKITQKVE GQLSKSQKEF LLRQQMRAIK EELGDNDDE
DDVAALERKM QNAGMPANIW KHAQREMRR LKMQPQQPGY SSSRAYLELL ADLPWQKVSE
ERELDLRVAK ESLDQDHYGL TKVKQRIIEY LAVRKLKPD RGPVLCFVGP PGVGKTSLAS
SIKALNRKF IRISLGGVKD EADIRGHRRT YIGSMPGRLI DGLKRVS VSN FMVLLDEIDK
TGSDVRGDPA SALLEVLDP E QNKAFNDHYL NVPFDL SKVI FVATANRMQP IPPPLDRME
IIEPLGYTPE EKLKIAMKHL IPRVLEQHGL STTNLQIPEA MVKLVIERYT REAGVRNLER
NLAALARAAA VKVAEQVKTL RLGKEIQPIT TTLDSRLAD GGEVEMEVIP MEHDISNTYE
NPSPMIVDEA MLEKVLGPPR FDDREAADRV ASPGVS VGLV WTSVGGEVQF VEATAMVGKG
DLHLTGQLGD VIKESAQLAL TWVRARAADL NLSPTSDINL LESRDIHIHF PAGAVPKDGP
SAGVTLV TAL VSLFSNRKVR ADTAMTGEMT LRGLVLPVGG VKDKVLAHR YGIKRVILPE
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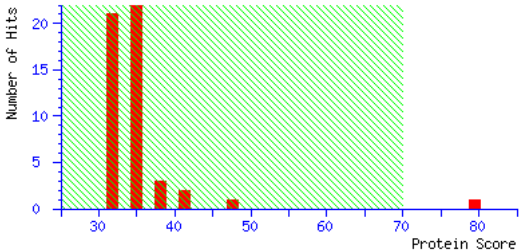
Mascot: <http://www.matrixscience.com/>

MATRIX SCIENCE Mascot Search Results

User : Fatin
Email : fatinkhan35@gmail.com
Search title :
MS data file : sa1.mgf
Database : SwissProt 2022_04 (568363 sequences; 205318884 residues)
Timestamp : 3 Mar 2023 at 11:07:19 GMT
Top Score : 79 for LONP2_MAIZE, Lon protease homolog 2, peroxisomal OS=Zea mays OX=4577 GN=LON1 PE=2 SV=1

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 70 are significant (p<0.05).



Protein Summary Report

Format As Protein Summary [Help](#)
Significance threshold p< 0.05 Max. number of hits 20
Preferred taxonomy All entries
Re-Search All Search Unmatched

Index

Accession	Mass	Score	Description
1. LONP2_MAIZE	97900	79	Lon protease homolog 2, peroxisomal OS=Zea mays OX=4577 GN=LON1 PE=2 SV=1
2. HIS4_CHLP8	29202	47	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Chlorobaculum par
3. GP53_BPSP1	25460	41	Putative gene 53 protein OS=Bacillus phage SP01 OX=10685 GN=53 PE=4 SV=1
4. AROA_CERS4	46526	40	3-phosphoshikimate 1-carboxyvinyltransferase OS=Cereibacter sphaeroides (strain ATCC 17023 / DSM 158 / JCM 6121 / CCUG
5. ISPG_ACAH1	45108	38	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin) OS=Acaryochloris marina (strain MBIC 11017) OX=329726
6. RGS14_MOUSE	60380	37	Regulator of G-protein signaling 14 OS=Mus musculus OX=10090 GN=Rgs14 PE=1 SV=2
7. TSPE_WOLNR	32054	37	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase OS=Wolbachia sp. subsp. Drosophila simulans (strain wRi) OX=66084 GN=
8. PUR9_BARBK	58384	36	Bifunctional purine biosynthesis protein PurH OS=Bartonella bacilliformis (strain ATCC 35685 / NCTC 12138 / KC583) OX=
9. Y2323_ALKCK	9622	36	Putative regulatory protein ABC2323 OS=Alkalihalobacillus clausii (strain KSM-K16) OX=66692 GN=ABC2323 PE=3 SV=1
10. FIXA_AZOVI	30892	36	Protein FixA OS=Azotobacter vinelandii OX=354 GN=fixA PE=3 SV=1
11. FOLD_DEHMB	31652	36	Bifunctional protein FOLD OS=Dehalococcoides mccartyi (strain ATCC BAA-2100 / JCM 16839 / KCTC 5957 / BAV1) OX=216389 (
12. FOLD_DEHMC	31683	36	Bifunctional protein FOLD OS=Dehalococcoides mccartyi (strain CBDB1) OX=255470 GN=fold PE=3 SV=1
13. SYC2_TROW8	51698	36	Putative cysteine--tRNA ligase 2 OS=Tropheryma whipplei (strain TW08/27) OX=218496 GN=cysS2 PE=3 SV=1
14. SYC2_TROWT	51698	36	Putative cysteine--tRNA ligase 2 OS=Tropheryma whipplei (strain Twist) OX=203267 GN=cysS2 PE=3 SV=1
15. VNS1_EHDV2	65480	36	Non-structural protein NS1 OS=Epizootic hemorrhagic disease virus 2 (strain Alberta) OX=10910 GN=Segment-5 PE=3 SV=1
16. CDK1_MOUSE	34142	35	Cyclin-dependent kinase 1 OS=Mus musculus OX=10090 GN=Cdk1 PE=1 SV=3
17. CDK1_RAT	34170	35	Cyclin-dependent kinase 1 OS=Rattus norvegicus OX=10116 GN=Cdk1 PE=1 SV=1
18. CYC_ASPNG	12061	35	Cytochrome c OS=Aspergillus niger OX=5061 GN=cycA PE=1 SV=1
19. TAF8_HUMAN	34298	34	Transcription initiation factor TFIID subunit 8 OS=Homo sapiens OX=9606 GN=TAF8 PE=1 SV=1
20. MSHD_CORDI	33582	34	Mycothiol acetyltransferase OS=Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis) OX=257306

Results List

1.	LONP2_MAIZE	Mass: 97900	Score: 79	Expect: 0.0065	Matches: 10
Lon protease homolog 2, peroxisomal OS=Zea mays OX=4577 GN=LON1 PE=2 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	1179.7573	1178.7500	1178.7499	0.09	19 - 29 1 R.NKVLLPGAIVR.I
	1233.9388	1232.9316	1232.5707	293	1 - 11 0 -.MSDSPVELPSR.L + Oxidation (M)
	1309.7839	1308.7766	1308.7765	0.07	49 - 60 1 K.EEKGLIGLVPVR.D
	1487.7278	1486.7205	1486.7793	-39.54	103 - 115 1 K.EPIHWHSKGVAAR.A
	1506.8497	1505.8424	1505.8426	-0.13	116 - 129 1 R.ALHLSRGVEKPSGR.V
	1551.7908	1550.7835	1550.7545	18.7	799 - 812 1 K.VRADTAMTGEMTLR.G
	1570.7965	1569.7893	1569.7899	-0.42	864 - 876 1 K.RIEEVLDAHFEGR.C
	1632.8273	1631.8200	1631.8155	2.76	371 - 384 1 K.ESLDQDHYGLTKVK.Q
	1648.8183	1647.8110	1647.8065	2.70	539 - 552 0 R.MEIIELPGYTPEEK.L
	2264.0525	2263.0452	2263.0452	-0.01	61 - 85 0 R.DSEATAVGSLSPGVGSDSGEGGSK.V
No match to: 842.7330, 2211.6135, 2705.7922					
2.	HIS4_CHLP8	Mass: 29202	Score: 47	Expect: 11	Matches: 5
1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase OS=Chlorobaculum parvum (strain DSM 263 / NC					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	1309.7839	1308.7766	1308.8017	-19.13	2 - 13 1 M.LIIPAIIDIKEGK.C
	1487.7278	1486.7205	1486.7264	-3.92	194 - 208 0 K.ITASGGVSTSDDLHK.L
	1570.7965	1569.7893	1569.7457	27.7	172 - 185 1 R.DGMLQGVGYETTKR.F + Oxidation (M)
	2264.0525	2263.0452	2263.0865	-18.24	46 - 65 0 K.MLHVVDLDAALTGEMVNFKEK.I + 2 Oxidation (M)
	2705.7922	2704.7850	2704.3200	172	42 - 65 1 K.QNAKMLHVVDLDAALTGEMVNFKEK.I + 2 Oxidation (M)
No match to: 842.7330, 1179.7573, 1233.9388, 1506.8497, 1551.7908, 1632.8273, 1648.8183, 2211.6135					

3.	GP53_BPSP1	Mass: 25460	Score: 41	Expect: 47	Matches: 4
Putative gene 53 protein OS=Bacillus phage SP01 OX=10685 GN=53 PE=4 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	842.7330	841.7258	841.5134	252	213 - 219 1 K.RLGEVLR.S
	1309.7839	1308.7766	1308.6575	91.0	2 - 11 1 M.RTYWNVSLDR.S
	1648.8183	1647.8110	1647.7927	11.1	66 - 79 0 R.TFSVNDIVHCSLEK.V
	2705.7922	2704.7850	2704.3829	149	20 - 42 0 R.LVHYICVPIISIHHAEDISMTR.K
No match to: 1179.7573, 1233.9388, 1487.7278, 1506.8497, 1551.7908, 1570.7965, 1632.8273, 2211.6135, 2264.0525					
4.	AROA_CERS4	Mass: 46526	Score: 40	Expect: 60	Matches: 5
3-phosphoshikimate 1-carboxyvinyltransferase OS=Cereibacter sphaeroides (strain ATCC 17023 / DSM 158 / JCM 6121 / CCUG 31486 / LMG 2827 / NBRC					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	1179.7573	1178.7500	1178.5350	182	354 - 363 1 K.ESDRIDAMAR.G + Oxidation (M)
	1309.7839	1308.7766	1308.6786	74.9	22 - 33 1 R.AEIPGDKSISHR.A
	1551.7908	1550.7835	1550.8491	-42.28	153 - 167 0 R.LPMTLVGAADPVPVR.Y + Oxidation (M)
	2211.6135	2210.6062	2210.1075	226	106 - 127 0 R.LVMGAMATSPLTATFTGDASLR.K
	2705.7922	2704.7850	2704.4986	106	153 - 178 1 R.LPMTLVGAADPVPVRYTVPVPSAQVK.S
No match to: 842.7330, 1233.9388, 1487.7278, 1506.8497, 1570.7965, 1632.8273, 1648.8183, 2264.0525					
5.	ISPG_ACAM1	Mass: 45108	Score: 38	Expect: 94	Matches: 5
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin) OS=Acaryochloris marina (strain MBIC 11017) OX=329726 GN=ispG PE=3 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	1179.7573	1178.7500	1178.6335	98.8	127 - 136 0 R.INPGLYVFEK.A
	1309.7839	1308.7766	1308.6938	63.2	369 - 379 1 K.QPGYISLYRGR.E
	1506.8497	1505.8424	1505.8210	14.2	226 - 238 1 R.VPVMLAAYRLMAR.R + Oxidation (M)
	1551.7908	1550.7835	1550.7247	37.9	1 - 14 0 -.MQTLSTPVTGTDER.S + Oxidation (M)
	2211.6135	2210.6062	2210.1154	222	94 - 113 0 K.LTATYQTVPLVADVHHNGMK.I + Oxidation (M)
No match to: 842.7330, 1233.9388, 1487.7278, 1570.7965, 1632.8273, 1648.8183, 2264.0525, 2705.7922					
6.	RGS14_MOUSE	Mass: 60380	Score: 37	Expect: 1.2e+002	Matches: 5
Regulator of G-protein signaling 14 OS=Mus musculus OX=10090 GN=Rgs14 PE=1 SV=2					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	842.7330	841.7258	841.4909	279	337 - 344 0 R.GLSLPDIK.V
	1309.7839	1308.7766	1308.5914	142	451 - 461 1 K.MSEARSISPCR.S + Oxidation (M)
	1487.7278	1486.7205	1486.8191	-66.28	1 - 14 1 -.MPGKPKHLGVPNGR.M
	1506.8497	1505.8424	1505.6958	97.4	289 - 303 0 K.SLGSGESESESRPGK.Y
	2264.0525	2263.0452	2263.0750	-13.20	15 - 37 0 R.MVLAVSDGELTSTAGSQAQGEGR.G
No match to: 1179.7573, 1233.9388, 1551.7908, 1570.7965, 1632.8273, 1648.8183, 2211.6135, 2705.7922					
7.	ISPE_WOLWR	Mass: 32054	Score: 37	Expect: 1.2e+002	Matches: 4
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase OS=Wolbachia sp. subsp. Drosophila simulans (strain wRi) OX=66084 GN=ispE PE=3 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	842.7330	841.7258	841.5637	193	207 - 213 1 K.DLLKLLK.E
	1551.7908	1550.7835	1550.7253	37.5	194 - 206 1 K.FSEPIKWSDDAEK.D
	1632.8273	1631.8200	1631.7315	54.3	53 - 66 0 R.YDNSTVEFINSESK.I
	2211.6135	2210.6062	2210.2019	183	98 - 121 1 K.NIPTAAGLSSGSDAGAVVRTLGK.L
No match to: 1179.7573, 1233.9388, 1309.7839, 1487.7278, 1506.8497, 1570.7965, 1648.8183, 2264.0525, 2705.7922					
8.	PUR9_BARBK	Mass: 58384	Score: 36	Expect: 1.3e+002	Matches: 5
Bifunctional purine biosynthesis protein PurH OS=Bartonella bacilliformis (strain ATCC 35685 / NCTC 12138 / KC583) OX=360095 GN=purH PE=3 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	1179.7573	1178.7500	1178.6077	121	469 - 478 1 K.RMGLTESLTR.G + Oxidation (M)
	1506.8497	1505.8424	1505.7926	33.1	525 - 537 1 R.GLAMVFTGVRHFR.H + Oxidation (M)
	2211.6135	2210.6062	2210.1113	224	431 - 452 1 K.SNAIVYAKNSATVGIGAGQMSR.L + Oxidation (M)
	2264.0525	2263.0452	2263.1267	-36.01	514 - 534 1 R.DQEVIEAADARGLAMVFTGVR.H + Oxidation (M)
	2705.7922	2704.7850	2704.4072	140	146 - 171 1 R.AAAKNHAYTGVTAVSDYDVLAELK.Q
No match to: 842.7330, 1233.9388, 1309.7839, 1487.7278, 1551.7908, 1570.7965, 1632.8273, 1648.8183					
9.	Y2323_ALKCK	Mass: 9622	Score: 36	Expect: 1.3e+002	Matches: 3
Putative regulatory protein ABC2323 OS=Alkalihalobacillus clausii (strain KSM-K16) OX=66692 GN=ABC2323 PE=3 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	1309.7839	1308.7766	1308.6608	88.5	41 - 51 1 R.NMLIDATYGRR.T
	1487.7278	1486.7205	1486.8256	-70.66	5 - 18 0 K.LINIGFGNIVSANR.I
	2705.7922	2704.7850	2704.4508	124	52 - 76 1 R.TRAVIVTDSHVILSAVQPETVAQR.L
No match to: 842.7330, 1179.7573, 1233.9388, 1506.8497, 1551.7908, 1570.7965, 1632.8273, 1648.8183, 2211.6135, 2264.0525					
10.	FIXA_AZOVI	Mass: 30892	Score: 36	Expect: 1.4e+002	Matches: 4
Protein FixA OS=Azotobacter vinelandii OX=354 GN=fixA PE=3 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	842.7330	841.7258	841.4480	330	2 - 8 0 M.HSVVCIK.Q
	1570.7965	1569.7893	1569.7999	-6.75	122 - 137 0 K.QTIDGDTAQVGPPIAK.R
	2211.6135	2210.6062	2211.1787	-258.89	139 - 157 1 R.LDYQLLTYVSRIVDVTAK.K
	2264.0525	2263.0452	2263.1341	-39.29	50 - 71 1 K.DKFGGTVTVTMGPPMAEALR.K + Oxidation (M)
No match to: 1179.7573, 1233.9388, 1309.7839, 1487.7278, 1506.8497, 1551.7908, 1632.8273, 1648.8183, 2705.7922					
11.	FOLD_DEHMB	Mass: 31652	Score: 36	Expect: 1.4e+002	Matches: 4
Bifunctional protein FoId OS=Dehalococcoides mccartyi (strain ATCC BAA-2100 / JCM 16839 / KCTC 5957 / BAV1) OX=216389 GN=foId PE=3 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	842.7330	841.7258	841.4657	309	199 - 205 0 K.NLPEITR.Q
	1179.7573	1178.7500	1178.6772	61.8	157 - 167 0 K.IEGTHVIVGR.S
	1506.8497	1505.8424	1505.7726	46.4	247 - 259 1 K.RILSGDVFEEVK.E
	2211.6135	2210.6062	2210.1477	207	1 - 20 1 -.MSAHIINGTEIAAAIREER.S + Oxidation (M)
No match to: 1233.9388, 1309.7839, 1487.7278, 1551.7908, 1570.7965, 1632.8273, 1648.8183, 2264.0525, 2705.7922					
12.	FOLD_DEHMC	Mass: 31683	Score: 36	Expect: 1.4e+002	Matches: 4
Bifunctional protein FoId OS=Dehalococcoides mccartyi (strain CBDB1) OX=255470 GN=foId PE=3 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Peptide
	842.7330	841.7258	841.4657	309	199 - 205 0 K.NLPEITR.Q

1179.7573 1178.7500 1178.6772 61.8 157 - 167 0 K.IEGTHVVIVGR.S
1506.8497 1505.8424 1505.7726 46.4 247 - 259 1 K.RILSGDVFEEVK.E
2211.6135 2210.6062 2210.1477 207 1 - 20 1 -.MSAHIINGTEIAAAIREEIR.S + Oxidation (M)
No match to: 1233.9388, 1309.7839, 1487.7278, 1551.7908, 1570.7965, 1632.8273, 1648.8183, 2264.0525, 2705.7922

13. [SYC2_TROWB](#) Mass: 51698 Score: 36 Expect: 1.6e+002 Matches: 5
Putative cysteine--tRNA ligase 2 OS=Tropheryma whipplei (strain TW08/27) OX=218496 GN=cysS2 PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1309.7839 1308.7766 1308.8129 -27.72 438 - 449 1 R.AVEKLLGIPLTR.V
1506.8497 1505.8424 1505.8242 12.1 327 - 339 1 R.LWKSALQEYIGAK.G
1551.7908 1550.7835 1550.7188 41.7 1 - 12 1 -.MYTFEVFDSRTR.S
1570.7965 1569.7893 1569.9090 -76.27 116 - 130 1 K.VLDGIKTGIEGLISR.N
1648.8183 1647.8110 1647.7601 30.9 343 - 357 1 R.STADQNKGQTQGAWER.I
No match to: 842.7330, 1179.7573, 1233.9388, 1487.7278, 1632.8273, 2211.6135, 2264.0525, 2705.7922

14. [SYC2_TROWT](#) Mass: 51698 Score: 36 Expect: 1.6e+002 Matches: 5
Putative cysteine--tRNA ligase 2 OS=Tropheryma whipplei (strain Twist) OX=203267 GN=cysS2 PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1309.7839 1308.7766 1308.8129 -27.72 438 - 449 1 R.AVEKLLGIPLTR.V
1506.8497 1505.8424 1505.8242 12.1 327 - 339 1 R.LWKSALQEYIGAK.G
1551.7908 1550.7835 1550.7188 41.7 1 - 12 1 -.MYTFEVFDSRTR.S
1570.7965 1569.7893 1569.9090 -76.27 116 - 130 1 K.VLDGIKTGIEGLISR.N
1648.8183 1647.8110 1647.7601 30.9 343 - 357 1 R.STADQNKGQTQGAWER.I
No match to: 842.7330, 1179.7573, 1233.9388, 1487.7278, 1632.8273, 2211.6135, 2264.0525, 2705.7922

15. [VNS1_EHDV2](#) Mass: 65480 Score: 36 Expect: 1.6e+002 Matches: 6
Non-structural protein NS1 OS=Epizootic hemorrhagic disease virus 2 (strain Alberta) OX=10910 GN=Segment-5 PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1179.7573 1178.7500 1178.5720 151 348 - 356 0 R.ETFYHIDVR.T
1233.9388 1232.9316 1232.6158 256 334 - 342 1 R.HKCQLCFLK.N
1487.7278 1486.7205 1486.6663 36.5 8 - 19 0 K.FNMNSYYANHVK.M
1570.7965 1569.7893 1569.6850 66.4 336 - 347 1 K.CQLCFCLKNGCDR.E
1648.8183 1647.8110 1647.8324 -12.98 67 - 80 1 R.LAEMAQITMLDREK.V
2705.7922 2704.7850 2704.3398 165 421 - 442 1 R.WIRGTGIWENDEWQEGIYLLAR.V
No match to: 842.7330, 1309.7839, 1506.8497, 1551.7908, 1632.8273, 2211.6135, 2264.0525

16. [CDK1_MOUSE](#) Mass: 34142 Score: 35 Expect: 1.7e+002 Matches: 4
Cyclin-dependent kinase 1 OS=Mus musculus OX=10090 GN=Cdk1 PE=1 SV=3
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1632.8273 1631.8200 1631.7944 15.7 284 - 296 1 K.HPYFDLDLNQIKK.M
2211.6135 2210.6062 2211.1463 -244.25 181 - 200 0 R.YSTPVDIWSIGTIFAELATK.K
2264.0525 2263.0452 2263.1406 -42.15 255 - 274 1 K.NLDENGLDLLSKMLVYDPAK.R + Oxidation (M)
2705.7922 2704.7850 2704.3497 161 216 - 238 1 R.IFRALGTPNNEVWPEVESLQDYK.N
No match to: 842.7330, 1179.7573, 1233.9388, 1309.7839, 1487.7278, 1506.8497, 1551.7908, 1570.7965, 1648.8183

17. [CDK1_RAT](#) Mass: 34170 Score: 35 Expect: 1.7e+002 Matches: 4
Cyclin-dependent kinase 1 OS=Rattus norvegicus OX=10116 GN=Cdk1 PE=1 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1632.8273 1631.8200 1631.7944 15.7 284 - 296 1 K.HPYFDLDLNQIKK.M
2211.6135 2210.6062 2211.1463 -244.25 181 - 200 0 R.YSTPVDIWSIGTIFAELATK.K
2264.0525 2263.0452 2263.1406 -42.15 255 - 274 1 K.NLDENGLDLLSKMLVYDPAK.R + Oxidation (M)
2705.7922 2704.7850 2704.3497 161 216 - 238 1 R.IFRALGTPNNEVWPEVESLQDYK.N
No match to: 842.7330, 1179.7573, 1233.9388, 1309.7839, 1487.7278, 1506.8497, 1551.7908, 1570.7965, 1648.8183

18. [CYC_ASPNG](#) Mass: 12061 Score: 35 Expect: 1.8e+002 Matches: 3
Cytochrome c OS=Aspergillus niger OX=5061 GN=cycA PE=1 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1551.7908 1550.7835 1550.6718 72.0 22 - 35 0 R.CAQCHTVEAGGPHK.V
1632.8273 1631.8200 1631.7427 47.4 47 - 61 1 R.KTGQSEGYAYTDANK.Q
2211.6135 2210.6062 2211.0484 -199.97 62 - 80 0 K.QAGVTWIDENTLFSYLENPK.K
No match to: 842.7330, 1179.7573, 1233.9388, 1309.7839, 1487.7278, 1506.8497, 1570.7965, 1648.8183, 2264.0525, 2705.7922

19. [TAF8_HUMAN](#) Mass: 34298 Score: 34 Expect: 2.1e+002 Matches: 4
Transcription initiation factor TFIID subunit 8 OS=Homo sapiens OX=9606 GN=TAF8 PE=1 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1233.9388 1232.9316 1232.5745 290 2 - 16 0 M.ADAAATAGAGGSGTR.S
1309.7839 1308.7766 1308.5881 144 75 - 85 1 R.SAKSYCEHTAR.T
1487.7278 1486.7205 1486.7490 -19.14 193 - 205 1 R.FMAKTGETQSLFK.D
2264.0525 2263.0452 2263.2060 -71.04 35 - 55 1 R.RTLQVVVSSLLTEAGFESA EK.A
No match to: 842.7330, 1179.7573, 1506.8497, 1551.7908, 1570.7965, 1632.8273, 1648.8183, 2211.6135, 2705.7922

20. [MSHD_CORDI](#) Mass: 33582 Score: 34 Expect: 2.1e+002 Matches: 4
Mycothiol acetyltransferase OS=Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis) OX=257309 GN=mshD PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1506.8497 1505.8424 1505.8089 22.2 200 - 212 1 R.ESDVLFLIDTAKR.T
1551.7908 1550.7835 1550.7954 -7.65 101 - 116 1 K.NVWAHGDGAGAKAVAK.A
1632.8273 1631.8200 1631.7904 18.2 69 - 83 1 R.DGDSAEVVDPAFRR.Q
1648.8183 1647.8110 1647.8052 3.52 255 - 267 1 R.MGLHHLEYEHARR.V
No match to: 842.7330, 1179.7573, 1233.9388, 1309.7839, 1487.7278, 1570.7965, 2211.6135, 2264.0525, 2705.7922

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted

Peptide Mass Tolerance : $\pm$ 350 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 13

Mascot: <http://www.matrixscience.com/>

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MASCOT Search Results

Protein View: ATP23_HUMAN

Mitochondrial inner membrane protease ATP23 homolog OS=Homo sapiens OX=9606
GN=ATP23 PE=1 SV=3

Database: SwissProt
Score: 50
Expect: 1.8
Monoisotopic mass (M_r): 28690
Calculated pI: 8.30
Taxonomy: Homo sapiens

Sequence similarity is available as an NCBI BLAST search of ATP23 HUMAN against nr.

Search parameters

MS data file: peaklist.xml
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Mass values searched: 15
Mass values matched: 4

Protein sequence coverage: 32%

Matched peptides shown in **bold red**.

1 MAGAPDERRR **GPAAGEQLQQ QHVSCQVFPE** RLAQGNPQQG FFSSFFTSNQ
51 KCQLRLLKTL ETNPYVKLLL DAMKHSGCAV NKDRHFSCED CNGNVSGGFD
101 ASTSQIVLCQ NNIHNQAHMN RVVTHELIHA FDHCR**AHVDW FTNIRHLACS**
151 **EVRAANLSGD CSLVNEIFRL HFGLK**QHHQT CVRDRATLSI LAVRNISKEV
201 AK**KAVDEVFE SCFNDHEPFG** RIPHNKTYAR YAHRDFENRD RYYSNI

Unformatted sequence string: **246 residues** (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass
Show ☒ matched peptides only ☐ predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
11 - 31	2366.2876	2365.2803	2365.1233	66.4	0	R.GPAAGEQLQQQHVSCQVFPER.L
136 - 153	2211.1582	2210.1509	2210.0803	31.9	1	R.AHVDWFTNIRHLACSEVR.A
154 - 175	2461.2268	2460.2195	2460.2583	-15.8	1	R.AANLSGDCSLVNEIFRLHFGLK.Q
203 - 221	2283.2300	2282.2227	2282.0062	94.9	1	K.KAVDEVFE SCFNDHEPFGR.I

No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357

Error: try setting browser cache to automatic.

ID ATP23_HUMAN Reviewed; 246 AA.
AC Q9Y6H3; Q1RLM4; Q96E81;
DT 29-APR-2008, integrated into UniProtKB/Swiss-Prot.
DT 03-MAR-2009, sequence version 3.
DT 12-OCT-2022, entry version 136.
DE RecName: Full=Mitochondrial inner membrane protease ATP23 homolog;
DE EC=3.4.24.-;
DE AltName: Full=Ku70-binding protein 3;

DE AltName: Full=XRCC6-binding protein 1;
GN Name=ATP23 {ECO:0000312|HGNC:HGNC:29452}; Synonyms=KUB3, XRCC6BP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], VARIANT CYS-48, AND INTERACTION WITH XRCC6.
RC TISSUE=Liver;
RX PubMed=10219089; DOI=10.1093/nar/27.10.2165;
RA Yang C.-R., Yeh S.-Y., Leskov K., Odegaard E., Hsu H.L., Chang C.,
RA Kinsella T.J., Chen D.J., Boothman D.A.;
RT "Isolation of Ku70-binding proteins (KUBs).";
RL Nucleic Acids Res. 27:2165-2174(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16541075; DOI=10.1038/nature04569;
RA Scherer S.E., Muzny D.M., Buhay C.J., Chen R., Cree A., Ding Y.,
RA Dugan-Rocha S., Gill R., Gunaratne P., Harris R.A., Hawes A.C.,
RA Hernandez J., Hodgson A.V., Hume J., Jackson A., Khan Z.M., Kovar-Smith C.,
RA Lewis L.R., Lozado R.J., Metzker M.L., Milosavljevic A., Miner G.R.,
RA Montgomery K.T., Morgan M.B., Nazareth L.V., Scott G., Sodergren E.,
RA Song X.-Z., Steffen D., Lovering R.C., Wheeler D.A., Worley K.C., Yuan Y.,
RA Zhang Z., Adams C.Q., Ansari-Lari M.A., Ayele M., Brown M.J., Chen G.,
RA Chen Z., Clerc-Blankenburg K.P., Davis C., Delgado O., Dinh H.H.,
RA Draper H., Gonzalez-Garay M.L., Havlak P., Jackson L.R., Jacob L.S.,
RA Kelly S.H., Li L., Li Z., Liu J., Liu W., Lu J., Maheshwari M.,
RA Nguyen B.-V., Okwuonu G.O., Pasternak S., Perez L.M., Plopper F.J.H.,
RA Santibanez J., Shen H., Tabor P.E., Verduzco D., Waldron L., Wang Q.,
RA Williams G.A., Zhang J., Zhou J., Allen C.C., Amin A.G., Anyalebechi V.,
RA Bailey M., Barbara J.A., Bimage K.E., Bryant N.P., Burch P.E.,
RA Burkett C.E., Burrell K.L., Calderon E., Cardenas V., Carter K., Casias K.,
RA Cavazos I., Cavazos S.R., Ceasar H., Chacko J., Chan S.N., Chavez D.,
RA Christopoulos C., Chu J., Cockrell R., Cox C.D., Dang M., Dathorne S.R.,
RA David R., Davis C.M., Davy-Carroll L., Deshazo D.R., Donlin J.E.,
RA D'Souza L., Eaves K.A., Egan A., Emery-Cohen A.J., Escotto M., Flagg N.,
RA Forbes L.D., Gabisi A.M., Garza M., Hamilton C., Henderson N.,
RA Hernandez O., Hines S., Hogues M.E., Huang M., Idlebird D.G., Johnson R.,
RA Jolivet A., Jones S., Kagan R., King L.M., Leal B., Lebow H., Lee S.,
RA LeVan J.M., Lewis L.C., London P., Lorensuhewa L.M., Loulseged H.,
RA Lovett D.A., Lucier A., Lucier R.L., Ma J., Madu R.C., Mapua P.,
RA Martindale A.D., Martinez E., Massey E., Mawhiney S., Meador M.G.,
RA Mendez S., Mercado C., Mercado I.C., Merritt C.E., Miner Z.L., Minja E.,
RA Mitchell T., Mohabbat F., Mohabbat K., Montgomery B., Moore N., Morris S.,
RA Munidasa M., Ngo R.N., Nguyen N.B., Nickerson E., Nwaokelemeh O.O.,
RA Nwokenkwo S., Obregon M., Oguh M., Oragunye N., Oviedo R.J., Parish B.J.,
RA Parker D.N., Parrish J., Parks K.L., Paul H.A., Payton B.A., Perez A.,
RA Perrin W., Pickens A., Primus E.L., Pu L.-L., Puazo M., Quiles M.M.,
RA Quiroz J.B., Rabata D., Reeves K., Ruiz S.J., Shao H., Sisson I.,
RA Sonaike T., Sorelle R.P., Sutton A.E., Svatek A.F., Svetz L.A.,
RA Tamerisa K.S., Taylor T.R., Teague B., Thomas N., Thorn R.D., Trejos Z.Y.,
RA Trevino B.K., Ukegbu O.N., Urban J.B., Vasquez L.I., Vera V.A.,
RA Villasana D.M., Wang L., Ward-Moore S., Warren J.T., Wei X., White F.,
RA Williamson A.L., Wleczyk R., Wooden H.S., Wooden S.H., Yen J., Yoon L.,
RA Yoon V., Zorrilla S.E., Nelson D., Kucherlapati R., Weinstock G.,
RA Gibbs R.A.;
RT "The finished DNA sequence of human chromosome 12.";
RL Nature 440:346-351(2006).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L., Mobarry C.M.,
RA Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R., Flanigan M.J.,
RA Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V., Hannenhalli S.,
RA Turner R., Yooseph S., Lu F., Nusskern D.R., Shue B.C., Zheng X.H.,
RA Zhong F., Delcher A.L., Huson D.H., Kravitz S.A., Mouchard L., Reinert K.,
RA Remington K.A., Clark A.G., Waterman M.S., Eichler E.E., Adams M.D.,
RA Hunkapiller M.W., Myers E.W., Venter J.C.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA project:
RT the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
CC -!- SUBUNIT: Interacts with XRCC6. {ECO:0000269|PubMed:10219089}.
CC -!- INTERACTION:
CC Q9Y6H3; Q9NYB9-2: ABI2; NbExp=3; IntAct=EBI-12811889, EBI-11096309;

CC Q9Y6H3; Q08043: ACTN3; NbExp=3; IntAct=EBI-12811889, EBI-2880652;
CC Q9Y6H3; Q9H1Y0: ATG5; NbExp=3; IntAct=EBI-12811889, EBI-1047414;
CC Q9Y6H3; Q95429: BAG4; NbExp=3; IntAct=EBI-12811889, EBI-2949658;
CC Q9Y6H3; P41182: BCL6; NbExp=3; IntAct=EBI-12811889, EBI-765407;
CC Q9Y6H3; Q9NX04: Clorf109; NbExp=3; IntAct=EBI-12811889, EBI-8643161;
CC Q9Y6H3; Q96HB5: CCDC120; NbExp=3; IntAct=EBI-12811889, EBI-744556;
CC Q9Y6H3; P33240: CSTF2; NbExp=3; IntAct=EBI-12811889, EBI-711360;
CC Q9Y6H3; Q9H0L4: CSTF2T; NbExp=3; IntAct=EBI-12811889, EBI-747012;
CC Q9Y6H3; Q9UI47-2: CTNNA3; NbExp=3; IntAct=EBI-12811889, EBI-11962928;
CC Q9Y6H3; Q9H596: DUSP21; NbExp=3; IntAct=EBI-12811889, EBI-7357329;
CC Q9Y6H3; Q14204: DYNC1H1; NbExp=3; IntAct=EBI-12811889, EBI-356015;
CC Q9Y6H3; Q8IYI6: EXOC8; NbExp=3; IntAct=EBI-12811889, EBI-742102;
CC Q9Y6H3; Q75593: FOXH1; NbExp=3; IntAct=EBI-12811889, EBI-1759806;
CC Q9Y6H3; Q12951-2: FOXI1; NbExp=3; IntAct=EBI-12811889, EBI-12018822;
CC Q9Y6H3; Q43559: FRS3; NbExp=3; IntAct=EBI-12811889, EBI-725515;
CC Q9Y6H3; Q8IVS8: GLYCTK; NbExp=3; IntAct=EBI-12811889, EBI-748515;
CC Q9Y6H3; Q96NT3-2: GUCD1; NbExp=3; IntAct=EBI-12811889, EBI-11978177;
CC Q9Y6H3; P52597: HNRNPF; NbExp=3; IntAct=EBI-12811889, EBI-352986;
CC Q9Y6H3; P49639: HOXA1; NbExp=3; IntAct=EBI-12811889, EBI-740785;
CC Q9Y6H3; Q43593: HR; NbExp=3; IntAct=EBI-12811889, EBI-2880706;
CC Q9Y6H3; Q6P597-3: KLC3; NbExp=3; IntAct=EBI-12811889, EBI-12076930;
CC Q9Y6H3; Q92876: KLK6; NbExp=3; IntAct=EBI-12811889, EBI-2432309;
CC Q9Y6H3; Q9NRQ2: PLSCR4; NbExp=3; IntAct=EBI-12811889, EBI-769257;
CC Q9Y6H3; Q96I34: PPP1R16A; NbExp=3; IntAct=EBI-12811889, EBI-710402;
CC Q9Y6H3; Q75716: STK16; NbExp=3; IntAct=EBI-12811889, EBI-749295;
CC Q9Y6H3; Q96PN8: TSSK3; NbExp=3; IntAct=EBI-12811889, EBI-3918381;
CC Q9Y6H3; Q15915: ZIC1; NbExp=3; IntAct=EBI-12811889, EBI-11963196;
CC -!- SIMILARITY: Belongs to the peptidase M76 family. {ECO:0000305}.
CC -!- SEQUENCE CAUTION:
CC Sequence=AAD31085.1; Type=Erroneous initiation; Evidence={ECO:0000305};
CC -----
CC Copyrighted by the UniProt Consortium, see <https://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution (CC BY 4.0) License
CC -----
DR EMBL; AF078164; AAD31085.1; ALT_INIT; mRNA.
DR EMBL; AC084033; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; CH471054; EAW97091.1; -; Genomic_DNA.
DR EMBL; BC012776; AAH12776.3; -; mRNA.
DR EMBL; BC115381; AAI15382.1; -; mRNA.
DR EMBL; BC115382; AAI15383.1; -; mRNA.
DR CCDS; CCDS41802.1; -.
DR RefSeq; NP_001307337.1; NM_001320408.1.
DR RefSeq; NP_001307338.1; NM_001320409.1.
DR RefSeq; NP_001307339.1; NM_001320410.1.
DR RefSeq; NP_150592.1; NM_033276.3.
DR AlphaFoldDB; Q9Y6H3; -.
DR BioGRID; 124830; 57.
DR IntAct; Q9Y6H3; 38.
DR STRING; 9606.ENSP00000300145; -.
DR MEROPS; M76.001; -.
DR iPTMnet; Q9Y6H3; -.
DR PhosphoSitePlus; Q9Y6H3; -.
DR BioMuta; ATP23; -.
DR DMDM; 224471894; -.
DR EPD; Q9Y6H3; -.
DR jPOST; Q9Y6H3; -.
DR MassIVE; Q9Y6H3; -.
DR MaxQB; Q9Y6H3; -.
DR PaxDb; Q9Y6H3; -.
DR PeptideAtlas; Q9Y6H3; -.
DR PRIDE; Q9Y6H3; -.
DR ProteomicsDB; 86679; -.
DR Antibodypedia; 28994; 97 antibodies from 16 providers.
DR DNASU; 91419; -.
DR Ensembl; ENST00000300145.4; ENSP00000300145.3; ENSG00000166896.9.
DR Ensembl; ENST00000571490.1; ENSP00000460944.1; ENSG00000262145.5.
DR GeneID; 91419; -.
DR KEGG; hsa:91419; -.
DR MANE-Select; ENST00000300145.4; ENSP00000300145.3; NM_033276.4; NP_150592.1.
DR UCSC; uc001sqp.4; human.
DR CTD; 91419; -.
DR DisGeNET; 91419; -.
DR GeneCards; ATP23; -.
DR HGNC; HGNC:29452; ATP23.
DR HPA; ENSG00000166896; Tissue enhanced (testis).
DR MIM; 619760; gene.
DR neXtProt; NX_Q9Y6H3; -.
DR OpenTargets; ENSG00000166896; -.
DR PharmGKB; PA142670557; -.
DR VEuPathDB; HostDB:ENSG00000166896; -.

DR eggNOG; KOG3314; Eukaryota.
 DR GeneTree; ENSGT00390000010948; -.
 DR HOGENOM; CLU_079125_1_0_1; -.
 DR InParanoid; Q9Y6H3; -.
 DR OMA; CFNDREP; -.
 DR OrthoDB; 1288109at2759; -.
 DR PhylomeDB; Q9Y6H3; -.
 DR TreeFam; TF327014; -.
 DR PathwayCommons; Q9Y6H3; -.
 DR Signalink; Q9Y6H3; -.
 DR BioGRID-ORCS; 91419; 60 hits in 1073 CRISPR screens.
 DR ChiTaRS; ATP23; human.
 DR GenomeRNAi; 91419; -.
 DR Pharos; Q9Y6H3; Tbio.
 DR PRO; PR:Q9Y6H3; -.
 DR Proteomes; UP000005640; Chromosome 12.
 DR RNAct; Q9Y6H3; protein.
 DR Bgee; ENSG00000166896; Expressed in right testis and 100 other tissues.
 DR ExpressionAtlas; Q9Y6H3; baseline and differential.
 DR Genevisible; Q9Y6H3; HS.
 DR GO; GO:0030054; C:cell junction; IDA:HPA.
 DR GO; GO:0005829; C:cytosol; IDA:HPA.
 DR GO; GO:0005958; C:DNA-dependent protein kinase-DNA ligase 4 complex; NAS:UniProtKB.
 DR GO; GO:0031314; C:extrinsic component of mitochondrial inner membrane; IBA:GO_Central.
 DR GO; GO:0043231; C:intracellular membrane-bounded organelle; IDA:HPA.
 DR GO; GO:0005886; C:plasma membrane; IDA:HPA.
 DR GO; GO:0004677; F:DNA-dependent protein kinase activity; TAS:UniProtKB.
 DR GO; GO:0046872; F:metal ion binding; IEA:UniProtKB-KW.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA:InterPro.
 DR GO; GO:0006303; P:double-strand break repair via nonhomologous end joining; TAS:UniProtKB.
 DR GO; GO:0034982; P:mitochondrial protein processing; IBA:GO_Central.
 DR GO; GO:0033615; P:mitochondrial proton-transporting ATP synthase complex assembly; IBA:GO_Central.
 DR InterPro; IPR019165; Peptidase_M76_ATP23.
 DR PANTHER; PTHR21711; PTHR21711; 1.
 DR Pfam; PF09768; Peptidase_M76; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 PE 1: Evidence at protein level;
 KW Hydrolase; Metal-binding; Metalloprotease; Protease; Reference proteome.
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 FT /note="Mitochondrial inner membrane protease ATP23 homolog"
 FT /id="PRO_0000330344"
 FT ACT_SITE 126
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU10095"
 FT BINDING 125
 FT /ligand="a divalent metal cation"
 FT /ligand_id="ChEBI:CHEBI:60240"
 FT /ligand_note="catalytic"
 FT /evidence="ECO:0000250"
 FT BINDING 129
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 FT /ligand_id="ChEBI:CHEBI:60240"
 FT /ligand_note="catalytic"
 FT /evidence="ECO:0000250"
 FT VARIANT 48
 FT /note="S -> C (in dbSNP:rs3751325)"
 FT /evidence="ECO:0000269|PubMed:10219089"
 FT /id="VAR_054489"
 SQ SEQUENCE 246 AA; 28081 MW; A9541CBEA299A35F CRC64;
 MAGAPDERRR GPAAGEQLQQ QHVSCQVFPE RLAQGNPQQG FFSSFFTSNQ KCQLRLKLT
 ETNPYVKLLL DAMKHSGCAV NKDRHFCED CNGNVSGGFD ASTSQIVLCQ NNIHNQAHMN
 RVVTHELIHA FDHCRADVW FTNIRHLACS EVRAANLSGD CSLVNEIFRL HFGLKQHHQT
 CVRDRATLSI LAVRNISKEV AKKAVDEVFE SCFNDHEPFG RIPHNKTYAR YHRDFENRD
 RYYSNI

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

User : Fatin

Email : fatinkhan35@gmail.com

Search title : sb1

MS data file : peaklist.xml

Database : SwissProt 2022_04 (568363 sequences; 205318884 residues)

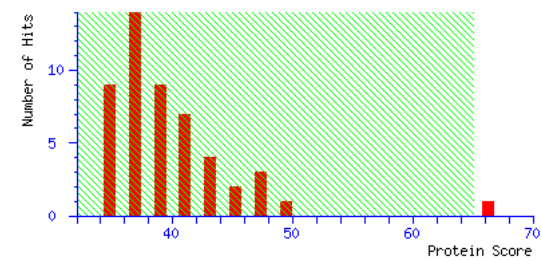
Taxonomy : Eukaryota (eucaryotes) (195824 sequences)

Timestamp : 22 Feb 2023 at 07:23:04 GMT

Top Score : 66 for **SUS2_ARATH**, Sucrose synthase 2 OS=Arabidopsis thaliana OX=3702 GN=SUS2 PE=2 SV=3

Mascot Search Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 65 are significant (p<0.05).



Protein Summary Report

Format As

Protein Summary

Help

Significance threshold p<

0.05

Max. number of hits

50

Preferred taxonomy

All entries

Re-Search All

Search Unmatched

Index

Accession	Mass	Score	Description
1. SUS2_ARATH	92348	66	Sucrose synthase 2 OS=Arabidopsis thaliana OX=3702 GN=SUS2 PE=2 SV=3
2. ATP23_HUMAN	28690	50	Mitochondrial inner membrane protease ATP23 homolog OS=Homo sapiens OX=9606 GN=ATP23 PE=1 SV=3
3. CHO2_AJECH	110398	47	Phosphatidylethanolamine N-methyltransferase OS=Ajellomyces capsulatus (strain H143) OX=544712 GN=CHO2 PE=3 SV=1
4. CHO2_AJECG	111373	47	Phosphatidylethanolamine N-methyltransferase OS=Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 24
5. KN4A_GOSHI	117026	47	Kinesin-like protein KIN-4A OS=Gossypium hirsutum OX=3635 GN=KIN4A PE=2 SV=1
6. AL1A1_RAT	54994	45	Aldehyde dehydrogenase 1A1 OS=Rattus norvegicus OX=10116 GN=Aldh1a1 PE=1 SV=3
7. AL1A1_MOUSE	55060	44	Aldehyde dehydrogenase 1A1 OS=Mus musculus OX=10090 GN=Aldh1a1 PE=1 SV=5
8. TENS4_RAT	78337	42	Tensin-4 OS=Rattus norvegicus OX=10116 GN=Tns4 PE=2 SV=1
9. RMGL_PICST	39097	42	L-rhamnono-gamma-lactonase OS=Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) OX=:
10. THEM5_MOUSE	28132	42	Acyl-coenzyme A thioesterase THEM5 OS=Mus musculus OX=10090 GN=Them5 PE=2 SV=1
11. NCKS1_MOUSE	139396	42	Nck-associated protein 5-like OS=Mus musculus OX=10090 GN=Nckap51 PE=1 SV=1
12. M2OM_RAT	34393	42	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a11 PE=1 SV=3
13. COQ4_PLACH	42308	41	Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial OS=Plasmodium chabaudi OX=5825 GN=PC000176.04.0 PE=3 SV=1
14. DACT1_HUMAN	91145	40	Dapper homolog 1 OS=Homo sapiens OX=9606 GN=DACT1 PE=1 SV=2
15. METK_ASCIM	43211	41	S-adenosylmethionine synthase OS=Ascobolus immersus OX=5191 PE=3 SV=1
16. TRXH_FAGES	13234	40	Thioredoxin H-type OS=Fagopyrum esculentum OX=3617 PE=3 SV=1
17. RL138_PLAVI	80727	40	Secreted RxLR effector protein 138 OS=Plasmopara viticola OX=143451 GN=RXLR138 PE=2 SV=1
18. MYH9_CHICK	227446	40	Myosin-9 OS=Gallus gallus OX=9031 GN=MYH9 PE=2 SV=1
19. DAAM1_HUMAN	123966	39	Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens OX=9606 GN=DAAM1 PE=1 SV=2
20. PDS5D_ARATH	93967	39	Sister chromatid cohesion protein PDS5 homolog D OS=Arabidopsis thaliana OX=3702 GN=PDS5D PE=2 SV=3
21. CSN3_DICDI	47749	39	COP9 signalosome complex subunit 3 OS=Dictyostelium discoideum OX=44689 GN=csn3 PE=1 SV=1
22. ENO_MASBA	48489	39	Enolase OS=Mastigamoeba balamuthi OX=108607 GN=ENOL PE=2 SV=1
23. ATAT_RAT	47469	38	Alpha-tubulin N-acetyltransferase 1 OS=Rattus norvegicus OX=10116 GN=Atat1 PE=1 SV=1
24. GRC14_ORYSJ	11420	38	Putative glutaredoxin-C14 OS=Oryza sativa subsp. japonica OX=39947 GN=GRXC14 PE=3 SV=2
25. Y4660_DICDI	17831	38	Uncharacterized protein DDB_G0281771 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0281771 PE=3 SV=1
26. ZN594_HUMAN	96698	38	Zinc finger protein 594 OS=Homo sapiens OX=9606 GN=ZNF594 PE=2 SV=3
27. RGAP7_ARATH	96582	38	Rho GTPase-activating protein 7 OS=Arabidopsis thaliana OX=3702 GN=ROPGAP7 PE=2 SV=1
28. ATG4_CANGA	55051	38	Probable cysteine protease ATG4 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) O
29. SGF11_DEBHA	11726	37	SAGA-associated factor 11 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 /
30. DDX21_RAT	86540	37	Nucleolar RNA helicase 2 OS=Rattus norvegicus OX=10116 GN=Ddx21 PE=2 SV=1
31. SPAST_DROMO	83699	37	Spastin OS=Drosophila mojavensis OX=7230 GN=spas PE=3 SV=1
32. CHIF_DROME	190471	37	Protein chifon OS=Drosophila melanogaster OX=7227 GN=chif PE=1 SV=2
33. TNF14_RAT	22518	37	Tumor necrosis factor ligand superfamily member 4 OS=Rattus norvegicus OX=10116 GN=Tnfsf4 PE=2 SV=1
34. MP2K2_CYPCA	44461	36	Dual specificity mitogen-activated protein kinase kinase 2 OS=Cyprinus carpio OX=7962 GN=map2k2 PE=2 SV=1
35. RL15_BRANA	10553	36	60S ribosomal protein L15 (Fragment) OS=Brassica napus OX=3708 GN=RPL15 PE=2 SV=1
36. EFGM_CANGA	84785	36	Elongation factor G, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65)
37. REHY_MHEAT	24178	36	1-Cys peroxiredoxin PER1 OS=Triticum aestivum OX=4565 GN=PER1 PE=2 SV=1
38. C7D94_MENGR	56557	36	Cytochrome P450 71D94 OS=Mentha gracilis OX=241069 GN=CYP71D94 PE=2 SV=1
39. CBS_DICDI	54936	36	Cystathionine beta-synthase OS=Dictyostelium discoideum OX=44689 GN=cysB PE=2 SV=2
40. RBS3_LEMGI	20074	36	Ribulose biphosphate carboxylase small subunit, chloroplastic 3 OS=Lemna gibba OX=4470 GN=RBCS3 PE=2 SV=1
41. RBS4_LEMGI	20146	36	Ribulose biphosphate carboxylase small subunit, chloroplastic 4 OS=Lemna gibba OX=4470 GN=RBCS4 PE=2 SV=1
42. REHYA_ORYSJ	24228	36	1-Cys peroxiredoxin A OS=Oryza sativa subsp. indica OX=39946 GN=OsI_27030 PE=2 SV=1
43. REHYA_ORYSJ	24198	36	1-Cys peroxiredoxin A OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0638300 PE=2 SV=1
44. RELB_CHICK	60896	36	Transcription factor RelB homolog OS=Gallus gallus OX=9031 GN=RELB PE=1 SV=2
45. VATB_CHICK	50536	36	V-type proton ATPase subunit B OS=Gallus gallus OX=9031 GN=ATP6V1B PE=3 SV=1
46. GPC1_DANRE	62169	35	Glypican-1 OS=Danio rerio OX=7955 GN=gpc1 PE=2 SV=1
47. YP033_HUMAN	16223	35	Putative uncharacterized protein FLJ42384 OS=Homo sapiens OX=9606 PE=2 SV=1
48. DGKI_MOUSE	119844	35	Diacylglycerol kinase iota OS=Mus musculus OX=10090 GN=Dgki PE=1 SV=1
49. CEP20_HUMAN	19765	35	Centrosomal protein 20 OS=Homo sapiens OX=9606 GN=CEP20 PE=1 SV=1
50. PLK4_BOVIN	101385	35	Serine/threonine-protein kinase PLK4 OS=Bos taurus OX=9913 GN=PLK4 PE=2 SV=1

Results List

1.	SUS2_ARATH	Mass: 92348	Score: 66	Expect: 0.046	Matches: 7
Sucrose synthase 2 OS=Arabidopsis thaliana OX=3702 GN=SUS2 PE=2 SV=3					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.4862	47.5	642 - 649	0 R.WIAAQMN.R.A + Oxidation (M)
1487.7792	1486.7719	1486.7562	10.6	337 - 349	1 R.LLPEAKGTTCNQR.L
1794.8629	1793.8556	1793.9822	-70.53	426 - 441	1 K.LGVIQCNIAHALEKTK.Y
1968.9867	1967.9794	1968.1044	-63.50	37 - 53	1 K.GILQSHQLIDEFLKTVK.V
2211.1582	2210.1509	2210.2422	-41.32	197 - 216	1 R.IQNIPILQGALARAEFLSK.L
2366.2876	2365.2803	2365.1961	35.6	149 - 169	1 R.SSSIGNGVQLNRHLSSIMFR.N + Oxidation (M)
2461.2268	2460.2195	2460.1671	21.3	217 - 237	0 K.LPLATPYSEFEFLQGMGFER.G
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1569.8661, 1842.8889, 2142.1357, 2283.2300					
2.	ATP23_HUMAN	Mass: 28690	Score: 50	Expect: 1.8	Matches: 4
Mitochondrial inner membrane protease ATP23 homolog OS=Homo sapiens OX=9606 GN=ATP23 PE=1 SV=3					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
2211.1582	2210.1509	2210.0803	31.9	136 - 153	1 R.AHVDWFTNIRHLACSEVR.A
2283.2300	2282.2227	2282.0062	94.9	203 - 221	1 K.KAVDEVFESCFNDHEPFGR.I
2366.2876	2365.2803	2365.1233	66.4	11 - 31	0 R.GPAAGEQLQQHVSCQVFPER.L
2461.2268	2460.2195	2460.2583	-15.78	154 - 175	1 R.AANLSDGCSLVNEIFRLHFGLK.Q
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357					
3.	CH02_AJECH	Mass: 110398	Score: 47	Expect: 3.7	Matches: 6
Phosphatidylethanolamine N-methyltransferase OS=Ajellomyces capsulatus (strain H143) OX=544712 GN=CH02 PE=3 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.5477	-13.79	142 - 149	1 R.TLVCWAKK.S
1233.6483	1232.6410	1232.6288	9.89	685 - 695	0 R.LEPDLAGYDLK.D
1794.8629	1793.8556	1793.9539	-54.75	235 - 249	0 R.WTTGMSLVLFNLWVK.L
1842.8889	1841.8816	1841.9424	-32.99	547 - 561	1 K.LTYSGIYRFLNNPER.V
2283.2300	2282.2227	2282.1470	33.2	639 - 657	0 K.ILDESFEFIEEFIEAARPK.L
2366.2876	2365.2803	2365.0492	97.7	948 - 969	1 K.VLAPYSMSRSGASTPTTHEED.- + Oxidation (M)
No match to: 842.5311, 861.0856, 1472.7454, 1487.7792, 1569.8661, 1968.9867, 2142.1357, 2211.1582, 2461.2268					
4.	CH02_AJECG	Mass: 111373	Score: 47	Expect: 3.9	Matches: 6
Phosphatidylethanolamine N-methyltransferase OS=Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) OX=447093 GN=CH02 PE=					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.5477	-13.79	142 - 149	1 R.TLVCWAKK.S
1233.6483	1232.6410	1232.6288	9.89	685 - 695	0 R.LEPDLAGYDLK.D
1794.8629	1793.8556	1793.9539	-54.75	235 - 249	0 R.WTTGMSLVLFNLWVK.L
1842.8889	1841.8816	1841.9424	-32.99	547 - 561	1 K.LTYSGIYRFLNNPER.V
2283.2300	2282.2227	2282.1470	33.2	639 - 657	0 K.ILDESFEFIEEFIEAARPK.L
2366.2876	2365.2803	2365.0492	97.7	957 - 978	1 K.VLAPYSMSRSGASTPTTHEED.- + Oxidation (M)
No match to: 842.5311, 861.0856, 1472.7454, 1487.7792, 1569.8661, 1968.9867, 2142.1357, 2211.1582, 2461.2268					
5.	KN4A_GOSHI	Mass: 117026	Score: 47	Expect: 4.3	Matches: 6
Kinesin-like protein KIN-4A OS=Gossypium hirsutum OX=3635 GN=KIN4A PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
842.5311	841.5238	841.4770	55.6	664 - 670	0 K.LQALNQR.Q
1005.5411	1004.5339	1004.4637	69.8	96 - 104	0 K.TYTMGTGFK.G
1569.8661	1568.8588	1568.8774	-11.82	293 - 308	0 K.GLLALGNVISALGDEK.K
1842.8889	1841.8816	1841.9231	-22.52	702 - 719	1 R.DNLAIANGNGTNGKINEK.G
2283.2300	2282.2227	2282.1875	15.4	962 - 983	1 K.MIPLGLPMKNLVANGQAGNGK.L + 2 Oxidation (M)
2461.2268	2460.2195	2460.3046	-34.59	105 - 127	1 K.GGSQTGIIPQVMNALFSKIENLK.H + Oxidation (M)
No match to: 861.0856, 1233.6483, 1472.7454, 1487.7792, 1794.8629, 1968.9867, 2142.1357, 2211.1582, 2366.2876					
6.	AL1A1_RAT	Mass: 54994	Score: 45	Expect: 6.1	Matches: 5
Aldehyde dehydrogenase 1A1 OS=Rattus norvegicus OX=10116 GN=Aldh1a1 PE=1 SV=3					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.5688	-34.81	491 - 499	1 K.TVAMKISQK.N
1233.6483	1232.6410	1232.5720	56.0	368 - 378	1 K.LECGGGRWGNK.G
1487.7792	1486.7719	1486.7793	-4.99	66 - 78	1 K.AARQAFQIGSPWR.T
2211.1582	2210.1509	2210.0929	26.3	477 - 495	1 R.ELGEHGLYEYTELKTVMAMK.I
2283.2300	2282.2227	2282.0889	58.6	38 - 57	0 K.FPVLNPATEEVICHVEEGDK.A
No match to: 842.5311, 861.0856, 1472.7454, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2366.2876, 2461.2268					
7.	AL1A1_MOUSE	Mass: 55060	Score: 44	Expect: 7.3	Matches: 5
Aldehyde dehydrogenase 1A1 OS=Mus musculus OX=10090 GN=Aldh1a1 PE=1 SV=5					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.5688	-34.81	491 - 499	1 K.TVAMKISQK.N
1233.6483	1232.6410	1232.5720	56.0	368 - 378	1 K.LECGGGRWGNK.G
1487.7792	1486.7719	1486.7793	-4.99	66 - 78	1 K.AARQAFQIGSPWR.T
2211.1582	2210.1509	2210.0929	26.3	477 - 495	1 R.ELGEHGLYEYTELKTVMAMK.I
2283.2300	2282.2227	2282.0889	58.6	38 - 57	0 K.FPVLNPATEEVICHVEEGDK.A
No match to: 842.5311, 861.0856, 1472.7454, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2366.2876, 2461.2268					
8.	TENS4_RAT	Mass: 78337	Score: 44	Expect: 8.4	Matches: 5
Tensin-4 OS=Rattus norvegicus OX=10116 GN=Tns4 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1487.7792	1486.7719	1486.7416	20.4	477 - 490	1 R.DSSSYRGSFGLALK.V
1842.8889	1841.8816	1841.9272	-24.72	467 - 482	1 R.TEKPGETFVIRDSSSYR.G
1968.9867	1967.9794	1967.9297	25.3	189 - 206	1 R.ETRSSSNESLIFSGNQGR.G
2142.1357	2141.1285	2140.9695	74.2	560 - 580	0 K.ELGGAEPASDSPHTGQTSCLK.I
2366.2876	2365.2803	2365.1308	63.2	163 - 184	1 R.CSSPCVTPPFSGPRSGGLFLSR.D
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1569.8661, 1794.8629, 2211.1582, 2283.2300, 2461.2268					
9.	RMGL_PICST	Mass: 39097	Score: 42	Expect: 11	Matches: 4
L-rhamnono-gamma-lactonase OS=Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) OX=322104 GN=LRA2 PE=1 SV=2					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.4967	37.0	325 - 332	0 K.IYYSNAFK.A

1472.7454 1471.7381 1471.8035 -44.42 89 - 101 1 K.LLPEEGVSTPFKR.R
1842.8889 1841.8816 1841.9887 -58.12 84 - 100 1 R.NINGKLLPEEGVSTPFK.R
2461.2268 2460.2195 2460.3160 -39.22 103 - 125 1 R.LIKAMIPFAPMPLGSAGVEEYVK.A
No match to: 842.5311, 861.0856, 1233.6483, 1487.7792, 1569.8661, 1794.8629, 1968.9867, 2142.1357, 2211.1582, 2283.2300, 2366.2876

10. THEM5_MOUSE Mass: 28132 Score: 42 Expect: 11 Matches: 4
Acyl-coenzyme A thioesterase THEM5 OS=Mus musculus OX=10090 GN=Them5 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
842.5311 841.5238 841.4480 90.1 21 - 27 0 R.SPCLLP.R.V
1233.6483 1232.6410 1232.6990 -46.99 4 - 14 1 R.TSFQGVRLVR.H
1487.7792 1486.7719 1486.6908 54.5 214 - 225 1 K.LYMSCIAQSRDK.Q + Oxidation (M)
1968.9867 1967.9794 1968.0316 -26.53 93 - 110 1 R.DHIQGLKLPFGLETASDK.Q
No match to: 861.0856, 1005.5411, 1472.7454, 1569.8661, 1794.8629, 1842.8889, 2142.1357, 2211.1582, 2283.2300, 2366.2876, 2461.2268

11. NCK5L_MOUSE Mass: 139396 Score: 42 Expect: 12 Matches: 6
Nck-associated protein 5-like OS=Mus musculus OX=10090 GN=Nckap5l PE=1 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1233.6483 1232.6410 1232.5786 50.7 375 - 386 0 K.SAWGASTPEATR.L
1472.7454 1471.7381 1471.7388 -0.47 773 - 785 1 K.SRLAGALCPQMPR.T + Oxidation (M)
1487.7792 1486.7719 1486.6583 76.4 617 - 630 1 K.SMDRAGESPASHR.R
2142.1357 2141.1285 2140.9735 72.4 596 - 616 0 R.SPGAPSPGLPESCPYSGPQEK.S
2283.2300 2282.2227 2282.2383 -6.82 428 - 450 1 K.SKLQIGPPSPGDAQGPLLPSPAR.G
2366.2876 2365.2803 2365.3118 -13.29 430 - 453 1 K.LQIGPPSPGDAQGPLLPSPARGLK.F
No match to: 842.5311, 861.0856, 1005.5411, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2211.1582, 2461.2268

12. M2OM_RAT Mass: 34393 Score: 42 Expect: 14 Matches: 4
Mitochondrial 2-oxoglutarate/malate carrier protein OS=Rattus norvegicus OX=10116 GN=Slc25a11 PE=1 SV=3
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.4709 62.7 1 - 11 0 -.MAATASPGAGR.M + Oxidation (M)
1794.8629 1793.8556 1793.8804 -13.79 247 - 260 1 R.IQNMRMIDEKPEYK.N
2283.2300 2282.2227 2282.2457 -10.06 123 - 146 0 K.ALIGMTAGTAGAFVGPAPAEVALIR.M
2366.2876 2365.2803 2365.2504 12.6 289 - 308 1 R.LGPHTVLTFIFLEQMNKAYK.R + Oxidation (M)
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1842.8889, 1968.9867, 2142.1357, 2211.1582, 2461.2268

13. COQ4_PLACH Mass: 42308 Score: 41 Expect: 16 Matches: 4
Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial OS=Plasmodium chabaudi OX=5825 GN=PC000176.04.0 PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1487.7792 1486.7719 1486.6827 60.0 205 - 216 0 K.DDNYIDEISLK.Q
1842.8889 1841.8816 1841.8988 -9.33 190 - 204 0 K.IPPNFLNPNFDYTYK.D
1968.9867 1967.9794 1968.1156 -69.19 72 - 87 1 K.NKPLLIRQDIQFNEK.K
2142.1357 2141.1285 2141.2686 -65.45 163 - 181 0 K.LPITLLAILVAPFMTPLYR.F
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1569.8661, 1794.8629, 2211.1582, 2283.2300, 2366.2876, 2461.2268

14. DACT1_HUMAN Mass: 91145 Score: 41 Expect: 17 Matches: 5
Dapper homolog 1 OS=Homo sapiens OX=9606 GN=DACT1 PE=1 SV=2
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5013 32.5 653 - 662 1 R.AGSRAHGHGR.E
1842.8889 1841.8816 1841.8578 13.0 298 - 315 0 R.LGNHASDICGGSELDVAVK.T
1968.9867 1967.9794 1967.9735 3.02 432 - 450 1 K.RVPLPEGCPGSAASDLQSK.H
2142.1357 2141.1285 2141.0575 33.1 397 - 417 0 K.QACLPSPGGIPSLNNGTFSPPK.Q
2283.2300 2282.2227 2282.1073 50.6 455 - 476 1 K.TAKPASQEHARCSAIGTGESPK.E
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 2211.1582, 2366.2876, 2461.2268

15. METK_ASCIM Mass: 43211 Score: 41 Expect: 17 Matches: 4
S-adenosylmethionine synthase OS=Ascobolus immersus OX=5191 PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1233.6483 1232.6410 1232.6223 15.2 1 - 11 0 -.MSIPVNPNSFK.G
1842.8889 1841.8816 1841.9160 -18.63 178 - 194 0 K.TQVTIEYHDGGAVVPK.K
2142.1357 2141.1285 2141.0964 15.0 198 - 216 1 K.TVVVSAQHSEDTTEELRK.E
2283.2300 2282.2227 2282.1439 34.5 58 - 77 1 K.TGMIMVFGIEITTKAHLDYQK.I
No match to: 842.5311, 861.0856, 1005.5411, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1968.9867, 2211.1582, 2366.2876, 2461.2268

16. TRXH_FAGES Mass: 13234 Score: 40 Expect: 18 Matches: 3
Thioredoxin H-type OS=Fagopyrum esculentum OX=3617 PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1233.6483 1232.6410 1232.6839 -34.74 78 - 88 0 K.VEAMPSFVILK.E
1794.8629 1793.8556 1793.8593 -2.05 29 - 43 0 K.LIVIDFTASWCGPCR.V
2142.1357 2141.1285 2140.9847 67.1 2 - 19 0 M.AEEAQVIACHTVQEWNEK.F
No match to: 842.5311, 861.0856, 1005.5411, 1472.7454, 1487.7792, 1569.8661, 1842.8889, 1968.9867, 2211.1582, 2283.2300, 2366.2876, 2461.2268

17. RL138_PLAVT Mass: 80727 Score: 40 Expect: 19 Matches: 5
Secreted RxLR effector protein 138 OS=Plasmodium viticola OX=143451 GN=RXLR138 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5039 29.8 540 - 548 0 K.SAHTTAVYR.Q
1842.8889 1841.8816 1841.8333 26.3 175 - 190 0 R.SVPQHDYHSAPQDSFK.I
1968.9867 1967.9794 1968.0001 -10.53 669 - 683 0 K.LVIMYDLFIIFCHER.V
2211.1582 2210.1509 2210.0089 64.3 368 - 385 0 R.EELVSVDELMLHDFEDFK.S + Oxidation (M)
2283.2300 2282.2227 2282.2457 -10.05 1 - 22 1 -.MRSAFYVAIVLLVAAGSQTAAC.C + Oxidation (M)
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 2142.1357, 2366.2876, 2461.2268

18. MYH9_CHICK Mass: 227446 Score: 40 Expect: 20 Matches: 7
Myosin-9 OS=Gallus gallus OX=9031 GN=MYH9 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1233.6483 1232.6410 1232.5408 81.3 1343 - 1352 0 K.EQLEEEEAQK.R
1487.7792 1486.7719 1486.7011 47.6 1877 - 1888 1 K.RQLEEEEAQK.R
1794.8629 1793.8556 1793.8175 21.3 1373 - 1388 1 K.MDDGLGCLIEAEEAKK.K + Oxidation (M)
1968.9867 1967.9794 1968.0779 -50.03 976 - 992 1 K.LEEDVIVLEDQNLKLAK.E
2142.1357 2141.1285 2141.0059 57.3 588 - 606 0 K.NMDPLNDNIATLLHQSSDK.F + Oxidation (M)

2211.1582 2210.1509 2210.0008 67.9 1898 - 1917 1 R.ELDDATETADAMNREVSSLK.S + Oxidation (M)
2461.2268 2460.2195 2460.1438 30.8 940 - 959 1 K.KMQQNIQELEEQLLEESAR.Q
No match to: 842.5311, 861.0856, 1005.5411, 1472.7454, 1569.8661, 1842.8889, 2283.2300, 2366.2876

19. DAAM1_HUMAN Mass: 123966 Score: 39 Expect: 24 Matches: 6
Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens OX=9606 GN=DAAM1 PE=1 SV=2
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5212 12.6 726 - 733 0 K.DMLEQLLK.F + Oxidation (M)
1569.8661 1568.8588 1568.7583 64.1 655 - 667 1 R.QQDFVNSNSKQK.E
1968.9867 1967.9794 1967.9952 -8.03 639 - 654 1 K.ILDLEDLERTFSAYQR.Q
2211.1582 2210.1509 2210.1769 -11.75 807 - 826 1 R.SGALKQLLEVLVAFGNMKNK.G + Oxidation (M)
2283.2300 2282.2227 2282.0677 67.9 331 - 348 1 R.HLDFFEMLRNEDELEFAK.R
2461.2268 2460.2195 2460.2972 -31.57 196 - 218 0 R.AHVLAHSEINVIAQSLSTENIK.T
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1794.8629, 1842.8889, 2142.1357, 2366.2876

20. PDS5D_ARATH Mass: 93967 Score: 39 Expect: 25 Matches: 5
Sister chromatid cohesion protein PDS5 homolog D OS=Arabidopsis thaliana OX=3702 GN=PDS5D PE=2 SV=3
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5437 -9.78 516 - 524 1 K.KMVSQVAAR.Q + Oxidation (M)
1233.6483 1232.6410 1232.6765 -28.74 127 - 137 1 K.KAEFVLDNVAK.V
1968.9867 1967.9794 1967.8960 42.4 590 - 606 0 R.VIYSDGDSEELNLTEER.W
2142.1357 2141.1285 2141.0350 43.6 91 - 108 1 R.ITAPETPYSDLMKEIFR.L + Oxidation (M)
2366.2876 2365.2803 2365.1372 60.5 340 - 359 1 R.KPNSLMNPEDYDISWLSGKR.D + Oxidation (M)
No match to: 842.5311, 861.0856, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 2211.1582, 2283.2300, 2461.2268

21. CSN3_DICDI Mass: 47749 Score: 39 Expect: 26 Matches: 4
COP9 signalosome complex subunit 3 OS=Dictyostelium discoideum OX=44689 GN=csn3 PE=1 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
842.5311 841.5238 841.5385 -17.48 15 - 21 1 K.NLKNLLK.Y
1842.8889 1841.8816 1841.7625 64.7 403 - 418 0 K.NTGQLSQYEDPMEDIS.- + Oxidation (M)
1968.9867 1967.9794 1968.0238 -22.53 301 - 317 1 K.KLTQTFTMTLSINDIAEK.V + Oxidation (M)
2283.2300 2282.2227 2282.0372 81.3 398 - 418 1 K.LASGKNTGQLSQYEDPMEDIS.-
No match to: 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 2142.1357, 2211.1582, 2366.2876, 2461.2268

22. ENO_MASBA Mass: 48489 Score: 39 Expect: 27 Matches: 4
Enolase OS=Mastigamoeba balamuthi OX=108607 GN=ENOL PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1487.7792 1486.7719 1486.8065 -23.27 269 - 282 1 K.KTPDMLVSGEGLIK.L
1794.8629 1793.8556 1793.9999 -80.43 317 - 332 1 R.NRIQIVGDDLVTNPK.R
2283.2300 2282.2227 2282.0485 76.3 34 - 55 1 R.SAVPSGASTGIYEACELRDGDK.S
2461.2268 2460.2195 2460.1631 22.9 232 - 254 1 K.QAGYTGKIEIGMDVAASSFWDAK.E + Oxidation (M)
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1569.8661, 1842.8889, 1968.9867, 2142.1357, 2211.1582, 2366.2876

23. ATAT_RAT Mass: 47469 Score: 38 Expect: 29 Matches: 4
Alpha-tubulin N-acetyltransferase 1 OS=Rattus norvegicus OX=10116 GN=Atat1 PE=1 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5655 -31.47 103 - 110 1 K.KLFLVDDR.E
1487.7792 1486.7719 1486.8078 -24.17 70 - 81 1 R.MQSNRHVIYVLK.D
1794.8629 1793.8556 1793.9828 -70.89 241 - 255 1 R.EFLKVAVEPPWPLNR.A
2366.2876 2365.2803 2365.2325 20.2 389 - 410 1 R.AQAPPAQSHMVGDIILNARVIR.N + Oxidation (M)
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1569.8661, 1842.8889, 1968.9867, 2142.1357, 2211.1582, 2283.2300, 2461.2268

24. GRC14_ORYSJ Mass: 11420 Score: 38 Expect: 29 Matches: 3
Putative glutaredoxin-C14 OS=Oryza sativa subsp. japonica OX=39947 GN=GRXC14 PE=3 SV=2
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5324 1.43 51 - 58 1 K.EMERALLK.L + Oxidation (M)
2142.1357 2141.1285 2140.9890 65.1 12 - 29 0 R.AVVIFTLSSCCMCHTVTR.L
2211.1582 2210.1509 2210.0790 32.5 30 - 48 0 R.LFCDLGVNALVHQLDQDPR.G
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2283.2300, 2366.2876, 2461.2268

25. Y4660_DICDI Mass: 17831 Score: 38 Expect: 30 Matches: 3
Uncharacterized protein DDB_G0281771 OS=Dictyostelium discoideum OX=44689 GN=DDB_G0281771 PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.4523 81.2 68 - 75 1 R.VDREDES.R
1968.9867 1967.9794 1968.0065 -13.75 33 - 50 1 R.KSIVSDHWMNVANSIDGK.T
2142.1357 2141.1285 2141.0310 45.5 71 - 88 1 R.EDESRIILNMYINVTSVK.A + Oxidation (M)
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 2211.1582, 2283.2300, 2366.2876, 2461.2268

26. ZN594_HUMAN Mass: 96698 Score: 38 Expect: 30 Matches: 5
Zinc finger protein 594 OS=Homo sapiens OX=9606 GN=ZNF594 PE=2 SV=3
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1472.7454 1471.7381 1471.7718 -22.89 232 - 243 1 R.IHSRGKPYLCNK.C
1569.8661 1568.8588 1568.7253 85.1 76 - 90 0 K.AIVGEIGHGNEGEK.I
1794.8629 1793.8556 1793.7713 47.0 645 - 659 0 R.IHTGKPYECSECGK.A
1842.8889 1841.8816 1841.8764 2.86 288 - 302 1 R.IHTGKPLKCNCEK.A
2211.1582 2210.1509 2209.9745 79.8 450 - 467 1 R.HHRVHTGKPYECSECGK.A
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1487.7792, 1968.9867, 2142.1357, 2283.2300, 2366.2876, 2461.2268

27. RGAP7_ARATH Mass: 96582 Score: 38 Expect: 32 Matches: 5
Rho GTPase-activating protein 7 OS=Arabidopsis thaliana OX=3702 GN=ROPGAP7 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1472.7454 1471.7381 1471.7644 -17.87 679 - 690 0 K.VAELHHQLNQQR.Q
1487.7792 1486.7719 1486.7528 12.8 271 - 283 1 R.SAIAETFPENRR.L
1842.8889 1841.8816 1841.9483 -36.18 193 - 208 1 K.IEGILRQSADVEEVER.R
2142.1357 2141.1285 2141.1076 9.74 615 - 632 1 R.LSLEQDVSRLEQLQAER.D
2211.1582 2210.1509 2210.0756 34.1 716 - 733 1 R.FLQQDFDSTLAYVNHKQ.Q
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1569.8661, 1794.8629, 1968.9867, 2283.2300, 2366.2876, 2461.2268

28.	ATG4_CANGA	Mass: 55051	Score: 38	Expect: 34	Matches: 4
Probable cysteine protease ATG4 OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) OX=284593 GN=ATG4 PE=3 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.4927	41.0	94 - 101	0 R.TNFEPIER.A
2211.1582	2210.1509	2210.1477	1.46	1 - 19	1 -.METIHNISNRLQEVLATNK.S
2283.2300	2282.2227	2282.1327	39.4	339 - 358	0 K.LNFSDLDPMSLLGLLPCSK.W + Oxidation (M)
2366.2876	2365.2803	2365.1889	38.7	199 - 219	1 R.IYNKIAPGEWFGPATTATCIR.Y
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2461.2268					
29.	SGF11_DEBHA	Mass: 11726	Score: 37	Expect: 36	Matches: 3
SAGA-associated factor 11 OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / BCRC 21394 / JCM 1990 / NBRC 0083 / IGC 2968) OX=284592 GN=SG					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.5138	20.0	34 - 42	1 K.STLGENEKK.S
1472.7454	1471.7381	1471.7228	10.4	42 - 54	1 K.KSVFIDDIIMSSSK.D + Oxidation (M)
2283.2300	2282.2227	2282.1286	41.2	1 - 19	0 -.MTEKPTVYQSLDMLNILR.Q + Oxidation (M)
No match to: 842.5311, 861.0856, 1233.6483, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2211.1582, 2366.2876, 2461.2268					
30.	DDX21_RAT	Mass: 86540	Score: 37	Expect: 39	Matches: 5
Nucleolar RNA helicase 2 OS=Rattus norvegicus OX=10116 GN=Ddx21 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
842.5311	841.5238	841.4545	82.3	174 - 180	0 K.EIPVEQK.E
1233.6483	1232.6410	1232.6917	-41.13	201 - 211	0 R.GVNFLFPIQAK.T
1487.7792	1486.7719	1486.7926	-13.93	301 - 314	1 R.MRSGIDILVGTPGR.I + Oxidation (M)
1842.8889	1841.8816	1841.9537	-39.10	212 - 227	1 K.TFHHVYSGKDLIAQAR.T
2142.1357	2141.1285	2140.9317	91.9	11 - 29	0 K.SESEGTEESMETLQKPSEK.K + Oxidation (M)
No match to: 861.0856, 1005.5411, 1472.7454, 1569.8661, 1794.8629, 1968.9867, 2211.1582, 2283.2300, 2366.2876, 2461.2268					
31.	SPAST_DROMO	Mass: 83699	Score: 37	Expect: 39	Matches: 5
Spastin OS=Drosophila mojavensis OX=7230 GN=spas PE=3 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
842.5311	841.5238	841.4419	97.3	214 - 219	1 K.QKHHHR.R
1005.5411	1004.5339	1004.4637	69.9	128 - 135	0 R.YLYCASTK.V
1569.8661	1568.8588	1568.8522	4.22	674 - 688	1 K.QGSPLDTEALARLAK.I
2142.1357	2141.1285	2141.0674	28.5	542 - 562	0 R.AVATECSATFLNISAASLTSK.Y
2211.1582	2210.1509	2210.1583	-3.33	580 - 598	0 R.HLQPSIIFIDEVDSLLSER.S
No match to: 861.0856, 1233.6483, 1472.7454, 1487.7792, 1794.8629, 1842.8889, 1968.9867, 2283.2300, 2366.2876, 2461.2268					
32.	CHIF_DROME	Mass: 190471	Score: 37	Expect: 42	Matches: 6
Protein chiffon OS=Drosophila melanogaster OX=7227 GN=chif PE=1 SV=2					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1569.8661	1568.8588	1568.8344	15.5	1041 - 1054	0 R.EHASTLALVSCIIR.Q
1794.8629	1793.8556	1793.8730	-9.69	988 - 1003	1 R.EFASGSMGDRVQLIER.V
2142.1357	2141.1285	2140.9436	86.3	1258 - 1275	0 K.EYDIEFDQISPEVESEGR.E
2211.1582	2210.1509	2210.0711	36.1	1218 - 1236	1 K.GLLEYEMETCALKDQAR.Q
2366.2876	2365.2803	2365.2311	20.8	1651 - 1674	1 K.AASSCAAEAATAAVKSLAISQFLK.K
2461.2268	2460.2195	2460.2195	0.03	41 - 59	1 K.RPLCHFIFYLDICDHQLAK.R
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1842.8889, 1968.9867, 2283.2300					
33.	TNFL4_RAT	Mass: 22518	Score: 37	Expect: 43	Matches: 3
Tumor necrosis factor ligand superfamily member 4 OS=Rattus norvegicus OX=10116 GN=Tnfsf4 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1472.7454	1471.7381	1471.7606	-15.27	125 - 137	0 R.SPIFVPMLNNGQR.V
2211.1582	2210.1509	2210.0022	67.3	1 - 20	0 -.MEGEGVQPDPENLENGSRPR.F
2283.2300	2282.2227	2282.1803	18.6	36 - 56	0 K.AAGLLLCVVYVCLQFSSSPAK.D
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2366.2876, 2461.2268					
34.	MP2K2_CYPCA	Mass: 44461	Score: 36	Expect: 44	Matches: 4
Dual specificity mitogen-activated protein kinase 2 OS=Cyprinus carpio OX=7962 GN=map2k2 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1233.6483	1232.6410	1232.6522	-9.05	359 - 368	1 K.MLMGHTFIKR.A
1569.8661	1568.8588	1568.7141	92.3	383 - 397	0 K.TMGLPQPSTPTTHSAE.- + Oxidation (M)
1842.8889	1841.8816	1841.8076	40.2	368 - 382	1 K.RAEVEEVDFAGWMCK.T + Oxidation (M)
2461.2268	2460.2195	2460.1528	27.1	330 - 349	1 K.LPHGVFTTDFEEFVMKCLMK.N + 2 Oxidation (M)
No match to: 842.5311, 861.0856, 1005.5411, 1472.7454, 1487.7792, 1794.8629, 1968.9867, 2142.1357, 2211.1582, 2283.2300, 2366.2876					
35.	RL15_BRANA	Mass: 10553	Score: 36	Expect: 46	Matches: 3
60S ribosomal protein L15 (Fragment) OS=Brassica napus OX=3708 GN=RPL15 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
842.5311	841.5238	841.5385	-17.51	80 - 87	0 R.GATVLLLR.S
1233.6483	1232.6410	1232.6006	32.8	62 - 71	0 K.VLCMVNPQTR.E + Oxidation (M)
1794.8629	1793.8556	1793.9757	-66.90	57 - 71	1 K.RPVPKVLCMVNPQTR.E
No match to: 861.0856, 1005.5411, 1472.7454, 1487.7792, 1569.8661, 1842.8889, 1968.9867, 2142.1357, 2211.1582, 2283.2300, 2366.2876, 2461.2268					
36.	EFGM_CANGA	Mass: 84785	Score: 36	Expect: 46	Matches: 5
Elongation factor G, mitochondrial OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) OX=284593 GN=MEF1 PE=3 S					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.5212	12.6	238 - 246	0 K.GVVDLLDMK.A + Oxidation (M)
1569.8661	1568.8588	1568.8198	24.9	379 - 391	1 K.LEEGKYGQLTYIR.V
1794.8629	1793.8556	1793.8836	-15.56	544 - 558	1 R.ESITIPSEFDYTHKK.Q
1842.8889	1841.8816	1841.8036	42.4	102 - 117	1 R.GRDNVGATMDFMDLER.E + Oxidation (M)
2366.2876	2365.2803	2365.1657	48.4	507 - 526	1 K.ETVISGMGELHLEIYVERMK.R + 2 Oxidation (M)
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1487.7792, 1968.9867, 2142.1357, 2211.1582, 2283.2300, 2461.2268					
37.	REHY_WHEAT	Mass: 24178	Score: 36	Expect: 47	Matches: 3
1-Cys peroxiredoxin PER1 OS=Triticum aestivum OX=4565 GN=PER1 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
2142.1357	2141.1285	2141.0059	57.3	109 - 127	1 K.QLNMVDPDKDAEQGLPSR.T

2211.1582 2210.1509 2210.0889 28.1 1 - 21 0 -.MPGLTIGDTPVNLELDSTHGK.I + Oxidation (M)
2366.2876 2365.2803 2365.1624 49.9 84 - 104 1 K.DIEAYKPGSKVTYPIADPDR.S
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2283.2300, 2461.2268

38. C7D94 MENG Mass: 56557 Score: 36 Expect: 47 Matches: 4
Cytochrome P450 71D94 OS=Mentha gracilis OX=241069 GN=CYP71D94 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
842.5311 841.5238 841.4922 37.5 24 - 29 1 K.QWRKPK.S
1794.8629 1793.8556 1793.8697 -7.82 92 - 107 1 K.VLDPNFADRFDSVSGR.I
1968.9867 1967.9794 1967.9159 32.3 367 - 382 1 R.QSREECEINGFYIPAR.T
2366.2876 2365.2803 2365.3899 -46.33 38 - 58 0 K.LPVIGHLHLWGLPPQHLLR.S
No match to: 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1842.8889, 2142.1357, 2211.1582, 2283.2300, 2461.2268

39. CBS DICDI Mass: 54936 Score: 36 Expect: 48 Matches: 4
Cystathionine beta-synthase OS=Dictyostelium discoideum OX=44689 GN=cysB PE=2 SV=2
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
842.5311 841.5238 841.5021 25.8 137 - 144 0 K.ALGAEIIR.T
1569.8661 1568.8588 1568.7729 54.8 76 - 89 1 R.IGHRMIVDAEESGR.I
1968.9867 1967.9794 1967.9952 -8.04 145 - 163 1 R.TPTEAAFDAPESHIGVAKK.L
2211.1582 2210.1509 2210.2093 -26.40 31 - 50 1 K.LIMDNILDNIGGTPLVRVKN.V + Oxidation (M)
No match to: 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1794.8629, 1842.8889, 2142.1357, 2283.2300, 2366.2876, 2461.2268

40. RBS3 LEMGI Mass: 20074 Score: 36 Expect: 52 Matches: 3
Ribulose biphosphate carboxylase small subunit, chloroplastic 3 OS=Lemna gibba OX=4470 GN=RBCS3 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1487.7792 1486.7719 1486.6578 76.8 1 - 15 0 -.MASSMMASTAAVAR.A + 2 Oxidation (M)
2211.1582 2210.1509 2210.0235 57.7 128 - 147 0 K.LPMFGCTDASQVIAEEVEAK.K + Oxidation (M)
2283.2300 2282.2227 2282.1041 52.0 86 - 103 1 K.EVDYLLRNDWVPCIEFSK.E
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2366.2876, 2461.2268

41. RBS4 LEMGI Mass: 20146 Score: 36 Expect: 52 Matches: 3
Ribulose biphosphate carboxylase small subunit, chloroplastic 4 OS=Lemna gibba OX=4470 GN=RBCS4 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1487.7792 1486.7719 1486.6578 76.8 1 - 15 0 -.MASSMMASTAAVAR.A + 2 Oxidation (M)
2211.1582 2210.1509 2210.0235 57.7 128 - 147 0 K.LPMFGCTDASQVIAEEVEAK.K + Oxidation (M)
2283.2300 2282.2227 2282.1041 52.0 86 - 103 1 K.EVDYLLRNDWVPCIEFSK.E
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2366.2876, 2461.2268

42. REHYA ORYSI Mass: 24228 Score: 36 Expect: 54 Matches: 3
1-Cys peroxiredoxin A OS=Oryza sativa subsp. indica OX=39946 GN=OsI_27030 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1968.9867 1967.9794 1967.9741 2.68 198 - 215 1 K.FPQGFDTADLPSGKGYLR.F
2142.1357 2141.1285 2141.0398 41.4 141 - 158 1 K.LSFLYPSCVGRNMDEVVR.A
2211.1582 2210.1509 2210.0889 28.1 1 - 21 0 -.MPGLTIGDTPVNLELDSTHGK.I + Oxidation (M)
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 2283.2300, 2366.2876, 2461.2268

43. REHYA ORYSJ Mass: 24198 Score: 36 Expect: 54 Matches: 3
1-Cys peroxiredoxin A OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0638300 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1968.9867 1967.9794 1967.9741 2.68 198 - 215 1 K.FPQGFDTADLPSGKGYLR.F
2142.1357 2141.1285 2141.0398 41.4 141 - 158 1 K.LSFLYPACVGRNMDEVVR.A + Oxidation (M)
2211.1582 2210.1509 2210.0889 28.1 1 - 21 0 -.MPGLTIGDTPVNLELDSTHGK.I + Oxidation (M)
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 2283.2300, 2366.2876, 2461.2268

44. RELB CHICK Mass: 60896 Score: 36 Expect: 55 Matches: 4
Transcription factor RelB homolog OS=Gallus gallus OX=9031 GN=RELB PE=1 SV=2
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1472.7454 1471.7381 1471.7922 -36.79 296 - 308 0 R.QLSPVLSEPIFDK.K
2142.1357 2141.1285 2141.0959 15.2 532 - 549 1 R.YRPPPLKKGWSQWAPPHQ.-
2283.2300 2282.2227 2282.0559 73.1 324 - 343 1 K.ESGPCTGGEELYLLCDKVQK.E
2366.2876 2365.2803 2365.1056 73.9 270 - 288 1 K.NHQEVDMMNVVRIQFQASYR.D
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2211.1582, 2461.2268

45. VATB CHICK Mass: 50536 Score: 36 Expect: 55 Matches: 4
V-type proton ATPase subunit B OS=Gallus gallus OX=9031 GN=ATP6V1B PE=3 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
842.5311 841.5238 841.4406 98.9 256 - 262 1 R.EEVPGR.R
1005.5411 1004.5339 1004.5728 -38.81 427 - 434 1 R.IFPKEMLK.R
1842.8889 1841.8816 1841.9166 -18.99 10 - 28 1 R.MVNGAGPGGAREQAAALTR.D + Oxidation (M)
1968.9867 1967.9794 1968.1230 -72.95 328 - 344 1 R.QIYPPINVLP.LSR.LMK.S
No match to: 861.0856, 1233.6483, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 2142.1357, 2211.1582, 2283.2300, 2366.2876, 2461.2268

46. GPC1 DANRE Mass: 62169 Score: 35 Expect: 56 Matches: 4
Glypican-1 OS=Danio rerio OX=7955 GN=gpc1 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5403 -6.42 80 - 87 1 R.REFEGLVR.E
1487.7792 1486.7719 1486.7528 12.8 194 - 206 0 K.QTETLRFPGDAPR.E
2142.1357 2141.1285 2140.9470 84.7 174 - 193 0 K.ASDPETASLLSDDFLDCASK.Q
2461.2268 2460.2195 2460.3145 -38.61 1 - 25 0 -.MDLTAVALLVSLVSVLSAENAGGK.A + Oxidation (M)
No match to: 842.5311, 861.0856, 1233.6483, 1472.7454, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2211.1582, 2283.2300, 2366.2876

47. YP033 HUMAN Mass: 16223 Score: 35 Expect: 58 Matches: 3
Putative uncharacterized protein FLJ42384 OS=Homo sapiens OX=9606 PE=2 SV=1
Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide
1005.5411 1004.5339 1004.5378 -3.93 1 - 7 1 -.MWPFR.LR.C
1233.6483 1232.6410 1232.6513 -8.34 103 - 113 1 R.ASPREQATVFK.R
1472.7454 1471.7381 1471.7064 21.5 115 - 126 0 R.ICAPLHAEVFCR.A
No match to: 842.5311, 861.0856, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2142.1357, 2211.1582, 2283.2300, 2366.2876, 2461.2268

48.	DGKI_MOUSE	Mass: 119844	Score: 35	Expect: 61	Matches: 5
Diacylglycerol kinase iota OS=Mus musculus OX=10090 GN=Dgki PE=1 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1472.7454	1471.7381	1471.7817	-29.63	1015 - 1028	0 R.AVCQLLV DAGASLR.Q
1794.8629	1793.8556	1793.8519	2.09	822 - 836	1 R.LSPRWCF LDATSADR.F
2142.1357	2141.1285	2141.0099	55.4	400 - 417	1 R.QVFDLSQEGPKDALEYR.K + Oxidation (M)
2211.1582	2210.1509	2209.9984	69.0	899 - 917	1 K.RMLSDSGMITPHYEDSDLK.D + Oxidation (M)
2366.2876	2365.2803	2365.1480	55.9	661 - 680	1 R.EVMLLTYKSI PMQVDGEPCL.L
No match to: 842.5311, 861.0856, 1005.5411, 1233.6483, 1487.7792, 1569.8661, 1842.8889, 1968.9867, 2283.2300, 2461.2268					
49.	CEP20_HUMAN	Mass: 19765	Score: 35	Expect: 65	Matches: 3
Centrosomal protein 20 OS=Homo sapiens OX=9606 GN=CEP20 PE=1 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1005.5411	1004.5339	1004.5291	4.76	120 - 128	0 K.DGIQNAFLK.G
1233.6483	1232.6410	1232.6077	27.0	59 - 67	1 R.EYLEFNKYK.Y
2142.1357	2141.1285	2141.1997	-33.26	101 - 119	1 K.DNTIPLLYGILAHFLRGTK.D
No match to: 842.5311, 861.0856, 1472.7454, 1487.7792, 1569.8661, 1794.8629, 1842.8889, 1968.9867, 2211.1582, 2283.2300, 2366.2876, 2461.2268					
50.	PLK4_BOVIN	Mass: 101385	Score: 35	Expect: 66	Matches: 5
Serine/threonine-protein kinase PLK4 OS=Bos taurus OX=9913 GN=PLK4 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Peptide
1233.6483	1232.6410	1232.6261	12.1	105 - 114	1 R.RKPFSENEAR.H
1569.8661	1568.8588	1568.7327	80.4	1 - 13	1 -.MATCIGEKIEDFR.V
1968.9867	1967.9794	1968.0026	-11.79	223 - 239	1 K.VVLADYEMPTFLSREAK.D
2142.1357	2141.1285	2141.0688	27.9	249 - 267	1 R.NPADRLSLSSVLDHPFMSR.N
2211.1582	2210.1509	2210.1405	4.71	218 - 236	1 K.NTLNKVVLADYEMPTFLSR.E
No match to: 842.5311, 861.0856, 1005.5411, 1472.7454, 1487.7792, 1794.8629, 1842.8889, 2283.2300, 2366.2876, 2461.2268					

Search Parameters

Type of search	: Peptide Mass Fingerprint
Enzyme	: Trypsin
Fixed modifications	: Carbamidomethyl (C)
Variable modifications	: Oxidation (M)
Mass values	: Monoisotopic
Protein Mass	: Unrestricted
Peptide Mass Tolerance	: ± 100 ppm
Peptide Charge State	: 1+
Max Missed Cleavages	: 1
Number of queries	: 15

Mascot: <http://www.matrixscience.com/>

Mitochondrial inner membrane protease ATP23



		/ligand="Zn(2+)"	
BINDING	125	/ligand_id="CHEBI:CHEBI:29105"	(condition: none)
		/ligand_note="catalytic"	
ACT_SITE	126		(condition: none)
		/ligand="Zn(2+)"	
BINDING	129	/ligand_id="CHEBI:CHEBI:29105"	(condition: none)