

**Table S2. List of all statistically significantly changed proteins in a comparative proteomics analysis of *P. aeruginosa* PA14 cells grown aerobically in AB medium with 2,3-butanediol or glucose as carbon source, respectively.**

Functional category	Label	log (B/G) down	log (B/G) up
Quorum sensing/Virulence factors/Biofilm formation	PA14_30800 Putative nitroreductase	-0.854	
	PA14_18180 Putative antibiotic biosynthesis monooxygenase	-0.750	
	PA14_61390 Putative lipoprotein	-0.658	
	PA14_27460 Thiopurine methyl transferase	-0.398	
	PA14_28450 Ecotin precursor		0.336
	PA14_7650 Putative sporulation protein		0.406
	PA14_65000 Azurin precursor		0.444
	PA14_62420 Zinc metallo peptidase		0.484
	PA14_1490 Putative hemolysin		0.486
	PA14_69370 Alginate regulatory protein AlgP		0.496
	PA14_36980 Putative outer membrane protein		0.568
	PA14_56070 Transcriptional regulator MvaT P-16 subunit		0.582
Transporter	PA14_3930 Putrescine ABC transporter putrescine-binding protein potF	-0.575	
	PA14_62650 TolA protein	-0.399	
	PA14_16510 Peptide chain release factor 2	-0.368	
	PA14_68260 TRAP-type C4-dicarboxylate transport system, periplasmic component		0.328
	PA14_51810 FIG000859 (not subsystem-based): hypothetical protein		0.372
	PA14_21175 Phosphonate ABC transporter phosphate-binding periplasmic component		0.399
	PA14_46910 Glutamate Aspartate periplasmic binding protein precursor gtlI		0.407
	PA14_50520 High-affinity leucine-specific transport system, periplasmic binding protein livK		0.415
Transporter	PA14_52790 Arginine/ornithine ABC transporter, periplasmic arginine/ornithine binding protein		0.448
	PA14_45930 GGDEF and EAL domain proteins		0.454
	PA14_24020 General secretion pathway protein G		0.501
	PA14_67840 Glutamate ABC transporter, periplasmic glutamine-binding protein		0.579
	PA14_57840 Uncharacterized ABC transporter, auxiliary component YrbC		0.613
	PA14_64900 Branched-chain amino acid ABC transporter, amino acid-binding protein		0.646
	PA14_7870 ABC transporter, periplasmic spermidine putrescine-binding protein potD		0.656
	PA14_46220 Putrescine ABC transporter putrescine-binding protein potF		1.113
	PA14_54540 Putative tricarboxylic transport TetC		1.122
	PA14_68070 Arginine/ornithine ABC transporter, periplasmic arginine/ornithine binding protein		1.210
	PA14_39350 Ribose ABC transport system, periplasmic ribose-binding protein RbsB		1.367
	PA14_14390 Putative ABC-type transport protein periplasmic c		1.399

	PA14_73120 Putative periplasmic transport protein		1.501
	PA14_33530 Putative ABC transporter periplasmic substrate binding protein		1.501
	PA14_67850 ABC type amino acid transport protein periplasmic component		1.656
Structure	PA14_14910 Outer membrane protein YfgL,	-0.832	
	PA14_68200 Glucose-1-phosphate thymidyltransferase	-0.758	
	PA14_68210 dTDP-4-dehydrorhamnose 3,5-epimerase	-0.548	
	PA14_50930 type IV pilus biogenesis protein PilE		0.307
	PA14_63030 Outer membrane lipoprotein SmpA,		0.447
Structure	PA14_30310 Outer membrane lipoprotein carrier protein LolA		0.561
Stress Response	PA14_34460 Alkylhydroperoxidase	-1.775	
	PA14_67090 Glucans biosynthesis protein G precursor	-0.775	
	PA14_56590 Universal stress protein family 4	-0.647	
	PA14_68380 ADP compounds hydrolase NudE	-0.565	
	PA14_56940 Copper sensory histidine kinase CusS	-0.503	
	PA14_4730 Gamma-glutamyltranspeptidase	-0.409	
	PA14_21220 Universal stress protein family	-0.332	
	PA14_48590 Trans-aconitate 2-methyltransferase	-0.304	
	PA14_62970 Chaperone protein DnaK		0.339
	PA14_24770 Probable transmembrane protein		0.368
	PA14_70740 Probable transmembrane protein		0.577
	PA14_49410 Cold shock protein		1.368
PA14_21760 Cold acclimation protein B		1.577	
Regulation	PA14_73020 C4-type zinc finger protein, DksA/TraR family	-1.099	
	PA14_23720 Putative translation initiation inhibitor, yjgF family	-0.440	
	PA14_64930 Nudix-related transcriptional regulator NrtR	-0.390	
	PA14_25800 Transcriptional regulator, TetR family	-0.390	
	PA14_65280 HflK protein	-0.306	
	PA14_52570 Carbon storage regulator		0.376
PA14_41250 Cell division trigger factor		0.397	
Redox	PA14_22710 Coenzyme F420-1:L-glutamate ligase	-0.759	
	PA14_14680 Myo-inositol-1(or 4)-monophosphatase	-0.576	
	PA14_69420 Homolog of E. coli HemY protein	-0.545	
	PA14_23380 UDP-N-acetyl-D-mannosaminuronate dehydrogenase	-0.503	
Redox	PA14_46980 Signal transduction histidine kinase HoxJ	-0.463	
	PA14_15120 Copper metallochaperone, bacterial analog of Cox17 protein	-0.374	
	PA14_20140 Ferredoxin--NADP(+) reductase	-0.334	
	PA14_69970 membrane c-type cytochrome cy		0.305
	PA14_31810 Thiol peroxidase, Tpx-type		0.337
	PA14_69200 Thioredoxin		0.424
	PA14_14750 Iron binding protein IscA for iron-sulfur cluster assembly		0.557
PA14_51980 Arsenate reductase		0.692	

	PA14_29020 Biotin synthesis protein bioH		0.778
Phosphorous metabolism	PA14_28960 PhnB protein	-0.305	
	PA14_46830 PhnB protein		0.341
	PA14_2450 NAD(P) transhydrogenase alpha subunit		0.493
	PA14_11690 Inorganic pyrophosphatase		0.537
	PA14_64460 Phosphate starvation inducible protein		1.537
Phenazines	PA14_39960 Phenazine biosynthesis protein PhzB		0.487
	PA14_9420 Phenazine biosynthesis protein PhzF		0.550
Chemotaxis/Motility	PA14_30700 Chemotaxis protein methyltransferase CheR	-1.413	
	PA14_68400 Flagellar hook-length control protein fliK	-0.343	
	PA14_67010 Aerotaxis sensor receptor protein	-0.338	
	PA14_58390 Dipeptide-binding ABC transporter, periplasmic substrate-binding component		0.366
	PA14_61200 Flagellar hook-length control protein fliK		0.482
	PA14_58350 Dipeptide-binding ABC transporter, periplasmic substrate-binding component		0.589
	PA14_45810 Flagellar biosynthesis protein fliL		0.808
Chemotaxis/Motility	PA14_69100 Flagellar biosynthesis protein fliL		0.822
Metabolism	PA14_53250 Chitin binding protein	-1.080	
	PA14_71720 Pyruvate carboxyl transferase subunit B	-0.956	
	PA14_67500 Lactoylglutathione lyase	-0.907	
	PA14_22910 Phosphogluconate dehydratase	-0.777	
	PA14_49660 Beta-galactosidase	-0.691	
	PA14_15340 GMP synthase	-0.587	
	PA14_37570 Benzoate 1,2-dioxygenase (EC 1.14.12.10)	-0.578	
	PA14_27960 Transaldolase (EC 2.2.1.2)	-0.472	
	PA14_25080 Enoyl-CoA hydratase (EC 4.2.1.17)	-0.471	
	PA14_53220 Fumarate hydratase class II (EC 4.2.1.2)	-0.449	
	PA14_54470 YgfY COG2938	-0.434	
	PA14_25660 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	-0.431	
	PA14_41670 Phosphoenolpyruvate synthase (EC 2.7.9.2)	-0.399	
	PA14_8460 Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9)	-0.398	
	PA14_56240 Pyruvate kinase (EC 2.7.1.40)	-0.383	
	PA14_57890 Arabinose 5-phosphate isomerase (EC 5.3.1.13)	-0.370	
	PA14_66290 Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	-0.367	
	PA14_10290 Transcriptional activator of acetoin dehydrogenase operon acoR	-0.366	
	PA14_40830 Alcohol dehydrogenase (EC 1.1.1.1)	-0.356	
	PA14_27730 Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)	-0.355	
	PA14_70370 Orotate phosphoribosyltransferase (EC 2.4.2.10)	-0.354	
	PA14_71850 diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)	-0.353	
Metabolism	PA14_57600 Putative oxido-reductase aldo-keto reductase family	-0.351	

	PA14_21540 3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41)	-0.335	
	PA14_25090 Acetyl-CoA acetyltransferase (EC 2.3.1.9)	-0.331	
	PA14_25650 Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	-0.323	
	PA14_4150 Fumarylacetoacetate hydrolase family protein	-0.315	
	PA14_10250 Acetoin dehydrogenase E1 component beta-subunit (EC 1.2.4.-)		0.316
	PA14_9550 6-phosphogluconolactonase (EC 3.1.1.31)		0.329
	PA14_49330 Candidate 1: diene lactone hydrolase		0.347
	PA14_11810 Aldehyde dehydrogenase (EC 1.2.1.3)		0.398
	PA14_10230 2,3-butanediol dehydrogenase, R-alcohol forming, (R)- and (S)-acetoin-specific (EC 1.1.1.4)		0.401
	PA14_73280 ATP synthase delta chain (EC 3.6.3.14)		0.435
	PA14_73230 ATP synthase epsilon chain (EC 3.6.3.14)		0.459
	PA14_10260 Acetoin dehydrogenase E1 component alpha-subunit (EC 1.2.4.-)		0.485
	PA14_64110 Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)		0.486
	PA14_10280 Short-chain alcohol dehydrogenase associated with acetoin utilization		0.615
	PA14_10240 Dihydroliipoamide acetyltransferase component (E2) of acetoin dehydrogenase complex (EC 2.3.1.-)		0.683
	PA14_51170 Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative		0.736
	PA14_24790 hydroxycinnamate specific porine		0.785
	PA14_25670 Acyl carrier protein		0.797
	PA14_38860 Quino(hemo)protein alcohol dehydrogenase, PQQ-dependent (EC 1.1.99.8)		1.077
Metabolism	PA14_66875 Polyhydroxyalkanoate synthesis protein PhaF		1.486
	PA14_25900 Putative short chain alcohol-dehydrogenase		
Iron acquisition	PA14_3800 Outer membrane porin, coexpressed with pyoverdine biosynthesis regulon	-0.967	
	PA14_9220 Pyochelin biosynthetic protein PchB	-0.589	
	PA14_42820 Isochorismatase (EC 3.3.2.1)	-0.429	
	PA14_62300 Periplasmic hemin-binding protein	-0.356	
	PA14_33710 PvdO, pyoverdine responsive serine/threonine kinase		0.380
	PA14_56830 Iron-regulated protein A precursor		0.397
DNA/RNA/protein	PA14_70190 LSU ribosomal protein L28p	-0.950	
	PA14_41380 Glutaminyl-tRNA synthetase (EC 6.1.1.18)	-0.749	
	PA14_19870 Leucine dehydrogenase (EC 1.4.1.9)	-0.742	
	PA14_70270 Phosphomannomutase (EC 5.4.2.8)	-0.646	
	PA14_58630 ArPA14nine decarboxylase (EC 4.1.1.19)	-0.580	
	PA14_72520 Ribonucleotide reductase of class II (coenzyme B12-dependent) (EC 1.17.4.1)	-0.560	
	PA14_12400 Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)	-0.545	
	PA14_49870 Peptide deformylase (EC 3.5.1.88)	-0.505	
	PA14_5230 Cystathionine gamma-lyase (EC 4.4.1.1)	-0.475	

	PA14_54640 Enoyl-CoA hydratase [valine degradation] (EC 4.2.1.17)	-0.459	
	PA14_23320 Cytidylate kinase (EC 2.7.4.14)	-0.449	
	PA14_54480 COG0354: Predicted aminomethyltransferase related to GcvT	-0.440	
	PA14_28650 Threonyl-tRNA synthetase (EC 6.1.1.3)	-0.407	
	PA14_3450 5-aminovalerate aminotransferase (EC 2.6.1.48)	-0.403	
	PA14_70440 Guanylate kinase (EC 2.7.4.8)	-0.403	
DNA/RNA/protein	PA14_23110 Pseudouridine synthase family protein	-0.392	
	PA14_12080 Membrane-bound lytic murein transglycosylase B (EC 3.2.1.-)	-0.390	
	PA14_25560 Ribonuclease E (EC 3.1.4.-)	-0.389	
	PA14_51310 tRNA 5-methylaminomethyl-2-thiouridine synthase TusA	-0.362	
	PA14_8760 DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	-0.361	
	PA14_67810 Carboxyl-terminal protease (EC 3.4.21.102)	-0.356	
	PA14_8790 SSU ribosomal protein S12p (S23e)	-0.351	
	PA14_24445 NADP-specific glutamate dehydrogenase (EC 1.4.1.4)	-0.347	
	PA14_24270 Membrane alanine aminopeptidase N (EC 3.4.11.2)	-0.341	
	PA14_64490 LSU ribosomal protein L21p	-0.332	
	PA14_67110 Proline iminopeptidase (EC 3.4.11.5)	-0.326	
	PA14_12230 Leucyl-tRNA synthetase (EC 6.1.1.4)	-0.316	
	PA14_57580 SSU ribosomal protein S9p (S16e)	-0.311	
	PA14_66790 ATP-dependent hsl protease ATP-binding subunit hslU	-0.303	
	PA14_20 DNA polymerase III beta subunit (EC 2.7.7.7)	-0.303	
	PA14_57010 Heat shock protein 60 family chaperone GroEL		0.323
	PA14_60460 LSU ribosomal protein L21p		0.326
	PA14_8990 SSU ribosomal protein S8p (S15Ae)		0.339
	PA14_9000 LSU ribosomal protein L6p (L9e)		0.351
	PA14_8940 SSU ribosomal protein S17p (S11e)		0.353
	PA14_45110 Sulfate and thiosulfate binding protein cysP		0.353
	PA14_30330 Seryl-tRNA synthetase (EC 6.1.1.11)		0.366
	PA14_21030 ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92)		0.375
PA14_62900 Transcription elongation factor GreA		0.405	
DNA/RNA/protein	PA14_17050 Methionine aminopeptidase (EC 3.4.11.18)		0.406
	PA14_22450 Peptidyl-prolyl cis-trans isomerase ppiA precursor (EC 5.2.1.8)		0.423
	PA14_17060 SSU ribosomal protein S2p (SAe)		0.440
	PA14_23330 SSU ribosomal protein S1p		0.444
	PA14_21880 Tail-specific protease precursor (EC 3.4.21.102)		0.449
	PA14_9010 LSU ribosomal protein L18p (L5e)		0.450
	PA14_46970 L-asparaginase (EC 3.5.1.1)		0.452
	PA14_62720 SSU ribosomal protein S15p (S13e)		0.499
	PA14_8720 LSU ribosomal protein L11p (L12e)		0.584
	PA14_41390 Peptidyl-prolyl cis-trans isomerase ppiB (EC 5.2.1.8)		0.658

	PA14_70600 DNA-binding protein HU-alpha		0.682
	PA14_68860 Glycine cleavage system H protein		0.841
	PA14_44620 conserved protein of unknown function likely to be involved in DNA repair		0.892
	PA14_8750 LSU ribosomal protein L7/L12 (L23e)		0.921
	PA14_9890 Peptidyl-prolyl cis-trans isomerase ppiC (EC 5.2.1.8)		0.979
	PA14_65310 RNA-binding protein Hfq		1.039
	PA14_27210 Translation elongation factor P		1.080
	PA14_8930 LSU ribosomal protein L29p (L35e)		1.110
	PA14_68710 TRANSCRIPTION ACCESSORY PROTEIN (S1 RNA binding domain)		1.225
	PA14_ Putative ribosomal protein L25		2.225
Miscellaneous	PA14_30800 Putative nitroreductase	-0.854	
	PA14_18180 Putative antibiotic biosynthesis monooxygenase	-0.750	
Miscellaneous	PA14_61390 Putative lipoprotein	-0.658	
	PA14_27460 Thiopurine methyl transferase	-0.398	
	PA14_28450 Ecotin precursor		0.336
	PA14_7650 Putative sporulation protein		0.406
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	PA14_62420 Zinc metallo peptidase		0.484
	PA14_1490 Putative hemolysin		0.486
	PA14_69370 AIPA14nate regulatory protein		0.496
	PA14_36980 Putative outer membrane protein		0.568
	PA14_56070 Transcriptional regulator MvaT P-16 subunit		0.582