

**Appendix 1.** Proteins detected in the clinical strain and ATCC10145 strain by LC-MS/MS along with their RefSeq accession number, scan count, fold change and p values, sorted based on their scan count from highest to lowest.

<b>RefSep Accession</b>	<b>Description</b>	<b>Clinical Isolate SC</b>	<b>ATCC10145 SC</b>	<b>NLOG-FoldR*</b>	<b>Np</b>	<b>Adj-Np</b>
15599581	molecular chaperone GroEL	230	604	-0.035750753	0.668408	1
15596974	porin	134.67	298	0.210275102	0.064567	1
15599955	molecular chaperone DnaK	106	284	-0.064906816	0.595382	1
218891724	putative non-ribosomal peptide synthetase	88.67	0	7.833194611	3.17E-68	0.00E+00
386058801	putative non-ribosomal peptide synthetase	87.33	0	7.811417668	3.36E-67	0.00E+00
15600747	ATP synthase F0F1 subunit beta	86.33	211	0.066946037	0.628863	1
15596289	flagellin type B	84	12	4.055052535	2.81E-49	0.00E+00
15599462	elongation factor G	78.33	229	-0.190348323	0.171004	1
15599465	DNA-directed RNA polymerase subunit beta~	74.67	176	0.11867432	0.429572	1
15599461	elongation factor Tu	66.33	186	-0.130539591	0.392351	1
15597819	isocitrate dehydrogenase	65.33	170	-0.023302017	0.881753	1
15598851	elongation factor Ts	63.33	0	7.349927507	9.37E-49	0.00E+00
15600018	Mg(2+) transport ATPase, P-type 2	56.67	214	-0.557841656	0.000273	0.135661
15596997	trigger factor	56.67	130	0.156928192	0.365677	1
15598505	hypothetical protein PA3309	54.33	138	0.011109611	0.948715	1
15596784	dihydrolipoamide dehydrogenase	53.33	187	-0.451173295	0.005047	0.907743
15599934	polynucleotide phosphorylase	53	150	-0.143977966	0.397673	1
15598888	Lipotoxon F, LptF	52.67	54	1.304021921	2.79E-09	0.000002
15598725	peroxidase	52.33	164	-0.290042787	0.082467	1
116049952	acetyl-CoA acetyltransferase	52	163	-0.290432577	0.083009	1
15596793	heat shock protein 90	51.33	125	0.071343161	0.69108	1
15596062	4-hydroxyphenylpyruvate dioxygenase	51.33	129	0.026255271	0.882822	1

15600749	ATP synthase F0F1 subunit alpha	51	146	-0.160387125	0.353939	1
15598264	NAD-dependent glutamate dehydrogenase	50.33	66	0.954337002	0.000006	0.003634
116052305	DNA-directed RNA polymerase subunit beta	50.33	205	-0.666074335	0.00003	0.016789
15595463	4-aminobutyrate aminotransferase	49.33	131	-0.05272692	0.768595	1
15596984	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase	48.67	189	-0.597684585	0.000272	0.135399
15598965	inosine 5--monophosphate dehydrogenase	48.33	112	0.142144275	0.447816	1
15600073	bacterioferritin	46.67	79	0.590121936	0.004162	0.863249
15599933	hypothetical protein PA4739	46	51	1.191000033	2.27E-07	0.000139
15598197	glyceraldehyde-3-phosphate dehydrogenase	43.67	105	0.088972344	0.648428	1
15599866	50S ribosomal protein L25	43.33	116	-0.064443039	0.735473	1
15599738	ClpB protein	42	87	0.301751747	0.143775	1
15598148	electron transfer flavoprotein subunit beta	42	111	-0.046171556	0.812203	1
116050197	dihydrolipoamide dehydrogenase	41.67	0	6.749778602	3.96E-32	0.00E+00
15597749	acyl-CoA thiolase	41	75	0.478767476	0.026238	0.999986
15596196	3-oxoacyl-ACP synthase	40.67	0	6.715013184	2.31E-31	0.00E+00
15600365	ornithine carbamoyltransferase	40.33	139	-0.426047001	0.021737	0.999916
15598358	30S ribosomal protein S1	40	131	-0.353032203	0.061482	1
15596067	aromatic amino acid aminotransferase	39.67	97	0.06467943	0.750968	1
15596195	PqsC	39	0	6.655141728	4.38E-30	0.00E+00
15596759	aconitate hydratase	38.67	118	-0.251954365	0.1972	1
15596084	acetyl-CoA synthetase	38.33	85	0.204214919	0.336227	1
15595337	alkyl hydroperoxide reductase	38	125	-0.359291194	0.063255	1
15597445	branched-chain alpha-keto acid dehydrogenase subunit E2	37.67	134	-0.471426904	0.013358	0.997482
15596786	succinyl-CoA synthetase subunit alpha	37.67	114	-0.240101358	0.226066	1
15596967	phosphoenolpyruvate synthase	37	79	0.257925506	0.237051	1

15596783	dihydrolipoamide succinyltransferase	36.33	140	-0.58569296	0.002072	0.644712
15599447	50S ribosomal protein L5	36	73	0.331229638	0.139126	1
15595462	succinate-semialdehyde dehydrogenase I	35.67	0	6.527386181	1.56E-27	0.00E+00
15595679	malate synthase G	35.33	73	0.3045123	0.175906	1
15596159	dna-binding stress protein	35	63	0.500419133	0.032361	0.999999
15596780	succinate dehydrogenase flavoprotein subunit	34.33	95	-0.112024104	0.597758	1
15596194	PqsB	33.67	0	6.444924021	5.31E-26	0.00E+00
15596271	branched-chain amino acid ABC transporter	33	130	-0.617068133	0.001867	0.607162
15598766	methylmalonate-semialdehyde dehydrogenase	33	124	-0.549429416	0.006193	0.944014
15595752	fructose-1,6-bisphosphate aldolase	33	67	0.328892027	0.159354	1
15598147	electron transfer flavoprotein subunit alpha	31.67	51	0.657021461	0.009262	0.985638
15600371	LysM domain/BON superfamily protein	31.33	47	0.757391786	0.00336	0.804573
15600209	dihydrolipoamide acetyltransferase	31.33	121	-0.58838305	0.00402	0.854787
15595629	S-adenosyl-L-homocysteine hydrolase	31	116	-0.543277189	0.008755	0.98234
15596539	ABC transporter	30.67	0	6.31165749	1.05E-23	0.00E+00
15596085	arginine/ornithine binding protein AotJ	30.33	111	-0.511294287	0.015214	0.998824
116050019	elongation factor G	29.67	0	6.264351775	6.10E-23	0.00E+00
15600505	aldehyde dehydrogenase	28.67	84	-0.193948761	0.396748	1
15599434	DNA-directed RNA polymerase subunit alpha	28.67	64	0.193074362	0.43017	1
116050368	hypothetical protein PA14_33310	28.33	8	3.028838432	3.46E-14	2.25E-11
15598049	Outer membrane lipoprotein OprI precursor	28.33	92	-0.340395378	0.129326	1
15598335	aromatic amino acid aminotransferase	28	0	6.181889615	1.15E-21	0.00E+00
15597830	isocitrate lyase	28	40	0.82433761	0.002841	0.754027
15596990	peptidyl-prolyl cis-trans isomerase B	27.67	73	-0.044637264	0.851855	1
15595620	hypothetical protein PA0423	27.67	72	-0.025008457	0.916952	1

386056781	pyochelin synthetase	27	0	6.130050683	6.66E-21	0.00E+00
15599469	50S ribosomal protein L1	27	58	0.247407634	0.330936	1
15600115	azurin	27	72	-0.059773875	0.804341	1
15595785	hypothetical protein PA0588	26.67	161	-1.227501321	5.95E-10	3.74E-07
15600239	malic enzyme	26.67	37	0.864421168	0.002414	0.699154
15599939	transcription elongation factor NusA	26.33	77	-0.190975445	0.423846	1
15596155	porin	26	0	6.076279427	3.87E-20	0.00E+00
15599421	pyochelin synthetase	26	0	6.076279427	3.87E-20	0.00E+00
15600364	arginine deiminase	26	121	-0.854457911	0.000066	0.036172
15598958	phosphoribosylformylglycinamidine synthase	26	43	0.616847808	0.025632	0.999983
15598937	50S ribosomal protein L19	26	62	0.098999504	0.695206	1
218893498	cell division protein FtsZ	25	0	6.020426192	2.24E-19	0.00E+00
15599938	translation initiation factor IF-2	25	78	-0.283354556	0.239895	1
15596785	succinyl-CoA synthetase subunit beta	25	72	-0.169398367	0.49091	1
15598964	GMP synthase	24.67	56	0.168427355	0.521064	1
15600125	50S ribosomal protein L9	24.67	56	0.168427355	0.521064	1
15599444	50S ribosomal protein L6	24.67	61	0.047121059	0.854528	1
15597641	glycine dehydrogenase	24.33	0	5.981952044	7.24E-19	0.00E+00
15600206	branched-chain amino acid aminotransferase	24.33	63	-0.018047956	0.943759	1
386068123	putative aldehyde dehydrogenase	24	0	5.962323238	1.30E-18	0.00E+00
15599548	hypothetical protein PA4352	23.67	33	0.854960839	0.004601	0.887601
15599582	co-chaperonin GroES	23.67	66	-0.12366551	0.627242	1
116048712	aconitate hydratase	23.67	62	-0.034856243	0.892783	1
15598887	hypothetical protein PA3691	23.33	4	3.600317703	8.69E-14	5.65E-11
15595200	DNA polymerase III subunit beta	23.33	55	0.114890876	0.667291	1
15599835	hypothetical protein PA4639	22.67	49	0.237166946	0.391753	1

15597905	cysteine synthase A	22.67	56	0.048133121	0.857464	1
15599442	30S ribosomal protein S5	22.33	41	0.467644097	0.10722	1
15600751	ATP synthase F0F1 subunit B	22.33	68	-0.248562937	0.332388	1
15599031	hypothetical protein PA3836	22.33	63	-0.14003848	0.592006	1
15599895	hypothetical protein PA4701	22	12	2.138148151	4.17E-08	0.000026
15597992	transaldolase B	22	32	0.79419375	0.010284	0.99065
15599463	30S ribosomal protein S7	22	37	0.590660356	0.048047	1
15598849	ribosome recycling factor	22	72	-0.35123669	0.166355	1
15599468	50S ribosomal protein L10	22	43	0.379156251	0.188037	1
116049276	hypothetical protein PA14_47120	21.67	4	3.494964703	1.24E-12	8.01E-10
152984968	carbamoyl phosphate synthase large subunit [PA PA7]	21.67	38	0.531490579	0.07446	1
15599691	hypothetical protein PA4495	21.67	44	0.325039702	0.258217	1
15599449	50S ribosomal protein L14	21.67	47	0.231930297	0.412292	1
15599432	catalase	21.33	99	-0.848989698	0.000328	0.159632
15600367	beta-ketoacyl synthase	21.33	25	1.094426774	0.000944	0.384473
15598882	adenylate kinase	21.33	36	0.585413126	0.053399	1
15599448	50S ribosomal protein L24	21.33	64	-0.227501321	0.387461	1
15599764	50S ribosomal protein L21	21.33	48	0.180156648	0.523668	1
15599456	50S ribosomal protein L2	21.33	51	0.094426774	0.734425	1
15599659	hypothetical protein PA4463	21.33	58	-0.087776558	0.744826	1
15597211	isovaleryl-CoA dehydrogenase	21	36	0.563045313	0.064215	1
15600041	acetyl-CoA carboxylase biotin carboxylase subunit	21	62	-0.204781245	0.441963	1
15597027	hypothetical protein PA1830	20.67	58	-0.132864447	0.624971	1
15598833	CTP synthetase	20.33	26	0.971807487	0.003399	0.807508
15599511	transcriptional regulator MvaT, P16 subunit	20.33	51	0.026255271	0.92573	1
15599452	50S ribosomal protein L16	20	44	0.21138292	0.470951	1

15596207	dihydrodipicolinate synthase	20	47	0.118273516	0.68185	1
15600244	arginyl-tRNA synthetase	20	52	-0.024684438	0.930113	1
116052737	ABC transporter ATP-binding protein	19.67	94	-0.890466334	0.000266	0.133117
15598163	3-ketoacyl-ACP reductase	19.67	33	0.591926433	0.060871	1
15595979	bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase	19.67	71	-0.490535727	0.060952	1
15595992	methylcitrate synthase	19.67	69	-0.449893743	0.08791	1
15596100	alanyl-tRNA synthetase	19.67	53	-0.075498228	0.788401	1
15599949	transcription elongation factor GreA	19.67	49	0.035533085	0.901387	1
218891424	Heavy metal translocating P-type ATPase	19.33	0	5.655141728	4.69E-15	3.05E-12
15600620	alcohol dehydrogenase	19.33	85	-0.771123027	0.002165	0.660119
15597204	fumarylacetoacetase	19.33	68	-0.453382729	0.087933	1
15598355	UDP-N-acetyl-d-glucosamine 6- dehydrogenase [	19	0	5.630479674	8.41E-15	5.52E-12
15597205	homogentisate 1,2-dioxygenase	19	95	-0.954482827	0.000102	0.054484
15596051	fumarate hydratase	19	27	0.823124752	0.013809	0.997858
15600035	hypothetical protein PA4842	18.67	17	1.435463692	0.000128	0.067826
15599458	50S ribosomal protein L4	18.67	30	0.651192383	0.04666	1
15598458	peptidyl-prolyl cis-trans isomerase, FkbP- type	18.67	37	0.35746118	0.250541	1
15596534	glutaminase-asparaginase	18.33	81	-0.777698404	0.002556	0.719046
15597771	hypothetical protein PA2575	18.33	40	0.222301596	0.468414	1
15595716	nitrite reductase	18	25	0.853418674	0.013402	0.997464
15595942	enoyl-CoA hydratase	18	45	0.030296436	0.919358	1
15596197	Quinolone signal response protein	17.67	0	5.527386181	8.70E-14	5.65E-11
15595644	glutaryl-CoA dehydrogenase	17.67	72	-0.662438378	0.013388	0.997483
116053247	urocanate hydratase	17.67	27	0.720031259	0.034376	0.999999

15597863	hypothetical protein PA2667	17.67	55	-0.279968741	0.327957	1
15596999	ATP-dependent protease ATP-binding subunit ClpX	17.67	38	0.241983962	0.439879	1
15595745	transketolase	17.33	44	0.008566037	0.977498	1
15599454	50S ribosomal protein L22	17	35	0.303013396	0.347662	1
15598831	phosphopyruvate hydratase	17	39	0.151010302	0.630857	1
116049954	3-hydroxybutyrate dehydrogenase	16.67	12	1.744484303	0.00003	0.016786
15597838	NADH dehydrogenase subunit G	16.67	67	-0.64253882	0.02016	0.999843
15599756	isoleucyl-tRNA synthetase	16.67	31	0.444924021	0.182706	1
15595749	phosphoglycerate kinase	16.67	53	-0.309963481	0.29005	1
15599445	30S ribosomal protein S8	16.67	34	0.315641004	0.333693	1
15599194	D-ala-D-ala-carboxypeptidase	16.33	62	-0.560925055	0.047698	1
15597210	methylcrotonyl-CoA carboxylase subunit beta	16.33	29	0.509464273	0.135195	1
15595513	D-3-phosphoglycerate dehydrogenase	16.33	46	-0.138233983	0.650193	1
15599888	ketol-acid reductoisomerase	16	51	-0.313231195	0.294368	1
15600515	phosphomannomutase	16	37	0.139281009	0.666397	1
15596266	hypothetical protein PA1069	15.67	0	5.35746118	2.88E-12	1.85E-09
15596777	type II citrate synthase	15.67	88	-1.118272251	0.00002	0.011559
15595497	polyamine transporter	15.67	60	-0.573276158	0.046921	1
15599182	leucyl-tRNA synthetase	15.67	27	0.550106257	0.11655	1
15599599	preprotein translocase subunit SecA	15.33	28	0.469106535	0.179261	1
15599525	pyruvate kinase	15.33	42	-0.099177224	0.754035	1
15597750	short-chain dehydrogenase	15.33	38	0.041685312	0.897739	1
15597526	hypothetical protein PA2330	15	0	5.296060635	9.23E-12	5.92E-09
15595257	osmotically inducible protein OsmC	15	11	1.711098134	0.000092	0.049631
15599435	30S ribosomal protein S4	15	34	0.166777618	0.618642	1
15596806	3-oxoacyl-ACP synthase	15	37	0.048133121	0.883412	1

15599440	50S ribosomal protein L15	15	37	0.048133121	0.883412	1
116048819	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase	14.67	0	5.264351775	1.65E-11	1.06E-08
15596169	translocation protein TolB	14.67	18	1.016424262	0.009597	0.987453
15597001	DNA-binding protein HU	14.67	59	-0.64253882	0.029079	0.999995
15599591	nucleotide-binding protein	14.67	54	-0.517007938	0.085753	1
15597443	2-oxoisovalerate dehydrogenase subunit alpha	14.67	52	-0.463568679	0.126902	1
15598926	hypothetical protein PA3731	14.33	13	1.424575375	0.000822	0.345724
15599505	chemotactic transducer PctA	14.33	23	0.646967797	0.082249	1
15600433	thioredoxin	14.33	46	-0.322658554	0.305256	1
15600312	glutamine synthetase	14.33	31	0.231930297	0.503229	1
15598311	Motility protein FimV	14.33	39	-0.089997797	0.783576	1
15598562	acylamide amidohydrolase	14	0	5.198763434	5.29E-11	3.37E-08
386063883	Lipid A 3-O-deacylase	14	0	5.198763434	5.29E-11	3.37E-08
15599585	3-ketoacyl-ACP reductase	14	17	1.028838432	0.010551	0.991547
15599002	nucleoside diphosphate kinase	14	54	-0.58259628	0.055576	1
15596356	cold-shock protein	14	39	-0.123164661	0.708605	1
15597638	glycine cleavage system protein T2	14	39	-0.123164661	0.708605	1
15595944	aldehyde dehydrogenase	14	37	-0.04916408	0.882909	1
15599436	30S ribosomal protein S11	13.67	14	1.257925506	0.002976	0.767877
15596986	hypothetical protein PA1789	13.67	41	-0.227501321	0.487243	1
15599649	hypothetical protein PA4453	13.67	41	-0.227501321	0.487243	1
15599679	aspartyl/glutamyl-tRNA amidotransferase subunit A	13.67	36	-0.044637264	0.894942	1
15597196	dehydrocarnitine CoA transferase subunit B	13.33	6	2.322695761	0.000006	0.003651
15599958	ferric uptake regulation protein	13.33	63	-0.869949317	0.003347	0.803954



15600069	OsmE family transcriptional regulator	13.33	20	0.737733261	0.059699	1
15599677	rod shape-determining protein MreB	13.33	32	0.085656564	0.806627	1
15599602	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	13.33	34	0.000767666	0.998224	0
15597380	hypothetical protein PA2184	13	0	5.094426774	3.03E-10	1.91E-07
15597527	hypothetical protein PA2331	13	3	3.094426774	1.74E-07	0.000107
15600541	DNA-binding protein	13	50	-0.577998568	0.067201	1
15599459	50S ribosomal protein L3	13	23	0.509464273	0.181482	1
15599455	30S ribosomal protein S19	13	44	-0.397426323	0.222566	1
15600128	30S ribosomal protein S6	13	31	0.094426774	0.790142	1
15599865	ribose-phosphate pyrophosphokinase	13	34	-0.034856243	0.919978	1
15595268	hypothetical protein PA0070	12.67	0	5.057900898	5.41E-10	3.41E-07
15599443	50S ribosomal protein L18	12.67	48	-0.556808946	0.082801	1
15600698	TonB-dependent receptor	12.67	48	-0.556808946	0.082801	1
15598980	hypothetical protein PA3785	12.67	41	-0.334416525	0.316134	1
15598835	acetyl-CoA carboxylase carboxyltransferase subunit alpha	12.67	39	-0.264027197	0.434307	1
15599956	heat shock protein GrpE	12.67	28	0.199919903	0.584877	1
15596782	2-oxoglutarate dehydrogenase E1	12.33	85	-1.405838562	0.000001	0.000328
15600682	thiol:disulfide interchange protein DsbA	12.33	38	-0.264976027	0.438544	1
15599453	30S ribosomal protein S3	12.33	26	0.26553869	0.478873	1
15599428	single-stranded DNA-binding protein	12.33	37	-0.227501321	0.508745	1
15598509	hypothetical protein PA3313	12.33	36	-0.189027173	0.585483	1
15600425	hypothetical protein PA5232	12	6	2.174597122	0.000038	0.021216
15598667	malate dehydrogenase	12	13	1.174597122	0.00827	0.978075
15600436	delta-aminolevulinic acid dehydratase	12	52	-0.74596841	0.019332	0.999782
15596170	peptidoglycan associated lipoprotein OprL precursor	12	47	-0.603010456	0.065109	1

15599627	iron-sulfur protein	12	44	-0.509901052	0.12485	1
15598809	hypothetical protein PA3613	12	42	-0.44431271	0.186102	1
15598279	aminopeptidase	12	34	-0.147330972	0.677089	1
15596160	aspartyl-tRNA synthetase	12	33	-0.105510797	0.76717	1
15599262	Outer membrane protein OprG precursor	12	33	-0.105510797	0.76717	1
15595496	aminotransferase	12	32	-0.062442075	0.86193	1
15599172	glutamate-1-semialdehyde aminotransferase	12	32	-0.062442075	0.86193	1
15597030	oxidoreductase	12	30	0.027755734	0.939333	1
15596092	bifunctional N-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein	11.67	55	-0.864931242	0.006315	0.946763
116050392	serine hydroxymethyltransferase	11.67	15	0.94242368	0.029587	0.999996
15595608	twitching motility protein PilJ	11.67	43	-0.517007938	0.124333	1
15596095	succinylglutamic semialdehyde dehydrogenase	11.33	0	4.901781696	5.51E-09	0.000003
15595550	dihydroxy-acid dehydratase	11.33	44	-0.590071401	0.079854	1
15598187	soluble pyridine nucleotide transhydrogenase	11.33	42	-0.524483059	0.123744	1
15600135	protease subunit HflK	11.33	41	-0.490535727	0.152381	1
15600339	hypothetical protein PA5146	11.33	19	0.579853601	0.159915	1
15598172	ribonuclease E	11.33	36	-0.30767167	0.384492	1
15597939	translation initiation factor IF-3	11.33	29	-0.0051089	0.989067	0.99988
15596198	anthranilate synthase component I	11	0	4.85996152	9.84E-09	0.000006
116051566	3-hydroxyisobutyrate dehydrogenase	11	0	4.85996152	9.84E-09	0.000006
15600253	polyhydroxyalkanoate synthesis protein PhaF	11	3	2.85996152	0.000004	0.002163
15599637	hypothetical protein PA4441	11	11	1.274999019	0.00692	0.959561
15600211	peptide methionine sulfoxide reductase	11	45	-0.663600436	0.049257	1
15598440	cell division inhibitor MinD	11	20	0.467644097	0.254695	1

15596998	ATP-dependent Clp protease proteolytic subunit	11	21	0.400529901	0.323661	1
15600746	ATP synthase F0F1 subunit epsilon	11	36	-0.349491846	0.326729	1
15596376	two-component response regulator PhoP	11	22	0.336399564	0.401919	1
15600208	pyruvate dehydrogenase subunit E1	10.67	99	-1.826963392	6.52E-11	4.14E-08
15599828	hypothetical protein PA4632	10.67	0	4.816892798	1.76E-08	0.000011
152983977	dihydroaeruginic acid synthetase	10.67	0	4.816892798	1.76E-08	0.000011
15598852	30S ribosomal protein S2	10.67	9	1.494964703	0.002667	0.732703
15597835	bifunctional NADH:ubiquinone oxidoreductase subunit C/D	10.67	54	-0.964466915	0.003013	0.771342
15598364	DNA gyrase subunit A	10.67	14	0.910002203	0.043113	1
15596068	pterin-4-alpha-carbinolamine dehydratase	10.67	44	-0.674960298	0.04835	1
15600040	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	10.67	15	0.816892798	0.065016	1
15598209	3-ketoacyl-CoA thiolase	10.67	41	-0.575424625	0.09806	1
15595221	quinone oxidoreductase	10.67	39	-0.505035297	0.15147	1
15600748	ATP synthase F0F1 subunit gamma	10.67	33	-0.270570043	0.460606	1
15599460	30S ribosomal protein S10	10.67	24	0.173036608	0.662141	1
15595265	oligopeptidase A	10.67	26	0.062005296	0.87318	1
15599117	hypothetical protein PA3922	10.33	100	-1.885712804	1.98E-11	1.27E-08
15595563	aldehyde dehydrogenase	10.33	7	1.772498679	0.000827	0.346775
15598844	outer membrane protein Opr86	10.33	11	1.187536178	0.013233	0.997371
15600366	carbamate kinase	10.33	37	-0.475428835	0.185886	1
15595993	2-methylisocitrate lyase	10.33	18	0.524571165	0.219686	1
116050970	malonyl-CoA-ACP transacylase	10.33	24	0.128642489	0.747177	1
15600497	D-amino acid dehydrogenase small subunit	10.33	25	0.072058961	0.855307	1
15596193	coenzyme A ligase	10	0	4.726694989	5.59E-08	0.000034
15599932	hypothetical protein PA4738	10	6	1.919340067	0.00051	0.235805

15596069	phenylalanine 4-monooxygenase	10	10	1.267263371	0.010271	0.990692
15596250	hypothetical protein PA1053	10	19	0.404766894	0.341257	1
15596208	hypothetical protein PA1011	10	20	0.334377566	0.426129	1
15599249	bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II-like protein	10	20	0.334377566	0.426129	1
15597395	dehydrogenase	9.67	0	4.679389274	9.96E-08	0.000061
15600628	pyruvate carboxylase subunit B	9.67	66	-1.386699916	0.000012	0.006887
15600247	ATP-dependent protease ATP-binding subunit HslU	9.67	7	1.679389274	0.001828	0.600853
15596053	hypothetical protein PA0856	9.67	8	1.509464273	0.003921	0.848857
15596353	ribonucleotide-diphosphate reductase subunit alpha	9.67	37	-0.568538239	0.119563	1
15596101	aspartate kinase	9.67	27	-0.127965648	0.745482	1
15596781	succinate dehydrogenase iron-sulfur subunit	9.67	27	-0.127965648	0.745482	1
15598813	recombinase A	9.33	8	1.460554673	0.005652	0.928743
15599566	Insulin-cleaving metalloproteinase outer membrane protein	9.33	9	1.308551579	0.010925	0.992791
15599202	gamma-glutamyl phosphate reductase	9.33	11	1.045517173	0.033339	0.999999
15600113	NAD synthetase	9.33	15	0.630479674	0.167961	1
15600385	phosphoenolpyruvate carboxykinase	9.33	16	0.543016833	0.227956	1
15597002	peptidyl-prolyl cis-trans isomerase D	9.33	23	0.045517173	0.912284	1
15600481	nitrogen regulatory protein P-II 2	9.33	23	0.045517173	0.912284	1
15595656	ClpA/B protease ATP binding subunit [	9	0	4.579853601	3.16E-07	0.000192
15596656	chemotaxis-specific methyltransferase	9	0	4.579853601	3.16E-07	0.000192
15597501	protein AmbB	9	0	4.579853601	3.16E-07	0.000192
15598344	UDP-N-acetylglucosamine 2-epimerase [	9	0	4.579853601	3.16E-07	0.000192
116052241	hypothetical protein PA14_09550	9	0	4.579853601	3.16E-07	0.000192
15595792	organic solvent tolerance protein OstA	9	1	3.579853601	0.000003	0.00177

15597203	maleylacetoacetate isomerase	9	10	1.120421982	0.02697	0.99999
15597812	thioredoxin reductase	9	13	0.772498679	0.105305	1
15597937	50S ribosomal protein L20	9	13	0.772498679	0.105305	1
15598308	acetyl-CoA carboxylase subunit beta	9	13	0.772498679	0.105305	1
15598930	threonine synthase	9	13	0.772498679	0.105305	1
15600532	hypothetical protein PA5339	9	14	0.672963005	0.151146	1
15600131	adenylosuccinate synthetase	9	33	-0.50760924	0.183994	1
15598236	hypothetical protein PA3040	9	19	0.257925506	0.55439	1
15600622	aspartate ammonia-lyase	9	26	-0.175033901	0.66541	1
15597748	acyl-CoA dehydrogenase	9	21	0.120421982	0.777425	1
15596758	aerotaxis receptor Aer	9	22	0.056291645	0.893707	1
15598047	elongation factor P	9	22	0.056291645	0.893707	1
15598636	hypothetical protein PA3440	9	23	-0.0051089	0.990221	0.990221
15599217	aldehyde dehydrogenase	8.67	123	-2.426810129	2.67E-18	0.00E+00
15599120	acyl-CoA thiolase	8.67	0	4.527386181	0.000001	0.000339
15598678	methionyl-tRNA synthetase	8.67	9	1.205458086	0.021286	0.9999
15599656	hypothetical protein PA4460	8.67	11	0.94242368	0.059551	1
15595498	polyamine transporter	8.67	12	0.826946463	0.091679	1
15599953	dihydrodipicolinate reductase	8.67	17	0.35746118	0.429049	1
15600256	ubiquinone/menaquinone biosynthesis methyltransferase	8.67	17	0.35746118	0.429049	1
15598356	O-antigen chain length regulator	8.33	0	4.472938397	0.000001	0.0006
15598063	chemotaxis transducer	8.33	39	-0.848989698	0.023098	0.99995
15600327	carboxyl-terminal protease	8.33	10	1.013506778	0.049524	1
15596375	PhoP/Q and low Mg <sup>2+</sup> inducible outer membrane protein H1	8.33	13	0.665583475	0.170731	1
15595206	glycyl-tRNA synthetase subunit beta	8.33	25	-0.227501321	0.584662	1
15596094	arginine/ornithine succinyltransferase AII	8.33	24	-0.170917793	0.684276	1

	subunit					
15599836	malate:quinone oxidoreductase	8.33	19	0.151010302	0.734023	1
15600127	30S ribosomal protein S18	8.33	19	0.151010302	0.734023	1
15595705	acyl-CoA dehydrogenase	8	0	4.416354869	0.000002	0.001064
15600676	two-component response regulator AlgB	8	6	1.608999947	0.005795	0.932954
15599529	fumarase	8	41	-0.975962554	0.008846	0.982917
15600435	polyphosphate kinase	8	11	0.831392368	0.103015	1
15597834	NADH dehydrogenase subunit B	8	30	-0.537841442	0.181181	1
15595791	peptidyl-prolyl cis-trans isomerase SurA	8	27	-0.391000053	0.343315	1
15598940	30S ribosomal protein S16	8	16	0.328892027	0.481667	1
15599014	hypothetical protein PA3819	8	22	-0.107207087	0.80463	1
386067392	putative glutamine synthetase	8	22	-0.107207087	0.80463	1
116051153	bifunctional cyclohexadienyl dehydrogenase/ 3-phosphoshikimate 1-carboxyvinyltransferase	8	21	-0.04307675	0.9217	1
15595283	hypothetical protein PA0085	7.67	0	4.35746118	0.000003	0.001868
15599375	acetolactate synthase	7.67	0	4.35746118	0.000003	0.001868
15599721	type 4 fimbrial PilA	7.67	0	4.35746118	0.000003	0.001868
15599009	cysteine desulfurase	7.67	5	1.772498679	0.003782	0.839019
15599638	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase	7.67	7	1.35746118	0.017234	0.999471
15599394	acyl-CoA dehydrogenase	7.67	8	1.187536178	0.031911	0.999998
15595625	ATP-dependent RNA helicase	7.67	11	0.772498679	0.13374	1
15596992	cysteinyl-tRNA synthetase	7.67	11	0.772498679	0.13374	1
15599248	6,7-dimethyl-8-ribityllumazine synthase	7.67	27	-0.449893743	0.280453	1
15598862	tetrahydrodipicolinate succinylase	7.67	25	-0.342978539	0.41926	1
15598149	electron transfer flavoprotein-ubiquinone oxidoreductase	7.67	22	-0.166100777	0.704424	1

15600454	alginate biosynthesis regulatory protein AlgR	7.67	20	-0.034856243	0.937973	1
15599385	monooxygenase	7.33	0	4.296060635	0.000006	0.003282
15598990	oxidoreductase	7.33	2	2.711098134	0.000217	0.109861
15598210	multifunctional fatty acid oxidation complex subunit alpha	7.33	41	-1.096256788	0.003976	0.852225
15596776	hypothetical protein PA1579	7.33	8	1.126135633	0.044116	1
15595657	hypothetical protein PA0460	7.33	33	-0.791402206	0.048611	1
116049897	ribose ABC transporter substrate-binding protein	7.33	31	-0.703939365	0.084052	1
15599446	30S ribosomal protein S14	7.33	12	0.595620917	0.243198	1
15599807	hypothetical protein PA4611	7.33	12	0.595620917	0.243198	1
15598995	hypothetical protein PA3800	7.33	13	0.488705713	0.329339	1
15595743	S-adenosylmethionine synthetase	7.33	24	-0.347795555	0.422279	1
15599017	preprotein translocase subunit YajC	7.33	16	0.208597794	0.662066	1
15598011	acyl-CoA dehydrogenase	7.33	18	0.048133121	0.917412	1
15597820	isocitrate dehydrogenase	7	0	4.231930297	0.00001	0.005758
15598218	hypothetical protein PA3022	7	0	4.231930297	0.00001	0.005758
116049963	alpha subunit of geranyl-CoA carboxylase, GnyA	7	0	4.231930297	0.00001	0.005758
119167454	nonspecific ribonucleoside hydrolase	7	0	4.231930297	0.00001	0.005758
152986789	long-chain-fatty-acid--CoA ligase	7	0	4.231930297	0.00001	0.005758
15599437	30S ribosomal protein S13	7	28	-0.626050698	0.138193	1
15596794	hypothetical protein PA1597	7	26	-0.522957205	0.223802	1
15599450	30S ribosomal protein S17	7	12	0.531490579	0.303074	1
15600450	hypothetical protein PA5257	7	13	0.424575375	0.401988	1
15599371	peptidyl-prolyl cis-trans isomerase C2	7	14	0.325039702	0.51391	1
15599625	cytochrome C1 precursor	7	22	-0.291631659	0.514581	1
15597940	threonyl-tRNA synthetase	7	17	0.062005296	0.896306	1

15599467	50S ribosomal protein L7/L12	7	18	-0.015997216	0.972812	1
15595734	hypothetical protein PA0537	6.67	0	4.164816102	0.000018	0.010051
15595666	hypothetical protein PA0469	6.67	9	0.842888007	0.130548	1
15596205	bacterioferritin comigratory protein	6.67	12	0.464376383	0.373783	1
15600509	50S ribosomal protein L28	6.67	14	0.257925506	0.608658	1
15595552	protease PfpI	6.67	18	-0.083111412	0.861062	1
15597393	hypothetical protein PA2197	6.33	0	4.094426774	0.000031	0.017591
15599420	pyochelin biosynthetic protein PchG	6.33	0	4.094426774	0.000031	0.017591
386061659	hypothetical protein PAM18_5602	6.33	0	4.094426774	0.000031	0.017591
15599680	aspartyl/glutamyl-tRNA amidotransferase subunit B	6.33	4	1.772498679	0.008206	0.977598
15599457	50S ribosomal protein L23	6.33	8	0.924501772	0.11056	1
15599628	30S ribosomal protein S9	6.33	11	0.509464273	0.34474	1
15600354	dTDP-D-glucose 4,6-dehydratase	6.33	11	0.509464273	0.34474	1
15596140	hypothetical protein PA0943	6.33	12	0.393987056	0.456003	1
15595526	hypothetical protein PA0329	6.33	19	-0.227501321	0.631662	1
15597956	hypothetical protein PA2760	6.33	14	0.187536178	0.713058	1
15600451	hypothetical protein PA5258	6.33	17	-0.075498228	0.876858	1
116051381	acylamide amidohydrolase	6	75	-2.227501321	8.92E-11	5.65E-08
15599927	acetyl-CoA synthetase	6	53	-1.73446131	0.000004	0.002152
15596743	coproporphyrinogen III oxidase	6	0	4.020426192	0.000056	0.03051
15598800	response regulator ErdR	6	0	4.020426192	0.000056	0.03051
15600470	diaminopimelate decarboxylase	6	3	2.020426192	0.004876	0.900447
15599183	hypothetical protein PA3988	6	31	-0.979573808	0.021897	0.99992
15597209	gamma-carboxygeranoyl-CoA hydratase	6	5	1.435463692	0.027038	0.99999
15600346	amino acid ABC transporter substrate-binding protein	6	29	-0.886464403	0.04125	1
15597778	hypothetical protein PA2582	6	6	1.21307127	0.052202	1



15596690	sulfate ABC transporter substrate-binding protein	6	7	1.020426192	0.091333	1
15598363	phosphoserine aminotransferase	6	7	1.020426192	0.091333	1
15600100	short-chain dehydrogenase	6	7	1.020426192	0.091333	1
15600134	protease subunit HflC	6	7	1.020426192	0.091333	1
15598303	O-succinylhomoserine sulfhydrylase	6	8	0.850501191	0.147275	1
15600408	glycine cleavage system aminomethyltransferase T	6	23	-0.564536308	0.218992	1
15595597	cystathionine gamma-lyase	6	9	0.698498097	0.221727	1
15597386	hypothetical protein PA2190	6	9	0.698498097	0.221727	1
15599917	suppressor protein DksA	6	11	0.435463692	0.425272	1
15595865	tyrosyl-tRNA synthetase	6	20	-0.371891231	0.433534	1
15599926	glucose-6-phosphate isomerase	6	13	0.21307127	0.685149	1
15600269	ABC transporter	6	17	-0.149498809	0.761948	1
15595596	cystathionine beta-synthase	5.67	0	3.94242368	0.000098	0.052788
15597960	hypothetical protein PA2764	5.67	0	3.94242368	0.000098	0.052788
15599417	Fe(III)-pyochelin outer membrane receptor	5.67	0	3.94242368	0.000098	0.052788
15600303	fructose-1,6-bisphosphatase	5.67	0	3.94242368	0.000098	0.052788
15600495	alanine racemase	5.67	5	1.35746118	0.039151	1
15597984	chemotaxis transducer	5.67	6	1.135068758	0.073109	1
15599562	superoxide dismutase	5.67	6	1.135068758	0.073109	1
15600714	short-chain dehydrogenase	5.67	7	0.94242368	0.123959	1
15598423	peptidyl-prolyl cis-trans isomerase A	5.67	23	-0.64253882	0.167501	1
15597840	NADH dehydrogenase subunit I	5.67	9	0.620495585	0.284211	1
15595623	Resistance-Nodulation-cell Division (RND) multidrug efflux transporter MexB	5.67	18	-0.305503833	0.535896	1
15599470	50S ribosomal protein L11	5.67	18	-0.305503833	0.535896	1
15595488	Anaerobically-induced outer membrane porin OprE precursor	5.67	17	-0.227501321	0.649261	1

15600324	phosphoglyceromutase	5.67	17	-0.227501321	0.649261	1
15600360	c4-dicarboxylate-binding protein	5.33	46	-1.694627332	0.000022	0.01217
15597500	protein AmbC	5.33	0	3.85996152	0.000174	0.090301
15597687	oxidoreductase	5.33	0	3.85996152	0.000174	0.090301
15598351	UDP-2-acetamido-2-dideoxy-d-ribo-hex-3- uluronic acid transaminase, wbpE	5.33	0	3.85996152	0.000174	0.090301
15598354	UDP-2-acetamido-2-deoxy-d-glucuronic acid 3-dehydrogenase, WbpB	5.33	0	3.85996152	0.000174	0.090301
15598924	hypothetical protein PA3729	5.33	0	3.85996152	0.000174	0.090301
15599324	hypothetical protein PA4129	5.33	0	3.85996152	0.000174	0.090301
15596030	hypothetical protein PA0833	5.33	38	-1.425440699	0.000651	0.287669
15595207	glycyl-tRNA synthetase subunit alpha	5.33	1	2.85996152	0.001067	0.41909
15600566	betaine aldehyde dehydrogenase	5.33	1	2.85996152	0.001067	0.41909
15596878	chorismate synthase	5.33	2	2.274999019	0.004086	0.858728
15595773	RNA polymerase sigma factor RpoD	5.33	3	1.85996152	0.011755	0.994995
15597825	adenylosuccinate lyase	5.33	6	1.052606598	0.101359	1
15598367	3-demethylubiquinone-9 3- methyltransferase	5.33	6	1.052606598	0.101359	1
15598721	argininosuccinate synthase	5.33	6	1.052606598	0.101359	1
15596951	transcriptional regulator CysB	5.33	23	-0.725000981	0.1247	1
15599619	hypothetical protein PA4423	5.33	20	-0.532355903	0.275564	1
15596750	cbb3-type cytochrome C oxidase subunit II	5.33	15	-0.14003848	0.788726	1
15598723	dihydroorotase	5.33	15	-0.14003848	0.788726	1
15598997	histidyl-tRNA synthetase	5.33	15	-0.14003848	0.788726	1
15595963	serine protease MucD	5.33	14	-0.046929076	0.929589	1
15596569	hypothetical protein PA1372	5	0	3.772498679	0.000307	0.150767
15599763	50S ribosomal protein L27	5	0	3.772498679	0.000307	0.150767
152985052	hypothetical protein PSPA7_3838	5	0	3.772498679	0.000307	0.150767

15599612	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	5	4	1.450570584	0.040859	1
15598677	hypothetical protein PA3481	5	7	0.772498679	0.220821	1
15595776	30S ribosomal protein S21	5	8	0.602573677	0.325338	1
15600615	hypothetical protein PA5422	5	11	0.187536178	0.742211	1
15596807	3-hydroxydecanoyl-ACP dehydratase	5	13	-0.034856243	0.949338	1
392985870	chemotactic transducer PctB	4.67	45	-1.844172682	0.000008	0.00478
15598019	hypothetical protein PA2823	4.67	0	3.679389274	0.000541	0.247545
15598873	Resistance-Nodulation-cell Division (RND) efflux membrane fusion protein	4.67	0	3.679389274	0.000541	0.247545
116054387	N-acetyl-gamma-glutamyl-phosphate reductase	4.67	0	3.679389274	0.000541	0.247545
152987372	transcriptional regulator Vfr	4.67	0	3.679389274	0.000541	0.247545
386057055	hypothetical protein PAM18_0988	4.67	0	3.679389274	0.000541	0.247545
15598322	heat-shock protein IbpA	4.67	2	2.094426774	0.010454	0.991257
15600271	glucan biosynthesis protein G	4.67	3	1.679389274	0.027527	0.999991
15597810	outer-membrane lipoprotein carrier protein	4.67	24	-0.964466915	0.045505	1
15596324	oxidoreductase	4.67	20	-0.712928148	0.157004	1
15597195	dehydrocarnitine CoA transferase subunit A	4.67	6	0.872034352	0.188389	1
15598823	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	4.67	6	0.872034352	0.188389	1
15596725	cell division protein ZipA	4.67	7	0.679389274	0.28936	1
15595622	Resistance-Nodulation-cell Division (RND) multidrug efflux membrane fusion protein MexA precursor	4.67	15	-0.320610726	0.552115	1
15595643	hypothetical protein PA0446	4.67	9	0.35746118	0.555564	1
15599952	carbamoyl phosphate synthase small subunit	4.67	13	-0.127965648	0.818458	1
15598304	amidophosphoribosyltransferase	4.67	12	-0.021050444	0.970434	1

15600230	hypothetical protein PA5037	4.67	12	-0.021050444	0.970434	1
15596133	lipopolysaccharide biosynthetic protein LpxO2	4.33	0	3.579853601	0.000952	0.386483
15597315	alcohol dehydrogenase	4.33	0	3.579853601	0.000952	0.386483
218893525	putative oxidoreductase	4.33	2	1.9948911	0.016559	0.999299
15599622	hypothetical protein PA4426	4.33	25	-1.120586117	0.021076	0.999893
15597935	phenylalanyl-tRNA synthetase subunit beta	4.33	3	1.579853601	0.041595	1
15599226	inorganic pyrophosphatase	4.33	21	-0.879578018	0.082509	1
15599920	two-component response regulator CbrB	4.33	20	-0.812463822	0.112909	1
15595514	hypothetical protein PA0317	4.33	5	0.9948911	0.15581	1
15597367	hypothetical protein PA2171	4.33	5	0.9948911	0.15581	1
15597903	hypothetical protein PA2707	4.33	5	0.9948911	0.15581	1
15598522	ATP-dependent Clp protease proteolytic subunit	4.33	6	0.772498679	0.252096	1
15598931	homoserine dehydrogenase	4.33	6	0.772498679	0.252096	1
15599671	hypothetical protein PA4475	4.33	6	0.772498679	0.252096	1
15598386	sugar ABC transporter substrate-binding protein	4.33	17	-0.590071401	0.267962	1
15598896	lysyl-tRNA synthetase	4.33	16	-0.50760924	0.347508	1
15599441	50S ribosomal protein L30	4.33	16	-0.50760924	0.347508	1
15599598	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	4.33	15	-0.420146399	0.443756	1
15600233	type 4 fimbrial biogenesis outer membrane protein PilQ precursor	4.33	15	-0.420146399	0.443756	1
116052451	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	4.33	15	-0.420146399	0.443756	1
15600017	hypothetical protein PA4824	4.33	14	-0.327036995	0.557473	1
15596969	ribonuclease activity regulator protein RraA	4.33	13	-0.227501321	0.688357	1
15597519	glyceraldehyde-3-phosphate dehydrogenase	4.33	13	-0.227501321	0.688357	1

15596153	prolyl-tRNA synthetase	4.33	10	0.120421982	0.841572	1
15600047	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	4.33	10	0.120421982	0.841572	1
15597660	hypothetical protein PA2464	4	0	3.472938397	0.001674	0.569377
15600755	chromosome partitioning protein Spo0J	4	2	1.887975896	0.026036	0.999985
15599532	hypothetical protein PA4336	4	23	-1.112024104	0.027633	0.999991
15598459	recombination associated protein	4	22	-1.050623559	0.039517	1
15596870	hypothetical protein PA1673	4	4	1.151010302	0.123517	1
15598362	chorismate mutase	4	4	1.151010302	0.123517	1
15600393	osmolarity response regulator	4	4	1.151010302	0.123517	1
15599135	DNA binding protein	4	6	0.665583475	0.332727	1
15599696	ABC transporter	4	6	0.665583475	0.332727	1
15599942	triosephosphate isomerase	4	6	0.665583475	0.332727	1
15598201	beta-hexosaminidase	4	7	0.472938397	0.476694	1
15598225	molybdopterin biosynthetic protein B2	4	7	0.472938397	0.476694	1
15600619	phosphoribosylaminoimidazole carboxylase catalytic subunit	4	7	0.472938397	0.476694	1
15595624	multidrug ABC transporter	4	13	-0.334416525	0.562754	1
15596400	hypothetical protein PA1203	4	12	-0.227501321	0.699129	1
15598146	trans-2-enoyl-CoA reductase	4	9	0.151010302	0.810129	1
15600410	iron ABC transporter	4	9	0.151010302	0.810129	1
15596294	transcriptional regulator FleQ	4	10	0.013506778	0.982442	0.999995
15597330	hypothetical protein PA2134	3.67	0	3.35746118	0.002937	0.76411
218892899	chaperone protein HchA	3.67	20	-1.034856243	0.052019	1
15597000	Lon protease	3.67	18	-0.890466334	0.102999	1
15597850	chemotaxis transducer	3.67	16	-0.730001662	0.193612	1
15599629	50S ribosomal protein L13	3.67	5	0.772498679	0.289001	1

15600432	transcription termination factor Rho	3.67	5	0.772498679	0.289001	1
15595606	twitching motility protein PilH	3.67	14	-0.549429416	0.343002	1
152985302	aminopeptidase N	3.67	14	-0.549429416	0.343002	1
15599635	tryptophanyl-tRNA synthetase	3.67	6	0.550106257	0.432623	1
15600334	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	3.67	6	0.550106257	0.432623	1
15599471	transcription antitermination protein NusG	3.67	12	-0.342978539	0.567909	1
15595493	glutamine synthetase	3.67	7	0.35746118	0.598045	1
15599433	50S ribosomal protein L17	3.67	7	0.35746118	0.598045	1
15599935	30S ribosomal protein S15	3.67	7	0.35746118	0.598045	1
15598330	glutamyl-tRNA synthetase	3.67	10	-0.101970439	0.870631	1
15596991	glutaminyl-tRNA synthetase	3.33	27	-1.575424625	0.001861	0.606726
15599029	valyl-tRNA synthetase	3.33	25	-1.468509421	0.004417	0.877862
15597365	hypothetical protein PA2169	3.33	0	3.231930297	0.005145	0.910567
116052260	ABC transporter ATP-binding protein	3.33	0	3.231930297	0.005145	0.910567
15600516	acetylglutamate kinase	3.33	1	2.231930297	0.02245	0.999936
15598313	aspartate-semialdehyde dehydrogenase	3.33	2	1.646967797	0.06271	1
15600273	prolyl aminopeptidase	3.33	2	1.646967797	0.06271	1
15598314	3-isopropylmalate dehydrogenase	3.33	17	-0.937994704	0.097314	1
15595534	phosphoenolpyruvate-protein phosphotransferase PtsP	3.33	4	0.910002203	0.242906	1
15595857	hypothetical protein PA0660	3.33	4	0.910002203	0.242906	1
15599980	3-ketoacyl-ACP reductase	3.33	4	0.910002203	0.242906	1
15595801	ABC transporter	3.33	14	-0.674960298	0.254349	1
15598200	5~-methylthioadenosine phosphorylase	3.33	5	0.646967797	0.384907	1
15595703	acyl-CoA dehydrogenase	3.33	12	-0.468509421	0.445234	1
15598870	hypothetical protein PA3674	3.33	12	-0.468509421	0.445234	1

15599621	phosphoheptose isomerase	3.33	11	-0.353032203	0.57287	1
15597629	hypothetical protein PA2433	3.33	7	0.231930297	0.737845	1
15600438	isoprenoid biosynthesis protein with amidotransferase-like domain	3.33	7	0.231930297	0.737845	1
15596655	two-component sensor	3.33	9	-0.089997797	0.890769	1
15597848	chemotaxis transducer	3.33	8	0.062005296	0.926574	1
15599651	ABC transporter permease	3.33	8	0.062005296	0.926574	1
15597837	NADH dehydrogenase I subunit F	3	31	-1.905573226	0.000143	0.075335
15599013	extragenic suppressor protein SuhB	3	0	3.094426774	0.008993	0.983889
15595956	hypothetical protein PA0759	3	1	2.094426774	0.036564	1
15600496	hypothetical protein PA5303	3	1	2.094426774	0.036564	1
15600629	acetyl-CoA carboxylase subunit A	3	18	-1.15350074	0.043568	1
15598843	hypothetical protein PA3647	3	15	-0.905573226	0.129103	1
15599646	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	3	14	-0.812463822	0.180316	1
15599741	competence protein ComL	3	4	0.772498679	0.333078	1
116052876	3-methyl-2-oxobutanoate hydroxymethyltransferase	3	12	-0.606012944	0.33495	1
15598317	isopropylmalate isomerase large subunit	3	11	-0.490535727	0.444275	1
15600745	glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridyltransferase	3	5	0.509464273	0.504068	1
386058262	putative peroxidase	3	5	0.509464273	0.504068	1
15599604	cell division protein FtsA	3	10	-0.365004845	0.577544	1
15599668	PmbA protein	3	10	-0.365004845	0.577544	1
15596093	arginine/ornithine succinyltransferase AI subunit	3	9	-0.227501321	0.734625	1
15600525	catabolite repression control protein	3	9	-0.227501321	0.734625	1
15597816	ATP-binding protease component ClpA	2.67	25	-1.758016038	0.001184	0.45158

15596945	enoyl-CoA hydratase	2.67	22	-1.581138276	0.004691	0.891819
15595848	indole-3-glycerol phosphate synthase	2.67	0	2.94242368	0.015676	0.999028
15597342	hypothetical protein PA2146	2.67	0	2.94242368	0.015676	0.999028
15599424	pyochelin biosynthesis protein PchD	2.67	0	2.94242368	0.015676	0.999028
15600634	hypothetical protein PA5441	2.67	0	2.94242368	0.015676	0.999028
15597936	phenylalanyl-tRNA synthetase subunit alpha	2.67	17	-1.227501321	0.039029	1
116053323	ADP-ribose diphosphatase NudE	2.67	1	1.94242368	0.059074	1
15599765	octaprenyl-diphosphate synthase	2.67	13	-0.864931242	0.1721	1
15597221	glutathione reductase	2.67	11	-0.64253882	0.329062	1
15598543	hypothetical protein PA3347	2.67	11	-0.64253882	0.329062	1
15600048	phosphoribosylamine--glycine ligase	2.67	4	0.620495585	0.448902	1
15598560	aliphatic amidase expression-regulating protein	2.67	5	0.35746118	0.647973	1
15598676	deoxycytidine triphosphate deaminase	2.67	5	0.35746118	0.647973	1
15598998	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	2.67	5	0.35746118	0.647973	1
15600417	aminopeptidase	2.67	8	-0.227501321	0.747768	1
15595218	hypothetical protein PA0020	2.67	6	0.135068758	0.857702	1
15600321	preprotein translocase subunit SecB	2.67	6	0.135068758	0.857702	1
15600562	phosphate ABC transporter substrate-binding protein	2.33	84	-3.636892257	7.39E-19	0.00E+00
15596752	cytochrome C oxidase cbb3-type, CcoP subunit	2.33	21	-1.68693294	0.003764	0.838188
15596947	phospho-2-dehydro-3-deoxyheptonate aldolase	2.33	0	2.772498679	0.02724	0.99999
15598301	general secretion pathway protein D	2.33	0	2.772498679	0.02724	0.99999
15597815	translation initiation factor IF-1	2.33	9	-0.549429416	0.438787	1
15599016	preprotein translocase subunit SecD	2.33	9	-0.549429416	0.438787	1



15598996	hypothetical protein PA3801	2.33	4	0.450570584	0.593403	1
15600614	glutathione-independent formaldehyde dehydrogenase	2	89	-3.911999495	5.67E-21	0.00E+00
15598764	acetyl-coa synthetase	2	33	-2.50760924	0.000003	0.001886
15597972	hypothetical protein PA2776	2	30	-2.37434271	0.000017	0.009466
15599692	ABC transporter	2	28	-2.278127394	0.000049	0.02689
15599783	cytochrome C551 peroxidase precursor	2	20	-1.812463822	0.002914	0.762123
15597836	NADH dehydrogenase subunit E	2	17	-1.590071401	0.012016	0.995501
15595202	DNA gyrase subunit B	2	14	-1.327036995	0.045267	1
15598657	hypothetical protein PA3461	2	0	2.579853601	0.047163	1
15596717	transcriptional regulator	2	12	-1.120586117	0.102884	1
15598207	DNA topoisomerase I	2	11	-1.0051089	0.151604	1
15595511	L-cysteine transporter of ABC system FliY	2	9	-0.742074494	0.311824	1
15595599	aspartate carbamoyltransferase	2	9	-0.742074494	0.311824	1
15598001	hypothetical protein PA2805	2	8	-0.590071401	0.433445	1
15599358	amidase	2	7	-0.420146399	0.588129	1
15597018	enoyl-CoA hydratase	1.67	22	-2.166100777	0.000456	0.214204
15598545	chemotaxis protein	1.67	16	-1.730001662	0.009523	0.987141
15596753	cbb3-type cytochrome C oxidase subunit II	1.67	12	-1.342978539	0.059955	1
15596261	hypothetical protein PA1064	1.67	0	2.35746118	0.08129	1
15598246	dihydroorotate dehydrogenase	1.67	10	-1.101970439	0.138832	1
15595943	acyl-CoA dehydrogenase	1.67	9	-0.964466915	0.205912	1
15599954	molecular chaperone DnaJ	1.67	9	-0.964466915	0.205912	1
15600330	hypothetical protein PA5137	1.67	9	-0.964466915	0.205912	1
15600590	hypothetical protein PA5397	1.33	16	-1.993036068	0.004297	0.871207
15598316	isopropylmalate isomerase small subunit	1.33	11	-1.490535727	0.050516	1
15598810	hypothetical protein PA3614	1.33	11	-1.490535727	0.050516	1
15598646	antioxidant protein	1.33	10	-1.365004845	0.079757	1

15598537	transcriptional regulator	1.33	6	-0.712928148	0.413884	1
15598498	hypothetical protein PA3302	1	21	-2.68693294	0.000098	0.052863
15600558	phosphate uptake regulatory protein PhoU	1	20	-2.619818744	0.000175	0.090137
15598850	uridylate kinase	1	17	-2.397426323	0.000966	0.389844
15599126	hypothetical protein PA3931	1	17	-2.397426323	0.000966	0.389844
15600738	hypothetical protein PA5545	1	12	-1.927941039	0.014586	0.998466
15598324	short-chain dehydrogenase	1	9	-1.549429416	0.066207	1
15600130	exoribonuclease R	1	9	-1.549429416	0.066207	1
15600456	argininosuccinate lyase	1	7	-1.227501321	0.168846	1
15596641	flagellar motor switch protein	1	6	-1.034856243	0.261956	1
15600761	inner membrane protein translocase component YidC	1	6	-1.034856243	0.261956	1
15600591	dimethylglycine catabolism protein DgcA	0.67	54	-4.423898534	1.71E-14	1.12E-11
15600603	protein GbcA	0.67	49	-4.28639501	4.56E-13	2.95E-10
15599167	acyl-CoA dehydrogenase	0.67	13	-2.449893743	0.003199	0.789927
15600189	bifunctional heptose 7-phosphate kinase/heptose 1-phosphate adenylyltransferase	0.67	10	-2.101970439	0.017406	0.999501
15599890	acetolactate synthase 3 catalytic subunit	0.67	7	-1.64253882	0.086496	1
15596238	hypothetical protein PA1041	0.33	37	-4.475428835	1.56E-10	9.85E-08
15598432	glycine betaine-binding protein	0.33	35	-4.397426323	5.87E-10	3.70E-07
15600589	hypothetical protein PA5396	0.33	11	-2.812463822	0.003192	0.789858
15598907	hypothetical protein PA3712	0.33	8	-2.397426323	0.019619	0.999804
15598096	hypothetical protein PA2900	0.33	6	-2.034856243	0.063237	1
386068630	putative ClpA/B protease ATP binding subunit	0	263	-8.271895441	2.48E-79	0.00E+00
392984201	dihydrolipoamide dehydrogenase	0	201	-7.885712804	1.04E-60	0.00E+00
152985351	A-type flagellin	0	186	-7.774395781	3.33E-56	0.00E+00

218890120	elongation factor Ts	0	179	-7.719354418	4.21E-54	0.00E+00
116049294	ABC transporter substrate-binding protein	0	123	-7.181697632	2.67E-37	0.00E+00
116053992	succinate-semialdehyde dehydrogenase I	0	106	-6.968968308	3.34E-32	0.00E+00
116050611	monomeric isocitrate dehydrogenase	0	85	-6.653766076	6.51E-26	0.00E+00
116051135	aromatic amino acid aminotransferase	0	80	-6.567351324	2.04E-24	0.00E+00
15597267	elongation factor G	0	76	-6.494287862	3.22E-23	0.00E+00
15599603	cell division protein FtsZ	0	49	-5.871357511	3.76E-15	2.48E-12
116052343	chemotactic transducer PctA	0	46	-5.782090173	2.95E-14	1.92E-11
218893071	Basic amino acid, basic peptide and imipenem outer membrane porin OprD precursor	0	42	-5.653766076	4.58E-13	2.97E-10
15600611	sarcosine oxidase subunit alpha	0	40	-5.585053326	1.81E-12	1.17E-09
15600106	ABC transporter	0	39	-5.549429416	3.59E-12	2.31E-09
218893133	succinylglutamic semialdehyde dehydrogenase	0	38	-5.51290354	7.12E-12	4.57E-09
218890204	3-hydroxyisobutyrate dehydrogenase	0	36	-5.436954687	2.80E-11	1.79E-08
15598614	leucine dehydrogenase	0	31	-5.227501321	8.57E-10	0.000001
15600179	oxidoreductase	0	30	-5.181697632	1.70E-09	0.000001
15598918	FMN oxidoreductase	0	28	-5.085482316	6.66E-09	0.000004
386059096	methylcrotonyl-CoA carboxylase subunit alpha	0	28	-5.085482316	6.66E-09	0.000004
116050457	anthranilate dioxygenase small subunit	0	26	-4.982388823	2.61E-08	0.000016
386059105	3-hydroxybutyrate dehydrogenase	0	26	-4.982388823	2.61E-08	0.000016
15596906	translocator outer membrane protein PopD precursor	0	24	-4.871357511	1.02E-07	0.000063
116050451	catechol 1,2-dioxygenase	0	24	-4.871357511	1.02E-07	0.000063
15599119	long-chain-fatty-acid--CoA ligase	0	22	-4.751063277	3.98E-07	0.00024
218893619	type 4 fimbrial Pila	0	21	-4.68693294	0.000001	0.000472
15600275	ABC transporter	0	20	-4.619818744	0.000002	0.000929

15597431	protein PslE	0	19	-4.549429416	0.000003	0.001822
15598613	pyruvate dehydrogenase E1 component subunit alpha	0	19	-4.549429416	0.000003	0.001822
116051435	branched-chain alpha-keto acid dehydrogenase subunit	0	19	-4.549429416	0.000003	0.001822
152986800	chemotaxis-specific methylesterase	0	19	-4.549429416	0.000003	0.001822
392984203	2-oxoisovalerate dehydrogenase subunit beta	0	19	-4.549429416	0.000003	0.001822
15597428	protein PslB	0	18	-4.475428835	0.000006	0.003516
386056371	hypothetical protein PAM18_0302	0	18	-4.475428835	0.000006	0.003516
15598985	copper transport outer membrane porin OprC	0	17	-4.397426323	0.000012	0.006796
15598579	phosphonate ABC transporter substrate-binding protein	0	15	-4.227501321	0.000046	0.025522
116049404	chemotaxis-specific methylesterase	0	15	-4.227501321	0.000046	0.025522
386060636	aspartyl/glutamyl-tRNA amidotransferase subunit B	0	15	-4.227501321	0.000046	0.025522
218891081	phenylalanyl-tRNA synthetase subunit beta	0	14	-4.134391917	0.00009	0.04894
15596905	translocator protein PopB	0	13	-4.034856243	0.000178	0.091087
15598421	transcriptional regulator	0	12	-3.927941039	0.000348	0.168227
15595859	N-acetyl-gamma-glutamyl-phosphate reductase	0	11	-3.812463822	0.000682	0.298641
15597958	hypothetical protein PA2762	0	11	-3.812463822	0.000682	0.298641
15598446	hypothetical protein PA3250	0	11	-3.812463822	0.000682	0.298641
15599856	lipid A 3-O-deacylase	0	11	-3.812463822	0.000682	0.298641
15596661	purine-binding chemotaxis protein	0	10	-3.68693294	0.001334	0.491075
15597700	hypothetical protein PA2504	0	10	-3.68693294	0.001334	0.491075
116053449	alanine racemase	0	10	-3.68693294	0.001334	0.491075
15599716	chemotaxis transducer	0	9	-3.549429416	0.002605	0.725094

15600571	hypothetical protein PA5378	0	8	-3.397426323	0.005079	0.908659
116049657	regulatory protein PcrH	0	8	-3.397426323	0.005079	0.908659
15599772	ATP-dependent protease	0	5	-2.812463822	0.037068	1

**Abbreviations:** RefSeq: reference sequence, SC: scan count, NLOG-FoldR: normalized log ratio, Np: normalized p value, Adj-NP: adjusted normalized p value  
 \*Normalized ratios are calculated from the ratio of the scans (clinical/ATCC10145) adjusted to the ratio of the total scans for all proteins detected in each group.