





3.85E+05	4.03E+05	2.63E+05	2.64E+05	0.00E+00	1.94E+07	1.14E+07	1.21E+07	1.34E+07	1.63E+07	>tr A0A0K2GB06 A0A0K2GB06_NITMO	Nitrospira moscoviensis	Sulfurtransferase	0	37,734	1,09E+09	23	1	1	1	1	1	9.8	13,911	A0A0K2GB06	A0A0K2GB06	107	0.18	0.00001
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.07E+06	1.42E+06	3.20E+05	7.20E+05	3.84E+05	>tr A0A0K2GCL8 A0A0K2GCL8_NITMO	Nitrospira moscoviensis	Uncharacterized protein	0	63,72	4,86E+08	20	1	1	1	1	1	9	14,959	A0A0K2GCL8	A0A0K2GCL8	108	3.86	0.00551
3.00E+04	7.73E+04	3.25E+04	1.15E+05	0.00E+00	1.27E+05	1.71E+05	6.27E+04	1.39E+05	0.00E+00	>tr A0A0K2GCW2 A0A0K2GCW2_NITMO	Nitrospira moscoviensis	Uncharacterized protein	0,0054152	6,0393	7,75E+06	2	1	1	1	13	12.5	11,215	A0A0K2GCW2;A0A1W18D1;A0A1	A0A0K2GCW2;A0A1W18D1;A0A1W9	109	1.53	#ZAHLI	
1.57E+05	2.13E+05	1.49E+05	1.51E+05	1.33E+05	0.00E+00	8.45E+05	4.82E+05	5.91E+05	8.36E+05	>tr D8PE89 D8PE89_9BACT	Nitrospira defluvi	Threonine synthase	0,0082781	5,8925	1,38E+08	1	1	1	1	13	3.6	44,49	D8PE89;A0A1W1893;A0A054L218	D8PE89;A0A1W1893;A0A054L218;A	110	0.24	0.00736	
7.17E+05	7.89E+05	7.99E+05	8.69E+05	7.02E+05	0.00E+00	1.88E+06	0.00E+00	0.00E+00	9.87E+06	>tr A0A0K2GF07 A0A0K2GF07_NITMO	Nitrospira moscoviensis	Rubrythrin	0	27,053	4,30E+08	11	3	3	3	2	2	15,701	A0A0K2GF07;A0A2C9C92	A0A0K2GF07	111	2.35	0.25450	
0.00E+00	0.00E+00	3.92E+05	4.71E+05	4.29E+05	9.55E+05	7.00E+05	4.05E+05	1.52E+05	0.00E+00	>tr A0A0K2GG72 A0A0K2GG72_NITMO	Nitrospira moscoviensis	Carboxy-terminal-processing protease	0	11,287	2,79E+08	3	2	2	2	11	6.3	47,922	A0A0K2GG72;A0A136JQ63;D8PHM	A0A0K2GG72;A0A136JQ63;D8PHM3;A	112	2.17	0.03509	
0.00E+00	0.00E+00	0.00E+00	0.68E+05	2.23E+05	6.62E+05	2.31E+05	0.00E+00	0.00E+00	0.00E+00	>tr A0A1W1HZT2 A0A1W1HZT2_9BACT	Nitrospira japonica	Metal-binding protein SmbP	0	166	1,98E+07	3	2	1	2	2	19.5	11,883	A0A1W1HZT2;A0A0K2GG80	A0A1W1HZT2;A0A0K2GG80	113	0.29	#ZAHLI	
1.50E+06	2.08E+06	1.25E+06	1.58E+06	1.27E+06	1.08E+07	8.19E+06	3.18E+06	4.40E+06	6.50E+06	>tr A0A1W9GG60 A0A1W9GG60_9BACT	Nitrospira sp. SG-bin2	Uncharacterized protein	0	323,31	2,69E+09	70	3	3	3	5	14.2	34,071	A0A1W9GG60;A0A0K2GGE5;A0A1	A0A1W9GG60;A0A0K2GGE5;A0A1W9	114	3.01	0.00120	
2.86E+05	4.49E+05	6.22E+05	8.04E+05	3.47E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A0K2GHA6 A0A0K2GHA6_NITMO	Nitrospira moscoviensis	Uncharacterized protein	0	7,3647	2,20E+07	4	1	1	1	1	16.2	11,68	A0A0K2GHA6	A0A0K2GHA6	115	#ZAHLI	#ZAHLI	
1.53E+06	1.52E+06	1.32E+06	1.34E+06	1.75E+06	1.04E+06	9.99E+05	6.59E+05	8.80E+05	1.62E+06	>tr A0A1W1HZY7 A0A1W1HZY7_9BACT	Nitrospira japonica	Uncharacterized protein	0	6,1381	6,00E+08	5	1	1	2	5.3	28,404	A0A1W1HZY7;A0A0K2GHF5	A0A1W1HZY7;A0A0K2GHF5	116	3.25	0.00018		
4.43E+06	2.76E+06	2.41E+06	3.90E+06	3.76E+06	1.15E+07	1.51E+07	3.19E+06	6.45E+06	9.49E+06	>tr A0A0K2GH6 A0A0K2GH6_NITMO	Nitrospira moscoviensis	Putative Monoheme cytochrome c	0	323,31	3,19E+09	9	4	4	1	1	4.3	15,99	A0A0K2GH6H	A0A0K2GH6H	117	3.16	0.00212	
1.95E+06	1.85E+06	1.07E+06	1.54E+06	1.58E+06	3.67E+06	5.26E+06	4.96E+06	3.67E+06	7.46E+06	>tr A0A256WY47 A0A256WY47_9BACT	Nitrospira sp. UW-LDO-01	Histidine Kinase	0,0069204	5,9859	2,62E+09	8	1	1	13	1.6	84,792	A0A256WY47;A0A1W9GJQ9;A0A0	A0A256WY47;A0A1W9GJQ9;A0A0S4L	118	0.46	0.00009		
8.10E+04	1.11E+05	2.65E+05	6.55E+04	1.44E+05	9.20E+06	8.27E+06	4.72E+06	7.39E+06	5.92E+06	>tr D8PHJ9 D8PHJ9_9BACT	Nitrospira defluvi	Uncharacterized protein	0	286,09	8,00E+08	47	1	1	1	12	13.4	12,52	D8PHJ9;A0A256W5I6;A0A1W9IK4	D8PHJ9;A0A256W5I6;A0A1W9IK4;A	119	1.15	0.00002	
5.27E+05	7.43E+05	5.52E+05	7.70E+05	6.65E+05	0.00E+00	0.00E+00	0.00E+00	2.47E+05	1.94E+05	>tr A0A1W9J574 A0A1W9J574_9BACT	Nitrospira sp. ST-bin5	Iron-sulfur cluster assembly scaffold protein k	0	323,31	2,21E+08	15	2	2	15	18.3	13,779	A0A1W9J574;A0A1W1185;A0A25	A0A1W9J574;A0A1W1185;A0A256W	120	5.94	#ZAHLI		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.67E+06	4.12E+06	3.90E+06	3.16E+06	4.14E+06	>tr D8P865 D8P865_9BACT	Nitrospira defluvi	Chaperone protein HscA (Hsc66)	0	6,5014	8,84E+08	6	1	1	13	2.3	65,432	D8P865;A0A256WVL8;A0A1W9J47	D8P865;A0A256WVL8;A0A1W9J47;A	121	-1.42	0.00039		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	8.05E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr D8P8H0 D8P8H0_9BACT	Nitrospira defluvi	Transcription termination/antitermination pro	0	11,546	1,11E+08	2	2	2	2	13	7.4	42,058	D8P8H0;A0A1W1HVM7;A0A1W9J45	D8P8H0;A0A1W1HVM7;A0A1W9J45;J	122	2.32	0.34665	
1.28E+06	1.67E+06	1.18E+06	9.69E+05	1.18E+06	1.25E+07	1.29E+07	9.37E+06	8.08E+06	1.36E+07	>tr A0A0K2GIT2 A0A0K2GIT2_NITMO	Nitrospira moscoviensis	Uncharacterized protein	0	88,569	1,21E+09	22	2	2	2	13	13.6	17,752	A0A0K2GIT2;A0A1W9J418;A0A1W7	A0A0K2GIT2;A0A1W9J418;A0A1W70	123	1.72	0.00001	
3.24E+05	5.96E+05	0.00E+00	3.89E+05	9.25E+04	1.47E+07	1.07E+07	4.2E+06	1.04E+07	1.44E+07	>tr A0A136JNW2 A0A136JNW2_9BACT	Nitrospira sp. OLB3	Rubrythrin	0	323,31	3,57E+09	27	2	2	2	14	27	15,607	A0A136JNW2;A0A0K2GJ4;D8P87	A0A136JNW2;A0A0K2GJ4;D8P87;A	124	3.31	0.00042	
2.67E+06	3.15E+06	2.37E+06	2.61E+06	2.48E+06	5.42E+06	5.18E+06	1.32E+06	3.34E+06	3.54E+06	>tr A0A1V6M208 A0A1V6M208_9BACT	Candidatus Brocadia saporovensis	Malate dehydrogenase	0	8,1127	1,75E+09	11	1	1	1	2	3.9	33,413	A0A1V6M208;A0A0M2UVM4	A0A1V6M208;A0A0M2UVM4	125	1.96	0.00095	
0.00E+00	0.00E+00	9.36E+05	7.25E+05	8.67E+05	4.08E+06	2.58E+06	1.67E+06	1.74E+06	2.69E+06	>tr A0A0M2UWM9 A0A0M2UWM9_9BACT	Candidatus Brocadia fulgida	Adenylate kinase	0	6,1225	1,95E+08	2	1	1	1	4.4	25,532	A0A0M2UWM9	A0A0M2UWM9	126	-2.48	0.00038		
1.11E+06	8.86E+05	1.65E+05	6.10E+05	3.77E+05	1.61E+06	1.34E+06	5.78E+05	1.06E+06	1.21E+06	>tr A0A0M2UYH7 A0A0M2UYH7_9BACT	Candidatus Brocadia fulgida	ATPase	0	11,831	1,96E+08	4	1	1	1	3.6	37,584	A0A0M2UYH7	A0A0M2UYH7	127	0.50	#ZAHLI		
1.71E+06	3.10E+06	3.77E+05	1.42E+06	2.35E+05	0.00E+00	0.00E+00	3.21E+05	0.00E+00	4.33E+05	>tr A0A1V4AXP1 A0A1V4AXP1_9BACT	Candidatus Brocadia carolinensis	2-dehydro-3-deoxyphosphonate aldolase	0	9,9393	8,84E+07	4	1	1	1	3	5.2	29,891	A0A1V4AXP1;A0A1V6M0Q9;A0A0	A0A1V4AXP1;A0A1V6M0Q9;A0A0M2U	128	2.76	0.04642	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	3.34E+05	1.11E+05	8.34E+04	9.89E+04	2.14E+05	>tr F9ZF09 F9ZF09_9PROT	Nitrosomonas sp. AL212	Rubrythrin	0	17,683	1,84E+08	7	3	3	3	11	18.7	15,15	F9ZF09;F8GF27;A0A114DMZ7;A0A1	F9ZF09;F8GF27;A0A114DMZ7;A0A1H9	129	5.15	0.00745	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	4.21E+05	2.73E+05	3.64E+05	3.64E+05	3.64E+05	>tr F9ZE99 F9ZE99_9PROT	Nitrosomonas sp. AL212	Lysine-tRNA ligase	0	20,375	1,66E+08	8	1	1	17	3.6	57,583	F9ZE99;A0A286A533;A0A285BYR5	F9ZE99;A0A286A533;A0A285BYR5;A	130	1.17	0.00002		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.37E+07	1.53E+07	3.20E+06	4.00E+05	1.66E+07	>tr F9ZE90 F9ZE90_9PROT	Nitrosomonas sp. AL212	Cold-shock DNA-binding domain protein	0	8,1127	1,69E+09	10	1	1	1	1	14.9	7,218	F9ZE90;F8GFU9;A0A1N6GF07;A0A1	F9ZE90;F8GFU9;A0A1N6GF07;A0A1I4C	131	2.92	0.01864	
7.88E+05	7.95E+05	1.26E+06	9.08E+05	1.14E+06	2.14E+06	1.83E+06	1.82E+06	0.00E+00	2.86E+06	>tr F9ZD19 F9ZD19_9PROT	Nitrosomonas sp. AL212	Ribulose-phosphate 3-epimerase	0	6,7162	3,76E+08	5	1	1	1	5.3	24,334	F9ZD19;A0A286A5V4;A0A1H8ZPD4	F9ZD19;A0A286A5V4;A0A1H8ZPD4;A	132	1.74	0.00638		
1.22E+06	1.05E+06	6.76E+05	1.97E+06	7.99E+05	0.00E+00	2.98E+05	0.00E+00	0.00E+00	0.00E+00	>tr A0A286A5B8 A0A286A5B8_9PROT	Nitrosomonas ureae	Acyl carrier protein	0	7,5407	8,00E+07	4	1	1	2	17.5	8,9038	A0A286A5B8;A0A0S3AGN4	A0A286A5B8;A0A0S3AGN4	133	5.72	0.34676		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.59E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr F9ZDG3 F9ZDG3_9PROT	Nitrosomonas sp. AL212	ATP synthase subunit alpha	0,0098039	5,8645	0.00E+00	0	5	1	10	11.7	55,311	F9ZDG3;A0A286A636;A0A285BYG	F9ZDG3;A0A286A636;A0A285BYG;A	135	#ZAHLI	#ZAHLI		
7.43E+06	7.74E+06	5.22E+06	7.49E+06	6.51E+06	2.32E+06	1.94E+06	2.10E+06	2.97E+06	2.10E+06	>tr F9ZIM9 F9ZIM9_9PROT	Nitrosomonas sp. AL212	Glutamate dehydrogenase	0	279,8	7,52E+08	41	1	7	4	4.5	48,526	F9ZIM9;F8GLW9;A0A285C053;A0A1	F9ZIM9;F8GLW9;A0A285C053;A0A1H9	136	0.49	0.00000		
2.56E+06	3.25E+06	1.55E+06	1.21E+06	2.00E+06	4.21E+07	4.03E+07	1.49E+07	3.00E+07	2.87E+07	>tr F9ZIM7 F9ZIM7_9PROT	Nitrosomonas sp. AL212	Glyceraldehyde-3-phosphate dehydrogenase	0	27,456	5,97E+09	8	1	3	37	10.5	36,078	F9ZIM7;F8GHX2;A0A285C095;A0A1	F9ZIM7;F8GHX2;A0A285C095;A0A1I	137	-0.28	0.00021		
1.30E+07	2.02E+07	1.23E+07	9.24E+06	1.46E+07	0.00E+00	0.00E+00	8.92E+04	0.00E+00	0.00E+00	>tr F9ZG12 F9ZG12_9PROT	Nitrosomonas sp. AL212	O-acetylthioester/O-acetylserine sulphydry	0,0083893	5,9087	2,36E+07	1	3	3	3	2.8	45,706	F9ZG12;A0A286A1F6;A0A1H9S60	F9ZG12;A0A286A1F6;A0A1H9S60;A	138	3.53	#ZAHLI		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.47E+06	3.99E+06	4.95E+06	3.78E+06	5.45E+06	>tr F9ZGW2 F9ZGW2_9PROT	Nitrosomonas sp. AL212	30S ribosomal protein S8	0	8,2672	5,82E+08	11	1	1	1	13	9.2	14,48	F9ZGW2;F8GHL8;B1Y8C3;A0A286A	F9ZGW2;F8GHL8;B1Y8C3;A0A286A	139	1.34	0.00004	
1.73E+06	1.98E+06	1.69E+05	1.44E+06	6.07E+05	6.40E+06	6.36E+06	6.51E+06	5.50E+06	9.15E+06	>tr A0A117YD8 A0A117YD8_9PROT	Nitrosomonas eutropha	Acetolactate synthase, small subunit	0	56,493	4,67E+08	11	1	1	1	21	12.3	17,315	A0A117YD8;A0A114KY27;A0A113Y	A0A117YD8;A0A114KY27;A0A113YQ	140	-1.33	0.00001	
1.57E+07	1.00E+07	7.79E+06	9.58E+06	7.45E+06	3.99E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A1H8GL3 A0A1H8GL3_9PROT	Nitrosomonas oligotropha	50S ribosomal protein L11	0,0083333	5,9041	4,19E+07	3	1	1	1	8.3	14,999	A0A1H8GL3;A0A1H5Y494;A0A0S5	A0A1H8GL3;A0A1H5Y494;A0A0S5A	141	3.10	0.34670		
4.25E+06	4.49E+06	3.92E+06	4.44E+06	2.21E+06	5.81E+05	2.87E+05	4.66E+05	3.65E+05	7.76E+05	>tr F9ZD08 F9ZD08_9PROT	Nitrosomonas sp. AL212	Urease subunit alpha	0	6,2796	1,37E+08	4	1	1	6	2.5	61,58	F9ZD08;A0A285B5W5;A0A114P9H	F9ZD08;A0A285B5W5;A0A114P9H;A	142	0.60	0.00042		
2.47E+07	2.51E+07	1.04E+07	2.51E+07	1.57E+07	3.44E+05	2.38E+05	0.00E+00	2.65E+05	2.70																			



0.00E+00	4.95E+05	3.14E+05	0.00E+00	1.97E+05	6.17E+06	8.24E+06	5.11E+06	5.82E+06	9.05E+06	>tr A0A1E4ERT1 A0A1E4ERT1_9RHOB	Paracoccus sp. SCN 68-21	Electron transfer flavoprotein subunit beta	0,0083195	5,8955	7,15E+08	6	1	1	1	1	1	1	26,804	A0A1E4ERT1	A0A1E4ERT1	217	-1,74	0,00002
2.41E+06	2.73E+06	3.14E+06	2.76E+06	1.68E+06	1.04E+07	1.68E+07	1.40E+07	2.02E+07	3.24E+07	>tr A0A1E4ET4 A0A1E4ET4_9RHOB	Paracoccus sp. SCN 68-21	Uncharacterized protein	0,0071174	6,0163	2,85E+09	3	2	1	1	1	1	12,4	9,6203	A0A1E4ET4	A0A1E4ET4	218	2,34	0,00109
2.06E+06	2.81E+06	1.25E+06	1.01E+06	1.25E+06	3.44E+06	2.55E+06	1.01E+06	1.16E+06	4.57E+05	>tr A0A238WGN0 A0A238WGN0_9RHOB	Paracoccus sediminis	NiTT/TauT family transport system substrate	0	13,978	2,06E+08	8	2	2	17	7,1	34,84	A0A238WGN0;A0A1N7KLG7;A0A1	A0A238WGN0;A0A1N7KLG7;A0A1N9B	219	0,24	0,01390		
2.77E+05	5.54E+05	3.55E+05	0.00E+00	2.67E+05	7.30E+07	3.38E+07	0.00E+00	6.36E+07	0.00E+00	>tr A0A1E4EWK3 A0A1E4EWK3_9RHOB	Paracoccus sp. SCN 68-21	Cytochrome c biogenesis ATP-binding export	0	10,28	5,74E+09	10	1	1	1	3,8	21,887	A0A1E4EWK3	A0A1E4EWK3	220	0,89	0,06775		
3.46E+05	4.67E+05	4.79E+05	5.64E+05	2.11E+05	9.62E+06	7.00E+06	4.92E+06	6.30E+06	7.05E+06	>tr A0A1H3N2L3 A0A1H3N2L3_9PROT	Nitrosomonas halophila	30S ribosomal protein S5	0	55,311	3,91E+08	26	1	1	1	11	11,117	A0A1H3N2L3;Q82X75;Q0AIH9;A0A1	A0A1H3N2L3;Q82X75;Q0AIH9;A0A17	221	-2,04	0,00002		
1.03E+07	1.16E+07	9.19E+06	1.18E+07	2.47E+06	4.03E+05	0.00E+00	0.00E+00	3.13E+05	2.19E+05	>tr Q82TQ0 Q82TQ0_NITEU	Nitrosomonas europaea (strain AT	Site-determining protein	0	6,4469	1,70E+07	4	1	1	1	7	6,3	29,478	Q82TQ0;Q0AG21;A0A1I4T4B4;A0A1	Q82TQ0;Q0AG21;A0A1I4T4B4;A0A13	222	-2,86	#ZAHU!	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.28E+05	0.00E+00	>sp Q0AIH9 CH60_NITEC	Nitrosomonas europaea (strain C9	60 kDa chaperonin	0	15,204	2,94E+08	2	3	1	1	1	7	6,9	57,461	Q0AIH9;A0A1I76Q2;A0A1G4W9W3	Q0AIH9;A0A1I76Q2;A0A1G4W9W3	223	4,77	0,16074
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.73E+07	2.96E+07	9.44E+06	1.58E+07	3.25E+07	>sp Q82Y61 CH10_NITEU	Nitrosomonas europaea (strain AT	10 kDa chaperonin	0	79,245	1,20E+09	16	1	1	1	7	26	10,544	Q82Y61;Q0AIH8;A0A1I4S94;A0A1	Q82Y61;Q0AIH8;A0A1I4S94;A0A1H9	224	0,36	0,00136	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.14E+05	1.28E+06	9.46E+05	4.75E+05	9.38E+05	6.49E+05	>tr Q82UN3 Q82UN3_NITEU	Nitrosomonas europaea (strain AT	Iron-regulated ABC transporter ATPase subun	0	27,972	7,33E+07	3	1	1	1	5	6,5	28,952	Q82UN3;Q0AGN9;A0A1I7FKD0;A0A1	Q82UN3;Q0AGN9;A0A1I7FKD0;A0A1H	225	-3,89	#ZAHU!	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	8.90E+04	7.15E+04	0.00E+00	7.75E+04	6.42E+04	>tr A0A2D2C5L6 A0A2D2C5L6_9RHOB	Paracoccus yeei	2-ketoglutarate dehydrogenase	0	16,566	8,11E+06	1	1	1	1	4	6,4	56,805	A0A2D2C5L6;A0A2Z2G8H1;A0A1V0G	A0A2D2C5L6;A0A2Z2G8H1;A0A1V0G	226	-3,08	#ZAHU!	
6.36E+05	1.16E+06	5.33E+05	4.73E+05	5.68E+05	8.91E+07	4.11E+07	5.94E+07	2.45E+07	7.43E+07	>tr A0A1G5DFJ5 A0A1G5DFJ5_9RHOB	Paracoccus tibetensis	ATP synthase subunit beta	0	7,1071	6,77E+09	28	3	1	1	3	8,6	50,266	A0A1G5DFJ5;A0A2H5EVS2;A0A2D8X2	A0A1G5DFJ5;A0A2H5EVS2;A0A2D8X2	227	-5,61	0,00103	
6.78E+05	6.15E+05	2.71E+05	3.95E+05	3.94E+06	4.89E+06	2.94E+06	4.89E+06	2.94E+06	4.89E+06	>tr A0A1G5DFT7 A0A1G5DFT7_9RHOB	Paracoccus tibetensis	ATP synthase subunit alpha	0	10,1	5,12E+08	8	2	1	1	1	6,2	55,493	A0A1G5DFT7	A0A1G5DFT7	228	#ZAHU!	#ZAHU!	
5.54E+05	0.00E+00	0.00E+00	2.49E+05	1.45E+06	1.39E+06	1.90E+06	1.07E+06	1.23E+06	1.31E+06	>tr A0A1G5HG74 A0A1G5HG74_9RHOB	Paracoccus tibetensis	Electron transfer flavoprotein beta subunit	0	257,56	2,86E+08	28	1	1	1	1	6,4	26,434	A0A1G5HG74	A0A1G5HG74	229	0,81	0,00001	
2.58E+05	3.19E+05	1.57E+05	1.61E+05	1.33E+05	1.17E+07	0.00E+00	4.15E+06	8.24E+06	8.89E+06	>tr A0A10EHV2 A0A10EHV2_9RHOB	Paracoccus homiensis	3-oxoacyl-[acyl-carrier-protein] reductase/acc	0	41,77	7,98E+08	7	1	1	1	9	6,4	25,391	A0A10EHV2;Q35N32;Q1QH81;A3	A0A10EHV2;Q35N32;Q1QH81;A3WQ2	230	-0,97	#ZAHU!	
0.00E+00	0.00E+00	2.06E+04	0.00E+00	3.55E+04	2.08E+06	1.33E+06	0.00E+00	8.15E+05	7.79E+05	>tr A0A1G5SB2 A0A1G5SB2_9RHOB	Nitrosomonas mobilis	Uncharacterized protein	0	17,407	4,46E+07	3	1	1	1	2	9	23,83	A0A1G5SB2;A0A1I4PYF4	A0A1G5SB2;A0A1I4PYF4	231	#ZAHU!	#ZAHU!	
3.23E+05	3.35E+05	2.52E+05	4.17E+05	3.25E+05	1.20E+05	1.17E+05	0.00E+00	7.16E+04	1.08E+05	>tr A0A1G5SBX2 A0A1G5SBX2_9PROT	Nitrosomonas mobilis	60 kDa chaperonin	0	18,314	5,78E+07	7	4	1	1	1	10,7	57,636	A0A1G5SBX2	A0A1G5SBX2	232	2,05	0,00610	
6.60E+04	1.01E+05	1.08E+05	1.08E+05	1.68E+05	0.00E+00	0.00E+00	0.00E+00	1.18E+06	2.02E+06	>tr A0A1G5SDA5 A0A1G5SDA5_9PROT	Nitrosomonas mobilis	Elongation factor Tu	0	314,77	2,05E+08	5	2	1	1	8	7,7	39,397	A0A1G5SDA5;A0A1N6HIM8;A0A1I3	A0A1G5SDA5;A0A1N6HIM8;A0A1N6G	233	1,25	#ZAHU!	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A1G5SG84 A0A1G5SG84_9PROT	Nitrosomonas mobilis	Thioredoxin reductase	0	10,132	2,23E+07	4	1	1	1	1	6	34,389	A0A1G5SG84	A0A1G5SG84	234	#ZAHU!	0,00000	
1.77E+06	2.15E+06	1.58E+06	1.66E+06	1.45E+06	0.00E+00	0.00E+00	5.65E+04	1.06E+05	1.10E+05	>tr A0A1G5S85 A0A1G5S85_9PROT	Nitrosomonas mobilis	Chaperone protein HspG	0	8,8661	1,12E+07	2	1	1	1	4	2	73,179	A0A1G5S85;A0A1I4K20;A0A1H3K	A0A1G5S85;A0A1I4K20;A0A1H3K12	235	#ZAHU!	#ZAHU!	
4.22E+06	4.69E+06	5.45E+06	0.00E+00	2.90E+06	0.00E+00	0.00E+00	5.28E+06	0.00E+00	3.52E+06	>tr A0A1G5S84 A0A1G5S84_9PROT	Nitrosomonas mobilis	Uncharacterized protein	0	7,9419	4,97E+07	2	1	1	1	7	2	2,8392	A0A1G5S84	A0A1G5S84	236	2,22	0,15244	
4.40E+05	4.83E+05	4.57E+05	5.36E+05	3.77E+05	1.99E+05	9.45E+05	1.58E+06	1.39E+06	0.00E+00	>tr A0A2H5EYF2 A0A2H5EYF2_9RHOB	Paracoccus zhejiangensis	Glyceroldehyde-3-phosphate dehydrogenase	0	6,1339	3,07E+08	3	1	1	1	2	4,5	35,529	A0A2H5EYF2;A0A1G7ATQ2	A0A2H5EYF2;A0A1G7ATQ2	237	1,45	0,03082	
7.90E+05	9.21E+05	6.83E+05	9.39E+05	6.40E+05	0.00E+00	0.00E+00	3.43E+05	2.72E+05	2.72E+05	>tr A0A1G7BKE7 A0A1G7BKE7_9RHOB	Paracoccus yeei	ATP synthase subunit alpha	0	96,726	1,49E+08	2	4	2	33	10,6	55,101	A0A1G7BKE7;A0A2Z3CCH9;A0A2D8X2	A0A1G7BKE7;A0A2Z3CCH9;A0A2D8X2	238	2,21	0,04795		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.77E+07	2.47E+07	5.61E+06	0.00E+00	>tr A0A1G7BLW8 A0A1G7BLW8_9RHOB	Paracoccus isopora	Hydroxyacylglutathione hydrolase	0	6,2331	8,02E+08	3	1	1	1	10,5	25,936	A0A1G7BLW8	A0A1G7BLW8	239	-0,90	#ZAHU!		
1.03E+07	1.29E+07	8.67E+06	1.05E+07	5.87E+06	7.49E+05	4.81E+05	0.00E+00	0.00E+00	0.00E+00	>tr A0A1G7HLF5 A0A1G7HLF5_9RHOB	Paracoccus isopora	Uncharacterized protein	0,0068376	5,9389	2,06E+07	0	1	1	1	7,6	20,731	A0A1G7HLF5	A0A1G7HLF5	240	0,13	#ZAHU!		
7.20E+06	1.20E+07	6.91E+06	6.76E+06	9.92E+06	1.04E+06	6.38E+05	0.00E+00	6.81E+05	7.78E+05	>tr A0A14N008 A0A14N008_9PROT	Nitrosomonas nitrosa	Iron-regulated ABC transporter ATPase subun	0	6,1737	1,23E+08	4	1	1	1	3	3,8	29,501	A0A14N008;A0A1I4JH9;A0A1I3G	A0A14N008;A0A1I4JH9;A0A1I3G8R4	241	0,53	0,00639	
0.00E+00	1.57E+04	3.41E+05	8.61E+05	4.64E+05	0.00E+00	1.15E+05	0.00E+00	1.24E+05	1.80E+05	>tr A0A14K246 A0A14K246_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	6,7325	4,60E+07	2	1	1	1	3	3,3	51,57	A0A14K246;A0A1H3K035;A0A1G7K	A0A14K246;A0A1H3K035;A0A1G7K28	242	1,61	0,04825	
3.44E+05	5.25E+05	1.32E+05	3.89E+05	2.45E+05	5.46E+06	0.00E+00	2.87E+06	5.01E+06	6.26E+06	>tr A0A1I4T28 A0A1I4T28_9PROT	Nitrosomonas nitrosa	Putative exosortase-associated protein, TIGR0	0	66,259	2,74E+08	9	1	1	1	4	14,2	13,232	A0A1I4T28;A0A1I4SF80;A0A1H3J	A0A1I4T28;A0A1I4SF80;A0A1H3JRT2	243	0,41	0,00844	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.70E+05	4.89E+05	2.64E+05	4.85E+05	7.75E+05	>tr A0A1G8C5M9 A0A1G8C5M9_9PROT	Nitrosomonas sp. Nm132	Cytochrome c-type biogenesis protein CcmH	0	10,017	8,52E+08	13	1	1	1	2	4,3	48,272	A0A1G8C5M9;A0A1H3LV63	A0A1G8C5M9;A0A1H3LV63	244	3,43	0,00044	
2.02E+05	3.68E+05	3.13E+05	3.57E+05	0.00E+00	1.52E+05	0.00E+00	7.93E+04	0.00E+00	1.03E+05	>tr A0A14NHQ6 A0A14NHQ6_9PROT	Nitrosomonas nitrosa	Peptidylglyoxylase	0	6,8664	1,00E+07	1	1	1	1	2	4,7	68,643	A0A14NHQ6;A0A1I4RY26;A0A1I3J	A0A14NHQ6;A0A1I4RY26;A0A1I3J8I3	245	#ZAHU!	#ZAHU!	
7.70E+05	8.70E+05	8.51E+05	6.07E+06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A1H3MM73 A0A1H3MM73_9PROT	Nitrosomonas sp. Nm58	Superoxide dismutase	0	6,6279	0,00E+00	1	1	1	1	7	10,4	23,364	A0A1H3MM73;A0A1I68G6B1;A0A1I4C	A0A1H3MM73;A0A1I68G6B1;A0A1I4C	246	#ZAHU!	#ZAHU!	
9.23E+05	2.22E+05	0.00E+00	0.00E+00	0.00E+00	3.33E+05	2.26E+05	0.00E+00	0.00E+00	0.00E+00	>tr A0A1H3P364 A0A1H3P364_9PROT	Nitrosomonas sp. Nm33	Uncharacterized protein	0	13,509	1,63E+07	4	1	1	1	6	25,6	9,4958	A0A1H3P364;F8GKU4;A0A1I4NLP4;A0	A0A1H3P364;F8GKU4;A0A1I4NLP4;A0	247	2,28	#ZAHU!	
2.46E+06	2.93E+06	2.25E+06	9.51E+06	3.52E+06	0.00E+00	0.00E+00	0.00E+00	1.75E+05	0.00E+00	>tr A0A1N6IDW7 A0A1N6IDW7_9PROT	Nitrosomonas cryotolerans ATCC	Uroporphyrinogen decarboxylase	0	6,4825	2,13E+07	3	1	1	1	5	4,2	39,108	A0A1N6IDW7;A0A1I4RR0;A0A1I4N	A0A1N6IDW7;A0A1I4RR0;A0A1I4N6J	248	3,33	#ZAHU!	
1.78E+06	1.71E+06	1.44E+06	1.90E+06	1.35E+06	2.16E+07	1.84E+07	8.86E+06	1.87E+07	2.50E+07	>tr A0A1I4UY44 A0A1I4UY44_9PROT	Nitrosomonas nitrosa	30S ribosomal protein S7	0	161,78	8,85E+08	11	2	2	26	16	17,956	A0A1I4UY44;A0A1H3NRM1;A0A1H3K	A0A1I4UY44;A0A1H3NRM1;A0A1H3K	249	-1,45	0,00013		
4.05E+05	3.52E+05	0.00E+00	5.54E+05	4.55E+05	9.76E+04	0.00E+00	0.00E+00	2.80E+05	2.80E+05	>tr A0A1G8I86G A0A1G8I86G_9PROT	Nitrosomonas sp. Nm132	Nitroxyamine dehydrogenase	0	10,106	1,03E+08	9	4	1	12	8,2	63,762	A0A1G8I86G;A0A1H3R5V0;A0A1G5D	A0A1G8I86G;A0A1H3R5V0;A0A1G5D5	250	1,41	0,09642		
8.25E+04	1.23E+05	1.08E+05	1.32E+05	7.18E+04	1.79E+06	1.97E+06	1.75E+06	2.10E+06	1.92E+06	>tr A0A1G9DRA9 A0A1G9DRA9_9RHOB	Paracoccus chinensis	Acetyltransferase component of pyruvate dehyd	0	10,886	2,84E+08	32	1	1	1	4,3	47,551	A0A1G9DRA9	A0A1G9DRA9	251	-1,50	0,00000		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	8.11E+04	9.38E+04	8.97E+04	8.72E+04	0.00E+00	>tr A0A2H5F242 A0A2H5F242_9RHOB	Paracoccus zhejiangensis																	



1.20E+08	1.62E+08	1.32E+08	1.17E+08	1.10E+08	6.64E+05	4.68E+05	2.32E+05	3.83E+05	6.43E+05	>tr AOA114LL08 AOA114LL08_9PROT	Nitrosomonas nitrosa	Apoptosis-inducing factor, C-term	0	19,579	7,65E+07	7	3	2	3	3	1	11.2	43.74	AOA114LL08	AOA114LL08	327	-0.55	0.00036
1.35E+07	1.58E+07	1.23E+07	1.55E+07	1.68E+07	0.00E+00	0.00E+00	0.00E+00	1.05E+05	0.00E+00	>tr AOA114LL47 AOA114LL47_9PROT	Nitrosomonas nitrosa	Dienelactone hydrolase	0	28,146	9,65E+07	9	2	2	2	1	1	13.5	25.78	AOA114LL47	AOA114LL47	328	6.51	0.34705
0.00E+00	2.88E+05	1.01E+05	1.55E+05	0.00E+00	2.64E+05	9.41E+04	0.00E+00	7.94E+04	5.32E+04	>tr AOA114LLU2 AOA114LLU2_9PROT	Nitrosomonas nitrosa	N-acetylneuraminic acid mutarotase	0	218,64	1,90E+08	13	2	2	2	1	1	15.5	36,257	AOA114LLU2	AOA114LLU2	329	4.20	0.05853
5.71E+04	1.02E+05	6.94E+04	1.12E+05	5.49E+04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr AOA114LNV3 AOA114LNV3_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	9,9485	1,68E+07	4	1	1	1	1	1	8.1	26,157	AOA114LNV3	AOA114LNV3	330	#ZAH!	0.00000
1.64E+06	2.38E+06	1.72E+06	1.40E+06	1.86E+06	1.75E+06	1.07E+06	7.10E+05	1.56E+06	1.87E+06	>tr AOA114LQ74 AOA114LQ74_9PROT	Nitrosomonas nitrosa	Chaperone protein DnaK	0	189,7	4,75E+08	24	5	1	4	17	11.2	70,259	AOA114LQ74;AOA113HHP9;AOA113H3E8	AOA114LQ74;AOA113HHP9;AOA113H3E8	331	-0.08	0.00022	
1.46E+06	1.91E+06	1.04E+06	1.17E+06	1.15E+06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.02E+05	>tr AOA114LQQ0 AOA114LQQ0_9PROT	Nitrosomonas nitrosa	Glutathione S-transferase	0	81,825	1,67E+07	3	1	1	1	1	1	7.3	23,212	AOA114LQQ0	AOA114LQQ0	332	3.23	#ZAH!
4.46E+06	1.88E+06	1.15E+06	1.40E+06	1.23E+06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr AOA114LY11 AOA114LY11_9PROT	Nitrosomonas nitrosa	Thiazole synthase	0	9,8523	2,93E+07	3	1	1	1	1	1	7.2	28,056	AOA114LY11	AOA114LY11	333	#ZAH!	0.00000
6.67E+06	8.96E+06	6.73E+06	0.00E+00	5.79E+06	1.43E+07	1.47E+07	6.15E+06	1.11E+07	1.46E+07	>tr AOA114LY25 AOA114LY25_9PROT	Nitrosomonas nitrosa	Thioredoxin	0	323,31	2,91E+09	63	4	4	4	4	14	38	12,074	AOA114LY25;AOA113K5R3;AOA113H3E8	AOA114LY25	334	3.10	0.00008
9.08E+06	1.14E+07	7.82E+06	9.06E+06	9.10E+06	2.60E+08	3.07E+08	2.73E+08	2.44E+08	3.28E+08	>tr AOA114LZ17 AOA114LZ17_9PROT	Nitrosomonas nitrosa	CHRD domain-containing protein	0	32,899	1,35E+10	15	2	2	2	1	1	21.7	18,734	AOA114LZ17	AOA114LZ17	335	0.48	0.00000
1.38E+05	1.04E+05	8.02E+04	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	2.79E+05	2.56E+05	>tr AOA114M5U7 AOA114M5U7_9PROT	Nitrosomonas nitrosa	Malate dehydrogenase	0	20,039	9,65E+07	6	3	3	3	5	13.4	35,956	AOA114M5U7;F8E8A4;AOA112AZM2	AOA114M5U7	336	3.28	0.04486	
2.54E+08	2.99E+08	1.87E+08	2.58E+08	2.86E+08	3.24E+05	6.42E+04	3.89E+04	5.88E+05	7.25E+05	>tr AOA114M6F6 AOA114M6F6_9PROT	Nitrosomonas nitrosa	Cytochrome c-type biogenesis protein CcmH	0	323,31	5,15E+08	37	3	3	3	1	9.9	48,123	AOA114M6F6	AOA114M6F6	337	3.50	0.03488	
3.77E+08	1.32E+08	1.63E+08	2.55E+08	2.40E+06	1.03E+05	9.43E+04	7.04E+04	0.00E+00	0.00E+00	>tr AOA114M38 AOA114M38_9PROT	Nitrosomonas nitrosa	Phospholipid transport system substrate-bind	0,0068611	5,9511	5,70E+07	2	1	1	1	1	5.8	23,43	AOA114M38	AOA114M38	338	3.95	0.04457	
3.80E+05	4.49E+05	1.39E+05	0.00E+00	1.82E+05	5.49E+06	6.16E+06	3.13E+06	0.00E+00	0.00E+00	>tr AOA114ME11 AOA114ME11_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	54,834	6,74E+08	13	1	1	1	1	11.9	16,928	AOA114ME11	AOA114ME11	339	2.72	0.05359	
4.37E+06	5.35E+06	4.62E+06	4.28E+06	3.70E+06	5.71E+06	4.12E+06	0.00E+00	3.15E+06	5.19E+06	>tr AOA114MHK6 AOA114MHK6_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	14,03	1,66E+08	2	1	1	1	1	11.6	16,064	AOA114MHK6	AOA114MHK6	340	0.36	#ZAH!	
4.89E+06	8.19E+06	1.17E+07	2.30E+06	6.28E+06	2.90E+05	2.42E+05	1.83E+05	0.00E+00	2.70E+05	>tr AOA114MNF9 AOA114MNF9_9PROT	Nitrosomonas nitrosa	Cytochrome c, mono- and dihem variants	0,0054348	6,0422	5,08E+07	2	1	1	1	1	2.8	47,09	AOA114MNF9	AOA114MNF9	341	0.09	0.00558	
1.53E+06	3.26E+06	3.38E+06	1.20E+06	2.97E+06	4.56E+05	6.14E+05	2.37E+05	5.21E+05	7.26E+05	>tr AOA114MQW9 AOA114MQW9_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	12,737	1,66E+08	7	2	2	2	2	13.4	22,388	AOA114MQW9;AOA113HT57	AOA114MQW9;AOA113HT57	342	3.58	0.00025	
6.66E+06	4.00E+06	3.12E+06	7.74E+06	3.03E+06	0.00E+00	0.00E+00	1.29E+05	3.62E+05	2.49E+05	>tr AOA114MRP1 AOA114MRP1_9PROT	Nitrosomonas nitrosa	Uncharacterized protein YjbJ, contains pentap	0	323,31	1,55E+08	12	3	3	3	1	18.5	27,233	AOA114MRP1	AOA114MRP1	343	4.47	0.06973	
6.73E+05	3.24E+06	2.27E+06	2.87E+06	2.11E+06	1.30E+05	1.41E+05	1.05E+05	8.99E+04	1.47E+05	>tr AOA114MZB4 AOA114MZB4_9PROT	Nitrosomonas nitrosa	Putative HEP-CTERM system TPR-repeat lipop	0	7,2206	4,57E+07	4	1	1	1	1	1.4	102,42	AOA114MZB4	AOA114MZB4	344	-1.47	0.00000	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	6.63E+05	2.59E+05	2.32E+05	3.47E+05	2.07E+05	0.00E+00	>tr AOA114N2B1 AOA114N2B1_9PROT	Nitrosomonas nitrosa	4-HYDROXY-3-METHYLBUT-2-EN-1-YL DIPHOSPHATE	0	6,574	3,16E+07	2	1	1	1	1	3.9	44,446	AOA114N2B1	AOA114N2B1	345	-1.94	#ZAH!	
9.86E+06	1.81E+07	1.33E+07	1.40E+07	4.60E+06	0.00E+00	0.00E+00	9.27E+04	0.00E+00	0.00E+00	>tr AOA114N2X8 AOA114N2X8_9PROT	Nitrosomonas nitrosa	Glucokinase	0	19,053	3,98E+07	5	2	2	2	2	10.2	36,272	AOA114N2X8	AOA114N2X8	346	5.12	0.34706	
9.16E+05	1.44E+06	1.65E+06	6.86E+05	1.19E+06	5.24E+05	7.17E+05	1.29E+05	2.58E+05	0.00E+00	>tr AOA114N348 AOA114N348_9PROT	Nitrosomonas nitrosa	Polyketide cyclase / dehydrase and lipid trans	0	34,294	3,10E+08	11	4	4	4	3	27.9	19,103	AOA114N348;AOA113PH93;AOA113H3E8	AOA114N348	347	4.17	0.03739	
3.81E+07	4.37E+07	4.04E+07	3.70E+07	3.62E+07	1.83E+05	1.83E+05	8.95E+04	1.69E+05	1.78E+05	>tr AOA114N3B7 AOA114N3B7_9PROT	Nitrosomonas nitrosa	Dimerisation domain-containing protein	0,0068143	5,9378	4,54E+07	6	1	1	1	1	4.9	17,7	AOA114N3B7	AOA114N3B7	348	0.75	#ZAH!	
3.57E+06	3.42E+06	1.65E+06	7.72E+05	2.37E+06	3.32E+05	2.53E+05	0.00E+00	3.20E+05	5.42E+05	>tr AOA114N6P0 AOA114N6P0_9PROT	Nitrosomonas nitrosa	Peptide methionine sulfoxide reductase MsrA	0	13,632	8,58E+07	6	1	1	1	1	8.7	25,865	AOA114N6P0	AOA114N6P0	349	2.02	0.01050	
1.35E+06	2.58E+06	2.32E+06	1.88E+06	1.86E+06	1.05E+06	1.16E+06	3.56E+05	1.42E+06	9.21E+05	>tr AOA114NDH3 AOA114NDH3_9PROT	Nitrosomonas nitrosa	Reactive intermediate/imine deaminase	0	323,31	6,98E+08	18	2	2	2	9	22.9	14,088	AOA114NDH3;Q82TN3;QOAF1;AOA114N2B1	AOA114NDH3;Q82TN3;QOAF1;AOA114N2B1	350	4.07	0.00055	
4.60E+06	3.66E+06	3.45E+06	4.61E+06	4.85E+06	2.19E+06	2.83E+06	1.09E+06	1.99E+06	2.47E+06	>tr AOA114NE55 AOA114NE55_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	38,082	1,77E+08	7	3	3	3	8	19.8	25,246	AOA114NE55;AOA114SX72;AOA113K5R3	AOA114NE55	351	-3.10	#ZAH!	
7.55E+06	1.09E+07	8.16E+06	1.18E+07	4.52E+06	6.25E+07	5.54E+07	2.06E+07	3.01E+07	5.07E+07	>tr AOA114NHR2 AOA114NHR2_9PROT	Nitrosomonas nitrosa	Bacterial nucleoid protein Hbs	0	323,31	1,03E+09	16	2	2	2	4	30	9,1096	AOA114NHR2;AOA113H3E8;AOA113H3E8	AOA114NHR2;AOA113H3E8;AOA113H3E8	352	-0.83	0.00055	
1.92E+07	2.45E+07	2.37E+07	1.24E+07	1.35E+07	1.02E+05	4.45E+05	0.00E+00	0.00E+00	0.00E+00	>tr AOA114NHS8 AOA114NHS8_9PROT	Nitrosomonas nitrosa	Enoyl-[acyl-carrier-protein] reductase [NADH	0,0070671	6,0074	7,20E+07	3	1	1	1	1	5	28,063	AOA114NHS8	AOA114NHS8	353	2.75	0.23999	
1.67E+07	2.12E+07	1.65E+07	2.09E+07	1.23E+07	0.00E+00	3.02E+05	0.00E+00	0.00E+00	0.00E+00	>tr AOA114NJF2 AOA114NJF2_9PROT	Nitrosomonas nitrosa	Ribose-5-phosphate isomerase A	0	27,36	1,06E+08	7	1	1	1	1	8.7	23,332	AOA114NJF2	AOA114NJF2	354	5.09	0.34675	
8.07E+05	7.79E+05	5.02E+05	3.95E+05	1.23E+05	1.07E+05	8.73E+04	4.31E+04	5.65E+04	0.00E+00	>tr AOA114NJN4 AOA114NJN4_9PROT	Nitrosomonas nitrosa	D-alanine--D-alanine ligase	0	6,5713	1,23E+07	1	1	1	1	1	5.2	33,156	AOA114NJN4	AOA114NJN4	355	0.40	0.31063	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.21E+06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr AOA114NP32 AOA114NP32_9PROT	Nitrosomonas nitrosa	Thiosulfate sulfurtransferase	0	55,062	2,16E+08	6	1	1	1	1	12.7	16,612	AOA114NP32	AOA114NP32	356	4.23	#ZAH!	
1.69E+07	2.30E+07	8.44E+06	5.03E+06	1.55E+07	1.93E+05	1.18E+05	1.55E+05	0.00E+00	0.00E+00	>tr AOA114NQJ8 AOA114NQJ8_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	14,167	2,13E+08	2	2	2	2	2	28.2	8,8851	AOA114NQJ8;AOA113H3E8	AOA114NQJ8;AOA113H3E8	357	7.83	0.04753	
3.94E+05	4.41E+05	2.72E+05	3.84E+05	8.08E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr AOA114NTE7 AOA114NTE7_9PROT	Nitrosomonas nitrosa	Uncharacterized protein	0	152,16	8,01E+07	3	1	1	1	1	20.2	13,792	AOA114NTE7	AOA114NTE7	358	#ZAH!	#ZAH!	
1.18E+06	1.27E+06	9.39E+05	1.20E+06	8.00E+05	2.14E+05	1.38E+05	9.18E+04	1.61E+05	1.95E+05	>tr AOA114NUJ8 AOA114NUJ8_9PROT	Nitrosomonas nitrosa	Tryptophan--tRNA ligase	0	303,6697	6,059	3,53E+07	2	1	1	1	3.5	45,494	AOA114NUJ8	AOA114NUJ8	359	-0.12	0.00008	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.29E+06	1.82E+05	0.00E+00	0.00E+00	0.00E+00	>tr AOA114NVP1 AOA114NVP1_9PROT	Nitrosomonas nitrosa	Cytochrome P450	0	219,76	1,03E+09	12	4	4	8	29.3	19,675	AOA114NVP1;AOA113H3E8;AOA113H3E8	AOA114NVP1;AOA113H3E8;AOA113H3E8	360	5.96	0.27555		
1.46E+06	1.89E+06	1.38E+06	1.36E+06	4.73E+05	4.84E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr AOA114NW6 AOA114NW6_9PROT	Nitrosomonas nitrosa	Cytochrome c553	0	23,126	8,55E+07	11	1	1	1	1	26.4	11,604	AOA114NW6	AOA114NW6	361	5.10	0.34669	
9.88E+05	1.25E+06	1.53E+06	8.59E+05	7.42E+05	2.07E+06	0.00E+00	6.80E+05	0.00E+00	1.06E+06	>tr AOA114NWU2 AOA114NWU2_9PROT	Nitrosomonas nitrosa	Heat shock protein Hsp20	0	7,0554	8,00E+07	3	1	1	1	1	11.7	16,27	AOA114NWU2	AOA114NWU2	362	0.70	0.38568	
1.09E+06	8.63E+05	5.69E+05	5.57E+05	1.04E+06	2.67E+05	3.26E+05	1.30E+05	2.54E+05	3.02E+05	>tr AOA114NY11 AOA114NY11_9PROT	Nitrosomonas nitrosa	Probable cytosol aminopeptidase	0	12,576	4,08E+07	5	2	2	2	17	5.6	53,271	AOA114NY11;AOA114PHL2;AOA113H3E8	AOA114NY11;AOA114PHL2;AOA113H3E8	363	-3.33	#ZAH!	





1.25E+07	1.61E+07	6.81E+06	1.14E+07	6.09E+06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A1W9J2W1 A0A1W9J2W1_9BACT	Nitrospira sp. ST-bin5	ATP synthase subunit beta	0	315,61	0,00E+00	0	4	3	0	8	14,2	52,892	A0A1W9J2W1:D8PA92;A0A1W9J0	A0A1W9J2W1:D8PA92;A0A1W9J0Y3;A	546	#ZAH!	#ZAH!	
4.73E+06	5.37E+06	2.86E+06	3.29E+06	9.47E+04	0.00E+00	2.38E+05	8.22E+04	1.41E+05	1.73E+05	>tr A0A1W9J4N3 A0A1W9J4N3_9BACT	Nitrospira sp. ST-bin5	Polyribonucleotide nucleotidyltransferase	0	6,5647	3,92E+07	2	1	1	1	1	1	2,1	75,756	A0A1W9J4N3	A0A1W9J4N3	547	-0,10	0,01391	
5.98E+07	9.64E+07	9.00E+07	1.40E+08	2.34E+07	1.67E+06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A1W9J4X2 A0A1W9J4X2_9BACT	Nitrospira sp. ST-bin5	Uncharacterized protein	0	7,8913	4,72E+08	4	1	1	1	1	1	5	24,165	A0A1W9J4X2	A0A1W9J4X2	548	4,37	0,34662	
3.55E+05	6.36E+05	3.34E+05	3.66E+05	2.80E+05	1.51E+05	1.90E+05	7.09E+04	1.13E+05	1.10E+05	>tr A0A1W9J589 A0A1W9J589_9BACT	Nitrospira sp. ST-bin5	Uncharacterized protein	0,0068847	5,9675	3,25E+07	3	1	1	1	1	1	4,9	41,045	A0A1W9J589	A0A1W9J589	549	0,41	0,00024	
2.37E+06	1.90E+06	1.59E+06	1.46E+06	1.07E+06	7.19E+05	2.01E+05	1.81E+06	5.01E+06	9.65E+06	>tr A0A1W9J7A5 A0A1W9J7A5_9BACT	Nitrospira sp. ST-bin5	Uncharacterized protein	0	15,556	2,58E+08	9	2	2	2	2	2	6	9,4	28,332	A0A1W9J7A5;A0A136JQL7;A0A1W	A0A1W9J7A5;A0A136JQL7;A0A1W9JIB	550	-1,52	0,08284
1.65E+06	1.75E+06	0.00E+00	1.66E+06	1.45E+06	2.86E+07	2.66E+07	1.36E+07	2.24E+07	0.43E+07	>tr A0A1W9J7H6 A0A1W9J7H6_9BACT	Nitrospira sp. ST-bin5	Uncharacterized protein	0	323,31	4,10E+09	31	3	3	3	3	3	9	23,9	31,737	A0A1W9J7H6;D8PI81;A0A1W1HY9	A0A1W9J7H6;D8PI81;A0A1W1HY9E	551	1,54	0,00002
3.71E+05	0.00E+00	2.42E+05	2.92E+05	1.95E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A1X7IY27 A0A1X7IY27_9RHOB	Paracoccus sp. J56	Predicted oxidoreductase	0	6,2719	1,72E+07	1	1	1	1	1	1	3,7	38,618	A0A1X7IY27	A0A1X7IY27	552	#ZAH!	0,00000	
1.74E+05	2.06E+05	1.97E+05	2.08E+05	3.28E+05	2.51E+05	2.25E+05	1.14E+05	1.67E+05	2.79E+05	>tr A0A1X7JG97 A0A1X7JG97_9RHOB	Paracoccus sp. J56	Amino acid/amide ABC transporter substrate	0	8,6633	9,52E+07	8	1	1	1	1	1	4	46,816	A0A1X7JG97	A0A1X7JG97	553	1,94	0,00012	
4.18E+05	0.00E+00	4.59E+05	4.16E+05	1.41E+05	3.57E+06	2.89E+06	3.65E+06	4.15E+06	4.18E+06	>tr A0A1X7JIS3 A0A1X7JIS3_9RHOB	Paracoccus sp. J56	ATP synthase subunit beta	0	46,947	6,08E+08	24	3	1	1	2	11,4	50,233	A0A1X7JIS3;A0A1G7BKN2	A0A1X7JIS3;A0A1G7BKN2	554	-1,00	0,00000		
1.22E+06	1.12E+06	0.00E+00	7.27E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A238VVT1 A0A238VVT1_9RHOB	Paracoccus sediminis	Isocitrate dehydrogenase [NADP]	0	29,264	0,00E+00	0	2	2	0	0	1	6,9	45,389	A0A238VVT1	A0A238VVT1	555	#ZAH!	#ZAH!	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A238W710 A0A238W710_9RHOB	Paracoccus sediminis	Polysaccharide pyruvyl transferase	0,0069808	5,9919	1,28E+07	1	1	1	1	1	1	3,1	42,402	A0A238W710	A0A238W710	556	#ZAH!	#ZAH!	
2.69E+05	3.93E+05	1.64E+05	3.16E+05	0.00E+00	7.39E+05	0.00E+00	9.81E+04	2.92E+05	2.64E+05	>tr A0A239PMM6 A0A239PMM6_9RHOB	Paracoccus seriniphilus	Catalase-peroxidase	0	15,288	2,09E+08	7	1	1	1	2	2	2	81,232	A0A239PMM6;SSY589	A0A239PMM6;SSY589	557	1,77	0,05961	
1.95E+06	2.20E+06	2.12E+06	3.39E+06	2.94E+06	1.98E+06	2.14E+06	1.67E+06	1.28E+06	0.00E+00	>tr A0A256WYH8 A0A256WYH8_9BACT	Nitrospira sp. UW-LDO-01	Uncharacterized protein	0,0069444	5,9864	5,27E+08	2	1	1	1	1	1	2,6	67,688	A0A256WYH8	A0A256WYH8	558	0,49	0,00604	
2.55E+05	2.32E+05	1.20E+05	0.00E+00	1.64E+05	2.08E+05	2.69E+05	5.94E+04	1.57E+05	1.53E+05	>tr A0A2A2GGF7 A0A2A2GGF7_9RHOB	Paracoccus sp. WN007	Microcin ABC transporter ATP-binding protein	0	6,4295	6,99E+07	3	1	1	1	1	1	2,3	55,892	A0A2A2GGF7	A0A2A2GGF7	559	1,04	0,00120	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.59E+06	7.40E+06	4.59E+06	6.25E+06	6.71E+06	>tr A0A2H5EWY1 A0A2H5EWY1_9RHOB	Paracoccus zhejiangensis	60 kDa chaperonin	0	323,31	1,69E+09	27	7	3	2	34	15,3	57,771	A0A2H5EWY1;A0A2A2GHN6;Q9Z4	A0A2H5EWY1;A0A2A2GHN6;Q9Z4G2;	560	-0,57	0,00000		
5.21E+05	6.26E+05	4.60E+05	6.22E+05	6.09E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A2A2GM46 A0A2A2GM46_9RHOB	Paracoccus sp. WN007	Chromosome segregation protein SMC (Fragm	0	6,3871	2,49E+07	2	1	1	1	1	1	1,8	91,458	A0A2A2GM46	A0A2A2GM46	561	#ZAH!	#ZAH!	
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.34E+06	0.00E+00	1.45E+05	>tr A0A2D2C7H2 A0A2D2C7H2_9RHOB	Paracoccus sp. Yee01	Sugar ABC transporter substrate-binding prot	0	7,0761	5,33E+07	1	1	1	1	1	1	5,6	53,048	A0A2D2C7H2	A0A2D2C7H2	562	#ZAH!	#ZAH!	
0.00E+00	0.00E+00	0.00E+00	3.41E+04	4.42E+04	0.00E+00	1.15E+06	0.00E+00	5.59E+05	8.70E+05	>tr A0A2E3CFP5 A0A2E3CFP5_9RHOB	Paracoccus sp.	PQQ-dependent dehydrogenase, methanol/et	0	6,2631	1,24E+08	4	1	1	1	1	2	2,1	67,305	A0A2E3CFP5;A0A2D8X0A6	A0A2E3CFP5;A0A2D8X0A6	563	-0,37	0,05573	
1.10E+06	1.49E+06	1.29E+06	1.11E+06	1.19E+06	3.94E+05	1.37E+05	2.96E+05	1.10E+05	0.00E+00	>tr A0A2E3CEI5 A0A2E3CEI5_9RHOB	Paracoccus sp.	Malate dehydrogenase	0,0018553	6,0847	2,00E+08	4	2	1	1	1	2	7,8	33,469	A0A2E3CEI5;A0A2D8X362	A0A2E3CEI5;A0A2D8X362	564	3,28	0,02818	
1.80E+05	1.21E+05	6.82E+04	1.67E+05	1.23E+05	4.49E+05	5.82E+05	0.00E+00	0.00E+00	0.00E+00	>tr A0A2G1YZ09 A0A2G1YZ09_9RHOB	Paracoccus sp.	ATP synthase subunit beta	0	17,755	7,90E+07	3	4	2	2	2	2	13,1	50,448	A0A2G1YZ09;A0A1N7MME2	A0A2G1YZ09;A0A1N7MME2	565	1,22	0,14592	
4.31E+05	6.60E+05	6.14E+05	4.14E+05	3.65E+05	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr A0A2G1Z1D0 A0A2G1Z1D0_9RHOB	Paracoccus sp.	Chaperone protein DnaK	0	22,931	0,00E+00	0	4	1	0	1	6,4	68,667	A0A2G1Z1D0	A0A2G1Z1D0	566	#ZAH!	#ZAH!		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	1.61E+07	1.89E+07	9.05E+06	1.35E+07	1.65E+07	>tr A0A2G1Z4R4 A0A2G1Z4R4_9RHOB	Paracoccus sp.	Transcriptional regulator	0	11,233	8,19E+08	3	2	2	2	41	19,6	12,255	A0A2G1Z4R4;SSXRT9;Q3SRC8;Q1C	A0A2G1Z4R4;SSXRT9;Q3SRC8;Q1C	567	-0,25	0,00002		
8.49E+05	8.11E+05	6.66E+05	5.18E+05	6.43E+05	0.00E+00	6.57E+05	2.87E+05	6.22E+05	4.81E+05	>tr A0A2H5EV53 A0A2H5EV53_9RHOB	Paracoccus zhejiangensis	ATP synthase subunit alpha	0	64,235	6,17E+07	5	3	1	1	1	1	8,2	55,151	A0A2H5EV53	A0A2H5EV53	568	-3,69	#ZAH!	
8.09E+05	1.32E+06	8.73E+05	1.87E+06	1.38E+06	2.61E+05	3.48E+05	0.00E+00	8.58E+04	2.99E+05	>tr A0A2H5EY37 A0A2H5EY37_9RHOB	Paracoccus zhejiangensis	Uncharacterized protein	0,0018762	6,1022	3,35E+08	1	1	1	1	1	1	0,8	146,73	A0A2H5EY37	A0A2H5EY37	569	1,96	#ZAH!	
5.83E+05	1.47E+06	1.00E+06	7.98E+05	5.00E+05	3.06E+05	2.28E+05	0.00E+00	1.69E+05	2.05E+05	>tr A0A2H5F1J9 A0A2H5F1J9_9RHOB	Paracoccus zhejiangensis	ABC transporter substrate-binding protein	0	10,689	4,46E+07	5	1	1	1	1	1	4,4	39,318	A0A2H5F1J9	A0A2H5F1J9	570	1,19	0,00713	
1.03E+05	1.59E+05	0.00E+00	9.13E+04	6.88E+04	8.28E+05	1.01E+06	6.46E+05	7.76E+05	9.43E+05	>tr A0A2H5F246 A0A2H5F246_9RHOB	Paracoccus zhejiangensis	Formate dehydrogenase	0	12,264	9,77E+08	5	2	2	2	2	2	2,6	109,92	A0A2H5F246;A0A1N7JPA7	A0A2H5F246;A0A1N7JPA7	571	1,94	0,00000	
3.31E+05	7.79E+05	8.30E+05	3.21E+05	0.00E+00	8.23E+06	6.07E+06	3.77E+06	8.24E+06	8.72E+06	>tr Q1QHY1 Q1QHY1_NITXH	Nitrobacter hamburgensis (strain	Cold-shock DNA-binding protein family	0	35,698	1,24E+09	8	1	1	1	1	2	15,9	7,3892	Q1QHY1;A3WV12	Q1QHY1;A3WV12	572	2,98	0,00007	
4.99E+05	1.13E+06	6.73E+05	6.63E+05	2.54E+05	1.87E+07	1.24E+07	1.17E+07	1.30E+07	1.65E+07	>tr A3X1N0 A3X1N0_9BRAD	Nitrobacter sp. Nb-311A	Uncharacterized protein	0	6,3386	1,93E+09	4	1	1	1	1	1	5,4	34,228	A3X1N0	A3X1N0	573	0,29	#ZAH!	
8.17E+05	1.11E+06	6.75E+05	0.00E+00	9.01E+05	6.27E+05	1.06E+06	0.00E+00	6.33E+05	1.33E+06	>sp B1XXY8 CH10_LEPCP	Leptothrix cholodnii (strain ATCC	10 kDa chaperonin	0	9,7547	5,05E+07	5	1	1	1	1	1	28,1	10,459	B1XXY8	B1XXY8	574	0,39	0,01208	
3.18E+07	3.38E+07	2.34E+07	2.53E+07	1.39E+07	2.38E+05	1.98E+04	0.00E+00	6.61E+05	2.13E+06	>sp B1XXY9 CH60_LEPCP	Leptothrix cholodnii (strain ATCC	60 kDa chaperonin	0	64,601	2,97E+08	7	8	5	3	1	16,4	57,309	B1XXY9	B1XXY9	575	1,17	0,16419		
2.24E+06	2.74E+06	2.36E+06	2.37E+06	1.53E+06	2.02E+06	1.98E+06	2.19E+06	2.49E+06	3.11E+06	>tr I4Z6D7 I4Z6D7_9BURK	Leptothrix ochracea L12	Isocitrate lyase	0	53,262	1,97E+09	13	1	1	2	2	2	7,7	47,793	I4Z6D7;B1XY22	I4Z6D7;B1XY22	576	2,00	0,00000	
1.48E+05	1.60E+05	1.30E+05	1.49E+05	1.40E+05	2.23E+05	4.36E+05	1.08E+05	2.29E+05	3.78E+05	>tr B1XZV7 B1XZV7_LEPCP	Leptothrix cholodnii (strain ATCC	Aldehyde ferredoxin oxidoreductase	0	6,3299	8,48E+07	4	1	1	1	1	1	2,3	65,907	B1XZV7	B1XZV7	577	0,27	0,00162	
2.69E+06	3.60E+05	1.16E+06	2.06E+06	1.45E+06	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	>tr B1Y042 B1Y042_LEPCP	Leptothrix cholodnii (strain ATCC	Acetyl-coenzyme A synthetase	0	6,2361	0,00E+00	2	1	1	1	1	1	1,8	71,191	B1Y042	B1Y042	578	#ZAH!	#ZAH!	
1.82E+06	1.72E+06	1.40E+06	2.01E+06	1.28E+06	2.08E+06	1.94E+06	1.61E+06	1.22E+06	0.00E+00	>tr B1Y0Z0 B1Y0Z0_LEPCP	Leptothrix cholodnii (strain ATCC	Formaldehyde-activating enzyme	0,0071048	6,0128	9,86E+07	2	1	1	1	1	1	6,5	17,691	B1Y0Z0	B1Y0Z0	579	-0,32	#ZAH!	
2.69E+06	2.67E+06	2.31E+06	3.03E+06	0.00E+00	4.54E+05	3.34E+05	3.74E+05	4.02E+05	0.00E+00	>tr I4Z5U7 I4Z5U7_9BURK	Leptothrix ochracea L12	Acetoacetyl-CoA reductase	0	7,6798	1,72E+07	1	1	1	1	2	7,3	26,11	I4Z5U7;B1Y253	I4Z5U7;B1Y253	580	#ZAH!	#ZAH!		
0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	7.83E+04	1.11E+05	4.68E+04	0.00E+00	0.00E+00	>tr B1Y3S7 B1Y3S7_LEPCP	Leptothrix cholodnii (strain ATCC	ATP synthase subunit beta	0	8,1473	8,38E+07	8	3	1	1	1	1	9,3	51,219	B1Y3S7	B1Y3S7	581	3,78	0,06241	
1.55E+07	1.67E+07	1.53E+07	1.61E+07	9.50E+06	1.62E+06	2.66E+06	1.26E+06	0.00E+00	1.13E+05	>sp B1Y3S9 ATPA_LEPCP	Leptothrix cholodnii (strain ATCC	ATP synthase subunit alpha	0	16,															