

Supplemental Data 1 Hörth et. al.

Information regarding all 670 proteins identified by auto validation criteria.

group Num = consecutive numbering of the identified proteins sorted by score

num Spec = number of measured spectra

num Peps = number of unique peptides

score Unique = non redundant sum of peptide scores

seqcov [%] = sequence coverage [%]

mean Intensity = mean intensity of measured precursor ions

mw = molecular weight of the identified protein

pI = calculated pI of the identified protein

acc num = Swiss Prot accession number of the identified protein

entry_name = Swiss Prot entry name of the identified protein

group Num	num Spec	num Peps	score Unique	seqcov [%]	mean Intensity	mw	pI	acc num	entry_name
1	59	36	546.09	31	5.93E+07	166710.8	6.27	P09831	Glutamate synthase [NADPH] large chain precursor (
2	63	25	434.19	42	1.14E+08	77450.5	5.24	P02996	Elongation factor G (EF-G).
3	69	25	408.13	46	1.59E+08	57198	4.85	P06139	60 kDa chaperonin (Protein Cpn60) (groEL protein).
4	52	24	381.89	58	2.31E+08	45524	5.32	P08324	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydrat
5	40	27	378.23	24	7.30E+07	155161.1	6.67	P00577	DNA-directed RNA polymerase beta' chain (EC 2.7.7.
6	41	27	377.95	31	5.02E+07	99063.1	5.52	P00864	Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEP
7	38	23	377.2	21	6.73E+07	141991.7	5.04	P11454	Enterobactin synthetase component F (EC 2.7.7.-) (
8	87	25	375.89	30	1.30E+08	84542.8	5.61	P25665	5-methyltetrahydropteroyltriglutamate--homocystein
9	43	24	352.95	28	1.01E+08	99537.8	5.46	P06958	Pyruvate dehydrogenase E1 component (EC 1.2.4.1).
10	29	24	339.97	21	8.16E+07	150633.1	5.15	P00575	DNA-directed RNA polymerase beta chain (EC 2.7.7.6
11	29	21	335.9	40	9.90E+07	61158.3	4.89	P02349	30S ribosomal protein S1.
12	34	23	333.08	46	2.02E+08	53938.2	5.2	P05793	Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohy
13	43	21	332.59	43	1.01E+08	68984.1	4.83	P04475	Chaperone protein dnaK (Heat shock protein 70) (He
14	42	21	307.11	29	8.34E+07	95996.6	6.34	P17547	Aldehyde-alcohol dehydrogenase [Includes: Alcohol

15	37	20	306.2	50	1.28E+08	51481.5	5.05	P00350	6-phosphogluconate dehydrogenase, decarboxylating
16	37	20	304.46	51	1.72E+08	45757	5.15	P08200	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) (Oxa
17	41	18	303.73	30	9.13E+07	63562.2	4.78	P08839	Phosphoenolpyruvate-protein phosphotransferase (EC
18	27	19	302.12	24	6.99E+07	117711.2	5.22	P00968	Carbamoyl-phosphate synthase large chain (EC 6.3.5
19	62	17	295.55	50	1.70E+08	47521.8	5.16	P05313	Isocitrate lyase (EC 4.1.3.1) (Isocitrase) (Isocit
20	68	17	288	54	4.30E+08	43182.6	5.3	P02990	Elongation factor Tu (EF-Tu) (P-43).
21	23	18	285.18	41	8.94E+07	57167	5.47	P09151	2-isopropylmalate synthase (EC 4.1.3.12) (Alpha-is
22	37	20	283.89	43	1.39E+08	48192.9	4.82	P22257	Trigger factor (TF).
23	35	19	282.4	53	1.04E+08	47214	5.32	P12283	Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--asp
24	29	19	275.31	31	4.12E+07	76682.1	5.29	P00961	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) (G
25	36	19	273.08	43	9.63E+07	55222.4	5.8	P00822	ATP synthase alpha chain (EC 3.6.3.14).
26	24	18	267.23	21	5.02E+07	105062.3	6.04	P07015	2-oxoglutarate dehydrogenase E1 component (EC 1.2.
27	41	16	259.96	53	1.46E+08	34358.6	5.83	P11096	Cysteine synthase A (EC 4.2.99.8) (O-acetylserine
28	20	16	253.97	17	6.12E+07	141403.5	5.23	P15254	Phosphoribosylformylglycinamide synthase (EC 6.3
29	17	16	248.42	24	8.01E+07	95585.5	5.37	P03815	ClpB protein (Heat shock protein F84.1).
30	20	14	242.32	40	1.37E+08	50194.5	4.9	P00824	ATP synthase beta chain (EC 3.6.3.14).
31	30	16	239.54	36	1.37E+08	60899.2	6.05	P23843	Periplasmic oligopeptide-binding protein precursor
32	24	16	236.89	28	5.63E+07	87378.6	5.17	P07395	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.
33	39	15	228.69	47	7.86E+07	34296.3	6.13	P00479	Aspartate carbamoyltransferase catalytic chain (EC
34	21	14	226.4	35	8.50E+07	50557.6	5.79	P00391	Dihydrolipoamide dehydrogenase (EC 1.8.1.4) (E3 co
35	18	15	226.35	38	1.21E+08	42042.8	5.68	P07023	T-protein [Includes: Chorismate mutase (EC 5.4.99.
36	23	14	225.76	22	1.01E+08	72202.1	5.43	P27302	Transketolase 1 (EC 2.2.1.1) (TK 1).
37	26	16	224.9	42	1.29E+08	50729.7	5.77	P14178	Pyruvate kinase I (EC 2.7.1.40) (PK-1).
38	30	15	224.68	59	1.86E+08	39046.5	5.54	P02917	Leu/Ile/Val-binding protein precursor (LIV-BP).
39	28	16	223.7	41	8.01E+07	43573.6	5.55	P00509	Aspartate aminotransferase (EC 2.6.1.1) (Transamin
40	23	15	220.27	36	6.94E+07	47004.5	6.75	P03002	Transcription termination factor rho.
41	32	14	219.56	53	9.62E+07	36511.9	4.98	P00574	DNA-directed RNA polymerase alpha chain (EC 2.7.7.
42	26	17	218.43	45	1.06E+08	35088.2	5.11	P30148	Transaldolase B (EC 2.2.1.2).
43	45	12	218.22	36	1.78E+08	40987.2	5.08	P11665	Phosphoglycerate kinase (EC 2.7.2.3).
44	19	14	214.02	26	5.91E+07	76124	5.56	P00959	Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionin
45	24	15	213.14	32	5.02E+07	63734	5.12	P16659	Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRN
46	32	15	212.51	43	7.91E+07	30292	5.22	P02997	Elongation factor Ts (EF-Ts).
47	37	13	209.39	39	9.49E+07	38804.2	5.42	P00888	Phospho-2-dehydro-3-deoxyheptonate aldolase, Tyr-s
48	24	12	207.23	39	1.18E+08	41392.9	5.37	P07460	Succinyl-CoA synthetase beta chain (EC 6.2.1.5) (S
49	32	13	206.41	42	9.37E+07	39652.3	5.37	P23721	Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT
50	29	14	204.37	47	1.07E+08	37200.9	5.99	P02934	Outer membrane protein A precursor (Outer membrane

51	17	13	201.96	22	7.53E+07	97234.3	5.16	P07813	Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA
52	24	14	201.33	33	6.28E+07	58679.5	5.24	P04079	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)
53	59	15	200.87	51	2.11E+08	35401.5	6.58	P06977	Glyceraldehyde 3-phosphate dehydrogenase A (EC 1.2
54	25	13	200.26	38	9.67E+07	48581.7	5.98	P00370	NADP-specific glutamate dehydrogenase (EC 1.4.1.4)
55	18	14	199.85	25	5.61E+07	71422.9	5.09	P10413	Chaperone protein htpG (Heat shock protein htpG) (
56	28	13	198.54	61	1.88E+08	32337.5	5.61	P06994	Malate dehydrogenase (EC 1.1.1.37).
57	34	14	195.43	35	2.13E+08	44044.8	5.93	P08328	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (
58	26	14	195.14	46	6.31E+07	38867.3	5.24	P23861	Spermidine/putrescine-binding periplasmic protein
59	16	10	193.67	33	9.01E+07	51884.4	5.54	P09832	Glutamate synthase [NADPH] small chain (EC 1.4.1.1
60	18	13	192.88	24	4.84E+07	73896.1	5.11	P17315	Colicin I receptor precursor.
61	20	11	190.45	48	1.40E+08	28724.3	5.32	P00928	Tryptophan synthase alpha chain (EC 4.2.1.20).
62	25	12	188.33	17	9.02E+07	89122.9	5.63	P00561	Bifunctional aspartokinase/homoserine dehydrogenas
63	28	12	186.97	23	4.96E+07	65965.2	5.09	P06959	Dihydrolipoamide acetyltransferase component of py
64	22	13	186.17	20	1.09E+08	85226.5	5.69	P09373	Formate acetyltransferase 1 (EC 2.3.1.54) (Pyruvat
65	28	12	184.51	44	2.24E+08	28425.3	5.86	P31217	2,3-bisphosphoglycerate-dependent phosphoglycerate
66	17	11	181.99	29	8.65E+07	52141.9	5.07	P25553	Aldehyde dehydrogenase A (EC 1.2.1.22) (Lactaldehy
67	23	12	180.26	27	4.94E+07	57494.8	5.32	P00895	Anthranilate synthase component I (EC 4.1.3.27).
68	24	11	179.26	35	1.26E+08	51772.9	5.27	P06711	Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammo
69	25	12	177.07	46	7.88E+07	26612.6	6.69	P02351	30S ribosomal protein S2.
70	14	11	176.97	17	1.10E+08	118183.2	5.48	P21513	Ribonuclease E (EC 3.1.4.-) (RNase E).
71	25	12	174.36	25	1.46E+08	60273.9	5.39	P08997	Malate synthase A (EC 4.1.3.2) (MSA).
72	19	12	174.33	17	3.71E+07	93498.6	5.24	P36683	Aconitate hydratase 2 (EC 4.2.1.3) (Citrate hydro-
73	18	13	173.99	19	6.36E+07	108192.9	5.2	P07118	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA l
74	17	11	173.14	60	1.14E+08	29431.8	5.13	P28635	D-methionine-binding lipoprotein metQ precursor.
75	16	11	172.3	30	6.34E+07	48532	5.02	P08660	Lysine-sensitive aspartokinase III (EC 2.7.2.4) (A
76	21	13	169.67	28	7.38E+07	60294	6.21	P23847	Periplasmic dipeptide transport protein precursor
77	14	11	169.56	26	1.03E+08	49767.5	5.23	P22767	Argininosuccinate synthase (EC 6.3.4.5) (Citrullin
78	27	12	165.21	60	2.83E+08	20630.3	5.03	P26427	Alkyl hydroperoxide reductase C22 protein (EC 1.6.
79	16	11	163.82	14	8.48E+07	96032.9	5.53	P00957	Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA
80	14	11	160.87	24	3.90E+07	82107.3	5.39	P05825	Ferrienterobactin receptor precursor (Enterobactin
81	16	11	159.82	33	5.31E+07	42931.9	5.49	P10377	Isochorismate synthase entC (EC 5.4.99.6) (Isochor
82	18	10	157.42	26	2.14E+08	45316.8	6.03	P00477	Serine hydroxymethyltransferase (EC 2.1.2.1) (Seri
83	27	10	155.59	50	2.94E+08	24762	5.91	P76344	Hypothetical protein yodA.
84	27	8	154.06	25	1.33E+08	39016.3	5.52	P11604	Fructose-bisphosphate aldolase class II (EC 4.1.2.
85	14	10	153.94	27	5.46E+07	40324.1	4.65	P06138	Cell division protein ftsZ.
86	15	10	153.64	18	5.29E+07	62312	5.43	P37797	ABC transporter ATP-binding protein yjjK.

87	14	10	153.14	29	9.64E+07	47114.1	5.24	P00934	Threonine synthase (EC 4.2.3.1).
88	31	11	151.97	43	1.13E+08	23338	10.05	P02354	30S ribosomal protein S4.
89	25	9	151.44	15	3.62E+07	61530.1	5.85	P11537	Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (
90	13	10	150.44	18	7.30E+07	87304.4	4.93	P23538	Phosphoenolpyruvate synthase (EC 2.7.9.2) (Pyruvat
91	24	10	149.88	57	1.20E+08	19888	10.37	P02359	30S ribosomal protein S7.
92	15	10	149.7	29	5.80E+07	41820.7	5.1	P04384	S-adenosylmethionine synthetase (EC 2.5.1.6) (Meth
93	16	9	149.03	26	9.83E+07	52022.7	6.02	P06981	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.2
94	14	11	146.4	16	5.52E+07	104166.2	5.66	P00956	Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine
95	13	10	144.07	17	4.54E+07	87438.6	6.01	P08177	ATP-dependent protease La (EC 3.4.21.53).
96	17	11	143.17	18	4.68E+07	65913.8	5.47	P21889	Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate-
97	14	10	139.74	36	1.04E+08	29039.3	6.22	P39174	Cystine-binding periplasmic protein precursor (CBP
98	12	9	139.36	17	6.85E+07	80024.2	5.14	P13029	Peroxidase/catalase HPI (EC 1.11.1.6) (Catalase-pe
99	29	8	139.02	37	6.41E+07	40018.1	5.37	P00353	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)
100	18	10	138.99	67	1.55E+08	15769.1	6.17	P02418	50S ribosomal protein L9.
101	13	9	138.04	15	3.66E+07	77013.2	5.23	P39184	Phosphate acetyltransferase (EC 2.3.1.8) (Phosphot
102	19	9	136.56	22	6.72E+07	43880.4	5.58	P07016	Dihydrolipoamide succinyltransferase component of
103	10	9	136.37	46	9.98E+07	17264	5.99	P00859	ATP synthase B chain (EC 3.6.3.14).
104	19	9	136	22	2.82E+07	57329.5	5.52	P15639	Bifunctional purine biosynthesis protein purH [Inc
105	20	9	135.97	63	1.55E+08	12968.3	10.78	P02369	30S ribosomal protein S13.
106	12	9	134.81	11	3.57E+07	102023.5	5.43	P10408	Preprotein translocase secA subunit.
107	30	9	134.53	48	9.40E+07	18772.7	9.71	P02390	50S ribosomal protein L6.
108	14	9	131.82	39	1.47E+08	26995.2	5.07	P21155	Phosphoribosylaminoimidazole-succinocarboxamide sy
109	11	9	131.3	23	4.35E+07	54871.2	4.53	P03003	N utilization substance protein A (nusA protein) (
110	16	9	129.08	24	7.24E+07	39386	5.14	P30125	3-isopropylmalate dehydrogenase (EC 1.1.1.85) (Bet
111	18	10	129.06	23	5.33E+07	57472.5	5.1	P13030	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA 1
112	13	8	128.67	14	8.85E+07	77101.4	5.11	P05055	Polyribonucleotide nucleotidyltransferase (EC 2.7.
113	12	8	127.91	55	5.94E+08	12164.1	4.6	P02392	50S ribosomal protein L7/L12 (L8).
114	12	10	127.2	17	3.74E+07	48414.3	5.34	P09156	Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA
115	14	9	126.55	47	7.73E+07	20170.5	9.49	P02389	50S ribosomal protein L5.
116	11	8	126.47	26	4.32E+07	35963.1	5.18	P39179	Unknown protein from 2D-page (Spot PR51).
117	21	9	126.31	41	6.46E+07	22243.6	9.9	P02386	50S ribosomal protein L3.
118	15	8	125.85	30	8.90E+07	29892.2	5.56	P03948	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-suc
119	10	9	125.25	26	5.01E+07	46225	5.24	P33138	ATP-dependent Clp protease ATP-binding subunit clp
120	14	8	125.12	21	4.48E+07	49419.5	5.61	P00909	Tryptophan biosynthesis protein trpCF [Includes: I
121	14	7	124.95	25	8.03E+07	42852.1	5.71	P00932	Tryptophan synthase beta chain (EC 4.2.1.20).
122	13	7	124.62	21	5.29E+07	41431.2	5.91	P00907	Carbamoyl-phosphate synthase small chain (EC 6.3.5

123	17	9	123.46	28	4.23E+07	43538	5.32	P04693	Aromatic-amino-acid aminotransferase (EC 2.6.1.57)
124	15	9	122.96	29	3.03E+07	39536.3	4.87	P31216	Probable GTP-binding protein ychF (ORF-3).
125	10	8	122.52	25	6.88E+07	49779	5.9	P30127	3-isopropylmalate dehydratase large subunit (EC 4.
126	16	8	121.34	18	7.10E+07	52439.5	5.17	P17242	Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparag
127	14	10	121.15	36	4.84E+07	34893.3	4.8	P17963	ADP-L-glycero-D-manno-heptose-6-epimerase (EC 5.1.
128	8	8	120.73	17	5.57E+07	51543.1	5.68	P25739	Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccin
129	13	7	119.05	34	5.73E+07	28882.1	8.39	P45523	FKBP-type peptidyl-prolyl cis-trans isomerase fkpA
130	9	8	119.01	26	6.50E+07	41137.8	4.98	P75902	Protein ycdO.
131	19	9	118.02	29	8.66E+07	29729.4	10.93	P02387	50S ribosomal protein L2.
132	11	7	117.44	40	8.95E+07	28483.5	5.47	P39182	Histidine-binding periplasmic protein precursor (H
133	11	8	117.24	51	3.74E+08	15408.5	5.43	P08936	DNA-binding protein H-NS (Histone-like protein HLP
134	14	8	116.49	24	2.38E+08	48063.3	6.21	P00891	Citrate synthase (EC 4.1.3.7).
135	8	7	116.4	14	6.00E+07	82417.9	5.34	P76558	NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME
136	8	7	115.79	11	8.28E+07	96964	5.09	P09097	DNA gyrase subunit A (EC 5.99.1.3).
137	13	7	115.49	22	2.39E+08	25852.2	10.27	P02352	30S ribosomal protein S3.
138	17	6	114.23	48	1.92E+08	17704.2	4.75	P37901	Thiol peroxidase (EC 1.11.1.-) (Scavengase P20).
139	19	8	113.81	46	1.62E+08	24598.6	9.64	P02384	50S ribosomal protein L1.
140	11	9	113.75	24	5.37E+07	47543.8	5.71	P31120	Protein mrsA.
141	11	8	113.43	9	4.88E+07	97350.4	5.8	P02995	Translation initiation factor IF-2.
142	16	8	113.15	34	5.62E+07	33366.9	5.47	P10366	ATP phosphoribosyltransferase (EC 2.4.2.17).
143	9	7	112.25	47	9.40E+07	19046.8	5.99	P77482	Protein yajQ.
144	9	7	111.97	44	6.86E+07	26892.6	5.07	P75743	Hypothetical protein ybgI.
145	7	7	111.7	16	4.36E+07	58361.2	5.43	P36938	Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomu
146	10	8	111.45	30	1.12E+08	33777.5	5.61	P39172	High-affinity zinc uptake system protein znuA prec
147	16	8	111.42	32	7.06E+07	30637	5.41	P18843	NH(3)-dependent NAD(+) synthetase (EC 6.3.5.1) (Ni
148	16	8	111.11	48	5.66E+07	22284.1	5.57	P10177	KHG/KDPG aldolase [Includes: 4-hydroxy-2-oxoglutar
149	9	8	109.18	20	5.92E+07	51226.3	6.24	P21599	Pyruvate kinase II (EC 2.7.1.40) (PK-2).
150	13	8	109.07	26	7.68E+07	36832	5.79	P08312	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1
151	10	6	108.14	44	1.58E+08	20564	9.54	P02999	Translation initiation factor IF-3.
152	11	7	107.99	29	9.04E+07	23586.1	5.55	P05082	Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosph
153	10	7	107.41	15	7.55E+07	59112.5	5.42	P10378	Enterobactin synthetase component E (Enterochelin
154	8	7	107.07	13	3.42E+07	84207.3	5.91	P15716	ATP-dependent clp protease ATP-binding subunit clp
155	9	7	106.89	15	2.44E+07	66149	4.92	P38038	Sulfite reductase [NADPH] flavoprotein alpha-compo
156	8	7	105.42	58	3.96E+07	16156.6	5.16	P25540	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.
157	16	8	105.15	20	9.97E+07	38613.1	9.22	P76116	Hypothetical protein yncE precursor.
158	23	7	105.03	57	1.30E+08	17472.3	10.11	P02356	30S ribosomal protein S5.

159	6	6	104.34	20	7.36E+07	50318.5	5.11	P11447	Argininosuccinate lyase (EC 4.3.2.1) (Argininosuccin
160	10	8	103.62	17	7.25E+07	62528.2	5.55	P22106	Asparagine synthetase B [glutamine-hydrolyzing] (E
161	14	6	102.32	53	1.98E+08	18120	4.73	P08837	PTS system, glucose-specific IIA component (EIIA-G
162	10	8	101.8	16	3.78E+07	55704.7	5.56	P22992	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
163	7	7	101.15	21	8.95E+07	45089.8	5.94	P39171	Cysteine desulfurase (EC 4.4.1.-) (ThiI transpersu
164	10	6	100.95	20	4.99E+07	46180.4	5.6	P37095	Peptidase B (EC 3.4.11.-) (Aminopeptidase B).
165	8	7	100.92	14	6.36E+07	89819.2	5.72	P06982	DNA gyrase subunit B (EC 5.99.1.3).
166	13	7	99.08	22	3.36E+07	30832.9	6.32	P17579	2-dehydro-3-deoxyphosphooctonate aldolase (EC 4.1.
167	14	6	98.93	35	1.03E+08	25560.4	6.76	P25716	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1
168	11	7	98.79	19	3.59E+07	45955.7	6.98	P19935	TolB protein precursor.
169	11	7	97.48	22	1.43E+08	22966	6.44	P00448	Superoxide dismutase [Mn] (EC 1.15.1.1) (MnSOD).
170	15	7	97.12	54	3.19E+08	17580.5	9.04	P02408	50S ribosomal protein L10 (L8).
171	7	7	96.49	36	9.59E+07	24350.3	7.72	P39811	Glutaredoxin 2 (Grx2).
172	8	7	94.54	14	3.71E+07	65446.7	5.1	P32132	GTP-binding protein typA/BipA (Tyrosine phosphoryl
173	9	7	93.78	27	1.00E+08	35395.7	5.5	P37666	2-ketogluconate reductase (EC 1.1.1.215) (2KR) (2-
174	8	7	93.46	28	4.31E+07	31791.2	4.5	P77395	Hypothetical protein ybbN.
175	11	6	92.36	28	6.11E+07	34087.3	5.23	P08330	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) (R
176	6	6	92.21	11	8.36E+07	72491.2	5.4	P30850	Exoribonuclease II (EC 3.1.13.1) (Ribonuclease II)
177	6	6	91.9	13	6.06E+07	77167.6	5.15	P27298	Oligopeptidase A (EC 3.4.24.70).
178	8	6	91.22	21	2.90E+07	47284	6.48	P21202	Survival protein surA precursor (Peptidyl-prolyl c
179	20	6	91.13	64	7.84E+07	9225.6	9.7	P02341	DNA-binding protein HU-beta (NS1) (HU-1).
180	9	6	90.45	14	7.93E+07	46096	5.37	P07638	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2
181	14	7	89.91	45	1.12E+08	16018.6	9.91	P02410	50S ribosomal protein L13.
182	10	8	89.17	22	4.22E+07	40278.2	5.76	P06987	Histidine biosynthesis bifunctional protein hisB [
183	9	6	88.88	28	4.11E+07	37842.4	5.09	P03017	RecA protein (Recombinase A).
184	7	6	88.83	26	8.36E+07	40839.9	5.84	P31133	Putrescine-binding periplasmic protein precursor.
185	7	6	87.6	62	5.86E+07	13002.4	6.13	P27827	Protein yifE.
186	10	6	87.34	25	5.92E+07	11185.1	10.21	P02425	50S ribosomal protein L24.
187	10	6	86.99	24	3.58E+07	36952.6	5.19	P13519	Rod shape-determining protein mreB.
188	16	6	86.67	50	8.77E+07	12226.4	10.23	P02423	50S ribosomal protein L22.
189	19	5	86.58	45	5.25E+07	15332.3	5.55	P24233	Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (
190	7	6	86.48	17	5.86E+07	42302.7	5.48	P33221	Phosphoribosylglycinamide formyltransferase 2 (EC
191	7	6	85.88	27	1.55E+08	32554.5	5.05	P15048	Isochorismatase (EC 3.3.2.1) (Isochorismate lyase)
192	10	6	85.3	33	1.46E+08	19572.5	5.03	P17288	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosph
193	7	6	85.08	15	6.50E+07	56177.4	5.47	P35340	Alkyl hydroperoxide reductase subunit F (EC 1.6.4.
194	12	5	84.94	63	4.01E+08	9535	9.57	P02342	DNA-binding protein HU-alpha (NS2) (HU-2).

195	10	6	84.39	18	4.97E+07	45366.4	4.73	P23893	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3
196	6	6	83.51	31	5.49E+07	27159.7	5.38	P11445	Acetylglutamate kinase (EC 2.7.2.8) (NAG kinase) (
197	9	5	83.22	22	5.79E+07	35110.5	5.76	P30867	Acetyl-coenzyme A carboxylase carboxyl transferase
198	10	5	83.14	57	5.39E+07	9190.6	10.54	P02372	30S ribosomal protein S16.
199	13	5	82.88	59	8.21E+07	11675.5	4.68	P00274	Thioredoxin 1 (TRX1) (TRX).
200	6	6	82.49	10	4.65E+07	74014.7	5.8	P00955	Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--
201	18	6	82.21	18	4.46E+07	38696.4	5.77	P05020	Dihydroorotase (EC 3.5.2.3) (DHOase).
202	11	6	80.74	13	3.46E+07	49321	6.65	P24182	Biotin carboxylase (EC 6.3.4.14) (A subunit of ace
203	8	6	80.7	34	2.13E+08	27732.9	5.58	P29132	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC
204	5	5	79.98	9	6.90E+07	66763.5	5.56	P17169	Glucosamine--fructose-6-phosphate aminotransferase
205	5	5	79.98	22	7.47E+07	32666.3	5.89	P39173	Unknown protein from 2D-page (Spots T26/PR37).
206	7	6	79.85	22	7.50E+07	31577.6	8.84	P00837	ATP synthase gamma chain (EC 3.6.3.14).
207	11	6	79.19	45	5.16E+07	16989.5	6.83	P00478	Aspartate carbamoyltransferase regulatory chain.
208	14	5	78.66	28	1.86E+07	11035.2	7.2	P25521	Hfq protein (Host factor-I protein) (HF-I) (HF-1).
209	8	6	77.97	32	7.16E+07	27292.2	5.21	P03026	Aerobic respiration control protein arcA (Dye resi
210	8	5	77.74	16	6.87E+07	48566.7	5.78	P00584	Glucose-1-phosphate adenyltransferase (EC 2.7.7.
211	9	6	77.26	43	9.32E+07	18755.7	8.91	P19494	Leucine-responsive regulatory protein.
212	8	6	77.07	24	7.09E+07	33623.9	5.45	P00547	Homoserine kinase (EC 2.7.1.39) (HK).
213	12	5	76.93	41	1.21E+08	9553.2	11.18	P02378	30S ribosomal protein S20.
214	14	5	76.65	45	9.41E+07	15703.6	4.93	P02358	30S ribosomal protein S6.
215	7	6	75.71	16	4.72E+07	41250.9	4.64	P07012	Peptide chain release factor 2 (RF-2).
216	6	5	75.54	18	4.19E+07	42850.2	5.29	P00946	Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosph
217	5	5	75.42	13	8.67E+07	70708.5	5.91	P28691	Cell division protein ftsH (EC 3.4.24.-).
218	8	5	74.02	26	5.18E+07	25096.9	6.16	P36857	Protein yadF.
219	7	5	73.97	8	2.85E+07	100168.6	5.85	P33602	NADH dehydrogenase I chain G (EC 1.6.5.3) (NADH-ub
220	13	5	73.18	24	4.43E+07	23640.6	8.38	P03020	Catabolite gene activator (cAMP receptor protein)
221	5	5	72.85	20	4.96E+07	35561.1	5.11	P04425	Glutathione synthetase (EC 6.3.2.3) (Glutathione s
222	5	5	72.76	30	5.24E+07	27734	5.5	P00882	Deoxyribose-phosphate aldolase (EC 4.1.2.4) (Phosp
223	10	6	72.59	51	1.56E+08	11735.6	9.68	P02364	30S ribosomal protein S10.
224	8	5	72.48	26	8.79E+07	18153.6	5.51	P23869	Peptidyl-prolyl cis-trans isomerase B (EC 5.2.1.8)
225	5	4	72.4	14	6.11E+07	44370.2	5.11	P07651	Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribom
226	13	5	72	27	9.72E+07	22086.6	9.72	P02388	50S ribosomal protein L4.
227	9	5	71.91	24	4.09E+07	26972	5.64	P04790	Triosephosphate isomerase (EC 5.3.1.1) (TIM).
228	12	5	71.84	37	6.55E+07	13713.8	11.33	P02366	30S ribosomal protein S11.
229	7	5	71.8	16	4.75E+07	41550.6	6.01	P00935	Cystathionine gamma-synthase (EC 4.2.99.9) (CGS) (
230	10	5	71.54	30	4.90E+07	24699.6	6.93	P27511	GTP cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I).

231	6	5	71	12	4.22E+07	68150.2	4.94	P77241	Peptidyl-prolyl cis-trans isomerase D (EC 5.2.1.8)
232	7	5	70.86	29	1.35E+08	22533.4	5.32	P25532	Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP
233	5	4	70.84	43	1.04E+08	14957	5.57	P23929	Osmotically inducible protein C.
234	9	4	70.26	27	1.02E+08	18534	5.73	P30746	Molybdenum cofactor biosynthesis protein B.
235	5	5	70.01	13	5.75E+07	52202.4	5.33	P21888	Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine-
236	8	5	69.76	24	3.17E+07	32811.3	5.11	P25520	UTP--glucose-1-phosphate uridylyltransferase (EC 2
237	8	6	69.39	46	4.27E+07	17641	4.71	P21346	Transcription elongation factor greA (Transcript c
238	7	5	69.39	57	6.66E+07	14905.9	9.5	P76002	Protein ycgK precursor.
239	6	5	69.32	23	9.20E+07	22860.5	5.2	P27252	Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosp
240	5	5	68.55	17	8.87E+07	33420.3	8.61	P37902	Glutamate/aspartate periplasmic binding protein pr
241	8	6	68.2	55	5.18E+07	14284.3	5.09	P33633	Protein yfiD.
242	6	4	67.98	29	8.53E+07	20059.1	6.32	P24250	Protein ydjA.
243	7	4	67.8	36	1.32E+08	17634	5.03	P23480	Bacterioferritin comigratory protein.
244	5	4	67.66	12	8.15E+07	47396	5.59	P00951	Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosine--tR
245	6	5	67.65	14	6.14E+07	39333.5	4.76	P02931	Outer membrane protein F precursor (Porin ompF) (O
246	4	4	67.57	8	1.38E+08	37497.1	6.47	P00954	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptop
247	5	5	67.05	16	5.16E+07	45766.3	6.2	P18133	Nicotinate phosphoribosyltransferase (EC 2.4.2.11)
248	6	5	66.89	22	6.45E+07	33903.4	9.27	P76177	Protein ydgH precursor.
249	6	5	66.79	12	3.86E+07	53816	5.6	P04805	Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate-
250	7	5	66.76	13	6.06E+07	56739.1	6.05	P00904	Anthranilate synthase component II (EC 4.1.3.27) [
251	6	5	66.25	11	5.75E+07	60243.3	5.63	P08398	CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (C
252	6	6	66.01	17	5.98E+07	36687.5	5.3	P16456	Selenide,water dikinase (EC 2.7.9.3) (Selenophosph
253	8	6	65.99	8	1.82E+07	98788.3	5.14	P04825	Aminopeptidase N (EC 3.4.11.2) (Alpha-aminoacylpep
254	7	4	65.93	17	8.22E+07	29483	5.25	P18197	Septum site-determining protein minD (Cell divisio
255	5	5	65.88	8	4.29E+07	92109.7	8.78	P21499	Ribonuclease R (EC 3.1.-.-) (RNase R) (VacB protei
256	9	5	65.65	13	1.86E+07	50176.4	5.6	P21165	Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptida
257	10	4	64.99	44	9.39E+07	8368.8	11.15	P02379	30S ribosomal protein S21.
258	6	4	64.94	13	6.53E+07	29646.4	6.31	P07459	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5) (
259	5	5	64.81	24	2.86E+07	37650.1	6.3	P25661	HflC protein (EC 3.4.-.-).
260	5	5	64.77	25	3.85E+07	27844.8	5.51	P17854	Phosphoadenosine phosphosulfate reductase (EC 1.8.
261	4	4	64.22	6	3.62E+07	85775.7	5.79	P00452	Ribonucleoside-diphosphate reductase 1 alpha chain
262	5	4	63.78	12	1.08E+08	52784.5	5.2	P15288	Aminoacyl-histidine dipeptidase (EC 3.4.13.3) (Xaa
263	4	4	63.76	33	8.29E+07	15096.2	6.61	P37048	Hypothetical protein yaeH.
264	5	4	63.74	21	5.55E+07	26249.8	4.97	P15047	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (E
265	9	4	63.65	34	9.68E+07	14980.5	11.19	P02413	50S ribosomal protein L15.
266	7	4	63.51	26	3.93E+07	24173.8	5.22	P05838	Stringent starvation protein A.

267	5	5	63.4	13	7.25E+07	43111.6	6.21	P07022	P-protein [Includes: Chorismate mutase (EC 5.4.99.
268	7	4	63.02	27	3.23E+07	23713.3	5.05	P75805	Hypothetical GST-like protein yliJ.
269	7	4	62.92	20	3.39E+07	33515.3	5.08	P24249	3-oxoacyl-[acyl-carrier-protein] synthase III (EC
270	6	4	62.15	38	5.33E+07	10693.5	9.6	P02426	50S ribosomal protein L25.
271	4	4	61.43	12	5.39E+07	49292.7	6.44	P31979	NADH dehydrogenase I chain F (EC 1.6.5.3) (NADH-ub
272	5	4	60.49	15	6.18E+07	38043.9	6.3	P15039	Purine nucleotide synthesis repressor.
273	4	4	60.45	25	1.22E+08	20638.7	6.44	P16174	Ribosome recycling factor (Ribosome releasing fact
274	7	4	60.39	33	1.12E+08	13848.7	4.82	P77310	NifU-like protein.
275	7	5	59.51	12	3.08E+07	72094	5.5	P27550	Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate
276	4	4	59.49	20	5.77E+07	33557.2	5.14	P16936	Agmatinase (EC 3.5.3.11) (Agmatine ureohydrolase)
277	7	4	59.41	25	2.92E+07	25535.3	5.1	P23836	Transcriptional regulatory protein phoP.
278	4	4	59.36	10	3.56E+07	49684.5	5.25	P15034	Xaa-Pro aminopeptidase (EC 3.4.11.9) (X-Pro aminop
279	4	3	59.03	18	1.98E+08	27190.2	8.44	P10344	Glutamine-binding periplasmic protein precursor (G
280	6	5	58.77	4	2.58E+07	135965.7	4.98	P13009	5-methyltetrahydrofolate--homocysteine methyltrans
281	8	4	58.62	22	5.96E+07	32286.2	4.95	P25715	Malonyl CoA-acyl carrier protein transacylase (EC
282	6	4	58.47	19	8.89E+07	32829.4	5.73	P78083	UTP--glucose-1-phosphate uridylyltransferase (EC 2
283	6	5	58.32	17	5.03E+07	37614.7	7.78	P16700	Thiosulfate-binding protein precursor.
284	4	4	58.18	10	4.35E+07	45545.1	6.19	P25662	HflK protein.
285	5	4	58.16	23	5.21E+07	23445	5.64	P29015	Riboflavin synthase alpha chain (EC 2.5.1.9).
286	4	4	58.1	12	4.35E+07	42196.9	7.69	P31223	Acriflavine resistance protein A precursor.
287	4	4	57.15	6	3.05E+07	103118.6	5.39	P00582	DNA polymerase I (EC 2.7.7.7) (POL I).
288	7	4	57.11	27	8.20E+07	20997.8	4.52	P46847	Protein yhgI.
289	4	4	57.09	9	9.27E+07	73984	4.86	P21170	Biosynthetic arginine decarboxylase (EC 4.1.1.19)
290	9	4	56.94	40	1.09E+08	15347.6	7.95	P30017	DNA-binding protein stpA (H-NS homolog stpA).
291	6	5	56.8	17	6.04E+07	35048.8	6.38	P30177	Hypothetical protein ybiB.
292	5	4	56.63	21	6.49E+07	33325.5	5.99	P75789	Protein ybiS precursor.
293	11	4	56.61	52	9.25E+07	10387	5.15	P05380	10 kDa chaperonin (Protein Cpn10) (groES protein).
294	6	4	56.25	57	8.78E+07	6240.4	10.25	P02436	50S ribosomal protein L33.
295	6	5	56.25	21	5.47E+07	31597.9	5.92	P31663	Pantoate--beta-alanine ligase (EC 6.3.2.1) (Pantot
296	4	4	56.07	8	5.63E+07	60824.3	5.47	P07024	Protein ushA precursor [Includes: UDP-sugar hydrol
297	5	3	55.94	10	7.29E+07	45940.6	4.96	P15640	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)
298	5	5	55.74	18	5.04E+07	32693.7	5.39	P37744	Glucose-1-phosphate thymidyltransferase (EC 2.7.
299	4	4	55.62	20	7.26E+07	28231.5	8.58	P45955	Hypothetical protein ybgF precursor.
300	6	4	55.56	9	3.13E+07	54623.7	5.65	P07001	NAD(P) transhydrogenase subunit alpha (EC 1.6.1.2)
301	4	4	55.45	20	4.51E+07	36776.1	5.46	P04391	Ornithine carbamoyltransferase chain I (EC 2.1.3.3
302	13	3	55.3	16	1.19E+08	13605.9	10.88	P02367	30S ribosomal protein S12.

303	6	4	55.25	25	3.26E+07	23670.7	6.85	P14374	Capsular synthesis regulator component B.
304	6	4	55.23	13	1.66E+07	36494.9	5.81	P75823	Low-specificity L-threonine aldolase (EC 4.1.2.5)
305	8	3	55.09	49	9.49E+07	7273.5	9.98	P02429	50S ribosomal protein L29.
306	4	4	54.67	11	4.07E+07	46898.5	5.65	P04804	Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine-
307	8	4	54.17	17	7.67E+07	31270.2	5.98	P05640	Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPS)
308	3	3	54.08	26	5.35E+07	13950.9	6.58	P80449	D-erythro-7,8-dihydroneopterin triphosphate epimer
309	5	4	53.87	14	5.29E+07	40654.7	6.24	P77349	PhoH-like protein.
310	5	4	53.65	4	2.86E+07	170231	5.24	P22523	Cell division protein mukB.
311	4	4	53.23	8	3.92E+07	85120.3	5.92	P46837	Protein yhgF.
312	6	4	53.07	19	4.00E+07	38897.4	5.96	P30178	Hypothetical oxidoreductase ybiC (EC 1.1.1.-).
313	7	3	52.81	32	2.61E+07	15281.3	11.23	P02414	50S ribosomal protein L16.
314	5	4	52.46	12	1.51E+07	47009	6.47	P04335	Hypothetical protein yafA.
315	3	3	52.46	10	3.06E+07	55361.1	5.58	Q46829	6-phospho-beta-glucosidase bglA (EC 3.2.1.86).
316	7	3	52.36	8	2.31E+07	49594.1	5.24	P32168	ATP-dependent hsl protease ATP-binding subunit hsl
317	5	3	52.3	9	6.96E+07	45978.4	5.19	P06988	Histidinol dehydrogenase (EC 1.1.1.23) (HDH).
318	4	3	52.26	11	3.56E+07	44630.3	5.42	P07004	Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1
319	4	4	52.24	65	1.15E+08	9006.4	6.95	P37687	Glutaredoxin 3 (Grx3).
320	3	3	51.77	18	3.11E+07	29172.3	6.45	P22783	Inositol-1-monophosphatase (EC 3.1.3.25) (IMPase)
321	5	4	51.01	25	1.20E+08	19285.1	5.18	P45578	Autoinducer-2 production protein luxS (EC 3.13.1.-
322	5	4	50.26	10	3.31E+07	63843.3	7.26	P17846	Sulfite reductase [NADPH] hemoprotein beta-compone
323	6	4	50.23	13	9.02E+07	57912.8	6.7	P33136	Periplasmic glucans biosynthesis protein mdoG prec
324	4	3	50.2	18	9.23E+07	20531.6	6.34	P16921	Transcription antitermination protein nusG.
325	4	3	50.2	6	3.84E+07	64683.3	5.32	P11875	Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--t
326	3	3	50.1	6	1.05E+08	66570.6	5.4	P07682	GTP-binding protein lepA.
327	6	3	50.09	5	3.47E+07	62984.7	5.88	P00893	Acetolactate synthase isozyme III large subunit (E
328	5	4	49.96	7	2.89E+07	70263.7	4.69	P00579	RNA polymerase sigma factor rpoD (Sigma-70).
329	7	4	49.84	10	3.99E+07	49354.5	8.65	P09376	Protease do precursor (EC 3.4.21.-).
330	12	3	49.7	57	1.14E+08	7271.2	6.82	P36996	Cold shock-like protein cspC (CSP-C).
331	5	4	49.66	7	2.49E+07	64422.2	5.85	P10444	Succinate dehydrogenase flavoprotein subunit (EC 1
332	3	3	49.59	9	3.03E+07	51580.1	4.61	P37349	Hypothetical protein ycgC.
333	5	4	49.56	15	7.68E+07	25818.9	5.42	P09743	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inos
334	4	4	49.54	32	2.21E+08	17688.3	9.69	P11457	Histone-like protein HLP-1 precursor (DNA-binding
335	6	4	49.34	13	4.24E+07	27582.5	4.84	P77499	Probable ATP-dependent transporter sufC.
336	7	4	49.32	43	6.05E+07	8855.3	10.59	P02374	30S ribosomal protein S18.
337	7	4	48.99	27	3.71E+07	20469.7	4.81	P06610	Vitamin B12 transport periplasmic protein btuE.
338	6	4	48.82	19	5.21E+07	32391.8	6.21	Q46845	Hypothetical GST-like protein yghU.

339	7	3	48.31	16	2.94E+07	21134.7	5.58	P09157	Superoxide dismutase [Fe] (EC 1.15.1.1).
340	4	4	48.27	11	4.59E+07	50972.2	6.05	P37350	Hypothetical protein ygdH.
341	4	3	48.03	12	5.79E+07	30680.8	4.56	P31142	3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2)
342	12	3	47.71	33	1.38E+08	8508.4	3.97	P02901	Acyl carrier protein (ACP) (Cytosolic activating f
343	5	4	47.64	11	2.98E+07	51050.9	5.29	P76658	ADP-heptose synthase (EC 2.7.-.-).
344	14	4	47.6	28	9.60E+07	14744.3	9.64	P02409	50S ribosomal protein L11.
345	5	4	47.42	13	4.86E+07	35562.5	5.76	P09169	Protease VII precursor (EC 3.4.21.87) (OmpT) (Ou
346	3	3	47.2	14	1.48E+07	33852	5.31	P06983	Porphobilinogen deaminase (EC 4.3.1.8) (PBG) (Hydr
347	3	3	47.07	15	5.87E+07	26253.3	5.62	P24223	Pyridoxal phosphate biosynthetic protein pdxJ (PNP
348	4	4	47	6	2.09E+07	77385	5.49	P24171	Peptidyl-dipeptidase dcp (EC 3.4.15.5) (Dipeptidyl
349	3	3	46.98	7	3.21E+07	60440.9	5.3	P08142	Acetolactate synthase isozyme I large subunit (EC
350	7	3	46.83	12	5.05E+07	33962.6	5.54	P00510	Branched-chain amino acid aminotransferase (EC 2.6
351	4	3	46.79	9	4.05E+07	29331	5.64	P07906	Methionine aminopeptidase (EC 3.4.11.18) (MAP) (Pe
352	5	3	46.76	23	1.60E+08	14725.1	10.94	P02363	30S ribosomal protein S9.
353	3	3	46.22	28	8.83E+07	12878.8	4.75	P37010	Protein ydhD.
354	3	3	46.19	10	7.43E+07	43290.7	5.85	P15046	Acetate kinase (EC 2.7.2.1) (Acetokinase).
355	3	3	46.13	11	4.17E+07	40902.2	5.14	P40874	N-methyl-L-tryptophan oxidase (EC 1.5.3.-) (MTOX).
356	3	3	46.07	12	1.05E+08	33322.1	7.58	P08193	Acetyl-coenzyme A carboxylase carboxyl transferase
357	3	3	45.84	29	1.13E+08	15239.3	5.65	P39436	Hypothetical protein yhcB.
358	3	3	45.71	15	7.54E+07	23905.3	5.8	P38489	Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.
359	3	3	45.54	10	2.61E+07	43387.9	5.54	P02928	Maltose-binding periplasmic protein precursor (Mal
360	3	3	45.34	11	3.47E+07	47227.7	8.96	P00393	NADH dehydrogenase (EC 1.6.99.3).
361	4	3	44.94	20	2.91E+07	19859	5.26	P07672	Adenine phosphoribosyltransferase (EC 2.4.2.7) (AP
362	4	4	44.85	33	1.13E+07	20375.7	5	P31465	Hypothetical protein yieF.
363	4	3	44.47	18	1.26E+08	22085.1	4.85	P39311	FKBP-type 22 kDa peptidyl-prolyl cis-trans isomera
364	4	3	44.29	12	1.42E+07	36443.4	4.67	P37146	Ribonucleoside-diphosphate reductase 2 beta chain
365	3	3	44.27	14	2.23E+07	26032.8	4.94	P10371	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)met
366	5	4	44.15	8	5.46E+07	34842.3	5.47	P06998	6-phosphofructokinase isozyme I (EC 2.7.1.11) (Pho
367	4	3	43.58	21	4.94E+07	20724.5	4.21	P75915	Hypothetical protein ycdY.
368	9	3	43.49	29	1.13E+08	13541.1	10.43	P02411	50S ribosomal protein L14.
369	4	3	43.44	16	1.91E+07	44067.5	5.03	P12281	Molybdopterin biosynthesis protein moeA.
370	4	3	43.33	15	6.56E+07	26287.5	7.89	P18783	Biopolymer transport exbB protein.
371	3	3	43.19	4	1.96E+07	53987.5	5.44	P42607	Uronate isomerase (EC 5.3.1.12) (Glucuronate isome
372	3	3	42.99	10	7.88E+07	39360.3	5.01	P06986	Histidinol-phosphate aminotransferase (EC 2.6.1.9)
373	3	3	42.82	24	4.21E+07	6547.7	8.96	P77695	GnsB protein.
374	5	4	42.61	13	2.34E+07	44434	5.89	P77444	Selenocysteine lyase (EC 4.4.1.16) (Selenocysteine

375	3	3	42.59	15	6.04E+07	36307.8	5.06	P52697	Hypothetical protein ybhE.
376	6	3	42.58	47	1.11E+08	7332.3	8.06	P36997	Cold shock-like protein cspE (CSP-E).
377	3	3	42.06	10	6.79E+07	43212.6	6.01	P06721	Cystathionine beta-lyase (EC 4.4.1.8) (CBL) (Beta-
378	6	3	42.03	27	6.01E+07	17277.5	4.27	P15040	Protein-export protein secB.
379	4	3	41.91	16	4.34E+07	30029.5	5.43	P76268	Transcriptional regulator kdgR.
380	3	3	41.81	15	5.82E+07	37784.6	8.94	P33635	Hypothetical tRNA/rRNA methyltransferase yfiF (EC
381	4	3	41.58	12	1.54E+08	37978.2	6.24	P71295	Fructose-bisphosphate aldolase class I (EC 4.1.2.1
382	6	3	41.52	8	7.25E+07	42613.6	5.35	P14926	3-oxoacyl-[acyl-carrier-protein] synthase I (EC 2.
383	4	3	41.47	10	2.31E+07	44817.9	5.81	P28909	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
384	4	3	41.41	26	1.02E+08	11287.9	5.09	P77225	Protein ydhR precursor.
385	14	3	41.07	20	1.02E+08	10299.1	10.53	P02375	30S ribosomal protein S19.
386	3	3	40.71	22	2.13E+07	15596.3	9.37	P37688	Hypothetical protein yibN.
387	3	3	40.44	10	3.70E+07	30812.1	5.87	P37192	Tagatose-bisphosphate aldolase gatY (EC 4.1.2.-).
388	5	3	40.16	10	3.52E+07	42579.1	4.69	P27431	Hypothetical protein ycfD.
389	6	2	40.05	5	2.42E+07	56194.2	5.14	P37689	2,3-bisphosphoglycerate-independent phosphoglycera
390	3	3	39.67	11	1.05E+08	38721.3	6.42	P00887	Phospho-2-dehydro-3-deoxyheptonate aldolase, Trp-s
391	4	3	39.21	21	3.38E+07	24554.4	5.13	P32661	Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Pento
392	2	2	39.17	13	1.53E+08	18843.9	5.45	P02339	Single-strand binding protein (SSB) (Helix-destabi
393	5	3	39.12	21	6.07E+07	13365.8	11.47	P02421	50S ribosomal protein L20.
394	4	3	38.76	15	3.61E+07	29721.3	5.11	P09997	Hypothetical protein yidA.
395	9	3	38.52	53	8.78E+07	9634.9	4.69	P32164	Hypothetical protein yiiU.
396	3	3	38.47	5	2.91E+07	81960.4	5.55	P75780	Probable tonB-dependent receptor ybiL precursor.
397	3	3	38.08	11	1.19E+07	36834.1	5.67	P09200	Fructose-1,6-bisphosphatase (EC 3.1.3.11) (D-fruct
398	3	3	38.05	11	1.89E+07	29436.9	5.49	P30863	2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.-
399	5	2	37.91	15	7.48E+07	20814.9	5.97	P51001	Phosphoheptose isomerase (EC 5.-.-.-).
400	3	3	37.3	18	3.00E+07	26770.1	6.31	P07014	Succinate dehydrogenase iron-sulfur protein (EC 1.
401	2	2	37.27	14	6.35E+07	17649.2	6.03	P09028	Phosphoribosylaminoimidazole carboxylase catalytic
402	2	2	37.23	4	3.45E+07	70401.3	8.76	P23304	Cold-shock DEAD-box protein A (ATP-dependent RNA h
403	4	3	37.03	7	2.39E+07	54846.1	6.76	P30848	Proline/betaine transporter (Proline porter II) (P
404	4	3	36.95	11	6.42E+07	29423.7	5.77	P04846	Lipoprotein-28 precursor.
405	3	2	36.94	10	2.74E+07	28454.6	5.04	P10373	Imidazole glycerol phosphate synthase subunit hisF
406	3	3	36.94	4	2.25E+07	93173	5.57	P13031	Glycogen phosphorylase (EC 2.4.1.1).
407	3	2	36.57	16	1.95E+08	19605.8	4.21	P23243	Flavodoxin 1.
408	6	2	36.53	40	3.62E+07	5095.8	11.04	P28690	30S ribosomal protein S22 (Stationary-phase-induce
409	5	3	36.2	12	2.19E+07	28073.4	7.77	P27851	Ubiquinone/menaquinone biosynthesis methyltransfer
410	2	2	36.15	25	9.70E+07	13241.4	5.73	P36950	HIT-like protein ycfF.

411	2	2	36.12	6	2.29E+07	43438.4	7.06	P24285 DNA/pantothenate metabolism flavoprotein.
412	12	3	35.62	14	6.90E+07	14364.7	11.05	P02416 50S ribosomal protein L17.
413	2	2	35.59	13	3.76E+07	26929.7	5.79	P30859 Arginine-binding periplasmic protein 1 precursor.
414	2	2	35.45	8	4.69E+07	51429.5	6.09	P27306 Soluble pyridine nucleotide transhydrogenase (EC 1
415	3	3	35.4	18	1.20E+08	19536.3	6.07	P76492 Protein yfbU.
416	3	3	35.33	9	2.01E+07	45517.6	5.85	P77727 Probable aminotransferase yfbQ (EC 2.6.1.-).
417	2	2	35.21	12	4.89E+07	36723.1	4.83	P08178 Phosphoribosylformylglycinamide cyclo-ligase (EC
418	8	4	35.13	23	1.36E+08	10137.6	10.4	P02371 30S ribosomal protein S15.
419	3	3	35.11	11	5.00E+07	37691.5	4.88	P33920 37 kDa nucleoid-associated protein.
420	4	3	35.09	8	3.51E+07	40683.8	5.87	P27433 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate syn
421	5	3	35.08	17	2.16E+07	19406.9	5.26	P24167 Shikimate kinase I (EC 2.7.1.71) (SKI).
422	4	3	34.98	9	6.22E+07	36535	5.29	P52643 D-lactate dehydrogenase (EC 1.1.1.28) (D-LDH) (Fer
423	3	3	34.07	13	3.79E+07	32534.7	4.35	P45803 33 kDa chaperonin (Heat shock protein 33) (HSP33).
424	3	3	34.05	8	1.13E+08	42966.1	6.61	P37747 UDP-galactopyranose mutase (EC 5.4.99.9).
425	3	2	33.92	14	3.08E+08	21798	4.68	P09372 GrpE protein (HSP-70 cofactor) (Heat shock protein
426	3	2	33.61	7	2.80E+07	52390.3	4.95	P03005 Replicative DNA helicase (EC 3.6.1.-).
427	4	2	33.57	9	3.27E+07	39495	4.93	P76015 Hypothetical protein ycgT.
428	10	3	33.56	27	3.77E+07	11564.4	9.84	P02422 50S ribosomal protein L21.
429	3	3	33.46	16	2.29E+07	20122.2	5.63	P76495 Hypothetical protein yfcE.
430	8	3	33.42	23	6.84E+07	12769.7	10.42	P02419 50S ribosomal protein L18.
431	3	3	33.17	10	1.50E+07	40586.8	5.25	P00583 DNA polymerase III, beta chain (EC 2.7.7.7).
432	2	2	33.12	32	7.77E+07	8820.8	4.43	P22938 Exodeoxyribonuclease VII small subunit (EC 3.1.11.
433	2	2	32.73	23	1.33E+07	13386.3	6.29	P76243 Hypothetical protein yeaO.
434	4	2	32.64	20	4.57E+07	12199.7	4.49	P25528 Ferredoxin, 2Fe-2S.
435	3	2	32.58	34	5.31E+07	6410.6	10.96	P02430 50S ribosomal protein L30.
436	4	3	32.44	14	4.50E+07	22981.7	4.67	P26428 Enhancing lycopene biosynthesis protein 2 (Sigma c
437	2	2	32.27	8	7.04E+07	40969.4	8.03	P08622 Chaperone protein dnaJ (Heat shock protein J) (HSP
438	3	2	32.25	15	5.46E+07	46177.5	5.63	P00861 Diaminopimelate decarboxylase (EC 4.1.1.20) (DAP d
439	3	2	32.24	5	9.80E+07	64270.9	5.2	P26616 NAD-dependent malic enzyme (EC 1.1.1.38) (NAD-ME).
440	3	3	32.08	7	4.41E+07	63347	5.89	P00962 Glutaminyl-tRNA synthetase (EC 6.1.1.18) (Glutamin
441	2	2	32.08	23	2.24E+08	8875.3	11.42	P02428 50S ribosomal protein L28.
442	4	2	32	18	1.25E+07	15473.2	5.57	P11555 Fucose operon fucU protein.
443	3	2	31.94	8	6.84E+07	34723.3	6.06	P46880 Glucokinase (EC 2.7.1.2) (Glucose kinase).
444	3	3	31.66	15	1.69E+07	42963.2	4.67	P09127 Putative uroporphyrin-III C-methyltransferase (EC
445	2	2	31.64	12	6.39E+07	25892.6	9.66	P45577 ProP effector.
446	3	2	31.52	13	4.62E+07	16594.4	7.03	P55740 Transcriptional regulator slyA.

447	2	2	31.49	8	4.97E+07	28871.7	5.53	Q46871 Hypothetical protein yqjH.
448	4	2	31.36	6	2.64E+07	47460	5.72	P25524 Cytosine deaminase (EC 3.5.4.1) (Cytosine aminohyd
449	3	3	31.35	21	1.66E+07	18564.2	5.72	P27430 DNA protection during starvation protein.
450	6	3	31.23	24	4.88E+07	13002.1	10.62	P02420 50S ribosomal protein L19.
451	4	2	31.09	6	2.26E+07	34774.6	4.89	P00960 Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14) (
452	2	2	31.04	31	3.14E+07	10235	5.15	P18198 Cell division topological specificity factor.
453	2	2	31.01	10	6.36E+07	25867.2	4.71	P76351 Hypothetical protein yeeN.
454	3	3	30.94	11	6.28E+07	40558.5	5.47	P37759 dTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
455	2	2	30.9	14	2.57E+07	19315	4.45	P14189 Hypothetical protein yceD (G30K).
456	3	2	30.85	17	6.63E+07	17527.9	5.06	P18274 DnaK suppressor protein.
457	3	2	30.7	11	6.66E+07	20563.6	5.82	P24201 Transcriptional repressor mprA (EmrR protein).
458	2	2	30.38	8	7.57E+07	21229.7	4.19	P25533 Hypothetical protein ygfB.
459	3	2	30.34	9	4.89E+07	26778.7	5.21	P25529 7-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159
460	2	2	30.25	5	5.62E+07	46697.5	5.65	P09053 Valine--pyruvate aminotransferase (EC 2.6.1.66) (T
461	5	3	30.18	31	3.73E+07	10273	5.18	P32126 Protein yihD.
462	3	3	30.13	8	5.07E+06	43778.1	5.69	P30010 Cyclopropane-fatty-acyl-phospholipid synthase (EC
463	2	2	29.98	11	1.08E+08	33102.9	6	P00394 5,10-methylenetetrahydrofolate reductase (EC 1.7.9
464	3	3	29.96	4	2.88E+07	76663.5	6.19	P23865 Tail-specific protease precursor (EC 3.4.21.102) (
465	4	2	29.72	12	7.36E+06	23592.8	6.07	P24234 Guanylate kinase (EC 2.7.4.8) (GMP kinase).
466	2	2	29.52	7	1.96E+07	33471.9	6.4	P24194 Chromosome initiation inhibitor (OriC replication
467	2	2	29.51	47	6.21E+07	8118.4	9.23	P02998 Translation initiation factor IF-1.
468	3	2	29.46	7	2.68E+07	40368.3	4.58	P06996 Outer membrane protein C precursor (Porin ompC) (O
469	2	2	28.9	15	3.90E+07	17033.1	6.84	P21774 (3R)-hydroxymyristoyl-[acyl carrier protein] dehyd
470	3	2	28.86	10	2.71E+07	30950.6	6.85	P02925 D-ribose-binding periplasmic protein precursor.
471	2	2	28.79	12	3.49E+07	23238.4	5.52	P08179 Phosphoribosylglycinamide formyltransferase (EC 2.
472	2	2	28.75	15	8.12E+07	16849.9	5.26	P30749 Molybdopterin converting factor subunit 2 (MPT syn
473	2	2	28.67	9	3.76E+07	30847.6	5.14	P40191 Pyridoxine kinase (EC 2.7.1.35) (Pyridoxal kinase)
474	3	2	28.59	27	6.29E+07	9920.2	9.3	P71302 50S ribosomal protein L31 type B-1.
475	2	2	28.56	23	2.10E+07	12009.6	5.4	P08338 Met repressor (Met regulon regulatory protein metJ
476	2	2	28.47	8	6.18E+07	31934.9	6.5	P37051 Formyltetrahydrofolate deformylase (EC 3.5.1.10) (
477	3	3	28.32	6	2.92E+07	80300.7	8.96	P28688 Polyphosphate kinase (EC 2.7.4.1) (Polyphosphoric
478	2	2	28.15	32	1.27E+08	9573.3	9.64	P02373 30S ribosomal protein S17.
479	2	2	28.02	19	1.09E+08	16155.6	5.03	P06968 Deoxyuridine 5'-triphosphate nucleotidohydrolase (
480	2	2	27.99	16	5.19E+07	19059.3	6.37	P32130 Hypothetical protein yihI.
481	2	2	27.94	9	3.32E+07	35575.9	5.16	P03807 Protein ydaA.
482	2	2	27.92	15	7.32E+07	18824.3	6.29	P07176 Peptidoglycan-associated lipoprotein precursor.

483	2	2	27.85	15	9.81E+07	24354.1	5.09	P24247	MTA/SAH nucleosidase (P46) [Includes: 5'-methylthi
484	2	2	27.76	7	6.09E+07	40015.7	5.37	P27248	Aminomethyltransferase (EC 2.1.2.10) (Glycine clea
485	2	2	27.66	22	2.88E+08	11354	9.34	P06984	Integration host factor alpha-subunit (IHF-alpha).
486	2	2	27.43	16	3.17E+07	18533.9	4.57	P45473	Hypothetical acetyltransferase yhbS (EC 2.3.1.-).
487	2	2	27.3	12	4.71E+07	23962.7	9.35	P45390	Protein yrbC precursor.
488	2	2	27.28	4	4.68E+07	59643.8	5.46	P22259	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.
489	2	2	27.22	4	8.73E+06	64481.5	6.19	P06149	D-lactate dehydrogenase (EC 1.1.1.28) (Respiratory
490	2	2	27.19	4	1.97E+07	49190.3	6.09	P17114	Bifunctional glmU protein [Includes: UDP-N-acetylgl
491	2	2	27.07	26	3.45E+07	10317.8	5.84	P55756	Hypothetical protein yaiN.
492	3	2	26.97	8	2.41E+07	31059.4	5.63	P31658	Protein yedU.
493	2	2	26.81	8	2.38E+07	32456.2	5.25	P06999	6-phosphofructokinase isozyme 2 (EC 2.7.1.11) (Pho
494	2	2	26.64	41	5.17E+07	6855	4.91	P75844	Protein ycaR.
495	2	2	26.58	29	1.42E+08	13398.7	5.89	P76569	Protein yfgD.
496	3	2	26.44	6	2.82E+07	43636	5.8	P18335	Acetylornithine aminotransferase (EC 2.6.1.11) (AC
497	2	2	26.25	7	5.23E+07	32708.7	4.77	P07862	D-alanine--D-alanine ligase B (EC 6.3.2.4) (D-alan
498	2	2	26.21	9	3.05E+07	34276.2	5.96	P11721	Hydrogen peroxide-inducible genes activator (Morph
499	3	2	26.16	13	2.23E+07	20315.6	8.82	P36658	SeqA protein.
500	2	2	25.95	3	1.21E+07	83716.1	5.58	P37177	Phosphoenolpyruvate-protein phosphotransferase pts
501	3	2	25.72	11	4.72E+07	22868.5	5.85	P39100	Glutathione S-transferase (EC 2.5.1.18).
502	2	2	25.48	4	3.39E+07	60167.7	6.11	P00923	Fumarate hydratase class I, aerobic (EC 4.2.1.2) (
503	2	2	25.41	9	2.68E+07	19576.3	4.79	P45391	Hypothetical protein yrbD precursor.
504	3	2	25.4	15	2.80E+07	21653	5.34	P10375	Imidazole glycerol phosphate synthase subunit hisH
505	3	2	25.37	14	9.57E+06	25787.6	6.09	P52054	Hypothetical protein yggS.
506	2	2	25.21	11	4.50E+07	21270.2	5.48	P37745	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)
507	2	2	25.13	11	1.67E+07	29586	6.86	P11288	Protein yaaA.
508	2	2	24.8	8	1.16E+07	36650.7	5.45	P00963	Aspartate--ammonia ligase (EC 6.3.1.1) (Asparagine
509	2	2	24.73	9	2.28E+07	29705.9	5.5	P34209	Protein ydcF.
510	4	2	24.66	15	2.50E+07	22497.2	6.28	P39178	Outer-membrane lipoproteins carrier protein precur
511	2	2	24.65	2	4.74E+07	88756.9	5.34	P00562	Bifunctional aspartokinase/homoserine dehydrogenas
512	2	2	24.42	4	8.07E+07	54880.1	6.82	P11648	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine amin
513	2	2	24.41	13	5.95E+07	15773.8	5.57	P29209	16 kDa heat shock protein A.
514	2	2	24.35	25	4.31E+07	11051.5	9.05	P42617	Hypothetical protein yqjD.
515	1	1	24.29	5	7.12E+07	43286.1	4.74	P42641	Hypothetical GTP-binding protein yhbZ.
516	2	2	24.03	11	8.49E+07	12777.9	9.3	P76367	Hypothetical protein yeeX.
517	3	2	24.02	10	3.06E+07	26635.4	6.1	P11668	Hypothetical protein yggE.
518	2	2	23.95	6	3.88E+07	37978.6	5.8	P75691	Hypothetical zinc-type alcohol dehydrogenase-like

519	2	2	23.94	8	3.67E+07	34724	5.63	P26646	Protein yhdH.
520	3	2	23.92	8	5.09E+07	38499.7	6.27	Q46933	Tas protein.
521	2	2	23.65	6	4.08E+07	52685.5	5.22	P80063	Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-a
522	2	2	23.43	6	3.44E+07	37440	6.27	P15344	GMP reductase (EC 1.7.1.7) (Guanosine 5'-monosp
523	1	1	23.37	7	4.16E+06	23431.2	6.06	P17113	Methyltransferase gidB (EC 2.1.-.-) (Glucose inhib
524	1	1	23.35	7	8.20E+07	32664.4	5.42	P16703	Cysteine synthase B (EC 4.2.99.8) (O-acetylserine
525	3	2	23.34	8	1.98E+07	14516.8	5.52	P24246	Hypothetical protein yhfA.
526	3	2	23.17	18	1.46E+08	11199.2	9.94	P02424	50S ribosomal protein L23.
527	1	1	22.83	17	1.85E+08	8323.5	9.3	P02937	Major outer membrane lipoprotein precursor (Murein
528	3	2	22.67	8	6.56E+07	30896.2	7.9	P11666	Hypothetical protein yggB.
529	3	2	22.56	17	5.45E+07	8993.3	10.59	P02427	50S ribosomal protein L27.
530	3	2	22.53	8	1.65E+07	27466.8	5.19	P05194	3-dehydroquinatase (EC 4.2.1.10) (3-dehy
531	1	1	22.14	2	1.67E+07	69521.6	6.2	P17112	Glucose inhibited division protein A.
532	2	2	22.1	13	2.24E+07	31464.2	7.79	P75960	CobB protein.
533	1	1	22.04	7	1.31E+08	22966.9	6.5	P77262	Hypothetical protein yagU.
534	2	2	22.03	12	4.44E+07	18838	6.17	P18391	3-hydroxydecanoyl-[acyl-carrier-protein] dehydrata
535	2	2	21.87	5	1.67E+07	37024.1	8.39	P06128	Phosphate-binding periplasmic protein precursor (P
536	1	1	21.7	11	1.12E+08	16016.6	5.61	P37903	Unknown protein 2D_000B3L from 2D-page.
537	3	2	21.66	29	1.26E+08	11449.4	11.16	P02370	30S ribosomal protein S14.
538	2	2	21.44	5	7.08E+07	42914.8	5.71	P39435	3-oxoacyl-[acyl-carrier-protein] synthase II (EC 2
539	2	2	21.41	3	5.78E+06	70832.5	5.45	P08331	2',3'-cyclic-nucleotide 2'-phosphodiesterase precu
540	1	1	21.41	7	1.23E+08	27249.1	5.65	P39831	Probable oxidoreductase ydfG (EC 1.-.-.-).
541	1	1	21.29	8	5.45E+07	22176.2	5.07	P76576	Hypothetical protein yfgM.
542	1	1	21.19	25	7.27E+08	11857.7	5.06	P26604	Protein hdeA precursor (10K-S protein).
543	1	1	21.16	5	1.31E+07	36774.7	7.66	P05021	Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydro
544	2	1	21.03	17	2.26E+07	14937.2	5.46	P00832	ATP synthase epsilon chain (EC 3.6.3.14) (ATP synt
545	2	2	20.91	5	6.45E+06	41367.9	6.23	P05459	Erythronate-4-phosphate dehydrogenase (EC 1.1.1.-)
546	2	1	20.82	7	2.44E+07	27636	5	P08187	PTS system, mannose-specific IIC component (EIIC-M
547	1	1	20.73	6	9.93E+07	42347.6	5.54	P23908	Acetylornithine deacetylase (EC 3.5.1.16) (Acetylo
548	1	1	20.69	6	1.77E+07	27048.1	5.69	P77438	Hypothetical tRNA/rRNA methyltransferase yfhQ (EC
549	1	1	20.65	11	9.02E+07	19423.9	4.77	P23887	Ferritin 1.
550	2	2	20.6	4	4.51E+07	54745.6	5.06	P77522	SufB protein.
551	3	2	20.57	9	1.04E+07	22487.6	5.16	P30126	3-isopropylmalate dehydratase small subunit (EC 4.
552	1	1	20.55	13	1.62E+07	17336.7	6.83	P77484	Hypothetical protein yfhP.
553	4	2	20.52	14	5.44E+06	20605.5	4.61	P21504	16S rRNA processing protein rimM (21K).
554	1	1	20.48	3	3.13E+07	42097.2	5.72	Q46856	Hypothetical oxidoreductase yqhD (EC 1.1.-.-).

555	2	2	20.41	3	6.94E+06	83460.5	5.85	P33363	Periplasmic beta-glucosidase precursor (EC 3.2.1.2)
556	2	2	20.39	12	6.42E+07	23104.7	5.95	P24991	Thiol:disulfide interchange protein dsbA precursor
557	1	1	20.32	16	3.87E+08	10236.6	4.87	P08374	DNA-directed RNA polymerase omega chain (EC 2.7.7.7)
558	2	2	20.26	10	2.98E+07	20912.6	5.57	P37904	Protein yceI precursor.
559	1	1	20.14	9	1.19E+07	20115.4	5.09	P36766	Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)
560	2	2	20.11	8	1.80E+07	46318	5.82	P31455	Hypothetical protein yidR.
561	2	1	19.47	10	6.70E+06	14701.2	6.72	P75874	Protein yccU.
562	1	1	19.37	3	7.48E+07	36689.5	6.35	P06997	Sulfate-binding protein precursor (Sulfate starvat
563	2	1	19.24	9	1.58E+07	36810.3	6.06	P32695	Hypothetical protein yjbN.
564	1	1	19.21	7	1.41E+07	22731.9	5.18	P32145	Hypothetical protein yihX.
565	1	1	19.2	7	4.17E+07	17108	9.04	P08367	CreA protein.
566	1	1	19.04	11	1.75E+08	21741.9	5.53	P37347	Hypothetical isochorismatase family protein yecD.
567	1	1	18.94	2	4.82E+07	50489.2	6.12	P05042	Fumarate hydratase class II (EC 4.2.1.2) (Fumarase
568	1	1	18.89	6	9.31E+07	26829.6	6.83	P30860	Arginine-binding periplasmic protein 2 precursor.
569	1	1	18.87	24	7.95E+07	7731.6	3.98	P37096	Hypothetical protein yfhJ.
570	1	1	18.79	3	3.64E+07	39006.5	5.82	P12008	Chorismate synthase (EC 4.2.3.5) (5-enolpyruvylshi
571	1	1	18.77	31	2.54E+08	9937.5	4.82	P21831	Hypothetical protein yaiB.
572	1	1	18.6	8	6.15E+07	16794.9	5.68	P06975	Ferric uptake regulation protein (Ferric uptake re
573	1	1	18.58	5	1.03E+07	37265.3	5.89	P09147	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowalde
574	1	1	18.52	4	7.71E+07	53995.2	5.9	P15272	AMP nucleosidase (EC 3.2.2.4).
575	2	1	18.03	12	2.02E+07	12493.3	4.97	P76258	Hypothetical protein yoaB.
576	1	1	17.92	39	4.75E+07	4809.6	7.93	P56549	Entericidin B precursor.
577	1	1	17.87	4	6.07E+07	37493.7	6	P39406	Ribosomal RNA small subunit methyltransferase C (E
578	3	1	17.81	3	1.17E+07	52558.7	4.98	P23845	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)
579	1	1	17.76	2	1.15E+07	68867.8	6.11	P14081	Selenocysteine-specific elongation factor (SelB tr
580	1	1	17.72	11	4.27E+07	11437	4.9	P75819	Hypothetical protein ybjQ.
581	1	1	17.64	10	7.50E+07	12100.6	4.11	P37026	Hypothetical protein yadR.
582	1	1	17.57	3	8.23E+07	49914.4	9.27	P21507	ATP-dependent RNA helicase srmB.
583	1	1	17.56	3	8.56E+07	46995	7.28	P24229	Putative ATP-dependent RNA helicase rhlB.
584	1	1	17.45	1	2.74E+07	102390.7	6.22	P27249	[Protein-P _{II}] uridylyltransferase (EC 2.7.7.59) (P
585	1	1	17.4	1	6.71E+06	149028.7	7.89	P43329	ATP-dependent helicase hrpA.
586	1	1	17.25	3	2.32E+07	41084.1	5.08	P39377	Isoaspartyl dipeptidase (EC 3.4.19.-).
587	1	1	17.24	2	5.75E+07	53212.7	5.43	P22188	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diamin
588	1	1	17.16	3	1.57E+07	53990	4.63	P24255	RNA polymerase sigma-54 factor.
589	1	1	17.13	1	2.63E+07	146663.4	4.91	P46889	Cell division protein ftsK.
590	1	1	17.11	18	5.31E+07	9122.6	4.89	P52092	Hypothetical protein yecJ.

591	1	1	17.08	4	3.20E+07	20950.1	8.68	P36671	Hypothetical lipoprotein yajG precursor.
592	1	1	17.05	7	1.40E+08	19332.3	4.95	P00831	ATP synthase delta chain (EC 3.6.3.14).
593	1	1	17.05	5	8.98E+07	25414.1	9.18	P28225	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PN
594	1	1	16.93	3	2.51E+07	41139.2	5.36	P09424	Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)
595	1	1	16.93	7	2.08E+07	29411.4	5.57	P56262	Putative carboxymethylenebutenolidase (EC 3.1.1.45
596	2	1	16.83	5	2.51E+07	27389.3	4.58	P32662	Phosphoglycolate phosphatase (EC 3.1.3.18) (PGP).
597	1	1	16.77	2	2.47E+07	53626.2	5.53	P17952	UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8)
598	1	1	16.63	4	7.54E+07	33175.1	5.1	P23839	Protein yicC.
599	1	1	16.62	5	6.05E+07	17360.4	4.07	P32165	S-adenosylmethionine:2-demethylmenaquinone methylt
600	1	1	16.48	20	1.76E+07	7871.1	9.46	P02432	50S ribosomal protein L31.
601	2	1	16.45	11	2.95E+07	12594.2	5.22	P45580	Hypothetical protein ygfE.
602	1	1	16.44	4	6.65E+07	20853	4.86	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD
603	1	1	16.42	6	3.42E+07	23784.2	4.95	P75849	Hypothetical protein ycbL.
604	1	1	16.41	4	8.24E+07	36364.3	4.38	P08390	USG-1 protein.
605	1	1	16.33	6	2.20E+07	17336.2	6.58	P30747	Molybdenum cofactor biosynthesis protein C.
606	1	1	16.27	2	4.15E+07	42569.8	6.14	P13039	Enterochelin esterase (Ferric enterobactin esteras
607	1	1	16.22	5	8.23E+07	39056.7	6.07	P07005	Glutamate 5-kinase (EC 2.7.2.11) (Gamma-glutamyl k
608	5	1	16.08	6	7.02E+07	13995.4	9.44	P02361	30S ribosomal protein S8.
609	2	1	16.02	10	3.17E+07	21038.9	5.22	P52061	HAM1 protein homolog.
610	1	1	16	17	5.05E+07	17663.2	7.88	P76062	Rac prophage repressor.
611	1	1	15.99	6	9.40E+07	22357.8	6.23	P03033	LexA repressor (EC 3.4.21.88).
612	1	1	15.96	5	1.77E+07	35712.8	5.68	P02927	D-galactose-binding periplasmic protein precursor
613	1	1	15.88	4	1.03E+07	27307.5	6.42	P32049	Hypothetical methyltransferase yggH (EC 2.1.1.-).
614	1	1	15.87	16	5.77E+07	11958.5	5.5	P39278	Hypothetical protein yjeI precursor.
615	1	1	15.84	9	4.42E+07	10602.1	5.18	P31070	Protein yciI.
616	1	1	15.83	6	4.38E+07	23561	6.86	P24253	Probable GTP-binding protein engB.
617	2	1	15.62	23	3.12E+07	11240	9.34	P11028	DNA-binding protein fis (Factor-for-inversion stim
618	1	1	15.59	4	4.58E+07	45245.3	8.52	P09128	HemY protein.
619	1	1	15.56	17	1.75E+08	10821.4	5.91	P52065	Protein yggX.
620	2	1	15.53	17	3.99E+07	6315.2	11.03	P02435	50S ribosomal protein L32.
621	1	1	15.51	5	1.52E+07	30912.7	5.75	P24186	Fold bifunctional protein [Includes: Methylene-tetr
622	1	1	15.43	6	2.67E+07	34492	5.3	P09625	Thioredoxin reductase (EC 1.8.1.9) (TRXR).
623	1	1	15.41	6	7.61E+07	24330.4	4.8	P77247	Hypothetical protein yniC.
624	1	1	15.3	6	1.36E+07	26731.1	6.09	P10346	Glutamine transport ATP-binding protein glnQ.
625	1	1	15.25	4	2.13E+07	38765.2	6.07	P46853	Putative oxidoreductase yhhX (EC 1.-.-.-).
626	1	1	15.24	16	1.24E+08	9827.4	5.5	P30977	Hypothetical protein ybeD.

627	1	1	15.18	9	9.76E+06	21356.7	8.73	P10101 Rare lipoprotein B precursor.
628	1	1	15.03	1	4.20E+07	65532	5.59	P05791 Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
629	1	1	15.02	20	4.98E+07	9385.7	5.47	P46132 Protein yciN.
630	1	1	14.96	6	6.42E+07	23310.7	6.51	P75950 Hypothetical protein ycfP.
631	1	1	14.93	3	1.13E+07	27028	5.81	P12758 Uridine phosphorylase (EC 2.4.2.3) (UDRPase).
632	1	1	14.79	8	2.98E+07	27171	5.69	P22255 CysQ protein.
633	1	1	14.72	5	5.84E+07	36361.8	6.09	P37606 Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1
634	1	1	14.68	10	4.15E+07	13300.2	4.85	P77667 SufA protein.
635	1	1	14.63	5	3.48E+07	31303.1	9.17	P08188 PTS system, mannose-specific IID component (EIID-M
636	1	1	14.61	2	1.10E+07	100372.7	5.06	P39838 Putative sensor-like histidine kinase yojN (EC 2.7
637	1	1	14.56	6	7.61E+06	28237.6	5.15	P31057 3-methyl-2-oxobutanoate hydroxymethyltransferase (
638	1	1	14.49	16	3.85E+07	11365.2	6.09	P33582 Protein-export membrane protein secG (Preprotein t
639	1	1	14.47	2	1.30E+07	54513.6	4.47	P10121 Cell division protein ftsY.
640	1	1	14.39	9	1.20E+07	17093	9.02	P37175 Protein ybaK.
641	1	1	14.37	16	1.40E+08	8673	4.88	P31992 Hypothetical protein ydcE.
642	1	1	14.37	11	1.61E+07	16293.1	6.37	P32163 Hypothetical protein yiiT.
643	1	1	14.34	3	3.75E+07	44838.3	5.39	P24215 Mannonate dehydratase (EC 4.2.1.8) (D-mannonate hy
644	1	1	14.29	7	1.39E+08	23184	4.99	P27110 Peptide methionine sulfoxide reductase msrA (EC 1.
645	1	1	14.28	2	1.56E+08	48723.3	5.72	P07002 NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)
646	1	1	14.27	7	1.66E+08	15689.1	6.6	P04381 N utilization substance protein B (NusB protein).
647	1	1	14.26	22	4.23E+07	12331.2	4.85	P36654 Periplasmic divalent cation tolerance protein cutA
648	1	1	14.25	9	8.16E+07	21891	5.85	P40717 Modulator of drug activity B.
649	1	1	14.21	2	2.07E+07	48389.2	5.73	P30871 Hypothetical protein ygiF (ORFXE).
650	1	1	14.05	7	5.22E+07	22545.2	5.1	P32105 Hypothetical GST-like protein yibF.
651	1	1	14.02	15	3.52E+07	12345.1	4.97	P16680 PhnA protein.
652	2	1	14	1	2.47E+07	90553.2	4.93	P39170 Unknown protein from 2D-page spots M62/M63/O3/O9/T
653	1	1	13.99	6	5.31E+06	25248.1	5.09	P03813 Hypothetical protein ygeA.
654	1	1	13.97	5	5.75E+07	24404	9.34	P27307 Hypothetical protein yijC.
655	1	1	13.96	6	3.93E+07	21073.8	6.32	P27291 Osmotically inducible protein Y precursor.
656	1	1	13.93	11	9.05E+07	15676.5	4.3	P03817 Protein mioC.
657	1	1	13.75	5	3.89E+07	20277.3	4.68	P76270 Protein yebR.
658	1	1	13.7	3	1.23E+07	47335.9	5.53	P12995 Adenosylmethionine-8-amino-7-oxononanoate aminotra
659	1	1	13.65	3	2.63E+07	35202.5	7.8	P21156 Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)
660	1	1	13.65	9	1.67E+07	15935.3	5.12	P28242 Universal stress protein A.
661	1	1	13.55	2	7.27E+07	54656.2	9.68	P13685 Poly(A) polymerase (EC 2.7.7.19) (PAP) (Plasmid co
662	1	1	13.53	3	2.44E+07	30615.3	5.68	P26282 Dihydropteroate synthase (EC 2.5.1.15) (DHPS) (Dih

663	1	1	13.46	4	2.46E+07	26312.2	5.39	P16244	Transcriptional regulatory protein cpxR.
664	1	1	13.41	13	5.04E+07	10317.7	4.25	P76504	Hypothetical protein yfcZ.
665	1	1	13.4	4	1.24E+07	36026.8	9.85	P23851	Ribosomal large subunit pseudouridine synthase C (
666	1	1	13.29	3	2.99E+06	29269.8	5.77	P77734	Negative regulator of allantoin and glyoxylate uti
667	1	1	13.29	2	4.42E+07	54689.3	5.07	P77804	Hypothetical protein ydgA.
668	1	1	13.27	19	6.68E+07	6855.9	8.16	P31803	Carbon storage regulator.
669	1	1	13.24	3	2.56E+07	40149.2	9.52	P33648	Lipoprotein nlpD precursor.
670	1	1	13.2	6	8.66E+07	26310.4	5.6	P22731	High-affinity branched-chain amino acid transport