

Supplementary table 1. The detailed information of identified proteins.

NO.	Protein Name	Accession No.	Protein MW	Protein PI	Protein score	Protein score	Total Ion score	Total Ion C. I. %
1	tyrosyl-tRNA synthetase	gi 116516055	47451.2	5.46	247	100	121	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	283	291	QFEAAPHER	17	82.811			
	1	10	MHIFDELKER	59	99.999			
	11	23	GLIFQTTDEEALR	27	98.269			
	11	24	GLIFQTTDEEALRI	18	84.432			
2	hypothetical protein SPD_0547	gi 116516393	38188.1	5.26	265	100	106	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	31	41	TLEGFGYQPVR	27	97.658			
	259	269	DASGPYHYDFR	39	99.874			
	61	74	YVTAHVDTLGAIVL	40	99.898			
3	catabolite control protein A	gi 116517109	37020.2	5.47	245	100	93	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	224	235	YSYDDGYALAER	75	100			
	1	14	MNADDTVTIYDVAI	17	78.651			
4	glutamate dehydrogenase	gi 116516965	48936.7	5.43	698	100	514	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	66	74	VPWVDRDGK	32	99.556			
	176	185	EIGYLYGQYK	45	99.975			
	176	186	EIGYLYGQYKR	61	100			
	98	108	FHPTVNGGILK	72	100			
	43	54	HPEYIEENILAR	68	100			
	158	175	HIGPSLDVDPAGDI	154	100			
	371	390	AAANAGVAVSALEI	82	100			
5	aromatic amino acid aminotransferase	gi 116516139	43259.4	5.16	478	100	336	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	347	358	AVAFIPGAAFGFR	68	100			
	186	196	EQLEALAAVLR	75	100			
	346	358	KAVAFIPGAAFGFR	18	87.877			
	10	20	QLDKIQVSLIR	50	99.992			
	21	34	QFDQVISEIPGVL	56	99.998			
	169	185	AVILNYPANPTGI	69	100			
6	inositol-5-monophosphate dehydrogenase	gi 116515965	52525.9	5.18	562	100	270	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	302	313	VGIGPGSICTTR	33	99.444			
	277	290	TLIAGNIATAEGAI	28	98.359			
	122	134	ISGVPVVETLENR	39	99.868			
	122	135	ISGVPVVETLENRI	16	70.958			
	209	222	VIEFPNAAKDFEFGI	83	100			
	223	238	LLVAGAVGVTSDTI	26	97.314			
	314	334	VIAGVGPVQTAI	47	99.979			
7	lactate oxidase	gi 116517149	41577.1	5.67	311	100	164	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	285	294	VPIVFDGSGVR	19	82.041			
	284	294	RVPIVFDGSGVR	20	87.998			
	94	105	LANEQGEVATAR	18	79.333			
	284	295	RVPIVFDGSGVRR	23	93.266			
	361	373	HNPYNPTFPVDPR	38	99.798			
	246	262	SLAAGASGIWVTNI	47	99.976			
8	recombinase A	gi 116516275	41923.9	5.13	129	100	35	99.525
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	200	209	TIAIFINQLR	35	99.525			
9	aminopeptidase C	gi 116516913	50281.2	5.09	357	100	215	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	224	230	KPDFAYR	55	99.997			
	292	299	YINVPMER	39	99.887			
	241	250	GITPQEFYKK	37	99.838			
	178	187	LLRQDAQILR	32	99.428			
	275	288	SYTVEMLGNVVGSI	52	99.995			
10	UDP-N-acetylglucosamine pyrophosphorylase	gi 116516172	49454.4	5.3	311	100	111	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	429	439	DVPADAIAGR	47	99.987			
	141	151	IVRNDNAEVLRL	21	94.832			
	167	179	EINTGTYYVFDNER	17	88.107			
	123	140	NVATILTAETDNPI	26	98.421			
11	acetyl-CoA carboxylase biotin carboxylase	gi 116515928	49862.3	5.16	226	100	91	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	284	293	NFYFMMNTR	24	97.095			
	356	369	ITNLYLPSGGVGLI	68	100			
12	glutamyl aminopeptidase PepA	gi 116516201	38166.4	5.46	307	100	238	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	284	290	YQYYCGK	12	18.471			
	10	25	EVTELAAVSGHEAI	27	97.509			
	85	100	VVEIGGWNPVVVS	82	100			
	107	124	DGHEIPVISGSVPI	77	100			
	201	218	LGNELYLGSNVQEI	41	99.914			
13	threonyl-tRNA synthetase	gi 116515338	74831.5	5.26	111	100	27	97.519
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	174	182	QGEYVDLCR	14	52.868			
	1	12	MINITFPDGAVR	14	44.257			
14	GTP-binding protein EngA	gi 116515879	49051.3	5.27	452	100	227	100
	Peptide Information							
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
	412	418	FLENQIR	23	93.717			
	412	419	FLENQIRK	20	86.19			

177	187	FSLIGRPNVGK	20	85.639			
28	39	ISIVEDVEGVTR	46	99.97			
94	105	EGITDADEYVAR	39	99.823			
2	16	ALPTIAIVGRPNV	42	99.951			
420	433	AFVFEPTPIHLIAI	37	99.846			
15	UDP-N-acetylglucosamine 1-carboxylase	gi 116516843	45922.9	5.38	55	99.336	35 99.732
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	97	108	ASIVVLGPILAR	18	86.985		
	358	375	IVGGQPLQGAEVL	17	83		
16	pneumolysin	gi 116515376	52923.9	5.14	543	100	349 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	289	301	AVILGGDPSSGAR	18	78.992		
	20	31	LLTHQGESIENR	27	97.686		
	307	319	VDMVEDLIQEGSR	87	100		
	35	48	EGNQLPDEFVVIIEI	100	100		
	134	147	WHQDYGVVNNVPAI	102	100		
17	pneumolysin	gi 116515376	52923.9	5.14	134	100	57 99.997
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	35	48	EGNQLPDEFVVIIEI	21	89.126		
	134	147	WHQDYGVVNNVPAI	37	99.813		
18	cell division protein DivIVA	gi 116515933	30223.4	4.63	57	99.618	26 97.652
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	89	102	SNNIHHQAEQDAQI	17	82.593		
19	hypothetical protein SPD_0310	gi 116516184	55087.5	5.51	153	100	46 99.97
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	38	46	MLEDPHAAAR	18	81.682		
	85	97	GDLGISYDQEVLR	27	97.863		
20	tyrosyl-tRNA synthetase	gi 116516055	47451.2	5.46	48	97.102	
21	UDP-N-acetylmuramate-L-alanine	gi 116515384	49842.7	5.43	243	100	134 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	240	251	STIGSTFTVHFR	24	94.787		
	201	212	GLFVYGEDAELR	38	99.793		
	148	158	YFVFESEDEYER	35	99.642		
	201	213	GLFVYGEDAELRK	20	88.855		
	252	265	GQNLGQFHPTFGI	17	77.086		
22	3-oxoacyl-(acyl carrier protein)	gi 116516059	44075.1	5.44	143	100	112 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	114	121	EIEDQVLR	19	87.69		
	218	226	ASIPFDKDR	30	98.992		
	159	176	SINTACSSSDAI	64	100		
23	hypothetical protein SPD_0310	gi 116516184	55087.5	5.51	130	100	27 97.594
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	85	97	GDLGISYDQEVLR	27	97.594		
24	metallo-beta-lactamase domain-c	gi 116516160	61195	5.67	359	100	176 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	107	116	GKLEEHGLLR	18	86.755		
	386	395	YFMPVHGEYR	16	77.969		
	478	490	SQMILSGPDLISR	34	99.606		
	168	181	FDFTPVGEPADLHI	38	99.843		
	432	447	IAGHFNAGDIYVDI	70	100		
25	adenylosuccinate synthetase	gi 116515772	47711.6	5.49	697	100	473 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	408	417	ISTFSVGPGR	30	99.109		
	147	157	IADLKDIDFR	63	100		
	19	32	ITDFLSANAIEVIAI	89	100		
	291	304	EVGHEYGTTGRPI	29	98.748		
	102	114	AHVILPYHIELDR	60	100		
	272	288	VGDGPFPELTFDEI	118	100		
	82	97	ELSYLHEGVTTDI	84	100		
26	PTS system, mannose-specific II	gi 116515792	35421.6	5.15	298	100	122 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	301	309	DLGVEFDVR	41	99.912		
	231	239	LIEISKDPR	13	48.834		
	196	210	IIVASDNVAKDDL	21	92.415		
	240	257	FGETHALILFETPI	48	99.982		
27	thiamine biosynthesis protein T	gi 116516659	45232.3	5.37	102	100	
28	capsular polysaccharide biosynt	gi 116516120	45833.4	5.33	223	100	50 99.995
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	319	327	VEGVSLER	29	99.114		
	284	297	DIVDRYDSGFAGSI	21	93.685		
29	Cof family protein/peptidyl-pro	gi 116515578	52160.3	4.82	213	100	131 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	56	65	GIFGVVPEIR	37	99.831		
	317	327	DGYVDGVIFHR	53	99.994		
	14	24	IVFFDIDTLR	41	99.899		
31	CTP synthetase	gi 116515581	59504.5	5.45	284	100	101 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	465	472	YEFNNAFR	19	80.503		
	447	459	AAAAAHNQEVVQR	25	95.889		
	473	490	EQFEAAGFVFSGV	57	99.997		
32	sugar ABC transporter, ATP-bind	gi 116515854	55029.2	5.47	162	100	27 97.43
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	433	445	GLDVGAIIEYIHKR	18	85.984		
	417	432	EIDRDPDLLIVSQI	10	18.414		
33	enoyl-CoA hydratase	gi 116516619	28831.2	5.84	175	100	85 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	83	93	IAELVNTISYK	18	88.555		
	236	248	SLAQTEDFKEGVR	66	100		
34	lysyl-tRNA synthetase	gi 116517090	56702.9	5.32	525	100	165 100
	Peptide Information						
	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %		
	321	328	VHMVDAIR	23	96.661		

165	172	YLDLISNR	24	97.105			
87	95	EGQIQIYVR	19	90.055			
151	162	FHGLTDVETIYR	27	100			
110	124	ADLGDFLVGEGEVI	38	100			
416	433	EYGNAFTELNDPII	36	100			
36	glyceraldehyde-3-phosphate dehydrogenase	gi 116516523	51101.9	5.2	335	100	226 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
109	116	YAAEGLR	41	99.931			
270	282	QIVAGAFYSYGQR	56	99.998			
221	236	EVNFINFTGSTPII	59	99.999			
191	208	AFEEAGIPAGVFN	71	100			
37	ATP-dependent Clp protease ATP-binding subunit ClpX	gi 116516310	84016.3	5.48	173	100	58 99.998
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
142	149	VIEILNRR	13	44.301			
192	204	LDVVSIVGQGTGIR	18	81.976			
258	272	GELQLVGATTLNE	27	98.033			
38	ribonucleotide-diphosphate reductase	gi 116516073	81825.9	5.32	357	100	200 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
197	209	IGGGVGITLSNLR	45	99.955			
151	163	YQPATPSFLNAGR	65	100			
563	575	DKVQEDGLYHQNR	17	74.009			
231	245	LFEDSFYSNQLG	47	99.972			
351	368	LQQESGYPPVVNI	26	96.173			
39	ATP-dependent Clp protease ATP-binding subunit ClpX	gi 116516310	84016.3	5.48	142	100	17 74.009
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
258	272	GELQLVGATTLNE	17	86.347			
40	phosphoglucosyltransferase/phosphomannosyltransferase	gi 116516422	48092.6	4.65	256	100	60 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
409	421	ILVRPSGTEPLLR	25	97.772			
230	245	ESGSAIGLAFDGD	27	98.368			
41	metallo-beta-lactamase superfamily class B	gi 116516084	61128	5.38	303	100	138 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
534	540	YLPDQTK	30	99.274			
382	391	YLPVQGEYR	37	99.78			
249	261	IVLTGFDIENIVR	27	97.873			
286	298	FEDHELIILETGR	45	99.96			
42	ribose-phosphate pyrophosphokinase	gi 116517035	35331.5	5.93	357	100	246 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
218	229	AILIDDLNTGR	64	100			
217	229	KAILIDDLNTGR	18	82.412			
37	52	QFSDGEIQVNIEE	21	91.601			
83	99	ASAHSINVLPPYF	83	100			
286	302	NVCYITASELIGD	54	99.996			
43	putative manganese-dependent inorganic pyrophosphatase	gi 116516825	33457.9	4.57	249	100	217 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
115	127	LEPVGSAIVYR	77	100			
102	114	VANFETASPLYMR	61	100			
218	232	VAQVNTVDIAEVL	180	100			
44	DNA-directed RNA polymerase subunit beta	gi 116516293	34242.8	4.64	164	100	70 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
21	28	FVIEPLER	21	76.645			
174	182	VNYQVEPAR	31	97.643			
250	259	TIEELDLSVR	18	56.309			
45	proline dipeptidase PepQ	gi 116516123	40347.3	4.73	101	100	76 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
281	290	AGYGEYFNHR	40	99.849			
87	96	HALPQLDFKR	18	75.153			
114	127	TVFETAEDNLTPI	17	70.941			
46	amino acid ABC transporter, ATP-binding subunit	gi 116516709	27350.4	6.01	240	100	147 100
Peptide Information							
Start Seq.	End Seq.	Sequence	Ion Score	C. I. %			
70	79	ITQEILALR	40	99.878			
235	244	TKEFFASYKR	27	97.486			
127	138	VGLSDRENHYPR	63	100			
217	234	IIESGTPDEIHTI	17	73.004			