

Supplementary Table S1

Table 1 Summary table of MHC II binding peptide sequences and protein identification in cell membrane debris suspensions treated by hypotonic swelling

Number	Protein names	Accession	Sequence	Score	intensity
1	IMP dehydrogenase	WP_087932817.1	AAAATSV GADGFER	79.693	50395
2	urease accessory protein UreE	WP_087909543.1	AASEELYE IR	64.485	24917
3	50S ribosomal protein L21	WP_002967949.1	ADAAEGE AAKPK	102.06	34653
4	DUF2333 family protein	WP_087932945.1	ADDRFWF AYGQLYA YYGLLR	8.1875	6019
5	urease subunit alpha	WP_004682812.1	ADGELLT CEPVDVV PMAQR	81.565	93831
6	ribosomal protein S3	WP_087909567.1	ADIDYGT AEAK	91.584	286730
7	hypothetical protein	WP_002967723.1	AEANINDI QQALEK	176.18	1960300*
8	Cytochrome b N-terminal domain-containing protein	WP_004684075.1	AEIAPVEIS AETKG	80.014	122160
9	Re/Si-specific NAD(P)(+)transhydrogenase subunit alpha,partial	WP_244563609.1	AETAPAA VTEK	99.815	54193
10	F0F1 ATP synthase subunit delta	WP_004684267.1	AETSSLIS GVAQR	93.058	71346
11	CobS cobaltochelata- se subunit CobS	WP_087932849.1	AFGVLEPE SAANIVLA	60.518	143080
12	YdcF family protein	WP_017750400.1	AFMQTVP APR	71.501	31350

Number	Protein names	Accession	Sequence	Score	intensity
13	CLPB ATP-dependent chaperone ClpB	WP_124737044.1	AGELAYG TIPQLEK	100.09	278280
14	Mrp/NBP35 family ATP-binding protein,partial	WP_206118526.1	AGILDADI YGPSMPR	63.184	517080
15	glucose-6-phosphate dehydrogenase	WP_004682109.1	AGQLSDP TR	136.8	112970
16	branched-chain amino acid ABC transporter substrate-binding protein	WP_023080355.1	AGSTDDS AAVAK	82.749	37189
17	trigger factor	WP_005973381.1	AGVEVTE EELQR	170.95	271560
18	CBS domain-containing protein	WP_004683933.1	ALAAQES QAMSK	78.655	30803
19	YebC/PmpR family DNA-binding transcriptional regulator	WP_002964805.1	ALEAALG EAESIK	143.5	239950
20	glycerol-3-phosphate dehydrogenase	WP_004684843.1	ALIGTTDI AYEGR	56.359	58109
21	tonB-system energizer ExbB	WP_006136925.1	ALLADAS AGVER	87.298	43701
22	pyruvate, phosphate dikinase	WP_006152532.1	ANAETPA DAR	106.42	28922
23	DUF883 family protein	WP_014489482.1	AQDVEAQ LTATVR	145.46	136110

Number	Protein names	Accession	Sequence	Score	intensity
24	50S ribosomal protein L9	WP_004683101.1	AQLEAQN LER	154.56	415910
25	SPFH/Band 7/PHB domain protein	WP_004681235.1	AQVLEAE GNR	114.89	326820
26	hypothetical protein	WP_006140655.1	ASGAPGIG EGTSTAAS TAGPGNPP SAQEQPV AVGQQAL LYEER	20.016	241810
27	DsbA family protein	WP_087909557.1	ATEESAIA DAVK	87.298	107680
28	NusG transcription termination/antitermination protein NusG	WP_087932883.1	ATPVDLE YGQVDKL	94.767	218820
29	FabI enoyl-ACP reductase FabI	WP_208936940.1	AVDAPDIS VVKD	63.32	86028
30	NhaA Na ⁺ /H ⁺ antiporter NhaA	WP_103053145.1	AVETEIPV VR	105.57	125570
31	30S ribosomal protein S5	WP_002964345.1	AVFETLG VQDVVAK	49.466	376920
32	tyrosine--tRNA ligase	WP_087913329.1	DAAEEAA ETAR	79.974	27567
33	DUF1476 domain-containing protein	WP_004683653.1	DAEAEAY AR	154.31	92139

Number	Protein names	Accession	Sequence	Score	intensity
34	ACP S-malonyltransferase	WP_069129796.1	DVSGAAV GSAEEIEA ALAALNA	44.511	291870
35	biosynthesis protein HemY	WP_004686704.1	DVVEAEVI VPAAEPVS ADEPVK	108.71	41898
36	bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ	WP_004684467.1	EATQATA EAAAK	105.2	24799
37	F0F1 ATP synthase subunit gamma	WP_087920822.1	ELIEIISGA EAL	89.298	219920
38	nucleoside-diphosphate kinase	WP_004683449.1	EVMGATN PANADEG TIR	74.326	39989
39	glycosyltransferase	WP_126981401.1	EVPPEDV NNANYFQ GR	134.75	227700
40	PLP-dependent aminotransferase family protein	WP_087932979.1	FAYLSADF SNPTGETV DR	102.66	68258
41	RseP RIP metalloprotease RseP	WP_006141584.1	FIGDESET SSPVGVNE SALSEEDR	2.4404	2295.1
42	acyl-CoA dehydrogenase C-terminal domain-containing protein	WP_006265927.1	FILDENG PGTR	72.643	25159
43	pyrimidine 5'-nucleotidase	WP_087913376.1	FLGAFGV DATRAVM FENLARN LVVPK	2.1945	11248

Number	Protein names	Accession	Sequence	Score	intensity
44	methionine adenosyltransferase	WP_011005450.1	FVIGGPDG DAGLTGR	84.718	76615
45	Rho transcription termination factor Rho	WP_002965128.1	GEVISSTF DEPAAR	92.611	45908
46	sugar ABC transporter ATP-binding protein	WP_087913374.1	GIIDDIR	137.5	2405.1
47	malate dehydrogenase	WP_087909583.1	GLDIAESS PVDGFDA K	136.53	290520
48	F0F1 ATP synthase subunit B	WP_004683012.1	IAQDLEQA AR	118.5	74482
49	dihydrolipoamide acetyltransferase family protein	WP_101457630.1	IAVGSELV R	162.5	112400
50	50S ribosomal protein L14	WP_004683923.1	IISLAPEVL	128.86	449940
51	phosphoribosylaminoimi dazolesuccinocarboxami de synthase	WP_002963974.1	IVVADEIS PDSAR	134.59	101330
52	alanine--tRNA ligase	WP_103053188.1	KGEGVFV HIGEVTEG TAK	3.4405	101180
53	saccharopine dehydrogenase family protein	WP_005973863.1	LAADDYL DEVK	79.974	60513

Number	Protein names	Accession	Sequence	Score	intensity
54	hypothetical protein	WP_004684078.1	LADYALA TTR	131.11	63911
55	protein translocase subunit SecDF	WP_247644351.1	LAELNIDS AR	108.98	25319
56	molybdopterin- dependent oxidoreductase	WP_002966561.1	LEGPGAL AR	64.803	119700
57	acetyl-CoA carboxylase biotin carboxylase subunit	WP_014490080.1	LGIPVVP SDGGVTD EVEAAR	68.972	42424
58	D-glycerate dehydrogenase	WP_118874249.1	LIANFGNG VDNIDVA AAARR	30.059	34344
59	GntR family transcriptional regulator	WP_101457049.1	LIDAYAV R	118.01	112170
60	thioredoxin	WP_087907738.1	LIGDPVEL ER	64.841	136940
61	PurS phosphoribosylformylgl ycinamidine synthase subunit PurS	WP_002963973.1	LLANTVIE DYSIAIA	103.7	163840
62	30S ribosomal protein S10	WP_002964363.1	LLDIVDPT PQTVDAL MK	50.222	915300
63	response regulator	WP_087924395.1	LLSTASGE ISR	87.298	54704

Number	Protein names	Accession	Sequence	Score	intensity
64	acyl-CoA dehydrogenase	QFP61583.1	LQAFGVT EPTSGTDT GALK	57.106	97135
65	30S ribosomal protein S7	WP_004686959.1	LSGELLDA ANNR	84.17	63796
66	IclR family transcriptional regulator	WP_006153697.1	LSMVYLD VVQGEGN MTMRR	9.7521	227320
67	50S ribosomal protein L2	WP_004683925.1	LVSGACF ASVGAVS NPDHGNI NDGK	94.449	1630400
68	amidase	WP_103053206.1	MANLDPF NALIAK	42.348	695120
69	hypothetical protein F9L69_14770	QFP68537.1	MAQFQNS GIR	23.32	14820
70	50S ribosomal protein L4	WP_002964361.1	MDLTITTL EGK	51.927	47802
71	murein L,D-transpeptidase	WP_004686459.1	MDPLTSG MSPIR	21.464	83305
72	AGE family epimerase/isomerase	WP_103053146.1	MNDVIRK LQVEVER	33.875	67820
73	pyruvate dehydrogenase complex E1 component subunit beta	WP_101456324.1	MPiEILMP ALSPTMEE GK	10.326	54289
74	nucleotidyltransferase family protein	WP_004684550.1	MRPITETM PKPLVNV AGK	52.344	1002100

Number	Protein names	Accession	Sequence	Score	intensity
75	transporter ATP-binding protein	WP_004682535.1	MSDVMTA NR	9.9869	50052
76	superoxide dismutase family protein	WP_006140982.1	MYEALPT GPGK	133.13	310510
77	ubiquinol-cytochrome c reductase iron-sulfur subunit	WP_002964648.1	NANLPTD AEATDLA R	151.98	188210
78	acetyl-CoA carboxylase biotin carboxyl carrier protein	WP_002964036.1	NAVPSPM VGTAYLA PAPGAR	111.79	73346
79	DNA starvation/stationary phase protection protein Dps	WP_004686203.1	NDLPSNT K	142.19	299370
80	acyl-CoA thioesterase	WP_002964616.1	NTENEPTG MLTIR	121.29	132590
81	FlhB flagellar biosynthesis protein FlhB	WP_004681320.1	NVVRLLV ANVLAIA AIAGFDLA WSRIHWR	0	5409.2
82	30S ribosomal protein S12	WP_004683928.1	PTVNQLIR	124.89	40413
83	0S ribosomal protein S2	WP_002964289.1	QASDIIAD AANR	102.55	181680

Number	Protein names	Accession	Sequence	Score	intensity
84	Asp-tRNA(Asn)/Glu-tRNA(Gln) amidotransferase subunit GatB	WP_087920610.1	QIAILEDG GVIDQETR	99.671	55566
85	50S ribosomal protein L24	WP_004683922.1	QTQTQEA GIISK	149.96	272660
86	RpiB/LacA/LacB family sugar-phosphate isomerase	WP_002965776.1	SAGNVNA INEVDAK	78.692	41283
87	RidA family protein	WP_002967716.1	SAVGVAS LPLNAPVE VEAIIIEVA	65.895	681250
88	50S ribosomal protein L25/general stress protein Ctc	WP_002964640.1	SEENAEG AAEEAKD GE	56.225	93024
89	50S ribosomal protein L19	WP_002964975.1	SGAGLNE NFTVR	176.6	155970
90	Hsp20 family protein	WP_002965411.1	SGDGYPP YNIER	82.831	54699
91	pyruvate kinase	WP_101419803.1	SIRCKVVS GTR	45.081	146100
92	DnaJ molecular chaperone DnaJ	WP_004684564.1	SLSVNIPA GIEDGTR	119.39	130640

Number	Protein names	Accession	Sequence	Score	intensity
93	electron transfer flavoprotein subunit beta/FixA family protein	WP_004684482.1	SPADFGA DIAPR	99.53	76537
94	Tim44/TimA family putative adaptor protein	WP_130137854.1	SSDAAPA GGGPDNV VSLPR	107.37	101170
95	30S ribosomal protein S11	WP_002964339.1	STPFAAQI AAEDCAK	82.362	180680
96	TonB-dependent receptor	WP_004685730.1	STSSVSVI DAADIER	65.574	39052
97	TIGR02300 family protein	WP_151039136.1	SYFEATVE SR	62.463	53371
98	translation elongation factor Ts	WP_002964288.1	TAAEGLV GVAASGN K	154.94	416590
99	dUTP diphosphatase	WP_002964766.1	TAASSSAP TLGIIR	127.42	88005
100	leucyl aminopeptidase	WP_011005277.1	TAEAIETT PAGVEK	103.91	83777
101	lipoprotein	WP_002964140.1	TAIPVTGT SNAAYVK	87.667	57395
102	transposase, partial	WP_206118522.1	TGDLELK QR	27.487	3764.3
103	integration host factor subunit alpha	WP_002963914.1	TGEEVPIL PR	199.02*	389890
104	integration host factor subunit beta	WP_014489310.1	TGETVDV EEK	101.65	36910

Number	Protein names	Accession	Sequence	Score	intensity
105	cytochrome c1	WP_005967752.1	TLEGLGYS PEQVK	122.57	123810
106	NADH-NADH-quinone oxidoreductase subunit J	WP_101457039.1	TPETAIEIR	114.89	60972
107	type IV secretion system protein VirB10	WP_087913357.1	TQENIPVQ PGTLDGE R	52.344	62543
108	2,3,4,5- tetrahydropyridine-2,6- dicarboxylate N- succinyltransferase	WP_004685944.1	TSINELLR D	72.23	74924
109	ferrochelatase	WP_005974740.1	TVPSYEAE PVYIDALA R	108.59	944840
110	leucine--tRNA ligase	WP_087907724.1	VATMLDS GAPVEIGS IEK	71.241	70291
111	hypothetical protein F9L69_10885	QFP67779.1	VFPANIKK QVASAPI LLTK	3.0979	10447
112	30S ribosomal protein S17	WP_002964353.1	VGDFVSIQ ESAPISK	108.35	341370
113	D-amino acid dehydrogenase	WP_101433153.1	VGGMAEV SGFTDDL AAR	94.191	49671
114	50S ribosomal protein L1	WP_101457031.1	VGTVTTD VAAAVAA SK	80.522	194490
115	S41 family peptidase	WP_118890819.1	VIAPIDDT PASK	85.29	48323

Number	Protein names	Accession	Sequence	Score	intensity
116	ABC transporter ATP-binding protein	WP_070329530.1	VIVLDEPT SALDR	96.89	76544
117	hypothetical protein	WP_004683155.1	VIYQAALT DTTR	111.06	119570
118	polyribonucleotide nucleotidyltransferase	WP_124737052.1	VLAVVEN DLR	64.654	38318
119	peroxiredoxin	WP_004686034.1	VLDALQT DELCPCN R	183*	213890
120	50S ribosomal protein L20	WP_002965185.1	VLDQAAG FR	67.903	46806
121	sigma-54 dependent transcriptional regulator	WP_006144450.1	VLVDQQF ER	103.56	38249
122	virB8 family protein	WP_002966517.1	VNAQTGA PDILTSLD EK	101.43	476170
123	30S ribosomal protein S13	WP_002964340.1	VNQLSDA EVLQIR	132.78	116590
124	methylated-DNA--[protein]-cysteine S-methyltransferase	WP_101415739.1	VRALLDG ASPDFSDT PLALDSVP DLNRR	0.63148	9984.5
125	GumC family protein	WP_087932900.1	VVGTELTP GQLPTDA SLAVAES QAR	28.951	68183

Number	Protein names	Accession	Sequence	Score	intensity
126	aldehyde dehydrogenase family protein	WP_118874233.1	YFENTSPV NGQVLCE VAR	109.22	124850
127	beta-ketoacyl-ACP synthase I	WP_011005448.1	YNDTPST ASR	107.15	24999
128	50S ribosomal protein L7/L12	WP_002964371.1	AQLEAAG AK DLVEGAP K	145.65 119.29	943350 118800
129	DUF1013 domain-containing protein	WP_002964823.1	AIADGEAS QGIK GLDPVITG QLSR	103.7 99.788	148250 112870
130	hypothetical protein	WP_002964396.1	AATAQITP EEK QAQEQTN ATLK	106.42 109.44	83176 31295
131	GrpE nucleotide exchange factor GrpE	WP_002965419.1	AEAAADE AEGEVDE TANR ALDAIPAD ALEADSN LK	112.51 81.92	260890 635400
132	30S ribosomal protein S1	WP_002965274.1	IENALGEA VLSR SEIVQNLE EGQVVEG VVK	112.13 111.91	120460 122770
133	catalase	WP_002966234.1	DAHGYDA NTIALNEK EPPLCISG NADR	62.357 75.294	47115 55903

Number	Protein names	Accession	Sequence	Score	intensity
134	co-chaperone GroES	WP_002966386.1	IGNDDYS QPR	107.57	65292
			TGNPDAY YEPNSFNG PVEQPSAK	18.699	72254
			EKPQEGE VVAAGAG AR	154.69	3179400*
			IGGEDLLI MK	136.27	1799900*
			TAGGHIIPD TAK	125.74	3072300*
135	Hsp20 family protein	WP_002966528.1	ADETASD VGEVLYR	112.15	100090
			AGSGTAQ PIEAK	90.108	112740
136	molecular chaperone DnaK	WP_002969217.1	DAEANA ADKK	213.53*	302330
			IINEPTAA ALAYGLD K	120.47	6082300*
			IQASGGLS DADIEK	145.91	901660
			SQTFSTAE DNQSAVTI R	105	336520
			TTPSIIAFT DGDER	157.97	2674400*
			VIENAEGA R	172.15	1959400*
			VIGIDLGT TNSCVAV MDGK	130.07	879510
			DTTACVM R	70.912	72075
137	invasion associated locus B family protein	WP_004682929.1			

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			QEQSSAQ AGQR	176.79*	221830
			VLTAELR	160.69	404730
138	3-deoxy-7-phosphoheptulonate synthase class II	WP_004683758.1	NVTECTG GAR	105.52	52716
			QVPFYPD AQALNDV EAR	68.809	143490
139	type I glyceraldehyde-3-phosphate dehydrogenase	WP_004684167.1	EVEVAGD TIDVGYGP IK	59.57	42089
			MSDTAVA LGK	68.224	46151
140	F0F1 ATP synthase subunit beta	WP_004684261.1	AALVYGQ MNEPPGA R	65.574	81811
			DTGEPIMV PVGVELT GR	198.32*	2400800*
			FTQAGSE VSALLGR	210.44*	1545200
			GIYPAVDP LDSTSR	155.11	854320
			IMNVIGEP VDEAGPIK	153.95	2348900*
			TIAMDAT EGLVR	154.56	424300
			TTAAAEA KPAAK	105.2	176670
			TTAAAKP AATK	97.965	31183
141	DegQ family serine endoprotease	WP_004685513.1	DIAASLGL AEEK	172.27	112580
			GAIVASPQ DDGPAAK	91.937	194050

Number	Protein names	Accession	Sequence	Score	intensity
			SGDVIVSV NNQTVK	88.596	73719
142	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine- residue succinyltransferase	WP_004685222.1	EEAKPAA AAPAAAP VASASSGP AMQPAPA AAK EGDTVEV GELLGQIS SDGAAVA AAPAQK LLAESGLS ADQVEGS GK	28.673 228.51* 224.24*	102470 1606800 263980
143	Outer membrane protein Omp31	WP_004685017.1	LGYTATE R NLVDVDN SFLESK	170.06 167.12	2321700* 31213000*
144	50S ribosomal protein L15	WP_004685698.1	AGGSIKLP EAAAE SGVSINGF EGGQMPI YR	73.885 85.288	318440 57969
145	25 kDa outer-membrane immunogenic protein	WP_004685536.1	LNNGLDD ESK LTDNILGR NYDLAGT TVR QGFEGSLR VGWTAGA GLEAK	138.98 175.75 182.53* 152.41 84.658	202740 67088 241610 2504700* 196680
146	30S ribosomal protein S8	WP_004686960.1	EQNVGGE LLCR	134.66	259410

Number	Protein names	Accession	Sequence	Score	intensity
			YYEGVPVI R	117.17	224860
147	protein translocase subunit SecD	WP_005968113.1	QEGGEEA QTAAVNK	70.942	32357
			TAEEGAIA QK	101.72	41343
			TNEPIVSF R	114.89	50111
			VVGDAVV VTIPDADQ R	109.6	28469
148	30S ribosomal protein S9	WP_004686488.1	TEAAAPV DVQK	109.29	493490
			VESINSLE ELGTVAK	174.24	1760700*
149	outer membrane protein assembly factor BamA	WP_006137216.1	EFDLNEG DAFNQVM VQR	110.66	75641
			NDVYDEG R	121.74	64878
			STGEFSIG GGYTTGG ESPGAQV EAAITER	35.923	121770
			TVDLGQG R	138.37	65234
			VNVVYEI NEGSR	125.97	113420
			YTFGDVS VESTVDG VDTQALD R	72.175	554610

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150	outer membrane protein Omp2a	WP_006142025.1	GGDDVYS GTDR	125.82	273530
			NTVAEDN AWGGIVR	97.813	81677
			VSTGSETE LGTLK	104.79	271150
151	peptidoglycan- associated lipoprotein Pal	WP_006267420.1	ADAQQTL SK	126.62	447550
			AVTVLNG AGR	100.45	59382
			EYNLALG QR	134.66	70672
152	DUF4167 domain- containing protein	WP_006152741.1	AEQPQPAI EAPAAAA R	56.225	40580
			VEEAAPA VVEAAPV EASAEAA GAPR	62.193	136590
153	HflK FtsH protease activity modulator HflK	WP_006213848.1	EVADAFD EVQR	91.867	68043
			VVQDAEG EAQR	147.2	56366
154	threonine--tRNA ligase	WP_006144467.1	LCEEATPP DLLR	93.111	54367
			SNTVSLQF PDGSR	89.548	77157
155	50S ribosomal protein L3	WP_029077456.1	AGAKAEA AATEGGE	67.726	26121
			VTTQNIEV VSTDSR	141.73	180860
156	fumarylacetoacetate hydrolase family protein	WP_029077452.1	AGDVVEL GIEGLGSQ K	93.011	158360

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			ATSAIVGP NDDLVIPR	140.78	251680
157	FtsH ATP-dependent zinc metalloprotease FtsH	WP_014489490.1	EISYSQFID DVSNGR	112.86	86853
			NVPLAPN VDLK	74.267	230760
			QVVVPNP DIVGR	75.652	68570
158	DNA-directed RNA polymerase subunit alpha	WP_065874193.1	AEDAPIGL IPVDSLYS PVR	147.7	796950
			GYVPADC NR	108.09	63104
159	elongation factor Tu	WP_040120183.1	AYDQIDA APEER	188.04*	977540
			TVGAGIVS SIIE	82.452	702220
			VGEEVEIV GIK	150.27	1641400
160	D-ribose ABC transporter substrate- binding protein	WP_069129862.1	DNVDKYN SPFVLEQ	89.805	228680
			YVELFGA PSDNNA TR	106.49	230480
161	mitofilin family membrane protein	WP_075630298.1	AIGEWEQ LPADAK	85.622	73073
			APVTGAS DNTTGEA PASSGQ	57.802	47702
			ATPAAEP VGGFSGK	129.82	187940

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			NPVTINLD PSEVK	93.096	55805
162	TonB-dependent receptor	WP_087910434.1	IAGLPNYD SQK	82.645	202660
			NGDGTEIL GTEPAAR	72.089	45535
			NNAFYTD PTFSPGR	124.67	115550
163	DNA-directed RNA polymerase subunit beta'	WP_087920739.1	GTPVNQG EAVGVIA AQSIGEPG TQLTMR	28.215	172070
			IIIEPNDDT IEPVEYLIP K	79.639	1188500
			SALTCETR	114.78	55419
164	peroxiredoxin	WP_087913324.1	SLNIEEQP GQAVTSA ASALLAQ L	97.203	589390
			TADGVTE MTTDDVF K	102.4	136120
			YSAIVEDG VVK	90.15	290620
167	OmpA family protein	WP_087924404.1	AASVASV LDSQGIDP R	83.397	50696
			AQLQGTG VSVTR	83.862	42503
168	tetratricopeptide repeat protein	WP_087932740.1	AIQLNPQY DAAYIGR	62.408	55976
			AISLNSTA PEPYNGR	80.763	60982

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169	sodium-translocating pyrophosphatase	WP_087932724.1	ATDALDA VGNTTK	159.83	73100
			SFEDGFTD ADGVK	72.006	21279
170	phosphopyruvate hydratase	WP_087932779.1	SGETEDST IADLAVAT NCGQIK	94.728	429270
			TAIIDIVGR	130.22	966470
171	chaperonin GroEL	WP_087932869.1	AAVEEGIV AGGGTAL LR	187.78*	8291800*
			ENTTIVDG AGQK	152.11	235080
			GVNADQE AGINIVR	261.65*	1673400*
			GYLSPYFV TNPEK	81.865	897180
			INTSEEVA QVGTISAN GEAEIGK	73.389	68255
			KINTSEEV AQVGTISA NGEAEIGK	119.01	2723000*
			MIAEAMQ K	113.1	403230
			QITTNAGE EASVIVGK	136.38	662630
			TAETELEV VEGMQFD R	342.62*	5666600*

Number	Protein names	Accession	Sequence	Score	intensity
			TNDTAGD GTTTATV LGQAIVQE GAK	189.81*	1472700
			VDDALNA TR	145.16	672800
			VGGATEV EVK	183.65*	1342600
			VGNEGVIT VEEAK	227.37*	3522900*
172	membrane protein insertase YidC	WP_101415741.1	DAAIAQSP R	117.4	45161
			YQSDLLS APLTVAP GQSQK	70.622	63322
173	NAD- glutamatedehydrogenase	WP_101419116.1	LVDGLPEP R	73.616	14122
			NAVIVPV GAK	70.919	66346
			SSAETDA QVGDR	132.91	84871
			VIGEGANL GVTQR	106.29	62053
174	aminopeptidase	WP_101419834.1	CFVDGAT LTPEEIR	100.72	119800
			LAIAADNP MLLSTQD AGK	52.555	32388
			VLDTDEG ACR	182.39*	36141

Number	Protein names	Accession	Sequence	Score	intensity
			YANAPDE SFDR	127.4	116460
175	pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase	WP_101419815.1	DVEAALA SGGAK	83.862	156020
			EAAAPAA APAPAR	169.44	146850
176	flagellar biosynthetic protein FliO	WP_101433138.1	IEPVVPFV AQEVR	98.353	1803600*
			LSVMDAA AVDSR	103.22	58017
177	NADP-dependent isocitrate dehydrogenase	WP_101457606.1	CATITPDE AR	176.79	139990
			DATNDQV TIDAANAI K	89.403	120930
178	porin family protein	WP_118874251.1	DFSVVDG DLSVEAR	156.51	143610
			NSVSLTD GIESIGVS QSK	222.29*	1157200
			STLSDEDT SIR	226.47*	3444100*
179	DUF1775 domain- containing protein	WP_110506816.1	VGDLVITD PSVR	120.45	264350
			VTVDLPE GFIMAQP QAK	78.653	1270900

Number	Protein names	Accession	Sequence	Score	intensity
180	DNA-directed RNA polymerase subunit beta	WP_124737035.1	AEAPFVG TGMEPIVA R	151.55	842660
			DIPNVSEE ALK	87.913	167490
			DSGAAIA AR	154.01	285950
			SLGLNVEL DDTR	129.7	115300
181	ribosome recycling factor	WP_130163227.1	ASASLLEP ITIEAYGS TMPINQV ANISVPES R	65.893	341120
			DSVISQDE SR	168.27	231410
182	25 kDa outer-membrane immunogenic protein	WP_247876854.1	DYGFDDA AVTNNFK	53.569	119050
			GEFEGTGF SQSK	114.4	239160
			NIDFLDEN NAAATFE NR	270.45*	1605800
183	elongation factor G, partial	WP_247872136.1	LAAEDPSF R	130.22	89222
			QSGGSGQ FAR	109.11	35708

Note: *Top 20 for peptide LFQ and score.