Protein Report

Project Info

Name:	UGR_Microbiologia_M.Manzanera	**Date:**	April 15, 2014

Sample Info & Protocols

Name:	140409C	**Date:**	April 15, 2014

Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
LIFT_NCBI_Viridiplantae_Mascot_2014-04-24 14:30:33	/UGR_Microbiologia_M.Manzanera/140409C/ 140409/geles ZT/36/CombinedLIFT	Mascot, 2.4.0	NCBInr, NCBInr_20140305.fasta	2/5 (FDR:0.00%)

Protein 1:	PREDICTED: 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Solanum tuberosum]		
Accession:	gi|565402329	**Score:**	71.05
Database:	NCBInr	**MW [kDa]:**	61.20
Seq. Coverage [%]:	2.10 %	**pI:**	5.37
		No. of Peptides:	1

10	20	30	40	50	60	70	80	90	100	110	120
MGSSGDAWKL	KDHPKLPKGK	TVAVIVLDGW	GEAKPNEYNA	ISVAETPVMD	SLKQGAPEHW	RLIKAHGNAV	GLPTEDDMGN	SEVGHNALGA	GRIFAQGAKL	VDLALASGKI	YDGEGFKYVQ
130	**140**	**150**	**160**	**170**	**180**	**190**	**200**	**210**	**220**	**230**	**240**
ECFEKGTLHL	IGLVSDGGVH	SRLDQLLLLL	KGAAERGAKR	ICVHALTDGR	DVLDGSSVGF	METLENDLAK	LREQGVDARV	ASGGGRMYVT	MDRYENDWDV	VKRGWDAQIL	GEAPHHFKDP
250	**260**	**270**	**280**	**290**	**300**	**310**	**320**	**330**	**340**	**350**	**360**
VEAIKKLRQE	PNATDQYLAP	FVIVDDNGKP	VGPILDGDAV	VTFNFRADRM	VMLAKALEYE	DFDKFDRVRV	PKIHYAGMLQ	YDGELKLPNK	YLVSPPEIDR	TSGEYLVRNG	VRTFACSETV
370	**380**	**390**	**400**	**410**	**420**	**430**	**440**	**450**	**460**	**470**	**480**
KFGHVTFFWN	GNRSGYFDEK	LEEYVEIPSD	SGITFNVKPK	MKALEIAERT	RDAILSHKFD	QVRVNIPNSD	MVGHTGDIKA	TIEACKAADD	GVKMILEAIE	QVGGIFLVTA	DHGNAEDMVK
490	**500**	**510**	**520**	**530**	**540**	**550**	**560**				
RNKKGEPLLD	KNGNIQILTS	HTLEPVPIAI	GGPGLLPGVR	FRTDLPTGGL	ANVAATFMNL	HGFEAPSDYE	PTLIEVVDN				

Cmpd.	m/z meas.	z	Rt [min]	Score	P	Range	Sequence	Modification
	1428.7656	1		71.05	1	412-423	R.DAILSHKFDQVR.V	

Protein 2: RecName: Full=2,3-bisphosphoglycerate-independent phosphoglycerate mutase; Short=BPG-independent PGAM; Short=Phosphoglyceromutase; AltName: Full=PGAM-I

Accession:	gi|548533	**Score:**	54.22
Database:	NCBInr	**MW [kDa]:**	61.00
Seq. Coverage [%]:	2.10 %	**pI:**	5.98
		No. of Peptides:	1

10	20	30	40	50	60	70	80	90	100	110	120
MGSSGDAWKL	KDHPKLPKGK	TVAVIVLDGW	GEAKPNEFNA	IHVAETPVMY	SLKNGAPEKW	RLIKAHGNAV	GLPTEDDMGN	SEVGHNALGA	GRIFAQGAKL	VDLALASGKI	YEGEGFKYVK
130	140	150	160	170	180	190	200	210	220	230	240
ECFEKGTLHL	IGLLSDGGVH	SRLDQVQLLL	KGAAKHGAKR	IRVHALTDGR	DVLDGSSVGF	METLENSLAQ	LREKGIDAQV	ASGGGRMYVT	MDRYENDWDV	VKRGWDAQVL	GEAPHKFKDP
250	260	270	280	290	300	310	320	330	340	350	360
VEAVKKLRQE	PNANDQYLAP	FVIVDDNGKP	VAAILDGDAV	VTFNFRADRM	VMLAKALEYE	NFDKFDRVRV	PKIRYAGMLQ	YHGELQLPSH	YLVSPPEIAR	HSGEYLVRNG	VRTFACSETV
370	380	390	400	410	420	430	440	450	460	470	480
KFGHVTFFWN	GNRSGYFNEK	LEEYVEIPSD	SGITFNVKPK	MKALEIAERT	RDAILSGKFD	QVRVNLPNGD	MVGHTGDIKA	TIEACKSADE	AVKMILEAIE	QVGGIYLVTA	DHGNAEDMVK
490	500	510	520	530	540	550	560				
RNKKGEPALD	KNGNIQILTS	HTCEPVPIAI	GGPGLAPGVR	FRQDLPTGGL	ANVAATFMNL	HGSEAPSDYE	PSLIEVVDN				

Cmpd.	m/z meas.	z	Rt [min]	Score	P	Range	Sequence	Modification
	1546.7262	1		54.22	1	296-307	K.ALEYENFDKFDR.V	