MASCOT Search Results

Protein View: PLP1_ORYSI

Patatin-like protein 1 OS=Oryza sativa subsp. indica OX=39946 GN=PLP1 PE=3 SV=1

Database:	SwissProt
Score:	53
Expect:	0.027
Monoisotopic mass (M_r):	44993
Calculated pI:	8.80
Taxonomy:	Oryza sativa Indica Group

Sequence similarity is available as an NCBI BLAST search of PLP1_ORYSI against nr.

Search parameters

MS data file:	SPOT_86.mgf
Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications:	Carbamidomethyl (C)
Variable modifications:	Oxidation (M)

Protein sequence coverage: 37%

Matched peptides shown in ***bold red***.

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  1 MAGCVVGEPA SAPGQRVTLL AIDGGGIRGL IPGTILAFLE ARLQELDGPD
 51 ARLADYFDCI AGTSTGGLIT AMLAAPGDHG RPLFAASDIN RFYLDNGPRI
101 FPQKRCGMAA AMAALTRPRY NGKYLQGKIR KMLGETRVRD TLTNVVIPTF
151 DVRLLQPTIF STYDAKSMPL KNALLSDICI STSAAPTYLP AHCFQTTDDA
201 TGKVREFDLI DGGVAANNPT MVAMTQITKK IMVKDKEELY PVKPSDCGKF
251 LVLSLGTGST SDQGMYTARQ CSRWGIVRWL RNKGMAPIID IFMAASSDLV
301 DIHAAVMFQS LHSDGDYLRI QDNTLHGDAA TVDAATRDNM RALVGIGERM
351 LAQRVSRVNV ETGRYVEVPG AGSNADALRG FARQLSEERR ARLGRRNACG
401 GGGEGEPSGV ACKR
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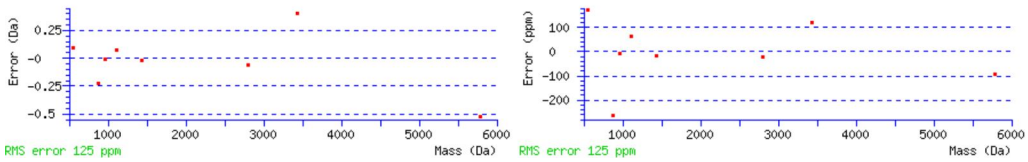
Unformatted sequence string: **414 residues** (for pasting into other applications).

Sort by ◉ residue number ○ increasing mass ○ decreasing mass
Show ◉ matched peptides only ○ predicted peptides also

Query	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Score	Peptide
23	43 – 52	1113.6242	1112.6170	1112.5462	0.0708	0		R.LQELDGPDAR.L
18	124 – 130	877.2956	876.2884	876.5181	-0.2298	1		K.YLQGKIR.K
22	132 – 139	961.5185	960.5112	960.5175	-0.0062	1		K.MLGETRVR.D
64	172 – 203	3440.0221	3439.0148	3438.6072	0.4076	0		K.NALLSDICISTSAAPTYLPAHCFQTTDDATGK.V
52	204 – 229	2807.3420	2806.3348	2806.3994	-0.0646	1		K.VREFDLIDGGVAANNPTMVAMTQITK.K + Oxidation (M)
3	270 – 273	550.3339	549.3267	549.2329	0.0937	0		R.QCSR.W
69	284 – 337	5788.2406	5787.2333	5787.7607	-0.5274	1		K.GMAPIIDIFMAASSDLVDIHAAVMFQSLHSDGDYLRIQDNTLHGDAATVDAATR.D + 2 Oxidation (M)
41	342 – 354	1429.7710	1428.7637	1428.7871	-0.0234	1		R.ALVGIGERMLAQR.V + Oxidation (M)

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ID   PLP1_ORYSI              Reviewed;         414 AA.
AC   B8AQW7;
DT   19-MAR-2014, integrated into UniProtKB/Swiss-Prot.
DT   03-MAR-2009, sequence version 1.
DT   31-JUL-2019, entry version 46.
DE   RecName: Full=Patatin-like protein 1;
DE            EC=3.1.1.-;
GN   Name=PLP1; ORFNames=OsI_11898;
OS   Oryza sativa subsp. indica (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BOP clade;
OC   Oryzoideae; Oryzeae; Oryzinae; Oryza; Oryza sativa.
OX   NCBI_TaxID=39946;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=cv. 93-11;
RX   PubMed=15685292; DOI=10.1371/journal.pbio.0030038;
RA   Yu J., Wang J., Lin W., Li S., Li H., Zhou J., Ni P., Dong W., Hu S.,
RA   Zeng C., Zhang J., Zhang Y., Li R., Xu Z., Li S., Li X., Zheng H.,
RA   Cong L., Lin L., Yin J., Geng J., Li G., Shi J., Liu J., Lv H., Li J.,
RA   Wang J., Deng Y., Ran L., Shi X., Wang X., Wu Q., Li C., Ren X.,
RA   Wang J., Wang X., Li D., Liu D., Zhang X., Ji Z., Zhao W., Sun Y.,
RA   Zhang Z., Bao J., Han Y., Dong L., Ji J., Chen P., Wu S., Liu J.,
RA   Xiao Y., Bu D., Tan J., Yang L., Ye C., Zhang J., Xu J., Zhou Y.,
RA   Yu Y., Zhang B., Zhuang S., Wei H., Liu B., Lei M., Yu H., Li Y.,
RA   Xu H., Wei S., He X., Fang L., Zhang Z., Zhang Y., Huang X., Su Z.,
RA   Tong W., Li J., Tong Z., Li S., Ye J., Wang L., Fang L., Lei T.,
RA   Chen C.-S., Chen H.-C., Xu Z., Li H., Huang H., Zhang F., Xu H.,
RA   Li N., Zhao C., Li S., Dong L., Huang Y., Li L., Xi Y., Qi Q., Li W.,
RA   Zhang B., Hu W., Zhang Y., Tian X., Jiao Y., Liang X., Jin J., Gao L.,
RA   Zheng W., Hao B., Liu S.-M., Wang W., Yuan L., Cao M., McDermott J.,
RA   Samudrala R., Wang J., Wong G.K.-S., Yang H.;
RT   "The genomes of Oryza sativa: a history of duplications.";
RL   PLoS Biol. 3:266-281(2005).
CC   -!- FUNCTION: Possesses non-specific lipolytic acyl hydrolase (LAH)
CC       activity. Hydrolyzes phospholipids as well as galactolipids. May
CC       play a role in disease resistance (By similarity). {ECO:0000250}.
CC   -!- DOMAIN: The nitrogen atoms of the two glycine residues in the GGXR
CC       motif define the oxyanion hole, and stabilize the oxyanion that
CC       forms during the nucleophilic attack by the catalytic serine
CC       during substrate cleavage. {ECO:0000250}.
CC   -!- SIMILARITY: Belongs to the patatin family. {ECO:0000305}.
DR   EMBL; CM000128; EEC75405.1; -; Genomic_DNA.
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DR   SMR; B8AQW7; -.
DR   EnsemblPlants; BGIOSGA012798-TA; BGIOSGA012798-PA; BGIOSGA012798.
DR   Gramene; BGIOSGA012798-TA; BGIOSGA012798-PA; BGIOSGA012798.
DR   eggNOG; KOG0513; Eukaryota.
DR   eggNOG; COG3621; LUCA.
DR   OMA; FPQKRCG; -.
DR   Proteomes; UP000007015; Chromosome 3.
DR   GO; GO:0016787; F:hydrolase activity; IEA:UniProtKB-KW.
DR   GO; GO:0006952; P:defense response; IEA:UniProtKB-KW.
DR   GO; GO:0016042; P:lipid catabolic process; IEA:UniProtKB-KW.
DR   InterPro; IPR016035; Acyl_Trfase/lysoPLipase.
DR   InterPro; IPR002641; PNPLA_dom.
DR   Pfam; PF01734; Patatin; 1.
DR   SUPFAM; SSF52151; SSF52151; 1.
DR   PROSITE; PS51635; PNPLA; 1.
PE   3: Inferred from homology;
KW   Complete proteome; Hydrolase; Lipid degradation; Lipid metabolism;
KW   Plant defense; Reference proteome.
FT   CHAIN         1    414       Patatin-like protein 1.
FT                                /FTId=PRO_0000425825.
FT   DOMAIN       20    224       PNPLA. {ECO:0000255|PROSITE-
FT                                ProRule:PRU01161}.
FT   MOTIF        24     29       GXGXXG. {ECO:0000255|PROSITE-
FT                                ProRule:PRU01161}.
FT   MOTIF        62     66       GXSXG. {ECO:0000255|PROSITE-
FT                                ProRule:PRU01161}.
FT   MOTIF       211    213       DGA/G. {ECO:0000255|PROSITE-
FT                                ProRule:PRU01161}.
FT   COMPBIAS    400    405       Poly-Gly.
FT   ACT_SITE     64     64       Nucleophile. {ECO:0000255|PROSITE-
FT                                ProRule:PRU01161}.
FT   ACT_SITE    211    211       Proton acceptor. {ECO:0000255|PROSITE-
FT                                ProRule:PRU01161}.
SQ   SEQUENCE   414 AA;  44508 MW;  FC886600CD0445FB CRC64;
     MAGCVVGEPA SAPGQRVTLL AIDGGGIRGL IPGTILAFLE ARLQELDGPD ARLADYFDCI
     AGTSTGGLIT AMLAAPGDHG RPLFAASDIN RFYLDNGPRI FPQKRCGMAA AMAALTRPRY
     NGKYLQGKIR KMLGETRVRD TLTNVVIPTF DVRLLQPTIF STYDAKSMPL KNALLSDICI
     STSAAPTYLP AHCFQTTDDA TGKVREFDLI DGGVAANNPT MVAMTQITKK IMVKDKEELY
     PVKPSDCGKF LVLSLGTGST SDQGMYTARQ CSRWGIVRWL RNKGMAPIID IFMAASSDLV
     DIHAAVMFQS LHSDGDYLRI QDNTLHGDAA TVDAATRDNM RALVGIGERM LAQRVSRVNV
     ETGRYVEVPG AGSNADALRG FARQLSEERR ARLGRRNACG GGGEGEPSGV ACKR
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