MASCOT Search Results

Protein View: XP_015614956.1

PREDICTED: probable galacturonosyltransferase 3 isoform X3 [Oryza sativa Japonica Group]

Database:	NCBIprot
Score:	86
Expect:	0.019
Monoisotopic mass (M_r):	79942
Calculated pI:	7.68
Taxonomy:	Oryza sativa Japonica Group

This protein sequence matches the following other entries:

- `XP_015614958.1` from **Oryza sativa Japonica Group**
- `ABB47337.1` from **Oryza sativa Japonica Group**

Sequence similarity is available as **an NCBI BLAST search of XP_015614956.1 against nr**.

Search parameters

Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications:	Carbamidomethyl (C)
Variable modifications:	Oxidation (M)
Mass values searched:	29
Mass values matched:	16

Protein sequence coverage: 27%

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

1 **MAFPSTSSVA** **YPRSLSPLR**R CPGFLALLVA VLLFLSFQLM IHVPSIR**LAV**

51 **SGWLFSDHQT** **GHKGPGSCPG** **CHNGMDNADK** **TIAYTNQDGR** **IR**LFKVTTRE

101 FLSSSIWK**NP** **LLPK**DTEPVA EIQEIAEEQL LATGSEVSNL SSTETLETRT

151 DPIKLKREVF RRKRKEHRIQ ELLQVDKEAE LHMRNVATNR SRNFSNKVRA

201 SYNIWR**LQFH** **HTNTDSTLRL** **MK**DQIIMAKV YATIAHSQKQ PDMYALLMKC

251 IKLCQEAIGD AHMDYELDSS ALERAK**AMGH** **ALSSARDVLY** **NSDEVSRR**LL

301 VMLQSTELNI DSVKKQNSFL VQHAAKTVPM PLHCLHMQLT TDYYFRDGMI

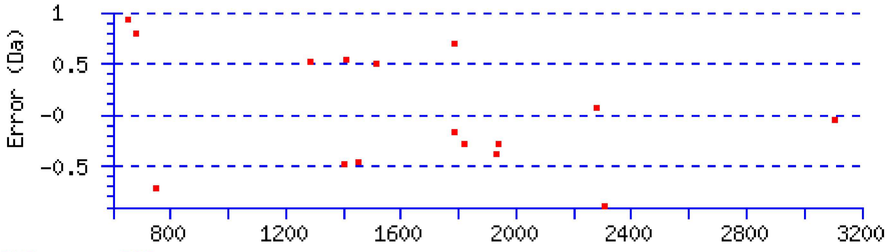
351 KEYFHDAALK **EEEDK**AKRED RSLYHYAIFS DNVLAASVVV RSTVTHAKEP
401 EKHVFHIVTD R**LNFAAMTMW** **FIR**HPPLPAT VHVENIDNFK WLNSSYCSVL
451 RQLESARLK**E** **YYFK**AHDPSS LSDGNENLKY RNPKYLSMLN HLRFYMPEIH
501 PKLDKILFLD DDVVVQKDLT PLWDVDLK**GM** **VNGAVETCKE** **SFHRFDTYLN**
551 **FSHPKIAENF** **DPR**ACGWAFG MNMFDLKEWK KQNITGIYHY WQDLNEDRKL
601 WKLGTLPPGL ITFYNLTYPL NRNWHVLGLG YDPAVDLAEI ENAAVVHYNG
651 NYKPWLDLAV SK**YKPYWSKY** **VDLDNSHIQH** **CYMSEQ**

Unformatted sequence string: **686 residues** (for pasting into other applications).

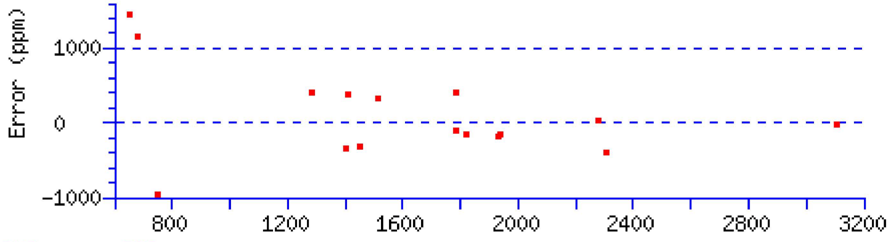
Sort by ● residue number ○ increasing mass ○ decreasing mass
Show ● matched peptides only ○ predicted peptides also

Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Peptide
1 – 13	1414.2130	1413.2057	1412.6758	0.5299	0	-.MAFPSTSSVAYPR.S
2 – 13	1283.1700	1282.1627	1281.6353	0.5274	0	M.AFPSTSSVAYPR.S
2 – 19	1935.6530	1934.6457	1935.0214	-0.3757	1	M.AFPSTSSVAYPRSLSPLR.R
48 – 63	1783.5950	1782.5877	1781.8849	0.7028	0	R.LAVSGWLFSDHQTGHK.G
64 – 80	1789.5050	1788.4977	1788.6614	-0.1637	0	K.GPGSCPGCHNGMDNADK.T + Oxidation (M)
81 – 92	1407.2470	1406.2397	1406.7266	-0.4869	1	K.TIAYTNQDGRIR.L
109 – 114	682.2220	681.2147	680.4221	0.7926	0	K.NPLLPK.D
207 – 222	1941.7100	1940.7027	1940.9891	-0.2863	1	R.LQFHHTNTDSTLRLMK.D
277 – 297	2278.1580	2277.1507	2277.0808	0.0700	1	K.AMGHALSSARDVLYNSDEVSR.R
287 – 298	1452.2430	1451.2357	1451.7005	-0.4647	1	R.DVLYNSDEVSRR.L
361 – 365	650.2080	649.2007	648.2602	0.9405	0	K.EEEDK.A
412 – 423	1517.2540	1516.2467	1515.7366	0.5101	0	R.LNFAAMTMWFIR.H + Oxidation (M)
460 – 464	748.6310	747.6237	748.3432	-0.7194	0	K.EYYFK.A
529 – 544	1821.5560	1820.5487	1820.8298	-0.2811	1	K.GMVNGAVETCKESFHR.F
545 – 563	2310.2160	2309.2087	2310.1069	-0.8982	1	R.FDTYLNFSHPKIAENFDPR.A
663 – 686	3107.3160	3106.3087	3106.3589	-0.0502	1	K.YKPYWSKYVDLDNSHIQHCYMSEQ.- + Oxidation (M)

No match to: 952.9410, 958.7960, 1312.0890, 1365.1830, 1393.2490, 1402.2770, 1436.2680, 1459.3440, 1745.6470, 1764.5250, 1807.4940, 1945.8520, 2071.9490



RMS error 582 ppm



RMS error 582 ppm

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LOCUS       XP_015614956             686 aa            linear   PLN 07-AUG-2018
DEFINITION  probable galacturonosyltransferase 3 isoform X2 [Oryza sativa
            Japonica Group].
ACCESSION   XP_015614956
VERSION     XP_015614956.1
DBLINK      BioProject: PRJNA122
DBSOURCE    REFSEQ: accession XM_015759470.2
KEYWORDS    RefSeq.
SOURCE      Oryza sativa Japonica Group (Japanese rice)
  ORGANISM  Oryza sativa Japonica Group
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BOP
            clade; Oryzoideae; Oryzeae; Oryzinae; Oryza.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from a genomic sequence
            (NC_029265.1) annotated using gene prediction method: Gnomon,
            supported by EST evidence.
            Also see:
                Documentation of NCBI's Annotation Process

            ##Genome-Annotation-Data-START##
            Annotation Provider         :: NCBI
            Annotation Status           :: Full annotation
            Annotation Name             :: Oryza sativa Japonica Group
                                           Annotation Release 102
            Annotation Version          :: 102
            Annotation Pipeline         :: NCBI eukaryotic genome annotation
                                           pipeline
            Annotation Software Version :: 8.1
            Annotation Method           :: Best-placed RefSeq; Gnomon
            Features Annotated          :: Gene; mRNA; CDS; ncRNA
            ##Genome-Annotation-Data-END##
            COMPLETENESS: full length.
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