Gene no.	Description	Gene name	Class[a]	GRAVY[b]	TMD[c]
PA0004	DNA gyrase subunit B		2	-0.411	0
PA0011	probable 2-OH-lauroyltransferase		3	-0.094	0
PA0040	conserved hypothetical protein		4	-0.593	0
PA0070	hypothetical protein		4	-0.481	1
PA0077	hypothetical protein	pvdS	4	-0.244	1
PA0126	hypothetical protein	gcd	4	-0.316	0
PA0139	alkyl hydroperoxide reductase subunit C		2	-0.182	0
PA0260	hypothetical protein		4	-0.37	0
PA0266	4-aminobutyrate aminotransferase		2	0.142	1
PA0290	hypothetical protein	fabB	4	-0.364	0
PA0295	probable periplasmic polyamine binding protein		3	-0.214	0
PA0341	prolipoprotein diacylglyceryl transferase		2	0.526	4
PA0389	hypothetical protein		4	-0.234	0
PA0520	regulatory protein NirQ	oprF	1	-0.166	0
PA0595	organic solvent tolerance protein OstA precursor		2	-0.599	0
PA0652	transcriptional regulator Vfr	pscC	1	-0.25	0
PA0658	probable short-chain dehydrogenase		3	0.039	0
PA0659	hypothetical protein		4	0.182	4
PA0716	hypothetical protein		4	-0.098	0
PA0789	probable amino acid permease		3	0.784	12
PA0809	probable transporter	nqrF	3	0.825	10
PA0867	hypothetical protein		4	-0.224	0
PA0892	arginine/ornithine transport protein AotP	serC	1	-0.17	0
PA0936	lipopolysaccharide biosynthetic protein LpxO2		2	-0.138	1
PA0944	phosphoribosylaminoimidazole synthetase	wbpB	2	-0.334	1
PA0949	Trp repressor binding protein WrbA	wbpG	2	0.031	1
PA1003	probable transcriptional regulator	wbpJ	3	-0.138	0
PA1064	hypothetical protein	xcpY	4	-0.381	0
PA1097	transcriptional regulator FleQ		1	-0.364	0
PA1222	probable membrane-bound lytic murein transglycolase A	nuoD	3	-0.265	0
PA1339	probable ATP-binding component of ABC transporter		3	-0.072	0
PA1361	probable transporter	fadD1	3	0.632	11
PA1430	transcriptional regulator LasR		1	-0.02	0
PA1454	flagellar synthesis regulator FleN	oprI	1	0.196	1
PA1482	cytochrome C-type biogenesis protein CcmH		2	-0.176	1
PA1549	probable cation-transporting P-type ATPase		3	0.161	5
PA1581	succinate dehydrogenase (C subunit)		2	0.841	3
PA1583	succinate dehydrogenase (A subunit)		2	-0.18	1
PA1584	succinate dehydrogenase (B subunit)		2	-0.212	0
PA1587	lipoamide dehydrogenase-glc		2	0.135	1

Gene no.	Description	Gene name	Class[a]	GRAVY[b]	TMD[c]
PA1609	beta-ketoacyl-ACP synthase I		1	-0.087	0
PA1641	hypothetical protein		4	-0.22	0
PA1662	probable ClpA/B-type protease		3	-0.201	0
PA1689	conserved hypothetical protein		4	0.003	5
PA1716	Type III secretion outer membrane protein PscC precursor		1	-0.231	0
PA1746	hypothetical protein	vfr	4	-0.031	0
PA1777	Major porin and structural outer membrane porin OprF precursor	ostA	1	-0.443	0
PA1807	probable ATP-binding component of ABC transporter	nirQ	3	-0.08	1
PA1822	hypothetical protein		4	-0.035	0
PA1901	phenazine biosynthesis protein PhzC	lgt	2	-0.259	0
PA1969	hypothetical protein	gyrB	4	-0.085	0
PA2042	probable transporter (membrane subunit)		3	1.024	9
PA2122	hypothetical protein		4	-0.239	2
PA2177	probable sensor/response regulator hybrid		3	-0.349	0
PA2290	glucose dehydrogenase	ahpC	2	-0.098	4
PA2426	sigma factor PvdS		1	-0.35	0
PA2537	probable acyltransferase		3	-0.044	0
PA2540	conserved hypothetical protein		4	-0.214	0
PA2587	probable FAD-dependent monooxygenase		3	-0.01	0
PA2627	conserved hypothetical protein	fleQ	4	-0.151	0
PA2639	NADH dehydrogenase I chain C,D	gabT	2	-0.351	1
PA2743	translation initiation factor IF-3		2	-0.608	0
PA2756	hypothetical protein	sdhB	4	-0.098	0
PA2776	conserved hypothetical protein	sdhA	4	-0.161	1
PA2793	hypothetical protein	sdhC	4	-0.398	0
PA2815	probable acyl-CoA dehydrogenase		3	0.03	2
PA2820	hypothetical protein	ccmH	4	-0.329	1
PA2853	Outer membrane lipoprotein OprI precursor		1	-0.541	0
PA2930	probable transcriptional regulator	lasR	3	-0.132	0
PA2953	electron transfer flavoprotein-ubiquinone oxidoreductase		2	-0.27	0
PA2983	probable tolQ-type transport protein		3	0.373	2
PA2994	Na+-translocating NADH:quinone oxidoreductase, subunit Nqr6		2	-0.186	0
PA3001	probable glyceraldehyde-3-phosphate dehydrogenase	lpdG	3	-0.168	0
PA3096	general secretion pathway protein L		1	-0.027	1
PA3147	probable glycosyl transferase WbpJ		3	0.119	2
PA3150	LPS biosynthesis protein WbpG	wrbA	1	-0.362	0
PA3158	probable oxidoreductase WpbB	purN	3	-0.266	0
PA3164	still frameshift 3-PHOSPHOSHIKIMATE 1-	lpxO2	2	0.074	4

Gene no.	Description	Gene name	Class[a]	GRAVY[b]	TMD[c]
	CARBOXYVINYLTRANSFERASE prephenate dehydrogenase				
PA3167	3-phosphoserine aminotransferase	aotP	2	-0.232	0
PA3242	probable lauroyl acyltransferase		3	-0.348	2
PA3299	long-chain-fatty-acid--CoA ligase	narH	2	-0.027	1
PA3391	regulatory protein NosR	atpH	2	0.074	6
PA3456	hypothetical protein	infC	4	-0.053	1
PA3468	conserved hypothetical protein	pilQ	4	0.145	4
PA3529	probable peroxidase		3	-0.077	0
PA3531	bacterioferritin		2	-0.52	0
PA3554	conserved hypothetical protein		4	-0.253	0
PA3602	conserved hypothetical protein	psd	4	-0.059	1
PA3617	RecA protein	osmE	1	-0.131	1
PA3626	conserved hypothetical protein	fdnG	4	-0.215	1
PA3648	probable outer membrane protein precursor	mreB	3	-0.368	0
PA3656	30S ribosomal protein S2	ftsH	2	-0.335	0
PA3694	hypothetical protein	ubiB	4	0.228	1
PA3716	hypothetical protein		4	-0.292	0
PA3736	homoserine dehydrogenase	prs	1	0.135	1
PA3790	Putative copper transport outer membrane porin OprC precursor	mqoB	1	-0.494	1
PA3816	O-acetylserine synthase		2	-0.15	0
PA3819	conserved hypothetical protein	pilA	4	-0.227	0
PA3856	hypothetical protein		4	-0.535	0
PA3874	respiratory nitrate reductase beta chain		2	-0.366	0
PA3875	respiratory nitrate reductase alpha chain		2	-0.482	0
PA4235	bacterioferritin	betA	1	-0.504	0
PA4239	30S ribosomal protein S4	fdnH	2	-0.677	0
PA4240	30S ribosomal protein S11	atpA	2	-0.437	0
PA4241	30S ribosomal protein S13	atpG	2	-0.681	0
PA4242	50S ribosomal protein L36	atpD	2	-0.634	0
PA4246	30S ribosomal protein S5		2	-0.193	0
PA4254	30S ribosomal protein S17		2	-0.44	0
PA4258	50S ribosomal protein L22	ltaA	2	-0.251	0
PA4260	50S ribosomal protein L2	sdaB	2	-0.604	0
PA4265	elongation factor Tu	mdoH	2	-0.146	0
PA4268	30S ribosomal protein S12	rpmB	2	-0.818	0
PA4307	chemotactic transducer PctC		1	-0.037	1
PA4323	hypothetical protein		4	-0.302	0
PA4362	hypothetical protein		4	-0.095	0

Gene no.	Description	Gene name	Class[a]	GRAVY[b]	TMD[c]
PA4372	hypothetical protein	ppk	4	-0.208	0
PA4385	GroEL protein		1	0.037	0
PA4408	cell division protein FtsA	envZ	2	0.038	1
PA4423	conserved hypothetical protein	arcB	4	-0.284	0
PA4429	probable cytochrome c1 precursor		3	-0.076	1
PA4431	probable iron-sulfur protein		3	-0.092	1
PA4456	probable ATP-binding component of ABC transporter		3	0.018	0
PA4481	rod shape-determining protein MreB		2	0.037	0
PA4494	probable two-component sensor		3	0.195	4
PA4506	probable ATP-binding component of ABC dipeptide transporter		3	-0.416	0
PA4525	type 4 fimbrial precursor PilA		1	0.13	0
PA4579	hypothetical protein	cysE	4	-0.429	0
PA4640	malate:quinone oxidoreductase	oprC	2	-0.249	0
PA4670	ribose-phosphate pyrophosphokinase	hom	2	0.097	1
PA4671	probable ribosomal protein L25		3	0.03	0
PA4715	probable aminotransferase		3	-0.194	0
PA4751	cell division protein FtsH	nosR	2	-0.251	2
PA4811	nitrate-inducible formate dehydrogenase, beta subunit		2	-0.359	1
PA4812	formate dehydrogenase-O, major subunit	narG	2	-0.371	0
PA4876	osmotically inducible lipoprotein OsmE	recA	2	-0.489	0
PA4957	phosphatidylserine decarboxylase		2	0.018	1
PA4972	hypothetical protein		4	-0.296	0
PA5004	probable glycosyl transferase	bfrB	3	-0.032	1
PA5005	probable carbamoyl transferase		3	-0.328	0
PA5040	Type 4 fimbrial biogenesis outer membrane protein PilQ precursor		1	-0.257	0
PA5044	type 4 fimbrial biogenesis protein PilM		1	0.085	2
PA5065	ubiquinone biosynthetic protein UbiB	tufA	2	-0.129	1
PA5077	periplasmic glucans biosynthesis protein MdoH	pctC	2	-0.019	6
PA5120	hypothetical protein	rpsB	4	-0.784	0
PA5146	hypothetical protein		4	-0.313	0
PA5172	ornithine carbamoyltransferase, catabolic		1	-0.404	0
PA5199	two-component sensor EnvZ	ftsA	2	-0.085	2
PA5231	probable ATP-binding/permease fusion ABC transporter	groEL	3	0.101	6
PA5242	polyphosphate kinase		1	-0.168	0
PA5257	hypothetical protein		4	-0.197	2
PA5291	probable choline transporter		3	0.419	10
PA5307	hypothetical protein	bfrA	4	-0.24	0
PA5316	50S ribosomal protein L28	rpsL	2	-0.655	0

Gene no.	Description	Gene name	Class[a]	GRAVY[b]	TMD[c]
PA5372	choline dehydrogenase		2	-0.414	0
PA5379	L-serine dehydratase	rplB	2	-0.005	0
PA5413	low specificity l-threonine aldolase	rplV	2	-0.092	0
PA5414	hypothetical protein	rpsQ	4	-0.142	0
PA5503	probable ATP-binding component of ABC transporter	rpsE	3	-0.043	0
PA5554	ATP synthase beta chain	rpmJ	2	-0.061	0
PA5555	ATP synthase gamma chain	rpsM	2	-0.134	0
PA5556	ATP synthase alpha chain	rpsK	2	-0.073	0
PA5557	ATP synthase delta chain	rpsD	2	-0.142	0
PA5568	conserved hypothetical protein	pilM	4	-0.09	5

Supplementary Table 2. Comprehensive list of all identified proteins of *P. aeruginosa* strain PAO1 from the labeled membrane protein sample.

a Class assigned according to the pseudoCAP database
1 -function experimentally demonstrated in *P. aeruginosa*.
2 **-**function of highly similar gene experimentally demonstrated in another organism.
3 -function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.
4 -homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.

b GRAVY value is calculated using ProtParam algorithm. Proteins and peptides showing positive values were classified as hydrophobic.

c Number of mapped transmembrane domains (TMDs) predicted by the PSORT algorithm.