

Protein View: XP_010066854.1

PREDICTED: beta-glucosidase 40 [Eucalyptus grandis]

Database:NCBIprot

Score:63

Expect:2.7

Monoisotopic mass (M_r):57772

Calculated pI:6.36

Taxonomy:[Eucalyptus grandis](#)

This protein sequence matches the following other entries:

- [KCW64896.1](#) from [Eucalyptus grandis](#)

Sequence similarity is available as [an NCBI BLAST search of XP_010066854.1 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:23

Mass values matched:7

Protein sequence coverage: 21%

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

1MERYRPR**AAA ASAMMAGLLA GLLVHACCAD AIGR**SSFFPKGFVFGTASSAF

51QYEGAVKEDGRGPSVWDTFSHQFGKVIDLSNADVAVDQYHRFNEDIQLMK

101DMGMDAYRFSISWSRIFFNGSQINQAGVDHYNLNINALLAKGIEPYVTL

151FHWDLFQALEDKYNGWLDPOIIKDFATYAE

201TLAIQGYDVG

251VYRKKYKQKQHGSIGVAFDVMWFEVPR**TNST DDIEATQ**RALDFQFGWFIEP

301LIFGNYPSSMISRVGSRLPAISSSESALLKGSLDFVGINHYTTYYGSDNT

351SDVIGSLLKDSLSDSGSVTL

401**NYIKTK**YGNPVVIITENGMDDPNPPLINIKEALKDEKR**IK YHNDYLTNLL**

451**ASIKEDGCNV KGYFVWSLLD NWEWAAGYTS**RFGLYFVDYNDKLKRYPK**DS**

501**VQWFK**NFLKST

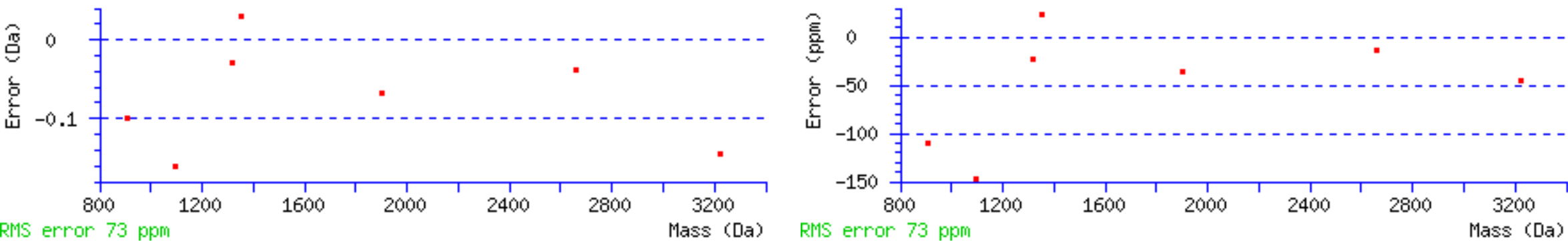
Unformatted sequence string: [511 residues](#) (for pasting into other applications).

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
8 – 34	2658.2607	2657.2535	2657.2910	-0.0375 0	R.AAAASAMMAGLLAGLLVHACCADAIGR.S + Oxidation (M)
217 – 226	1318.6462	1317.6389	1317.6686	-0.0297 0	R.CSILLHLFCR.A
277 – 288	1350.6440	1349.6367	1349.6059	0.0308 0	R.TNSTDDIEATQR.A
398 – 406	1097.4415	1096.4342	1096.5950	-0.1608 1	R.SLMNYIKTK.Y
439 – 454	1905.9754	1904.9681	1905.0359	-0.0679 1	R.IKYHNDYLTNLLASIK.E
455 – 481	3223.3126	3222.3054	3222.4505	-0.1452 1	K.EDGCNVKGYFVWSLLDNWEWAAGYTSR.F
499 – 505	909.3471	908.3398	908.4392	-0.0994 0	K.DSVQWFK.N

No match to: 842.3830, 856.3992, 870.4262, 948.3295, 1125.4659, 1187.6122, 1232.5516, 1326.6202, 1339.5863, 1372.6291, 1650.8046, 1766.7704, 1794.7974, 2055.9753, 2211.1043, 3621.4175



LOCUS	XP_010066854	511 aa	linear	PLN 25-OCT-2016
DEFINITION	PREDICTED: beta-glucosidase 40 [Eucalyptus grandis].			
ACCESSION	XP_010066854			
VERSION	XP_010066854.1			
DBLINK	BioProject: PRJNA264012			
DBSOURCE	REFSEQ: accession XM_010068552.2			
KEYWORDS	RefSeq.			
SOURCE	Eucalyptus grandis			
ORGANISM	Eucalyptus grandis			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Myrtales; Myrtaceae; Myrtoideae; Eucalypteae; Eucalyptus.			
COMMENT	MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from a genomic sequence (NW_010092444.1) 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 Version :: Eucalyptus grandis Annotation Release 101 Annotation Pipeline :: NCBI eukaryotic genome annotation pipeline Annotation Software Version :: 7.2 Annotation Method :: Best-placed RefSeq; Gnomon Features Annotated :: Gene; mRNA; CDS; ncRNA ##Genome-Annotation-Data-END## COMPLETENESS: full length.			
FEATURES	Location/Qualifiers			
source	1..511 /organism="Eucalyptus grandis" /cultivar="BRASUZ1" /db_xref="taxon:71139" /chromosome="Unknown" /tissue_type="leaf extractions" /country="Brazil" /collection_date="Dec-2008" /note="individual tree from a line of selfed trees grown from seeds collected in Coffs Harbor, Australia"			
Protein	1..511 /product="beta-glucosidase 40" /calculated_mol_wt=57335			
Region	34..510 /region_name="Glyco_hydro_1" /note="Glycosyl hydrolase family 1; c123725" /db_xref="CDD:304882"			
CDS	1..511 /gene="LOC104453907" /coded_by="XM_010068552.2:286..1821" /db_xref="GeneID:104453907"			