

Protein View: XP_022553271.1

glutathione S-transferase T3-like [Brassica napus]

Database: NCBIprot
Score: 54
Expect: 21
Monoisotopic mass (M_r): 23636
Calculated pI: 8.83
Taxonomy: [Brassica napus](#)

Sequence similarity is available as [an NCBI BLAST search of XP_022553271.1 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: 10
Mass values matched: 4

Protein sequence coverage: 22%

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

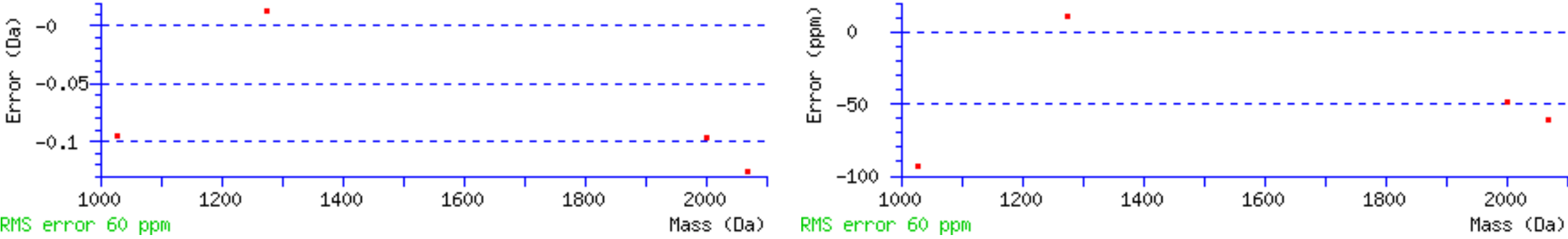
1 MVNSSTSFIN LLASQGVIDL DSSEPPCVSS QGVASQCSDE ATVKEKRK**WS**
51 **PKEDIILIGA WLNTSKDPIV SNEQK**GLAFW KRIVENYNSS PLLVGTIPRE
101 LGQVKKR**WAR INDLVCKFSG SYEMAL**REQR SGQNDNDVMK AALEIFFNDK
151 GFKFNLEHAW RELRHDVKWC STFLGKDSGK DKRKTGASDA GGSVTEPQER
201 PIGVKAAKAA GG

Unformatted sequence string: [212 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
49 – 66	2070.9956	2069.9883	2070.1149	-0.1266 1	K.WSPKEDIILIGAWLNTSK.D
67 – 75	1029.4253	1028.4180	1028.5138	-0.0958 0	K.DPIVSNEQK.G
108 – 117	1274.6806	1273.6734	1273.6601	0.0132 1	R.WARINDLVCK.F
111 – 127	2002.8759	2001.8687	2001.9652	-0.0965 1	R.INDLVCKFSGSYEMALR.E

No match to: 1306.6755, 1406.7560, 1529.7144, 1819.8732, 1980.9026, 2211.1028



LOCUS	XP_022553271	212 aa	linear	PLN 04-OCT-2017
DEFINITION	glutathione S-transferase T3-like [Brassica napus].			
ACCESSION	XP_022553271			
VERSION	XP_022553271.1			
DBLINK	BioProject: PRJNA293435			
DBSOURCE	REFSEQ: accession XM_022697550.1			
KEYWORDS	RefSeq; includes ab initio.			
SOURCE	Brassica napus (rape)			
ORGANISM	Brassica napus			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Brassicales; Brassicaceae; Brassiceae; Brassica.			
COMMENT	MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from a genomic sequence (NC_027769.2) annotated using gene prediction method: Gnomon. Also see: Documentation of NCBI's Annotation Process			
	##Genome-Annotation-Data-START##			
	Annotation Provider :: NCBI			
	Annotation Status :: Full annotation			
	Annotation Version :: Brassica napus Annotation Release 101			
	Annotation Pipeline :: NCBI eukaryotic genome annotation pipeline			
	Annotation Software Version :: 7.4			
	Annotation Method :: Best-placed RefSeq; Gnomon			
	Features Annotated :: Gene; mRNA; CDS; ncRNA			
	##Genome-Annotation-Data-END##			
	##RefSeq-Attributes-START##			
	ab initio :: 100% of CDS bases			
	##RefSeq-Attributes-END##			
	COMPLETENESS: full length.			
FEATURES	Location/Qualifiers			
source	1..212			
	/organism="Brassica napus"			
	/cultivar="ZS11"			
	/db_xref="taxon:3708"			
	/chromosome="C3"			
Protein	1..212			
	/product="glutathione S-transferase T3-like"			
	/calculated_mol_wt=23291			
Region	<80..108			
	/region_name="GT1"			
	/note="myb-like, SANT family; cl23759"			
	/db_xref="CDD:329061"			
Region	153..>210			
	/region_name="NAM-associated"			
	/note="No apical meristem-associated C-terminal domain; pfam14303"			
	/db_xref="CDD:316794"			
CDS	1..212			
	/gene="LOC111203635"			
	/coded_by="XM_022697550.1:1..639"			
	/db_xref="GeneID:111203635"			