

Appendix

Table A1. Interaction partners found for NorB, NorC and NosR involved in the respiratory chains and other crucial cellular processes. For experimental details consult Table 1 and the experimental procedures section.

PA N°	Interaction Partners	NorB	NorC	NosR
1. Primary dehydrogenases (electron donating)				
PA2638	NADH dehydrogenase subunit B NuoB	3.59	29.01	11.47
PA2639	NADH:dehydrogenase NuoD	16.63	148.76	19.72
PA2644	NADH dehydrogenase subunit I Nuol	3.40	18.98	7.62
PA2951	Electron transfer flavoprotein alpha-subunit EtfA	0.70	0.97	ND
PA2952	Electron transfer flavoprotein beta-subunit EtfB	0.51	1.21	ND
PA4771	L-lactate dehydrogenase LldD	0.89	11.33	ND
PA0782	Bifunctional proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase PutA	0.74	17.03	4.03
PA4640	Malate:quinone oxidoreductase MqoB	1.75	6.63	ND
PA5304	D-amino acid dehydrogenase small subunit DadA	0.33	3.09	1.12
PA1583	Succinate dehydrogenase flavoprotein subunit SdhA	4.01	12.38	4.08
PA1584	Succinate dehydrogenase Fe-S-subunit SdhB	7.60	17.30	6.00
PA1582	Succinate dehydrogenase D subunit SdhD	ND	5.78	3.04
2 ATP synthase				
PA5556	F0F1 ATP synthase subunit alpha AtpA	0.87	4.43	1.92
PA5558	F0F1 ATP synthase subunit B AtpF	1.27	3.49	2.60
PA5553	F0F1 ATP synthase subunit epsilon AtpC	1.67	9.69	3.70
PA5554	F0F1 ATP synthase subunit beta AtpD	1.32	6.76	2.25
PA5555	F0F1 ATP synthase subunit gamma AtpG	1.13	7.52	ND
PA5557	F0F1 ATP synthase subunit delta AtpH	0.24	2.83	1.40

3 Cytochrome oxidases				
PA1552	Cytochrome <i>c</i> oxidase, <i>cbb</i> ₃ -type, CcoP subunit	0.96	1.43	ND
PA1553	Cytochrome <i>c</i> oxidase, <i>cbb</i> ₃ -type, CcoO subunit	0.88	2.46	2.02
PA1554	Cytochrome oxidase subunit (<i>cbb</i> ₃ -type) CcoN1	ND	6.17	ND
PA4429	Putative cytochrome <i>c</i> ₁ precursor	0.42	1.44	0.97
PA5300	Cytochrome <i>c</i> ₅ CycB	0.45	0.69	ND
PA5490	Cytochrome <i>c</i> ₄ precursor Cc4	0.52	1.17	2.24
4 Fermentation				
PA0835	Phosphate acetyltransferase Pta	1.43	4.22	ND
PA5427	Alcohol dehydrogenase AdhA	0.42	4.94	ND
PA0888	Arginine/ornithine binding protein AotJ	0.29	0.55	ND
PA5171	Arginine deiminase ArcA	2.14	3.09	ND
PA5172	Ornithine carbamoyltransferase ArcB	3.80	3.69	ND
5 Cofactor formation				
PA3813	Scaffold protein IscU	1.73	2.17	0.63
PA3814	Cysteine desulfurase IscS	1.33	2.63	ND
PA1479	Cytochrome <i>c</i> -type biogenesis protein CcmE	2.08	4.20	2.14
PA1483	Cytochrome <i>c</i> -type biogenesis protein Cych	1.44	40.78	ND
PA3977	Glutamate-1-semialdehyde aminotransferase HemL	3.76	29.64	ND
PA5243	Delta-aminolevulinic acid dehydratase HemB	0.38	1.95	ND
PA1546	Coproporphyrinogen III oxidase HemN	0.31	10.32	2.65
PA0024	Coproporphyrinogen III oxidase HemF	1.49	11.99	ND
PA5257	Heme biosynthesis associated protein PA5257	3.41	18.98	ND
PA5258	Potential enzyme of heme biosynthesis HemX	0.89	6.71	2.52
PA3915	Molybdopterin biosynthetic protein B1 MoaB1	2.81	16.59	9.00
PA5063	Ubiquinone/menaquinone biosynthesis methyltransferase UbiE	0.89	13.05	ND
PA0546	S-adenosylmethionine synthetase MetK	0.94	2.74	ND
6 Cell division				
PA4751	Cell division protein FtsH	30.05	76.99	19.69
PA4408	Cell division protein FtsA	1.82	4.98	ND
PA1528	Cell division protein ZipA	13.88	54.62	ND
PA5037	Potential cell division protein	5.39	27.55	9.64
PA4407	Cell division protein FtsZ	3.04	11.54	1.48
PA3244	Cell division inhibitor MinD	2.55	7.07	ND

PA1847	Potential iron-sulfur cluster assembly protein NfuA	2.61	5.27	ND
PA4481	Rod-shape-determining protein MreB	6.59	23.13	7.46

7 TCA cycle and pyruvate knot

PA1770	Phosphoenolpyruvate synthase PpsA	1.09	3.04	ND
PA5192	Phosphoenolpyruvate carboxykinase PckA	1.09	2.79	ND
PA3635	Phosphopyruvate hydratase Eno	1.28	1.96	ND
PA4329	Pyruvate kinase PykA	7.11	12.42	ND
PA5015	Pyruvate dehydrogenase subunit E1 AceE	1.55	5.19	ND
PA4848	Acetyl-CoA carboxylase biotin carboxylase subunit AccC	3.93	8.47	1.72
PA3112	Acetyl-CoA carboxylase subunit beta AccD	19.11	23.44	4.64
PA3639	Acetyl-CoA carboxylase carboxyltransferase subunit alpha AccA	15.90	12.76	ND
PA1587	Dihydrolipoamide dehydrogenase Lpd	3.54	6.26	ND
PA1580	Type II citrate synthase GltA	0.71	3.45	ND
PA1562	Aconitate hydratase AcnA	0.73	1.44	ND
PA1787	Bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase AcnB	0.55	3.61	0.72
PA2623	Isocitrate dehydrogenase Icd	0.30	1.03	ND
PA2634	Isocitrate lyase AceA	2.58	ND	ND
PA2624	Isocitrate dehydrogenase Idh	1.27	2.96	ND
PA5016	Dihydrolipoamide acetyltransferase AceF	9.06	18.79	ND
PA1585	2-oxoglutarate dehydrogenase E1 component SucA	9.14	30.46	ND
PA1586	Dihydrolipoamide succinyltransferase SucB	2.30	8.79	ND
PA1588	Succinyl-CoA synthetase subunit beta SucC	2.11	6.15	1.27
PA1589	Succinyl-CoA synthetase subunit alpha SucD	0.72	2.50	0.54

8 Cell wall/membrane/envelope

PA4749	Phosphoglucosamine mutase GlmM	0.90	3.62	1.90
PA5077	Gucosyltransferase MdoH	1.09	17.85	10.85
PA4460	Periplasmic LPS transport OstA	13.60	36.42	20.34
PA3299	Acyl-CoA synthetase FadD1	11.48	23.92	6.54
PA3148	UDP-N-acetylglucosamine 2-epimerase WbpL	3.38	22.32	4.62
PA2966	Acyl carrier protein AcpP	6.57	18.88	ND
PA5134	Putative carboxyl-terminal protease CtpA	4.13	5.08	0.70
PA0425	RND multidrug efflux membrane fusion protein MexA	2.11	2.96	1.06
PA3692	Outer membrane protein precursor LptF	2.17	7.34	ND
PA3158	Oxidoreductase WbpB	0.95	8.86	ND
PA3999	D-ala-D-ala-carboxypeptidase DacC	5.19	10.72	ND
PA1777	Major porin and structural outer membrane porin OprF precursor OprF	0.08	0.14	0.07
PA3159	UDP-glucose/GDP-mannose dehydrogenase WbpA	2.64	22.78	1.21

PA5475	Hypothetical protein PA5475	1.58	18.57	3.02
PA0070	Outer membrane lipoprotein TagQ1	0.10	1.67	0.24
PA0745	Enoyl-CoA hydratase	5.31	5.19	1.23
PA3014	Multifunctional fatty acid oxidation complex subunit alpha FaoA	1.33	4.17	ND
PA2968	Malonyl-CoA-[acyl-carrier-protein] transacylase FabD	2.36	3.27	ND
PA2967	3-ketoacyl-(acyl-carrier-protein) reductase FabG	2.31	3.79	0.68
PA1609	3-oxoacyl-(acyl carrier protein) synthase I FabB	1.72	3.80	ND

9 Chemotaxis/motility

PA0413	Component of chemotactic signal transduction system ChpA	11.00	58.67	8.18
PA1457	Chemotaxis protein CheZ	3.39	41.83	7.32
PA1458	Two-component sensor CheA	3.11	22.24	ND
PA2788	Putative chemotaxis transducer	1.75	19.01	4.38
PA4307	Chemotactic transducer PctC	2.07	13.99	2.83
PA2654	Putative chemotaxis transducer	1.92	9.42	2.65
PA3115	Motility protein FimV	0.59	ND	ND
PA1092	Flagellin type B FliC	0.18	0.25	0.15
PA0411	Twitching motility protein PilJ	0.55	1.60	0.42
PA4525	Type 4 fimbrial precursor PilA	2.23	4.92	1.58
PA4493	Putative two-component response regulator RoxR	1.94	8.38	ND
PA5043	Type 4 fimbrial biogenesis protein PilN	0.87	1.87	ND
PA1094	Flagellar capping protein FliD	2.22	8.60	ND
PA3805	Type 4 fimbrial biogenesis protein PilF	0.71	2.30	ND
PA1179	Two-component response regulator PhoP	15.25	16.75	ND
PA2867	Putative chemotaxis transducer	2.74	8.19	1.29
PA2652	Putative chemotaxis transducer	1.20	7.25	1.67

10 Protein transport

PA3822	Preprotein translocase subunit YajC	13.35	30.23	12.57
PA4403	Preprotein translocase subunit SecA	7.55	23.72	7.29
PA3821	Preprotein translocase subunit SecD	3.56	18.39	8.21
PA3820	Preprotein translocase subunit SecE	1.59	13.39	3.81
PA5568	Putative inner membrane protein translocase component YidC	0.65	2.60	2.01

11 Amino acid metabolism

PA4694	Ketol-acid reductoisomerase IlvC	190.75	225.30	86.39
PA0316	D-3-phosphoglycerate dehydrogenase SerA	1.27	10.61	2.39

PA3068	NAD-dependent glutamate dehydrogenase GdhB	5.29	48.85	8.04
PA5508	Putative glutamine synthetase PauA7	0.79	8.78	ND
PA1339	Amino acid ABC transporter ATP binding protein AatP	1.53	20.61	4.15
PA3814	Cysteine desulfurase IscS	1.33	2.63	ND
PA5173	Carbamate kinase ArcC	2.74	3.16	0.59
PA0316	D-3-phosphoglycerate dehydrogenase SerA	1.27	10.61	2.39
PA5119	Glutamine synthetase GlnA	9.67	9.23	2.25
PA1342	Putative binding protein component of ABC transporter AatJ	10.91	0.59	0.17
PA3816	O-acetylserine synthase CysE	1.85	5.30	4.05
PA0895	Bifunctional succinylornithine transaminase/acetylornithine aminotransferase AruC	1.38	6.17	ND

12 Iron metabolism

PA4764	Ferric uptake regulation protein Fur	7.80	3.53	1.55
PA3531	Bacterioferritin BfrB	13.60	27.23	ND
PA4235	Bacterioferritin FtnA	6.07	45.75	14.20

13 Proteases/chaperones

PA4542	ClpB protein	6.28	9.64	1.17
PA4941	Protease subunit HflC	13.92	14.04	11.57
PA1805	Peptidyl-prolyl <i>cis-trans</i> isomerase D PpiD	6.29	22.33	4.38
PA0459	Putative ClpA/B protease ATP binding subunit ClpC	3.15	8.56	1.31
PA5054	ATP-dependent protease ATP-binding subunit HslU	18.23	13.06	ND
PA4632	Potential Zn-dependent protease with chaperone function	1.60	1.90	0.69
PA4760	Chaperone protein DnaJ	8.84	6.06	ND
PA1793	Peptidyl-prolyl <i>cis-trans</i> isomerase B PpiB	1.62	4.10	0.63
PA1802	ATP-dependent protease ATP-binding subunit ClpX	2.74	11.17	3.05
PA1801	ATP-dependent Clp protease proteolytic subunit ClpP	0.91	8.76	ND
PA1800	Trigger factor Tig	1.15	2.01	0.85
PA4942	Protease subunit HflK	6.51	7.96	5.62
PA4386	Co-chaperonin GroES	1.89	5.33	1.15
PA4385	Chaperonin GroEL	0.95	2.27	0.71
PA0766	Serine protease MucD precursor	8.16	17.06	ND
PA3262	Putative peptidyl-prolyl <i>cis-trans</i> isomerase, FkbP-type	1.54	7.74	1.41
PA1596	Heat shock protein 90 HtpG	3.75	5.15	1.13
PA4761	Molecular chaperone DnaK	3.12	3.09	ND
PA4370	Metalloproteinase outer membrane protein precursor IcmP	0.98	2.44	ND

14 Stress/detoxification

PA2664	Nitric oxide dioxygenase Fhp	19.04	8.22	ND
PA0139	Alkyl hydroperoxide reductase subunit C AhpC	2.81	5.82	ND
PA0652	cAMP-regulatory protein Vfr	5.82	19.98	9.54
PA4236	Catalase KatA	3.19	17.03	ND
PA2582	Activator of osmoprotectant ProP	5.50	17.69	5.47
PA0456	Putative cold-shock protein	2.71	5.16	1.57
PA3309	Universal stress protein UspK	7.87	11.42	6.22
PA4352	Universal stress protein UspA	2.07	5.69	ND
PA4762	Heat shock protein GrpE	3.17	3.19	ND
PA1561	Aerotaxis receptor Aer	2.50	16.48	3.24
PA2582	Potential activator of osmoprotectant transporter ProP	5.50	17.69	5.47

15 DNA/RNA metabolism

PA1155	Ribonucleotide-diphosphate reductase (Nrd) subunit beta NrdB	0.08	3.24	1.07
PA1156	Ribonucleotide-diphosphate reductase subunit alpha NrdA	0.65	7.27	1.37
PA5497	NrdJa	0.23	4.78	1.20
PA5496	NrdJb	0.29	5.10	1.15
PA3637	CTP synthetase PyrG	5.94	9.26	ND
PA3770	Inosine 5'-monophosphate dehydrogenase GuaB	4.25	5.66	ND
PA4670	Ribose-phosphate pyrophosphokinase Prs	8.94	12.94	ND
PA3168	DNA gyrase subunit A GyrA	1.87	7.54	ND
PA0004	DNA gyrase subunit B GyrB	3.05	20.06	6.46
PA5562	Chromosome partitioning protein Spo0J	2.35	10.20	ND
PA3940	Putative DNA binding protein	0.26	ND	ND
PA3617	Recombinase A RecA	2.64	8.76	3.08
PA0428	Putative ATP-dependent RNA helicase RhIE	3.52	21.93	5.80
PA4232	Single-stranded DNA-binding protein Ssb	4.12	10.40	1.96
PA3266	Cold acclimation protein B CapB	3.74	6.89	3.43
PA5239	Transcription termination factor Rho	4.74	10.61	2.61
PA4270	DNA-directed RNA polymerase subunit beta RpoB	2.68	12.60	2.65
PA4238	DNA-directed RNA polymerase subunit alpha RpoA	3.39	8.86	1.78
PA4269	DNA-directed RNA polymerase subunit beta' RpoC	2.97	16.96	3.18
