

Gene ID	Locus tag	Annotation	Fold change	Rank abundance	
				NH ₃ -limited growth	O ₂ -limited growth
Energy conservation					
<i>amoC</i>	NE1411	Ammonia monooxygenase subunit C singleton	1.9	229	115
<i>amoC</i>	NE0945 / 2064	Ammonia monooxygenase subunit C	-3.3	2	2
<i>amoA</i>	NE0944 / 2063	Ammonia monooxygenase subunit A	-1.6	5	4
<i>amoB</i>	NE0943 / 2062	Ammonia monooxygenase subunit B	-1.3	6	6
<i>amoE</i>	NE0942 / 2061	Ammonia monooxygenase subunit E	1.0	66	81
<i>amoD</i>	NE0941 / NE2060	Ammonia monooxygenase subunit D	-1.2	42	59
<i>haoA</i>	NE0962 / NE2044 / NE2339	Hydroxylamine dehydrogenase subunit A	1.33	245	183
<i>haoB</i>	NE0961 / NE2043 / NE2338	Hydroxylamine dehydrogenase subunit B	1.2	422	387
<i>cycA</i>	NE0960 / NE2042 / NE2337	Cytochrome c-554	-1.07	91	117
<i>cycX</i>	NE0959 / NE2336	Tetraheme cytochrome c-type cm552	-1.03	75	93
<i>ncy</i>	NE0143	Nitrosocyanin	1.7	36	27
<i>cycB</i>	NE0102	Cytochrome c-552	1.3	100	89
<i>cytL</i>	NE0011	Cytochrome P460	-1.6	271	522
<i>cytS</i>	NE0824	Cytochrome c' beta	-2.3**	120	360

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Carbon fixation and storage compound metabolism					
<i>cbbO</i>	NE1918	von Willebrand factor type A / RuBisCO activation protein	-19.71	25	891
<i>cbbQ</i>	NE1919	RuBisCO activation protein	-8.18	26	351
<i>cbbS</i>	NE1920	Ribulose biphosphate carboxylase small chain	-9.89*	3	16
<i>cbbL</i>	NE1921	Ribulose biphosphate carboxylase large chain	-4.02**	4	9
<i>cbbR</i>	NE1922	LysR transcription regulator	4.50**	2086	1173
<i>cbbA</i>	NE0324	Fructose-bisphosphate aldolase	1.14	368	348
<i>pykA1</i>	NE0325	Pyruvate kinase	1.18	862	1048
<i>pgk</i>	NE0326	Phosphoglycerate kinase	1.63	207	423
<i>cbbG</i>	NE0327	Glyceraldehyde-3-phosphate dehydrogenase	1.06	266	278
<i>cbbT</i>	NE0328	Transketolase	2.06*	610	304
<i>cah</i>	NE0606	Carbonic anhydrase	-1.20	652	861
<i>cah</i>	NE1926	Carbonic anhydrase	-1.43	310	512
<i>ppk</i>	NE0323	Polyphosphate kinase	2.08**	1084	607
<i>ppx</i>	NE1745	Exopolyphosphatase	-1.05	1085	1223

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Universal and oxidative stress response					
<i>cspD</i>	NE1312	Cold-shock protein	4.9	1172	256
<i>hsp</i>	NE2074	Heat-shock protein	1.6	538	346
<i>sodB</i>	NE0870	Superoxide dismutase	-2.9**	105	421
<i>katA</i>	NE1886	Catalase	-1.5	1414	1756
<i>rubA</i>	NE1426	Rubredoxin	2.78**	965	362
<i>trxA</i>	NE2328	Thioredoxin	1.75**	123	73
Nitrifier denitrification					
<i>nirK</i>	NE0924	Nitrite reductase	-4.2**	9	43
<i>ncgC</i>	NE0925	Cytochrome c class I	-2.0	61	156
<i>ncgB</i>	NE0926	Cytochrome c class I	-1.3	57	92
<i>ncgA</i>	NE0927	Multicopper oxidase type I	2.6*	99	30
<i>nrsA</i>	NE0928	Nitrite-sensitive transcriptional repressor	2.1**	656	320
<i>norC</i>	NE2003	Nitric oxide reductase subunit C	1.5*	695	476
<i>norB</i>	NE2004	Nitric oxide reductase subunit B	1.2	749	662
<i>norQ</i>	NE2005	Nitric oxide reductase activation ATPase	1.2	1651	1618
<i>norD</i>	NE2006	Nitric oxide reductase activation protein	1.2	1398	1329

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Respiration					
<i>senC</i>	NE0682	senC (sNOR associated)	2.7**	1356	631
<i>norY</i>	NE0683	sNOR subunit 1	5.5*	428	64
<i>norS</i>	NE0684	sNOR subunit 2	10.8*	1200	102
<i>coxC</i>	NE1013	Cyt c oxidase aa ₃ sub 3	1.9**	27	13
<i>coxA</i>	NE1016	Cyt c oxidase aa ₃ sub 1	1.7*	50	24
<i>coxB</i>	NE1017	Cyt c oxidase aa ₃ sub 2	3.0*	60	16
<i>ctaG</i>	NE1015	Cyt c oxidase aa ₃ sub 4	1.9**	86	45
<i>petA</i>	NE0809	Ubiquinol-cytochrome c reductase	3.0**	389	110
<i>petB</i>	NE0810	Cytochrome b	2.2*	112	44
<i>petC</i>	NE0811	Cytochrome c	1.1	114	118
<i>nuoN</i>	NE1764	NADH-quinone oxidoreductase subunit N	1.2	494	448
<i>nuoM</i>	NE1765	NADH:ubiquinone oxidoreductase subunit M	1.2	659	612
<i>nuoL</i>	NE1766	NADH:ubiquinone oxidoreductase subunit L	1.3	391	323
<i>nuoK</i>	NE1767	NADH-quinone oxidoreductase subunit K	-1.2	498	681
<i>nuoJ</i>	NE1768	NADH:ubiquinone oxidoreductase subunit J	-1.0	336	381

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<i>nuoI</i>	NE1769	NADH-quinone oxidoreductase subunit I	-2.8	131	500
<i>nuoH</i>	NE1770	NADH-quinone oxidoreductase subunit H	-1.6**	119	236
<i>nuoG</i>	NE1771	NADH dehydrogenase subunit G	-1.1	240	288
<i>nuoF</i>	NE1772	NADH dehydrogenase	1.0	355	379
<i>nuoE</i>	NE1773	NADH dehydrogenase	1.4**	485	377
<i>nuoD</i>	NE1774	NADH-quinone oxidoreductase subunit D	1.2*	321	299
<i>nuoC</i>	NE1775	NADH-quinone oxidoreductase subunit C	-1.4	253	424
<i>nuoB</i>	NE1776	NADH-quinone oxidoreductase subunit B	1.0	323	349
<i>nuoA</i>	NE1777	NADH:ubiquinone oxidoreductase subunit A	1.2	201	173
<i>atpI</i>	NE0199	ATP synthase unit I	5.2**	516	85
<i>atpB</i>	NE0200	ATP synthase subunit A	2.8*	345	148
<i>atpE</i>	NE0201	ATP synthase subunit C	1.1	87	96
<i>atpF</i>	NE0202	ATP synthase subunit B	-1.2	244	342
<i>atpH</i>	NE0203	ATP synthase subunit delta	1.0	208	221
<i>atpA</i>	NE0204	ATP synthase subunit alpha	-1.1	133	158
<i>atpG</i>	NE0205	ATP synthase subunit gamma	1.2	390	343
<i>atpD</i>	NE0206	ATP synthase subunit beta	1.1	102	103
<i>atpC</i>	NE0207	ATP synthase epsilon chain	1.3	101	87