

**Supplemental materials for** Complete genome sequence of *Nitrosospira multiformis*, an ammonia-oxidizing bacterium from the soil environment by Jeanette M. Norton, \* Martin G. Klotz, Lisa Y. Stein, Daniel J. Arp, Peter J. Bottomley, Patrick S.G. Chain, Loren J. Hauser, Miriam L. Land, Frank W. Larimer, Maria W. Shin, Shawn R. Starkenburg

**Supplemental Table 1.** Detail list of the 187 regulatory proteins in *N. multiformis*

<b>Transcription/Elongation/Termination Factors</b>	<b>98</b>
<b>Sigma Factors</b>	<b>8</b>
RNA polymerase, sigma 28 subunit, FliA/WhiG	1
RNA polymerase, sigma 32 subunit, RpoH	1
RNA polymerase, sigma 54 subunit, RpoN	1
RNA polymerase, sigma 70 subunit, RpoD	1
RNA polymerase, sigma 70 subunit, RpoD family	1
RNA polymerase, sigma-24 subunit, ECF subfamily	3
<b>Anti/Anti-Anti Sigma Factors</b>	<b>6</b>
anti sigma-E protein, RseA	1
anti-sigma-28 factor, FlgM	1
anti-sigma-factor antagonist	1
putative sigma 54 modulation protein/ribosomal protein S30EA	1
sigma 54 modulation protein/ribosomal protein S30EA	1
sigma E regulatory protein, MucB/RseB	1
<b>Termination/Antitermination Factor</b>	<b>4</b>
NusA antitermination factor	1
NusB antitermination factor	1
NusG antitermination factor	1
transcription termination factor Rho	1
<b>Elongation Factors</b>	<b>3</b>
GreA/GreB family elongation factor	1
transcription elongation factor GreA	1
transcription elongation factor GreB	1
<b>Transcription Factors</b>	<b>77</b>
Flagellar transcriptional activator, FlhC subunit	1
Flagellar transcriptional activator, FlhD subunit	1
cold-shock DNA-binding domain protein	4
ferric uptake regulator, Fur family	2
heat-inducible transcription repressor HrcA	1
phage transcriptional regulator, AlpA	2
phosphate uptake regulator, PhoU	1
putative prophage repressor	1
putative transcriptional activator, Baf family	1

putative transcriptional regulator	4
putative transcriptional regulator, CopG family	2
putative transcriptional regulator, Crp/Fnr family	3
putative transcriptional regulator, TetR family	1
putative transcriptional regulator, XRE family	2
sigma54 specific transcriptional regulator, Fis family	1
transcriptional regulator, AraC family	1
transcriptional regulator, ArsR family	1
transcriptional regulator, BadM/Rrf2 family	3
transcriptional regulator, Crp/Fnr family	4
transcriptional regulator, Fis family	1
transcriptional regulator, GntR family	1
transcriptional regulator, HxIR family	2
transcriptional regulator, LuxR family	5
transcriptional regulator, LysR family	6
transcriptional regulator, MerR family	1
transcriptional regulator, TetR family	5
transcriptional regulator, XRE family	8
transcriptional regulator, putative ATPase, winged helix family	1
transcriptional regulator/antitoxin, MazE	1
two component transcriptional regulator, Fis family	1
two component transcriptional regulator, LuxR family	4
two component transcriptional regulator, winged helix family	2
two component, sigma54 specific, transcriptional regulator, Fis family	3
<b>Signal Transduction proteins</b>	<b>89</b>
<b>Chemotaxis Signal Transduction Proteins</b>	<b>6</b>
<b>Chemotaxis Sensory Transducers (receptors)</b>	<b>1</b>
methyl-accepting chemotaxis sensory transducer	1
<b>Other Chemotaxis Signal Transduction Proteins</b>	<b>5</b>
CheA signal transduction histidine kinases	1
CheW protein	2
MCP methyltransferase, CheR-type with TPR repeats	1
response regulator receiver modulated CheB methylesterase	1
<b>NON-Chemotaxis Signal Transduction</b>	<b>83</b>
<b>Signal Transduction Histidine Kinases (STHK)</b>	<b>23</b>
PAS/PAC sensor hybrid histidine kinase	3
PAS/PAC sensor signal transduction histidine kinase	3
histidine kinase	3
integral membrane sensor hybrid histidine kinase	1
integral membrane sensor signal transduction histidine kinase	6
multi-sensor hybrid histidine kinase	3
multi-sensor signal transduction histidine kinase	3
putative signal transduction histidine kinase	1

<b>Cyclic Nucleotide Signal Transduction</b>	<b>21</b>
cyclic nucleotide-binding protein	1
diguanylate cyclase	2
diguanylate cyclase with PAS/PAC sensor	2
diguanylate cyclase/phosphodiesterase	1
diguanylate cyclase/phosphodiesterase with PAS/PAC and Chase sensor(s)	1
diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	6
diguanylate phosphodiesterase	2
response regulator receiver modulated diguanylate cyclase	2
response regulator receiver modulated diguanylate cyclase/phosphodiesterase	1
response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)	2
response regulator receiver modulated diguanylate phosphodiesterase	1
<b>PTS NTR Regulator</b>	<b>2</b>
HPr kinase	1
Phosphotransferase system, phosphocarrier protein HPr	1
<b>Miscellaneous</b>	<b>37</b>
(p)ppGpp synthetase I, SpoT/RelA	2
N-acetylmuramyl-L-alanine amidase, negative regulator of AmpC, AmpD	1
Ppx/GppA phosphatase	1
UTP-GlnB uridylyltransferase, GlnD	1
UTP-glucose-1-phosphate uridylyltransferase GalU	2
bis(5'nucleosyl)-tetrphosphatase, ApaH	1
metal dependent phosphohydrolase	1
nitrogen regulatory protein P-II	4
phosphohistidine phosphatase, SixA	1
polynucleotide adenylyltransferase/metal dependent phosphohydrolase	1
protein serine/threonine phosphatases	1
protein tyrosine phosphatase	1
putative PAS/PAC sensor protein	1
response regulator receiver modulated PAS/PAC sensor protein	1
putative signal-transduction protein with CBS domains	2
response regulator receiver protein	13
transcriptional regulator, TraR/DksA family	2

**Supplemental Table 2.** Sensory Transduction and Regulatory Response Systems arranged by location.

<b>gene # Nmul_A</b>	<b>response regulator receiver proteins</b>	<b>gene # Nmul_A</b>	<b>histidine kinases</b>	<b>Comment</b>
0007	two component transcriptional regulator, Fis family	0008	integral membrane sensor signal transduction histidine kinase	
0163	response regulator receiver protein (CheY)			
0238	two-component response regulator degradative enzyme and competence regulation NarL family			
0334	response regulator receiver modulated CheB methyltransferase	0333	CheA signal transduction histidine kinases	
0335	response regulator receiver modulated diguanylate cyclase/phosphodiesterase			
0389	two component, sigma54 specific, transcriptional regulator, Fis family	0390	multi-sensor signal transduction histidine kinase	Nitrogen assimilation ntrX
0542	response regulator receiver protein (CheY)			
0543	response regulator receiver protein (CheY)			
		0553	histidine kinase	
0706	two component transcriptional regulator, winged helix family	0707	integral membrane sensor signal transduction histidine kinase	OmpR
0728	two component transcriptional regulator, LuxR family	0727	putative signal transduction histidine kinase	NarL
0823	response regulator receiver protein (CheY)			PleD
0826	response regulator receiver protein (CheY)			
0827	pseudogene with frame shift GGDEF & EAL domains			
0828	diguanylate cyclase/ phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s)			
0829	response regulator receiver protein (CheY)			
0831	cyclic nucleotide-binding domain protein, regulatory subunit	0832	histidine kinase	Flanked by transposases IS4
		1000	histidine kinase	OmpR aerobic/anaerobic respiration

1138	response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)			
1161	two component, sigma54 specific, transcriptional regulator, Fis family	1159	integral membrane sensor signal transduction histidine kinase	NtrC
		1191	integral membrane sensor hybrid histidine kinase	
1235	two component transcriptional regulator, LuxR family	1236	integral membrane sensor signal transduction histidine kinase	NarL
1279	response regulator receiver protein (CheY)			
		1287	multi-sensor signal transduction histidine kinase	
1288	response regulator receiver protein (CheY)	1289	multi-sensor signal transduction histidine kinase	
		1334	Histidine kinase, dimerisation and phosphoacceptor region	
1336	two component transcriptional regulator, LuxR family	1335	putative signal transduction histidine kinase	Flagellar cluster, NarL
		1490	PAS/PAC sensor hybrid histidine kinase	Dehydrogenase/reductase
		1491	PAS/PAC sensor hybrid histidine kinase	
		1492	PAS/PAC sensor hybrid histidine kinase	
1555	response regulator receiver modulated diguanylate phosphodiesterase	1556	multi-sensor hybrid histidine kinase	
		1636	histidine kinase (pseudogene)	transposase
1860	response regulator receiver modulated diguanylate cyclase			
1861	response regulator receiver modulated PAS/PAC sensor protein			
		2015	PAS/PAC sensor signal transduction histidine kinase	
2037	response regulator receiver protein (CheY)			
		2207	multi-sensor hybrid histidine kinase	
2231	two component transcriptional regulator, winged helix family	2232	PAS/PAC sensor signal transduction histidine kinase	Pho regulon
2297	response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s)			
2298	response regulator receiver protein (CheY)	2299	PAS/PAC sensor signal transduction histidine kinase	

2355	response regulator receiver protein (CheY)			
2385	response regulator receiver protein (CheY)			
2411	response regulator receiver protein (CheY)	2410	integral membrane sensor signal transduction histidine kinase	OmpR
2671	two component, sigma54 specific, transcriptional regulator, Fis family	2672	integral membrane sensor signal transduction histidine kinase	Outer membrane proteins, asparagine synthase, NtrC
2674	two component transcriptional regulator, LuxR family			NarL
2675	response regulator receiver protein (CheY)			
2693	response regulator receiver modulated diguanylate cyclase	2694	multi-sensor hybrid histidine kinase	PleD

**Supplemental Table 3.** Detail of transport and efflux as analyzed by COG categories, scores and probabilities. C=categories including: C, energy production and conversion; E, amino acid transport and metabolism; H, coenzyme transport; M, cell envelope biogenesis, outer membrane; N cell motility and secretion, O, posttranslational modification or chaperones; P, inorganic ion transport; Q, secondary metabolite transport and catabolism; R, general function prediction only; U, biopolymer transport V, defense mechanism.

<b>ABC Transporters</b>	<b>C</b>	<b>Locus Tag</b>	<b>COG</b>	<b>Score</b>	<b>P</b>
ABC-type (unclassified) transport system ATPase subunit	R	Nmul_A0085	COG1137	392	1.00E-110
ABC-type Fe <sup>3+</sup> -hydroxamate transport system periplasmic subunit	P	Nmul_A0090	COG0614	133	1.00E-32
ABC-type sulfate transport system periplasmic subunit, pseudogene	P	Nmul_A0100	COG1613	45.3	9.00E-07
ABC-type antimicrobial peptide transport system ATPase subunit	V	Nmul_A0367	COG1136	272	2.00E-74
ABC-type transport system involved in lipoprotein release inner membrane subunit	M	Nmul_A0369	COG4591	167	1.00E-42
ABC-type transport system involved in lipoprotein release inner membrane subunit	M	Nmul_A0370	COG4591	182	6.00E-47
ABC-type phosphate transport system periplasmic subunit	P	Nmul_A0486	COG0226	207	1.00E-54
ABC-type sulfate/molybdate transport systems ATPase subunit	P	Nmul_A0503	COG1118	413	1.00E-116
ABC-type sulfate transport system inner membrane subunit	P	Nmul_A0504	COG4208	398	1.00E-112
ABC-type sulfate transport system inner membrane subunit	O	Nmul_A0505	COG0555	267	5.00E-73
ABC-type sulfate transport system periplasmic subunit	P	Nmul_A0507	COG1613	508	1.00E-145
ABC-type uncharacterized transport system - periplasmic binding protein	N	Nmul_A0583	COG3225	61.5	1.00E-10
ABC-type Na <sup>+</sup> efflux pump inner membrane subunit	C	Nmul_A0584	COG1668	39	3.00E-04
ABC-type multidrug transport system ATPase subunit	V	Nmul_A0585	COG1131	229	1.00E-61
ABC-type multidrug transport system, fused ATPase and inner membrane subunits	V	Nmul_A0629	COG1132	332	4.00E-92
ABC-type transport system involved in Fe-S cluster assembly, fused inner membrane and ATPase subunits	O	Nmul_A0682	COG5265	649	0
ABC-type transport system involved in Fe-S cluster assembly inner membrane subunit	O	Nmul_A0696	COG0719	433	1.00E-122
ABC-type transport system involved in Fe-S cluster assembly ATPase subunit	O	Nmul_A0697	COG0396	347	5.00E-97

ABC-type transport system involved in Fe-S cluster assembly inner membrane subunit	O	Nmul_A0698	COG0719	284	1.00E-77
ABC-type spermidine/putrescine transport systems ATPase subunits	E	Nmul_A0730	COG3842	356	1.00E-99
ABC-type Fe <sup>3+</sup> transport system inner membrane subunit	P	Nmul_A0731	COG1178	306	3.00E-84
ABC-type Fe <sup>3+</sup> transport system periplasmic subunit	P	Nmul_A0732	COG1840	178	5.00E-46
ABC-type cobalamin/Fe <sup>3+</sup> -siderophores transport systems ATPase subunits	P	Nmul_A0883	COG1120	219	2.00E-58
ATPase subunits of ABC transporters with duplicated ATPase domains	R	Nmul_A0889	COG0488	567	1.00E-163
ABC-type transport system involved in lipoprotein release inner membrane subunit	M	Nmul_A0894	COG4591	82	2.00E-16
ABC-type antimicrobial peptide transport system ATPase subunit	V	Nmul_A0895	COG1136	243	6.00E-66
ABC-type phosphate transport system periplasmic subunit	P	Nmul_A0897	COG0226	206	2.00E-54
Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis inner membrane subunit	Q	Nmul_A0948	COG3127	639	0
ABC-type antimicrobial peptide transport system ATPase subunit	V	Nmul_A0951	COG1136	282	2.00E-77
ABC-type antimicrobial peptide transport system inner membrane subunit	V	Nmul_A0953	COG0577	115	5.00E-27
ABC-type antimicrobial peptide transport system inner membrane subunit	V	Nmul_A0954	COG0577	122	3.00E-29
spermidine/putrescine transport system substrate-binding protein (potD)	E	Nmul_A0979	COG0687	273	1.00E-74
ABC-type spermidine/putrescine transport system inner membrane subunit II	E	Nmul_A0980	COG1177	215	2.00E-57
ABC-type spermidine/putrescine transport system inner membrane subunit I	E	Nmul_A0981	COG1176	231	4.00E-62
ABC-type spermidine/putrescine transport systems ATPase subunits	E	Nmul_A0982	COG3842	392	1.00E-110
ABC-type phosphate transport system inner membrane subunit	P	Nmul_A1086	COG0573	238	3.00E-64
ABC-type phosphate transport system inner membrane subunit	P	Nmul_A1087	COG0581	224	5.00E-60
ABC-type phosphate transport system ATPase subunit	P	Nmul_A1088	COG1117	428	1.00E-121
ABC-type bacteriocin/lantibiotic exporters, fused inner membrane and ATPase subunits	V	Nmul_A1174	COG2274	258	1.00E-69
ABC-type sulfate transport system periplasmic subunit	P	Nmul_A1192	COG1613	380	1.00E-107



ABC-type transport system involved in cytochrome c biogenesis inner membrane subunit	O	Nmul_A1212	COG0755	134	7.00E-33
ABC-type transport system involved in cytochrome c biogenesis inner membrane subunit	O	Nmul_A1216	COG2386	156	1.00E-39
ABC-type transport system involved in cytochrome c biogenesis (heme) ATPase subunit	O	Nmul_A1217	COG4133	199	1.00E-52
ABC-type Mn <sup>2+</sup> /Zn <sup>2+</sup> transport systems inner membrane subunits	P	Nmul_A1230	COG1108	177	1.00E-45
ABC-type Mn/Zn transport systems ATPase subunit	P	Nmul_A1231	COG1121	237	5.00E-64
ABC-type metal ion transport system periplasmic subunit/surface adhesin	P	Nmul_A1232	COG0803	218	5.00E-58
ABC-type protease/lipase transport system, fused ATPase and inner membrane subunits	R	Nmul_A1280	COG4618	706	0
ABC-type multidrug transport system inner membrane subunit	V	Nmul_A1419	COG0842	88	9.00E-19
ABC-type multidrug transport system inner membrane subunit	V	Nmul_A1420	COG0842	92.3	6.00E-20
ABC-type multidrug transport system ATPase subunit	V	Nmul_A1421	COG1131	253	3.00E-68
ABC-type multidrug transport system ATPase , fused inner membrane subunits	V	Nmul_A1487	COG1132	381	1.00E-107
ABC-type antimicrobial peptide transport system ATPase subunit	V	Nmul_A1504	COG1136	240	9.00E-65
ABC-type transport system involved in lipoprotein, release inner membrane subunit	M	Nmul_A1505	COG4591	61.4	1.00E-10
ABC-type branched-chain amino acid transport systems periplasmic subunit	E	Nmul_A1557	COG0683	195	5.00E-51
ABC-type uncharacterized transport system auxiliary subunit	R	Nmul_A1609	COG3218	116	1.00E-27
ABC-type transport system involved in resistance to organic solvents periplasmic subunit	Q	Nmul_A1610	COG1463	125	6.00E-30
ABC-type transport system involved in resistance to organic solvents ATPase subunit	Q	Nmul_A1611	COG1127	339	1.00E-94
ABC-type transport system involved in resistance to organic solvents inner membrane subunit	Q	Nmul_A1612	COG0767	221	5.00E-59
ABC-type multidrug transport system, fused ATPase inner membrane subunits	V	Nmul_A1740	COG1132	407	1.00E-114
ATPase subunits of ABC transporters with duplicated ATPase domains	R	Nmul_A1811	COG0488	575	1.00E-165
ABC-type siderophore export system, fused ATPase inner membrane subunits	P	Nmul_A1823	COG4615	355	5.00E-99
ABC-type phosphate transport system periplasmic subunit	P	Nmul_A1955	COG0226	38.5	2.00E-04

Predicted ABC-type transport system involved in lysophospholipase L1 biosynthesis ATPase subunit	Q	Nmul_A1972	COG4181	279	1.00E-76
ABC-type transport system involved in resistance to organic solvents inner membrane subunit	Q	Nmul_A1981	COG0767	206	2.00E-54
ABC-type transport system involved in resistance to organic solvents ATPase subunit	Q	Nmul_A1982	COG1127	302	1.00E-83
ABC-type transport system involved in resistance to organic solvents periplasmic subunit	Q	Nmul_A1983	COG1463	118	6.00E-28
ABC-type uncharacterized transport system auxiliary subunit	R	Nmul_A1984	COG3218	70	1.00E-13
ABC-type sulfate transport system periplasmic subunit	P	Nmul_A2032	COG1613	339	2.00E-94
ABC-type uncharacterized transport system inner membrane subunit	R	Nmul_A2133	COG4137	194	6.00E-51
ABC-type polysaccharide/polyol phosphate transport system ATPase subunit	M	Nmul_A2200	COG1134	286	2.00E-78
ABC-type multidrug transport system, fused ATPase and inner membrane subunits	V	Nmul_A2254	COG1132	498	1.00E-141
ABC-type dipeptide/oligopeptide/nickel transport system ATPase subunit	P	Nmul_A2331	COG0444	411	1.00E-116
ABC-type dipeptide/oligopeptide/nickel transport systems inner membrane subunits	P	Nmul_A2332	COG1173	176	2.00E-45
ABC-type dipeptide/oligopeptide/nickel transport systems inner membrane subunits	P	Nmul_A2333	COG0601	182	4.00E-47
ABC-type dipeptide transport system periplasmic subunit	E	Nmul_A2334	COG0747	139	6.00E-34
ABC-type polysaccharide/polyol phosphate export systems inner membrane subunit	M	Nmul_A2397	COG1682	147	7.00E-37
ABC-type polysaccharide/polyol phosphate transport system ATPase subunit	M	Nmul_A2398	COG1134	294	1.00E-80
ABC-type antimicrobial peptide transport system ATPase subunit	V	Nmul_A2508	COG1136	273	5.00E-75
ABC-type transport system involved in lipoprotein release inner membrane subunit	M	Nmul_A2509	COG4591	391	1.00E-110
ABC-type transport system involved in resistance to organic solvents auxiliary subunit	Q	Nmul_A2559	COG2854	88	7.00E-19
ABC-type Fe <sup>3+</sup> -siderophore transport system inner membrane subunit	P	Nmul_A2614	COG0609	166	1.00E-42
ATPase subunits of ABC transporters with duplicated ATPase domains	R	Nmul_A2700	COG0488	537	1.00E-153
ABC-type polysaccharide/polyol phosphate export systems inner membrane subunit	M	Nmul_A2743	COG1682	57.1	1.00E-09
ABC-type multidrug transport system ATPase subunit	V	Nmul_A2744	COG1131	260	1.00E-70

ABC-type transport system involved in resistance to organic solvents auxiliary subunit	Q	Nmul_A2746	COG2854	154	4.00E-39
ABC-type transport system involved in resistance to organic solvents periplasmic subunit	Q	Nmul_A2747	COG1463	114	4.00E-27
ABC-type transport system involved in resistance to organic solvents inner membrane subunit	Q	Nmul_A2748	COG0767	234	5.00E-63
ABC-type transport system involved in resistance to organic solvents ATPase subunit	Q	Nmul_A2749	COG1127	342	2.00E-95
<b>P-Type ATPase</b>					
Cation transport ATPase	P	Nmul_A0037	COG0474	690	0
Cation transport ATPase	P	Nmul_A1528	COG0474	779	0
Cation transport ATPase	P	Nmul_A1648	COG0474	579	1.00E-166
Cation transport ATPase	P	Nmul_A2005	COG2217	705	0
Cation transport ATPase	P	Nmul_A2276	COG2217	750	0
<b>TonB/ExbB/ExbD or TolA/TolQ/TolR</b>					
Biopolymer transport protein ExbD/TolR	U	Nmul_A1028	COG0848	106	8.00E-25
Biopolymer transport protein ExbD/TolR	U	Nmul_A1047	COG0848	128	2.00E-31
Biopolymer transport protein ExbD/TolR	U	Nmul_A2301	COG0848	81	2.00E-17
Biopolymer transport protein ExbD/TolR	U	Nmul_A2569	COG0848	105	1.00E-24
Biopolymer transport protein ExbD/TolR	U	Nmul_A2716	COG0848	111	2.00E-26
MotA/TolQ/ExbB proton channel	U	Nmul_A1029	COG0811	135	2.00E-33
MotA/TolQ/ExbB proton channel	U	Nmul_A1048	COG0811	146	1.00E-36
MotA/TolQ/ExbB proton channel	U	Nmul_A2300	COG0811	106	1.00E-24
MotA/TolQ/ExbB proton channel	U	Nmul_A2570	COG0811	117	3.00E-27
MotA/TolQ/ExbB proton channel	U	Nmul_A2717	COG0811	187	4.00E-49
TonB protein	M	Nmul_A0537	COG0810	46	6.00E-06
TonB protein	M	Nmul_A1049	COG0810	53	2.00E-08
TolA protein	A	Nmul_A2715	COG3064	50	3.00E-07
Tol-pal system protein YbgF	S	Nmul_A2712	COG1729	128	4.00E-31
peptidoglycan-associated lipoprotein	M	Nmul_A2713	COG2885	122	1.00E-29
Tol-Pal system beta propeller repeat protein TolB	U	Nmul_A2714	COG0823	308	7.00E-85
<b>Ton B dependent receptors</b>					
Outer membrane receptor for monomeric catechols	P	Nmul_A1260	COG4774	314	2.00E-86
Outer membrane receptor for monomeric catechols	P	Nmul_A2391	COG4774	221	2.00E-58
ferrichrome iron receptor KO: K02014 iron complex outermembrane receptor protein	H	Nmul_A0628	COG4206	162	9.00E-42

Outer membrane receptor proteins mostly Fe transport	P	Nmul_A0635	COG1629	105	2.00E-23
Outer membrane receptor proteins mostly Fe transport	P	Nmul_A1233	COG1629	73.4	5.00E-14
Outer membrane receptor proteins mostly Fe transport	P	Nmul_A1426	COG1629	150	2.00E-37
Outer membrane receptor proteins mostly Fe transport	P	Nmul_A1826	COG1629	224	1.00E-59
Outer membrane hemin receptor TonB cobalamin	H	Nmul_A0973	COG4206	94	2.00E-20
Outer membrane cobalamin receptor protein		Nmul_A2510	COG4206	125	8.00E-30
<b>RND - efflux</b>					
Cation/multidrug efflux pump	V	Nmul_A0043	COG0841	951	0
Cation/multidrug efflux pump	V	Nmul_A0688	COG0841	985	0
Cation/multidrug efflux pump	V	Nmul_A0691	COG0841	969	0
Cation/multidrug efflux pump	V	Nmul_A0850	COG0841	912	0
Cation/multidrug efflux pump	V	Nmul_A1727	COG0841	827	0
Cation/multidrug efflux pump	V	Nmul_A1842	COG0841	500	1.00E-142
Cation/multidrug efflux pump	V	Nmul_A1970	COG0841	891	0
Predicted exporters of the RND superfamily	R	Nmul_A1652	COG1033	113	7.00E-26
Predicted exporters of the RND superfamily	R	Nmul_A2558	COG1033	103	8.00E-23
Putative silver efflux pump	P	Nmul_A1113	COG3696	1125	0
Putative silver efflux pump	P	Nmul_A1406	COG3696	1121	0
Putative silver efflux pump	P	Nmul_A1639	COG3696	1008	0
Putative silver efflux pump	P	Nmul_A2108	COG3696	1211	0
<b>DMT efflux superfamily</b>					
Small multidrug resistance protein	P	Nmul_A0642	COG2076	45.1	1.00E-06
Drug/metabolite exporter, DME family		Nmul_A1849	COG2962	48	1.00E-06
Predicted permease DMT superfamily	R	Nmul_A2637	COG5006	219	3.00E-58
Small multidrug resistance protein		Nmul_A0286			
<b>Efflux accessory proteins, membrane fusion proteins</b>					
Membrane-fusion protein, HlyD subfamily	V	Nmul_A0950	COG1566	102	5.00E-23
Membrane-fusion protein, HlyD subfamily	V	Nmul_A1281	COG1566	56.5	4.00E-09
Membrane-fusion protein, HlyD subfamily	V	Nmul_A1422	COG1566	117	1.00E-27
Membrane-fusion protein, HlyD subfamily	V	Nmul_A1503	COG1566	77	2.00E-15
RND efflux system, membrane-fusion protein	M	Nmul_A0042	COG0845	131	1.00E-31
RND efflux system, membrane-fusion protein	M	Nmul_A0689	COG0845	156	4.00E-39
RND efflux system, membrane-fusion protein	M	Nmul_A0692	COG0845	136	2.00E-33
RND efflux system, membrane-fusion protein	M	Nmul_A0849	COG0845	142	6.00E-35
RND efflux system, membrane-fusion protein	M	Nmul_A1640	COG0845	112	5.00E-26

RND efflux system, membrane-fusion protein	M	Nmul_A1728	COG0845	113	2.00E-26
RND efflux system, membrane-fusion protein	M	Nmul_A1971	COG0845	117	1.00E-27
RND efflux system, membrane-fusion protein	M	Nmul_A2107	COG0845	90	4.00E-19
RND efflux system, membrane-fusion protein	M	Nmul_A1112	COG0845	87	2.00E-18
<b>Efflux accessory proteins, outer membrane proteins</b>					
RND efflux system, outer membrane lipoprotein, NodT	M	Nmul_A0690	COG1538	238	6.00E-64
RND efflux system, outer membrane lipoprotein, NodT	M	Nmul_A0851	COG1538	259	4.00E-70
RND efflux system, outer membrane lipoprotein, NodT	M	Nmul_A1502	COG1538	227	2.00E-60
RND efflux system, outer membrane lipoprotein, NodT	M	Nmul_A1726	COG1538	184	2.00E-47
RND efflux system, outer membrane lipoprotein, NodT	M	Nmul_A1840	COG1538	199	3.00E-52
outer membrane efflux channel	M	Nmul_A1408	COG1538	134	2.00E-32
outer membrane efflux channel	M	Nmul_A1641	COG1538	126	4.00E-30
outer membrane efflux channel	M	Nmul_A2106	COG1538	142	4.00E-35
outer membrane efflux channel	M	Nmul_A1282	COG1538	166	4.00E-42
type I secretion outer membrane protein, TolC	M	Nmul_A2283	COG1538	170	2.00E-43
<b>Predicted Permeases</b>					
Predicted permeases	R	Nmul_A0402	COG0795	143	2.00E-35
Predicted permeases	R	Nmul_A0403	COG0795	133	3.00E-32
Ammonia permease	P	Nmul_A0516	COG0004	107	1.00E-24
Predicted permeases	R	Nmul_A0613	COG0730	63.1	2.00E-11
Sulfate permease and related transporters	P	Nmul_A0710	COG0659	244	2.00E-65
Predicted permease	R	Nmul_A0737	COG0628	128	4.00E-31
Amino acid transporters	E	Nmul_A0940	COG0531	116	5.00E-27
Amino acid transporters	E	Nmul_A1252	COG0531	144	1.00E-35
Predicted permease	R	Nmul_A1509	COG0628	129	4.00E-31
Predicted permeases	R	Nmul_A1681	COG0730	49.6	2.00E-07
Tellurite resistance protein and related permeases	P	Nmul_A2613	COG1275	46.8	3.00E-06
Predicted permease	R	Nmul_A2644	COG0628	138	5.00E-34
Predicted permeases	R	Nmul_A2681	COG0730	77.7	1.00E-15
<b>Outer membrane proteins / Porins</b>					
Phosphate-selective porin	P	Nmul_A0898	COG3746	174	2.00E-44
Phosphate-selective porin	P	Nmul_A1267	COG3746	128	7.00E-31

Phosphate-selective porin	P	Nmul_A2678	COG3746	163	4.00E-41
Carbohydrate-selective porin	M	Nmul_A2120	COG3659	41	3.00E-04
Porin, OmpC family	M	Nmul_A2561	COG3203	85	7.00E-18
Polysaccharide export protein	M	Nmul_A0242	COG1596	107	1.00E-24
Polysaccharide export protein	M	Nmul_A2529	COG1596	93	2.00E-20
polypeptide-transport-associated, ShlB-type	U	Nmul_A2576	COG2831	194	2.00E-50
surface antigen D15	M	Nmul_A0665	COG4775	693	0
NlpBDapX family lipoprotein	M	Nmul_A1539	COG3317	225	4.00E-60
rare lipoprotein B	M	Nmul_A0512	COG2980	108	2.00E-25
organic solvent tolerance protein	M	Nmul_A0521	COG1452	388	1.00E-108
outer membrane lipoprotein LolB	M	Nmul_A0587	COG3017	109	2.00E-25
outer membrane lipoprotein carrier protein LolA	M	Nmul_A0178	COG2834	139	1.00E-34
<b>CDF</b>					
Co/Zn/Cd efflux system subunit	P	Nmul_A1744	COG1230	262	4.00E-71
<b>FNT</b>					
Formate/nitrite family of transporters	P	Nmul_A2663	COG2116	164	8.00E-42
<b>Trk</b>					
Kef-type K <sup>+</sup> transport system predicted NAD-binding subunit	P	Nmul_A1156	COG4651	423	1.00E-119
Kef-type K <sup>+</sup> transport systems membrane subunits	P	Nmul_A1547	COG0475	73	4.00E-14
K <sup>+</sup> transporter	P	Nmul_A0201	COG3158	774	0
Predicted flavoprotein involved in K <sup>+</sup> transport	P	Nmul_A1368	COG2072	211	6.00E-56
<b>Mechanosensitive Ion Channels</b>					
Small-conductance mechanosensitive channel	M	Nmul_A1514	COG3264	117	4.00E-27
Small-conductance mechanosensitive channel	M	Nmul_A2622	COG3264	178	4.00E-46
<b>Possible Ion Channels</b>					
K <sup>+</sup> Ion channel	P	Nmul_A0076	COG1226	37	.002
Ion channel		Nmul_A1615			
K <sup>+</sup> Ion channel	P	Nmul_A1690	COG1226		0.002
Ion channel pore region		Nmul_A1691			
<b>TerC</b>					
Membrane protein TerC possibly involved in tellurium resistance	P	Nmul_A1926	COG0861	199	2.00E-52
Membrane protein TerC possibly involved in tellurium resistance	P	Nmul_A2473	COG0861	130	1.00E-31
<b>Mg<sup>2+</sup>/Co<sup>2+</sup> Transporters</b>					
Mg <sup>2+</sup> and Co <sup>2+</sup> transporters, CorA	P	Nmul_A0433	COG0598	258	4.00E-70

Mg <sup>2+</sup> and Co <sup>2+</sup> transporters, CorA	P	Nmul_A0576	COG0598	145	4.00E-36
Mg/Co/Ni transporter MgtE (contains CBS domain)	P	Nmul_A0540	COG2239	396	1.00E-111
Putative Mg <sup>2+</sup> and Co <sup>2+</sup> transporter CorB	P	Nmul_A2132	COG4536	458	1.00E-130
Putative Mg <sup>2+</sup> and Co <sup>2+</sup> transporter CorC	P	Nmul_A2698	COG4535	336	8.00E-94
<b>Nha</b>					
Na <sup>+</sup> /H <sup>+</sup> antiporter	P	Nmul_A1537	COG3004	333	2.00E-92
<b>Symporter</b>					
Na <sup>+</sup> -dependent symporter	R	Nmul_A1633	COG0385	203	1.00E-53
Divalent anion symporter	P	Nmul_A1105	COG1055	81.4	1.00E-16
Na <sup>+</sup> :dicarboxylate symporter	C	Nmul_A0633	COG1301	277	8.00E-76
<b>Antiporters - MOP family efflux flippases</b>					
Polysaccharide biosynthesis efflux pump	R	Nmul_A0292	COG2244	62	9.00E-11
MviN family protein	R	Nmul_A1036	COG0728	427	1.00E-121
Polysaccharide biosynthesis efflux pump	R	Nmul_A0248	COG2244	50	3.00E-7
<b>MFS</b>					
Nitrate/nitrite transporter	P	Nmul_A0026	COG2223	53.7	2.00E-08
Major facilitator superfamily transporter	G	Nmul_A0223			
Major facilitator superfamily transporter	G	Nmul_A0899			
MFS efflux pump	G	Nmul_A0966	COG2814	67	3.00E-12
MFS efflux pump	G	Nmul_A1807	COG2814	77.5	2.00E-15
MFS efflux pump	G	Nmul_A1922	COG2814	41	1.00E-04
MFS efflux pump	G	Nmul_A2103	COG2814	41.7	9.00E-05
MFS efflux pump	G	Nmul_A2116	COG2814	35.6	0.006
MFS efflux pump	G	Nmul_A2228	COG2814	87	3.00E-18
Major facilitator superfamily transporter	R	Nmul_A2758	COG2270	195	5.00E-51
<b>ZIP - Zinc</b>					
Predicted divalent heavy-metal cations transporter	P	Nmul_A1978	COG0428	104	8.00E-24
<b>CopD</b>					
Putative copper export protein	P	Nmul_A2320	COG1276	71	2.00E-13
Putative copper export protein	P	Nmul_A2760	COG1276	71.5	2.00E-13
<b>Urea</b>					
Urea transporter	E	Nmul_A1245	COG4413	186	2.00E-48
<b>Phosphotransferase</b>					
Phosphotransferase system mannose/fructose-specific subunit IIA	G	Nmul_A0218	COG2893	99.6	6.00E-23

Phosphotransferase system HPr-related proteins	G	Nmul_A0219	COG1925	96.8	3.00E-22
Phosphoenolpyruvate-protein kinase (PTS system EI subunit in bacteria)	G	Nmul_A0220	COG1080	614	1.00E-177
<b>Type II Secretion</b>					
Type II secretory pathway subunit ExeA (predicted ATPase)	U	Nmul_A0215	COG3267	128	1.00E-158
Type II secretory pathway subunit PulM	U	Nmul_A1892	COG3149	58	2.00E-84
Type II secretory pathway subunit PulL	U	Nmul_A1893	COG3297	64	2.00E-84
Type II secretory pathway subunit PulK	U	Nmul_A1894	COG3156	170	2.00E-47
Type II secretory pathway subunit PulJ	U	Nmul_A1895	COG4795	53	2.00E-47
Type II secretory pathway pseudopilin PulG	U	Nmul_A1896	COG2165	49	7.00E-79
Type II secretory pathway pseudopilin PulG	U	Nmul_A1897	COG2165	44	3.00E-92
Type II secretory pathway pseudopilin PulG	U	Nmul_A1898	COG2165	94	7.00E-79
general secretion pathway protein C		Nmul_A1901	none	31	4.00E-12
Type II secretory pathway subunit PulD	U	Nmul_A1902	COG1450	307	5.00E-36
Type II secretory pathway ATPase Pule/Tfp pilus assembly pathway ATPase PilB	U	Nmul_A1903	COG2804	552	1.00E-158
Type II secretory pathway subunit PulF	U	Nmul_A1904	COG1459	332	2.00E-30
Type II secretory pathway prepilin signal peptidase PulO and related peptidases	U	Nmul_A2131	COG1989	147	3.00E-92
Flp pilus assembly protein ATPase CpaF	U	Nmul_A2354	COG4962	405	1.00E-114
Flp pilus assembly protein ATPase CpaE	U	Nmul_A2355	COG4963	172	3.00E-44
Flp pilus assembly protein secretin CpaC	U	Nmul_A2360	COG4964	283	2.00E-77
Flp pilus assembly protein CpaB	U	Nmul_A2361	COG3745	135	4.00E-33
Flp pilus assembly protein protease CpaA	U	Nmul_A2362	COG4960	51	6.00E-08
Flp pilus assembly protein pilin Flp	U	Nmul_A2363	COG3847	46	4.00E-07
Tfp pilus assembly protein major pilin Pila	U	Nmul_A2475	COG4969	54	6.00E-09
Type II secretory pathway subunit ExeA (predicted ATPase)	U	Nmul_A2525	COG3267	145	1.00E-136
Type II secretory pathway pseudopilin PulG	U	Nmul_A2580	COG2165	49	2.00E-08
Tfp pilus assembly protein Pile	U	Nmul_A2581	COG4968	59	2.00E-10
Type II secretory pathway pseudopilin PulG	U	Nmul_A2582	COG2165	62	2.00E-08
Type II secretory pathway subunit HofQ	U	Nmul_A2583	COG4796	184	2.00E-30
Type II secretory pathway ATPase Pule/Tfp pilus assembly pathway ATPase PilB	U	Nmul_A2588	COG2804	478	1.00E-136
Type II secretory pathway subunit PulF	U	Nmul_A2589	COG1459	287	5.00E-36
Type II secretory pathway pseudopilin PulG	U	Nmul_A2590	COG2165	89	9.00E-44

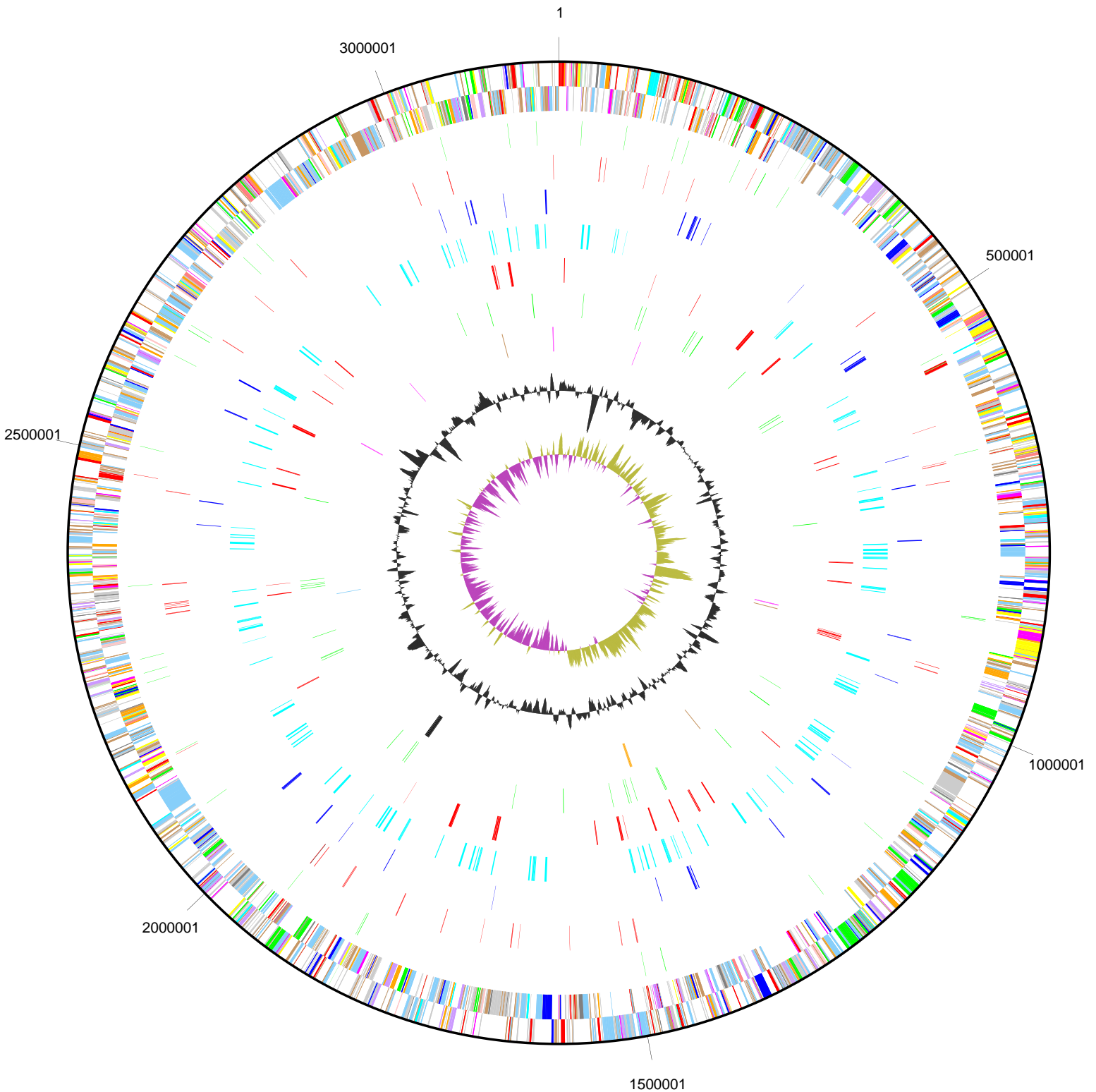


<b>Type III Secretion</b>					
Flagellar biosynthesis pathway subunit FlhB	U	Nmul_A1309	COG1377	397	1.00E-112
Flagellar biosynthesis pathway subunit FlhA	U	Nmul_A1310	COG1298	849	0
Flagellar biosynthesis/type III secretory pathway chaperone	N	Nmul_A1316	COG3418	40	6.00E-05
Flagellar biosynthesis/type III secretory pathway lipoprotein	U	Nmul_A1345	COG1766	414	1.00E-117
Flagellar biosynthesis/type III secretory pathway protein	U	Nmul_A1347	COG1317	95.8	2.00E-21
Flagellar biosynthesis/type III secretory pathway ATPase	U	Nmul_A1348	COG1157	588	1.00E-169
Flagellar motor switch/type III secretory pathway protein	U	Nmul_A1353	COG1886	95.5	2.00E-21
Flagellar biosynthesis pathway, FliO		Nmul_A1354	COG3190	76	1.00E-15
Flagellar biosynthesis pathway subunit FliP	U	Nmul_A1355	COG1338	287	5.00E-79
Flagellar biosynthesis pathway subunit FliQ	U	Nmul_A1356	COG1987	82	4.00E-18
Flagellar biosynthesis pathway subunit FliR	U	Nmul_A1357	COG1684	169	2.00E-43
<b>Type IV Secretion</b>					
Type IV secretory pathway VirD4 subunit	U	Nmul_C2793	COG3505	222	4.00E-59
predicted amidophosphoribosyltransferases KO: K02242 competence protein ComFC	R	Nmul_A1128	COG1040	157	1.00E-39
DNA uptake protein and related DNA-binding proteins	L	Nmul_A1771	COG1555	68	2.00E-13
putative DNA-binding protein KO: K02237 competence protein ComEA	L	Nmul_A2222	COG1555	84	3.00E-18
related to ComE operon protein 3 KO: K02238 competence protein ComEC	R	Nmul_A2506	COG2333	224	1.00E-59
<b>Sec-Dependent Translocase</b>					
Preprotein translocase subunit SecE	U	Nmul_A0753	COG0690	52	1.00E-08
Preprotein translocase subunit SecY	U	Nmul_A0787	COG0201	461	1.00E-131
Preprotein translocase subunit SecA (ATPase RNA helicase)	U	Nmul_A0924	COG0653	522	1.00E-149
Preprotein translocase subunit SecG	U	Nmul_A1090	COG1314	75	1.00E-15
Preprotein translocase subunit SecB	U	Nmul_A1124	COG1952	166	9.00E-43
Signal peptidase I	U	Nmul_A1752	COG0681	64	9.00E-12
Signal recognition particle GTPase	U	Nmul_A2134	COG0541	584	1.00E-168
Preprotein translocase subunit SecF	U	Nmul_A2426	COG0341	299	2.00E-82
Preprotein translocase subunit SecD	U	Nmul_A2427	COG0342	482	1.00E-137
Preprotein translocase subunit YajC	U	Nmul_A2428	COG1862	49	5.00E-08
Preprotein translocase subunit SecA (ATPase RNA helicase)	U	Nmul_A2485	COG0653	1095	0

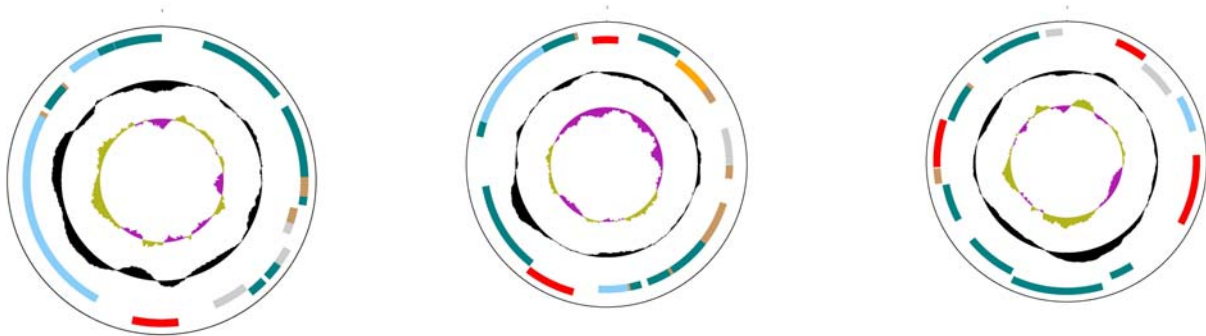
Lipoprotein signal peptidase	U	Nmul_A2655	COG0597	122	2.00E-29
Signal recognition particle GTPase	U	Nmul_A2738	COG0552	371	1.00E-104
Preprotein translocase subunit YidC	U	Nmul_A2776	COG0706	256	3.00E-69
<b>Twin-arginine protein translocation (Tat) system</b>					
Twin-arginine protein translocation, subunit TatC	U	Nmul_A0808	COG0805	221	3.00E-59
Twin-arginine protein translocation, subunit TatB	U	Nmul_A0809	COG1826	63	6.00E-12
Twin-arginine protein translocation, subunit TatA	U	Nmul_A0810	COG1826	67	3.00E-13

Supplemental Fig. 1A. Circle diagram of *N. multiformis* chromosome.

Rings from outside to the center: 1) Genes on forward strand (color by COG categories\*); 2) Genes on reverse strand (color by COG categories); 3) RNA genes (tRNAs green, sRNAs red); 4 IS elements (red); ring 5 cytochrome and related (blue), ring 6 transporters (cyan), ring 7 response regulators (red), ring 8 pep\_anchor elements (green), ring 9 amo (magenta), hao (brown), hyd/hyp (black), ure (gold), nirK (skyblue), ring 10 GC content ring 11 GC skew.



**Supplemental Figure 1B.** Plasmids 1, 2 and 3 of *N. multiformis*. Rings from outside to the center: 1) Genes on forward strand (color by COG categories\*); 2) Genes on reverse strand (color by COG categories); 3) GC content ring 4) GC skew.

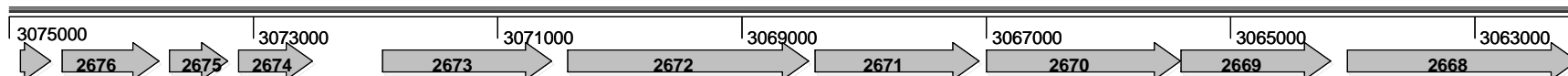


\*Key to COG Code Colors

COG Code	COG Function Definition
[A]	RNA processing and modification
[B]	Chromatin structure and dynamics
[C]	Energy production and conversion
[D]	Cell cycle control, cell division, chromosome partitioning
[E]	Amino acid transport and metabolism
[F]	Nucleotide transport and metabolism
[G]	Carbohydrate transport and metabolism
[H]	Coenzyme transport and metabolism
[I]	Lipid transport and metabolism
[J]	Translation, ribosomal structure and biogenesis
[K]	Transcription
[L]	Replication, recombination and repair
[M]	Cell wall/membrane/envelope biogenesis
[N]	Cell motility
[O]	Posttranslational modification, protein turnover, chaperones
[P]	Inorganic ion transport and metabolism
[Q]	Secondary metabolites biosynthesis, transport and catabolism
[R]	General function prediction only
[S]	Function unknown
[T]	Signal transduction mechanisms
[U]	Intracellular trafficking, secretion, and vesicular transport
[V]	Defense mechanisms
[W]	Extracellular structures
[Y]	Nuclear structure
[Z]	Cytoskeleton

**Supplemental Figure 2.** Nmul\_ A2677-2668. Doubled two component systems in front of genes related to oligosaccharide synthesis, decarboxylase, and asparagine synthase.

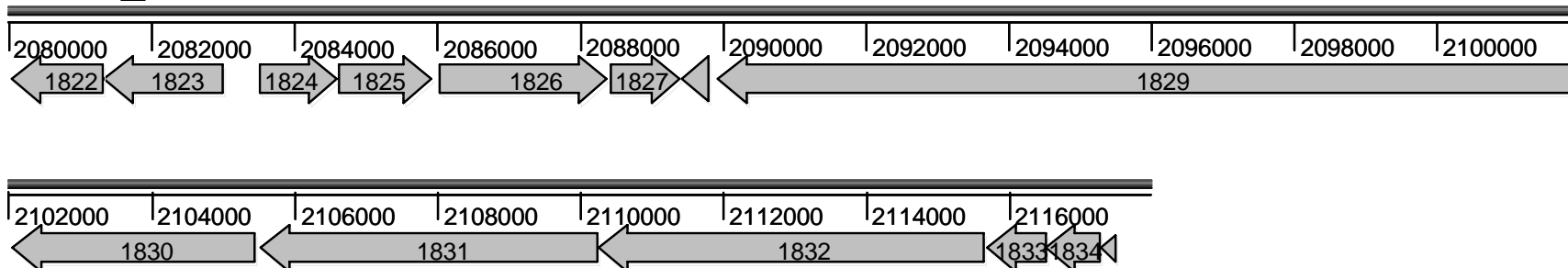
## Nmul\_ 2677-2668



<b>Locus</b> Nmul_A	<b>Putative Encoded Function</b>
2676	periplasmic serine protease/peptidase with signal peptide PDZ domain, possible membrane anchor for signaling complex
2675	response regulator receiver protein CheY-like
2674	two-component transcriptional regulator LuxR family
2673	Sugar transferase involved in LPS synthesis (Undecaprenyl-phosphate galactosephosphotransferase) 5 TM helices
2672	periplasmic sensor signal transduction, histidine kinase regulating C4-dicarboxylate transport system (COG4191), signal peptide and 8 TM helices
2671	Response regulator containing CheY-like receiver AAA-type ATPase and DNA-binding domains, Sigma -54
2670	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II
2669	Orn/DAP/Arg decarboxylase family 2, polyamine synthesis
2668	asparagine synthase, glutamine hydrolyzing.

**Supplemental Fig. 3.** Putative pyoverdine cluster in *N. multiformis* and comparison to genes identified in *Pseudomonas aeruginosa* Pa01 (PA), *Pseudomonas putida* KT2440 (PP), *Pseudomonas fluorescens* PfO-1 (Pfl), and *Pseudomonas syringe* DC3000 (PSPTO).

## Nmul\_A1822-1835



CDS in <i>N. multiformis</i>	Amino Acids	Putative Encoded Function	Similar CDS and Gene Designations in <i>Pseudomonas</i>
Nmul_A1822	428	4 TM helices PepSY-associated, Fe responsive membrane protein	PA2465
Nmul_A1823	555	Cyclic peptide transporter, 6 TM helices, siderophore export	PA2397, PP_4216, PSPTO_2153, <i>pvdE</i>
Nmul_A1824	364	Hypothetical acetylase	Pfl_3942
Nmul_A1825	435	Signal peptide, Lysine/ornithine N5 monooxygenase [EC:1.14.13.-]	PP3796, PA2384 <i>pvdA</i>
Nmul_A1826	784	TonB-dependent outer membrane siderophore receptor	PA2398, PP_4217, <i>fpvA</i>
Nmul_A1827	323	Lipolytic enzyme, esterase/lipase	PP_4218
Nmul_A1828	129	hypothetical	
Nmul_A1829	4037	Non-ribosomal peptide synthase (NRPS) siderophore sidechain	PA2402, PSPTO_2150, PP_4219; <i>pvdI</i>
Nmul_A1830	3417	NRPS siderophore sidechain	PSPTO_2147, PP4221, <i>pvdJ</i>
Nmul_A1831	1574	Polyketide synthase modules, beta-ketoacyl synthase:acyl transferase; Short-chain dehydrogenase; Phosphopantetheine-binding, acyl transferase	Matches in Cyanobacteria
Nmul_A1832	1801	NRPS	PSPTO_2135, PP_4243 (these are longer)
Nmul_A1833	280	4'-phosphopantetheinyl transferase	Matches in <i>Delftia</i> , <i>Burkholderia</i>
Nmul_A1834	253	Thioesterase involved in NRPS	PA2411, Psyr_1944
Nmul_A1835	76	MbtH-like protein	PA2412, Psyr_1947
Nmul_A1839	169	Sigma factor Fec-I like	PA2426, PP4244, <i>pvdS</i>