

MA6926 LC-MS run 1: 6926_220709_1a2_01

Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A2R4	DNA directed RNA polymerase subunit beta	155136	6.41	933.97	40	119	43.50	10.51	196	5	24.91	0.028
P0A1H3	Elongation factor G	77550	5.00	1592.45	37	47	72.59	9.07	335	3	19.48	0.025
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	840.11	32	60	51.99	9.30	212	3	19.89	0.026
P41031	Thiosulfate binding protein	37559	9.19	1328.42	31	32	81.36	7.95	270	0	16.20	0.024
P06202	Periplasmic oligopeptide binding protein	61254	6.03	1297.60	31	42	79.01	7.64	298	1	18.92	0.027
P0A1D3	60 kDa chaperonin	57249	4.65	1736.10	31	44	68.25	9.00	354	5	17.93	0.025
P66932	Trigger factor	48036	4.64	781.14	30	43	63.89	9.60	165	2	18.85	0.029
P64076	Enolase	45570	5.08	1813.48	30	34	77.55	9.24	345	1	18.27	0.025
Q7CPE1	ATP synthase subunit alpha	55078	5.61	988.57	28	40	71.35	9.60	243	3	20.67	0.026
P0A1P6	Glutamine synthetase	51752	5.25	944.64	28	33	79.53	10.48	209	2	21.01	0.026
Q7CPE2	ATP synthase subunit beta	50251	4.71	1027.95	28	32	72.61	9.45	199	1	17.81	0.026
P0A1E3	Cysteine synthase A	34514	5.72	1222.86	25	20	80.19	7.70	256	3	19.67	0.024
P52616	Phase 2 flagellin	52504	4.55	795.53	25	37	72.13	10.29	198	3	20.75	0.025
Q7CQ01	Chaperone protein clpB	95377	5.15	605.21	25	65	47.37	8.40	147	7	23.28	0.029
P0A1H5	Elongation factor Tu	43256	5.15	2221.17	25	30	82.23	9.19	394	1	15.82	0.022
P65702	Phosphoglycerate kinase	41106	4.90	1527.46	24	30	75.97	7.61	244	0	18.53	0.024
Q8ZQT5	Protein tolB	46120	8.73	609.01	23	21	62.56	8.98	141	0	20.34	0.026
P55900	Phosphoserine aminotransferase	39806	5.17	358.91	23	28	68.78	8.90	107	0	22.56	0.025
Q7CPK0	sn glycerol 3 phosphate binding periplasmic protein ugpB	48362	7.33	632.04	23	38	67.12	10.48	142	4	20.33	0.028
P05989	Ketol acid reductoisomerase	53907	4.96	622.75	22	47	63.34	7.53	164	4	22.46	0.028
Q8ZLT3	Polyribonucleotide nucleotidyltransferase	76990	4.86	414.73	22	51	47.68	12.50	112	3	24.18	0.029
P37412	3 isopropylmalate dehydrogenase	39488	5.14	356.58	22	25	66.12	9.03	114	1	24.33	0.031
P64052	Elongation factor Ts	30338	4.95	680.36	22	33	80.57	10.20	169	3	17.29	0.026
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1212.90	21	29	72.21	9.87	258	0	16.54	0.022
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	1211.58	21	21	75.17	8.97	200	2	17.10	0.024
P06179	Flagellin	51581	4.60	1074.49	21	36	68.08	8.63	236	3	18.99	0.027
Q7CR87	Chaperone surA	47221	6.88	606.78	21	31	67.29	7.44	137	0	17.44	0.027
P40720	Fumarate hydratase class I aerobic	63784	7.48	546.44	21	51	40.69	9.11	97	3	21.76	0.026
P25077	Malate dehydrogenase	32455	5.97	1221.40	21	22	71.79	9.04	217	1	15.61	0.023
O33921	Glucose 1 phosphatase	45530	6.64	742.70	20	25	74.82	10.50	184	1	17.89	0.022
P00924	Enolase 1	46773	6.15	732.09	20	28	48.05	9.58	156	2	20.62	0.026
Q56073	Chaperone protein dnaK	69215	4.64	662.18	20	59	49.84	8.92	141	2	22.02	0.026
Q8ZQM3	Glutathione binding protein gsiB	56502	8.98	547.59	20	40	59.77	7.85	128	1	20.21	0.027
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	929.78	20	22	71.47	10.23	180	1	18.84	0.025
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	484.89	19	28	78.42	11.35	125	1	20.81	0.025
Q8ZQU3	Succinate dehydrogenase flavoprotein subunit	64421	5.88	429.73	19	44	45.58	8.79	94	1	22.18	0.029
P51066	Isocitrate lyase	47532	5.06	411.91	19	29	61.75	9.27	83	1	22.02	0.030
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	395.26	19	27	68.06	12.16	99	0	22.69	0.025
Q8ZPS5	UPF0061 protein ydiU	54906	5.67	303.73	19	39	46.46	10.97	107	5	21.20	0.028
P23905	D galactose binding periplasmic protein	35791	5.75	622.31	19	30	62.05	8.18	143	4	19.11	0.027
P14062	6 phosphogluconate dehydrogenase decarboxylating	51363	5.04	609.41	18	38	60.47	9.06	111	3	21.26	0.028
P66869	Succinyl CoA ligase ADP forming subunit beta	41454	5.12	535.48	18	39	67.27	8.97	104	2	21.98	0.028
Q8ZL56	2 3 bisphosphoglycerate independent phosphoglycerate mutase	56219	4.88	416.55	18	37	55.84	8.21	101	1	23.50	0.028

P11003	5 10 methylenetetrahydrofolate reductase	33151	6.44	340.16	18	30	67.91	10.11	95	2	23.04	0.031
P65215	2 dehydro 3 deoxyphosphooctonate aldolase	30775	5.86	325.17	18	25	73.24	10.38	104	5	25.21	0.029
P02906	Sulfate binding protein	36517	7.72	662.92	18	28	68.69	10.73	148	0	23.00	0.026
P0A1W6	Leucine specific binding protein	39375	5.84	625.19	17	27	65.04	9.38	143	2	21.00	0.024
P41033	Phosphoenolpyruvate carboxykinase ATP	59539	5.58	528.77	17	45	50.19	7.14	116	2	20.64	0.027
P66764	S adenosylmethionine synthetase	41926	4.91	469.47	17	32	71.35	8.63	124	2	20.45	0.028
Q8ZP20	Periplasmic trehalase	63469	5.15	448.32	17	44	41.05	8.74	99	4	20.84	0.026
P0A269	Exopolyposphatase	58108	7.80	402.69	17	38	48.15	9.81	76	2	25.30	0.031
P15717	3 isopropylmalate dehydratase large subunit 1	49754	5.92	321.97	17	27	55.15	7.06	93	0	26.21	0.028
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	274.32	17	27	73.37	7.90	79	2	23.08	0.030
O68883	Citrate synthase	48074	6.26	631.11	17	33	59.95	8.10	129	1	19.89	0.027
P02910	Histidine binding periplasmic protein	28361	5.95	848.76	16	23	66.92	8.10	153	1	17.63	0.024
P26982	Protease do	49284	9.19	684.07	16	29	49.89	10.80	153	1	18.36	0.025
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	471.24	16	36	59.47	9.13	114	2	20.12	0.028
P58661	Aspartate aminotransferase	43494	5.29	354.35	16	34	52.78	9.57	84	0	23.84	0.029
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	249.97	16	19	58.41	10.55	75	2	22.04	0.030
P17215	Leu Ile Val Thr binding protein	38762	5.69	1254.58	16	21	78.90	8.34	241	1	17.52	0.022
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	435.99	15	25	76.64	8.09	94	1	21.29	0.028
P60446	50S ribosomal protein L3	22233	10.25	402.63	15	20	63.64	9.72	97	0	19.61	0.025
P02911	Lysine arginine ornithine binding periplasmic protein	28182	5.90	374.60	15	23	65.38	8.35	87	1	20.94	0.027
P0A2C5	D ribose binding periplasmic protein	30943	9.20	505.46	15	25	64.53	8.30	110	1	19.82	0.024
P65882	Adenylosuccinate synthetase	47347	5.15	426.71	14	42	53.01	6.94	92	3	21.15	0.027
P0A249	Phosphoenolpyruvate protein phosphotransferase	63328	4.56	400.16	14	51	46.78	12.54	101	4	25.62	0.029
P0A297	50S ribosomal protein L10	17789	9.46	374.37	14	15	76.36	9.10	93	4	19.80	0.029
P66955	Transaldolase B	35149	4.91	352.89	14	26	53.31	9.71	69	0	19.91	0.027
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	339.50	14	19	54.43	8.20	95	1	20.06	0.026
P67912	ADP L glycerol D mannose 6 epimerase	34827	4.72	464.66	14	33	51.29	8.57	74	1	23.77	0.027
P0A2A3	50S ribosomal protein L1	24713	10.10	585.47	13	19	60.26	7.84	110	2	18.19	0.023
P0A7W4	30S ribosomal protein S5	17592	10.56	565.04	13	13	70.06	9.46	112	3	15.57	0.026
P66313	50S ribosomal protein L6	18848	10.09	488.32	13	13	76.27	9.30	91	0	19.54	0.023
P26976	Non specific acid phosphatase	28364	9.22	331.54	13	19	58.80	10.08	77	1	19.97	0.028
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	633.48	13	16	82.35	9.33	108	0	17.65	0.026
P02936	Outer membrane protein A	37491	5.50	518.86	12	25	49.14	8.49	94	1	18.71	0.022
Q8ZK80	50S ribosomal protein L9	15774	7.73	498.65	12	14	68.46	9.80	91	2	19.02	0.025
Q8ZQD4	Outer membrane lipoprotein carrier protein	22467	7.39	395.45	12	17	88.18	9.25	103	3	18.57	0.025
O54297	30S ribosomal protein S4	23470	10.38	374.51	12	19	54.85	8.92	68	0	22.61	0.026
Q8ZRN1	D methionine binding lipoprotein metQ	29417	5.23	343.30	12	30	50.92	9.68	74	3	22.46	0.028
P24900	DNA replication and repair protein recF	40488	6.87	281.82	12	26	57.70	11.68	67	3	21.47	0.029
P00929	Tryptophan synthase alpha chain	28652	5.29	216.74	12	19	80.22	8.54	57	0	22.85	0.027
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	210.48	12	15	78.36	12.38	78	4	23.49	0.025
Q7CR64	UPF0325 protein yaeH	15084	7.17	155.66	12	11	75.78	8.03	48	0	20.79	0.025
P0A1S2	DNA binding protein H NS	15532	5.09	620.01	12	14	78.10	9.01	164	2	15.10	0.022
P63411	Acetate kinase	43230	5.91	498.49	11	25	49.75	9.92	86	1	20.59	0.025
P0A1V4	Adenylate kinase	23473	5.39	360.32	11	24	57.01	7.84	77	1	19.95	0.025
P65692	6 phosphofructokinase	34892	5.47	345.63	11	28	53.44	12.48	78	3	21.54	0.028
Q8ZRC9	UPF0234 protein yajQ	18307	5.42	333.04	11	14	71.78	9.20	72	1	19.21	0.027
Q8ZKP7	Triosephosphate isomerase	26899	5.61	331.47	11	22	75.69	9.99	98	0	19.88	0.023
Q7CQV9	DNA protection during starvation protein	18705	5.66	287.80	11	18	69.46	8.81	63	0	20.17	0.028

P0A2B3	30S ribosomal protein S7	17579	10.73	213.50	11	10	70.51	9.37	75	0	19.05	0.026
Q8ZP65	Probable thiol peroxidase	18014	4.74	566.63	11	12	95.83	6.51	144	1	18.56	0.024
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	345.99	10	16	64.90	9.19	74	1	17.99	0.021
P0A7X0	30S ribosomal protein S8	14117	9.85	268.39	10	12	76.15	8.55	53	0	19.65	0.024
P67091	Universal stress protein F	15704	5.92	512.90	10	11	87.50	8.53	96	0	18.64	0.024
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	541.00	9	12	66.27	9.31	125	0	18.51	0.021
P67904	30S ribosomal protein S10	11759	10.33	472.94	9	11	53.40	10.62	77	0	20.61	0.022
P0A1Z2	Chaperone protein skp	17894	10.25	451.78	9	10	58.39	9.36	105	1	16.73	0.023
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	327.47	9	15	66.14	9.60	99	0	16.66	0.024
P67093	Universal stress protein G	15891	6.20	249.18	9	9	88.73	9.60	79	2	18.96	0.024
P0A7V6	30S ribosomal protein S3	25967	10.72	233.71	9	20	50.21	10.92	47	0	21.67	0.025
P0A2D1	Oxidoreductase ucpA	27852	4.86	179.93	9	20	29.66	7.19	39	0	24.92	0.033
P66593	30S ribosomal protein S6	15163	5.08	667.51	9	9	67.94	9.76	128	0	17.41	0.024
Q7CPE5	ATP synthase subunit delta	19399	4.69	273.48	8	13	54.80	12.44	62	0	22.63	0.026
P0A2C7	Spermidine putrescine binding periplasmic protein	38996	4.99	269.26	8	28	47.99	8.22	41	0	27.18	0.030
P66738	Ribosome recycling factor	20542	8.60	266.66	8	16	54.59	6.34	63	2	19.08	0.028
Q8ZLD7	Universal stress protein A	16070	4.92	251.48	8	9	86.81	7.43	61	0	17.21	0.023
Q8ZQ40	Flavoprotein wrbA	20854	5.74	229.45	8	12	79.29	5.34	47	0	23.51	0.023
Q8ZRM2	Hydroxyacylglutathione hydrolase	28614	6.32	133.47	8	16	47.41	11.58	43	1	21.73	0.030
P0A2T6	Catabolite gene activator	23641	8.44	127.33	8	22	49.52	12.94	48	2	23.95	0.027
P66541	30S ribosomal protein S2	26741	6.73	286.04	8	23	58.92	7.83	59	1	19.84	0.030
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	537.89	7	8	61.54	10.90	86	0	16.70	0.023
P0A7K0	50S ribosomal protein L11	14865	10.09	298.37	7	11	68.31	10.73	49	1	18.12	0.022
Q8ZQS2	2 3 bisphosphoglycerate dependent phosphoglycerate mutase	28475	5.71	289.29	7	19	37.20	9.59	46	1	19.40	0.025
P0A9Y9	Cold shock like protein cspC	7397	7.70	271.01	7	5	92.75	8.45	45	0	19.20	0.024
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	253.69	7	19	56.85	8.63	35	0	19.50	0.027
P20753	Peptidyl prolyl cis trans isomerase A	20319	9.59	221.40	7	15	63.16	10.15	54	0	16.66	0.027
P0A1G5	DnaK suppressor protein	17504	4.87	204.34	7	12	63.58	7.95	37	0	17.43	0.026
P0A1P8	Glutaredoxin 1	9917	5.54	201.42	7	10	88.51	11.60	42	0	20.56	0.025
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	147.06	7	10	75.71	10.35	75	0	21.08	0.025
P58627	Maf like protein yceF	21479	5.84	145.44	7	16	53.61	11.30	35	0	19.68	0.031
P61179	50S ribosomal protein L22	12218	10.71	143.98	7	8	59.09	9.79	36	1	18.82	0.033
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	562.79	7	14	55.56	8.67	94	1	19.44	0.025
P0A1D5	10 kDa chaperonin	10311	5.19	581.58	6	7	56.70	7.71	88	0	15.79	0.022
P66692	Ribose 5 phosphate isomerase A	22881	4.89	470.49	6	15	49.77	8.21	85	2	18.47	0.026
P0AA28	Thioredoxin 1	11799	4.47	419.90	6	8	55.05	9.73	77	1	17.51	0.024
Q7CQ71	50S ribosomal protein L25	10534	9.94	255.67	6	8	69.15	5.77	54	0	20.44	0.023
Q7CPH8	Protein export protein secB	17234	4.06	232.72	6	12	65.16	13.10	48	0	21.52	0.025
P0A1B7	ATP synthase epsilon chain	15054	5.82	174.02	6	7	53.96	7.32	38	2	20.03	0.029
P63601	Shikimate kinase 1	19458	5.08	121.21	6	14	52.60	7.22	30	1	24.68	0.029
O68926	Bacterioferritin	18343	4.42	115.88	6	15	51.90	10.75	27	1	23.88	0.031
P0A1R6	DNA binding protein HU alpha	9515	10.12	717.89	6	7	64.44	3.76	101	0	19.02	0.019
P0A2F0	RNA polymerase sigma E factor	21698	5.20	231.93	5	17	55.50	5.24	45	2	20.69	0.026
Q7CPL4	50S ribosomal protein L16	15184	11.65	230.39	5	6	36.76	9.34	34	1	18.34	0.022
Q7CPB2	UPF0337 protein yjbJ	8454	7.16	167.96	5	11	60.00	8.71	18	0	20.41	0.027
P63727	Soluble cytochrome b562	13903	9.10	167.74	5	9	29.69	7.81	33	0	19.40	0.025
P0A1S4	DNA binding protein stpA	15477	9.24	148.99	5	12	55.64	7.02	35	1	19.78	0.024
P0A9Z4	Nitrogen regulatory protein P II 1	12417	4.98	133.70	5	8	42.86	8.08	29	0	25.60	0.031

Q7CQ70	UPF0352 protein yejL	8226	5.31	110.08	5	4	56.00	7.54	33	0	20.03	0.027
P0A299	50S ribosomal protein L7 L12	12291	4.40	417.15	5	20	55.37	9.33	60	3	19.10	0.025
P0A2F6	Single stranded DNA binding protein	19062	5.29	166.79	4	11	31.82	10.51	31	0	18.84	0.033
Q8ZK81	30S ribosomal protein S18	9065	11.11	118.37	4	4	48.00	11.48	23	0	22.27	0.027
P0A2A7	50S ribosomal protein L30	6509	11.41	91.58	4	6	71.19	10.59	19	0	17.82	0.025
Q8ZKP1	Cell division protein zapB	9306	4.38	348.58	4	13	59.49	7.00	39	0	17.27	0.027
P66643	30S ribosomal protein S9	14817	11.34	145.64	3	14	23.08	6.77	14	0	20.35	0.027
Q7CQN4	Major outer membrane lipoprotein I	8386	9.82	138.65	3	6	48.72	8.00	26	0	15.01	0.024
P66451	30S ribosomal protein S17	9716	10.08	119.29	3	4	39.29	11.70	19	0	16.38	0.017
Q8ZLM1	30S ribosomal protein S13	13153	11.22	146.93	3	12	15.25	6.73	21	0	15.81	0.027
P0A6B1	Acyl carrier protein	8634	3.75	126.04	2	4	32.05	12.68	19	0	12.75	0.025

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P0A1D3	60 kDa chaperonin	57249	4.65	1861.83	33	44	77.01	9.11	372	4	18.81	0.026
P64076	Enolase	45570	5.08	1562.70	32	34	80.56	9.48	325	0	18.71	0.025
P0A1H3	Elongation factor G	77550	5.00	1185.69	30	47	64.63	6.28	232	2	19.76	0.025
P52616	Phase 2 flagellin	52504	4.55	665.20	29	37	67.79	9.60	194	0	21.21	0.028
P06202	Periplasmic oligopeptide binding protein	61254	6.03	1046.33	29	42	64.27	9.08	240	0	16.96	0.028
P40720	Fumarate hydratase class I aerobic	63784	7.48	444.44	28	51	61.55	9.10	142	2	24.07	0.032
P0A1H5	Elongation factor Tu	43256	5.15	1815.10	28	30	81.73	9.77	360	3	15.65	0.024
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	626.03	25	60	44.43	9.08	148	1	19.39	0.027
P66932	Trigger factor	48036	4.64	592.61	24	43	44.68	9.95	135	1	22.14	0.029
Q7CPE1	ATP synthase subunit alpha	55078	5.61	697.02	24	40	64.72	8.52	169	1	19.90	0.027
Q8ZRP0	Outer membrane protein assembly factor yaeT	89471	4.80	460.85	23	58	36.19	8.44	121	1	23.07	0.031
P41031	Thiosulfate binding protein	37559	9.19	1221.15	23	32	68.34	7.07	248	2	16.65	0.026
P0A1P6	Glutamine synthetase	51752	5.25	685.47	22	33	71.43	7.29	146	2	19.97	0.028
Q8ZQU3	Succinate dehydrogenase flavoprotein subunit	64421	5.88	528.14	22	44	48.98	10.22	132	4	24.12	0.026
Q7CPE2	ATP synthase subunit beta	50251	4.71	690.92	22	32	69.13	9.81	161	2	19.53	0.028
O33921	Glucose 1 phosphatase	45530	6.64	685.63	21	25	79.66	9.00	188	2	17.72	0.028
P64052	Elongation factor Ts	30338	4.95	669.25	21	33	69.61	9.52	134	2	17.94	0.027
Q56073	Chaperone protein dnaK	69215	4.64	590.11	21	59	48.43	9.94	110	2	22.15	0.028
Q7CR87	Chaperone surA	47221	6.88	485.08	21	31	70.79	6.88	123	0	20.55	0.029
P65702	Phosphoglycerate kinase	41106	4.90	1344.65	21	30	72.61	6.28	208	0	18.10	0.024
P26982	Protease do	49284	9.19	565.12	20	29	56.63	8.15	143	0	18.55	0.026
P25077	Malate dehydrogenase	32455	5.97	1250.96	19	22	86.22	6.90	226	2	18.15	0.025
P0A1E3	Cysteine synthase A	34514	5.72	1022.17	19	20	70.90	5.42	176	0	18.08	0.026
P00924	Enolase 1	46773	6.15	582.36	19	28	46.00	10.37	131	3	19.07	0.027
Q7CPK0	sn glycerol 3 phosphate binding periplasmic protein ugpB	48362	7.33	516.95	19	38	57.31	7.64	100	0	22.01	0.028
P41033	Phosphoenolpyruvate carboxykinase ATP	59539	5.58	497.24	19	45	63.57	9.44	127	2	24.12	0.031
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	398.55	19	36	50.60	9.11	111	3	21.32	0.027
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1284.61	19	29	75.53	9.70	250	1	18.18	0.024
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	751.73	18	22	63.82	9.43	144	0	20.84	0.027

Q8ZQT5	Protein tolB	46120	8.73	542.54	18	21	51.40	8.87	130	1	19.03	0.028
P05989	Ketol acid reductoisomerase	53907	4.96	463.20	18	47	52.14	7.43	132	4	23.09	0.029
P55900	Phosphoserine aminotransferase	39806	5.17	429.72	18	28	58.56	8.19	115	2	21.07	0.030
Q8ZP20	Periplasmic trehalase	63469	5.15	411.98	18	44	49.47	9.07	129	3	21.74	0.028
Q8ZL56	2 3 bisphosphoglycerate independent phosphoglycerate mutase	56219	4.88	341.01	18	37	55.84	8.99	82	1	27.14	0.027
P06179	Flagellin	51581	4.60	806.71	18	36	52.53	8.92	163	0	18.78	0.027
Q8ZQM3	Glutathione binding protein gsiB	56502	8.98	444.30	17	40	43.75	8.06	79	0	21.05	0.028
P02906	Sulfate binding protein	36517	7.72	430.34	17	28	73.56	10.68	99	1	21.08	0.028
P65882	Adenylosuccinate synthetase	47347	5.15	427.67	17	42	52.31	7.77	117	2	20.01	0.026
P58661	Aspartate aminotransferase	43494	5.29	310.49	17	34	51.52	8.75	93	0	23.85	0.029
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	282.82	17	27	51.27	9.70	80	2	20.62	0.031
P0A1F8	Aspartate semialdehyde dehydrogenase	40110	5.21	262.02	17	27	75.82	8.18	94	4	22.99	0.029
P14062	6 phosphogluconate dehydrogenase decarboxylating	51363	5.04	548.20	17	38	61.32	7.67	101	3	21.57	0.026
P23905	D galactose binding periplasmic protein	35791	5.75	611.46	16	30	58.13	10.41	122	1	19.33	0.028
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	948.26	16	21	68.21	8.25	164	4	19.46	0.028
P0A2B3	30S ribosomal protein S7	17579	10.73	231.24	15	10	83.33	9.99	85	0	19.49	0.028
P17215	Leu Ile Val Thr binding protein	38762	5.69	1097.61	15	21	76.16	7.48	248	5	18.44	0.026
P0A1V4	Adenylate kinase	23473	5.39	408.48	14	24	49.53	9.47	100	0	19.73	0.029
P0A297	50S ribosomal protein L10	17789	9.46	396.79	14	15	75.15	8.31	107	3	19.82	0.029
O68883	Citrate synthase	48074	6.26	382.28	14	33	56.21	8.56	81	2	21.05	0.029
P66869	Succinyl CoA ligase ADP forming subunit beta	41454	5.12	353.47	14	39	62.63	9.08	90	2	18.97	0.030
P0A1W6	Leucine specific binding protein	39375	5.84	348.49	14	27	65.04	10.03	101	2	20.82	0.028
P77983	Pyruvate kinase I	50625	5.53	323.94	14	33	44.68	8.66	86	1	23.71	0.029
P60446	50S ribosomal protein L3	22233	10.25	279.70	14	20	63.16	8.70	80	2	19.56	0.030
Q8ZNV1	tRNA mo5U34 methyltransferase	37087	5.66	218.29	14	29	68.73	10.03	72	2	26.09	0.032
P63411	Acetate kinase	43230	5.91	457.49	14	25	50.75	10.85	98	2	23.16	0.030
P0A2C5	D ribose binding periplasmic protein	30943	9.20	542.18	13	25	54.73	7.21	121	3	19.66	0.027
P66955	Transaldolase B	35149	4.91	382.40	13	26	57.10	8.19	77	2	23.85	0.032
P15717	3 isopropylmalate dehydratase large subunit I	49754	5.92	254.65	13	27	40.56	8.13	59	0	21.66	0.030
P14146	Virulence transcriptional regulatory protein phoP	25617	5.14	205.84	13	21	73.21	9.67	78	2	21.99	0.028
P02910	Histidine binding periplasmic protein	28361	5.95	689.84	13	23	66.92	7.15	140	3	19.16	0.028
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	352.06	12	15	80.32	8.76	114	0	17.44	0.023
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	328.76	12	28	55.32	8.90	70	0	20.48	0.027
P02911	Lysine arginine ornithine binding periplasmic protein	28182	5.90	269.25	12	23	51.92	10.23	56	1	20.46	0.031
P37412	3 isopropylmalate dehydrogenase	39488	5.14	267.98	12	25	47.66	12.18	63	1	24.38	0.031
P0A2C7	Spermidine putrescine binding periplasmic protein	38996	4.99	259.46	12	28	63.22	10.57	58	0	22.63	0.028
P02936	Outer membrane protein A	37491	5.50	368.72	12	25	44.29	9.37	74	1	18.43	0.030
Q8ZK80	50S ribosomal protein L9	15774	7.73	514.24	11	14	73.15	11.24	91	1	21.09	0.029
Q8ZP65	Probable thiol peroxidase	18014	4.74	457.75	11	12	80.95	6.46	110	1	16.70	0.023
Q8ZRN1	D methionine binding lipoprotein metQ	29417	5.23	377.95	11	30	52.40	8.17	65	2	25.10	0.029
Q8ZKP7	Triosephosphate isomerase	26899	5.61	335.51	11	22	62.75	7.76	121	1	17.28	0.024
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	318.93	11	25	57.66	8.62	64	1	24.51	0.028
P66764	S adenosylmethionine synthetase	41926	4.91	269.37	11	32	57.55	10.57	66	2	22.34	0.030
P26976	Non specific acid phosphatase	28364	9.22	186.66	11	19	46.80	9.51	48	0	22.44	0.030
P0A7W4	30S ribosomal protein S5	17592	10.56	577.88	11	13	69.46	9.25	98	1	15.38	0.023
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	273.07	10	26	43.69	8.79	52	1	26.02	0.029
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	257.97	10	15	74.27	9.71	78	4	21.09	0.029
P16657	Enoyl acyl carrier protein reductase NADH	27742	5.47	255.03	10	21	49.62	10.09	58	0	23.83	0.032

Q8ZJV7	Purine nucleoside phosphorylase deoD type	25961	5.45	236.46	10	23	47.28	8.23	43	1	20.68	0.032
Q9ZFU6	Uncharacterized protein ypfL	48359	4.45	224.38	10	25	32.24	12.02	38	0	25.20	0.031
P65215	2 dehydro 3 deoxyphosphooctonate aldolase	30775	5.86	295.82	10	25	54.23	10.22	70	4	20.11	0.032
P0A2A3	50S ribosomal protein L1	24713	10.10	483.58	9	19	55.13	9.50	77	0	17.30	0.025
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	449.61	9	16	74.87	9.93	77	0	18.85	0.027
P66593	30S ribosomal protein S6	15163	5.08	444.47	9	9	67.94	7.38	74	0	18.33	0.026
P66313	50S ribosomal protein L6	18848	10.09	422.54	9	13	67.23	8.49	62	0	21.47	0.024
P0A1S0	Integration host factor subunit alpha	11360	9.88	241.02	9	13	61.62	7.51	52	0	20.75	0.030
P66541	30S ribosomal protein S2	26741	6.73	235.27	9	23	53.11	9.07	58	2	21.96	0.028
Q8ZNA5	Long chain fatty acid transport protein	47445	4.72	227.40	9	20	37.24	5.54	37	0	21.74	0.032
P65933	Uridylate kinase	25938	7.26	224.32	9	23	51.04	8.77	41	1	24.79	0.031
P0A7V6	30S ribosomal protein S3	25967	10.72	178.59	9	20	47.64	10.72	49	1	18.49	0.029
P0A8B8	UPF0133 protein ybaB	12006	4.82	174.06	9	11	93.58	7.66	49	1	22.08	0.033
P0A2F4	Superoxide dismutase Fe	21294	5.52	113.76	9	14	71.50	11.72	56	1	21.09	0.033
P0A1S2	DNA binding protein H NS	15532	5.09	596.29	9	14	71.53	8.80	132	1	14.79	0.025
P40783	Quinone oxidoreductase	35129	6.79	261.56	8	27	44.04	10.51	48	3	22.41	0.030
P67093	Universal stress protein G	15891	6.20	245.58	8	9	75.35	9.76	49	0	21.58	0.026
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	225.41	8	19	43.17	9.61	48	2	25.14	0.033
P62405	50S ribosomal protein L5	20304	9.76	218.55	8	14	59.22	7.27	43	1	19.56	0.030
P04787	3 isopropylmalate dehydratase small subunit I	22492	4.89	113.05	8	11	56.72	8.75	43	0	21.61	0.027
Q7CQV9	DNA protection during starvation protein	18705	5.66	284.66	8	18	55.09	9.05	40	0	19.60	0.029
O54297	30S ribosomal protein S4	23470	10.38	386.10	7	19	44.66	10.98	54	0	18.37	0.025
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	308.20	7	16	60.58	10.74	44	1	21.01	0.026
P22107	TraT complement resistance protein	26261	9.35	281.89	7	18	38.27	9.79	49	2	17.13	0.028
Q8ZQD4	Outer membrane lipoprotein carrier protein	22467	7.39	273.58	7	17	58.13	7.73	50	1	19.32	0.029
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	206.44	7	19	60.08	8.49	47	2	23.34	0.033
Q8ZQ40	Flavoprotein wrbA	20854	5.74	166.18	7	12	71.72	6.29	61	0	23.69	0.032
P65599	Oligoribonuclease	20619	4.85	156.68	7	21	37.57	7.68	40	1	21.54	0.031
P58663	Capsular synthesis regulator component B	23699	7.71	147.99	7	19	39.81	9.89	35	0	24.20	0.024
P41784	Protein prgI	8851	4.56	95.01	7	8	86.25	10.19	37	1	23.95	0.028
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	399.16	7	12	57.99	11.35	102	0	16.38	0.024
P0A299	50S ribosomal protein L7 L12	12291	4.40	441.86	6	20	52.07	6.89	68	2	17.30	0.026
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	364.19	6	14	43.48	10.72	76	1	18.45	0.024
P67091	Universal stress protein F	15704	5.92	361.81	6	11	53.47	8.00	68	0	17.69	0.026
P66692	Ribose 5 phosphate isomerase A	22881	4.89	351.95	6	15	42.47	7.58	52	0	18.93	0.026
P67904	30S ribosomal protein S10	11759	10.33	321.81	6	11	44.66	10.02	59	0	19.44	0.022
Q8ZLD7	Universal stress protein A	16070	4.92	228.57	6	9	72.92	6.82	50	0	16.32	0.031
Q8ZNW0	Pyruvate kinase II	51354	6.11	221.81	6	34	26.46	6.89	31	1	21.57	0.030
Q8ZRC9	UPF0234 protein yajQ	18307	5.42	219.65	6	14	56.44	9.66	57	2	22.84	0.027
P0A9Y9	Cold shock like protein cspC	7397	7.70	215.66	6	5	78.26	7.97	45	0	18.38	0.027
P0A7K0	50S ribosomal protein L11	14865	10.09	208.69	6	11	59.86	8.82	40	0	20.55	0.025
P00929	Tryptophan synthase alpha chain	28652	5.29	206.69	6	19	50.37	6.56	46	3	22.09	0.027
O54296	30S ribosomal protein S11	13822	11.74	169.75	6	9	54.26	8.82	35	1	23.86	0.033
P0A1G5	DnaK suppressor protein	17504	4.87	168.19	6	12	64.24	8.50	24	0	21.24	0.031
P0A277	Xanthine phosphoribosyltransferase	16958	5.74	167.11	6	11	42.11	6.56	28	0	21.20	0.032
P20753	Peptidyl prolyl cis trans isomerase A	20319	9.59	142.94	6	15	55.79	8.64	45	0	17.88	0.026
Q7CPD8	UPF0438 protein yifE	13069	6.23	137.24	6	13	31.25	8.70	30	0	19.46	0.031
P66738	Ribosome recycling factor	20542	8.60	137.05	6	16	41.08	8.08	42	2	19.48	0.034

P0A212	DNA gyrase inhibitory protein homolog	18050	4.28	131.64	6	8	65.16	9.76	29	0	19.40	0.033
P66643	30S ribosomal protein S9	14817	11.34	109.07	6	14	45.38	11.99	25	0	28.67	0.028
P43019	Superoxide dismutase Mn	23064	6.51	99.72	6	15	45.63	10.53	31	0	19.34	0.032
Q8ZK81	30S ribosomal protein S18	9065	11.11	82.80	6	4	52.00	7.27	31	0	22.67	0.031
P64267	Protein gns	6478	6.13	76.81	6	7	63.16	10.38	26	1	24.00	0.031
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	497.11	6	8	54.49	9.34	72	1	19.87	0.024
P0A1D5	10 kDa chaperonin	10311	5.19	628.68	5	7	71.13	6.11	89	1	18.65	0.022
P0A1Z2	Chaperone protein skp	17894	10.25	385.29	5	10	51.55	7.11	74	1	20.00	0.025
P0AA28	Thioredoxin 1	11799	4.47	382.44	5	8	58.72	10.37	63	1	16.77	0.024
Q8ZPU5	NH 3 dependent NAD synthetase	30464	5.21	157.40	5	22	20.73	11.64	24	0	25.49	0.029
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	154.39	5	10	43.50	10.02	57	1	18.47	0.028
O68926	Bacterioferritin	18343	4.42	112.56	5	15	53.80	9.55	24	0	27.25	0.028
Q7CQN4	Major outer membrane lipoprotein 1	8386	9.82	98.29	5	6	48.72	6.85	21	0	19.64	0.029
P0A1P8	Glutaredoxin 1	9917	5.54	95.77	5	10	52.87	7.48	28	0	17.84	0.023
P0A1R6	DNA binding protein HU alpha	9515	10.12	796.38	5	7	65.56	7.07	98	0	18.06	0.019
P58683	Class B acid phosphatase	26298	6.51	166.62	4	14	32.49	10.39	30	1	21.01	0.030
P0A1B7	ATP synthase epsilon chain	15054	5.82	160.11	4	7	53.24	8.04	30	0	20.68	0.023
Q9F7A2	GDP mannose mannosyl hydrolase	17638	4.80	145.95	4	11	31.85	9.10	22	0	24.27	0.030
P0A2S0	Leucine responsive regulatory protein	18845	9.15	133.76	4	14	35.37	3.74	18	0	17.98	0.029
Q7CPP7	50S ribosomal protein L21	11571	10.29	101.02	4	7	56.31	7.98	26	1	24.39	0.034
P0A7X0	30S ribosomal protein S8	14117	9.85	202.69	4	12	23.08	5.64	29	0	16.91	0.024
P0A1S4	DNA binding protein stpA	15477	9.24	219.83	3	12	35.34	7.55	36	2	18.81	0.029
Q7CPG1	Uncharacterized protein yicS	10975	8.86	168.17	3	8	23.71	6.04	20	1	19.47	0.028
P69226	Translation initiation factor IF 1	8244	9.74	131.40	3	5	55.56	8.57	33	1	21.32	0.027
Q9L9J1	Thiazole biosynthesis protein thiG	26837	5.08	107.12	3	18	21.09	11.78	15	1	28.08	0.032
P37589	Signal transduction protein pmrD	9742	8.74	98.03	3	5	51.76	9.83	29	2	21.44	0.026
P66170	50S ribosomal protein L29	7255	10.52	252.45	3	4	55.56	10.09	51	0	16.38	0.027

MA6926 LC-MS run 3: 6926_220709_1a2_03												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P06173	DNA directed RNA polymerase subunit beta	150506	4.96	964.27	46	112	44.78	9.73	192	1	24.55	0.042
P0A1D3	60 kDa chaperonin	57249	4.65	1637.82	34	44	74.09	7.74	319	2	16.45	0.033
P0A1H3	Elongation factor G	77550	5.00	964.76	31	47	71.73	7.90	237	3	21.01	0.035
P06202	Periplasmic oligopeptide binding protein	61254	6.03	968.61	31	42	64.46	8.79	240	0	18.05	0.035
Q56073	Chaperone protein dnaK	69215	4.64	705.48	30	59	57.99	9.72	170	1	22.81	0.037
P06179	Flagellin	51581	4.60	1007.55	28	36	70.71	8.69	243	1	20.31	0.033
P0A1P6	Glutamine synthetase	51752	5.25	572.96	26	33	75.27	8.83	161	4	21.49	0.038
P0A1H5	Elongation factor Tu	43256	5.15	1874.45	26	30	77.92	9.83	347	3	14.46	0.028
Q8ZQZ6	Leucyl tRNA synthetase	96923	5.02	488.58	24	66	44.65	11.20	127	4	24.19	0.042
Q7CPE1	ATP synthase subunit alpha	55078	5.61	764.94	24	40	57.70	8.01	183	2	20.57	0.037
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	600.96	23	60	43.37	8.11	118	1	21.16	0.032
P64076	Enolase	45570	5.08	1224.41	23	34	75.93	8.54	240	3	19.04	0.032
P41031	Thiosulfate binding protein	37559	9.19	1131.23	22	32	77.81	5.54	231	2	16.07	0.033
P52616	Phase 2 flagellin	52504	4.55	903.68	22	37	62.85	8.86	188	1	21.33	0.035

P65702	Phosphoglycerate kinase	41106	4.90	1325.22	22	30	74.16	7.65	228	1	17.65	0.032
Q7CPK0	sn glycerol 3 phosphate binding periplasmic protein ugpB	48362	7.33	435.13	21	38	65.30	9.14	103	1	21.54	0.038
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	403.15	21	36	56.59	9.75	124	2	19.96	0.039
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1368.62	21	29	67.98	8.03	269	1	18.52	0.030
P23905	D galactose binding periplasmic protein	35791	5.75	556.09	20	30	66.87	8.62	124	0	17.65	0.037
P25077	Malate dehydrogenase	32455	5.97	1176.74	20	22	82.05	7.35	210	2	17.53	0.031
P14062	6 phosphogluconate dehydrogenase decarboxylating	51363	5.04	497.12	19	38	73.72	8.84	119	3	23.29	0.038
Q8ZQM3	Glutathione binding protein gsiB	56502	8.98	439.40	19	40	57.23	7.85	124	4	20.53	0.041
Q8ZP20	Periplasmic trehalase	63469	5.15	436.85	19	44	47.02	8.85	105	1	21.50	0.038
P05989	Ketol acid reductoisomerase	53907	4.96	401.74	19	47	60.49	6.84	116	6	20.33	0.040
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	733.45	19	22	72.65	9.46	160	1	19.21	0.034
O33921	Glucose 1 phosphatase	45530	6.64	685.44	18	25	66.59	7.93	168	1	17.71	0.032
Q7CR87	Chaperone surA	47221	6.88	513.94	18	31	65.65	9.27	110	0	19.64	0.037
Q8ZL56	2 3 bisphosphoglycerate independent phosphoglycerate mutase	56219	4.88	406.36	18	37	56.23	9.78	108	3	22.80	0.036
P00924	Enolase 1	46773	6.15	714.06	18	28	50.34	11.02	139	4	19.29	0.033
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	869.47	17	21	61.26	8.26	189	4	17.27	0.035
P0A1E3	Cysteine synthase A	34514	5.72	791.01	17	20	65.02	6.30	147	1	18.27	0.031
P26982	Protease do	49284	9.19	589.41	17	29	46.53	9.50	144	2	19.78	0.034
P64052	Elongation factor Ts	30338	4.95	555.87	17	33	68.90	8.78	143	6	17.83	0.037
P65882	Adenylosuccinate synthetase	47347	5.15	424.07	17	42	55.56	9.50	113	6	22.51	0.039
P17215	Leu Ile Val Thr binding protein	38762	5.69	1063.42	17	21	79.73	8.63	222	1	17.71	0.033
P77983	Pyruvate kinase I	50625	5.53	420.26	16	33	41.91	7.62	88	1	19.71	0.039
O68883	Citrate synthase	48074	6.26	320.95	16	33	57.14	8.83	104	2	20.76	0.035
P60446	50S ribosomal protein L3	22233	10.25	253.35	16	20	65.07	9.15	77	0	19.08	0.036
P02910	Histidine binding periplasmic protein	28361	5.95	688.99	16	23	68.85	7.41	139	1	17.41	0.032
Q7CPE2	ATP synthase subunit beta	50251	4.71	652.48	15	32	49.78	6.01	112	2	17.69	0.036
P0A1W6	Leucine specific binding protein	39375	5.84	308.58	15	27	53.93	10.73	77	0	21.74	0.039
P15717	3 isopropylmalate dehydratase large subunit 1	49754	5.92	224.64	15	27	45.92	11.26	77	2	27.05	0.039
P0A7W4	30S ribosomal protein S5	17592	10.56	699.82	15	13	70.66	7.88	117	1	17.57	0.032
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	425.71	14	15	88.98	8.93	114	0	14.45	0.033
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	411.71	14	27	52.88	11.24	75	1	23.28	0.036
P55900	Phosphoserine aminotransferase	39806	5.17	360.93	14	28	50.83	6.56	86	2	20.68	0.035
P66932	Trigger factor	48036	4.64	561.47	14	43	42.13	9.49	93	2	18.73	0.037
P02906	Sulfate binding protein	36517	7.72	391.54	13	28	56.23	10.84	78	0	23.00	0.037
P58661	Aspartate aminotransferase	43494	5.29	317.35	13	34	41.67	10.11	80	0	21.93	0.042
Q8ZKF5	Cytochrome c 552	53782	6.43	247.90	13	31	36.82	9.62	64	1	19.99	0.039
P66764	S adenosylmethionine synthetase	41926	4.91	240.18	13	32	48.70	10.69	79	2	23.07	0.039
P02911	Lysine arginine ornithine binding periplasmic protein	28182	5.90	225.25	13	23	56.54	5.41	58	1	21.87	0.040
P0A2C5	D ribose binding periplasmic protein	30943	9.20	483.06	13	25	55.74	7.50	96	1	17.39	0.037
P0A297	50S ribosomal protein L10	17789	9.46	408.84	12	15	64.85	7.62	77	0	17.00	0.034
P0A2C7	Spermidine putrescine binding periplasmic protein	38996	4.99	274.68	12	28	45.69	9.28	55	0	24.94	0.038
Q7CR64	UPF0325 protein yaeH	15084	7.17	212.60	12	11	71.09	8.08	53	0	18.59	0.037
Q8ZQT5	Protein tolB	46120	8.73	522.77	12	21	40.70	8.12	96	0	17.46	0.032
P66869	Succinyl CoA ligase ADP forming subunit beta	41454	5.12	356.09	11	39	42.53	8.04	73	1	19.98	0.032
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	263.44	11	19	39.24	9.67	67	1	22.27	0.036
P65215	2 dehydro 3 deoxyphosphooctonate aldolase	30775	5.86	241.12	11	25	66.55	8.47	61	3	19.25	0.038
P16657	Enoyl acyl carrier protein reductase NADH	27742	5.47	231.51	11	21	53.05	7.95	64	1	22.92	0.036
P0A2B3	30S ribosomal protein S7	17579	10.73	213.01	11	10	77.56	8.34	61	0	18.26	0.035

P63411	Acetate kinase	43230	5.91	537.36	11	25	42.00	7.01	77	1	20.17	0.034
P0A1S2	DNA binding protein H NS	15532	5.09	545.52	10	14	67.88	9.38	119	1	16.48	0.035
P0A1V4	Adenylate kinase	23473	5.39	370.26	10	24	56.07	10.59	83	1	19.23	0.034
P66692	Ribose 5 phosphate isomerase A	22881	4.89	327.00	10	15	67.12	9.67	71	1	20.70	0.035
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	252.07	10	19	71.77	10.66	67	4	24.10	0.040
P66541	30S ribosomal protein S2	26741	6.73	226.26	10	23	53.53	12.28	62	1	22.64	0.034
P60726	50S ribosomal protein L4	22072	10.19	204.42	10	18	49.25	8.69	53	1	20.48	0.036
P63351	Vitamin B12 import ATP binding protein btuD	27092	8.82	147.04	10	17	63.45	10.63	54	2	21.99	0.039
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	581.22	10	16	76.47	8.66	80	0	16.52	0.034
P02936	Outer membrane protein A	37491	5.50	306.88	9	25	37.14	12.34	61	0	22.31	0.036
Q8ZRC9	UPF0234 protein yajQ	18307	5.42	281.94	9	14	60.12	7.77	59	1	19.35	0.041
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	242.35	9	19	44.76	7.86	49	1	17.63	0.036
P66738	Ribosome recycling factor	20542	8.60	196.98	9	16	55.14	8.63	61	1	17.56	0.036
O68901	Superoxide dismutase Cu Zn 2	17726	6.04	192.26	9	9	91.91	9.13	92	3	19.75	0.032
P0A2F4	Superoxide dismutase Fe	21294	5.52	191.07	9	14	66.32	10.29	52	0	20.24	0.041
P0A1Z2	Chaperone protein skp	17894	10.25	451.49	9	10	69.57	7.06	94	1	20.72	0.031
Q8ZK80	50S ribosomal protein L9	15774	7.73	527.40	8	14	51.01	6.93	76	0	17.96	0.033
P15111	NADP specific glutamate dehydrogenase	48543	6.29	433.70	8	38	25.95	8.39	63	2	19.87	0.043
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	305.47	8	16	62.02	6.83	47	0	16.88	0.035
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	217.80	8	26	34.63	8.61	56	2	22.96	0.041
Q7CPP7	50S ribosomal protein L21	11571	10.29	156.18	8	7	75.73	9.32	46	1	20.84	0.040
Q7CPD8	UPF0438 protein yifE	13069	6.23	116.49	8	13	70.54	12.82	40	0	27.73	0.039
P0A2A3	50S ribosomal protein L1	24713	10.10	528.87	8	19	35.90	5.87	76	0	16.41	0.029
P0A1D5	10 kDa chaperonin	10311	5.19	531.20	7	7	82.47	5.86	83	1	15.37	0.030
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	488.94	7	12	57.99	10.28	94	0	15.94	0.028
Q8ZQD4	Outer membrane lipoprotein carrier protein	22467	7.39	332.22	7	17	51.72	7.58	63	1	19.11	0.040
P67093	Universal stress protein G	15891	6.20	296.58	7	9	87.32	9.95	63	3	22.59	0.036
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	279.27	7	10	46.89	9.70	59	1	19.07	0.036
Q8ZQ40	Flavoprotein wrbA	20854	5.74	257.95	7	12	71.21	6.69	57	0	22.14	0.037
P0A9Y9	Cold shock like protein cspC	7397	7.70	246.84	7	5	92.75	10.04	50	0	19.16	0.030
Q7CQV9	DNA protection during starvation protein	18705	5.66	225.16	7	18	55.09	9.17	41	0	23.47	0.040
P62405	50S ribosomal protein L5	20304	9.76	211.56	7	14	35.20	6.97	47	0	18.82	0.033
P66593	30S ribosomal protein S6	15163	5.08	168.83	7	9	56.49	10.01	40	0	20.76	0.036
P0A1R6	DNA binding protein HU alpha	9515	10.12	603.81	7	7	70.00	6.34	101	0	15.63	0.027
P0A299	50S ribosomal protein L7 L12	12291	4.40	396.36	6	20	48.76	9.77	63	1	18.47	0.035
P67091	Universal stress protein F	15704	5.92	258.67	6	11	35.42	6.17	47	0	18.67	0.034
O54297	30S ribosomal protein S4	23470	10.38	234.10	6	19	34.95	9.63	46	0	24.11	0.035
P0A7K0	50S ribosomal protein L11	14865	10.09	223.74	6	11	47.18	7.33	53	1	18.99	0.034
P0A7X0	30S ribosomal protein S8	14117	9.85	194.78	6	12	49.23	7.61	41	0	18.93	0.031
P0A2F6	Single stranded DNA binding protein	19062	5.29	190.44	6	11	45.45	9.15	48	2	19.17	0.039
P0AA07	Phosphocarrier protein HPr	9113	5.51	180.69	6	7	95.29	6.88	63	0	13.21	0.029
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	146.36	6	15	49.12	9.54	30	0	19.86	0.035
O68926	Bacterioferritin	18343	4.42	122.50	6	15	43.04	8.97	35	0	22.56	0.035
Q7CPZ4	Protein grpE	21827	4.49	111.75	6	18	52.04	10.86	30	0	24.39	0.036
Q8ZP65	Probable thiol peroxidase	18014	4.74	473.03	6	12	67.86	8.60	86	0	17.63	0.028
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	306.71	5	8	46.79	9.20	49	0	18.38	0.030
P66313	50S ribosomal protein L6	18848	10.09	229.03	5	13	36.72	4.93	37	1	17.34	0.032
P0A7V6	30S ribosomal protein S3	25967	10.72	182.30	5	20	37.77	4.75	33	0	19.88	0.035

Q8ZR01	Rare lipoprotein A	39083	7.82	132.43	5	17	16.54	7.34	23	0	22.78	0.040
P67904	30S ribosomal protein S10	11759	10.33	356.90	5	11	38.83	7.77	44	0	16.94	0.027
P0AA28	Thioredoxin 1	11799	4.47	384.04	4	8	38.53	8.44	53	1	13.06	0.031
P66170	50S ribosomal protein L29	7255	10.52	251.68	4	4	65.08	9.14	46	0	16.33	0.037
P0A1S0	Integration host factor subunit alpha	11360	9.88	190.71	4	13	29.29	10.68	30	0	20.48	0.036
P0A1B7	ATP synthase epsilon chain	15054	5.82	189.94	4	7	53.24	5.53	29	0	19.06	0.039
P0A1R8	DNA binding protein HU beta	9234	10.24	175.99	4	9	52.22	11.37	35	1	16.54	0.028
P0A275	Protein mucA	16516	6.24	170.07	4	12	34.93	6.67	26	1	23.47	0.038
Q7CPL4	50S ribosomal protein L16	15184	11.65	143.27	4	6	25.00	8.44	30	0	20.03	0.038
P61179	50S ribosomal protein L22	12218	10.71	135.40	4	8	45.45	9.05	25	1	21.79	0.039
P0A1P8	Glutaredoxin 1	9917	5.54	105.55	4	10	48.28	9.47	24	0	24.46	0.030
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	459.37	4	14	39.61	8.00	78	1	16.86	0.033
Q7CQN4	Major outer membrane lipoprotein 1	8386	9.82	137.93	3	6	48.72	5.67	23	1	17.81	0.039

MA6926 + Zn(II) LC-MS run 1: 6926_Zn_220709_1a2_01												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1H3	Elongation factor G	77550	5.00	814.26	37	47	74.72	8.33	227	4	22.05	0.030
P0A1D3	60 kDa chaperonin	57249	4.65	1363.05	34	44	72.81	9.94	319	5	19.12	0.029
P0A1H5	Elongation factor Tu	43256	5.15	1725.35	32	30	86.55	10.12	365	2	17.49	0.025
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	680.71	31	60	51.19	9.65	168	2	21.54	0.028
P06202	Periplasmic oligopeptide binding protein	61254	6.03	1307.44	30	42	65.75	8.62	293	0	17.01	0.028
Q7CPE1	ATP synthase subunit alpha	55078	5.61	744.85	27	40	60.23	7.73	170	1	20.43	0.029
Q8ZQM3	Glutathione binding protein gsiB	56502	8.98	574.98	26	40	66.99	9.71	156	3	21.87	0.031
P52616	Phase 2 flagellin	52504	4.55	673.78	26	37	67.19	9.17	182	0	22.38	0.029
Q7CPK0	sn glycerol 3 phosphate binding periplasmic protein ugpB	48362	7.33	681.14	25	38	76.71	9.88	161	1	20.41	0.027
P41031	Thiosulfate binding protein	37559	9.19	1273.06	25	32	73.67	7.81	263	0	17.67	0.024
O33921	Glucose 1 phosphatase	45530	6.64	1010.44	24	25	75.06	7.89	237	1	17.31	0.024
P00924	Enolase 1	46773	6.15	683.67	24	28	53.32	9.53	156	3	20.64	0.029
P0A1P6	Glutamine synthetase	51752	5.25	625.96	24	33	68.23	10.00	142	1	22.34	0.031
P64076	Enolase	45570	5.08	1347.64	24	34	68.29	9.25	283	2	19.85	0.026
P06179	Flagellin	51581	4.60	793.54	23	36	58.99	7.43	184	3	21.58	0.029
Q8ZRP0	Outer membrane protein assembly factor yaeT	89471	4.80	502.83	23	58	36.19	9.49	95	1	24.85	0.036
P65702	Phosphoglycerate kinase	41106	4.90	1292.81	23	30	79.07	5.05	215	0	20.41	0.025
P64052	Elongation factor Ts	30338	4.95	609.80	22	33	64.66	10.06	149	1	17.65	0.031
Q8ZQT5	Protein tolB	46120	8.73	600.75	22	21	71.63	9.02	178	3	19.36	0.030
Q56073	Chaperone protein dnaK	69215	4.64	567.23	22	59	60.66	10.31	129	1	22.55	0.030
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	933.80	22	22	71.76	9.27	192	0	18.48	0.027
P06196	Silent protein ushA 0	60518	5.73	584.82	21	40	62.36	10.39	112	1	23.02	0.034
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	391.30	21	28	62.31	7.88	104	1	20.27	0.032
Q8ZP20	Periplasmic trehalase	63469	5.15	677.32	21	44	56.67	8.39	148	2	21.32	0.029
P66932	Trigger factor	48036	4.64	568.18	20	43	46.99	8.89	111	1	21.28	0.034
P05989	Ketol acid reductoisomerase	53907	4.96	352.00	20	47	57.84	9.68	112	2	21.71	0.029
P25077	Malate dehydrogenase	32455	5.97	1049.24	20	22	73.08	7.28	209	2	17.48	0.025
P0A1E3	Cysteine synthase A	34514	5.72	831.50	19	20	85.76	8.35	165	1	19.77	0.027
Q7CPE2	ATP synthase subunit beta	50251	4.71	713.51	19	32	66.30	8.12	149	3	18.33	0.030

Q7CR87	Chaperone surA	47221	6.88	590.42	19	31	59.35	7.92	135	1	18.22	0.026
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	920.69	19	21	66.89	9.11	182	4	18.41	0.029
P23905	D galactose binding periplasmic protein	35791	5.75	649.98	18	30	79.22	9.38	144	1	20.63	0.030
P0A2C5	D ribose binding periplasmic protein	30943	9.20	573.66	18	25	63.18	8.50	123	1	17.08	0.028
P66764	S adenosylmethionine synthetase	41926	4.91	257.89	18	32	78.39	9.04	84	0	24.03	0.031
P26982	Protease do	49284	9.19	832.75	18	29	52.84	7.17	166	2	18.96	0.026
P77983	Pyruvate kinase I	50625	5.53	368.82	17	33	56.81	8.72	90	3	26.60	0.031
P0A7W4	30S ribosomal protein S5	17592	10.56	638.02	17	13	86.23	8.53	135	2	19.69	0.028
P17215	Leu Ile Val Thr binding protein	38762	5.69	1157.05	16	21	76.16	8.30	238	2	16.25	0.025
P11003	5 10 methylenetetrahydrofolate reductase	33151	6.44	347.04	16	30	69.59	9.81	83	1	25.11	0.033
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	234.85	16	27	63.74	10.58	68	1	22.84	0.029
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1237.99	16	29	58.91	8.77	244	0	15.52	0.021
O68883	Citrate synthase	48074	6.26	370.13	15	33	54.57	10.58	76	0	22.67	0.031
P55900	Phosphoserine aminotransferase	39806	5.17	355.07	15	28	50.28	11.25	88	3	20.66	0.031
P0A1V4	Adenylate kinase	23473	5.39	243.71	15	24	75.23	8.57	88	1	18.44	0.029
P02906	Sulfate binding protein	36517	7.72	613.29	15	28	60.49	9.24	110	0	19.01	0.027
P0A1W6	Leucine specific binding protein	39375	5.84	470.11	14	27	59.35	10.15	106	1	20.37	0.029
P0A2C7	Spermidine putrescine binding periplasmic protein	38996	4.99	371.53	14	28	63.79	8.60	86	3	21.97	0.031
P63411	Acetate kinase	43230	5.91	349.48	14	25	54.75	8.23	68	1	24.72	0.031
P16657	Enoyl acyl carrier protein reductase NADH	27742	5.47	246.51	14	21	66.41	9.66	81	1	21.43	0.029
P00929	Tryptophan synthase alpha chain	28652	5.29	241.01	14	19	80.22	10.45	71	1	23.88	0.035
P60446	50S ribosomal protein L3	22233	10.25	173.88	14	20	65.55	7.28	60	0	18.81	0.030
P0A1S2	DNA binding protein H NS	15532	5.09	555.90	14	14	76.64	9.22	159	1	15.86	0.028
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	381.11	13	15	88.98	9.32	130	0	16.85	0.027
P02911	Lysine arginine ornithine binding periplasmic protein	28182	5.90	296.03	13	23	57.69	8.44	70	1	22.58	0.030
P0A297	50S ribosomal protein L10	17789	9.46	288.87	13	15	72.12	9.70	76	2	21.06	0.024
Q8ZP84	Universal stress protein E	35616	5.01	261.50	13	23	52.38	11.42	73	0	23.86	0.035
P14062	6 phosphogluconate dehydrogenase decarboxylating	51363	5.04	475.24	13	38	42.52	7.62	74	2	20.82	0.030
P65882	Adenylosuccinate synthetase	47347	5.15	492.64	12	42	44.21	8.37	91	6	21.21	0.032
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	440.24	12	16	80.75	11.85	100	1	19.16	0.029
P26976	Non specific acid phosphatase	28364	9.22	352.50	12	19	64.80	9.96	75	0	20.02	0.030
P66955	Transaldolase B	35149	4.91	288.33	12	26	46.06	8.34	44	0	19.58	0.030
Q8ZIV7	Purine nucleoside phosphorylase deoD type	25961	5.45	241.28	12	23	56.90	10.63	60	2	23.11	0.032
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	239.34	12	19	57.46	7.61	63	2	24.10	0.029
Q8ZJW6	Ribosomal RNA small subunit methyltransferase C	37592	6.39	185.47	12	22	63.16	13.30	64	3	25.66	0.034
P02910	Histidine binding periplasmic protein	28361	5.95	805.70	12	23	63.85	6.95	143	2	19.43	0.027
P02936	Outer membrane protein A	37491	5.50	410.45	11	25	36.00	12.47	64	0	21.62	0.030
P40827	Lipoprotein nlpD	39616	9.79	348.75	11	19	53.05	7.42	54	0	20.88	0.032
P22107	TraT complement resistance protein	26261	9.35	293.07	11	18	50.62	5.71	72	2	19.72	0.031
P58661	Aspartate aminotransferase	43494	5.29	264.40	11	34	40.91	10.58	55	1	24.55	0.029
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	234.73	11	19	54.43	9.04	71	0	20.87	0.032
Q8ZRC9	UPF0234 protein yajQ	18307	5.42	203.47	11	14	76.07	4.81	62	1	23.35	0.033
P0A2N2	Virulence protein vsdE	24829	6.48	196.35	11	22	56.02	10.98	61	1	22.77	0.030
P66313	50S ribosomal protein L6	18848	10.09	478.21	11	13	58.76	6.96	77	0	18.72	0.024
P0A1Z2	Chaperone protein skp	17894	10.25	377.18	10	10	57.76	7.78	89	0	17.53	0.026
Q7CQV9	DNA protection during starvation protein	18705	5.66	318.30	10	18	62.87	10.70	66	0	24.45	0.030
P67912	ADP L glycerol D mannose 6 epimerase	34827	4.72	297.85	10	33	47.42	8.47	50	2	24.92	0.036
Q8ZQD4	Outer membrane lipoprotein carrier protein	22467	7.39	225.03	10	17	81.28	6.89	58	0	19.80	0.028

Q8ZR01	Rare lipoprotein A	39083	7.82	212.47	10	17	38.85	6.03	52	1	24.47	0.030
Q8ZQ40	Flavoprotein wrbA	20854	5.74	195.21	10	12	86.36	8.26	63	0	23.42	0.029
Q7CR64	UPF0325 protein yaeH	15084	7.17	186.69	10	11	57.03	10.97	51	0	22.44	0.029
Q8ZK80	50S ribosomal protein L9	15774	7.73	496.78	10	14	68.46	9.21	82	1	18.58	0.026
Q8ZP65	Probable thiol peroxidase	18014	4.74	389.82	9	12	95.24	6.71	105	2	18.75	0.025
Q8ZRN1	D methionine binding lipoprotein metQ	29417	5.23	321.13	9	30	43.17	8.56	59	2	19.75	0.030
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	276.03	9	16	73.56	8.98	56	1	19.50	0.030
P14146	Virulence transcriptional regulatory protein phoP	25617	5.14	254.42	9	21	59.38	9.93	57	2	21.66	0.026
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	225.99	9	15	73.68	8.75	63	2	17.43	0.032
P0A8B8	UPF0133 protein ybaB	12006	4.82	219.69	9	11	87.16	6.32	45	1	20.78	0.031
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	204.50	9	19	72.98	10.41	56	4	18.93	0.030
P66541	30S ribosomal protein S2	26741	6.73	194.06	9	23	67.63	6.48	52	2	20.63	0.034
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	415.82	9	25	37.96	8.59	54	0	19.28	0.027
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	510.63	8	12	72.78	9.39	93	1	18.61	0.023
P67091	Universal stress protein F	15704	5.92	475.42	8	11	65.97	7.60	85	1	16.25	0.026
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	423.62	8	27	47.91	9.00	61	3	20.35	0.032
Q8ZKP7	Triosephosphate isomerase	26899	5.61	280.36	8	22	52.94	8.30	90	1	18.75	0.028
Q8ZQS2	2 3 bisphosphoglycerate dependent phosphoglycerate mutase	28475	5.71	251.30	8	19	41.60	7.56	48	0	20.60	0.027
P67093	Universal stress protein G	15891	6.20	238.81	8	9	78.87	12.29	71	1	19.72	0.028
Q8ZK57	Inositol 2 dehydrogenase	37243	4.92	238.49	8	25	47.62	13.21	57	3	26.60	0.033
P0AA19	Transcriptional regulatory protein ompR	27336	5.99	217.82	8	23	46.44	10.33	51	3	23.34	0.031
P0A2B3	30S ribosomal protein S7	17579	10.73	197.28	8	10	52.56	10.14	41	0	20.81	0.024
P66738	Ribosome recycling factor	20542	8.60	170.35	8	16	57.30	11.50	47	1	19.16	0.033
P15888	Oxygen insensitive NAD P H nitroreductase	23940	5.27	165.92	8	18	47.47	7.53	45	0	19.82	0.033
P66593	30S ribosomal protein S6	15163	5.08	535.20	8	9	58.78	10.64	109	0	16.42	0.022
P66869	Succinyl CoA ligase ADP forming subunit beta	41454	5.12	325.60	7	39	37.11	7.65	37	0	21.23	0.026
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	296.94	7	8	56.41	9.26	56	0	17.07	0.023
P0A2A3	50S ribosomal protein L1	24713	10.10	279.40	7	19	42.74	7.80	70	2	19.35	0.025
P0A1S4	DNA binding protein stpA	15477	9.24	176.69	7	12	53.38	8.81	45	1	21.48	0.033
P65554	RNA pyrophosphohydrolase	20792	10.35	133.75	7	16	46.02	6.92	32	1	25.45	0.030
P66643	30S ribosomal protein S9	14817	11.34	113.25	7	14	47.69	7.89	34	0	22.02	0.034
P0A1D5	10 kDa chaperonin	10311	5.19	568.35	7	7	56.70	7.57	88	1	17.34	0.027
P0A299	50S ribosomal protein L7 L12	12291	4.40	438.54	6	20	71.07	7.36	80	2	18.44	0.030
P67904	30S ribosomal protein S10	11759	10.33	370.96	6	11	33.98	8.19	55	0	19.17	0.023
P66692	Ribose 5 phosphate isomerase A	22881	4.89	311.21	6	15	46.12	8.40	45	0	18.89	0.028
P20753	Peptidyl prolyl cis trans isomerase A	20319	9.59	258.48	6	15	55.26	6.40	49	0	18.88	0.027
Q8ZL48	Phosphopantetheine adenyllyltransferase	17944	8.05	196.29	6	14	61.64	10.09	40	1	20.60	0.031
P66170	50S ribosomal protein L29	7255	10.52	182.03	6	4	58.73	7.08	43	1	17.07	0.029
Q8ZLD7	Universal stress protein A	16070	4.92	178.80	6	9	80.56	6.71	61	0	15.52	0.030
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	150.70	6	10	43.50	10.68	57	0	19.47	0.028
P0AA28	Thioredoxin 1	11799	4.47	443.28	6	8	55.96	9.21	70	0	17.27	0.023
P0A1S0	Integration host factor subunit alpha	11360	9.88	222.00	5	13	37.37	9.98	36	0	21.42	0.031
P0A7K0	50S ribosomal protein L11	14865	10.09	219.75	5	11	43.66	8.15	43	0	20.91	0.024
Q7CPH8	Protein export protein secB	17234	4.06	201.33	5	12	52.26	9.11	31	0	23.49	0.028
P0A1R8	DNA binding protein HU beta	9234	10.24	188.10	5	9	58.89	11.69	29	0	17.98	0.027
P58663	Capsular synthesis regulator component B	23699	7.71	185.55	5	19	22.69	9.66	34	2	19.65	0.036
P64267	Protein gns	6478	6.13	115.31	5	7	59.65	10.13	25	0	21.40	0.033
Q56109	Protein nrdI	15314	9.68	102.65	5	13	57.35	7.05	25	0	23.92	0.028

P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	640.54	5	14	39.61	7.47	106	3	17.43	0.028
P0A7X0	30S ribosomal protein S8	14117	9.85	276.48	4	12	27.69	10.21	34	0	21.43	0.019
O54297	30S ribosomal protein S4	23470	10.38	269.71	4	19	20.39	9.55	35	0	16.51	0.029
P0AA07	Phosphocarrier protein HPr	9113	5.51	248.80	4	7	82.35	8.43	65	1	16.82	0.026
P0AA02	Transcription antitermination protein nusG	20532	6.40	179.41	4	13	27.62	8.14	36	2	22.12	0.031
P67617	Probable Fe 2 trafficking protein	10892	5.87	158.44	4	15	40.66	8.75	28	1	22.65	0.032
P0A1P8	Glutaredoxin 1	9917	5.54	109.03	4	10	45.98	7.85	24	0	17.25	0.035
P0A1U6	Uncharacterized protein yjgD	15687	3.44	107.46	4	8	34.78	6.86	28	0	18.84	0.027
P67551	UPF0253 protein yaeP	7151	4.37	75.86	4	5	83.33	5.21	15	0	16.33	0.030
P0A9Y9	Cold shock like protein cspC	7397	7.70	379.11	4	5	47.83	6.51	47	0	14.91	0.023
Q7CR46	Anti adapter protein iraP	9876	5.50	201.05	3	7	46.51	5.33	26	0	16.89	0.025
Q7CPL6	50S ribosomal protein L18	12761	10.88	141.78	3	9	35.04	10.83	20	0	19.34	0.031
Q7CQN4	Major outer membrane lipoprotein 1	8386	9.82	138.66	3	6	48.72	3.81	21	0	16.71	0.031
P0A1R6	DNA binding protein HU alpha	9515	10.12	638.82	3	7	46.67	2.51	78	0	14.67	0.016

MA6926 + Zn(II) LC-MS run 2: 6926_Zn_220709_1a2_02												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1D3	60 kDa chaperonin	57249	4.65	1348.42	34	44	70.62	8.33	295	2	18.84	0.031
P06202	Periplasmic oligopeptide binding protein	61254	6.03	1052.47	29	42	64.27	7.14	244	0	18.80	0.031
P0A1H3	Elongation factor G	77550	5.00	562.20	28	47	53.55	8.99	163	2	23.42	0.034
P0A1H5	Elongation factor Tu	43256	5.15	1535.21	27	30	84.52	9.62	303	3	16.85	0.032
P64076	Enolase	45570	5.08	961.52	25	34	73.38	8.84	244	1	21.61	0.031
P52616	Phase 2 flagellin	52504	4.55	548.61	23	37	70.75	7.54	153	0	21.59	0.035
Q7CPK0	sn glycerol 3 phosphate binding periplasmic protein ugpB	48362	7.33	481.67	23	38	65.07	9.71	136	3	23.07	0.034
O86090	Polyphosphate kinase	80406	8.89	470.88	23	67	39.97	11.14	125	2	25.19	0.037
Q7CPE2	ATP synthase subunit beta	50251	4.71	654.08	23	32	71.09	8.52	150	2	21.58	0.033
Q56073	Chaperone protein dnaK	69215	4.64	458.62	22	59	47.18	9.55	122	2	22.55	0.034
P00924	Enolase 1	46773	6.15	556.19	22	28	57.21	9.88	136	2	21.70	0.033
O33921	Glucose 1 phosphatase	45530	6.64	766.46	21	25	78.21	8.65	203	1	19.80	0.032
P06179	Flagellin	51581	4.60	618.47	20	36	60.61	7.11	167	4	21.24	0.031
P06196	Silent protein ushA 0	60518	5.73	460.11	20	40	65.27	9.55	117	3	21.49	0.036
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1188.38	20	29	71.90	8.60	267	1	18.14	0.026
P66932	Trigger factor	48036	4.64	628.12	19	43	50.46	9.34	140	3	20.42	0.035
P0A1P6	Glutamine synthetase	51752	5.25	434.06	19	33	60.55	9.71	107	3	24.48	0.035
P65702	Phosphoglycerate kinase	41106	4.90	1108.06	19	30	70.80	7.88	185	0	20.73	0.031
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	885.14	18	22	71.18	7.56	173	2	18.69	0.030
Q8ZP20	Periplasmic trehalase	63469	5.15	487.39	18	44	49.12	9.46	141	3	24.29	0.034
P02906	Sulfate binding protein	36517	7.72	486.98	18	28	72.64	9.00	117	0	20.69	0.036
P0A1E3	Cysteine synthase A	34514	5.72	462.82	18	20	75.85	8.57	123	2	22.27	0.034
P64052	Elongation factor Ts	30338	4.95	416.87	18	33	63.60	10.55	112	3	20.81	0.034
P55900	Phosphoserine aminotransferase	39806	5.17	393.63	18	28	59.12	7.40	107	3	21.88	0.036
P58661	Aspartate aminotransferase	43494	5.29	230.75	18	34	55.30	8.25	96	0	22.33	0.038
P41031	Thiosulfate binding protein	37559	9.19	1050.56	18	32	61.24	7.32	240	2	17.76	0.031
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	650.56	17	21	58.28	8.39	143	1	19.32	0.035
Q8ZQT5	Protein tolB	46120	8.73	546.50	17	21	48.37	8.33	119	0	16.81	0.034

P0A1W6	Leucine specific binding protein	39375	5.84	359.60	17	27	63.69	10.64	111	2	20.97	0.035
Q7CR87	Chaperone surA	47221	6.88	339.25	17	31	65.19	7.67	102	1	20.88	0.032
P66764	S adenosylmethionine synthetase	41926	4.91	283.30	17	32	69.01	7.21	94	3	24.37	0.036
P26982	Protease do	49284	9.19	662.14	17	29	45.05	7.86	162	2	20.31	0.031
Q7CPE1	ATP synthase subunit alpha	55078	5.61	519.36	16	40	43.08	8.34	103	1	20.02	0.033
P0A2C5	D ribose binding periplasmic protein	30943	9.20	475.62	16	25	67.23	9.61	122	1	21.71	0.032
P65882	Adenylosuccinate synthetase	47347	5.15	466.09	16	42	49.07	9.27	93	2	22.28	0.034
P25077	Malate dehydrogenase	32455	5.97	964.64	16	22	74.68	8.24	176	0	18.53	0.027
P23905	D galactose binding periplasmic protein	35791	5.75	487.97	15	30	66.87	9.12	112	3	21.50	0.033
P0A297	50S ribosomal protein L10	17789	9.46	444.39	15	15	73.33	7.14	107	4	19.66	0.036
P02910	Histidine binding periplasmic protein	28361	5.95	688.45	15	23	65.00	9.94	123	0	20.18	0.034
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	393.60	14	36	48.20	9.58	89	3	21.16	0.036
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	445.87	13	15	88.19	8.20	125	1	17.05	0.029
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	310.80	13	27	49.29	9.58	89	2	22.40	0.038
P0A1V4	Adenylate kinase	23473	5.39	299.84	13	24	64.49	7.04	96	2	19.49	0.037
Q8ZRC9	UPF0234 protein yajQ	18307	5.42	285.13	13	14	70.55	7.12	83	1	22.06	0.035
P26976	Non specific acid phosphatase	28364	9.22	250.71	13	19	61.20	9.50	69	2	20.77	0.035
P37412	3 isopropylmalate dehydrogenase	39488	5.14	232.37	13	25	52.89	11.46	61	0	27.50	0.034
P0A7W4	30S ribosomal protein S5	17592	10.56	657.27	13	13	75.45	11.84	138	0	22.93	0.033
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	420.91	12	27	57.59	9.63	81	3	22.51	0.035
P11003	5 10 methylenetetrahydrofolate reductase	33151	6.44	386.25	12	30	55.07	10.89	70	0	20.07	0.033
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	359.06	12	28	51.06	9.42	73	3	21.07	0.038
P0A2A3	50S ribosomal protein L1	24713	10.10	339.98	12	19	61.11	6.68	88	2	18.70	0.031
P67912	ADP L glycerol D mannose 6 epimerase	34827	4.72	303.12	12	33	44.52	8.95	59	1	24.79	0.037
Q8ZQD4	Outer membrane lipoprotein carrier protein	22467	7.39	290.09	12	17	79.31	11.02	68	0	19.09	0.037
Q8ZQR4	6-phosphogluconolactonase	36314	5.07	197.68	12	18	71.90	12.13	57	0	25.69	0.039
P17215	Leu Ile Val Thr binding protein	38762	5.69	815.92	12	21	69.86	7.62	179	1	18.81	0.028
Q8ZRP4	2,3,4,5-tetrahydropyridine 2,6-dicarboxylate N-succinyltransferase	29833	5.39	327.88	11	25	58.03	10.64	56	0	25.23	0.034
P02936	Outer membrane protein A	37491	5.50	277.50	11	25	46.57	9.08	61	1	19.38	0.038
P65692	6-phosphofructokinase	34892	5.47	271.71	11	28	48.13	8.52	62	2	24.71	0.035
P0AA02	Transcription antitermination protein nusG	20532	6.40	134.93	11	13	61.88	10.34	61	1	22.74	0.039
P66955	Transaldolase B	35149	4.91	399.34	11	26	49.84	8.45	58	1	19.89	0.038
P63411	Acetate kinase	43230	5.91	328.83	10	25	61.75	10.86	75	2	24.60	0.036
P66313	50S ribosomal protein L6	18848	10.09	322.02	10	13	51.98	8.57	63	1	19.97	0.035
Q8ZKP7	Triosephosphate isomerase	26899	5.61	287.49	10	22	55.29	11.03	107	1	21.16	0.030
P22107	TraT complement resistance protein	26261	9.35	271.35	10	18	44.86	12.00	57	0	21.39	0.035
P60446	50S ribosomal protein L3	22233	10.25	211.23	10	20	61.72	10.80	57	2	22.50	0.034
P0A299	50S ribosomal protein L7 L12	12291	4.40	429.26	10	20	90.08	7.91	95	1	16.39	0.036
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	364.37	9	12	56.21	7.82	81	1	21.47	0.031
Q8ZP65	Probable thiol peroxidase	18014	4.74	308.00	9	12	84.52	7.77	92	0	18.87	0.031
P66593	30S ribosomal protein S6	15163	5.08	274.19	9	9	64.12	7.68	66	1	16.26	0.033
P20753	Peptidyl prolyl cis-trans isomerase A	20319	9.59	182.00	9	15	70.00	7.52	55	0	21.83	0.035
P0A1D5	10 kDa chaperonin	10311	5.19	484.98	9	7	82.47	7.80	90	0	17.91	0.027
P0A1Z2	Chaperone protein skp	17894	10.25	371.66	8	10	56.52	5.75	78	0	18.99	0.032
P66692	Ribose 5-phosphate isomerase A	22881	4.89	290.62	8	15	47.03	10.34	53	0	22.15	0.030
Q7CQV9	DNA protection during starvation protein	18705	5.66	249.51	8	18	59.88	10.09	41	0	21.49	0.034
P67093	Universal stress protein G	15891	6.20	244.55	8	9	77.46	10.34	58	3	21.26	0.031
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	239.77	8	19	46.98	9.76	53	1	23.31	0.039

P55890	Thiol disulfide interchange protein dsbC	25819	7.34	228.89	8	15	42.19	13.24	51	1	24.49	0.037
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	227.01	8	16	64.71	9.11	57	0	20.89	0.036
O54297	30S ribosomal protein S4	23470	10.38	224.50	8	19	48.54	7.29	43	0	24.78	0.040
P66541	30S ribosomal protein S2	26741	6.73	182.94	8	23	39.83	8.11	34	0	25.07	0.037
P0A1S2	DNA binding protein H NS	15532	5.09	488.72	8	14	51.82	8.55	127	2	16.92	0.031
Q8ZK80	50S ribosomal protein L9	15774	7.73	250.86	7	14	57.72	8.05	46	0	23.90	0.031
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	237.86	7	16	58.17	11.13	35	0	19.45	0.026
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	186.67	7	15	69.59	8.37	52	3	19.98	0.038
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	259.33	7	26	33.66	10.91	50	2	22.24	0.032
P0A7K0	50S ribosomal protein L11	14865	10.09	216.47	6	11	40.14	8.94	41	0	17.99	0.026
P0A2F4	Superoxide dismutase Fe	21294	5.52	198.43	6	14	54.40	9.92	42	0	18.26	0.033
P67904	30S ribosomal protein S10	11759	10.33	179.72	6	11	43.69	7.89	38	0	18.61	0.032
P67617	Probable Fe 2 trafficking protein	10892	5.87	131.38	6	15	73.63	10.06	30	1	26.56	0.034
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	441.05	6	8	53.85	9.15	62	0	19.03	0.027
P0AA28	Thioredoxin 1	11799	4.47	325.79	5	8	55.96	7.54	60	0	17.04	0.029
P0A9Y9	Cold shock like protein cspC	7397	7.70	265.42	5	5	72.46	7.14	41	0	19.02	0.034
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	237.15	5	19	64.11	9.16	46	4	20.15	0.035
O54296	30S ribosomal protein S11	13822	11.74	142.30	5	9	48.84	6.48	26	0	24.66	0.038
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	409.11	5	14	50.72	8.05	68	1	20.51	0.032
P0AA07	Phosphocarrier protein HPr	9113	5.51	184.59	4	7	85.88	10.20	57	0	18.15	0.030
Q8ZM79	UPF0267 protein yqfB	11891	4.68	171.33	4	10	41.75	6.23	32	0	20.86	0.034
P0A1B7	ATP synthase epsilon chain	15054	5.82	162.85	4	7	49.64	8.58	37	1	22.89	0.034
P0A1G5	DnaK suppressor protein	17504	4.87	121.09	4	12	56.29	9.09	23	1	16.59	0.035
P67091	Universal stress protein F	15704	5.92	219.98	4	11	45.14	6.87	40	0	15.81	0.026
P0A7X0	30S ribosomal protein S8	14117	9.85	167.74	3	12	32.31	7.18	30	1	16.73	0.031
P0A6B1	Acyl carrier protein	8634	3.75	129.02	2	4	32.05	7.43	18	0	18.27	0.030
P0A1R6	DNA binding protein HU alpha	9515	10.12	571.56	2	7	46.67	4.92	66	0	15.57	0.023

MA6926 + Zn(II) LC-MS run 3: 6926_Zn_220709_1a2_03												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1D3	60 kDa chaperonin	57249	4.65	1151.54	41	44	79.01	9.25	327	4	18.21	0.041
P06202	Periplasmic oligopeptide binding protein	61254	6.03	1333.73	29	42	65.56	8.43	274	0	19.05	0.039
P41031	Thiosulfate binding protein	37559	9.19	877.02	28	32	85.80	7.91	247	1	20.36	0.039
P52616	Phase 2 flagellin	52504	4.55	460.50	26	37	61.46	9.76	154	0	22.80	0.041
P0A1H5	Elongation factor Tu	43256	5.15	1457.46	25	30	79.95	10.59	282	3	17.17	0.035
Q56073	Chaperone protein dnaK	69215	4.64	536.76	24	59	50.31	8.33	153	3	21.64	0.042
P0A1H3	Elongation factor G	77550	5.00	642.07	24	47	64.35	8.04	162	4	20.68	0.038
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	527.47	23	60	35.81	9.58	121	2	22.70	0.044
P65702	Phosphoglycerate kinase	41106	4.90	1136.97	23	30	71.58	7.47	209	1	18.84	0.035
P64076	Enolase	45570	5.08	984.60	22	34	75.46	7.19	201	1	20.07	0.040
Q7CPE1	ATP synthase subunit alpha	55078	5.61	626.79	22	40	52.63	9.08	137	1	22.52	0.041
P23905	D galactose binding periplasmic protein	35791	5.75	615.03	22	30	75.00	8.99	146	2	21.47	0.040
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1138.79	22	29	69.79	7.44	230	1	18.25	0.035
P64052	Elongation factor Ts	30338	4.95	536.81	21	33	82.33	11.15	134	3	21.02	0.041
P26982	Protease do	49284	9.19	601.90	20	29	60.63	7.44	154	3	19.64	0.040

Q8ZQT5	Protein tolB	46120	8.73	633.12	20	21	56.28	9.56	137	0	20.97	0.040
Q8ZP20	Periplasmic trehalase	63469	5.15	557.23	19	44	45.79	6.76	147	2	22.20	0.038
P41033	Phosphoenolpyruvate carboxykinase ATP	59539	5.58	447.04	19	45	52.42	9.64	101	1	22.47	0.045
Q7CPK0	sn glycerol 3 phosphate binding periplasmic protein ugpB	48362	7.33	444.11	19	38	60.73	8.82	116	4	24.12	0.042
P65882	Adenylosuccinate synthetase	47347	5.15	349.96	19	42	52.55	9.17	94	2	24.13	0.040
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	1025.31	19	22	74.71	7.04	201	2	20.35	0.041
O33921	Glucose 1 phosphatase	45530	6.64	730.05	18	25	66.34	8.44	168	1	19.70	0.035
Q7CPE2	ATP synthase subunit beta	50251	4.71	522.53	18	32	52.17	9.05	116	1	18.66	0.042
P0A1E3	Cysteine synthase A	34514	5.72	493.32	18	20	76.16	6.32	120	2	19.01	0.040
P0A1P6	Glutamine synthetase	51752	5.25	382.94	18	33	61.83	7.06	108	1	21.93	0.043
Q7CR87	Chaperone surA	47221	6.88	378.17	18	31	66.36	9.71	134	1	21.89	0.040
P25077	Malate dehydrogenase	32455	5.97	819.07	18	22	84.94	7.34	172	0	17.02	0.034
P0A1W6	Leucine specific binding protein	39375	5.84	319.74	17	27	53.93	9.45	97	0	19.92	0.043
P06179	Flagellin	51581	4.60	472.50	17	36	53.54	7.73	126	1	21.34	0.042
P66932	Trigger factor	48036	4.64	439.25	16	43	41.20	9.46	85	1	23.39	0.043
P00924	Enolase I	46773	6.15	677.76	16	28	55.38	10.14	133	4	20.08	0.036
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	441.79	15	15	88.98	7.81	118	0	16.42	0.040
P02906	Sulfate binding protein	36517	7.72	416.38	15	28	56.54	10.06	103	0	20.61	0.045
P58661	Aspartate aminotransferase	43494	5.29	249.75	15	34	38.13	10.89	76	0	23.23	0.040
P60446	50S ribosomal protein L3	22233	10.25	246.02	15	20	69.38	10.10	67	0	21.56	0.038
Q9Zf60	Glutamate aspartate periplasmic binding protein	33381	9.16	743.43	15	21	69.87	8.83	143	1	18.77	0.039
P67557	Glucans biosynthesis protein G	57808	8.77	384.53	14	40	53.62	9.25	84	3	21.42	0.043
P02936	Outer membrane protein A	37491	5.50	375.58	14	25	44.29	11.68	74	0	21.28	0.038
P17215	Leu Ile Val Thr binding protein	38762	5.69	732.55	14	21	79.73	8.70	183	2	16.64	0.034
P02911	Lysine arginine ornithine binding periplasmic protein	28182	5.90	197.56	13	23	57.31	7.33	52	1	23.80	0.045
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	288.71	13	27	45.33	9.68	67	0	21.16	0.044
P0A2C5	D ribose binding periplasmic protein	30943	9.20	543.42	12	25	69.93	8.76	120	3	18.28	0.037
Q8ZKP7	Triosephosphate isomerase	26899	5.61	370.65	12	22	50.98	10.17	127	0	20.64	0.038
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	368.64	12	27	55.50	9.73	61	1	23.13	0.047
P26976	Non specific acid phosphatase	28364	9.22	339.07	12	19	62.80	10.53	75	2	19.41	0.042
Q8ZRN1	D methionine binding lipoprotein metQ	29417	5.23	330.03	12	30	72.32	9.01	70	1	23.88	0.043
P02910	Histidine binding periplasmic protein	28361	5.95	653.63	12	23	50.38	6.38	110	0	16.07	0.036
P0A297	50S ribosomal protein L10	17789	9.46	419.68	11	15	56.97	9.45	74	2	20.66	0.039
P55900	Phosphoserine aminotransferase	39806	5.17	293.48	11	28	38.12	8.91	63	3	25.03	0.039
Q8ZK80	50S ribosomal protein L9	15774	7.73	289.50	11	14	69.13	7.19	85	1	21.76	0.039
P63411	Acetate kinase	43230	5.91	267.22	11	25	62.25	8.82	87	3	21.00	0.044
P0A7W4	30S ribosomal protein S5	17592	10.56	647.98	11	13	70.66	7.12	102	2	17.84	0.034
P0A2A3	50S ribosomal protein L1	24713	10.10	461.63	10	19	44.02	9.67	76	1	20.86	0.040
Q8ZP65	Probable thiol peroxidase	18014	4.74	273.04	10	12	80.36	9.99	85	1	19.16	0.032
P0A1V4	Adenylate kinase	23473	5.39	272.88	10	24	44.39	9.09	70	2	15.53	0.041
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	258.18	10	26	38.51	10.40	51	0	19.66	0.042
P05989	Ketol acid reductoisomerase	53907	4.96	255.31	10	47	36.25	8.63	53	2	22.97	0.046
Q8ZQ40	Flavoprotein wrbA	20854	5.74	233.24	10	12	84.85	11.85	71	0	23.70	0.044
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	195.27	10	19	53.02	8.81	43	0	24.26	0.039
O54297	30S ribosomal protein S4	23470	10.38	189.20	10	19	43.69	9.31	56	0	23.62	0.043
Q7CR64	UPF0325 protein yaeH	15084	7.17	156.57	10	11	56.25	10.58	39	0	21.04	0.049
P0A1S2	DNA binding protein H NS	15532	5.09	547.94	10	14	64.96	10.04	120	1	16.83	0.035
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	129.77	9	15	70.18	10.86	47	2	21.97	0.043

P0A299	50S ribosomal protein L7 L12	12291	4.40	341.20	9	20	84.30	9.97	60	1	21.06	0.041
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	302.61	8	25	37.96	6.70	48	0	20.64	0.040
P0A1Z2	Chaperone protein skp	17894	10.25	263.15	8	10	57.76	5.14	57	0	19.32	0.040
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	237.37	8	19	53.23	11.34	73	4	23.78	0.044
P22107	TraT complement resistance protein	26261	9.35	234.29	8	18	41.56	11.60	54	3	17.88	0.042
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	221.04	8	16	48.08	7.61	50	1	17.76	0.039
P66541	30S ribosomal protein S2	26741	6.73	159.83	8	23	51.45	9.43	54	2	22.24	0.048
P60726	50S ribosomal protein L4	22072	10.19	139.12	8	18	52.24	6.49	47	2	22.81	0.045
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	407.86	8	12	50.30	8.50	83	0	16.62	0.034
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	498.52	7	14	54.11	8.64	98	2	18.32	0.036
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	323.21	7	16	51.34	7.21	45	0	19.35	0.040
P67093	Universal stress protein G	15891	6.20	261.82	7	9	71.83	11.09	54	1	22.80	0.044
P66593	30S ribosomal protein S6	15163	5.08	193.07	7	9	51.15	10.27	35	0	18.81	0.043
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	163.30	7	19	35.87	7.34	39	0	19.37	0.042
P0A8B8	UPF0133 protein ybaB	12006	4.82	129.39	7	11	71.56	8.01	40	0	23.21	0.052
P0A1D5	10 kDa chaperonin	10311	5.19	600.77	7	7	85.57	6.74	90	1	17.27	0.036
P0A9Y9	Cold shock like protein cspC	7397	7.70	227.92	6	5	86.96	7.42	46	0	20.07	0.041
P67091	Universal stress protein F	15704	5.92	215.59	6	11	53.47	4.77	37	0	21.90	0.042
P66692	Ribose 5 phosphate isomerase A	22881	4.89	199.88	6	15	53.88	6.21	40	0	18.42	0.040
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	198.50	6	10	48.02	7.92	37	0	18.23	0.033
Q8ZR01	Rare lipoprotein A	39083	7.82	187.04	6	17	32.81	10.53	33	0	22.03	0.049
Q7CQV9	DNA protection during starvation protein	18705	5.66	120.75	6	18	42.52	12.19	30	0	21.66	0.043
P66313	50S ribosomal protein L6	18848	10.09	271.55	6	13	35.59	7.86	42	0	19.66	0.033
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	249.93	5	8	51.28	10.15	40	0	19.09	0.035
Q7CPH8	Protein export protein secB	17234	4.06	214.59	5	12	56.77	11.91	36	0	22.15	0.044
P67904	30S ribosomal protein S10	11759	10.33	183.60	5	11	47.57	7.34	29	0	20.04	0.038
Q8ZLD7	Universal stress protein A	16070	4.92	169.69	5	9	63.19	7.53	29	0	20.29	0.047
P0AA28	Thioredoxin 1	11799	4.47	344.55	5	8	44.04	8.85	64	1	16.49	0.033
P0A7K0	50S ribosomal protein L11	14865	10.09	128.62	4	11	30.28	7.63	24	0	15.50	0.037
Q7CQJ0	Stationary phase induced ribosome associated protein	5365	11.74	104.76	4	3	51.06	9.70	27	0	16.47	0.034
P0A1S0	Integration host factor subunit alpha	11360	9.88	201.55	4	13	44.44	11.35	30	0	21.81	0.039
P0A7X0	30S ribosomal protein S8	14117	9.85	206.28	3	12	22.31	6.91	31	0	15.46	0.044
Q7CPZ4	Protein grpE	21827	4.49	142.04	3	18	38.27	8.30	18	0	23.27	0.041
P0A1R6	DNA binding protein HU alpha	9515	10.12	480.13	3	7	46.67	12.30	66	0	19.21	0.030
P0A7V6	30S ribosomal protein S3	25967	10.72	154.11	2	20	21.03	6.52	22	2	17.82	0.045
y67286	UPF0145 protein ybjQ	11429	4.72	148.09	2	14	13.08	2.99	17	0	17.08	0.038
P66491	30S ribosomal protein S19	10409	11.00	109.40	2	8	25.00	7.17	12	0	14.13	0.042
Q7CR46	Anti adapter protein iraP	9876	5.50	178.46	2	7	41.86	7.28	22	1	18.50	0.045

SA123 LC-MS run 1: 123_220709_1a2_01												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1D3	60 kDa chaperonin	57249	4.65	1428.88	39	44	82.48	8.71	376	5	18.00	0.034
Q56073	Chaperone protein dnaK	69215	4.64	621.41	31	59	62.07	8.83	168	2	22.25	0.041
P0A1H3	Elongation factor G	77550	5.00	764.17	30	47	65.34	9.82	215	2	21.07	0.037
P41031	Thiosulfate binding protein	37559	9.19	421.14	25	32	71.89	9.74	173	1	22.33	0.039

P0A1H5	Elongation factor Tu	43256	5.15	1486.65	25	30	73.60	8.80	294	2	17.09	0.035
P65702	Phosphoglycerate kinase	41106	4.90	1107.84	24	30	83.20	7.11	213	0	17.80	0.036
P06202	Periplasmic oligopeptide binding protein	61254	6.03	289.64	23	42	67.04	10.95	134	0	23.44	0.037
P64076	Enolase	45570	5.08	1239.06	23	34	75.23	7.91	301	4	19.48	0.034
P65882	Adenylosuccinate synthetase	47347	5.15	427.21	21	42	49.54	8.51	140	3	21.02	0.039
P64052	Elongation factor Ts	30338	4.95	575.35	20	33	80.92	10.02	155	2	17.47	0.038
P0A1E3	Cysteine synthase A	34514	5.72	648.33	20	20	64.40	8.75	193	4	18.59	0.037
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1120.50	19	29	62.54	9.00	270	2	16.11	0.033
P66932	Trigger factor	48036	4.64	431.91	18	43	49.77	10.41	106	2	24.62	0.038
P58661	Aspartate aminotransferase	43494	5.29	349.11	18	34	45.71	8.52	85	0	22.80	0.038
Q7CPE2	ATP synthase subunit beta	50251	4.71	567.36	18	32	60.00	8.58	130	3	20.41	0.038
Q7CPE1	ATP synthase subunit alpha	55078	5.61	488.39	17	40	56.53	8.42	119	3	20.35	0.039
P60446	50S ribosomal protein L3	22233	10.25	314.96	17	20	72.73	9.22	113	0	19.88	0.040
P77983	Pyruvate kinase I	50625	5.53	294.10	17	33	45.74	7.98	75	0	17.82	0.040
P0A7W4	30S ribosomal protein S5	17592	10.56	898.36	17	13	89.22	8.83	164	1	16.29	0.037
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	518.43	16	27	67.02	10.36	127	4	20.29	0.038
P00499	ATP phosphoribosyltransferase	33190	5.31	510.74	16	24	69.57	9.83	116	0	22.84	0.037
Q8ZL96	Glycyl tRNA synthetase beta subunit	76405	5.35	452.35	16	54	38.17	11.27	118	3	24.89	0.041
P10370	Histidinol dehydrogenase	45860	4.83	406.68	16	26	63.36	8.48	114	1	19.96	0.035
P40732	Acetylornithine succinyldiaminopimelate aminotransferase	43642	5.91	379.13	16	24	64.20	7.44	113	3	21.09	0.038
P0A1P6	Glutamine synthetase	51752	5.25	651.91	16	33	49.25	9.57	115	1	20.24	0.035
P00924	Enolase 1	46773	6.15	421.50	15	28	31.81	9.94	87	0	21.53	0.036
P63411	Acetate kinase	43230	5.91	404.53	15	25	58.50	7.72	108	1	21.86	0.039
P05989	Ketol acid reductoisomerase	53907	4.96	370.88	15	47	41.34	10.31	89	2	21.44	0.037
P02936	Outer membrane protein A	37491	5.50	271.79	15	25	49.71	7.72	83	0	22.98	0.036
Q8ZQT5	Protein tolB	46120	8.73	227.15	15	21	46.28	10.39	78	0	20.80	0.035
P02910	Histidine binding periplasmic protein	28361	5.95	556.67	15	23	66.54	7.44	141	2	18.66	0.036
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	233.86	14	27	41.36	10.82	80	1	19.85	0.042
P0A1V4	Adenylate kinase	23473	5.39	299.97	14	24	60.75	8.13	85	2	17.90	0.041
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	372.30	13	36	48.44	10.35	95	3	21.63	0.037
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	297.73	13	16	81.82	10.99	88	1	19.78	0.037
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	270.14	13	21	57.95	9.11	71	1	20.80	0.043
Q7CR87	Chaperone surA	47221	6.88	225.55	13	31	54.21	10.07	96	2	24.49	0.043
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	489.00	13	15	78.74	10.06	141	0	13.45	0.031
Q8ZP65	Probable thiol peroxidase	18014	4.74	605.33	12	12	77.38	7.86	148	1	18.25	0.031
Q8ZK80	50S ribosomal protein L9	15774	7.73	562.67	12	14	71.81	8.29	96	0	18.88	0.034
P26976	Non specific acid phosphatase	28364	9.22	451.86	12	19	49.20	8.42	111	4	19.90	0.037
P66313	50S ribosomal protein L6	18848	10.09	450.53	12	13	61.58	9.14	91	0	18.26	0.035
P55900	Phosphoserine aminotransferase	39806	5.17	442.18	12	28	54.42	9.09	103	3	18.58	0.038
O54297	30S ribosomal protein S4	23470	10.38	422.31	12	19	59.71	11.54	85	1	20.60	0.037
P0A2C7	Spermidine putrescine binding periplasmic protein	38996	4.99	396.11	12	28	46.84	11.35	81	2	22.07	0.033
P66541	30S ribosomal protein S2	26741	6.73	366.29	12	23	70.12	10.62	93	2	20.52	0.038
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	322.51	12	26	49.19	7.58	78	2	19.92	0.038
P65215	2 dehydro 3 deoxyphosphooctonate aldolase	30775	5.86	313.33	12	25	56.34	9.38	82	1	21.62	0.041
P0A2A3	50S ribosomal protein L1	24713	10.10	788.61	12	19	51.28	7.48	137	3	17.19	0.034
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	397.63	11	28	46.50	11.41	79	1	20.85	0.037
Q8ZQS2	2 3 bisposphoglycerate dependent phosphoglycerate mutase	28475	5.71	259.40	11	19	51.60	10.46	62	1	21.08	0.040
P26982	Protease do	49284	9.19	250.92	11	29	32.00	11.93	97	5	26.45	0.042

P0A2B3	30S ribosomal protein S7	17579	10.73	228.42	11	10	67.31	9.67	89	0	16.86	0.034
P65692	6 phosphofructokinase	34892	5.47	219.23	11	28	57.50	9.81	49	1	23.06	0.038
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	199.34	11	19	46.41	9.62	70	1	21.01	0.038
P25077	Malate dehydrogenase	32455	5.97	424.76	11	22	52.56	6.76	79	2	15.66	0.035
Q8ZRN1	D methionine binding lipoprotein metQ	29417	5.23	302.51	10	30	52.40	11.21	59	0	24.06	0.039
P10372	1 5 phosphoribosyl 5 5 phosphoribosylamino methylideneamino imidazole 4 carboxamide isomerase	26072	5.50	280.23	10	19	54.29	9.68	57	0	21.80	0.036
P0A1S0	Integration host factor subunit alpha	11360	9.88	277.06	10	13	60.61	10.31	57	0	20.35	0.037
P65226	Homoserine kinase	33264	6.32	217.47	10	21	55.34	8.16	69	1	23.83	0.038
P0AA02	Transcription antitermination protein nusG	20532	6.40	206.71	10	13	61.88	9.23	59	0	20.86	0.040
Q8ZRX8	Dihydrodipicolinate reductase	28832	5.73	195.39	10	24	64.84	10.43	56	3	23.59	0.038
P0A297	50S ribosomal protein L10	17789	9.46	416.21	10	15	59.39	9.75	89	2	20.63	0.036
P67904	30S ribosomal protein S10	11759	10.33	333.66	9	11	58.25	7.69	61	0	18.70	0.035
P66593	30S ribosomal protein S6	15163	5.08	311.95	9	9	70.99	10.29	77	2	17.43	0.038
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	258.31	9	19	72.58	10.44	71	2	22.54	0.043
P16657	Enoyl acyl carrier protein reductase NADH	27742	5.47	243.51	9	21	46.95	10.63	78	2	24.75	0.040
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	237.82	9	16	53.85	10.62	49	0	20.34	0.034
P10367	Histidine biosynthesis bifunctional protein hisIE	22660	5.37	232.86	9	15	79.31	9.20	70	2	25.33	0.041
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	212.16	9	19	35.87	10.98	45	0	24.84	0.041
P0A2F6	Single stranded DNA binding protein	19062	5.29	162.80	9	11	54.55	8.78	54	1	17.42	0.034
P66738	Ribosome recycling factor	20542	8.60	138.97	9	16	48.11	6.00	53	0	20.75	0.043
Q8ZKP7	Triosephosphate isomerase	26899	5.61	416.96	9	22	57.65	8.84	136	2	18.78	0.031
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	430.36	8	12	44.38	11.29	100	0	19.72	0.033
P0A1R2	Imidazole glycerol phosphate synthase subunit hisF	28350	4.80	366.26	8	20	46.51	7.80	56	1	22.51	0.042
P0A7K0	50S ribosomal protein L11	14865	10.09	267.45	8	11	63.38	11.35	74	1	19.30	0.032
Q56026	Cell invasion protein sipD	37089	4.83	265.98	8	24	47.81	11.03	69	3	23.03	0.040
P0A1Z2	Chaperone protein skp	17894	10.25	245.59	8	10	71.43	6.75	69	1	21.25	0.037
Q7CPL6	50S ribosomal protein L18	12761	10.88	243.07	8	9	64.10	10.55	58	0	18.88	0.038
Q7CPL7	50S ribosomal protein L17	14385	11.46	195.22	8	8	47.24	9.56	44	0	18.73	0.032
Q8ZQR4	6 phosphogluconolactonase	36314	5.07	182.77	8	18	55.29	8.79	60	2	22.29	0.041
Q8ZRC9	UPF0234 protein yajQ	18307	5.42	166.88	8	14	58.28	10.44	42	0	22.61	0.038
Q8ZQ40	Flavoprotein wrbA	20854	5.74	155.39	8	12	73.23	12.31	67	1	20.14	0.038
P0A1D5	10 kDa chaperonin	10311	5.19	525.38	8	7	74.23	7.15	98	0	18.59	0.032
P0AA28	Thioredoxin 1	11799	4.47	398.66	7	8	65.14	8.89	82	1	15.38	0.032
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	334.07	7	25	39.42	7.98	67	3	21.40	0.039
P0A299	50S ribosomal protein L7 L12	12291	4.40	324.35	7	20	55.37	6.23	51	1	15.95	0.039
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	319.39	7	14	50.72	5.22	72	1	19.89	0.037
P22107	TraT complement resistance protein	26261	9.35	250.06	7	18	45.68	7.84	58	1	20.64	0.036
P14146	Virulence transcriptional regulatory protein phoP	25617	5.14	244.23	7	21	47.77	10.40	64	3	21.87	0.038
P0A2C9	3 oxoacyl acyl carrier protein reductase	25529	7.19	241.87	7	16	52.05	12.93	55	1	22.46	0.037
Q9L9I8	Thiamine phosphate pyrophosphorylase	22969	4.95	237.82	7	16	44.55	8.93	43	0	18.35	0.040
P66032	3 4 dihydroxy 2 butanone 4 phosphate synthase	23295	4.70	231.91	7	15	47.93	11.48	55	1	23.11	0.035
O54296	30S ribosomal protein S11	13822	11.74	218.56	7	9	58.14	10.86	48	0	19.62	0.036
Q8ZLJ2	Transcription elongation factor greB	18497	6.89	175.78	7	17	42.04	12.03	49	1	24.89	0.035
P0A2C1	Ribonuclease HII	21493	7.63	166.97	7	17	45.45	9.78	57	2	24.10	0.039
Q7CQC4	tRNA cmo5U34 methyltransferase	27830	5.73	145.52	7	20	42.11	11.77	42	1	20.75	0.042
Q7CPP7	50S ribosomal protein L21	11571	10.29	104.09	7	7	62.14	13.30	37	1	21.64	0.035

P0A1S2	DNA binding protein H NS	15532	5.09	446.81	7	14	52.55	6.63	105	1	15.89	0.034
Q7CPL5	50S ribosomal protein L14	13559	10.89	186.77	6	14	38.21	9.30	55	0	24.93	0.035
P67617	Probable Fe 2 trafficking protein	10892	5.87	183.84	6	15	82.42	9.77	53	0	24.21	0.029
P67605	UPF0265 protein yeeX	13064	9.60	182.80	6	8	57.66	8.61	31	0	20.77	0.041
P0AA07	Phosphocarrier protein HPr	9113	5.51	172.34	6	7	89.41	9.24	87	0	19.39	0.036
P66193	50S ribosomal protein L31 type B	9808	9.67	130.43	6	9	81.40	9.41	58	0	17.79	0.038
Q7CPZ4	Protein grpE	21827	4.49	122.64	6	18	48.98	4.34	43	0	18.34	0.040
P61179	50S ribosomal protein L22	12218	10.71	116.14	6	8	54.55	10.36	33	1	20.88	0.033
P0A1R6	DNA binding protein HU alpha	9515	10.12	282.07	6	7	62.22	8.27	64	1	18.76	0.036
P66491	30S ribosomal protein S19	10409	11.00	91.11	5	8	58.70	12.38	33	1	22.37	0.046
P66643	30S ribosomal protein S9	14817	11.34	297.82	5	14	38.46	9.53	48	1	20.44	0.036
P0A7X0	30S ribosomal protein S8	14117	9.85	213.77	4	12	32.31	10.27	36	0	14.24	0.036
P0A2A9	30S ribosomal protein S16	9229	11.05	163.18	4	6	36.59	9.57	28	0	13.80	0.037
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	430.00	4	8	45.51	9.41	65	1	18.18	0.031
P60626	50S ribosomal protein L24	11309	10.72	129.65	3	11	28.85	10.40	15	0	20.04	0.037
P0A2B1	30S ribosomal protein S20	9649	11.63	154.09	3	3	27.59	7.01	31	0	15.78	0.036

SA123 LC-MS run 2: 123_220709_1a2_02												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1D3	60 kDa chaperonin	57249	4.65	1208.85	33	44	76.09	7.02	285	4	17.94	0.048
Q56073	Chaperone protein dnaK	69215	4.64	678.92	28	59	57.68	8.63	195	5	20.90	0.055
P64076	Enolase	45570	5.08	1274.79	22	34	69.21	7.04	240	1	18.27	0.046
P0A1H5	Elongation factor Tu	43256	5.15	1511.82	22	30	75.13	10.43	306	3	18.08	0.047
P0A1P6	Glutamine synthetase	51752	5.25	483.84	20	33	56.08	10.49	130	1	22.22	0.049
P65702	Phosphoglycerate kinase	41106	4.90	985.14	20	30	71.32	8.30	189	0	17.57	0.046
P0A1H3	Elongation factor G	77550	5.00	548.52	19	47	43.61	8.40	113	1	24.20	0.053
P0A1E3	Cysteine synthase A	34514	5.72	516.53	17	20	68.73	6.05	132	2	19.37	0.049
P66932	Trigger factor	48036	4.64	435.33	17	43	45.37	11.03	88	0	22.08	0.057
Q7CPE1	ATP synthase subunit alpha	55078	5.61	404.87	17	40	52.24	10.32	107	3	22.30	0.054
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1075.34	17	29	64.05	9.30	217	0	17.96	0.043
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	448.82	16	27	60.99	9.53	98	1	22.08	0.053
P00924	Enolase 1	46773	6.15	369.27	16	28	44.85	8.42	91	4	23.19	0.056
P06202	Periplasmic oligopeptide binding protein	61254	6.03	261.50	16	42	49.91	7.53	85	0	23.17	0.050
P00499	ATP phosphoribosyltransferase	33190	5.31	579.71	16	24	63.21	9.11	124	1	19.45	0.049
P40732	Acetylornithine succinyldiaminopimelate aminotransferase	43642	5.91	388.52	15	24	58.02	11.30	94	1	24.74	0.057
P41031	Thiosulfate binding protein	37559	9.19	366.33	15	32	54.44	8.01	86	1	16.09	0.056
P0A1V4	Adenylate kinase	23473	5.39	226.31	15	24	55.14	8.98	66	0	19.16	0.052
P64052	Elongation factor Ts	30338	4.95	524.88	15	33	57.95	9.92	115	2	20.96	0.057
P0A2C7	Spermidine putrescine binding periplasmic protein	38996	4.99	318.32	14	28	60.06	11.71	70	1	22.40	0.055
P66955	Transaldolase B	35149	4.91	302.17	14	26	59.31	7.66	76	0	21.83	0.057
P55900	Phosphoserine aminotransferase	39806	5.17	248.71	14	28	48.07	10.42	67	0	29.09	0.064
P02936	Outer membrane protein A	37491	5.50	226.23	14	25	34.57	9.40	80	0	20.99	0.057
P41782	Transcriptional regulator hiiD	35195	8.77	208.31	14	29	51.46	10.24	65	0	23.07	0.053
Q7CPE2	ATP synthase subunit beta	50251	4.71	540.90	14	32	42.39	9.91	99	4	21.00	0.053
Q8ZRN1	D methionine binding lipoprotein metQ	29417	5.23	270.23	13	30	64.58	8.18	57	0	27.48	0.061
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	229.32	13	15	87.72	10.14	91	2	24.54	0.056

Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	408.24	13	60	24.54	8.70	67	1	23.60	0.053
P02910	Histidine binding periplasmic protein	28361	5.95	399.62	12	23	53.08	9.15	81	0	20.63	0.049
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	395.96	12	36	35.97	7.71	104	3	19.70	0.057
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	305.23	12	28	44.07	10.29	61	0	20.70	0.051
P26976	Non specific acid phosphatase	28364	9.22	302.19	12	19	59.20	9.60	73	1	21.51	0.053
P60446	50S ribosomal protein L3	22233	10.25	295.53	12	20	59.33	11.54	77	2	18.54	0.051
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	446.25	12	15	85.04	9.97	139	0	15.08	0.041
Q8ZP65	Probable thiol peroxidase	18014	4.74	696.32	11	12	92.86	7.66	159	1	17.34	0.045
P0A297	50S ribosomal protein L10	17789	9.46	442.58	11	15	64.85	8.13	76	0	19.24	0.054
P66541	30S ribosomal protein S2	26741	6.73	329.34	11	23	68.46	9.37	79	1	18.58	0.046
P0A1F8	Aspartate semialdehyde dehydrogenase	40110	5.21	301.55	11	27	62.23	6.26	60	1	19.41	0.053
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	234.99	11	21	57.62	7.47	68	1	20.36	0.052
P65215	2 dehydro 3 deoxyphosphooctonate aldolase	30775	5.86	184.60	11	25	64.08	10.94	58	2	24.47	0.055
Q8ZQT5	Protein tolB	46120	8.73	160.01	11	21	41.16	9.81	60	1	22.18	0.049
P0A7W4	30S ribosomal protein S5	17592	10.56	828.43	11	13	70.66	9.66	122	1	18.38	0.036
P0A1S2	DNA binding protein H NS	15532	5.09	602.39	10	14	62.77	6.69	116	0	15.76	0.042
O54297	30S ribosomal protein S4	23470	10.38	420.33	10	19	47.09	8.09	76	1	19.93	0.050
P40810	Dihydroxy acid dehydratase	65660	5.73	301.03	10	41	23.86	9.26	46	0	23.33	0.058
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	299.89	10	25	35.04	5.79	55	0	20.11	0.051
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	259.41	10	27	35.98	9.93	58	1	21.75	0.056
P37418	2 succinylbenzoate CoA ligase	50212	7.80	213.56	10	35	36.04	13.09	53	1	25.39	0.062
P60726	50S ribosomal protein L4	22072	10.19	192.79	10	18	62.69	8.21	64	3	24.74	0.053
P0A2A3	50S ribosomal protein L1	24713	10.10	616.85	10	19	57.69	5.98	96	0	20.97	0.045
Q7CR87	Chaperone surA	47221	6.88	195.22	9	31	36.22	7.89	48	0	21.09	0.049
P58661	Aspartate aminotransferase	43494	5.29	192.04	9	34	38.89	10.36	49	1	26.18	0.052
Q8ZN71	Dihydrodipicolinate synthase	31274	5.61	187.12	9	21	48.63	11.20	46	1	24.51	0.060
P0A1R2	Imidazole glycerol phosphate synthase subunit hisF	28350	4.80	167.59	9	20	54.65	9.17	49	1	20.02	0.055
Q9L6M9	Putative carboxymethylenebutenolidase	29043	5.59	198.95	9	18	70.00	11.76	59	1	22.67	0.053
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	325.61	8	12	66.86	9.07	61	0	20.93	0.051
Q8ZKP7	Triosephosphate isomerase	26899	5.61	322.06	8	22	54.51	7.50	103	1	18.01	0.046
P25077	Malate dehydrogenase	32455	5.97	316.48	8	22	39.42	5.94	70	0	16.64	0.043
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	312.91	8	26	38.51	10.11	52	2	21.05	0.051
P0A299	50S ribosomal protein L7 L12	12291	4.40	306.95	8	20	90.08	9.04	66	1	20.65	0.056
P66032	3 4 dihydroxy 2 butanone 4 phosphate synthase	23295	4.70	285.24	8	15	57.14	9.98	47	0	25.51	0.058
P14146	Virulence transcriptional regulatory protein phoP	25617	5.14	244.42	8	21	58.48	12.54	52	2	22.72	0.048
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	225.54	8	16	63.94	6.48	43	1	19.83	0.053
P16326	Flagellar hook associated protein 3	34153	4.64	223.30	8	21	51.42	11.41	53	2	24.42	0.068
P37412	3 isopropylmalate dehydrogenase	39488	5.14	198.37	8	25	30.30	9.90	43	0	25.22	0.057
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	195.98	8	19	40.93	7.53	38	0	25.18	0.052
P0A2F6	Single stranded DNA binding protein	19062	5.29	189.55	8	11	52.84	7.94	52	1	21.27	0.055
P02906	Sulfate binding protein	36517	7.72	181.85	8	28	37.69	4.58	42	1	18.24	0.055
P66193	50S ribosomal protein L31 type B	9808	9.67	174.67	8	9	83.72	9.25	52	0	15.01	0.049
P0A2C5	D ribose binding periplasmic protein	30943	9.20	162.64	8	25	47.30	8.47	47	1	21.39	0.053
P10372	1 5 phosphoribosyl 5 5 phosphoribosylamino methylidenamino imidazole 4 carboxamide isomerase	26072	5.50	161.14	8	19	54.69	12.92	39	0	23.16	0.040
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	505.41	8	16	74.33	9.63	70	0	19.93	0.050
P66313	50S ribosomal protein L6	18848	10.09	378.23	7	13	45.20	6.51	56	0	16.61	0.050

P63411	Acetate kinase	43230	5.91	355.41	7	25	33.75	7.13	52	1	21.48	0.055
P58580	Glutathione synthetase	35410	4.88	231.12	7	29	35.56	6.88	40	1	20.61	0.063
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	215.20	7	19	50.40	8.64	39	1	22.26	0.058
P66643	30S ribosomal protein S9	14817	11.34	191.75	7	14	56.15	6.47	40	0	20.47	0.045
P67617	Probable Fe 2 trafficking protein	10892	5.87	189.98	7	15	80.22	9.95	36	0	21.94	0.046
P0A1Z2	Chaperone protein skp	17894	10.25	152.91	7	10	60.87	6.62	46	2	18.37	0.056
Q7CPD8	UPF0438 protein yifE	13069	6.23	136.80	7	13	40.18	9.36	31	0	24.09	0.045
Q9L9I8	Thiamine phosphate pyrophosphorylase	22969	4.95	132.87	7	16	50.71	8.25	30	0	24.53	0.053
P65559	Uncharacterized Nudix hydrolase yfcD	20893	4.48	68.59	7	12	47.83	11.23	34	1	21.25	0.061
Q8ZK80	50S ribosomal protein L9	15774	7.73	457.63	7	14	56.38	7.89	65	0	21.06	0.045
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	356.51	6	8	54.49	8.85	60	0	19.60	0.047
P0A9Y9	Cold shock like protein cspC	7397	7.70	325.26	6	5	78.26	6.56	50	0	15.44	0.050
Q7CPL5	50S ribosomal protein L14	13559	10.89	215.45	6	14	47.97	11.22	44	1	18.90	0.047
P66593	30S ribosomal protein S6	15163	5.08	209.99	6	9	75.57	12.52	44	1	17.48	0.045
O54296	30S ribosomal protein S11	13822	11.74	208.80	6	9	66.67	8.10	45	1	19.83	0.059
Q7CPL6	50S ribosomal protein L18	12761	10.88	175.93	6	9	54.70	10.49	35	1	21.09	0.054
P0A2F4	Superoxide dismutase Fe	21294	5.52	175.73	6	14	43.52	10.38	43	1	24.08	0.054
P0A7V6	30S ribosomal protein S3	25967	10.72	161.81	6	20	39.49	10.29	36	0	24.52	0.047
P0A1W6	Leucine specific binding protein	39375	5.84	149.15	6	27	28.73	10.10	28	0	24.02	0.064
P66692	Ribose 5 phosphate isomerase A	22881	4.89	135.05	6	15	42.47	10.05	34	0	22.28	0.050
P02911	Lysine arginine ornithine binding periplasmic protein	28182	5.90	124.30	6	23	31.54	8.37	28	0	20.22	0.055
P61179	50S ribosomal protein L22	12218	10.71	108.50	6	8	52.73	8.86	40	2	19.33	0.039
P0A1D5	10 kDa chaperonin	10311	5.19	617.26	6	7	74.23	7.79	97	0	16.79	0.043
P67904	30S ribosomal protein S10	11759	10.33	255.69	5	11	51.46	9.47	39	1	16.66	0.045
Q8ZLM1	30S ribosomal protein S13	13153	11.22	246.84	5	12	40.68	9.36	41	0	21.38	0.051
P0A2A1	50S ribosomal protein L19	13122	11.24	169.51	5	11	40.00	11.33	35	0	22.33	0.055
Q7CPL7	50S ribosomal protein L17	14385	11.46	153.32	5	8	37.80	8.14	26	0	20.63	0.051
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	150.68	5	14	40.10	7.03	54	2	21.27	0.060
P0A1S4	DNA binding protein stpA	15477	9.24	146.66	5	12	42.11	8.80	24	0	26.51	0.055
P0AA28	Thioredoxin 1	11799	4.47	406.33	5	8	49.54	7.75	76	0	16.65	0.045
Q7CPL4	50S ribosomal protein L16	15184	11.65	220.70	4	6	27.94	13.26	32	0	20.19	0.047
P67093	Universal stress protein G	15891	6.20	195.67	4	9	44.37	10.91	37	2	20.29	0.054
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	179.18	4	10	28.25	7.83	22	0	12.43	0.056
P67605	UPF0265 protein yeeX	13064	9.60	147.78	4	8	26.13	7.96	28	0	18.94	0.054
Q8ZK81	30S ribosomal protein S18	9065	11.11	127.27	4	4	46.67	7.95	25	0	19.95	0.054
P67537	UPF0250 protein ybeD	9793	5.04	71.82	4	4	91.95	8.16	21	0	26.95	0.057
P0A7X0	30S ribosomal protein S8	14117	9.85	254.96	4	12	23.08	11.40	48	1	14.20	0.050
P0A1P8	Glutaredoxin 1	9917	5.54	121.76	3	10	40.23	7.48	21	0	19.04	0.051
P0A6B1	Acyl carrier protein	8634	3.75	102.33	3	4	41.03	7.10	17	0	19.32	0.038
Q7CPP7	50S ribosomal protein L21	11571	10.29	99.17	3	7	40.78	9.65	18	1	21.25	0.046
P67551	UPF0253 protein yaeP	7151	4.37	86.73	3	5	57.58	3.83	15	0	23.56	0.057
P0A7K0	50S ribosomal protein L11	14865	10.09	231.80	3	11	43.66	8.05	43	2	17.93	0.043
Q7CR46	Anti adapter protein iraP	9876	5.50	165.74	2	7	41.86	9.68	19	0	16.85	0.051
P68684	30S ribosomal protein S21	8494	11.56	125.83	2	9	28.17	6.87	16	0	21.55	0.056
P0A1R6	DNA binding protein HU alpha	9515	10.12	296.34	2	7	46.67	5.05	39	0	14.83	0.041

Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1D3	60 kDa chaperonin	57249	4.65	1287.24	33	44	69.71	7.89	264	1	18.07	0.049
P14846	Carbamoyl phosphate synthase large chain	118064	4.94	382.18	23	83	31.72	10.03	120	2	22.89	0.063
P0A1H3	Elongation factor G	77550	5.00	477.00	22	47	46.59	9.33	121	1	19.64	0.054
P64076	Enolase	45570	5.08	1410.86	21	34	75.23	6.69	241	1	17.42	0.047
Q8ZMB5	Protease 3	107418	6.12	255.07	20	65	32.74	8.86	102	5	24.16	0.060
P65702	Phosphoglycerate kinase	41106	4.90	1155.43	18	30	63.31	8.32	187	0	17.52	0.045
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	985.06	16	29	62.84	10.27	205	0	17.24	0.038
Q56073	Chaperone protein dnaK	69215	4.64	598.02	16	59	39.97	9.35	109	2	20.26	0.050
P26978	Bifunctional purine biosynthesis protein purH	57431	5.48	229.44	16	50	51.80	10.21	95	3	20.30	0.052
P0A1H5	Elongation factor Tu	43256	5.15	1373.90	16	30	65.23	7.91	229	2	17.44	0.048
P0A1E3	Cysteine synthase A	34514	5.72	520.76	15	20	42.72	5.95	114	0	17.17	0.047
Q7CPE2	ATP synthase subunit beta	50251	4.71	516.91	15	32	49.35	8.40	98	3	18.21	0.051
P06202	Periplasmic oligopeptide binding protein	61254	6.03	247.79	15	42	48.43	7.62	81	0	23.41	0.054
P0A1P6	Glutamine synthetase	51752	5.25	557.16	15	33	51.81	8.00	114	2	22.96	0.052
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	343.95	14	36	43.65	8.67	91	1	16.69	0.049
Q7CPE1	ATP synthase subunit alpha	55078	5.61	298.14	14	40	43.47	7.28	75	0	18.48	0.052
P55900	Phosphoserine aminotransferase	39806	5.17	268.79	14	28	44.75	10.37	69	0	24.98	0.061
O54297	30S ribosomal protein S4	23470	10.38	373.72	14	19	48.06	9.84	81	0	19.62	0.046
P00499	ATP phosphoribosyltransferase	33190	5.31	504.13	13	24	53.18	8.19	96	0	19.16	0.052
P41031	Thiosulfate binding protein	37559	9.19	426.88	13	32	54.14	7.87	78	0	21.12	0.049
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	320.18	13	26	53.40	9.08	84	2	25.44	0.054
P05989	Ketol acid reductoisomerase	53907	4.96	289.85	13	47	42.36	8.71	81	2	20.67	0.054
Q8ZL56	2 3 bisposphoglycerate independent phosphoglycerate mutase	56219	4.88	257.53	13	37	53.50	9.65	76	2	25.36	0.055
P64052	Elongation factor Ts	30338	4.95	527.40	13	33	62.90	9.11	102	2	18.40	0.056
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	318.47	12	60	25.73	7.58	53	1	19.65	0.059
P0A1V4	Adenylate kinase	23473	5.39	304.04	12	24	50.47	8.13	71	2	19.34	0.059
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	286.01	12	27	52.09	6.87	73	1	23.46	0.054
P66932	Trigger factor	48036	4.64	280.24	12	43	42.36	9.89	63	2	20.20	0.053
P0A1F8	Aspartate semialdehyde dehydrogenase	40110	5.21	277.50	12	27	50.54	8.90	70	1	20.75	0.058
P40732	Acetylornithine succinyldiaminopimelate aminotransferase	43642	5.91	215.76	12	24	50.12	7.25	67	0	21.80	0.052
P00924	Enolase 1	46773	6.15	345.78	12	28	43.25	10.97	68	1	25.41	0.052
Q8ZP65	Probable thiol peroxidase	18014	4.74	423.84	11	12	95.83	8.96	129	3	18.66	0.047
P10370	Histidinol dehydrogenase	45860	4.83	299.04	11	26	59.22	4.50	80	0	22.12	0.051
P26976	Non specific acid phosphatase	28364	9.22	255.84	11	19	60.40	8.72	67	1	20.25	0.047
P0A1R2	Imidazole glycerol phosphate synthase subunit hisF	28350	4.80	223.74	11	20	56.98	10.04	54	0	23.39	0.056
P26973	DNA topoisomerase 4 subunit A	83984	6.10	218.44	11	52	24.20	11.67	55	2	24.50	0.055
P40861	Gamma glutamyl phosphate reductase	44637	5.56	193.91	11	28	39.42	12.75	75	1	27.42	0.050
P0A2A3	50S ribosomal protein L1	24713	10.10	568.73	11	19	57.69	6.19	105	1	17.27	0.047
Q8ZK80	50S ribosomal protein L9	15774	7.73	493.77	10	14	77.18	8.89	78	0	17.92	0.047
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	438.91	10	15	74.80	9.24	128	0	14.46	0.036
P0A297	50S ribosomal protein L10	17789	9.46	333.57	10	15	50.91	7.71	75	2	19.02	0.052
P66541	30S ribosomal protein S2	26741	6.73	305.15	10	23	48.96	9.47	76	2	19.38	0.048
P66955	Transaldolase B	35149	4.91	204.81	10	26	36.59	6.47	42	0	22.33	0.056
P60446	50S ribosomal protein L3	22233	10.25	202.25	10	20	46.89	10.65	52	0	16.38	0.049
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	179.59	10	21	42.38	10.06	62	0	24.67	0.050

P26366	N acetylmuramoyl L alanine amidase amiB	46761	9.47	157.41	10	32	54.90	12.04	65	2	25.28	0.059
P0A7W4	30S ribosomal protein S5	17592	10.56	935.44	10	13	73.65	8.74	128	1	17.61	0.045
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	262.37	9	16	61.54	6.35	48	0	18.21	0.055
P65215	2 dehydro 3 deoxyphosphooctonate aldolase	30775	5.86	260.86	9	25	53.17	8.97	60	1	23.49	0.054
Q8ZQK4	Putative transport protein ybjL	60141	8.35	244.68	9	32	23.53	7.43	40	1	25.06	0.059
Q08016	Ornithine carbamoyltransferase	36717	5.25	239.16	9	26	30.24	10.35	50	1	20.21	0.052
P26982	Protease do	49284	9.19	224.28	9	29	41.26	9.32	62	1	18.06	0.055
P25924	Siroheme synthase	50115	6.35	218.58	9	39	30.85	7.44	41	1	19.20	0.058
P60726	50S ribosomal protein L4	22072	10.19	186.21	9	18	60.20	9.56	50	1	18.86	0.056
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	184.68	9	19	36.29	9.10	50	0	20.02	0.049
P0A2B3	30S ribosomal protein S7	17579	10.73	175.14	9	10	68.59	11.52	44	0	18.47	0.050
Q8ZNF3	UDP 4 amino 4 deoxy L arabinose oxoglutarate aminotransferase	41138	5.83	168.74	9	22	35.36	11.32	44	0	25.35	0.061
P0A2C5	D ribose binding periplasmic protein	30943	9.20	103.66	9	25	36.49	11.56	33	0	26.76	0.058
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	291.15	9	12	71.60	9.63	77	0	19.17	0.054
Q8ZKP7	Triosephosphate isomerase	26899	5.61	338.42	8	22	52.94	9.55	86	0	17.65	0.047
P0A9Y9	Cold shock like protein cspC	7397	7.70	287.33	8	5	86.96	8.19	51	0	15.11	0.048
P0A2C7	Spermidine putrescine binding periplasmic protein	38996	4.99	271.38	8	28	24.14	11.05	50	1	21.93	0.058
P25077	Malate dehydrogenase	32455	5.97	252.62	8	22	42.95	6.39	69	1	20.78	0.053
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	199.29	8	28	20.06	9.08	35	0	19.63	0.051
P14146	Virulence transcriptional regulatory protein phoP	25617	5.14	187.75	8	21	54.91	9.59	50	1	23.43	0.051
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	186.64	8	25	36.13	11.21	55	1	26.04	0.055
P10372	1 5 phosphoribosyl 5 5 phosphoribosylamino methylideneamino imidazole 4 carboxamide isomerase	26072	5.50	162.57	8	19	53.88	7.65	35	0	21.88	0.056
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	125.56	8	15	70.18	12.10	49	1	23.14	0.061
P0A1R4	Imidazole glycerol phosphate synthase subunit hisH	21689	5.75	122.91	8	19	50.00	10.43	33	1	22.09	0.053
P02910	Histidine binding periplasmic protein	28361	5.95	378.72	8	23	47.31	8.24	67	0	17.46	0.047
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	438.21	7	16	58.29	8.19	57	1	17.23	0.053
P66593	30S ribosomal protein S6	15163	5.08	288.27	7	9	62.60	7.47	67	2	14.26	0.059
O54296	30S ribosomal protein S11	13822	11.74	277.03	7	9	52.71	7.22	47	1	16.65	0.056
Q8ZQT5	Protein tolB	46120	8.73	220.97	7	21	27.44	7.15	48	0	17.68	0.044
P02906	Sulfate binding protein	36517	7.72	190.81	7	28	27.05	8.12	32	0	19.48	0.053
Q8ZKW8	ATP synthase gamma chain	31535	9.26	159.25	7	26	45.64	12.00	45	2	26.13	0.063
P66032	3 4 dihydroxy 2 butanone 4 phosphate synthase	23295	4.70	158.01	7	15	53.00	12.73	35	1	24.05	0.061
P0AA02	Transcription antitermination protein nusG	20532	6.40	147.69	7	13	61.33	5.64	46	1	23.54	0.067
Q8ZRP3	1 deoxy D xylulose 5 phosphate reductoisomerase	43324	5.85	132.86	7	28	24.87	13.54	36	1	21.19	0.059
P0A1V6	Ribose phosphate pyrophosphokinase	34194	5.06	121.99	7	19	26.98	7.53	24	0	21.42	0.050
P10367	Histidine biosynthesis bifunctional protein hisIE	22660	5.37	115.94	7	15	39.90	5.38	36	1	21.39	0.053
Q8ZRT5	GMP reductase	37114	6.09	114.64	7	20	24.21	5.81	22	0	17.19	0.064
P62405	50S ribosomal protein L5	20304	9.76	102.01	7	14	42.46	7.31	34	0	17.88	0.056
P0A1S2	DNA binding protein H NS	15532	5.09	510.41	7	14	60.58	5.51	110	3	17.15	0.048
P0AA28	Thioredoxin 1	11799	4.47	476.89	6	8	49.54	8.02	84	0	14.68	0.041
P66313	50S ribosomal protein L6	18848	10.09	333.12	6	13	52.54	9.53	56	0	16.89	0.038
P0A7X0	30S ribosomal protein S8	14117	9.85	323.84	6	12	52.31	8.30	65	1	17.19	0.055
P0A1Z2	Chaperone protein skp	17894	10.25	289.75	6	10	56.52	8.23	62	1	18.82	0.057
Q7CPL5	50S ribosomal protein L14	13559	10.89	227.74	6	14	47.97	9.70	57	2	19.72	0.054
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	218.02	6	19	42.34	11.58	32	0	25.63	0.056
Q8ZQS2	2 3 bisphosphoglycerate dependent phosphoglycerate mutase	28475	5.71	211.22	6	19	26.40	6.50	28	0	19.81	0.052

Q8ZPD6	Uncharacterized protein yncE	38480	9.55	192.41	6	27	25.78	7.61	37	0	17.94	0.055
Q7CPL6	50S ribosomal protein L18	12761	10.88	161.86	6	9	49.57	10.81	32	0	18.74	0.052
P66692	Ribose 5 phosphate isomerase A	22881	4.89	139.51	6	15	38.36	4.22	38	0	21.03	0.055
P0A7V6	30S ribosomal protein S3	25967	10.72	135.26	6	20	45.92	8.46	34	0	18.83	0.055
P66193	50S ribosomal protein L31 type B	9808	9.67	120.13	6	9	69.77	12.41	36	0	16.33	0.046
P0A1D5	10 kDa chaperonin	10311	5.19	510.96	6	7	74.23	6.84	80	1	14.59	0.042
P0A299	50S ribosomal protein L7 L12	12291	4.40	318.82	5	20	67.77	3.61	54	2	16.06	0.056
P63411	Acetate kinase	43230	5.91	263.83	5	25	27.50	4.40	36	2	19.65	0.043
P67904	30S ribosomal protein S10	11759	10.33	256.97	5	11	35.92	8.79	42	0	19.12	0.050
P21267	Glutamate 1 semialdehyde 2 1 aminomutase	45295	4.62	199.65	5	24	23.24	9.01	38	2	21.18	0.056
Q7CR64	UPF0325 protein yaeH	15084	7.17	188.34	5	11	35.16	9.68	30	0	15.75	0.058
P67179	UPF0082 protein yebC	26401	4.53	165.89	5	16	27.24	4.36	25	0	17.29	0.049
P0A2A1	50S ribosomal protein L19	13122	11.24	145.08	5	11	45.22	11.89	30	0	23.59	0.055
P0A1W6	Leucine specific binding protein	39375	5.84	129.53	5	27	31.17	9.11	30	1	26.55	0.060
Q9L9I8	Thiamine phosphate pyrophosphorylase	22969	4.95	118.47	5	16	41.23	6.38	23	0	21.49	0.047
Q7CPH8	Protein export protein secB	17234	4.06	105.75	5	12	52.26	8.66	19	0	20.80	0.070
Q8ZNK6	Probable endonuclease 4	31176	5.02	76.21	5	17	24.56	10.03	24	0	20.32	0.061
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	389.26	5	8	51.28	10.31	60	0	17.48	0.041
P0A1R6	DNA binding protein HU alpha	9515	10.12	240.97	4	7	57.78	12.51	39	0	16.92	0.046
Q8ZLM1	30S ribosomal protein S13	13153	11.22	215.90	4	12	34.75	7.48	30	0	17.45	0.051
P37168	Virulence factor mvIM	33987	6.88	177.84	4	27	22.15	4.93	17	0	23.81	0.052
P0A2F6	Single stranded DNA binding protein	19062	5.29	173.35	4	11	36.93	6.06	33	0	15.94	0.051
P0A7K0	50S ribosomal protein L11	14865	10.09	172.82	4	11	23.24	6.75	34	0	13.72	0.052
P02936	Outer membrane protein A	37491	5.50	172.67	4	25	20.86	8.70	29	0	20.97	0.054
P66643	30S ribosomal protein S9	14817	11.34	155.13	4	14	33.85	8.52	26	0	13.21	0.050
P68684	30S ribosomal protein S21	8494	11.56	146.61	4	9	42.25	9.17	22	0	19.26	0.056
Q7CPL7	50S ribosomal protein L17	14385	11.46	139.94	4	8	26.77	5.96	26	0	15.34	0.058
P67093	Universal stress protein G	15891	6.20	135.27	4	9	47.89	11.92	25	1	23.07	0.055
Q8ZK81	30S ribosomal protein S18	9065	11.11	128.19	4	4	42.67	13.02	22	0	23.17	0.061
P0A1S4	DNA binding protein stpA	15477	9.24	126.75	4	12	42.11	5.83	35	2	21.58	0.055
P0A7S6	30S ribosomal protein S12	13728	11.28	96.44	4	15	22.58	8.84	19	0	20.83	0.046
Q8ZRM7	2 5 diketo D gluconic acid reductase B	29135	5.17	92.94	4	24	41.57	8.04	24	2	27.79	0.056
Q7CPP7	50S ribosomal protein L21	11571	10.29	79.82	4	7	40.78	6.26	18	0	18.09	0.048
Q7CPZ4	Protein grpE	21827	4.49	72.19	4	18	36.22	12.32	17	0	22.91	0.059
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	245.67	4	14	39.61	6.88	55	2	20.99	0.048
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	167.53	3	10	23.16	10.81	24	0	17.95	0.053
Q7CR46	Anti adapter protein iraP	9876	5.50	157.93	3	7	73.26	6.64	23	0	15.28	0.045
P67617	Probable Fe 2 trafficking protein	10892	5.87	118.47	3	15	72.53	8.39	30	2	20.94	0.058
P66431	30S ribosomal protein S15	10191	10.82	96.70	3	8	22.47	6.81	15	0	15.66	0.055
P67537	UPF0250 protein ybeD	9793	5.04	50.20	3	4	74.71	3.30	16	0	27.07	0.052
P16657	Enoyl acyl carrier protein reductase NADH	27742	5.47	167.72	3	21	17.56	10.15	16	1	21.40	0.041
P0A2A7	50S ribosomal protein L30	6509	11.41	75.14	2	6	33.90	7.82	16	0	19.08	0.048
P0A2B1	30S ribosomal protein S20	9649	11.63	148.08	2	3	22.99	7.66	22	0	15.31	0.046

SA123 + Zn(II) LC-MS run 1: 123_Zn_220709_1a2_01												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)

P0A1H3	Elongation factor G	77550	5.00	707.19	42	47	79.83	10.24	262	5	23.27	0.043
P0A1D3	60 kDa chaperonin	57249	4.65	1205.81	42	44	85.04	9.40	351	6	20.15	0.040
Q8ZQZ6	Leucyl tRNA synthetase	96923	5.02	653.96	38	66	54.07	9.81	242	7	24.85	0.044
Q8ZP54	Exoribonuclease 2	72394	5.40	608.29	32	50	49.22	10.89	184	4	22.14	0.042
P06202	Periplasmic oligopeptide binding protein	61254	6.03	553.09	29	42	60.59	8.91	171	0	22.56	0.045
Q56073	Chaperone protein dnaK	69215	4.64	668.70	29	59	56.11	9.29	195	5	21.92	0.043
P0A1P6	Glutamine synthetase	51752	5.25	521.08	28	33	75.91	9.39	171	3	23.92	0.042
P64076	Enolase	45570	5.08	1116.74	27	34	83.33	8.10	260	0	19.93	0.041
Q7CPE2	ATP synthase subunit beta	50251	4.71	617.96	26	32	66.09	10.35	162	3	22.09	0.045
P52616	Phase 2 flagellin	52504	4.55	801.50	25	37	68.58	10.03	183	1	22.84	0.042
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	566.79	25	60	38.46	9.11	156	5	22.74	0.044
P0A1H5	Elongation factor Tu	43256	5.15	1224.33	25	30	81.47	10.26	307	3	17.67	0.037
P65702	Phosphoglycerate kinase	41106	4.90	1147.75	24	30	77.78	8.72	222	1	20.23	0.036
P23905	D galactose binding periplasmic protein	35791	5.75	361.32	23	30	77.11	9.20	149	3	24.90	0.037
P41031	Thiosulfate binding protein	37559	9.19	747.19	23	32	77.81	9.52	198	1	19.14	0.043
P64052	Elongation factor Ts	30338	4.95	517.34	22	33	76.68	10.09	155	2	21.64	0.046
P05989	Ketol acid reductoisomerase	53907	4.96	525.92	21	47	53.56	8.99	133	4	20.95	0.043
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	949.83	21	29	64.65	7.99	258	3	18.91	0.037
P26982	Protease do	49284	9.19	377.87	20	29	66.32	9.96	153	5	22.03	0.044
O33921	Glucose 1 phosphatase	45530	6.64	343.22	20	25	65.62	9.70	138	1	21.64	0.041
P06179	Flagellin	51581	4.60	650.58	20	36	49.90	9.78	181	3	22.90	0.042
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	447.69	19	15	91.34	9.41	155	1	18.18	0.040
P02936	Outer membrane protein A	37491	5.50	365.99	19	25	56.86	11.30	137	1	26.67	0.041
Q8ZRC0	ATP dependent Clp protease ATP binding subunit clpX	46147	5.05	350.40	19	38	68.56	10.19	116	1	22.95	0.043
P66955	Transaldolase B	35149	4.91	456.49	19	26	62.78	9.66	104	1	22.28	0.038
Q7CR87	Chaperone surA	47221	6.88	394.92	18	31	61.45	7.81	129	1	22.38	0.036
P65215	2 dehydro 3 deoxyphosphooctonate aldolase	30775	5.86	347.24	18	25	67.96	9.18	105	3	22.31	0.044
P60446	50S ribosomal protein L3	22233	10.25	314.24	18	20	77.99	11.34	120	0	23.36	0.037
P0A1E3	Cysteine synthase A	34514	5.72	723.81	18	20	57.89	6.46	162	4	20.00	0.043
P0A297	50S ribosomal protein L10	17789	9.46	484.45	17	15	67.88	7.64	123	3	20.88	0.041
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	501.67	17	21	66.89	6.41	114	1	22.36	0.039
P02910	Histidine binding periplasmic protein	28361	5.95	564.11	16	23	71.54	9.30	132	1	21.16	0.041
P17215	Leu Ile Val Thr binding protein	38762	5.69	500.96	16	21	74.79	6.85	131	1	19.76	0.040
P66541	30S ribosomal protein S2	26741	6.73	408.33	16	23	70.12	9.31	123	2	20.74	0.043
Q8ZQT5	Protein tolB	46120	8.73	386.11	16	21	51.16	9.03	99	1	20.69	0.040
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	358.23	16	28	53.19	10.40	116	2	19.90	0.040
P02911	Lysine arginine ornithine binding periplasmic protein	28182	5.90	281.31	16	23	51.54	10.08	87	1	22.77	0.044
P25077	Malate dehydrogenase	32455	5.97	716.02	16	22	72.44	7.61	157	2	17.53	0.039
P02906	Sulfate binding protein	36517	7.72	432.53	15	28	55.93	9.63	99	0	20.65	0.046
Q8ZKP7	Triosephosphate isomerase	26899	5.61	340.56	15	22	57.65	7.91	120	0	18.60	0.035
P67179	UPF0082 protein yebC	26401	4.53	304.77	15	16	57.72	9.98	109	2	22.43	0.040
Q8ZLR8	UPF0042 protein yhbJ	32443	8.19	254.67	15	20	48.59	8.55	83	2	25.27	0.044
P0A7W4	30S ribosomal protein S5	17592	10.56	567.92	15	13	76.65	9.42	121	2	17.86	0.040
P0A2C5	D ribose binding periplasmic protein	30943	9.20	289.71	14	25	57.77	9.50	73	0	20.05	0.045
P29768	Sialidase	42046	8.46	325.81	13	27	48.43	10.54	101	4	23.69	0.042
P0A1S2	DNA binding protein H NS	15532	5.09	515.64	13	14	82.48	9.01	125	2	16.90	0.040
P0A2A3	50S ribosomal protein L1	24713	10.10	333.59	12	19	53.85	7.99	65	1	21.64	0.047

P00929	Tryptophan synthase alpha chain	28652	5.29	314.53	12	19	71.27	8.69	81	1	22.20	0.044
P0A1V4	Adenylate kinase	23473	5.39	360.26	12	24	49.53	10.52	78	0	19.35	0.041
P66313	50S ribosomal protein L6	18848	10.09	373.03	11	13	61.58	7.88	91	1	19.38	0.041
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	325.51	11	16	86.63	9.45	85	1	21.63	0.042
P0A1Z2	Chaperone protein skp	17894	10.25	284.99	11	10	73.29	9.94	106	2	20.93	0.038
P0A299	50S ribosomal protein L7 L12	12291	4.40	472.49	11	20	80.99	7.20	117	4	18.27	0.039
P0A1R2	Imidazole glycerol phosphate synthase subunit hisF	28350	4.80	208.69	10	20	63.95	11.64	49	0	24.71	0.047
P0A8B8	UPF0133 protein ybaB	12006	4.82	183.11	10	11	89.91	8.70	73	3	22.06	0.046
Q7CPD8	UPF0438 protein yifE	13069	6.23	156.81	10	13	66.96	8.74	69	0	24.45	0.037
Q8ZK80	50S ribosomal protein L9	15774	7.73	360.36	10	14	59.73	9.48	89	2	22.03	0.042
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	280.87	9	19	76.21	10.87	91	6	19.16	0.046
P0A1S0	Integration host factor subunit alpha	11360	9.88	271.35	9	13	58.59	7.46	60	0	21.64	0.039
P0A7K0	50S ribosomal protein L11	14865	10.09	221.69	9	11	53.52	8.41	75	1	17.57	0.034
P67093	Universal stress protein G	15891	6.20	201.14	9	9	91.55	8.49	51	2	19.31	0.040
P66593	30S ribosomal protein S6	15163	5.08	196.97	9	9	70.23	8.40	65	2	19.44	0.041
P22107	TraT complement resistance protein	26261	9.35	391.56	9	18	42.39	9.28	77	2	22.39	0.038
O54297	30S ribosomal protein S4	23470	10.38	352.92	8	19	38.35	6.92	58	0	18.56	0.047
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	264.86	8	25	38.69	11.28	65	1	20.39	0.041
P0A2A9	30S ribosomal protein S16	9229	11.05	261.35	8	6	73.17	8.33	53	0	19.98	0.037
P66193	50S ribosomal protein L31 type B	9808	9.67	204.94	8	9	70.93	10.27	51	0	22.73	0.038
P0A2F6	Single stranded DNA binding protein	19062	5.29	178.60	8	11	56.82	8.09	59	1	18.55	0.044
Q8ZP65	Probable thiol peroxidase	18014	4.74	452.92	8	12	95.83	7.27	106	2	16.88	0.032
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	260.31	7	10	49.72	10.44	60	2	18.60	0.042
P0AA28	Thioredoxin 1	11799	4.47	417.09	6	8	53.21	8.59	97	2	20.31	0.034
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	377.61	6	12	36.69	7.37	83	2	19.01	0.033
P0A9Y9	Cold shock like protein cspC	7397	7.70	290.49	6	5	92.75	10.78	58	0	18.36	0.038
P0AA07	Phosphocarrier protein HPr	9113	5.51	153.10	6	7	95.29	9.51	69	1	18.70	0.037
P0A1D5	10 kDa chaperonin	10311	5.19	458.51	6	7	79.38	5.74	92	0	16.47	0.036
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	242.85	5	16	36.54	9.90	37	1	21.09	0.041
P0A7X0	30S ribosomal protein S8	14117	9.85	210.20	5	12	32.31	8.08	40	0	17.16	0.037
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	181.14	5	8	47.44	9.63	42	1	16.25	0.043
Q8ZRE7	UPF0345 protein yaiE	10151	4.82	107.57	5	6	67.02	7.59	29	0	25.52	0.042
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	315.91	5	14	39.61	5.41	77	2	20.41	0.037
P26983	Probable sigma 54 modulation protein	10850	6.72	121.29	4	7	74.74	8.63	32	0	20.30	0.038
P66170	50S ribosomal protein L29	7255	10.52	93.91	4	4	41.27	8.55	20	0	16.53	0.045
P0A2A7	50S ribosomal protein L30	6509	11.41	194.44	4	6	50.85	7.66	33	0	19.04	0.038
P69226	Translation initiation factor IF 1	8244	9.74	80.22	3	5	52.78	7.65	16	0	25.74	0.050
P0A1P8	Glutaredoxin 1	9917	5.54	113.71	3	10	45.98	10.92	23	0	22.13	0.045

SA123 + Zn(II) LC-MS run 2: 123_Zn_220709_1a2_02												
Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1D3	60 kDa chaperonin	57249	4.65	1259.88	31	44	76.28	6.88	257	0	16.55	0.052
P06202	Periplasmic oligopeptide binding protein	61254	6.03	558.16	23	42	53.41	7.67	148	1	20.89	0.059
P0A1H3	Elongation factor G	77550	5.00	449.13	22	47	55.11	10.50	124	2	20.87	0.055
P64076	Enolase	45570	5.08	1277.59	21	34	60.88	7.64	224	2	17.77	0.050

P0A1H5	Elongation factor Tu	43256	5.15	1529.91	21	30	71.32	9.05	289	2	16.34	0.048
P52616	Phase 2 flagellin	52504	4.55	433.97	20	37	59.68	8.86	120	2	19.90	0.062
P65702	Phosphoglycerate kinase	41106	4.90	1215.59	20	30	66.15	6.37	196	0	17.22	0.046
Q56073	Chaperone protein dnaK	69215	4.64	681.08	19	59	43.42	8.56	108	1	19.22	0.059
P00924	Enolase 1	46773	6.15	520.64	18	28	48.05	9.92	113	4	22.15	0.056
Q7CPE2	ATP synthase subunit beta	50251	4.71	618.02	17	32	55.87	7.38	109	2	19.58	0.060
P64052	Elongation factor Ts	30338	4.95	553.40	17	33	68.90	8.86	118	3	18.73	0.058
P0A1E3	Cysteine synthase A	34514	5.72	502.48	17	20	60.37	6.84	107	0	16.90	0.053
P06179	Flagellin	51581	4.60	412.43	17	36	49.29	7.29	97	1	20.84	0.059
Q9L6N1	5 methyltetrahydropteroyltriglutamate homocysteine methyltransferase	84615	5.67	363.94	17	60	29.44	9.43	89	1	20.97	0.057
P41031	Thiosulfate binding protein	37559	9.19	619.23	17	32	61.24	6.56	121	0	18.74	0.055
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	466.68	16	36	45.08	6.88	106	1	19.59	0.060
Q7CPE1	ATP synthase subunit alpha	55078	5.61	374.92	16	40	53.02	8.56	105	3	25.03	0.054
Q7CR87	Chaperone surA	47221	6.88	357.39	16	31	55.84	8.52	100	1	19.94	0.060
Q8ZQT5	Protein tolB	46120	8.73	308.16	16	21	55.35	7.53	90	1	20.01	0.058
O33921	Glucose 1 phosphatase	45530	6.64	276.99	16	25	57.39	10.16	90	0	23.38	0.062
P05989	Ketol acid reductoisomerase	53907	4.96	270.89	16	47	47.05	10.46	95	2	21.23	0.065
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1107.19	16	29	59.21	7.84	218	0	16.15	0.045
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	411.16	15	21	63.58	6.25	115	1	19.79	0.050
P66932	Trigger factor	48036	4.64	309.26	14	43	46.99	11.23	80	1	24.45	0.058
P02936	Outer membrane protein A	37491	5.50	292.12	14	25	48.00	9.68	88	1	22.85	0.058
Q8ZQM3	Glutathione binding protein gsiB	56502	8.98	313.55	14	40	32.81	6.88	73	0	19.78	0.062
P60446	50S ribosomal protein L3	22233	10.25	255.83	13	20	70.81	9.15	70	1	20.28	0.056
Q8ZP20	Periplasmic trehalase	63469	5.15	230.68	13	44	37.54	8.41	64	1	28.09	0.061
P60726	50S ribosomal protein L4	22072	10.19	186.10	13	18	71.14	9.36	82	3	21.50	0.061
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	366.59	13	22	66.18	8.62	86	1	25.30	0.063
P17215	Leu Ile Val Thr binding protein	38762	5.69	407.63	12	21	71.51	9.64	98	0	20.57	0.052
P26982	Protease do	49284	9.19	319.96	12	29	47.58	6.88	99	2	23.03	0.053
P65882	Adenylosuccinate synthetase	47347	5.15	250.41	12	42	43.29	7.43	75	3	23.47	0.062
P25077	Malate dehydrogenase	32455	5.97	718.59	12	22	58.33	6.90	129	0	15.69	0.046
P02910	Histidine binding periplasmic protein	28361	5.95	458.39	11	23	51.15	4.15	92	1	18.78	0.043
P0A1P6	Glutamine synthetase	51752	5.25	440.12	11	33	37.95	6.90	83	2	20.84	0.057
P23905	D galactose binding periplasmic protein	35791	5.75	266.60	11	30	45.78	10.60	56	0	25.23	0.061
Q8ZN75	Succinyl diaminopimelate desuccinylase	41552	5.89	214.97	11	26	54.93	10.31	63	2	19.47	0.060
P0A2B3	30S ribosomal protein S7	17579	10.73	196.10	11	10	61.54	8.64	51	1	15.56	0.054
Q7CQ05	Autonomous glycyl radical cofactor	14335	4.92	548.28	11	15	83.46	6.32	136	0	14.14	0.045
P0A2I5	DNA topoisomerase 4 subunit B	70044	5.44	329.89	10	52	27.46	8.81	56	1	23.19	0.063
Q8ZKP7	Triosephosphate isomerase	26899	5.61	327.62	10	22	58.43	8.94	122	2	17.87	0.047
P0A299	50S ribosomal protein L7 L12	12291	4.40	296.45	10	20	64.46	7.02	58	1	17.25	0.056
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	289.14	10	28	36.17	10.67	61	1	20.45	0.061
P58661	Aspartate aminotransferase	43494	5.29	229.41	10	34	36.11	9.54	43	0	22.67	0.057
P63411	Acetate kinase	43230	5.91	352.33	10	25	48.50	6.86	69	1	21.87	0.057
P66313	50S ribosomal protein L6	18848	10.09	373.76	9	13	53.11	4.83	68	0	16.62	0.051
P0A297	50S ribosomal protein L10	17789	9.46	332.16	9	15	53.33	9.69	69	1	20.41	0.054
P66541	30S ribosomal protein S2	26741	6.73	311.38	9	23	61.83	9.19	66	2	19.35	0.056
P02906	Sulfate binding protein	36517	7.72	277.05	9	28	39.51	9.59	72	1	21.19	0.060
Q8ZQD4	Outer membrane lipoprotein carrier protein	22467	7.39	223.51	9	17	71.92	9.62	48	0	21.43	0.059

P0A2C5	D ribose binding periplasmic protein	30943	9.20	204.24	9	25	41.22	9.37	48	0	17.87	0.062
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	194.58	9	15	73.10	10.13	51	0	24.42	0.059
P0A1V4	Adenylate kinase	23473	5.39	191.89	9	24	37.85	7.65	47	1	19.91	0.060
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	171.47	9	19	40.93	8.04	45	0	26.92	0.058
P0A7W4	30S ribosomal protein S5	17592	10.56	715.24	9	13	60.48	5.45	98	0	15.43	0.046
P0A2A3	50S ribosomal protein L1	24713	10.10	493.52	8	19	50.85	7.66	80	1	16.93	0.049
Q8ZP65	Probable thiol peroxidase	18014	4.74	446.36	8	12	91.67	7.34	98	1	16.99	0.046
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	413.54	8	16	64.17	8.91	50	0	17.95	0.055
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	333.73	8	12	79.88	8.39	77	0	19.72	0.045
P77983	Pyruvate kinase I	50625	5.53	252.87	8	33	27.45	8.24	49	2	19.98	0.059
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	235.44	8	16	44.23	8.34	45	1	21.03	0.050
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	214.27	8	19	55.24	11.53	66	4	24.22	0.065
P0A1S2	DNA binding protein H NS	15532	5.09	659.38	8	14	62.77	9.11	112	1	14.59	0.047
Q8ZK80	50S ribosomal protein L9	15774	7.73	511.71	7	14	61.75	8.35	66	0	19.07	0.053
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	430.16	7	14	48.79	9.14	82	2	20.84	0.053
P0A1R8	DNA binding protein HU beta	9234	10.24	428.06	7	9	73.33	8.61	73	0	16.11	0.050
P67904	30S ribosomal protein S10	11759	10.33	338.35	7	11	58.25	9.18	55	0	21.15	0.049
Q8ZRP4	2 3 4 5 tetrahydropyridine 2 6 dicarboxylate N succinyltransferase	29833	5.39	224.01	7	25	33.58	7.23	37	1	19.17	0.066
O54297	30S ribosomal protein S4	23470	10.38	203.32	7	19	36.89	9.03	43	0	20.30	0.052
Q7CR64	UPF0325 protein yaeH	15084	7.17	195.00	7	11	40.63	8.56	41	0	19.41	0.060
P61179	50S ribosomal protein L22	12218	10.71	172.27	7	8	44.55	8.95	32	0	20.11	0.058
P66643	30S ribosomal protein S9	14817	11.34	160.06	7	14	44.62	7.98	34	0	18.34	0.062
P0A1S0	Integration host factor subunit alpha	11360	9.88	113.35	7	13	63.64	11.65	32	0	20.93	0.061
Q7CPP7	50S ribosomal protein L21	11571	10.29	100.06	7	7	72.82	10.16	36	1	19.42	0.057
P0A1D5	10 kDa chaperonin	10311	5.19	574.56	7	7	83.51	5.29	96	0	16.25	0.049
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	231.25	6	8	51.28	9.66	48	0	24.94	0.060
P0A1Z2	Chaperone protein skp	17894	10.25	218.13	6	10	45.96	8.58	47	0	20.00	0.052
P66955	Transaldolase B	35149	4.91	189.44	6	26	21.45	4.26	20	0	21.00	0.053
P66692	Ribose 5 phosphate isomerase A	22881	4.89	143.32	6	15	49.77	4.01	35	0	21.37	0.060
P22107	TraT complement resistance protein	26261	9.35	267.72	6	18	31.28	8.35	49	2	18.96	0.057
P66593	30S ribosomal protein S6	15163	5.08	229.58	5	9	43.51	6.35	35	0	14.75	0.059
P66193	50S ribosomal protein L31 type B	9808	9.67	191.28	5	9	62.79	8.54	44	1	15.36	0.063
P67093	Universal stress protein G	15891	6.20	157.42	5	9	61.97	8.43	42	2	21.70	0.050
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	130.45	5	10	29.38	8.02	39	2	19.86	0.059
P0A1R6	DNA binding protein HU alpha	9515	10.12	373.28	5	7	73.33	8.55	84	1	17.24	0.048
P0A7K0	50S ribosomal protein L11	14865	10.09	258.23	4	11	44.37	6.81	49	1	15.97	0.047
P0A9Y9	Cold shock like protein cspC	7397	7.70	233.40	4	5	78.26	6.37	41	0	16.95	0.053
P0A7X0	30S ribosomal protein S8	14117	9.85	207.22	4	12	27.69	7.29	36	0	12.90	0.051
O54296	30S ribosomal protein S11	13822	11.74	136.06	4	9	50.39	7.40	25	0	20.75	0.059
P0AA28	Thioredoxin 1	11799	4.47	407.51	4	8	38.53	7.52	65	0	15.15	0.037
P66170	50S ribosomal protein L29	7255	10.52	165.13	3	4	55.56	7.32	35	0	12.74	0.046
P67179	UPF0082 protein yebC	26401	4.53	130.03	3	16	20.33	4.69	19	0	16.00	0.056
P0A1P8	Glutaredoxin 1	9917	5.54	90.06	3	10	60.92	7.67	19	1	17.09	0.061
Q7CPL7	50S ribosomal protein L17	14385	11.46	88.51	3	8	22.05	9.28	15	0	12.33	0.052
P0A2A7	50S ribosomal protein L30	6509	11.41	84.81	3	6	45.76	6.76	15	0	18.26	0.054
P67091	Universal stress protein F	15704	5.92	184.30	3	11	40.28	11.91	29	0	16.42	0.061

SA123 + Zn(II) LC-MS run 3: 123_Zn_220709_1a2_03

Accession	Description	mW (Da)	pI (pH)	PLGS Score	Peptides	Theoretical Peptides	Coverage (%)	Precursor RMS Mass Error (ppm)	Products	Modified Peptides	Products RMS Mass Error (ppm)	Products RMS RT Error (min)
P0A1D3	60 kDa chaperonin	57249	4.65	1199.69	28	44	74.09	6.49	231	2	17.72	0.058
P06202	Periplasmic oligopeptide binding protein	61254	6.03	586.64	23	42	54.70	7.96	156	0	18.14	0.066
P0A1H3	Elongation factor G	77550	5.00	499.57	21	47	52.27	7.08	143	2	21.35	0.064
P41031	Thiosulfate binding protein	37559	9.19	652.53	20	32	72.49	7.08	153	2	16.69	0.063
P10503	Bifunctional protein putA	143999	5.69	471.48	20	91	24.02	10.49	91	1	24.42	0.069
P52616	Phase 2 flagellin	52504	4.55	352.85	20	37	62.85	8.43	107	0	22.81	0.070
Q7CPE1	ATP synthase subunit alpha	55078	5.61	310.69	20	40	49.32	9.30	107	1	23.77	0.065
P64076	Enolase	45570	5.08	1114.49	20	34	73.15	7.82	202	0	19.08	0.055
P0A1H5	Elongation factor Tu	43256	5.15	1435.78	19	30	70.81	8.10	277	2	15.91	0.055
Q56073	Chaperone protein dnaK	69215	4.64	566.00	18	59	51.10	9.24	101	0	20.38	0.065
Q7CPE2	ATP synthase subunit beta	50251	4.71	599.23	17	32	55.00	8.18	110	1	19.03	0.063
P65702	Phosphoglycerate kinase	41106	4.90	1031.61	17	30	54.78	6.76	175	0	16.53	0.053
P00924	Enolase 1	46773	6.15	385.62	16	28	53.09	8.55	90	2	21.44	0.054
P17215	Leu Ile Val Thr binding protein	38762	5.69	377.83	16	21	72.88	9.03	108	1	20.54	0.066
P0A1P6	Glutamine synthetase	51752	5.25	485.92	16	33	54.16	6.89	97	1	21.26	0.068
Q7CR87	Chaperone surA	47221	6.88	274.23	15	31	57.01	8.26	85	0	19.24	0.057
P64052	Elongation factor Ts	30338	4.95	579.70	15	33	74.56	6.98	101	1	18.18	0.063
P25077	Malate dehydrogenase	32455	5.97	549.44	14	22	55.77	5.29	126	1	16.56	0.061
Q8ZL56	2 3 bisphosphoglycerate independent phosphoglycerate mutase	56219	4.88	306.20	14	37	53.31	8.96	88	3	21.01	0.073
P55900	Phosphoserine aminotransferase	39806	5.17	206.55	14	28	40.33	9.62	67	2	24.27	0.066
P0A1P0	Glyceraldehyde 3 phosphate dehydrogenase	35564	6.36	1035.44	14	29	51.66	7.64	205	1	16.91	0.055
Q7CQ05	Autonomous glycyI radical cofactor	14335	4.92	522.15	13	15	84.25	8.04	137	0	15.25	0.053
P06179	Flagellin	51581	4.60	374.61	13	36	42.42	5.99	74	0	19.25	0.061
P67912	ADP L glycerol D mannose 6 epimerase	34827	4.72	314.39	13	33	47.10	10.59	76	1	24.64	0.065
P0A7W4	30S ribosomal protein S5	17592	10.56	601.97	13	13	83.23	7.46	113	0	18.97	0.055
Q8ZQT5	Protein tolB	46120	8.73	336.94	11	21	37.91	9.59	65	0	19.37	0.058
P0A2E1	Serine hydroxymethyltransferase	45426	6.02	324.27	11	36	36.21	10.89	64	0	17.81	0.069
O33921	Glucose 1 phosphatase	45530	6.64	300.82	11	25	54.24	6.04	82	1	20.02	0.067
P23905	D galactose binding periplasmic protein	35791	5.75	205.77	11	30	56.33	9.26	67	2	22.72	0.064
P77983	Pyruvate kinase I	50625	5.53	204.47	11	33	35.11	8.65	52	1	23.55	0.069
Q8ZRN1	D methionine binding lipoprotein metQ	29417	5.23	194.55	11	30	50.18	7.59	46	1	21.78	0.068
Q8ZP20	Periplasmic trehalase	63469	5.15	191.03	11	44	27.89	9.35	48	2	22.17	0.067
P65889	Phosphoribosylaminoimidazole succinocarboxamide synthase	26890	5.02	178.89	11	19	53.16	6.60	51	0	24.26	0.062
P0A1E3	Cysteine synthase A	34514	5.72	606.01	11	20	43.34	5.40	92	1	15.43	0.058
Q9ZF60	Glutamate aspartate periplasmic binding protein	33381	9.16	378.80	10	21	63.58	6.82	90	2	14.82	0.063
P14845	Carbamoyl phosphate synthase small chain	41625	6.00	338.00	10	27	43.98	6.87	57	1	20.64	0.067
P0A1Z2	Chaperone protein skp	17894	10.25	316.16	10	10	61.49	6.33	78	1	15.53	0.059
P63411	Acetate kinase	43230	5.91	305.39	10	25	45.00	9.67	61	0	25.64	0.067
P58661	Aspartate aminotransferase	43494	5.29	259.04	10	34	33.08	6.26	49	0	25.07	0.062
P66541	30S ribosomal protein S2	26741	6.73	163.84	10	23	48.55	9.00	50	0	22.42	0.062
Q8ZP65	Probable thiol peroxidase	18014	4.74	431.43	10	12	91.67	7.10	109	1	18.65	0.060
P0A2C5	D ribose binding periplasmic protein	30943	9.20	214.55	9	25	34.46	7.92	49	1	17.85	0.066
P0A7Z7	DNA directed RNA polymerase subunit alpha	36489	4.78	167.50	9	28	37.39	11.52	40	0	21.32	0.072
P0A1C3	Acetyl coenzyme A carboxylase carboxyl transferase subunit	35321	5.21	125.70	9	24	43.26	6.97	55	1	20.04	0.065

	alpha											
Q9L4T0	S ribosylhomocysteine lyase	19295	5.68	121.93	9	15	73.10	9.90	42	1	20.15	0.071
P26982	Protease do	49284	9.19	352.83	9	29	30.95	7.15	77	3	17.85	0.055
P0A297	50S ribosomal protein L10	17789	9.46	489.25	8	15	53.33	8.05	75	1	17.82	0.065
P02910	Histidine binding periplasmic protein	28361	5.95	475.21	8	23	44.23	7.69	73	1	16.49	0.050
Q8ZK80	50S ribosomal protein L9	15774	7.73	453.16	8	14	71.81	7.52	67	0	18.17	0.050
P0A299	50S ribosomal protein L7 L12	12291	4.40	357.15	8	20	74.38	7.86	68	1	18.64	0.071
P0A283	Glucose specific phosphotransferase enzyme IIA component	18235	4.54	327.61	8	12	71.60	11.88	73	0	18.19	0.057
P0A1V4	Adenylate kinase	23473	5.39	305.34	8	24	37.38	8.13	60	2	17.72	0.063
P02906	Sulfate binding protein	36517	7.72	224.17	8	28	40.12	9.14	41	0	27.20	0.059
Q8ZKQ1	Autoinducer 2 binding protein lsrB	36736	6.53	193.89	8	22	45.29	7.78	50	0	18.92	0.066
P0A1A5	Branched chain amino acid aminotransferase	34031	5.47	174.38	8	26	33.66	7.88	35	1	28.52	0.072
P26219	CDP diacylglycerol pyrophosphatase	28349	6.86	163.77	8	21	61.75	7.47	36	1	23.45	0.068
O68883	Citrate synthase	48074	6.26	162.26	8	33	33.49	7.58	49	0	19.12	0.066
P60726	50S ribosomal protein L4	22072	10.19	134.45	8	18	44.78	10.84	48	0	20.43	0.058
P0A2A3	50S ribosomal protein L1	24713	10.10	500.88	8	19	38.46	6.37	79	1	17.58	0.062
P0AA28	Thioredoxin 1	11799	4.47	419.50	7	8	62.39	8.28	77	0	16.32	0.050
P60446	50S ribosomal protein L3	22233	10.25	224.72	7	20	38.28	6.74	44	0	19.04	0.059
Q8ZRC9	UPF0234 protein yajQ	18307	5.42	164.92	7	14	48.47	9.61	35	0	23.69	0.069
P0A2B3	30S ribosomal protein S7	17579	10.73	126.60	7	10	42.31	10.47	39	0	19.91	0.068
P66643	30S ribosomal protein S9	14817	11.34	121.33	7	14	49.23	5.77	27	0	13.23	0.062
P0AA19	Transcriptional regulatory protein ompR	27336	5.99	100.52	7	23	49.79	12.70	40	1	18.28	0.065
P0A1S2	DNA binding protein H NS	15532	5.09	511.21	7	14	49.64	8.28	107	3	14.51	0.051
P0A2H9	Thiol disulfide interchange protein dsbA	22896	5.55	360.89	6	14	45.41	7.25	70	1	19.43	0.058
P66593	30S ribosomal protein S6	15163	5.08	310.77	6	9	63.36	7.54	59	2	13.76	0.062
O54297	30S ribosomal protein S4	23470	10.38	294.62	6	19	36.89	7.76	53	1	21.34	0.057
P0A251	Alkyl hydroperoxide reductase subunit C	20734	4.85	287.14	6	16	56.68	9.72	42	0	17.12	0.067
P66313	50S ribosomal protein L6	18848	10.09	284.87	6	13	42.37	6.83	47	0	15.63	0.048
P0A7X0	30S ribosomal protein S8	14117	9.85	281.45	6	12	47.69	8.16	56	0	18.28	0.058
Q8ZKP7	Triosephosphate isomerase	26899	5.61	263.70	6	22	34.51	8.78	86	1	16.69	0.049
P69936	NADP dependent L serine L allo threonine dehydrogenase ydfG	27025	5.78	219.32	6	19	49.60	6.95	39	1	17.82	0.069
P53636	Superoxide dismutase Cu Zn 1	18358	6.55	204.98	6	10	24.86	9.89	40	1	17.04	0.058
P35891	Chromosomal replication initiator protein dnaA	52565	9.11	195.38	6	51	19.10	10.93	27	0	23.77	0.068
P0A2M5	Uracil phosphoribosyltransferase	22518	5.17	162.49	6	16	50.00	6.87	34	1	15.13	0.061
P0A1R8	DNA binding protein HU beta	9234	10.24	158.80	6	9	68.89	10.88	49	0	15.14	0.044
P66692	Ribose 5 phosphate isomerase A	22881	4.89	156.15	6	15	37.90	8.08	38	0	20.24	0.064
O54296	30S ribosomal protein S11	13822	11.74	116.67	6	9	65.12	8.39	28	0	24.67	0.063
P0A8B8	UPF0133 protein ybaB	12006	4.82	100.29	6	11	74.31	9.94	29	0	20.49	0.071
P0A1D5	10 kDa chaperonin	10311	5.19	600.55	6	7	74.23	5.78	88	0	14.73	0.055
P0A9Y9	Cold shock like protein cspC	7397	7.70	279.34	5	5	78.26	6.83	45	0	12.68	0.060
Q7CPL5	50S ribosomal protein L14	13559	10.89	189.98	5	14	44.72	9.20	50	2	18.23	0.057
Q8ZPD6	Uncharacterized protein yncE	38480	9.55	164.75	5	27	22.66	9.91	26	0	27.34	0.069
Q7CPL7	50S ribosomal protein L17	14385	11.46	149.26	5	8	32.28	7.76	27	0	18.62	0.063
P67093	Universal stress protein G	15891	6.20	138.15	5	9	64.08	10.20	29	0	23.06	0.067
P67904	30S ribosomal protein S10	11759	10.33	300.83	5	11	48.54	11.06	42	0	20.99	0.055
P67091	Universal stress protein F	15704	5.92	217.64	4	11	48.61	7.98	34	1	17.97	0.061
P61179	50S ribosomal protein L22	12218	10.71	107.54	4	8	27.27	7.74	21	0	13.66	0.071
Q7CPZ4	Protein grpE	21827	4.49	102.32	4	18	41.33	5.87	19	0	23.03	0.066

Q8ZRE7	UPF0345 protein yaiE	10151	4.82	88.65	4	6	53.19	6.75	14	0	19.79	0.066
P66038	6 7 dimethyl 8 ribityllumazine synthase	15998	4.91	269.69	4	8	36.54	7.44	41	0	20.57	0.068
Q7CPL6	50S ribosomal protein L18	12761	10.88	135.74	3	9	19.66	7.09	16	0	20.09	0.053
Q7CPD8	UPF0438 protein yifE	13069	6.23	116.79	3	13	18.75	9.43	15	0	22.05	0.059
P0A2F0	RNA polymerase sigma E factor	21698	5.20	116.63	3	17	30.89	2.44	23	1	20.94	0.072
P0A2F4	Superoxide dismutase Fe	21294	5.52	93.27	3	14	39.90	3.59	32	1	17.57	0.073
P0A1R6	DNA binding protein HU alpha	9515	10.12	273.02	3	7	56.67	6.53	40	0	13.10	0.054