

Protein View: AFC75531.1

granule bound starch synthase, partial [Triticum spelta]

Database: NCBIprot
Score: 399
Expect: 7.3e-34
Monoisotopic mass (M_r): 64252
Calculated pI: 8.61
Taxonomy: [Triticum spelta](#)

Sequence similarity is available as [an NCBI BLAST search of AFC75531.1 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: 43
Mass values matched: 37

Protein sequence coverage: 55%

Matched peptides shown in **bold red**.

```

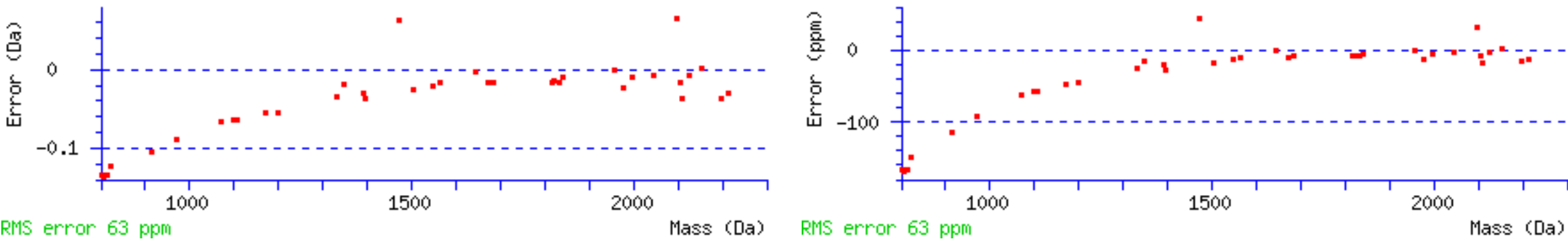
1  MAALVTSQLA  TSGTVLGITD  RFRRAGFQGV  RPRSPADAAL  GMRTVGASAA
51  PTQSRKAHRG  TRRCLSMVVR  ATGSGGMNLV  FVGAEMAPWS  KTGGLGDVLG
101 GLPPAMAANG  HRVMVISPRY  DQYKDAWDTs  VVSEIKVVVK  YERVRYFHCY
151 KRGVDRVFVD  HPCFLEKVRG  KTKEKIYGPD  AGTDYEDNQQ  RFSLLCQAAL
201 EVPRILNLDN  NPYFSGPYED  VVFCNDWHT  GLLACYLKSN  YQSNGIYRAA
251 KVAFCIHNIS  YQGRFSDDF  AQLNLPDRFK  SSFDFIDGYD  KPVEGRKINW
301 MKAGILQADK  VLTVPSPYAE  ELISGEARGC  ELDNIMRLTG  ITGIVNGMDV
351 SEWDPTKDKF  LAVNYDITTA  LEGKALNKEA  LQAEVGLPVD  RKVPLVAFIG
401 RLEEQKGPDV  MIAAIPEILK  EEDVQIVLLG  TGKKKFERLL  KSIEEKFPSK
451 VRAVVRFNAP  LAHQMMAGAD  VLAVTSRFEP  CGLIQLQGMR  YGTPCACAST
501 GGLVDTIVEG  KTGFHMGRLS  VDCNVVEPAD  VKKVVTTLKR  AVKVVGTPAY
551 HEMVKNCMIQ  DLSWKGPAKN  WEDVLL
```

Unformatted sequence string: [576 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
71 – 91	2109.9739	2108.9666	2109.0023	-0.0357 0	R.ATGSGGMNLV FVGAEMAPWSK.T
71 – 91	2125.9971	2124.9898	2124.9973	-0.0075 0	R.ATGSGGMNLV FVGAEMAPWSK.T + Oxidation (M)
92 – 112	1976.9737	1975.9664	1975.9898	-0.0234 0	K.TGGLGDVLG GLPPAMAANGHR.V + Oxidation (M)
113 – 119	801.3313	800.3240	800.4578	-0.1338 0	R.VMVISPR.Y
120 – 136	2046.9584	2045.9511	2045.9582	-0.0071 1	R.YDQYKDAWDT SVVSEIK.V
144 – 151	1172.5121	1171.5048	1171.5597	-0.0549 1	R.VRYFHCYK.R
146 – 151	917.2917	916.2844	916.3902	-0.1057 0	R.YFHCYK.R
146 – 152	1073.4323	1072.4250	1072.4913	-0.0663 1	R.YFHCYKR.G
153 – 167	1817.8849	1816.8776	1816.8931	-0.0154 1	R.GVDRV FVDHPCFLEK.V
157 – 167	1390.6532	1389.6459	1389.6751	-0.0292 0	R.VFVDHPCFLEK.V
157 – 169	1645.8496	1644.8423	1644.8447	-0.0023 1	R.VFVDHPCFLEKVR.G
174 – 191	2098.9956	2097.9884	2097.9239	0.0645 1	K.EKIYGP DAGTDYEDNQQR.F
176 – 191	1841.7834	1840.7761	1840.7864	-0.0103 0	K.IYGP DAGTDYEDNQQR.F
239 – 248	1201.5049	1200.4976	1200.5523	-0.0547 0	K.SNYQ SNGIYR.A
239 – 251	1471.7928	1470.7856	1470.7215	0.0641 1	K.SNYQ SNGIYRAAK.V
265 – 278	1684.7812	1683.7739	1683.7893	-0.0154 0	R.FS DDFAQLNL PD R.F
265 – 280	1959.9585	1958.9513	1958.9527	-0.0014 1	R.FS DDFAQLNL PD RFK.S
279 – 296	2106.9959	2105.9886	2106.0058	-0.0172 1	R.FK SS FD FID GYDKP VEGR.K
281 – 296	1831.8337	1830.8264	1830.8425	-0.0161 0	K.SS FD FID GYDKP VEGR.K
298 – 310	1503.7733	1502.7660	1502.7915	-0.0255 1	K.INWMKAGILQADK.V + Oxidation (M)
311 – 328	1997.0123	1996.0051	1996.0153	-0.0102 0	K.VLTVPSPYAE ELISGEAR.G
329 – 337	1107.4274	1106.4202	1106.4848	-0.0647 0	R.GCELDNIMR.L
375 – 391	1822.9875	1821.9802	1821.9948	-0.0146 1	K.ALNKEALQAEVGLP VDR.K
379 – 391	1396.7055	1395.6982	1395.7358	-0.0376 0	K.EALQAEVGLP VDR.K
392 – 401	1099.6348	1098.6275	1098.6913	-0.0638 1	R.KVPLVAFIGR.L
393 – 401	971.5152	970.5079	970.5964	-0.0885 0	K.VPLVAFIGR.L
457 – 477	2200.0641	2199.0568	2199.0929	-0.0360 0	R.FNAPLAHQMMAGAD VLA VT SR.F
457 – 477	2216.0657	2215.0584	2215.0878	-0.0293 0	R.FNAPLAHQMMAGAD VLA VT SR.F + Oxidation (M)
478 – 490	1548.7453	1547.7381	1547.7588	-0.0208 0	R.FEPCGLIQLQGMR.Y
478 – 490	1564.7453	1563.7380	1563.7538	-0.0158 0	R.FEPCGLIQLQGMR.Y + Oxidation (M)
491 – 511	2156.0014	2154.9941	2154.9926	0.0015 0	R.YGTPCACA ST GGLVD TIVEGK.T
512 – 518	805.2412	804.2339	804.3701	-0.1362 0	K.TGFHMGR.L
512 – 518	821.2493	820.2420	820.3650	-0.1230 0	K.TGFHMGR.L + Oxidation (M)
519 – 533	1672.8402	1671.8329	1671.8502	-0.0172 1	R.LS VD CNV VEPAD VKK.V
534 – 540	816.3950	815.3877	815.5229	-0.1352 1	K.VV TT LKR.A
544 – 555	1330.6479	1329.6406	1329.6751	-0.0345 0	K.VVGT PAYHEMVK.N
544 – 555	1346.6577	1345.6505	1345.6700	-0.0196 0	K.VVGT PAYHEMVK.N + Oxidation (M)

No match to: 1319.6901, 1326.6402, 1412.7463, 1430.7624, 1446.7509, 2211.1040



LOCUS	AFC75531	576 aa	linear	PLN 06-MAR-2012
DEFINITION	granule bound starch synthase, partial [Triticum spelta].			
ACCESSION	AFC75531			
VERSION	AFC75531.1			
DBSOURCE	accession JN935594.1			
KEYWORDS	.			
SOURCE	Triticum spelta			
ORGANISM	Triticum spelta			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BOP clade; Pooideae; Triticeae; Triticeae; Triticeae; Triticum.			
REFERENCE	1 (residues 1 to 576)			
AUTHORS	Guzman,C., Leonor,C., Martin,L.M. and Alvarez,J.B.			
TITLE	Comparative analysis of the waxy genes present in Spanish spelt wheat with their homologous genes in polyploid wheat and relatives			
JOURNAL	Unpublished			
REFERENCE	2 (residues 1 to 576)			
AUTHORS	Guzman,C., Leonor,C., Martin,L.M. and Alvarez,J.B.			
TITLE	Direct Submission			
JOURNAL	Submitted (26-OCT-2011) Genetics, University of Cordoba, Edificio C5 Gregor Mendel, Campus de Rabanales, Cordoba 14071, Spain			
FEATURES	Location/Qualifiers			
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Region	77..575			
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	/note="glycogen/starch synthase, ADP-glucose type; TIGR02095"			
	/db_xref="CDD:273969"			
Region	78..575			
	/region_name="GT1 Glycogen synthase_DULL1 like"			
	/note="This family is most closely related to the GT1 family of glycosyltransferases. Glycogen synthase catalyzes the formation and elongation of the alpha-1,4-glucose backbone using ADP-glucose, the second and key step of glycogen biosynthesis. This family...; cd03791"			
	/db_xref="CDD:99965"			
Site	order(91,399..401,456..457,462,479,484)			
	/site_type="other"			
	/note="ADP-binding pocket [chemical binding]"			
Site	order(320,499,504..505,507,536)			
	/site_type="other"			
	/note="homodimer interface [polypeptide binding]"			
	/db_xref="CDD:99965"			
CDS	1..576			
	/gene="Waxy"			
	/coded_by="join(JN935594.1:32..352,JN935594.1:443..523,JN935594.1:619..717,JN935594.1:822..975,JN935594.1:1131..1228,JN935594.1:1370..1723,JN935594.1:1809..1988,JN935594.1:2071..2262,JN935594.1:2347..2433,JN935594.1:2532..2660,JN935594.1:2777..>2810)"			