

**SUPPLEMENTARY TABLE 3** Proteins identified by ESI-MS/MS

spot No	NCBI nr accession no.	Locus	Protein Description	Sequence Coverage %	Matched Peptide number	Peptide sequence	Total Score <sup>b</sup>	% Identify <sup>a</sup>	Delta
32	gi 23465645	BL1076	glutamine synthetase 1	10	4	DGKPLFYDEK	206	100	0.01
						LVPGFEPVNLVYSAR	100		
						IPLAGTSPAACK	100		
						LSPTPLEYELYFHI	100		
70	gi 23465952	BL1392	narrowly conserved hypothetical protein	23	5	AESAETVLAEPASEYQGR	427	100	0.07
						AASEVDGVFGTELK	100		
						AAIDPDSPETEALNK	100		
						GPLSQDQQTEVK	100		
						GPMFSEVR	100		
45	gi 23465295	BL0715	transaldolase	18	5	IESGSLQDLIANK	452	100	0.09
						NVVGVTTNPSIFQK	100		
						ALSQVGPYDAQLK	100		
						EIAEATDFVDGR	100		
						DVTDKLEADGVAAFIK	100		
52	gi 23464630	BL0002	chaperone	5	2	VGAATEVEAK	118	100	0.1
						AAIEEGLLPGGGVALVQAAAK	100		
193	gi 23464630	BL0002	chaperone	5	1	AAIEEGLLPGGGVALVQAAAK	67	100	0.14
261	gi 23466203	BL1656	phosphoglycerate mutase	54	9	TVLIAAHGNSLR	773	100	0.09
						MLDNLSEEEIAK	100		
						AINTANIALDAADR	100		
						NVLPDIVFTSLLR	100		
						VKPYFESAIEPELK	100		

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						YAGDPVPEAECLANVVER	100		
						GEYLDPEAAAAGAAAVAAQGQK	100		
						TNQFTGWVDVPLTEQGAEAK	100		
313	gi 23466203	BL1656	phosphoglycerate mutase	54	9	TVLIAAHGNSLR	773	100	0.09
						MLDNLSEEEIAK	100		
						AINTANIALDAADR	100		
						NVLPDIVFTSLLR	100		
						VKPYFESAIEPELK	100		
						YAGDPVPEAECLANVVER	100		
						GEYLDPEAAAAGAAAVAAQGQK	100		
						TNQFTGWVDVPLTEQGAEAK	100		
153	gi 23465372	BL0796	choloylglycine hydrolase	24	6	FSDDEGNTYFGR	486	100	0.06
						NFDSVDEVEEALR	100		
						MGDGQFER	100		
						TLFTSGYSSK	100		
						TNTYYMNTYDDPAIR	100		
						SYAMADYDMDSSELISVAR	100		
593	gi 23465199	BL0615	alkyl hydroperoxide reductase C22 protein	22	3	IEYPMLADPTALLAK	203	100	0.04
						DLDTYNEADGVAER	100		
						VVAYEVISSNVGR	100		
120	gi 23465540	BL0969	acetate kinase	13	4	TVLVINSGSSSIK	339	100	0.03
						DLAVLAPLHNGPEAK	100		
						EIADQYHIR	100		
						SAAIAEAGTDTYGNTFAK	100		
816	gi 23465331	BL0753	ribulose-phosphate 3-epimerase	13	2	SNIAIAPSILSADFCNLER	131	100	0.04
						IQVDGGVSPK	100		

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33	gi 23465532	BL0959	xylulose-5-phosphate/fructose -6-phosphate phosphoketolase	13	2	VANYLSIGQIYLR TDGIVLPILHLDGYK	100 93	0.08
381	gi 23464661	BL0033	probable solute binding protein of ABC transporter system possibly for sugars	11	3	TVGFVAVGPEGGFR AAEAEIPVFTVDR TVEKDIEIESK	133 100 100	0.16
571	gi 23464661	BL0033	probable solute binding protein of ABC transporter system possibly for sugars	21	5	TVGFVAVGPEGGFR AAEAEIPVFTVDR NFPDGANGFILEGPAGLSVVK TVTAGLLDKYK TVEKDIEIESK	350 100 100 100 100	0.24

a) Percentage of identity between the amino acids present in MS/MS tag and the sequences in databases.

b) Ion scores greater than 44 are significant ( $p < 0.05$ ), total score is the sum of every ion score.