

# **Additional File 1. List of selected *Pseudomonas aeruginosa* target proteins**

ORF Number	Gene Name	Protein Name	#TM	%Inside	GRAVY	Express	Highest Score	BL21 14°C	BL21 20°C	BL21 30°C	BL21 37°C	C43 30°C	C43 37°C
PA0113	none	probable cytochrome C oxidase assembly factor	8	54	0.807	n	0	0	0	0	0	0	0
PA0205	PotB homologue	probable ABC transporter	6	46	0.752	y	2	2	2	1	0	1	1
PA0255	none	hypothetical	6	57	0.800	y	2	1	2	1	0	0	1
PA0288	speB2	agmatinase	2	13	-0.013	n	0	0	0	0	0	0	0
PA0303	PotH	polyamine ABC transporter	7	51	0.857	y	2	0	0	2	0	0	0
PA0325	PotB homologue	probable ABC transporter	6	43	0.618	n	0	0	0	0	0	0	0
PA0341	lgt homologue	prolipoprotein diacylglycerol transferase	7	53	0.526	y	1	0	1	0	0	0	1
PA0379	ygdD homologue	hypothetical	4	65	1.115	y	1	0	0	1	0	0	0
PA0385	none	hypothetical	3	56	1.059	y	2	0	0	2	0	0	0
PA0397	CzcD homologue	cation efflux system protein	6	39	0.619	y	2	1	2	2	0	0	2
PA0426	mexB	multidrug transporter MexB	13	28	0.274	y	2	0	2	1	1	1	1
PA0435	none	hypothetical	4	17	-0.134	y	2	1	2	1	1	0	1
PA0465	CreD	inner membrane protein CreD	6	26	0.216	y	2	n/a	n/a	n/a	n/a	2	2
PA0563	none	conserved hypothetical protein	3	49	0.426	y	3	0	3	2	1	1	0
PA0661	none	hypothetical	4	61	0.684	y	1	1	0	0	0	0	0
PA0790	none	hypothetical	7	52	0.912	n	0	0	0	0	0	0	0
PA0809	MntH	manganese transporter	10	47	0.825	n	0	0	0	0	0	0	0
PA0918	CybB homologue	bacterial cytochrome b561	4	42	0.341	y	3	3	3	3	0	3	3
PA0984	none	colicin immunity protein	3	55	0.721	y	1	0	0	1	0	0	0
PA1279	CobU, cobT homologue	nicotinate-nucleotide dimethylbenzimidazole phosphoribosyl transferase	4	26	0.219	y	3	1	3	2	3	0	1
PA1552	CcoP homologue	probable cytochrome C	2	14	-0.211	y	2	0	0	0	0	1	2
PA1581	sdhC	cytochrome b556	3	47	0.823	y	3	2	1	1	0	3	2
PA1651	BenE homologue	probable transporter	11	60	0.823	y	1	1	1	0	0	0	1
PA1691	unknown	unknown	6	48	1.090	n	0	0	0	0	0	0	0
PA1693	YopR homologue	unknown	4	42	0.672	n	0	0	0	0	0	0	0
PA1773	Cmax	Cmax	2	13	-0.163	y	2	2	1	2	1	1	1
PA1775	none	hypothetical	5	38	0.983	y	3	2	3	1	0	1	2
PA1820	NhaB	sodium/proton antiporter	12	50	0.802	n	0	0	0	0	0	0	0
PA1882	SugE homologue	probable transporter	4	70	1.305	y	1	0	1	0	0	0	0
PA1883	NuoA homologue	probable NADH-ubiquinone/plastoquinone oxidoreductase	3	47	0.507	y	1	0	1	1	0	1	1
PA1948	rbsC	ribose ABC transporter	7	43	0.940	y	1	0	1	0	0	1	1
PA2059	none	probable permease of	6	34	0.591	n	0	0	0	0	0	0	0

Accession	Gene	Protein	Length	Score	Model	1	2	3	4	5	6	7	8
PA2128	cupA1	ABC transporter fimbrial subunit CupA1	3	34	0.421	y	3	3	3	3	3	1	2
PA2340	mtlG homologue	probable maltose/mannitol transporter	7	55	0.727	n	0	0	0	0	0	0	0
PA2397	PvdE	pyoverdine ABC transporter biosynthesis protein	6	27	0.155	y	3	2	3	3	0	0	1
PA2533	none	probable sodium/alanine symporter	10	48	0.809	y	1	0	1	0	0	0	0
PA2541	none	probable CDP-alcohol phosphatidyl transferase	3	28	0.697	y	3	2	3	3	0	1	2
PA2628	none	hypothetical	9	60	0.741	n	0	0	0	0	0	0	0
PA2777	yfdC homologue	hypothetical	6	39	0.251	y	3	0	3	1	0	0	1
PA2811	YodH homologue	probable ABC transporter	7	54	0.893	y	1	0	1	1	0	0	0
PA2830	htpX	heat shock protein and zinc metallopeptidase	4	28	0.417	n	0	0	0	0	0	0	0
PA3039	none	probable transporter	11	51	0.752	n	0	0	0	0	0	0	0
PA3107	MetZ	O-succinylhomoserine sulfhydrylase	2	12	-0.038	y	3	3	3	3	3	1	2
PA3141	WbpM (LpsB homologue)	nucleotide sugar epimerase/dehydratase	7	23	0.096	n	0	0	0	0	0	0	0
PA3176	glts	sodium/glutamate symporter	12	62	0.857	y	1	0	0	0	0	0	1
PA3189	glfF	probable ABC transporter	6	44	0.585	n	0	0	0	0	0	0	0
PA3210	trkH	potassium uptake protein	13	55	0.743	y	1	0	1	0	0	0	0
PA3217	CyaB	adenylate cyclase	4	19	0.124	y	3	3	3	3	3	2	2
PA3331	none	cytochrome P450	2	10	-0.210	y	3	2	3	3	3	1	3
PA3391	NosR	regulatory protein NosR	8	25	0.074	y	2	1	2	1	0	1	1
PA3395	NosY	NosY	6	45	1.120	y	1	0	0	0	0	0	1
PA3474	YigM homologue	hypothetical	10	70	0.741	n	0	0	0	0	0	0	0
PA3553	ArnC	probable glycosyl transferase	2	15	0.193	y	3	2	3	0	0	2	3
PA3603	dgkA	diacylglycerol kinase	3	45	0.743	y	1	0	1	1	0	0	0
PA3651	CdsA	phosphatidate cytidyl transferase	7	54	0.897	n	0	0	0	0	0	0	0
PA3690	none	probable metal-transporting P-type ATPase	5	14	0.177	y	3	1	2	3	1	1	1
PA3773	none	hypothetical	12	62	1.042	y	2	0	0	2	0	0	0
PA3890	None	probable ABC transporter	5	52	1.157	n	0	0	0	0	0	0	0
PA3929	CiaB	cyanide insensitive terminal oxidase	8	49	0.863	y	2	0	2	0	0	0	1
PA3936	TauC	probable ABC taurine transporter	5	38	0.800	y	1	0	1	1	0	0	1
PA3955	none	hypothetical	5	53	0.845	n	0	0	0	0	0	0	0
PA4083	CupB4	Chaperone cupB4	2	19	0.003	y	3	1	2	3	2	0	1
PA4153	none	2,3-butanedial dehydrogenase	2	13	0.255	y	3	3	3	3	3	3	3
PA4276	SecE	Secretion protein	3	48	0.990	y	2	0	2	1	0	1	1

PA4417	MurE	UDP-MurNac-tripeptide synthetase	2	8	0.044	y	3	2	2	3	3	2	2
PA4455	yrbE homologue	probable ABC transporter	6	49	0.762	n	0	0	0	0	0	0	0
PA4467	None	hypothetical	8	52	1.037	n	0	0	0	0	0	0	0
PA4479	mrcD	rod shape-determining protein	5	67	0.956	y	1	0	1	1	0	0	1
PA4528	XcpA, PilD	type 4 prepilin peptidase	5	34	0.637	y	2	1	2	1	0	0	1
PA4559	lspA	prolipoprotein signal peptidase	5	64	0.615	y	3	1	3	2	1	1	2
PA4598	MexD	multidrug transporter MexD	14	29	0.401	y	3	0	0	3	2	0	0
PA4614	MscL	mechanosensitive channel	2	31	0.693	y	3	3	3	3	3	3	2
PA4740	Pnp	polyribonucleotide nucleotidyltransferase	3	10	-0.073	y	3	3	3	3	3	0	0
PA4779	none	hypothetical	10	66	1.219	n	0	0	0	0	0	0	0
PA4834	none	hypothetical	9	61	1.163	n	0	n/a	n/a	n/a	n/a	0	0
PA4838	None	hypothetical	8	45	0.665	y	1	0	0	1	0	0	0
PA4990	QacE homologue	SMR multidrug efflux transporter	4	72	1.444	y	2	0	2	1	1	0	0
PA5132	none	hypothetical	7	53	1.031	n	0	0	0	0	0	0	0
PA5168	DctQ homologue	probable dicarboxylate transporter	4	37	0.732	y	2	1	2	1	0	0	0
PA5199	Env2	two-component sensor Env2	2	9	-0.085	y	3	1	2	3	2	2	2
PA5249	None	hypothetical	5	56	0.822	n	0	0	0	0	0	0	0
PA5256	DsbH, DsbB homologue	disulfide bond formation protein	4	50	0.971	y	3	2	3	2	1	0	1
PA5262	AlgZ/FimS	alginate biosynthesis protein	4	21	0.241	y	3	2	3	3	3	3	3
PA5291	BetT homologue	probable choline transporter	12	37	0.419	y	3	0	2	3	2	0	0
PA5361	PhoR	two-component sensor PhoR	2	8	-0.334	y	2	2	1	1	0	2	2
PA5501	ZnuB	ABC zinc transporter	7	65	1.303	n	0	0	0	0	0	0	0
PA5529	YbaL homologue	probable sodium/proton antiporter	16	56	0.989	y	2	0	2	1	0	0	0

Gene name and Protein name were taken from the PseudoCap database. #TM = transmembrane helices predicted by TMPRED, %inside = percentage of amino acids predicted to be inside the transmembrane helices, GRAVY = grand average hydrophobicity, Express = expressed in at least one condition (y = yes, n = no), The Western blots were scored visually, and bands migrating near the predicted molecular weight were scored qualitatively. The scores are given as 0 = no expression, 1 = minimal expression, 2 = medium expression, 3 = highest level of expression. Highest score = highest level of expression in any of the conditions tested.