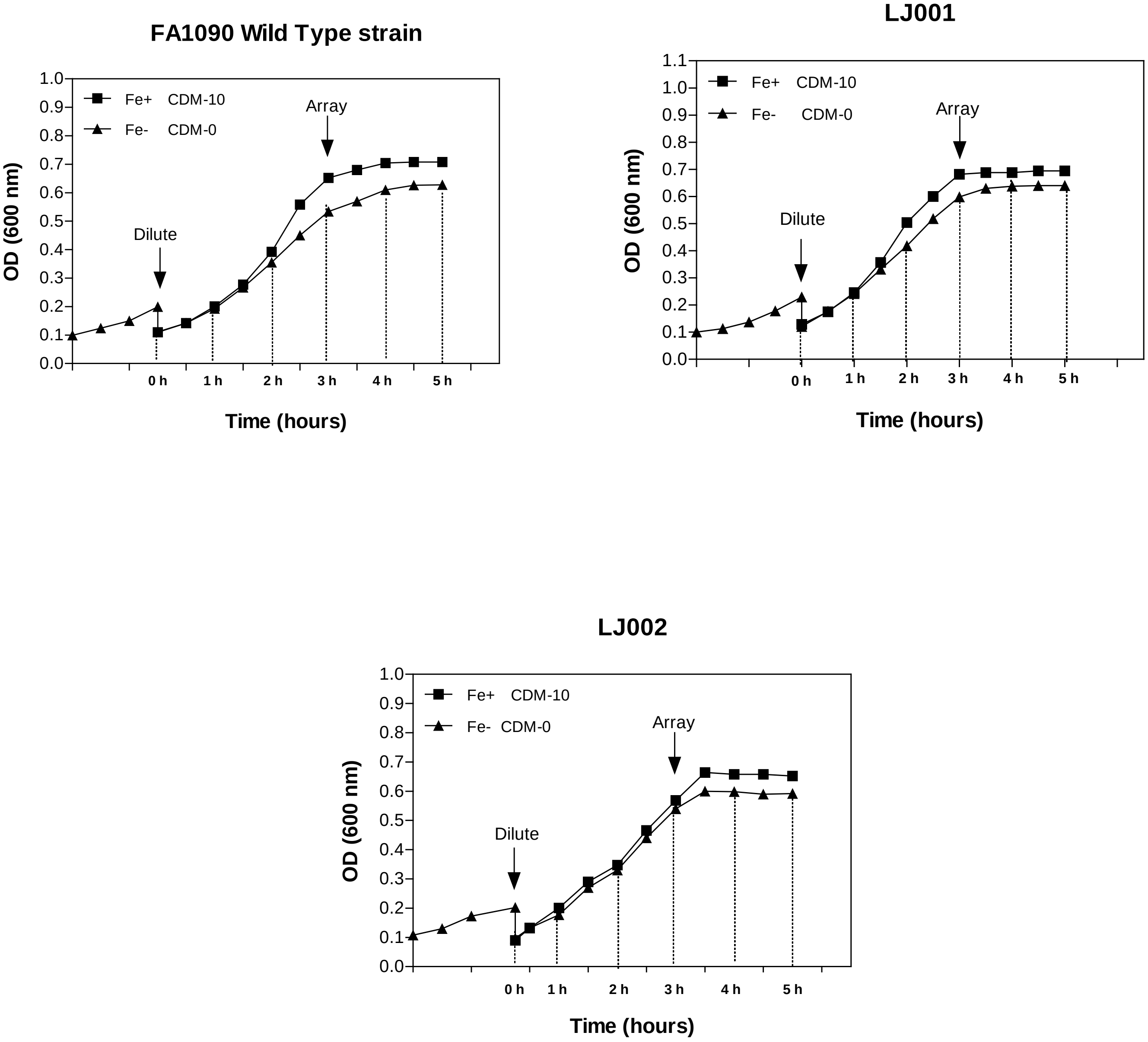
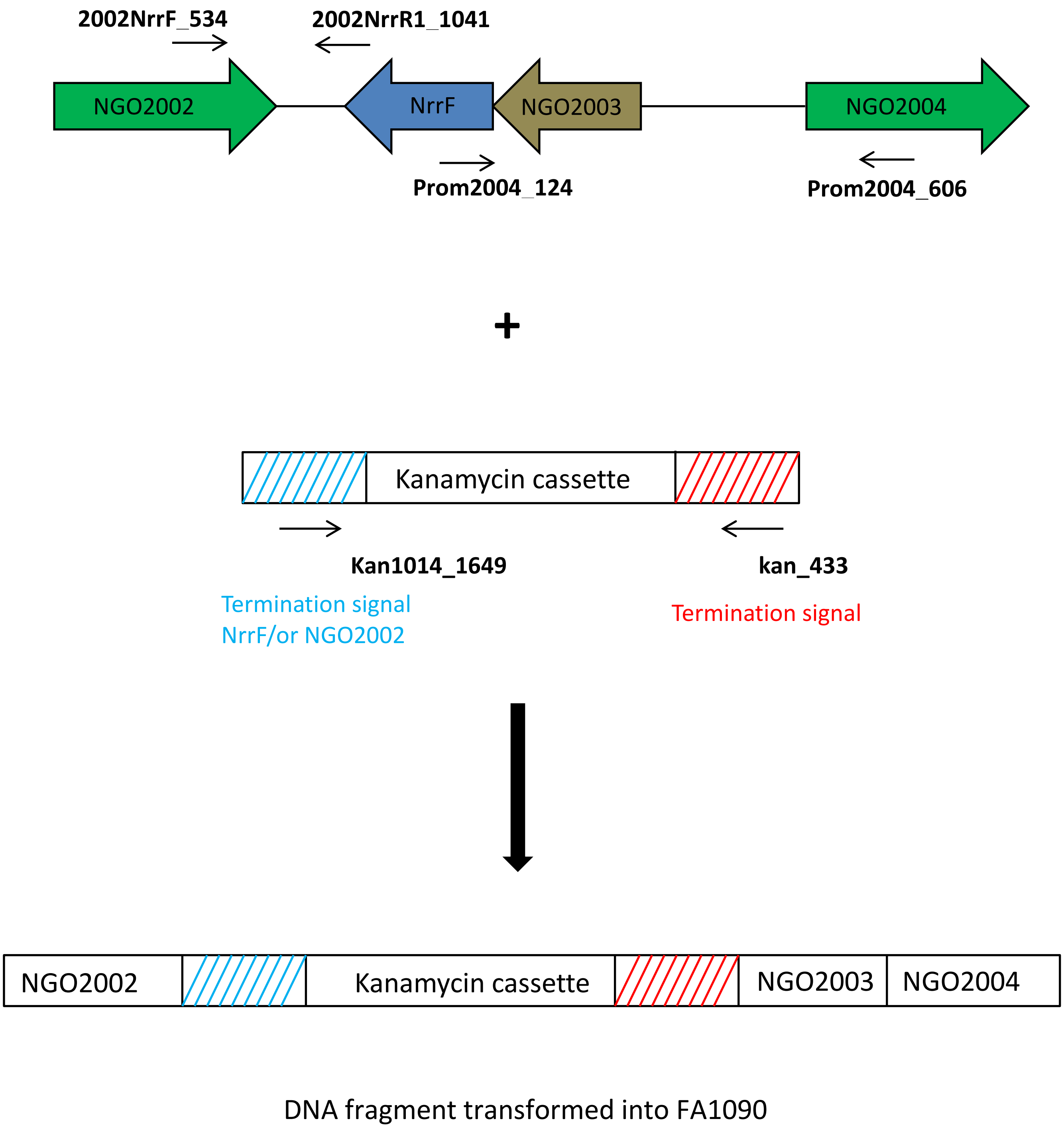


**Fig. S1.** Growth curves for FA1090, *nrrF* deletion mutant (LJ001) and complemented mutant strain (LJ002). Cells from overnight growth on GCB agar were inoculated into Fe-depleted medium (CDM-0) to $OD_{600}$ =0.1 and then grown to $OD_{600}$ =0.2 to iron starve the cells. At this point, denoted as 0h, the cells were split into two flasks and fresh CDM-0 added. Ferrous iron was added to one flask at 10 $\mu$M (CDM-10). Cells were harvested at 3 hours for array studies. Growth curves are representative of 3 separate experiments.

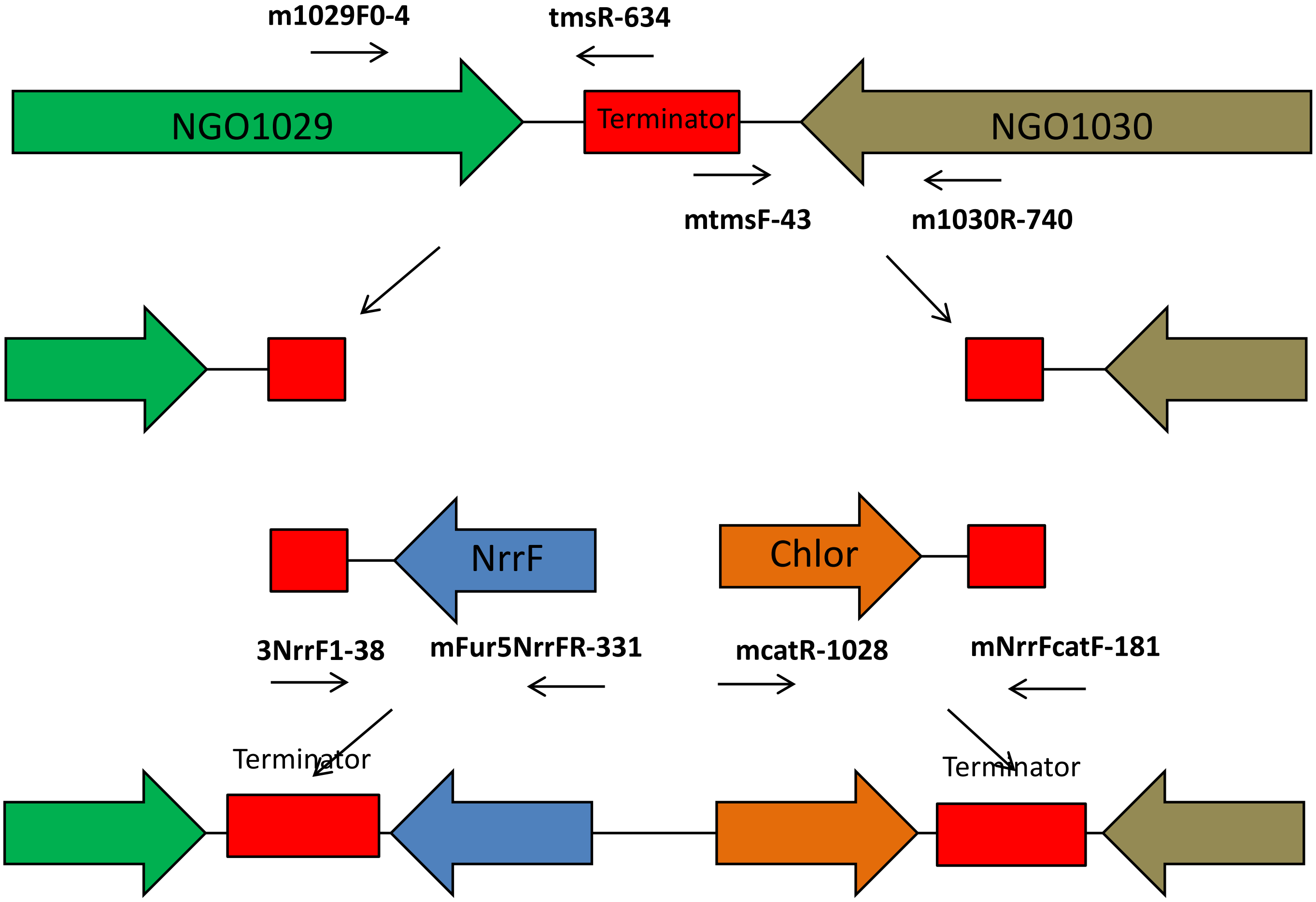
.


2002NrrF_534
2002NrrR1_1041
NGO2002
NrrF
NGO2003
NGO2004
Prom2004_124
Prom2004_606
+
Kanamycin cassette
Kan1014_1649
kan_433
Termination signal
NrrF/or NGO2002
Termination signal
NGO2002
Kanamycin cassette
NGO2003
NGO2004
DNA fragment transformed into FA1090

## Primers and template used in nrrF deletion mutant construction

| Primers | Amplicon | Sequence | Comments | Template |
|---|---|---|---|---|
| 2002NrrF_534 | NGO2002 | aggcaagcctcacgatggac | | FA1090 |
| 2002NrrF_1041 | | ggtttggcgtttttggtctgcac | overlapping in blue | |
| Kan1014_1649 | Kanamycin cassette | ccaaaaacgccaaaccggggaaagccacgttgtg | overlapping in blue | pUC4k |
| Kan_433 | | *ctgaactcaagcttcggacggcattttt*gcgctgaggtctgcctcg | Overlapping in pink; termination signal in italics | |
| Prom2004_124 | Fur box/NGO2003/2004 | *cgaagcttgagttcagacggcatttt*gttttgattatacgctaata | Overlapping in pink; termination signal in italics | FA1090 |
| Prom2004_606 | | gctttgtcgtgaggaacagg | | |

## Fig. S2 *nrrF* deletion mutant construction



DNA fragment transformed into FA1090

## Primers and templates used in nrrF complemented strain construction

| Primers | Amplicon | Sequence | Comments | Template |
|---|---|---|---|---|
| m1029F004 | NGO1029/termination signal | ttgccgcttcgggcgcattgaa | | FA1090 |
| tmsR-634 | | gctagttcgcaggcaacggaa | overlapping in blue | |
| 3NrrF1-38 | NrrF/Fur box | ttgcctgcgaactagccctcaagtcttgcaaataagtgcagacc | overlapping in blue | FA1090 |
| mFur5NrrFR-331 | | cctgcagcaacatcggcggacaggtt | Overlapping in pink | |
| mNrrFcatF-181 | Chloramphenicol cassette | gtccgccgatgttgctgcaggcgcagaactg | Overlapping in pink | pGCC5[a] |
| mcatR-1028 | | gatgaaccatatcggtagcaaccaggcgtttaagggcac | Overlapping in green | |
| mtmsF-43 | Termination signal/NGO1030 | gttgctaccgatatggttcatccgcgcta | Overlapping in green | FA1090 |
| m1030R-740 | | ggcagatttcgccgtttacga | | |

[a] Wiehr IJ, Seifert HS (1997) Random shuttle mutagenesis: gonococcal mutants deficient in pilin antigenic variation. Molecular Microbiology 23: 1121-1131.

## Fig. S3 complemented mutant strain construction

.

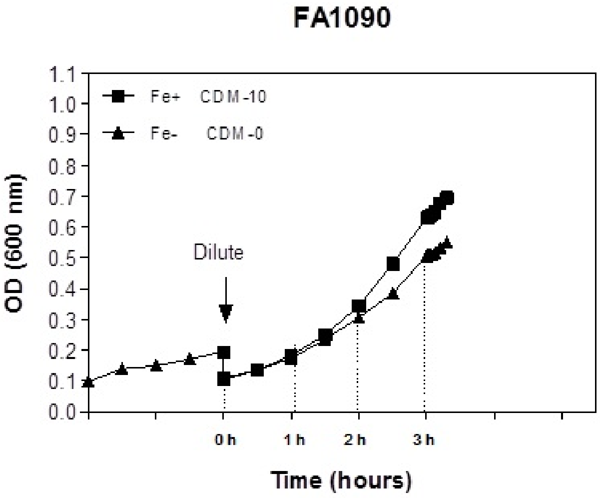


**Fig. S4.** Rifampin studies: Cells were grown to 3hrs in iron-deplete and –replete conditions. Rifampin was added to stop transcription at a final concentration of 200ug/ml and RNA isolated at 0, 2, 4, 8, 12, and 20 minutes. Growth was terminated immediately following addition of rifampin. Similar results were seen for *nrrF* mutant strain

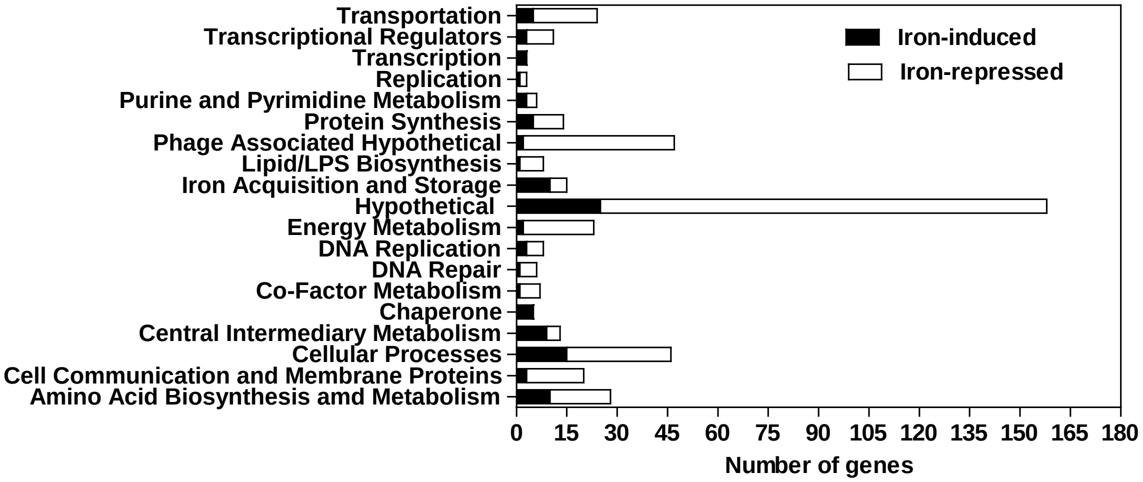


**Fig. S5.** Biological categories of Fe-repressed and –induced genes in the *nrrF* mutant. Normalized gene expression changes at 3 hours in Fe$^-$ vs. Fe$^+$ growth conditions that were 1.5-fold or greater and having a P value of $\leq$ 0.05 were categorized according to biological function. Bars represent the actual number of genes.

**Table S1.** Primers used in this study

| | Forward (5′ to 3′) | Reverse (5′ to 3′) |
|---|---|---|
| **qRTPCR and Rifampin Studies** | | |
| NGO0224 | AAGGATTTTGGCAGTCGGTAAC | CGTTTGGGCGACGGTTT |
| NGO0588 | CGCGATGCGCGTTG | CGACCTGATGAACGCTCGTA |
| NGO0797 | GCGTGGCGGCGTATCA | ATCGGCGGAATTGGTCATC |
| NGO0802 | AAAGGCGTATCCCTTCAAACAA | CGGTATCGGGTTCGGTTTC |
| NGO0920 | CTGCCGCGAAGGGATTT | CCGTTTTTGCCGTTGATGT |
| NGO0921 | GGCGTAACCGCCATGGA | GGCCTTGGCGTGGAAAATA |
| NGO0922 | CGACTGCGGTTATTATGTTGATTTA | AGGCAGGGCAAATAGAACCA |
| NGO0923 | CAGTATTCAGCTCAAGGCCTTTG | TCGCCGGTATCCGCTTT |
| NGO1024 | TGCCCGATGCGATTGTAGT | AACGGTTGATGCACCCAAA |
| NGO1368 | AGGCACGCTGATTTCTATGATGT | TAAGGCGATCCATGCAATTAAGA |
| NGO1446 | TTCTTTGGGCTTTGGAAGCTAT | CACCGCCCCCATTGC |
| NGO1561 | AGGCGCGTTCTATACCTGGTT | CGATACGCAGGCCCAGTTT |
| NGO1861 | CGGATTTGTCGGGATTCG | CACATCGTTAATCTGCAACACCAT |
| NGO2075 | CCACGCCGACCTGTTTAAA | AAATCGATGAAGCCCGATACC |
| NrrF | TCCGTTCCGAACCATTAAA | GCGTTTCGGTTTTGAGTATCT |
| por1 | TGTCCGTACGCTACGATTCTCC | AGCCAACGTGGTAAGATTCGC |
| **EMSA** | | |
| NrrF | TGTTTATTTTTCATCGCATTACA | TGAATTGTGAGGGAATACAGTG |
| NGO1809 | ATGGAAGAACAAGGCTCTATGTG | TGTAACGTTCATCTTCTGGATTG |
| NGO1779 | CAAATCGGGATGTCTAGTGT | ACCATAGCAGTTCGCAATAG |

**Table S2_FA1090_*nrrF* mutant_ complemented nrrF mutant_array fold changes_3hr**

| Locus Tag | p value | FA1090 Fe-/ Fe+ Fold Change | Regulation | p value | *nrrF* mutant Fe-/Fe+ Fold Change | Regulation | p value | Complemented mutant Fe-/Fe+ Fold Change | Regulation | Probe Comment |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0001 | 0.6881 | -1.20 | down | 0.7369 | -1.16 | down | 0.6087 | -1.16 | down | putative chromosomal replication protein (DnaA)\ Context:(NC_002946)+[159-1715]\ Notes:Best Blastp Hit: emb\|CAB83845.1\| (AL162753) putative chromosomal replication initiator protein [Neisseria meningitidis] COG0593 ATPase involved in DNA replication |
| NGO0002 | 0.1894 | 1.95 | up | 0.2868 | 1.47 | up | 0.4484 | 1.28 | up | DNA polymerase III subunit beta\ Context:(NC_002946)+[1795-2898]\ Notes:binds the polymerase to DNA and acts as a sliding clamp |
| NGO0003 | 0.5506 | 1.42 | up | 0.4724 | 1.74 | up | 0.0106 | 3.57 | up | polyphosphate kinase\ Context:(NC_002946)-[3047-5104]\ Notes:catalyzes the reversible transfer of the terminal phosphate of ATP to form a long chain polyphosphate |
| NGO0004 | 0.1265 | -2.43 | down | 0.6638 | -1.32 | down | 0.9466 | -1.04 | down | hypothetical protein\ Context:(NC_002946)-[5273-5716]\ Notes:Best Blastp Hit: pir\|\|D81974 probable periplasmic protein NMA0556 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379295\|emb\|CAB83849.1\| (AL162753) putative periplasmic protein [Neisseria meningitidis] |
| NGO0006 | 0.5894 | 1.29 | up | 0.2296 | 2.04 | up | 0.2264 | 2.06 | up | leucyl-tRNA synthetase\ Context:(NC_002946)+[6500-9136]\ Notes:leucine--tRNA ligase; LeuRS; class-I aminoacyl-tRNA synthetase; charges leucine by linking carboxyl group to alpha-phosphate of ATP and then transfers aminoacyl-adenylate to its tRNA; due to the large number of codons that tRNA(Leu) recognizes; the leucyl-tRNA synthetase does not recognize the anticodon loop of the tRNA |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0007 | 0.8843 | 1.11 | up | 0.8913 | -1.19 | down | 0.9083 | 1.14 | up | putative type II restriction endonuclease\ Context:(NC_002946)+[9365-10294]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0338 Site-specific DNA methylase dam |
| NGO0008 | 0.3836 | 2.17 | up | 0.8856 | 1.13 | up | 0.3673 | -1.64 | down | putative modification methylase\ Context:(NC_002946)+[10394-11071]\ Notes:Best Blastp Hit: sp\|P09358\|MT22_STRPN modification methylase DpnII 2 (adenine-specific methyltransferase DpnII 2) (M.DPNII 2) >gi\|6978344\|gb\|AAA88581.2\| (M14339) DNA adenine methyltransferase [Streptococcus pneumoniae] COG0863 Adenine-specific DNA methylase |
| NGO0009 | 0.0166 | -6.25 | down | 0.0476 | -4.50 | down | 0.0210 | -4.69 | down | hypothetical protein\ Context:(NC_002946)+[11091-11546]\ Notes:Best Blastp Hit: sp\|P54298\|LUXM_VIBHA LUXM protein >gi\|487037\|pir\|\|S37349 luxM protein - Vibrio harveyi >gi\|295433\|gb\|AAC36807.1\| (L13940) Lux M [Vibrio harveyi] |
| NGO0010 | 0.3343 | 2.28 | up | 0.0273 | -3.09 | down | 0.3889 | -1.77 | down | hypothetical protein\ Context:(NC_002946)-[12107-12307]\ Notes:Best Blastp Hit: gb\|AAF42226.1\| (AE002539) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0011 | 0.1391 | -2.57 | down | 0.1249 | -2.47 | down | 0.0220 | -5.46 | down | hypothetical protein\ Context:(NC_002946)-[12417-12728]\ Notes:Best Blastp Hit: pir\|\|B81975 probable DNA-binding protein NMA0564 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379301\|emb\|CAB83856.1\| (AL162753) putative DNA-binding protein [Neisseria meningitidis] |
| NGO0015 | 0.1344 | 7.92 | up | 0.6676 | -2.21 | down | 0.1836 | 12.12 | up | hypothetical protein\ Context:(NC_002946)+[13341-13625]\ Notes:Best Blastp Hit: emb\|CAB83858.1\| (AL162753) hypothetical protein NMA0567 [Neisseria meningitidis] |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0016 | 0.5404 | 1.45 | up | 0.5373 | 1.33 | up | 0.5539 | 1.26 | up | preprotein translocase subunit SecG\ Context:(NC_002946)-[14081-14431]\ Notes:SecG; Best Blastp Hit: pir\|\|F81031 protein-export membrane protein SecG NMB1888 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227147\|gb\|AAF42222.1\| (AE002538) protein-export membrane protein SecG [Neisseria meningitidis MC58] >gi\|7379305\|emb\|CAB83860.1\| (AL162753) putative protein-export integral membrane protein [Neisseria meningitidis] |
| NGO0017 | 0.8487 | 1.10 | up | 0.9342 | -1.04 | down | 0.3632 | -1.27 | down | triosephosphate isomerase\ Context:(NC_002946)-[14438-15211]\ Notes:Reversibly isomerizes the ketone sugar dihydroxyacetone phosphate to the aldehyde sugar glyceraldehyde-3-phosphate |
| NGO0018 | 0.1789 | -2.14 | down | 0.0752 | -2.20 | down | 0.1417 | -1.81 | down | hypothetical protein\ Context:(NC_002946)+[15370-15897]\ Notes:Best Blastp Hit: pir\|\|H81975 hypothetical protein NMA0571 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379307\|emb\|CAB83862.1\| (AL162753) hypothetical protein NMA0571 [Neisseria meningitidis] COG1956 GAF domain-containing proteins |
| NGO0019 | 0.1667 | -2.02 | down | 0.0964 | -2.28 | down | 0.2096 | -1.51 | down | putative protein-L-isoaspartate O-methyltransferase\ Context:(NC_002946)+[16000-16656]\ Notes:PimT; Best Blastp Hit: gb\|AAF42219.1\| (AE002538) protein-L-isoaspartate O-methyltransferase [Neisseria meningitidis MC58] |
| NGO0020 | 0.1304 | -2.87 | down | 0.1519 | -5.22 | down | 0.0517 | -6.00 | down | hypothetical protein\ Context:(NC_002946)+[16737-17060]\ Notes:Best Blastp Hit: emb\|CAB83864.1\| (AL162753) hypothetical protein NMA0573 [Neisseria meningitidis] |
| NGO0021 | 0.0392 | -3.01 | down | 0.0135 | -11.85 | down | 0.1065 | 1.84 | up | putative TonB-dependent receptor protein; iron related\ Context:(NC_002946)-[17323-19500]\ Notes:Best Blastp Hit: pir\|\|D81976 probable ferric siderophore receptor protein NMA0575 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379311\|emb\|CAB83866.1\| (AL162753) putative ferric siderophore receptor protein [Neisseria meningitidis] COG1629 Outer membrane receptor proteins; mostly Fe |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0022 | 0.2977 | -2.02 | down | 0.3939 | -1.52 | down | 0.6600 | -1.46 | down | hypothetical protein\ Context:(NC_002946)-[19763-20086]\ Notes:Best Blastp Hit: pir\|\|E81976 hypothetical protein NMA0576 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379312\|emb\|CAB83867.1\| (AL162753) hypothetical protein NMA0576 [Neisseria meningitidis] COG0662 Mannose-6-phosphate isomerase |
| NGO0023 | 0.2246 | -2.59 | down | 0.0307 | -10.58 | down | 0.7581 | 1.44 | up | putative ABC transporter; periplasmic binding protein;iron related\ Context:(NC_002946)-[20119-21090]\ Notes:Best Blastp Hit: gb\|AAF42214.1\| (AE002538) ABC transporter; periplasmic solute-binding protein; putative [Neisseria meningitidis MC58] COG0614 Ferrichrome-binding periplasmic proteins |
| NGO0024 | 0.0640 | -3.29 | down | 0.1070 | -3.92 | down | 0.9098 | -1.07 | down | hypothetical protein\ Context:(NC_002946)-[21087-21251]\ Notes: |
| NGO0025 | 0.0645 | 6.88 | up | 0.0443 | 3.77 | up | 0.0073 | 9.10 | up | AraC family transcriptional regulator\ Context:(NC_002946)+[21326-22282]\ Notes:Best Blastp Hit: emb\|CAB83869.1\| (AL162753) putative araC-family transcriptional regulator [Neisseria meningitidis] COG2207 AraC-type DNA-binding domain-containing |
| NGO0026 | 0.0068 | 6.86 | up | 0.1685 | 4.16 | up | 0.9420 | -1.04 | down | putative prolyl endopeptidase\ Context:(NC_002946)-[22395-24410]\ Notes:Best Blastp Hit: emb\|CAB83870.1\| (AL162753) putative prolyl endopeptidase [Neisseria meningitidis] COG1505 Serine proteases of the peptidase family |
| NGO0027 | 0.2161 | 1.89 | up | 0.9920 | 1.01 | up | 0.2019 | 2.96 | up | N-acetylglutamate synthase\ Context:(NC_002946)-[24506-25816]\ Notes:catalyzes the formation of N-acetyl-L-glutamate from L-glutamate and acetyl-CoA in arginine biosynthesis |
| NGO0028 | 0.4969 | 1.45 | up | 0.3142 | 1.43 | up | 0.9776 | -1.01 | down | hypothetical protein\ Context:(NC_002946)-[25813-26241]\ Notes:Best Blastp Hit: pir\|\|A81033 hypothetical protein NMB1875 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227133\|gb\|AAF42209.1\| (AE002537) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0029 | 0.8772 | -1.08 | down | 0.8229 | 1.08 | up | 0.9833 | 1.01 | up | orotate phosphoribosyltransferase\ Context:(NC_002946)-[26309-26950]\ Notes:involved in fifth step of pyrimidine biosynthesis; converts orotidine 5'-phosphate and diphosphate to orotate and 5-phospho-alpha-D-ribose 1-diphosphate |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0030 | 0.1402 | -2.45 | down | 0.0621 | -3.35 | down | 0.0585 | -2.46 | down | hypothetical protein\ Context:(NC_002946)-[27012-27749]\ Notes:Best Blastp Hit: pir\|\|G81032 DNA polymerase; bacteriophage-type; probable NMB1873 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227131\|gb\|AAF42207.1\| (AE002537) DNA polymerase; bacteriophage-type; putative [Neisseria meningitidis MC58] COG1573 Uracil-DNA glycosylase |
| NGO0031 | 0.7753 | 1.13 | up | 0.6419 | 1.33 | up | 0.9883 | 1.00 | up | putative acetyltransferase\ Context:(NC_002946)-[27743-28183]\ Notes:Best Blastp Hit: emb\|CAB83875.1\| (AL162753) putative acetyltransferase [Neisseria meningitidis] COG0456 Acetyltransferases |
| NGO0032 | 0.0506 | -4.02 | down | 0.0025 | -8.44 | down | 0.5766 | -1.27 | down | hypothetical protein\ Context:(NC_002946)-[28180-28857]\ Notes:Best Blastp Hit: pir\|\|F81977 hypothetical protein NMA0585 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379321\|emb\|CAB83876.1\| (AL162753) hypothetical protein NMA0585 [Neisseria meningitidis] COG1214 Inactive homologs of metal-dependent |
| NGO0033 | 0.4484 | -1.95 | down | 0.0201 | -15.38 | down | 0.6980 | -1.87 | down | hypothetical protein\ Context:(NC_002946)-[28996-29853]\ Notes:Best Blastp Hit: pir\|\|D81032 hypothetical protein NMB1870 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227128\|gb\|AAF42204.1\| (AE002537) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0034 | 0.3658 | -1.71 | down | 0.7983 | -1.11 | down | 0.2679 | -1.56 | down | fructose-1;6-bisphosphate aldolase\ Context:(NC_002946)-[29992-31056]\ Notes:class II aldolase; catalyzes the reversible aldol condensation of dihydroxyacetonephosphate and glyceraldehyde 3-phosphate in the Calvin cycle; glycolysis and gluconeogenesis |
| NGO0035 | 0.1244 | 2.23 | up | 0.0800 | -4.29 | down | 0.7132 | 1.19 | up | putative site-specific recombinase\ Context:(NC_002946)+[31250-32167]\ Notes:XerC; Best Blastp Hit: pir\|\|A81978 probable integrase/recombinase NMA0588 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379324\|emb\|CAB83879.1\| (AL162753) putative integrase/recombinase [Neisseria meningitidis] COG0582 Integrase |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0036 | 0.1376 | 2.23 | up | 0.2618 | 2.44 | up | 0.1742 | 2.09 | up | 1-deoxy-D-xylulose-5-phosphate synthase\ Context:(NC_002946)+[32252-34165]\ Notes:catalyzes the formation of 1-deoxy-D-xylulose 5-phosphate from pyruvate and D-glyceraldehyde 3-phosphate |
| NGO0037 | 0.0548 | -5.18 | down | 0.3639 | -1.71 | down | 0.5187 | -1.58 | down | hypothetical protein\ Context:(NC_002946)-[34412-35740]\ Notes:Best Blastp Hit: pir\|\|C81034 conserved hypothetical protein NMB1866 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227123\|gb\|AAF42200.1\| (AE002536) conserved hypothetical protein [Neisseria meningitidis MC58] COG0621 Fe-S oxidoreductases family 1 |
| NGO0039 | 0.1392 | -4.02 | down | 0.5012 | -1.25 | down | 0.0390 | -3.23 | down | hypothetical protein\ Context:(NC_002946)+[36107-36460]\ Notes:Best Blastp Hit: pir\|\|D81978 hypothetical protein NMA0591 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379327\|emb\|CAB83882.1\| (AL162753) hypothetical protein NMA0591 [Neisseria meningitidis] |
| NGO0040 | 0.2921 | -1.62 | down | 0.6914 | 1.19 | up | 0.7172 | 1.17 | up | glutamate-1-semialdehyde aminotransferase\ Context:(NC_002946)+[36524-37804]\ Notes:Converts (S)-4-amino-5-oxopentanoate to 5-aminolevulinate during the porphyrin biosynthesis pathway |
| NGO0042 | 0.1953 | 2.25 | up | 0.3965 | 2.45 | up | 0.1525 | 3.36 | up | oligoribonuclease\ Context:(NC_002946)-[39110-39673]\ Notes:3'-5' exoribonuclease specific for small oligoribonuclotides |
| NGO0043 | 0.0543 | 2.67 | up | 0.0551 | 3.89 | up | 0.1203 | 2.60 | up | ribosomal protein L11 methyltransferase\ Context:(NC_002946)-[39691-40578]\ Notes:methylates ribosomal protein L11 at multiple amino acid positions; mutations of these genes in Escherichia coli or Thermus thermophilus has no apparent phenotype |
| NGO0044 | 0.2309 | 1.72 | up | 0.5228 | 1.24 | up | 0.1311 | 1.66 | up | acetyl-CoA carboxylase; biotin carboxylase\ Context:(NC_002946)-[40682-42043]\ Notes:Best Blastp Hit: pir\|\|F81033 acetyl-CoA carboxylase; biotin carboxylase NMB1861 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227118\|gb\|AAF42195.1\| (AE002536) acetyl-CoA carboxylase; biotin carboxylase [Neisseria meningitidis MC58] COG0439 Biotin carboxylase |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0045 | 0.5342 | 1.38 | up | 0.9840 | 1.01 | up | 0.4894 | 1.28 | up | acetyl-CoA carboxylase biotin carboxyl carrier protein subunit\ Context:(NC_002946)-[42157-42618]\ Notes:composes the biotin carboxyl carrier protein subunit of the acetyl-CoA carboxylase complex; the enzyme that catalyzes the carboxylation of acetyl-CoA to malonyl-CoA; which in turn controls the rate of fatty acid metabolism |
| NGO0046 | 0.1468 | 3.67 | up | 0.6018 | -1.26 | down | 0.0225 | 2.11 | up | hypothetical protein\ Context:(NC_002946)-[42600-42857]\ Notes: |
| NGO0047 | 0.8858 | 1.11 | up | 0.4193 | -1.41 | down | 0.9387 | -1.03 | down | S-adenosylmethionine:tRNAribosyltransferase-isomerase\ Context:(NC_002946)+[42974-44014]\ Notes:Synthesizes oQ from preQ1 in a single S-adenosylmethionine-requiring step |
| NGO0048 | 0.3312 | 1.82 | up | 0.0276 | 2.83 | up | 0.1429 | 2.28 | up | carbamoyl phosphate synthase large subunit\ Context:(NC_002946)-[44215-47430]\ Notes:four CarB-CarA dimers form the carbamoyl phosphate synthetase holoenzyme that catalyzes the production of carbamoyl phosphate; CarB is responsible for the amidotransferase activity |
| NGO0049 | 0.1303 | 2.81 | up | 0.0101 | 4.24 | up | 0.2328 | 1.97 | up | hypothetical protein\ Context:(NC_002946)-[47441-47974]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO0050 | 0.5971 | -1.28 | down | 0.7362 | -1.18 | down | 0.7774 | -1.26 | down | hypothetical protein\ Context:(NC_002946)-[49539-49928]\ Notes:Best Blastp Hit: gb\|AAC78450.1\| (AF029362) similar to E. coli ORF; encoded by GenBank Accession Number X97282; and to H. influenzae protein HI0925; encoded by GenBank Accession Number U32774; and to H. influenzae protein HI1162; encoded by GenBank Accession Number U32796 [Neisseria g> |
| NGO0053 | 0.9144 | 1.06 | up | 0.1702 | 1.88 | up | 0.8677 | -1.05 | down | carbamoyl phosphate synthase small subunit\ Context:(NC_002946)-[50524-51657]\ Notes:catalyzes production of carbamoyl phosphate from bicarbonate and glutamine in pyrimidine and arginine biosynthesis pathways; forms an octamer composed of four CarAB dimers |
| NGO0054 | 0.4342 | 1.83 | up | 0.4647 | -3.53 | down | 0.4108 | -3.36 | down | hypothetical protein\ Context:(NC_002946)+[51927-52244]\ Notes:Best Blastp Hit: gb\|AAD38303.1\|AF036242_3 (AF036242) unknown [Neisseria meningitidis] |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| NGO0055 | 0.1165 | 2.47 | up | 0.0971 | 1.90 | up | 0.2637 | 1.55 | up | pilus-associated protein\ Context:(NC_002946)-[52527-55670]\ Notes:PilC1; Best Blastp Hit: possibly phase variable - 13G residue homopolymer repeat in the coding sequence (ON) |
| NGO0056 | 0.2644 | 1.82 | up | 0.7071 | -1.24 | down | 0.3483 | 1.38 | up | putative atpase\ Context:(NC_002946)-[57122-58201]\ Notes:Mrp; Best Blastp Hit: pir\|\|G81980 hypothetical protein NMA0611 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379346\|emb\|CAB83901.1\| (AL162753) hypothetical protein NMA0611 [Neisseria meningitidis] COG0489 ATPases involved in chromosome partitioning |
| NGO0057 | 0.0851 | -4.91 | down | 0.0008 | -13.27 | down | 0.2898 | -2.27 | down | putative thioredoxin\ Context:(NC_002946)+[58575-59084]\ Notes:Best Blastp Hit: emb\|CAB83902.1\| (AL162753) putative periplasmic thioredoxin [Neisseria meningitidis] COG0526 Thiol-disulfide isomerase and thioredoxins |
| NGO0058 | 0.7012 | 1.22 | up | 0.9979 | 1.00 | up | 0.8043 | -1.08 | down | MarR family transcriptional regulator\ Context:(NC_002946)+[59488-59865]\ Notes:Best Blastp Hit: gb\|AAF42178.1\| (AE002534) transcriptional regulator; MarR family [Neisseria meningitidis MC58] >gi\|7379348\|emb\|CAB83903.1\| (AL162753) putative marR-family transcriptional regulator [Neisseria meningitidis] COG1846 Transcriptional regulators; MarR/EmrR |
| NGO0059 | 0.5731 | -1.50 | down | 0.0006 | -6.19 | down | 0.0258 | -5.54 | down | putative flavoprotein oxidoreductase\ Context:(NC_002946)+[59981-60481]\ Notes:Best Blastp Hit: pir\|\|B81981 probable 4-hydroxyphenylacetate 3-monooxygenase (EC 1.14.13.3) small chain NMA0614 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379349\|emb\|CAB83904.1\| (AL162753) putative NADH:FMN oxidoreductase [Neisseria meningitidis] COG1853 Conserved protein/domain typically |
| NGO0060 | 0.0358 | -5.10 | down | 0.0445 | -4.04 | down | 0.7433 | -1.22 | down | putative sugar-phosphate transferase\ Context:(NC_002946)+[60497-61192]\ Notes:Best Blastp Hit: gb\|AAF42176.1\| (AE002534) mannose-1-phosphate guanyltransferase-related protein [Neisseria meningitidis MC58] COG1208 Nucleoside-diphosphate-sugar |

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| NGO0062 | 0.0243 | -4.69 | down | 0.1574 | -2.06 | down | 0.0677 | -2.92 | down | formate--tetrahydrofolate ligase\ Context:(NC_002946)+[61831-63507]\ Notes:catalyzes the formation of 10-formyltetrahydrofolate from formate and tetrahydrofolate |
| NGO0063 | 0.2758 | 1.94 | up | 0.7649 | 1.11 | up | 0.8895 | -1.04 | down | translation-associated GTPase\ Context:(NC_002946)+[63621-64712]\ Notes:the crystal structure of the Haemophilus influenzae YchF protein showed similarity to the yeast structure (PDB: 1NI3); fluorescence spectroscopy revealed nucleic acid binding; the yeast protein YBR025c interacts with the translation elongation factor eEF1 |
| NGO0064 | 0.4668 | 1.48 | up | 0.2585 | 1.55 | up | 0.3079 | -1.61 | down | hypothetical protein\ Context:(NC_002946)+[64750-64989]\ Notes:Best Blastp Hit: gb\|AAF42172.1\| (AE002533) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0065 | 0.2245 | -3.68 | down | 0.0425 | -6.12 | down | 0.2686 | -2.37 | down | putative lipo-oligosaccharide acyltransferase\ Context:(NC_002946)+[64986-66860]\ Notes:Best Blastp Hit: gb\|AAF42171.1\| (AE002533) lipopolysaccharide biosynthesis protein WbpC; putative [Neisseria meningitidis MC58] COG1835 Predicted acyltransferases |
| NGO0066 | 0.3643 | 1.58 | up | 0.5871 | 1.18 | up | 0.7206 | -1.18 | down | putative tyrosyl-tRNA synthase\ Context:(NC_002946)+[66922-68217]\ Notes:TyrRS Best Blastp Hit: pir\|\|A81037 tyrosyl-tRNA synthetase NMB1835 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227090\|gb\|AAF42170.1\| (AE002533) tyrosyl-tRNA synthetase [Neisseria meningitidis MC58] COG0162 Tyrosyl-tRNA synthetase |
| NGO0068 | 0.8800 | -1.08 | down | 0.5519 | -1.29 | down | 0.6213 | -1.26 | down | bifunctional riboflavin kinase/FMN adenylyltransferase\ Context:(NC_002946)+[70214-71173]\ Notes:catalyzes the formation of FMN from riboflavin and the formation of FAD from FMN; in Bacillus the ribC gene has both flavokinase and FAD synthetase activities |
| NGO0069 | 0.0211 | 5.16 | up | 0.1028 | 4.22 | up | 0.1161 | 3.50 | up | isoleucyl-tRNA synthetase\ Context:(NC_002946)+[71315-74104]\ Notes:IleRS; catalyzes the formation of isoleucyl-tRNA(Ile) from isoleucine and tRNA(Ile); since isoleucine and other amino acids such as valine are similar |

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| NGO0070 | 0.1098 | 3.05 | up | 0.0987 | 2.19 | up | 0.1926 | 1.81 | up | outer membrane opacity protein B\ Context:(NC_002946)-[74783-75580]\ Notes:OpaB; Best Blastp Hit: phase variable - 10 tandem repeats of CTCTT in the coding sequence (ON) |
| NGO0071 | 0.7725 | -1.15 | down | 0.2557 | -1.76 | down | 0.4911 | -1.26 | down | lipoprotein signal peptidase\ Context:(NC_002946)+[76565-77059]\ Notes:lipoprotein signal peptidase; integral membrane protein that removes signal peptides from prolipoproteins during lipoprotein biosynthesis |
| NGO0072 | 0.3147 | 1.65 | up | 0.8147 | -1.10 | down | 0.9370 | -1.02 | down | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase\ Context:(NC_002946)+[77089-78057]\ Notes:catalyzes the conversion of 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP); functions in the nonmevalonate isoprenoid biosynthesis pathway |
| NGO0073 | 0.5390 | 1.38 | up | 0.5598 | 1.49 | up | 0.5372 | 1.58 | up | putative phosphatase\ Context:(NC_002946)-[78813-79472]\ Notes:Best Blastp Hit: gb\|AAF42165.1\| (AE002532) phosphoglycolate phosphatase; putative [Neisseria meningitidis MC58] COG0546 Predicted phosphatases |
| NGO0076 | 0.0625 | -7.15 | down | 0.0240 | -14.83 | down | 0.9396 | -1.11 | down | hypothetical protein\ Context:(NC_002946)+[80406-80726]\ Notes:Best Blastp Hit: gb\|AAF42163.1\| (AE002532) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0077 | 0.0277 | -9.23 | down | 0.1379 | -4.92 | down | 0.7532 | -1.45 | down | hypothetical protein\ Context:(NC_002946)+[80714-81337]\ Notes:Best Blastp Hit: gb\|AAF42163.1\| (AE002532) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0078 | 0.7490 | -1.24 | down | 0.7873 | -1.27 | down | 0.3668 | 1.70 | up | putative DNA polymerase III; alpha subunit\ Context:(NC_002946)-[81989-85423]\ Notes:Best Blastp Hit: pir\|\|H81037 DNA polymerase III; alpha chain NMB1827 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227081\|gb\|AAF42162.1\| (AE002532) DNA polymerase III; alpha subunit [Neisseria meningitidis MC58] COG0587 DNA-dependent DNA polymerase III alpha |
| NGO0079 | 0.4227 | 1.47 | up | 0.7975 | -1.11 | down | 0.8333 | 1.07 | up | hypothetical protein\ Context:(NC_002946)+[85956-86189]\ Notes:Best Blastp Hit: emb\|CAB83923.1\| (AL162753) hypothetical protein NMA0633 [Neisseria meningitidis] |

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| NGO0080 | 0.9669 | 1.02 | up | 0.5717 | -1.32 | down | 0.9219 | -1.03 | down | hypothetical protein\ Context:(NC_002946)+[86167-86370]\ Notes:Best Blastp Hit: gb\|AAF42160.1\| (AE002532) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0081 | 0.3315 | -2.06 | down | 0.5153 | -1.67 | down | 0.0373 | -3.44 | down | hypothetical protein\ Context:(NC_002946)+[86665-87501]\ Notes:Best Blastp Hit: pir\|\|A81040 conserved hypothetical protein NMB1824 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227077\|gb\|AAF42159.1\| (AE002531) conserved hypothetical protein [Neisseria meningitidis MC58] COG0613 Predicted metal-dependent phosphoesterases |
| NGO0082 | 0.1615 | -2.98 | down | 0.0289 | -5.37 | down | 0.7629 | -1.18 | down | valine--pyruvate transaminase\ Context:(NC_002946)-[87553-88845]\ Notes:transaminase C; catalyzes transamination of alanine; valine; and 2-aminobutyrate with their respective 2-keto acids; also catalyzes terminal step in valine biosynthesis |
| NGO0083 | 0.1280 | -2.39 | down | 0.1251 | -3.68 | down | 0.2730 | -1.91 | down | pilin glycosylation protein\ Context:(NC_002946)-[88901-90811]\ Notes:PglD; Best Blastp Hit: pir\|\|G81039 pilin glycosylation protein PglD NMB1822 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|3299891\|gb\|AAC25981.1\| (AF014804) PglD [Neisseria meningitidis] >gi\|7227075\|gb\|AAF42157.1\| (AE002531) pilin glycosylation protein PglD [Neisseria meningitidis MC58] COG1086 Predicted nucleoside-diphosphate sugar |
| NGO0084 | 0.0356 | -3.09 | down | 0.0127 | -5.14 | down | 0.0264 | -2.97 | down | PglC\ Context:(NC_002946)-[90859-92034]\ Notes:Best Blastp Hit: pir\|\|H81983 pilin glycosylation protein NMA0638 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379371\|emb\|CAB83928.1\| (AL162753) |
| NGO0085 | 0.9090 | -1.12 | down | 0.7108 | -1.25 | down | 0.2605 | 2.32 | up | PglB\ Context:(NC_002946)-[92165-93406]\ Notes:Best Blastp Hit: gb\|AAC25979.1\| (AF014804) PglB [Neisseria meningitidis] >gi\|7227073\|gb\|AAF42155.1\| (AE002531) pilin glycosylation protein PglB [Neisseria meningitidis MC58] COG2148 Sugar transferases involved in |
| NGO0086 | 0.6571 | 1.28 | up | 0.9556 | -1.07 | down | 0.8425 | 1.18 | up | hypothetical protein\ Context:(NC_002946)-[93399-94565]\ Notes:Best Blastp Hit: possibly phase variable - 10C residue homopolymer repeat in the coding sequence (ON) COG0438 Glycosyltransferases I |

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| NGO0087 | 0.4380 | 1.67 | up | 0.2408 | 1.94 | up | 0.1234 | 3.12 | up | hypothetical protein\ Context:(NC_002946)-[94579-95643]\ Notes:Best Blastp Hit: gb\|AAF84279.1\|AE003977_2 (AE003977) conserved hypothetical protein [Xylella fastidiosa] COG0438 Glycosyltransferases I |
| NGO0088 | 0.8940 | -1.11 | down | 0.9684 | 1.03 | up | 0.5193 | -1.35 | down | hypothetical protein\ Context:(NC_002946)-[95640-97061]\ Notes:Best Blastp Hit: pir\|\|C81984 probable lipopolysaccharide biosynthesis translocase NMA0643 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379374\|emb\|CAB83932.1\| (AL162753) putative lipopolysaccharide biosynthesis translocase [Neisseria meningitidis] COG2244 Membrane protein involved in the export of |
| NGO0089 | 0.7939 | 1.12 | up | 0.4855 | -1.35 | down | 0.7444 | 1.14 | up | putative diaminohydroxyphosphoribosylaminopyrimidine deaminase\ Context:(NC_002946)-[97256-98365]\ Notes:Best Blastp Hit: pir\|\|D81984 riboflavin bifunctional biosynthesis protein ribD NMA0644 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379375\|emb\|CAB83933.1\| (AL162753) putative diaminohydroxyphosphoribosylaminopyrimidine deaminase/phosphoribosylamino)uracil reductase [Neisseria meningitidis] COG0117 Pyrimidine deaminase; riboflavin |
| NGO0090 | 0.7798 | 1.18 | up | 0.0006 | -13.01 | down | 0.8284 | 1.11 | up | transcriptional regulator NrdR\ Context:(NC_002946)-[98397-98849]\ Notes:Best Blastp Hit: pir\|\|A81039 conserved hypothetical protein NMB1816 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227069\|gb\|AAF42151.1\| (AE002531) conserved hypothetical protein [Neisseria meningitidis MC58] COG1327 Uncharacterized BCR |
| NGO0091 | 0.0758 | -2.51 | down | 0.1742 | -2.12 | down | 0.2521 | -2.11 | down | hypothetical protein\ Context:(NC_002946)-[98878-99720]\ Notes:Best Blastp Hit: pir\|\|H81038 conserved hypothetical protein NMB1815 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227068\|gb\|AAF42150.1\| (AE002531) conserved hypothetical protein [Neisseria meningitidis MC58] COG0121 Predicted glutamine amidotransferase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0092 | 0.6038 | -1.28 | down | 0.8658 | 1.08 | up | 0.7204 | -1.11 | down | 3-dehydroquinate synthase\ Context:(NC_002946)-[100459-101538]\ Notes:catalyzes the formation of 3-dehydroquinate from 3-deoxy-arabino-heptulonate 7-phosphate; functions in aromatic amino acid biosynthesis |
| NGO0093 | 0.1166 | -2.18 | down | 0.3086 | -1.61 | down | 0.1940 | -1.98 | down | shikimate kinase\ Context:(NC_002946)-[101618-102130]\ Notes:catalyzes the formation of shikimate 3-phosphate from shikimate in aromatic amino acid biosynthesis |
| NGO0094 | 0.0626 | 3.93 | up | 0.0218 | 7.26 | up | 0.0875 | 3.29 | up | hypothetical protein\ Context:(NC_002946)-[103398-105569]\ Notes:Best Blastp Hit: pir\|\|S70838 pilQ protein - Neisseria gonorrhoeae >gi\|1173875\|gb\|AAC43603.1\| (U40596) PilQ [Neisseria gonorrhoeae] >gi\|1589217\|prf\|\|2210365A pilQ gene [Neisseria gonorrhoeae] COG1450 General secretion pathway protein D |
| NGO0095 | 0.3837 | 1.64 | up | 0.4590 | 1.30 | up | 0.4044 | 1.34 | up | PilP\ Context:(NC_002946)-[105588-106133]\ Notes:Best Blastp Hit: pir\|\|C81041 pilus assembly protein NMA0651 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227064\|gb\|AAF42147.1\| (AE002530) pilP protein [Neisseria meningitidis MC58] >gi\|7379381\|emb\|CAB83939.1\| (AL162753) pilus assembly protein [Neisseria meningitidis]; pilin assembly protein |
| NGO0096 | 0.3289 | 1.83 | up | 0.6561 | 1.17 | up | 0.4099 | 1.39 | up | hypothetical protein\ Context:(NC_002946)-[106151-106798]\ Notes:Best Blastp Hit: gb\|AAB52533.1\| (U72876) PilO [Neisseria gonorrhoeae] |
| NGO0097 | 0.6471 | 1.24 | up | 0.7861 | 1.10 | up | 0.9060 | 1.04 | up | PilN\ Context:(NC_002946)-[106799-107398]\ Notes:Best Blastp Hit: pir\|\|D81985 probable pilus assembly protein NMA0653 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379383\|emb\|CAB83941.1\| (AL162753) putative pilus assembly protein [Neisseria meningitidis] |
| NGO0098 | 0.3927 | 1.69 | up | 0.5134 | 1.28 | up | 0.6779 | 1.17 | up | hypothetical protein\ Context:(NC_002946)-[107401-108516]\ Notes:Best Blastp Hit: gb\|AAB52535.1\| (U72876) PilM [Neisseria gonorrhoeae] COG0849 Predicted ATPases of the HSP70 class |

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| NGO0099 | 0.0588 | 2.94 | up | 0.3597 | 1.49 | up | 0.1844 | 1.51 | up | PonA\ Context:(NC_002946)+[108668-111064]\ Notes:Best Blastp Hit: gb\|AAB52536.1\| (U72876) penicillin-binding protein 1 [Neisseria gonorrhoeae] COG0744 Membrane carboxypeptidase |
| NGO0100 | 0.9785 | -1.01 | down | 0.7440 | -1.15 | down | 0.7602 | -1.11 | down | GTPase EngB\ Context:(NC_002946)-[111184-111819]\ Notes:binds guanine nucleotides; in Escherichia coli depletion results in defective cell division and filamentation; in Bacillus subtilis this gene is essential; |
| NGO0101 | 0.3698 | -1.76 | down | 0.2552 | -1.80 | down | 0.0526 | -2.00 | down | putative cytochrome precursor\ Context:(NC_002946)+[112020-112643]\ Notes:Best Blastp Hit: pir\|\|F81040 cytochrome C4 NMB1805 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227059\|gb\|AAF42142.1\| (AE002530) cytochrome c4 [Neisseria meningitidis MC58] >gi\|7379387\|emb\|CAB83945.1\| (AL162753) putative cytochrome C [Neisseria meningitidis] |
| NGO0102 | 0.9612 | -1.03 | down | 0.0081 | -3.11 | down | 0.2220 | -1.95 | down | putative cytochrome biogenesis protein\ Context:(NC_002946)+[112858-114873]\ Notes:Best Blastp Hit: pir\|\|E81040 cytochrome c-type biogenesis protein; probable NMB1804 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227058\|gb\|AAF42141.1\| (AE002530) cytochrome c-type biogenesis protein; putative [Neisseria meningitidis MC58] COG1333 ResB protein required for cytochrome c |
| NGO0103 | 0.0100 | -6.41 | down | 0.0345 | -7.32 | down | 0.1140 | -2.76 | down | putative cytochrome synthesis protein\ Context:(NC_002946)+[114866-116053]\ Notes:Best Blastp Hit: emb\|CAB83947.1\| (AL162753) putative membrane protein [Neisseria meningitidis] COG0755 Cytochrome c biogenesis factors; CcmC |
| NGO0104 | 0.9769 | -1.02 | down | 0.0048 | -6.22 | down | 0.1266 | -2.27 | down | O-sialoglycoprotein endopeptidase\ Context:(NC_002946)+[116169-117233]\ Notes:in most organisms; only the N-terminal domain is present in a single polypeptide; in some archaea this domain is fused to a kinase domain; this gene is essential for growth in Escherichia coli and Bacillus subtilis; the secreted glycoprotese from Pasteurella haemolytica showed specificity for O-sialoglycosylated proteins |

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| NGO0105 | 0.0864 | -2.56 | down | 0.2853 | -1.71 | down | 0.6625 | -1.29 | down | lipid A biosynthesis lauroyl acyltransferase\ Context:(NC_002946)-[117278-118171]\ Notes:Acylates the intermediate (KDO)2-lipid IVA to form (KDO)2-(lauroyl)-lipid IVA |
| NGO0106 | 0.0112 | 5.42 | up | 0.0009 | 6.43 | up | 0.0041 | 4.98 | up | S-adenosylmethionine synthetase\ Context:(NC_002946)+[118517-119686]\ Notes:methionine adenosyltransferase; catalyzes the formation of S-adenosylmethionine from methionine and ATP; methionine adenosyltransferase |
| NGO0107 | 0.1618 | 2.29 | up | 0.1353 | 2.63 | up | 0.8411 | 1.08 | up | putative carboxypeptidase; penicillin binding protein\ Context:(NC_002946)-[119751-121160]\ Notes:Best Blastp Hit: gb\|AAC24040.1\| (AF071224) penicillin binding protein 3 [Neisseria gonorrhoeae] COG2027 D-alanyl-D-alanine carboxypeptidase |
| NGO0108 | 0.3288 | 1.83 | up | 0.4333 | 1.37 | up | 0.4608 | 1.35 | up | hypothetical protein\ Context:(NC_002946)+[121405-121890]\ Notes:Best Blastp Hit: pir\|\|B81042 conserved hypothetical protein NMB1796 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227050\|gb\|AAF42134.1\| (AE002529) conserved hypothetical protein [Neisseria meningitidis MC58] COG0431 Predicted flavoprotein |
| NGO0109 | 0.4904 | 1.77 | up | 0.0427 | -9.37 | down | 0.3002 | -2.17 | down | hypothetical protein\ Context:(NC_002946)+[121880-122068]\ Notes: |
| NGO0110 | 0.1099 | -2.96 | down | 0.1930 | -3.00 | down | 0.6263 | -1.70 | down | putative magnesium citrate secondary transporter\ Context:(NC_002946)+[122259-123572]\ Notes:Best Blastp Hit: gb\|AAF42132.1\| (AE002529) citrate transporter [Neisseria meningitidis MC58] >gi\|7379397\|emb\|CAB83955.1\| (AL162753) putative transmembrane transport protein [Neisseria meningitidis] |
| NGO0112 | 0.0192 | -3.82 | down | 0.0053 | -12.40 | down | 0.1691 | -2.06 | down | putative two-component system sensor kinase\ Context:(NC_002946)+[124550-125800]\ Notes:Best Blastp Hit: gb\|AAG24266.1\|AF139612_3 (AF139612) BasS [Neisseria gonorrhoeae] COG0642 Sensory transduction histidine kinases |
| NGO0113 | 0.0187 | 5.18 | up | 0.0545 | 4.15 | up | 0.0809 | 2.84 | up | putative ribonuclease G / cytoplasmic axial filament protein\ Context:(NC_002946)-[125835-127328]\ Notes:Best Blastp Hit: emb\|CAB83959.1\| (AL162753) hypothetical protein NMA0672 [Neisseria meningitidis] COG1530 Ribonucleases G and E |

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| NGO0114 | 0.1631 | 2.19 | up | 0.2867 | 1.57 | up | 0.4553 | 1.29 | up | putative glutaredoxin\ Context:(NC_002946)+[127547-127804]\ Notes:Best Blastp Hit: gb\|AAF42129.1\|(AE002529) glutaredoxin 3 [Neisseria meningitidis MC58] COG0695 Glutaredoxin and related proteins |
| NGO0115 | 0.1898 | -3.01 | down | 0.0532 | -12.69 | down | 0.3027 | -3.30 | down | hypothetical protein\ Context:(NC_002946)-[127801-128310]\ Notes:Best Blastp Hit: sp\|P15041\|YZSB_ECOLI very hypothetical 17.7 kD protein in SecB region>gi\|76221\|pir\|\|QQEC17 hypothetical 17.7K protein (secB region) - Escherichia coli >gi\|1128972\|gb\|AAA83908.1\| (M24489) ORF; putative [Escherichia coli] |
| NGO0116 | 0.1619 | 2.41 | up | 0.1834 | 1.62 | up | 0.2937 | 1.58 | up | preprotein translocase subunit SecB\ Context:(NC_002946)+[127825-128268]\ Notes:molecular chaperone that is required for the normal export of envelope proteins out of the cell cytoplasm; in Escherichia coli this proteins forms a homotetramer in the cytoplasm and delivers proteins to be exported to SecA |
| NGO0117 | 0.0051 | 5.40 | up | 0.7255 | 1.37 | up | 0.8598 | 1.14 | up | hypothetical protein\ Context:(NC_002946)+[128354-130396]\ Notes:Best Blastp Hit: pir\|\|E81043 ATP-dependent DNA helicase RecG NMB1788 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227042\|gb\|AAF42127.1\| (AE002528) ATP-dependent DNA helicase RecG [Neisseria meningitidis MC58] COG1200 RecG-like helicases |
| NGO0118 | 0.5648 | -1.29 | down | 0.0236 | -3.33 | down | 0.1863 | -1.88 | down | N-acetyl-gamma-glutamyl-phosphate reductase\ Context:(NC_002946)-[130990-132033]\ Notes:catalyzes the reduction of N-acetyl-5-glutamyl phosphate to N-acetyl-L-glutamate 5-semialdehyde in arginine biosynthesis and the reduction of N-acetyl-gamma-aminoadipyl-phosphate to N-acetyl-L-aminoadipate-semialdehyde in lysine biosynthesis; involved in both the arginine and lysine biosynthetic pathways; lysine is produced via the AAA pathway; lysine from alpha-aminoadipate |
| NGO0119 | 0.5410 | 1.49 | up | 0.5710 | -1.52 | down | 0.4326 | -1.51 | down | hypothetical protein\ Context:(NC_002946)-[132030-132323]\ Notes:Best Blastp Hit: emb\|CAB83964.1\|(AL162753) hypothetical protein NMA0677 [Neisseria meningitidis] |
| NGO0120 | 0.7922 | -1.33 | down | 0.0115 | -20.23 | down | 0.0817 | -4.37 | down | hypothetical protein\ Context:(NC_002946)+[132347-132475]\ Notes: |

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| NGO0121 | 0.0022 | -18.44 | down | 0.0003 | -50.71 | down | 0.0177 | -8.74 | down | hypothetical protein\ Context:(NC_002946)+[132575-133729]\ Notes:Best Blastp Hit: gb\|AAF42125.1\| (AE002528) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0122 | 0.8599 | -1.09 | down | 0.8784 | -1.07 | down | 0.5191 | -1.30 | down | hypothetical protein\ Context:(NC_002946)+[133904-134311]\ Notes:Best Blastp Hit: pir\|\|F81988 hypothetical protein NMA0681 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379409\|emb\|CAB83968.1\| (AL162753) hypothetical protein NMA0681 [Neisseria meningitidis] |
| NGO0123 | 0.0077 | -8.32 | down | 0.0520 | -4.42 | down | 0.1136 | -3.72 | down | putative secretion protein\ Context:(NC_002946)+[134372-135646]\ Notes:Best Blastp Hit: gb\|AAF61809.1\| (AF129811) unknown [Moraxella catarrhalis] COG1566 Multidrug resistance efflux pump |
| NGO0124 | 0.3674 | 1.58 | up | 0.5794 | -1.23 | down | 0.9328 | -1.02 | down | hypothetical protein\ Context:(NC_002946)+[135831-136178]\ Notes:Best Blastp Hit: sp\|O24528\|MT1_FESRU metallothionein-like protein 1 >gi\|2317922\|gb\|AAB70464.1\| (U96646) mcMT1 [Festuca rubra] |
| NGO0125 | 0.1965 | 2.20 | up | 0.2842 | 5.10 | up | 0.5743 | -1.20 | down | hypothetical protein\ Context:(NC_002946)+[136192-136407]\ Notes:Best Blastp Hit: pir\|\|B70183 conserved hypothetical protein BB0667 - Lyme disease spirochete >gi\|2688586\|gb\|AAC67004.1\| (AE001167) conserved hypothetical protein [Borrelia burgdorferi] |
| NGO0127 | 0.8056 | 1.17 | up | 0.1158 | -1.86 | down | 0.5837 | -1.37 | down | fused ribonuclease BN/uncharacterized domain-containing protein\ Context:(NC_002946)-[137771-138997]\ Notes:RNase BN; required for 3' maturation of certain phage T4-encoded tRNAs; forms a dimer; specific for immature tRNA substrates containing incorrect residues within the universal CCA sequence; 3' to 5' exoribonuclease; this protein contains a C-terminal extension of unknown function |
| NGO0128 | 0.7868 | 1.14 | up | 0.6614 | -1.17 | down | 0.9936 | 1.00 | up | hypothetical protein\ Context:(NC_002946)+[139096-139476]\ Notes:Best Blastp Hit: gb\|AAC33457.1\| (AF067083) Trp repressor binding protein [Vitreoscilla sp.] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0129 | 0.5950 | 1.30 | up | 0.6663 | -1.23 | down | 0.7562 | -1.09 | down | YbaX\ Context:(NC_002946)+[139485-140159]\ Notes:Best Blastp Hit: pir\|\|C81913 hypothetical protein NMA0702 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379427\|emb\|CAB83989.1\| (AL162754) hypothetical protein NMA0702 [Neisseria meningitidis] COG0603 Predicted ATPase (PP-loop superfamily); putative aluminum resistance protein |
| NGO0130 | 0.2031 | 1.84 | up | 0.9599 | 1.02 | up | 0.8715 | -1.04 | down | hypothetical protein\ Context:(NC_002946)+[140187-140702]\ Notes:Best Blastp Hit: pir\|\|D81913 hypothetical protein NMA0703 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379428\|emb\|CAB83990.1\| (AL162754) hypothetical protein NMA0703 [Neisseria meningitidis] |
| NGO0131 | 0.3031 | 1.66 | up | 0.7482 | -1.16 | down | 0.9651 | -1.01 | down | putative 6-pyruvoyl-tetrahydropterin synthase\ Context:(NC_002946)+[140790-141212]\ Notes:Best Blastp Hit: pir\|\|E81913 hypothetical protein NMA0704 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379429\|emb\|CAB83991.1\| (AL162754) hypothetical protein NMA0704 [Neisseria meningitidis] COG0720 6-pyruvoyl-tetrahydropterin synthase |
| NGO0132 | 0.0778 | 2.91 | up | 0.9867 | 1.01 | up | 0.2728 | -1.45 | down | hypothetical protein\ Context:(NC_002946)+[141478-142485]\ Notes:Best Blastp Hit: emb\|CAB83993.1\| (AL162754) hypothetical protein NMA0707 [Neisseria meningitidis] COG0602 Organic radical activating enzymes |
| NGO0133 | 0.1254 | 3.36 | up | 0.1432 | -2.97 | down | 0.7695 | 1.25 | up | hypothetical protein\ Context:(NC_002946)+[142700-142903]\ Notes:Best Blastp Hit: dbj\|BAA98955.1\| (AP002547) CT631 hypothetical protein [Chlamydophila pneumoniae] |
| NGO0135 | 0.1659 | 3.27 | up | 0.2989 | -2.95 | down | 0.8960 | -1.13 | down | beta-hexosaminidase\ Context:(NC_002946)-[142978-144063]\ Notes:hydrolyzes the terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl-beta-D-hexosaminides |
| NGO0136 | 0.5104 | -1.42 | down | 0.3820 | -1.49 | down | 0.6524 | -1.29 | down | hypothetical protein\ Context:(NC_002946)-[144120-145640]\ Notes:Best Blastp Hit: gb\|AAF40961.1\| (AE002408) conserved hypothetical protein [Neisseria meningitidis MC58] COG1757 Na+/H+ antiporter NhaC |
| NGO0137 | 0.0006 | 10.98 | up | 0.7273 | -1.75 | down | 0.7778 | 1.74 | up | hypothetical protein\ Context:(NC_002946)+[145668-145817]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0138 | 0.0647 | 2.84 | up | 0.2787 | 1.91 | up | 0.4894 | 1.21 | up | putative serine protease\ Context:(NC_002946)-[145843-147342]\ Notes:Best Blastp Hit: pir\|\|B81914 probable periplasmic serine proteinase (EC 3.4.21.-) NMA0710 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379434\|emb\|CAB83996.1\| (AL162754) putative periplasmic serine protease [Neisseria meningitidis] COG0265 Trypsin-like serine proteases; typically |
| NGO0139 | 0.0077 | -4.61 | down | 0.0060 | -13.41 | down | 0.1531 | -2.28 | down | putative endonuclease III\ Context:(NC_002946)-[147480-148109]\ Notes:Best Blastp Hit: pir\|\|D81187 endonuclease III NMB0533 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225758\|gb\|AAF40962.1\| (AE002409) endonuclease III [Neisseria meningitidis MC58] COG0177 Predicted EndoIII-related endonuclease |
| NGO0140 | 0.0015 | -22.08 | down | 0.0120 | -24.19 | down | 0.0015 | -7.05 | down | hypothetical protein\ Context:(NC_002946)-[148156-148692]\ Notes:Best Blastp Hit: pir\|\|D81914 probable membrane protein NMA0712 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379436\|emb\|CAB83998.1\| (AL162754) putative membrane protein [Neisseria meningitidis] COG1238 Uncharacterized membrane protein |
| NGO0141 | 0.4350 | 2.96 | up | 0.0007 | -80.65 | down | 0.7331 | -1.44 | down | hypothetical protein\ Context:(NC_002946)+[148719-148865]\ Notes: |
| NGO0142 | 0.3269 | 1.78 | up | 0.6858 | 1.18 | up | 0.3083 | 1.51 | up | putative sugar transporter\ Context:(NC_002946)+[148948-150228]\ Notes:Best Blastp Hit: pir\|\|F81187 glucose/galactose transporter NMB0535 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225760\|gb\|AAF40964.1\| (AE002409) glucose/galactose transporter [Neisseria meningitidis MC58] COG0738 Fucose permease |
| NGO0143 | 0.3583 | 2.45 | up | 0.4326 | -2.61 | down | 0.0967 | -2.82 | down | hypothetical protein\ Context:(NC_002946)+[150518-151897]\ Notes:Best Blastp Hit: pir\|\|F81914 probable transmembrane transport protein NMA0715 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379438\|emb\|CAB84000.1\| (AL162754) putative transmembrane transport protein [Neisseria meningitidis] COG1757 Na+/H+ antiporter NhaC |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0144 | 0.7673 | 1.13 | up | 0.9012 | -1.04 | down | 0.8442 | 1.06 | up | hypothetical protein\ Context:(NC_002946)-[152040-152864]\ Notes:Best Blastp Hit: pir\|\|G81914 hypothetical protein NMA0716 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379439\|emb\|CAB84001.1\| (AL162754) hypothetical protein NMA0716 [Neisseria meningitidis] COG1253 Uncharacterized CBS domain-containing |
| NGO0145 | 0.9533 | 1.03 | up | 0.5683 | -1.32 | down | 0.3519 | -1.32 | down | hypothetical protein\ Context:(NC_002946)-[152866-153501]\ Notes:Best Blastp Hit: emb\|CAB84002.1\| (AL162754) hypothetical protein NMA0717 [Neisseria meningitidis] COG0319 Uncharacterized BCR (putative metal-binding |
| NGO0146 | 0.3133 | 1.57 | up | 0.3243 | 1.40 | up | 0.5474 | 1.17 | up | porphobilinogen deaminase\ Context:(NC_002946)+[153500-154435]\ Notes:transformation of porphobilinogen to hydroxymethylbilane in porphyrin biosynthesis |
| NGO0147 | 0.1927 | -1.95 | down | 0.4628 | -1.65 | down | 0.2992 | 1.39 | up | hypothetical protein\ Context:(NC_002946)-[156345-157430]\ Notes:Best Blastp Hit: emb\|CAB84865.1\| (AL162756) hypothetical protein [Neisseria meningitidis] COG0644 Dehydrogenases (flavoproteins) |
| NGO0148 | 0.3591 | -1.62 | down | 0.6425 | -1.23 | down | 0.5896 | 1.15 | up | hypothetical protein\ Context:(NC_002946)-[157367-157582]\ Notes: |
| NGO0149 | 0.1437 | 2.03 | up | 0.0978 | 2.58 | up | 0.1186 | 1.56 | up | putative ATP-dependent RNA helicase\ Context:(NC_002946)-[157762-159135]\ Notes:Best Blastp Hit: gb\|AAF41783.1\| (AE002491) ATP-dependent RNA helicase; putative [Neisseria meningitidis MC58] COG0513 Superfamily II DNA and RNA helicases |
| NGO0150 | 0.1542 | -2.88 | down | 0.7180 | -1.37 | down | 0.1769 | -2.42 | down | hypothetical protein\ Context:(NC_002946)-[159159-159347]\ Notes: |
| NGO0151 | 0.2727 | -1.84 | down | 0.2245 | 1.80 | up | 0.3278 | -2.03 | down | hypothetical protein\ Context:(NC_002946)+[159349-160353]\ Notes:Best Blastp Hit: pir\|\|G81085 nifR3 protein NMB1421 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226660\|gb\|AAF41782.1\| (AE002491) nifR3 protein [Neisseria meningitidis MC58] COG0042 Predicted TIM-barrel enzymes; possibly |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0152 | 0.0930 | -3.26 | down | 0.1072 | -3.08 | down | 0.0028 | -6.42 | down | hypothetical protein\ Context:(NC_002946)+[160452-160781]\ Notes:Best Blastp Hit: gb\|AAF41781.1\| (AE002491) factor-for-inversion stimulation protein Fis; putative [Neisseria meningitidis MC58] >gi\|7380274\|emb\|CAB84860.1\| (AL162756) factor-for-inversion-stimulation protein [Neisseria meningitidis] |
| NGO0153 | 0.4202 | -2.28 | down | 0.3532 | -2.18 | down | 0.1113 | -2.21 | down | Holliday junction resolvase\ Context:(NC_002946)+[160784-161320]\ Notes:endonuclease; resolves Holliday structures; forms a complex of RuvABC; the junction binding protein RuvA forms a hexameric ring along with the RuvB helicase and catalyzes branch migration; RuvC then interacts with RuvAB to resolve the Holliday junction by nicking DNA strands of like polarity |
| NGO0154 | 0.2458 | -2.33 | down | 0.1284 | -6.97 | down | 0.1491 | -3.09 | down | lipid A biosynthesis lauroyl acyltransferase\ Context:(NC_002946)+[161371-162240]\ Notes:Acylates the intermediate (KDO)2-lipid IVA to form (KDO)2-(lauroyl)-lipid IVA |
| NGO0155 | 0.6411 | 1.33 | up | 0.8436 | -1.11 | down | 0.4492 | -1.30 | down | hypothetical protein\ Context:(NC_002946)+[162894-163028]\ Notes:Best Blastp Hit: emb\|CAB84857.1\| (AL162756) hypothetical DNA-binding protein [Neisseria meningitidis] |
| NGO0156 | 0.8272 | -1.10 | down | 0.2594 | -2.00 | down | 0.7814 | -1.08 | down | hypothetical protein\ Context:(NC_002946)+[163144-163938]\ Notes:Best Blastp Hit: pir\|\|H81856 hypothetical protein NMA1628 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380270\|emb\|CAB84856.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0158 | 0.2866 | 1.68 | up | 0.3766 | 1.35 | up | 0.0397 | 2.48 | up | putative aminopeptidase N\ Context:(NC_002946)+[164163-166766]\ Notes:Best Blastp Hit: pir\|\|F81086 aminopeptidase N NMB1416 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226654\|gb\|AAF41777.1\| (AE002490) aminopeptidase N [Neisseria meningitidis MC58] COG0308 Aminopeptidase N |
| NGO0160 | 0.0981 | 3.98 | up | 0.9742 | -1.02 | down | 0.7599 | -1.10 | down | hypothetical protein\ Context:(NC_002946)-[167614-167805]\ Notes:Best Blastp Hit: emb\|CAB84331.1\| (AL162755) hypothetical protein NMA1067 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0161 | 0.7429 | 1.60 | up | 0.7608 | -1.29 | down | 0.3141 | -3.52 | down | hypothetical protein\ Context:(NC_002946)-[167838-168305]\ Notes:Best Blastp Hit: emb\|CAB84332.1\| (AL162755) hypothetical protein NMA1068 [Neisseria meningitidis] |
| NGO0162 | 0.5780 | -1.28 | down | 0.3035 | -1.74 | down | 0.0418 | -2.10 | down | hypothetical protein\ Context:(NC_002946)-[168362-168742]\ Notes:Best Blastp Hit: gb\|AAF41269.1\| (AE002438) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0163 | 0.7543 | 1.27 | up | 0.2013 | 2.33 | up | 0.0746 | -2.12 | down | hypothetical protein\ Context:(NC_002946)-[168745-169122]\ Notes:Best Blastp Hit: pir\|\|F81150 hypothetical protein NMB0859 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226095\|gb\|AAF41270.1\| (AE002438) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0164 | 0.3031 | -1.94 | down | 0.0586 | -2.75 | down | 0.0477 | -2.59 | down | hypothetical protein\ Context:(NC_002946)-[169180-169545]\ Notes:Best Blastp Hit: emb\|CAB84335.1\| (AL162755) hypothetical protein NMA1072 [Neisseria meningitidis] |
| NGO0165 | 0.0996 | 2.57 | up | 0.7266 | -1.24 | down | 0.0145 | -3.08 | down | hypothetical protein\ Context:(NC_002946)-[169527-170066]\ Notes:Best Blastp Hit: gb\|AAF41272.1\| (AE002438) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379768\|emb\|CAB84336.1\| (AL162755) hypothetical protein NMA1073 [Neisseria meningitidis] |
| NGO0166 | 0.1695 | -2.89 | down | 0.0031 | -23.40 | down | 0.8425 | -1.11 | down | hypothetical protein\ Context:(NC_002946)-[170109-170975]\ Notes:Best Blastp Hit: pir\|\|A81874 probable periplasmic protein NMA1084 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379779\|emb\|CAB84347.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] |
| NGO0167 | 0.3255 | -3.74 | down | 0.1069 | -11.01 | down | 0.1010 | 3.73 | up | hypothetical protein\ Context:(NC_002946)+[171011-171226]\ Notes: |
| NGO0168 | 0.1696 | 2.36 | up | 0.1857 | 1.58 | up | 0.2847 | 1.50 | up | MntC\ Context:(NC_002946)-[171195-172121]\ Notes:Best Blastp Hit: gb\|AAG30300.1\| (AY010757) periplasmic binding protein MntC [Neisseria gonorrhoeae] COG0803 Zn-binding (lipo) protein of the ABC-type Zn; putative ABC transporter; periplasmic binding protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0169 | 0.5296 | -1.62 | down | 0.6784 | -1.35 | down | 0.8028 | -1.16 | down | putative ABC transporter; membrane protein\ Context:(NC_002946)-[172198-173025]\ Notes:Best Blastp Hit: gb\|AAF41015.1\| (AE002415) membrane protein [Neisseria meningitidis MC58] COG1108 ABC-type Mn/Zn transport systems; ATPase |
| NGO0170 | 0.5827 | 1.32 | up | 0.7667 | 1.14 | up | 0.8326 | -1.06 | down | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)-[173108-173863]\ Notes:Best Blastp Hit: gb\|AAF41016.1\| (AE002415) ABC transporter; ATP-binding protein [Neisseria meningitidis MC58] COG1121 ABC-type iron (III) transport system; ATPase |
| NGO0171 | 0.0977 | 2.53 | up | 0.4656 | 1.38 | up | 0.4586 | 1.25 | up | 50S ribosomal protein L19\ Context:(NC_002946)-[174154-174519]\ Notes:this protein is located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site |
| NGO0172 | 0.0796 | 2.70 | up | 0.2293 | 1.65 | up | 0.3435 | 1.37 | up | putative tRNA (guanine-N1)-methyltransferase\ Context:(NC_002946)-[174534-175283]\ Notes:Best Blastp Hit: pir\|\|C81180 tRNA (guanine-N1)-methyltransferase NMB0590 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225820\|gb\|AAF41018.1\| (AE002415) tRNA (guanine-N1)-methyltransferase [Neisseria meningitidis MC58] COG0336 tRNA-(guanine-N1)-methyltransferase |
| NGO0173 | 0.0626 | 3.37 | up | 0.2510 | 1.57 | up | 0.3645 | 1.43 | up | 16S rRNA-processing protein\ Context:(NC_002946)-[175283-175792]\ Notes:Essential for efficient processing of 16S rRNA |
| NGO0174 | 0.0857 | 2.98 | up | 0.2498 | 1.61 | up | 0.3251 | 1.47 | up | 30S ribosomal protein S16\ Context:(NC_002946)-[175808-176053]\ Notes:binds to lower part of 30S body where it stabilizes two domains; required for efficient assembly of 30S; in Escherichia coli this protein has nuclease activity |
| NGO0176 | 0.0739 | 3.93 | up | 0.1821 | 4.30 | up | 0.2011 | 2.23 | up | putative two-component system sensor kinase\ Context:(NC_002946)-[178639-180045]\ Notes:Best Blastp Hit: gb\|AAF41022.1\| (AE002415) sensor histidine kinase [Neisseria meningitidis MC58] COG0642 Sensory transduction histidine kinases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0177 | 0.2488 | 1.88 | up | 0.8124 | 1.11 | up | 0.3355 | 1.37 | up | putative two-component system transcriptional response regulator\ Context:(NC_002946)-[180058-180735]\ Notes:Best Blastp Hit: pir\|\|H81180 DNA-binding response regulator NMB0595 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225825\|gb\|AAF41023.1\| (AE002415) DNA-binding response regulator [Neisseria meningitidis MC58] >gi\|7379518\|emb\|CAB84081.1\| (AL162754) putative two-component system regulator [Neisseria meningitidis] COG0745 Response regulators consisting of a |
| NGO0178 | 0.1947 | 3.44 | up | 0.6080 | 2.00 | up | 0.1756 | 6.08 | up | hypothetical protein\ Context:(NC_002946)-[180925-182739]\ Notes:Best Blastp Hit: pir\|\|A81181 hypothetical protein NMB0596 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225826\|gb\|AAF41024.1\| (AE002415) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0179 | 0.3542 | 2.33 | up | 0.5607 | -1.92 | down | 0.8651 | 1.09 | up | hypothetical protein\ Context:(NC_002946)-[182729-183082]\ Notes:Best Blastp Hit: pir\|\|B81181 hypothetical protein NMB0597 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225827\|gb\|AAF41025.1\| (AE002415) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0180 | 0.0329 | 5.02 | up | 0.1393 | 7.11 | up | 0.8040 | 1.14 | up | hypothetical protein\ Context:(NC_002946)-[183091-183738]\ Notes:Best Blastp Hit: pir\|\|C81181 Maf/YceF/YhdE family protein NMB0598 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225828\|gb\|AAF41026.1\| (AE002415) Maf/YceF/YhdE family protein [Neisseria meningitidis MC58] COG0424 Putative inhibitor of septum formation |
| NGO0181 | 0.1453 | 3.70 | up | 0.2443 | 4.94 | up | 0.1075 | 1.63 | up | putative sec-independent protein translocase component\ Context:(NC_002946)-[183743-184513]\ Notes:Best Blastp Hit: pir\|\|C81925 probable sec-independent protein translocase component NMA0803 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379523\|emb\|CAB84086.1\| (AL162754) putative sec-independent protein translocase component [Neisseria meningitidis] COG0805 Sec-independent protein secretion pathway |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0182 | 0.2283 | 2.00 | up | 0.3090 | 1.39 | up | 0.6748 | -1.11 | down | putative sec-independent protein translocase component\ Context:(NC_002946)-[184526-185212]\ Notes:Best Blastp Hit: pir\|\|E81181 hypothetical protein NMB0600 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225830\|gb\|AAF41028.1\| (AE002415) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0183 | 0.1219 | 2.48 | up | 0.3043 | 1.47 | up | 0.2030 | 1.46 | up | hypothetical protein\ Context:(NC_002946)-[185216-185419]\ Notes:Best Blastp Hit: sp\|P57049\|TATA_NEIMA Sec-independent protein translocase protein TATA/E homolog >gi\|7379525\|emb\|CAB84088.1\| (AL162754) putative sec-independent protein translocase component [Neisseria meningitidis] COG1826 Component of Sec-independent protein |
| NGO0184 | 0.3822 | 1.61 | up | 0.6172 | 1.22 | up | 0.7012 | 1.12 | up | HitA\ Context:(NC_002946)-[185466-185789]\ Notes:Best Blastp Hit: sp\|O07817\|HITA_NEIGO HITA protein >gi\|2197079\|gb\|AAB61288.1\| (AF003550) HitA [Neisseria gonorrhoeae] COG0537 Diadenosine tetraphosphate (Ap4A) hydrolase; putative histidine triad-family protein |
| NGO0185 | 0.2308 | 1.99 | up | 0.7748 | 1.11 | up | 0.8236 | 1.06 | up | putative phosphoribosyl-ATP cyclohydrolase\ Context:(NC_002946)-[185863-186186]\ Notes:Best Blastp Hit: pir\|\|G81925 probable phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) NMA0807 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379527\|emb\|CAB84090.1\| (AL162754) putative phosphoribosyl-ATP cyclohydrolase [Neisseria meningitidis] COG0140 Phosphoribosyl-ATP pyrophosphohydrolase |
| NGO0186 | 0.0928 | 3.04 | up | 0.0358 | 2.33 | up | 0.1463 | 2.11 | up | putative zinc-binding alcohol dehydrogenas\ Context:(NC_002946)-[186327-187391]\ Notes:Best Blastp Hit: pir\|\|H81925 probable alcohol dehydrogenase (EC 1.1.1.-) NMA0808 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379528\|emb\|CAB84091.1\| (AL162754) putative zinc-binding alcohol dehydrogenase [Neisseria meningitidis] COG1065 Zn-dependent oxidoreductases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0187 | 0.7947 | -1.27 | down | 0.0428 | -7.92 | down | 0.5159 | -1.67 | down | hypothetical protein\ Context:(NC_002946)-[188256-189374]\ Notes:Best Blastp Hit: gb\|AAF41032.1\| (AE002416) histone deacetylase family protein [Neisseria meningitidis MC58] COG0123 Deacetylases; including yeast histone |
| NGO0188 | 0.1143 | 2.52 | up | 0.1662 | 1.63 | up | 0.3352 | 1.48 | up | hypothetical protein\ Context:(NC_002946)+[189505-189771]\ Notes:Best Blastp Hit: gb\|AAF41033.1\| (AE002416) conserved hypothetical protein [Neisseria meningitidis MC58] COG1862 Uncharacterized secreted proteins; YajC |
| NGO0189 | 0.0435 | 3.16 | up | 0.0349 | 2.24 | up | 0.2684 | 1.46 | up | preprotein translocase subunit SecD\ Context:(NC_002946)+[189979-191835]\ Notes:part of the preprotein secretory system; when complexed with proteins SecF and YajC; SecDFyajC stimulates the proton motive force-driven protein translocation; and appears to be required for the release of mature proteins from the extracytoplasmic side of the membrane |
| NGO0190 | 0.0219 | 4.38 | up | 0.0937 | 5.02 | up | 0.1428 | 1.64 | up | preprotein translocase subunit SecF\ Context:(NC_002946)+[191839-192774]\ Notes:forms a complex with SecD and YajC; SecDFyajC stimulates the proton motive force-driven protein translocation; seems to modulate the cycling of SecA by stabilizing its membrane-inserted state and appears to be required for the release of mature proteins from the extracytoplasmic side of the membrane; in some organisms; such as Bacillus subtilis; SecD is fused to SecF |
| NGO0191 | 0.3547 | 2.28 | up | 0.2745 | -1.56 | down | 0.5312 | -1.19 | down | 30S ribosomal protein S15\ Context:(NC_002946)+[192979-193248]\ Notes:primary rRNA binding protein; helps nucleate assembly of 30S; binds directly to the 16S rRNA and an intersubunit bridge to the 23S rRNA; autoregulates translation through interactions with the mRNA leader sequence |
| NGO0192 | 0.6086 | -1.25 | down | 0.7796 | -1.13 | down | 0.3856 | -1.53 | down | putative ABC transporter; ATP-binding protein; polyamine\ Context:(NC_002946)+[193358-194650]\ Notes:Best Blastp Hit: gb\|AAF41037.1\| (AE002416) spermidine/putrescine ABC transporter; ATP-binding protein [Neisseria meningitidis MC58] COG1128 ABC-type spermidine/putrescine transport |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0195 | 0.1180 | -2.19 | down | 0.1490 | -3.21 | down | 0.5107 | -1.27 | down | putative ABC transporter; permease protein; polyamine\ Context:(NC_002946)+[194984-195949]\ Notes:Best Blastp Hit: gb\|AAF41038.1\| (AE002416) spermidine/putrescine ABC transporter; permease protein [Neisseria meningitidis MC58] COG1176 ABC-type spermidine/putrescine transport |
| NGO0196 | 0.0590 | 3.45 | up | 0.4998 | 1.38 | up | 0.7063 | 1.10 | up | putative ABC transporter; permease protein; polyamine\ Context:(NC_002946)+[195949-196836]\ Notes:Best Blastp Hit: pir\|\|E81179 spermidine/putrescine ABC transporter; permease protein NMB0612 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225842\|gb\|AAF41039.1\| (AE002416) spermidine/putrescine ABC transporter; permease protein [Neisseria meningitidis MC58] COG1177 ABC-type spermidine/putrescine transport |
| NGO0197 | 0.1992 | -3.95 | down | 0.0982 | -5.29 | down | 0.3851 | 1.34 | up | putative oxidoreductase\ Context:(NC_002946)+[196858-198258]\ Notes:Best Blastp Hit: possible phase variable - 8T residue homopolymer repeat in the coding sequence (ON) COG0665 Predicted oxidoreductases |
| NGO0198 | 0.0078 | -15.54 | down | 0.0026 | -13.55 | down | 0.0279 | -4.88 | down | putative transporter; ammonium\ Context:(NC_002946)-[198352-199818]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0004 Ammonia permeases |
| NGO0199 | 0.8733 | 1.11 | up | 0.2295 | 1.65 | up | 0.7947 | 1.08 | up | transcription termination factor Rho\ Context:(NC_002946)-[200272-201531]\ Notes:An RNA-DNA helicase that actively releases nascent mRNAs from paused transcription complexes |
| NGO0200 | 0.6040 | 1.42 | up | 0.7894 | 1.11 | up | 0.3727 | 1.39 | up | phosphoenolpyruvate synthase\ Context:(NC_002946)-[201752-204136]\ Notes:catalyzes the formation of phosphoenolpyruvate from pyruvate |
| NGO0202 | 0.8908 | 1.07 | up | 0.9523 | 1.02 | up | 0.6954 | 1.11 | up | hypothetical protein\ Context:(NC_002946)+[205270-206091]\ Notes:Best Blastp Hit: pir\|\|H81177 conserved hypothetical protein NMB0619 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225849\|gb\|AAF41045.1\| (AE002417) conserved hypothetical protein [Neisseria meningitidis MC58] COG1806 Uncharacterized BCR; YdiA family |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0203 | 0.0109 | -4.70 | down | 0.0223 | -2.74 | down | 0.1775 | -2.05 | down | putative phosphatase\ Context:(NC_002946)-[206177-206887]\ Notes:Best Blastp Hit: gb\|AAF41046.1\| (AE002417) phosphoglycolate phosphatase [Neisseria meningitidis MC58] COG0546 Predicted phosphatases |
| NGO0204 | 0.7799 | 1.31 | up | 0.0307 | -16.97 | down | 0.2371 | -2.42 | down | hypothetical protein\ Context:(NC_002946)-[206877-207704]\ Notes:Best Blastp Hit: pir\|\|B81178 conserved hypothetical protein NMB0621 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225851\|gb\|AAF41047.1\| (AE002417) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0205 | 0.0180 | -4.76 | down | 0.0013 | -15.18 | down | 0.1195 | -2.64 | down | LolA\ Context:(NC_002946)+[208087-208710]\ Notes:Best Blastp Hit: sp\|P57068\|LOLA_NEIMB outer-membrane lipoproteins carrier protein precursor >gi\|11281795\|pir\|\|C81178 outer membrane lipoprotein carrier protein NMB0622 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225852\|gb\|AAF41048.1\| (AE002417) outer membrane lipoprotein carrier protein [Neisseria meningitidis MC58]; putative lipoprotein carrier precursor; periplasmic binding |
| NGO0206 | 0.0421 | 3.79 | up | 0.0824 | 1.92 | up | 0.3965 | 1.29 | up | putative ABC transporter; periplasmic binding protein; polyamine\ Context:(NC_002946)+[208983-210119]\ Notes:Best Blastp Hit: pir\|\|D81176 spermidine/putrescine ABC transporter; periplasmic spermidine/putrescine-binding protein NMB0623 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225854\|gb\|AAF41049.1\| (AE002418) spermidine/putrescine ABC transporter; periplasmic spermidine/putrescine-binding protein [Neisseria meningitidis MC58] COG0687 Spermidine/putrescine-binding periplasmic |
| NGO0207 | 0.1063 | 2.97 | up | 0.1719 | 1.71 | up | 0.5896 | 1.17 | up | putative sugar transferase\ Context:(NC_002946)+[210214-211197]\ Notes:Best Blastp Hit: possibly phase variable - 5 tandem repeats of CAAACAC in the coding sequence (ON) COG0463 Glycosyl transferases involved in cell wall |

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| NGO0208 | 0.8904 | -1.07 | down | 0.9170 | -1.05 | down | 0.8114 | -1.07 | down | hypothetical protein\ Context:(NC_002946)+[211238-211768]\ Notes:Best Blastp Hit: pir\|\|E81176 conserved hypothetical protein NMB0625 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225855\|gb\|AAF41050.1\| (AE002418) conserved hypothetical protein [Neisseria meningitidis MC58] COG0663 Carbonic anhydrases/acetyltransferases |
| NGO0209 | 0.2466 | -2.30 | down | 0.9803 | 1.01 | up | 0.6071 | -1.40 | down | peptide chain release factor 3\ Context:(NC_002946)-[211936-213531]\ Notes:stimulates the release of release factors 1 and 2 from the ribosome after hydrolysis of the ester bond in peptidyl-tRNA has occurred; GDP/GTP-binding protein |
| NGO0210 | 0.3167 | 2.07 | up | 0.5073 | -1.28 | down | 0.8059 | -1.10 | down | phosphoribosyl-AMP cyclohydrolase\ Context:(NC_002946)-[213638-214033]\ Notes:PR-AMP cyclohydrolase; functions in histidine biosynthesis from PRPP; converts 1-(5-phosphoribosyl)-AMP to 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxyamide during the histidine biosynthesis pathway; binds zinc and magnesium; forms homodimers |
| NGO0211 | 0.7221 | 1.16 | up | 0.5207 | 1.24 | up | 0.4071 | -1.44 | down | imidazole glycerol phosphate synthase subunit HisF\ Context:(NC_002946)-[214064-214831]\ Notes:catalyzes the conversion of 5-[(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]- 1-(5-phosphoribosyl)imidazole-4-carboxamideand glutamine to imidazole-glycerolphosphate; 5-aminoimidazol-4-carboxamideribonucleotide and glutamate; the HisF subunit acts as a cyclase |
| NGO0212 | 0.9883 | -1.01 | down | 0.5968 | -1.23 | down | 0.8723 | 1.04 | up | 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase\ Context:(NC_002946)-[214844-215581]\ Notes:catalyzes the formation of 5-(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino-l- (5-phosphoribosyl)imidazole-4-carboxamide from 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0213 | 0.1644 | -2.04 | down | 0.1818 | -2.01 | down | 0.3163 | -1.63 | down | imidazole glycerol phosphate synthase subunit HisH\ Context:(NC_002946)-[215614-216252]\ Notes:with HisF IGPS catalyzes the conversion of phosphoribulosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide phosphate and glutamine to imidazole-glycerol phosphate; 5-aminoimidazol-4-carboxamide ribonucleotide; and glutamate in histidine biosynthesis; the HisH subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to HisF for the synthesis of imidazole-glycerol phosphate and 5-aminoimidazol-4-carboxamide ribonucleotide |
| NGO0214 | 0.8124 | -1.12 | down | 0.5077 | -1.37 | down | 0.5883 | -1.18 | down | putative phosphotransacetylase\ Context:(NC_002946)-[216382-217884]\ Notes:Best Blastp Hit: emb\|CAB84122.1\| (AL162754) putative phosphate acyltransferase [Neisseria meningitidis] COG0280 Phosphotransacetylase |
| NGO0215 | 0.0956 | 2.92 | up | 0.1078 | 5.94 | up | 0.0269 | 2.86 | up | ABC transporter; ATP-binding protein; iron related\ Context:(NC_002946)-[218069-219127]\ Notes:Best Blastp Hit: emb\|CAB84123.1\| (AL162754) putative iron-uptake permease ATP-binding protein [Neisseria meningitidis] COG1101 ATPase components of various transport; FbpC |
| NGO0216 | 0.0032 | 9.26 | up | 0.1079 | 5.89 | up | 0.0431 | 3.40 | up | ABC transporter; permease protein; iron related\ Context:(NC_002946)-[219148-220677]\ Notes:Best Blastp Hit: R] COG1081 Uncharacterized permeases |
| NGO0217 | 0.0388 | 5.24 | up | 0.0077 | 3.41 | up | 0.0185 | 4.05 | up | ABC transporter; periplasmic binding protein; iron related\ Context:(NC_002946)-[220733-221728]\ Notes:Best Blastp Hit: gb\|AAB63559.1\| (U33937) binds iron in a manner similar to transferrin; periplasmic iron-binding protein; Method: conceptual translation supplied by author [Neisseria gonorrhoeae] >gi\|1588872\|prf\|\|2209379A fbpA gene [Neisseria gonorrhoeae] COG1840 Thiamine-binding periplasmic proteins; FbpA |
| NGO0218 | 0.4096 | -1.58 | down | 0.5704 | -1.28 | down | 0.7171 | -1.15 | down | hypothetical protein\ Context:(NC_002946)-[222119-222460]\ Notes:Best Blastp Hit: pir\|\|A81175 hypothetical protein NMB0636 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225865\|gb\|AAF41059.1\| (AE002419) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0219 | 0.7285 | 1.24 | up | 0.8041 | 1.08 | up | 0.3637 | 1.60 | up | argininosuccinate lyase\ Context:(NC_002946)-[222518-223894]\ Notes:catalyzes the formation of arginine from (N-L-arginino)succinate |
| NGO0220 | 0.8729 | -1.08 | down | 0.8456 | -1.07 | down | 0.9203 | 1.03 | up | putative UTP--glucose-1-phosphate uridylyltransferase\ Context:(NC_002946)-[223913-224782]\ Notes:Best Blastp Hit: pir\|\|C81175 UTP--glucose-1-phosphate uridylyltransferase NMB0638 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225867\|gb\|AAF41061.1\| (AE002419) UTP--glucose-1-phosphate uridylyltransferase [Neisseria meningitidis MC58] COG1210 UDP-glucose pyrophosphorylase |
| NGO0221 | 0.0470 | -3.82 | down | 0.2558 | -1.64 | down | 0.2274 | -2.08 | down | putative deoxyribonucleotide triphosphate pyrophosphatase\ Context:(NC_002946)-[224810-225409]\ Notes:HAM1-like protein; Rec-dependent growth; RgdB; yggV; it is suspected that this protein functions to remove misincorporated bases such as xanthine or hypoxanthine |
| NGO0222 | 0.6589 | -1.29 | down | 0.8707 | -1.07 | down | 0.5166 | 1.18 | up | hypothetical protein\ Context:(NC_002946)-[225402-225635]\ Notes:Best Blastp Hit: gb\|AAF41063.1\| (AE002419) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0223 | 0.1697 | 2.06 | up | 0.3253 | 1.46 | up | 0.4693 | 1.28 | up | inorganic pyrophosphatase\ Context:(NC_002946)-[225743-226276]\ Notes:catalyzes the hydrolysis of pyrophosphate to phosphate |
| NGO0224 | 0.0289 | -3.34 | down | 0.2296 | -1.70 | down | 0.2475 | -1.47 | down | dATP pyrophosphohydrolase\ Context:(NC_002946)-[226378-226836]\ Notes:converts dATP to dAMP and pyrophosphate |
| NGO0225 | 0.6803 | 1.32 | up | 0.3684 | 1.33 | up | 0.9838 | -1.01 | down | MafB1\ Context:(NC_002946)+[227386-229272]\ Notes:Best Blastp Hit: gb\|AAF62313.1\| (AE002419) MafB-related protein [Neisseria meningitidis MC58]; putative MafB-like protein |
| NGO0226 | 0.5653 | 1.36 | up | 0.8987 | 1.06 | up | 0.4681 | -1.29 | down | hypothetical protein\ Context:(NC_002946)+[229300-229722]\ Notes:Best Blastp Hit: pir\|\|C81176 hypothetical protein NMB0648 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225875\|gb\|AAF41069.1\| (AE002419) hypothetical protein [Neisseria meningitidis MC58] |

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| NGO0227 | 0.6811 | 1.26 | up | 0.7498 | -1.14 | down | 0.3581 | -1.35 | down | hypothetical protein\ Context:(NC_002946)+[230200-230445]\ Notes:Best Blastp Hit: emb\|CAB84136.1\|(AL162754) hypothetical protein NMA0855 [Neisseria meningitidis] |
| NGO0228 | 0.8241 | -1.16 | down | 0.4078 | -1.49 | down | 0.3840 | -1.44 | down | hypothetical protein\ Context:(NC_002946)+[230448-230834]\ Notes:Best Blastp Hit: pir\|\|E81931 hypothetical protein NMA0857 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379573\|emb\|CAB84138.1\|(AL162754) hypothetical protein NMA0857 [Neisseria meningitidis] |
| NGO0229 | 0.1710 | -2.16 | down | 0.1337 | -2.01 | down | 0.1722 | -2.48 | down | hypothetical protein\ Context:(NC_002946)+[231055-231444]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO0230 | 0.0194 | 4.54 | up | 0.4108 | -1.84 | down | 0.5431 | -1.39 | down | putative transport protein; potassium\ Context:(NC_002946)-[231484-232941]\ Notes:Best Blastp Hit: pir\|\|G81931 probable transmembrane potassium transporter NMA0859 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379575\|emb\|CAB84140.1\|(AL162754) putative transmembrane potassium transporter [Neisseria meningitidis] COG0168 Potassium uptake system component TrkG |
| NGO0231 | 0.8161 | 1.11 | up | 0.8337 | -1.08 | down | 0.1533 | 1.50 | up | diadenosine tetraphosphatase\ Context:(NC_002946)-[232956-233786]\ Notes:hydrolyzes P(1);P(4)-bis(5'-adenosyl) tetraphosphate to form 2 ADP |
| NGO0232 | 0.0765 | 2.45 | up | 0.1586 | 1.59 | up | 0.1907 | 1.46 | up | hypothetical protein\ Context:(NC_002946)-[233863-234252]\ Notes:Best Blastp Hit: pir\|\|F81174 ribonuclease; probable NMB0662 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225887\|gb\|AAF41080.1\|(AE002420) ribonuclease; putative [Neisseria meningitidis MC58] COG0251 Putative translation initiation inhibitor |
| NGO0233 | 0.9091 | 1.08 | up | 0.9882 | -1.00 | down | 0.9668 | -1.02 | down | outer membrane protein\ Context:(NC_002946)-[234399-234926]\ Notes:Best Blastp Hit: gb\|AAB41581.1\| (U52069) outer membrane protein [Neisseria gonorrhoeae] |

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| NGO0234 | 0.2403 | 2.05 | up | 0.6198 | -1.59 | down | 0.5747 | 1.37 | up | coproporphyrinogen III oxidase\ Context:(NC_002946)-[235369-236544]\ Notes:catalyzes the oxygen-independent formation of protoporphyrinogen-IX from coproporphyrinogen-III |
| NGO0235 | 0.5487 | -1.48 | down | 0.3141 | -2.07 | down | 0.7192 | 1.41 | up | putative DNA ligase\ Context:(NC_002946)-[236601-239072]\ Notes:Best Blastp Hit: pir\|\|F81172 DNA ligase NMB0666 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225892\|gb\|AAF41084.1\| (AE002421) DNA ligase [Neisseria meningitidis MC58] COG0272 NAD-dependent DNA ligase (contains BRCT |
| NGO0236 | 0.1654 | 2.18 | up | 0.0195 | 4.53 | up | 0.0828 | 2.57 | up | hypothetical protein\ Context:(NC_002946)-[239206-240492]\ Notes:Best Blastp Hit: pir\|\|G81172 hypothetical protein NMB0667 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225893\|gb\|AAF41085.1\| (AE002421) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0237 | 0.0095 | -6.43 | down | 0.0083 | -16.59 | down | 0.0705 | -3.28 | down | N-acetyl-anhydromuranmyl-L-alanine amidase\ Context:(NC_002946)-[240686-241258]\ Notes:Best Blastp Hit: pir\|\|F81932 probable anhydro-N-acetylmuramyl-tripeptide amidase NMA0867 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379582\|emb\|CAB84147.1\| (AL162754) putative anhydro-N-acetylmuramyl-tripeptide amidase [Neisseria meningitidis] |
| NGO0238 | 0.4916 | -1.40 | down | 0.2692 | -1.81 | down | 0.2483 | -1.55 | down | hypothetical protein\ Context:(NC_002946)+[241342-242289]\ Notes:Best Blastp Hit: pir\|\|A81173 conserved hypothetical protein NMB0669 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225895\|gb\|AAF41087.1\| (AE002421) conserved hypothetical protein [Neisseria meningitidis MC58] COG1559 Uncharacterized BCR; YceG family |
| NGO0239 | 0.6812 | 1.24 | up | 0.9971 | -1.00 | down | 0.0263 | -2.41 | down | thymidylate kinase\ Context:(NC_002946)+[242398-243018]\ Notes:catalyzes the reversible phosphoryl transfer from adenosine triphosphate (ATP) to thymidine monophosphate (dTMP) to form thymidine diphosphate (dTDP) |

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| NGO0240 | 0.2744 | -1.80 | down | 0.2075 | -1.81 | down | 0.5652 | -1.22 | down | putative malic enzyme; malate dehydrogenase/oxaloacetate-decarboxylating\ Context:(NC_002946)+[243240-244520]\ Notes:Best Blastp Hit: pir\|\|A81933 probable malate dehydrogenase (oxaloacetate-decarboxylating) (EC 1.1.1.38) NMA0870 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379585\|emb\|CAB84150.1\| (AL162754) putative malate oxidoreductase [Neisseria meningitidis] COG0281 Malic enzyme |
| NGO0241 | 0.5726 | 1.33 | up | 0.6886 | 1.37 | up | 0.2238 | -1.68 | down | hypothetical protein\ Context:(NC_002946)+[244633-244836]\ Notes:Best Blastp Hit: emb\|CAB84151.1\| (AL162754) hypothetical protein NMA0871 [Neisseria meningitidis] |
| NGO0242 | 0.0038 | -11.53 | down | 0.0067 | -9.40 | down | 0.0806 | -3.27 | down | tetraacyldisaccharide 4'-kinase\ Context:(NC_002946)+[244922-245953]\ Notes:transfers the gamma-phosphate of ATP to the 4' position of a tetraacyldisaccharide 1-phosphate intermediate to form tetraacyldisaccharide 1;4'-bis-phosphate |
| NGO0243 | 0.8190 | -1.16 | down | 0.9597 | -1.02 | down | 0.2259 | -1.60 | down | hypothetical protein\ Context:(NC_002946)+[246159-246692]\ Notes:Best Blastp Hit: pir\|\|G81170 probable periplasmic protein NMA0873 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225900\|gb\|AAF41091.1\| (AE002422) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379588\|emb\|CAB84153.1\| (AL162754) putative periplasmic protein [Neisseria meningitidis] |
| NGO0244 | 0.7547 | 1.17 | up | 0.9414 | -1.03 | down | 0.5908 | -1.22 | down | hypothetical protein\ Context:(NC_002946)+[246914-247096]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO0245 | 0.8919 | -1.06 | down | 0.3337 | -1.55 | down | 0.6012 | -1.14 | down | 3-deoxy-manno-octulosonate cytidylyltransferase\ Context:(NC_002946)+[247093-247854]\ Notes:CMP-2-keto-3-deoxyoctulosonic acid synthetase; catalyzes the formation of CMP-3-deoxy-D-manno-octulosonate from CTP and 3-deoxy-D-manno-octulosonate which is incorporated into LPS |

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| NGO0246 | 0.9392 | -1.04 | down | 0.3412 | -1.37 | down | 0.6581 | -1.13 | down | hypothetical protein\ Context:(NC_002946)+[247877-248173]\ Notes:Best Blastp Hit: pir\|\|G81933 hypothetical protein NMA0876 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379591\|emb\|CAB84156.1\|(AL162754) hypothetical protein NMA0876 [Neisseria meningitidis] |
| NGO0247 | 0.0056 | -6.59 | down | 0.0055 | -3.36 | down | 0.0021 | -3.77 | down | hypothetical protein\ Context:(NC_002946)+[248228-248392]\ Notes:Best Blastp Hit: emb\|CAB84157.1\|(AL162754) hypothetical protein NMA0877 [Neisseria meningitidis] |
| NGO0248 | 0.3742 | -1.56 | down | 0.7941 | -1.14 | down | 0.1382 | -2.10 | down | tryptophan synthase subunit alpha\ Context:(NC_002946)+[248915-249700]\ Notes:catalyzes the formation of indole and glyceraldehyde 3-phosphate from indoleglycerol phosphate in tryptophan biosynthesis |
| NGO0249 | 0.6910 | -1.19 | down | 0.3200 | -1.66 | down | 0.1954 | -1.49 | down | acetyl-CoA carboxylase subunit beta\ Context:(NC_002946)+[249737-250609]\ Notes:catalyzes the carboxylation of acetyl-CoA to malonyl-CoA; forms a tetramer of AccA2D2 subunits |
| NGO0252 | 0.8282 | -1.18 | down | 0.3702 | 1.78 | up | 0.4884 | -1.30 | down | hypothetical protein\ Context:(NC_002946)+[251643-252029]\ Notes:Best Blastp Hit: pir\|\|F81934 probable lipoprotein NMA0883 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379598\|emb\|CAB84163.1\|(AL162754) putative lipoprotein [Neisseria meningitidis] |
| NGO0255 | 0.9076 | -1.06 | down | 0.0595 | -3.92 | down | 0.2539 | -1.85 | down | dihydroorotase\ Context:(NC_002946)+[253334-254368]\ Notes:catalyzes the formation of N-carbamoyl-L-aspartate from (S)-dihydroorotate in pyrimidine biosynthesis |
| NGO0256 | 0.0270 | -4.21 | down | 0.0189 | -4.07 | down | 0.4620 | -1.70 | down | transcription antitermination protein NusB\ Context:(NC_002946)-[254447-254872]\ Notes:Regulates rRNA biosynthesis by transcriptional antitermination |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0257 | 0.3264 | 1.86 | up | 0.4602 | 1.56 | up | 0.4939 | -1.22 | down | riboflavin synthase subunit beta\ Context:(NC_002946)-[254950-255426]\ Notes:RibE; 6;7-diimethyl-8-ribityllumazine synthase; DMRL synthase; lumazine synthase; beta subunit of riboflavin synthase; condenses 5-amino-6-(1'-D)-ribityl-amino-2;4(1H;3H)-pyrimidinedione with L-3;4-dihydrohy-2-butanone-4-phosphate to generate 6;6-dimethyl-8-lumazine (DMRL); riboflavin synthase then uses 2 molecules of DMRL to produce riboflavin (vitamin B12); involved in the last steps of riboflavin biosynthesis; forms a 60mer (icosahedral shell) in both Bacillus subtilis and Escherichia coli; in Bacillus subtilis this 60mer is associated with the riboflavin synthase subunit (alpha) while in Escherichia coli it is not |
| NGO0258 | 0.5266 | -1.39 | down | 0.0980 | -2.28 | down | 0.5644 | -1.21 | down | hypothetical protein\ Context:(NC_002946)-[255473-255796]\ Notes:Best Blastp Hit: pir\|\|C81172 hypothetical protein NMB0685 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225912\|gb\|AAF41103.1\|(AE002422) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0259 | 0.8666 | -1.12 | down | 0.5710 | -1.61 | down | 0.0004 | -6.27 | down | ribonuclease III\ Context:(NC_002946)+[255967-256686]\ Notes:cytoplasmic enzyme involved in processing rRNA and some mRNAs; substrates typically have dsRNA regions; forms a homodimer; have N-terminal nuclease and C-terminal RNA-binding domains; requires magnesium as preferred ion for activity; |
| NGO0260 | 0.0927 | 5.19 | up | 0.6817 | -1.61 | down | 0.2449 | -2.28 | down | GTP-binding protein Era\ Context:(NC_002946)+[256721-257656]\ Notes:Era; Escherichia coli Ras-like protein; Bex; Bacillus Era-complementing segment; essential protein in Escherichia coli that is involved in many cellular processes; GTPase; binds the cell membrane through apparent C-terminal domain; mutants are arrested during the cell cycle; Streptococcus pneumoniae Era binds to RNA and Escherichia coli Era binds 16S rRNA and 30S ribosome |
| NGO0261 | 0.0297 | -5.15 | down | 0.0001 | -36.92 | down | 0.0143 | -7.61 | down | N-(5'-phosphoribosyl)anthranilate isomerase\ Context:(NC_002946)-[260589-261215]\ Notes:catalyzes the formation of 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate from N-(5-phospho-beta-D-ribosyl)-anthranilate in tryptophan biosynthesis |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0262 | 0.1138 | -4.69 | down | 0.0251 | -2.98 | down | 0.3736 | -1.56 | down | transcription elongation factor GreB\ Context:(NC_002946)-[261274-261765]\ Notes:necessary for efficient RNA polymerase transcription elongation past template-encoded arresting sites; arresting sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that pass through; resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as GreA or GreB allows the resumption of elongation from the new 3'terminus |
| NGO0263 | 0.0300 | -4.69 | down | 0.0299 | -3.57 | down | 0.0151 | -2.31 | down | amidophosphoribosyltransferase\ Context:(NC_002946)-[261865-263409]\ Notes:Catalyzes first step of the de novo purine nucleotide biosynthetic pathway |
| NGO0264 | 0.0095 | 10.48 | up | 0.0404 | 12.25 | up | 0.1270 | 3.11 | up | putative bacteriocin production protein\ Context:(NC_002946)-[263603-264100]\ Notes:Best Blastp Hit: gb\|AAF62316.1\| (AE002423) colicin V production protein; putative [Neisseria meningitidis MC58] COG1286 Uncharacterized membrane protein; required |
| NGO0265 | 0.1656 | 1.90 | up | 0.0419 | 2.33 | up | 0.1761 | 1.50 | up | tetrapac protein\ Context:(NC_002946)-[264093-265133]\ Notes:Best Blastp Hit: emb\|CAA92429.1\| (Z68205) tpc [Neisseria gonorrhoeae] |
| NGO0266 | 0.8744 | -1.07 | down | 0.7366 | -1.17 | down | 0.5472 | -1.18 | down | putative folylpolyglutamate synthase/dihydrofolate synthase\ Context:(NC_002946)-[265147-266421]\ Notes:Best Blastp Hit: pir\|\|S63583 tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) / dihydrofolate synthase (EC 6.3.2.12) - Neisseria gonorrhoeae (strain MS11) >gi\|1237077\|emb\|CAA92428.1\| (Z68205) folC [Neisseria gonorrhoeae] COG0285 Folylpolyglutamate synthase |
| NGO0267 | 0.3374 | 1.56 | up | 0.9882 | -1.01 | down | 0.6304 | -1.14 | down | FolI\ Context:(NC_002946)-[266452-266892]\ Notes:Best Blastp Hit: pir\|\|S63582 folI protein - Neisseria gonorrhoeae (strain MS11) >gi\|1237076\|emb\|CAA92427.1\| (Z68205) folI [Neisseria gonorrhoeae]; putative folC transcriptional regulator |

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| NGO0268 | 0.6710 | -1.19 | down | 0.6509 | -1.23 | down | 0.2332 | -1.76 | down | hypothetical protein\ Context:(NC_002946)-[266897-267271]\ Notes:Best Blastp Hit: pir\|\|D81936 hypothetical protein NMA0899 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379612\|emb\|CAB84177.1\|(AL162754) hypothetical protein NMA0899 [Neisseria meningitidis] |
| NGO0269 | 0.7041 | 1.23 | up | 0.7622 | -1.15 | down | 0.8668 | -1.06 | down | putative ABC transporter; ATP-binding protein; amino acid\ Context:(NC_002946)-[267329-268057]\ Notes:Best Blastp Hit: pir\|\|E81936 probable amino acid permease ATP-binding protein NMA0900 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379613\|emb\|CAB84178.1\| (AL162754) putative amino acid permease ATP-binding protein [Neisseria meningitidis] COG1126 ABC-type polar amino acid transport system |
| NGO0270 | 0.8889 | 1.07 | up | 0.9195 | 1.04 | up | 0.2837 | -1.38 | down | hypothetical protein\ Context:(NC_002946)-[268099-268554]\ Notes: |
| NGO0271 | 0.5802 | 1.32 | up | 0.2180 | 1.65 | up | 0.8056 | -1.07 | down | hypothetical protein\ Context:(NC_002946)-[268665-269234]\ Notes: |
| NGO0272 | 0.3929 | 1.50 | up | 0.9962 | 1.00 | up | 0.8535 | 1.05 | up | dimethyladenosine transferase\ Context:(NC_002946)-[269249-270028]\ Notes:catalyzes the transfer of a total of four methyl groups from S-adenosyl-l-methionine (S-AdoMet) to two adjacent adenosine bases A1518 and A1519 in 16S rRNA; mutations in ksgA causes resistance to the translation initiation inhibitor kasugamycin |
| NGO0274 | 0.0334 | -4.74 | down | 0.1160 | -2.36 | down | 0.0475 | -2.69 | down | tryptophan synthase subunit beta\ Context:(NC_002946)+[271016-272218]\ Notes:catalyzes the formation of L-tryptophan from L-serine and 1-(indol-3-yl)glycerol 3-phosphate |
| NGO0275 | 0.0054 | 7.42 | up | 0.0591 | 4.25 | up | 0.1912 | 2.56 | up | IgA-specific metalloendopeptidase\ Context:(NC_002946)-[272294-277075]\ Notes:Best Blastp Hit: prf\|\|1303333A protease Ig A [Neisseria gonorrhoeae] |
| NGO0276 | 0.2559 | 2.30 | up | 0.8000 | -1.21 | down | 0.8891 | -1.07 | down | ComA\ Context:(NC_002946)+[277605-279680]\ Notes:Best Blastp Hit: sp\|P51973\|COMA_NEIGO competence protein ComA >gi\|481875\|pir\|\|S39867 competence protein comA - Neisseria gonorrhoeae >gi\|913748\|gb\|AAB32261.1\| (S75490) ComA=inner membrane protein [Neisseria gonorrhoeae; MS11; Peptide; 691 aa] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0277 | 0.5202 | 1.43 | up | 0.6474 | 1.21 | up | 0.5200 | 1.23 | up | ComL\ Context:(NC_002946)-[279750-280553]\ Notes:Best Blastp Hit: sp\|Q50985\|COML_NEIGO competence lipoprotein ComL precursor >gi\|2120876\|pir\|\|S71020 peptidoglycan-linked lipoprotein precursor - Neisseria gonorrhoeae >gi\|1107833\|emb\|CAA90076.1\| (Z49895) ComL; competence lipoprotein [Neisseria gonorrhoeae] >gi\|1588996\|prf\|\|2209423A lipoprotein [Neisseria gonorrhoeae] COG0457 TPR-repeat-containing proteins |
| NGO0278 | 0.1031 | 2.82 | up | 0.4588 | -1.34 | down | 0.3941 | -1.41 | down | RluD\ Context:(NC_002946)+[280552-281676]\ Notes:Best Blastp Hit: pir\|\|A81168 ribosomal large chain pseudouridine synthase D NMB0704 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225933\|gb\|AAF41121.1\| (AE002425) ribosomal large subunit pseudouridine synthase D [Neisseria meningitidis MC58] COG0564 Predicted pseudouridylate synthase family 2; putative ribosomal large subunit pseudouridine synthase D |
| NGO0280 | 0.4844 | 1.61 | up | 0.5500 | -1.65 | down | 0.6745 | -1.43 | down | hypothetical protein\ Context:(NC_002946)-[282855-283175]\ Notes: |
| NGO0281 | 0.3195 | 1.57 | up | 0.8178 | -1.12 | down | 0.6998 | -1.16 | down | hypothetical protein\ Context:(NC_002946)+[283231-284010]\ Notes:Best Blastp Hit: pir\|\|F81937 hypothetical protein NMA0911 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379622\|emb\|CAB84187.1\| (AL162754) hypothetical protein NMA0911 [Neisseria meningitidis] COG1496 Uncharacterized ACR; YfiH family |
| NGO0282 | 0.3130 | 1.70 | up | 0.5992 | 1.22 | up | 0.5453 | 1.19 | up | hypothetical protein\ Context:(NC_002946)+[284062-284541]\ Notes:Best Blastp Hit: emb\|CAB84188.1\| (AL162754) putative lipoprotein [Neisseria meningitidis] |
| NGO0283 | 0.3103 | 1.56 | up | 0.6284 | -1.22 | down | 0.8138 | -1.07 | down | DNA polymerase III subunit delta\ Context:(NC_002946)+[284543-285541]\ Notes:required for the assembly and function of the DNAX complex which is required for the assembly of the beta subunit onto primed DNA |

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| NGO0284 | 0.6630 | -1.26 | down | 0.2634 | -1.62 | down | 0.5543 | -1.24 | down | hypothetical protein\ Context:(NC_002946)+[285662-286081]\ Notes:Best Blastp Hit: pir\|\|A81938 probable membrane protein NMA0914 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379625\|emb\|CAB84190.1\| (AL162754) putative membrane protein [Neisseria meningitidis] >gi\|7413439\|gb\|AAF62317.1\| (AE002425) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0285 | 0.4256 | -2.01 | down | 0.0061 | -6.53 | down | 0.0014 | -3.65 | down | hypothetical protein\ Context:(NC_002946)+[286106-286672]\ Notes:Best Blastp Hit: gb\|AAF62318.1\| (AE002425) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0286 | 0.0575 | 2.73 | up | 0.3043 | 1.41 | up | 0.0833 | 2.04 | up | hypothetical protein\ Context:(NC_002946)-[286763-287647]\ Notes:Best Blastp Hit: pir\|\|F81168 conserved hypothetical protein NMB0711 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225938\|gb\|AAF41126.1\| (AE002425) conserved hypothetical protein [Neisseria meningitidis MC58] COG1561 Uncharacterized stress-induced protein; YicC |
| NGO0288 | 0.9272 | 1.05 | up | 0.8276 | -1.09 | down | 0.9645 | 1.01 | up | RNA polymerase factor sigma-32\ Context:(NC_002946)-[288380-289252]\ Notes:binds with the catalytic core of RNA polymerase to produce the holoenzyme; this sigma factor is responsible for the expression of heat shock promoters |
| NGO0289 | 0.7444 | 1.24 | up | 0.7974 | -1.21 | down | 0.3838 | -2.17 | down | apolipoprotein N-acyltransferase\ Context:(NC_002946)-[289507-291045]\ Notes:Transfers the fatty acyl group on membrane lipoproteins |
| NGO0290 | 0.6817 | 1.73 | up | 0.1399 | -9.24 | down | 0.2958 | -1.67 | down | hypothetical protein\ Context:(NC_002946)-[291115-291855]\ Notes:Best Blastp Hit: gb\|AAG05246.1\|AE004611_11 (AE004611) conserved hypothetical protein [Pseudomonas aeruginosa] |
| NGO0291 | 0.8917 | -1.06 | down | 0.1962 | -2.07 | down | 0.7375 | 1.10 | up | potassium/proton antiporter\ Context:(NC_002946)+[292059-293780]\ Notes:the Vibrio parahaemolyticus gene VP2867 was found to be a potassium/proton antiporter; can rapidly extrude potassium against a potassium gradient at alkaline pH when cloned and expressed in Escherichia coli |

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| NGO0292 | 0.0640 | -3.32 | down | 0.0708 | -2.76 | down | 0.3683 | -1.42 | down | hypothetical protein\ Context:(NC_002946)-[293777-294244]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO0293 | 0.8014 | 1.19 | up | 0.3169 | 2.33 | up | 0.4012 | 1.54 | up | HemZ\ Context:(NC_002946)-[294435-295445]\ Notes:Best Blastp Hit: emb\|CAB84199.1\| (AL162754) putative ferrochelatase [Neisseria meningitidis] COG0276 Protoheme ferro-lyase (ferrochelatase) |
| NGO0294 | 0.2296 | -1.95 | down | 0.9710 | -1.01 | down | 0.8907 | -1.04 | down | queuine tRNA-ribosyltransferase\ Context:(NC_002946)-[295527-296642]\ Notes:Exchanges the guanine residue with 7-aminomethyl-7-deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp; -Asn; -His and -Tyr) |
| NGO0295 | 0.2048 | 2.35 | up | 0.4913 | 1.31 | up | 0.5391 | 1.21 | up | putative threonyl-tRNA synthetase\ Context:(NC_002946)+[296950-298863]\ Notes:Best Blastp Hit: pir\|\|E81167 threonyl-tRNA synthetase NMB0720 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225946\|gb\|AAF41133.1\| (AE002426) threonyl-tRNA synthetase [Neisseria meningitidis MC58] COG0441 Threonyl-tRNA synthetase |
| NGO0296 | 0.0178 | 7.67 | up | 0.9322 | -1.06 | down | 0.2177 | 1.44 | up | translation initiation factor IF-3\ Context:(NC_002946)+[298881-299402]\ Notes:IF-3 has several functions that are required and promote translation initiation including; preventing association of 70S by binding to 30S; monitoring codon-anticodon interactions by promoting disassociation of fMet-tRNA(fMet) from initiation complexes formed on leaderless mRNAs or incorrectly bound noninitiatior tRNAs and complexes with noncanonical start sites; stimulates codon-anticodon interactions at P-site; involved in moving mRNA to the P-site; and in recycling subunits |

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| NGO0297 | 0.0619 | 3.40 | up | 0.3690 | 1.44 | up | 0.4601 | 1.36 | up | 50S ribosomal protein L35\ Context:(NC_002946)+[299549-299746]\ Notes:Best Blastp Hit: pir\|\|E81165 50S ribosomal protein L35 NMB0722 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225949\|gb\|AAF41135.1\| (AE002427) 50S ribosomal protein L35 [Neisseria meningitidis MC58] >gi\|7379636\|emb\|CAB84203.1\| (AL162754) putative 50S ribosomal protein L35 [Neisseria meningitidis] COG0291 Ribosomal protein L35 |
| NGO0298 | 0.0797 | 3.09 | up | 0.3109 | 1.59 | up | 0.2145 | 1.51 | up | 50S ribosomal protein L20\ Context:(NC_002946)+[299759-300118]\ Notes:binds directly to 23S ribosomal RNA prior to in vitro assembly of the 50S ribosomal subunit |
| NGO0299 | 0.3583 | 1.87 | up | 0.9523 | -1.02 | down | 0.3998 | -1.58 | down | phenylalanyl-tRNA synthetase subunit alpha\ Context:(NC_002946)+[300359-301348]\ Notes:catalyzes a two-step reaction; first charging a phenylalanine molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA; forms a heterotetramer of alpha(2)beta(2); binds two magnesium ions per tetramer; type 1 subfamily |
| NGO0300 | 0.5959 | -1.26 | down | 0.9665 | 1.02 | up | 0.6009 | -1.17 | down | putative very-short-patch-repair endonuclease\ Context:(NC_002946)+[301365-301778]\ Notes:Best Blastp Hit: emb\|CAB59896.1\| (AJ238948) putative very short patch repair endonuclease [Neisseria meningitidis] |
| NGO0302 | 0.2693 | 1.78 | up | 0.5749 | 1.30 | up | 0.4381 | 1.28 | up | hypothetical protein\ Context:(NC_002946)+[302132-302377]\ Notes: |
| NGO0303 | 0.2676 | 2.03 | up | 0.5715 | 1.22 | up | 0.9969 | -1.00 | down | hypothetical protein\ Context:(NC_002946)+[302383-303132]\ Notes:Best Blastp Hit: gb\|AAD19409.1\| (AF102543) unknown [Zymomonas mobilis] |
| NGO0304 | 0.9513 | 1.03 | up | 0.1792 | -2.01 | down | 0.5967 | -1.24 | down | phenylalanyl-tRNA synthetase subunit beta\ Context:(NC_002946)+[303223-305586]\ Notes:catalyzes a two-step reaction; first charging a phenylalanine molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA; forms a tetramer of alpha(2)beta(2); binds two magnesium ions per tetramer; type 2 subfamily |

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| NGO0305 | 0.1816 | 2.26 | up | 0.1809 | 1.66 | up | 0.1410 | 1.84 | up | IfhA\ Context:(NC_002946)+[305660-305962]\ Notes:Best Blastp Hit: pir\|\|D81166 integration host factor; alpha chain NMB0729 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225956\|gb\|AAF41142.1\| (AE002427) integration host factor; alpha subunit [Neisseria meningitidis MC58] >gi\|7379642\|emb\|CAB84209.1\| (AL162754) putative integration host factor alpha-subunit [Neisseria meningitidis] COG0776 Histone-like DNA-binding protein; integration host factor alpha subunit |
| NGO0306 | 0.3764 | 1.57 | up | 0.4138 | 1.38 | up | 0.5153 | 1.22 | up | hypothetical protein\ Context:(NC_002946)+[305946-306254]\ Notes:Best Blastp Hit: emb\|CAB84210.1\| (AL162754) hypothetical protein NMA0939 [Neisseria meningitidis] |
| NGO0307 | 0.8507 | -1.09 | down | 0.0847 | -2.93 | down | 0.6908 | 1.31 | up | FxsA\ Context:(NC_002946)+[306430-306915]\ Notes:F exclusion of bacteriophage T7; overproduction of this protein in Escherichia coli inhibits the F plasmid-mediated exclusion of bacteriophage T7; interacts with the F plasmid-encoded PifA protein; inner membrane protein |
| NGO0308 | 0.0078 | -7.26 | down | 0.0025 | -20.60 | down | 0.1902 | -2.56 | down | putative adenosylmethionine-8-amino-7-oxononanoate aminotranferase\ Context:(NC_002946)+[307549-308850]\ Notes:Best Blastp Hit: pir\|\|D81164 adenosylmethionine-8-amino-7-oxononanoate aminotransferase NMB0732 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225960\|gb\|AAF41145.1\| (AE002428) adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Neisseria meningitidis MC58] COG0161 Adenosylmethionine-8-amino-7-oxononanoate |
| NGO0309 | 0.2318 | -1.92 | down | 0.0039 | -11.97 | down | 0.1568 | -2.17 | down | dithiobiotin synthetase\ Context:(NC_002946)+[308847-309494]\ Notes:DTB synthetase; dethiobiotin synthase; involved in production of dethiobiotin from ATP and 7;8-diaminononanoate and carbon dioxide; contains magnesium |

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| NGO0310 | 0.5932 | 1.36 | up | 0.4133 | -2.30 | down | 0.2101 | -2.37 | down | hypothetical protein\ Context:(NC_002946)+[309428-309985]\ Notes:Best Blastp Hit: pir\|\|H81940 hypothetical protein NMA0944 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379648\|emb\|CAB84215.1\|(AL162754) hypothetical protein NMA0944 [Neisseria meningitidis] |
| NGO0311 | 0.5344 | -1.59 | down | 0.8169 | -1.20 | down | 0.6206 | -1.86 | down | hypothetical protein\ Context:(NC_002946)+[310109-310516]\ Notes: |
| NGO0312 | 0.4534 | -1.40 | down | 0.2957 | -1.83 | down | 0.8307 | 1.07 | up | 4-hydroxybenzoate octaprenyltransferase\ Context:(NC_002946)+[310506-311396]\ Notes:catalyzes the conversion of 4-Hydroxybenzoate into 3-octaprenyl-4-hydroxybenzoate; as part of the ubiquinone biosynthesis pathway |
| NGO0313 | 0.5806 | 1.34 | up | 0.7948 | 1.11 | up | 0.8872 | 1.05 | up | putative two-component system transcriptional response regulator\ Context:(NC_002946)+[311581-312030]\ Notes:Best Blastp Hit: pir\|\|B81941 probable regulatory protein NMA0946 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379650\|emb\|CAB84217.1\|(AL162754) putative regulatory protein [Neisseria meningitidis] COG1762 Phosphotransferase system |
| NGO0314 | 0.5626 | 1.30 | up | 0.7059 | 1.16 | up | 0.9118 | 1.03 | up | HPr kinase/phosphorylase\ Context:(NC_002946)+[312034-312996]\ Notes:catalyzes the phosphorylation of the phosphocarrier protein HPr of the bacterial phosphotransferase system |
| NGO0315 | 0.3608 | 1.52 | up | 0.9443 | -1.03 | down | 0.7168 | 1.10 | up | hypothetical protein\ Context:(NC_002946)+[312977-313831]\ Notes:Best Blastp Hit: pir\|\|D81941 hypothetical protein NMA0948 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379652\|emb\|CAB84219.1\|(AL162754) hypothetical protein NMA0948 [Neisseria meningitidis] COG1660 Uncharacterized BCR; YhbJ/UPF0042 family |
| NGO0316 | 0.8406 | 1.10 | up | 0.4519 | 1.51 | up | 0.5940 | -1.35 | down | ribosomal biogenesis GTPase\ Context:(NC_002946)+[313912-314853]\ Notes:essential GTPase; functions in ribosome assembly; binds a unique part of the 23S rRNA; interacts with ribosomal protein L25(Ctc) |

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| NGO0317 | 0.6132 | 1.46 | up | 0.1278 | 3.08 | up | 0.8709 | 1.09 | up | hypothetical protein\ Context:(NC_002946)+[314954-315556]\ Notes:Best Blastp Hit: pir\|\|F81941 hypothetical protein NMA0951 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379654\|emb\|CAB84221.1\|(AL162754) hypothetical protein NMA0951 [Neisseria meningitidis] COG1386 Uncharacterized ACR |
| NGO0318 | 0.5538 | 1.42 | up | 0.0194 | -2.59 | down | 0.4106 | -1.27 | down | hypothetical protein\ Context:(NC_002946)+[315740-317413]\ Notes:Best Blastp Hit: pir\|\|D81165 DNA repair protein RecN NMB0740 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225968\|gb\|AAF41153.1\|(AE002428) DNA repair protein RecN [Neisseria meningitidis MC58] COG0497 ATPases involved in DNA repair |
| NGO0319 | 0.0029 | -9.59 | down | 0.1448 | -5.76 | down | 0.8788 | -1.13 | down | hypothetical protein\ Context:(NC_002946)-[318158-319777]\ Notes:Best Blastp Hit: emb\|CAB84224.1\|(AL162754) hypothetical protein NMA0954 [Neisseria meningitidis] COG0500 SAM-dependent methyltransferases |
| NGO0320 | 0.8869 | -1.07 | down | 0.9648 | -1.02 | down | 0.9562 | -1.02 | down | hypothetical protein\ Context:(NC_002946)+[319873-320265]\ Notes:Best Blastp Hit: pir\|\|B81942 hypothetical protein NMA0955 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379658\|emb\|CAB84225.1\|(AL162754) hypothetical protein NMA0955 [Neisseria meningitidis] |
| NGO0321 | 0.6154 | 1.27 | up | 0.9824 | 1.01 | up | 0.7221 | -1.10 | down | ubiquinone/menaquinone biosynthesis methyltransferase\ Context:(NC_002946)+[320308-321045]\ Notes:Catalyzes the carbon methylation reaction in the biosynthesis of ubiquinone |
| NGO0322 | 0.0107 | 6.81 | up | 0.0199 | 4.67 | up | 0.0095 | 4.03 | up | hypothetical protein\ Context:(NC_002946)+[321265-321744]\ Notes:Best Blastp Hit: pir\|\|G81162 hypothetical protein NMB0744 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225973\|gb\|AAF41157.1\|(AE002429) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0323 | 0.0006 | -10.21 | down | 0.0125 | -6.67 | down | 0.0299 | -5.32 | down | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine-pyrophosphokinase\ Context:(NC_002946)-[321872-322366]\ Notes:Best Blastp Hit: H]COG08017; 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0324 | 0.0249 | -4.58 | down | 0.0050 | -6.08 | down | 0.0765 | -3.47 | down | hypothetical protein\ Context:(NC_002946)-[322376-322750]\ Notes:Best Blastp Hit: pir\|\|A81163 conserved hypothetical protein NMB0746 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225975\|gb\|AAF41159.1\| (AE002429) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0326 | 0.4716 | 1.57 | up | 0.8977 | 1.05 | up | 0.8616 | 1.06 | up | hypothetical protein\ Context:(NC_002946)-[323455-323748]\ Notes:Best Blastp Hit: pir\|\|C81163 host factor-I NMB0748 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225977\|gb\|AAF41161.1\| (AE002429) host factor-I [Neisseria meningitidis MC58] >gi\|7379664\|emb\|CAB84231.1\| (AL162754) putative regulator [Neisseria meningitidis] COG1923 Uncharacterized ACR; host factor I protein |
| NGO0327 | 0.3706 | 1.54 | up | 0.8963 | 1.05 | up | 0.3437 | 1.33 | up | putative D-alanyl-D-alanine-endopeptidase\ Context:(NC_002946)-[323877-324815]\ Notes:Best Blastp Hit: gb\|AAD38860.1\|AF156692_1 (AF156692) penicillin-binding protein 4 [Neisseria gonorrhoeae] COG1686 D-alanyl-D-alanine carboxypeptidase |
| NGO0328 | 0.7993 | 1.14 | up | 0.8617 | -1.07 | down | 0.8526 | -1.05 | down | hypothetical protein\ Context:(NC_002946)+[325073-325576]\ Notes:Best Blastp Hit: pir\|\|B81943 hypothetical protein NMA0963 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379666\|emb\|CAB84233.1\| (AL162754) hypothetical protein NMA0963 [Neisseria meningitidis] COG12 25 Peroxiredoxins |
| NGO0329 | 0.4717 | -1.84 | down | 0.6825 | -1.19 | down | 0.0457 | -2.92 | down | hypothetical protein\ Context:(NC_002946)+[325628-326503]\ Notes:Best Blastp Hit: pir\|\|F81163 integrase/recombinase XerD NMB0751 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225980\|gb\|AAF41164.1\| (AE002429) integrase/recombinase XerD [Neisseria meningitidis MC58] COG0582 Integrase |
| NGO0330 | 0.2644 | -2.15 | down | 0.0920 | -7.00 | down | 0.0428 | 6.38 | up | hypothetical protein\ Context:(NC_002946)-[326609-326962]\ Notes:Best Blastp Hit: >pir\|\|B81163 conserved hypothetical protein NMB0747 [imported] - Neisseria meningitidis (group B strain MD58) gb\|AAF41160.1\| (AE002429) conserved hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0331 | 0.0870 | 5.18 | up | 0.1395 | 4.39 | up | 0.7629 | -1.15 | down | hypothetical protein\ Context:(NC_002946)+[327041-327274]\ Notes:Best Blastp Hit: >pir\|\|B81163 conserved hypothetical protein NMB0747 [imported] - Neisseria meningitidis (group B strain MD58) gb\|AAF41160.1\|(AE002429) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0332 | 0.0336 | -3.43 | down | 0.1470 | -2.17 | down | 0.2141 | -2.04 | down | putative reductase\ Context:(NC_002946)-[327646-328509]\ Notes:Best Blastp Hit: pir\|\|F81943 probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133) NMA0967 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379670\|emb\|CAB84237.1\| (AL162754) putative dTDP-4-dehydrorhamnose reductase [Neisseria meningitidis] COG1091 dTDP-4-dehydrorhamnose reductase |
| NGO0333 | 0.5644 | -1.39 | down | 0.0381 | -3.38 | down | 0.1434 | -2.10 | down | phosphoribosylaminoimidazole-succinocarboxamidesynthase\ Context:(NC_002946)+[328606-329565]\ Notes:catalyzes the formation of (S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4- carboxamido)succinate from 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate and L-aspartate in purine biosynthesis; SAICAR synthase |
| NGO0335 | 0.3138 | 1.64 | up | 0.1573 | 1.63 | up | 0.0967 | 2.42 | up | polynucleotide phosphorylase/polyadenylase\ Context:(NC_002946)+[329799-331922]\ Notes:Best Blastp Hit: pir\|\|C81161 polyribonucleotide nucleotidyltransferase NMB0758 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225988\|gb\|AAF41171.1\| (AE002430) polyribonucleotide nucleotidyltransferase [Neisseria meningitidis MC58] COG1185 Polyribonucleotide nucleotidyltransferase |
| NGO0336 | 0.6955 | 1.22 | up | 0.0252 | -2.92 | down | 0.2606 | -2.42 | down | hypothetical protein\ Context:(NC_002946)-[331995-332663]\ Notes:Best Blastp Hit: pir\|\|D81161 conserved hypothetical protein NMB0759 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225989\|gb\|AAF41172.1\| (AE002430) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0337 | 0.2805 | -2.34 | down | 0.5353 | -2.70 | down | 0.2491 | -2.75 | down | hypothetical protein\ Context:(NC_002946)-[332660-332974]\ Notes:Best Blastp Hit: emb\|CAB84241.1\|(AL162754) putative lipoprotein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0338 | 0.6087 | 1.37 | up | 0.5274 | 1.35 | up | 0.5471 | -1.19 | down | diaminopimelate epimerase\ Context:(NC_002946)+[333111-333962]\ Notes:involved in lysine biosynthesis; DAP epimerase; produces DL-diaminopimelate from LL-diaminopimelate |
| NGO0339 | 0.0173 | -3.48 | down | 0.0341 | -2.48 | down | 0.0818 | -3.50 | down | hypothetical protein\ Context:(NC_002946)+[333959-334564]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) |
| NGO0340 | 0.2185 | 1.96 | up | 0.3520 | 1.54 | up | 0.4293 | 1.33 | up | putative cysteine synthase/cystathionine beta-synthase\ Context:(NC_002946)+[334760-335692]\ Notes:Best Blastp Hit: confirmed inframe stop |
| NGO0342 | 0.5350 | 1.99 | up | 0.1538 | -2.93 | down | 0.0424 | -2.40 | down | hypothetical protein\ Context:(NC_002946)+[337103-337339]\ Notes:Best Blastp Hit: pir\|\|T30271 surface protein - fluke (Schistosoma mansoni) (fragment) >gi\|501209\|gb\|AAA73556.1\| (M99494) surface protein [Schistosoma mansoni] |
| NGO0343 | 0.5677 | 1.31 | up | 0.9225 | -1.06 | down | 0.9534 | 1.03 | up | Lep\ Context:(NC_002946)-[337539-338558]\ Notes:Best Blastp Hit: gb\|AAF41178.1\| (AE002430) signal peptidase I [Neisseria meningitidis MC58] COG0681 Signal peptidase I; putative signal peptidase I |
| NGO0344 | 0.1143 | 2.54 | up | 0.0532 | 2.32 | up | 0.1670 | 1.52 | up | GTP-binding protein LepA\ Context:(NC_002946)-[338704-340497]\ Notes:binds to the ribosome on the universally-conserved alpha-sarcin loop |
| NGO0345 | 0.0907 | 2.22 | up | 0.4228 | 1.31 | up | 0.5882 | 1.16 | up | putative nucleoside phosphorylase\ Context:(NC_002946)-[340639-341340]\ Notes:Best Blastp Hit: pir\|\|D81159 5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase NMB0767 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225998\|gb\|AAF41180.1\| (AE002431) 5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase [Neisseria meningitidis MC58] COG0775 Nucleoside phosphorylase |
| NGO0346 | 0.5815 | 1.34 | up | 0.6650 | 1.18 | up | 0.9772 | 1.01 | up | putative twitching motility-like protein\ Context:(NC_002946)+[341526-342638]\ Notes:Best Blastp Hit: pir\|\|B81945 probable pilus retraction protein NMA0979 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379682\|emb\|CAB84249.1\| (AL162754) putative pilus retraction protein [Neisseria meningitidis] COG0630 Predicted ATPases involved in pili |

<table>
<tr><td>NGO0347</td><td>0.3205</td><td>1.65</td><td>up</td><td>0.1305</td><td>1.75</td><td>up</td><td>0.7701</td><td>1.09</td><td>up</td><td>DNA polymerase III subunit delta'\ Context:(NC_002946)+[342672-343649]\ Notes:catalyzes the DNA-template-directed extension of the 3'-end of a DNA strand; the delta' subunit seems to interact with the gamma subunit to transfer the beta subunit on the DNA</td></tr>
<tr><td>NGO0348</td><td>0.1748</td><td>1.95</td><td>up</td><td>0.0610</td><td>2.36</td><td>up</td><td>0.4586</td><td>1.31</td><td>up</td><td>putative type 4 pilus biogenesis protein\ Context:(NC_002946)+[343653-344003]\ Notes:Best Blastp Hit: pir||D81945 probable pilus biogenesis protein NMA0981 [imported] - Neisseria meningitidis (group A strain Z2491) >gi|7379684|emb|CAB84251.1| (AL162754) putative pilus biogenesis protein [Neisseria meningitidis]</td></tr>
<tr><td>NGO0349</td><td>0.2339</td><td>1.83</td><td>up</td><td>0.3722</td><td>1.40</td><td>up</td><td>0.5814</td><td>1.19</td><td>up</td><td>hypothetical protein\ Context:(NC_002946)+[344008-344787]\ Notes:Best Blastp Hit: pir||E81945 hypothetical protein NMA0982 [imported] - Neisseria meningitidis (group A strain Z2491) >gi|7379685|emb|CAB84252.1| (AL162754) hypothetical protein NMA0982 [Neisseria meningitidis] COG0084 Predicted hydrolases of PHP superfamily</td></tr>
<tr><td>NGO0350</td><td>0.5168</td><td>1.34</td><td>up</td><td>0.2339</td><td>1.47</td><td>up</td><td>0.6893</td><td>-1.12</td><td>down</td><td>hypothetical protein\ Context:(NC_002946)+[344813-345028]\ Notes:Best Blastp Hit: gb|AAF41185.1| (AE002431) conserved hypothetical protein [Neisseria meningitidis MC58]</td></tr>
<tr><td>NGO0351</td><td>0.2069</td><td>1.81</td><td>up</td><td>0.4997</td><td>-1.54</td><td>down</td><td>0.6437</td><td>1.15</td><td>up</td><td>glutaredoxin-like protein GrlA\ Context:(NC_002946)+[345129-345440]\ Notes:Best Blastp Hit: pir||B81160 conserved hypothetical protein NMB0773 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi|7226004|gb|AAF41186.1| (AE002431) conserved hypothetical protein [Neisseria meningitidis MC58] >gi|7379687|emb|CAB84254.1| (AL162754) hypothetical protein NMA0984 [Neisseria meningitidis] COG0278 Glutaredoxin-related proteins</td></tr>
<tr><td>NGO0352</td><td>0.2755</td><td>1.75</td><td>up</td><td>0.9201</td><td>-1.04</td><td>down</td><td>0.7956</td><td>1.07</td><td>up</td><td>hypothetical protein\ Context:(NC_002946)+[345440-345556]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON)</td></tr>
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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0353 | 0.3870 | 1.59 | up | 0.9293 | -1.04 | down | 0.9351 | -1.03 | down | uracil phosphoribosyltransferase\ Context:(NC_002946)+[345546-346172]\ Notes:Catalyzes the formation of uracil and 5-phospho-alpha-D-ribosy 1-diphosphate from UMP and diphosphate |
| NGO0354 | 0.2317 | 1.85 | up | 0.7644 | 1.10 | up | 0.6601 | -1.12 | down | hypothetical protein\ Context:(NC_002946)+[346195-346515]\ Notes:Best Blastp Hit: pir\|\|D81160 hypothetical protein NMB0775 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226006\|gb\|AAF41188.1\|(AE002431) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0356 | 0.0318 | -3.02 | down | 0.5772 | -1.21 | down | 0.1656 | -2.13 | down | hypothetical protein\ Context:(NC_002946)+[347355-348179]\ Notes:Best Blastp Hit: sp\|Q07605\|T4BA_BACCO restriction enzyme BGCI alpha subunit [includes: adenine-specific methyltransferase activity ] >gi\|1075788\|pir\|\|A53125 restriction enzyme BcgI alpha chain - Bacillus coagulans >gi\|304140\|gb\|AAA16626.1\|(L17341) restriction endonuclease alpha subunit [Bacillus coagulans] COG0286 Type I restriction-modification system |
| NGO0357 | 0.6344 | -1.23 | down | 0.4156 | 1.31 | up | 0.1378 | -1.71 | down | hypothetical protein\ Context:(NC_002946)+[348179-349147]\ Notes:Best Blastp Hit: sp\|Q07606\|T4BB_BACCO restriction enzyme BGCI beta subunit >gi\|1075789\|pir\|\|B53125 restriction enzyme BcgI beta chain - Bacillus coagulans >gi\|304141\|gb\|AAA16627.1\|(L17341) restriction endonuclease beta subunit [Bacillus coagulans] |
| NGO0358 | 0.1850 | 1.82 | up | 0.4615 | 1.30 | up | 0.2590 | 1.41 | up | hypothetical protein\ Context:(NC_002946)+[349426-349851]\ Notes:Best Blastp Hit: gb\|AAD13642.1\|(AF003941) Gly1ORF1 [Neisseria gonorrhoeae] |
| NGO0359 | 0.9610 | -1.03 | down | 0.7416 | 1.18 | up | 0.4451 | -1.32 | down | uroporphyrinogen-III synthase\ Context:(NC_002946)+[349869-350633]\ Notes:catalyzes the formation of uroporphyrinogen-III from hydroxymethylbilane; functions in tetrapyrrole and heme biosynthesis |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0360 | 0.7519 | 1.16 | up | 0.0741 | 2.30 | up | 0.7434 | 1.16 | up | hypothetical protein\ Context:(NC_002946)+[350705-351979]\ Notes:Best Blastp Hit: pir\|\|G81160 uroporphyrin-III C-methyltransferase HemX; probable NMB0778 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226009\|gb\|AAF41191.1\| (AE002431) uroporphyrin-III C-methyltransferase HemX; putative [Neisseria meningitidis MC58] |
| NGO0361 | 0.0436 | 2.81 | up | 0.0668 | 4.51 | up | 0.1498 | 1.77 | up | hypothetical protein\ Context:(NC_002946)+[351976-353193]\ Notes:Best Blastp Hit: pir\|\|E81946 hypothetical protein NMA0990 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379693\|emb\|CAB84260.1\| (AL162754) hypothetical protein NMA0990 [Neisseria meningitidis] |
| NGO0362 | 0.0234 | 3.59 | up | 0.0742 | 2.66 | up | 0.4896 | 1.53 | up | putative uroporphyrinogen decarboxylase\ Context:(NC_002946)+[353268-354332]\ Notes:Best Blastp Hit: pir\|\|F81946 probable uroporphyrinogen decarboxylase (EC 4.1.1.37) NMA0991 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379694\|emb\|CAB84261.1\| (AL162754) putative uroporphyrinogen decarboxylase [Neisseria meningitidis] COG0407 Uroporphyrinogen-III decarboxylase |
| NGO0363 | 0.0271 | -6.89 | down | 0.3727 | -2.87 | down | 0.4533 | 1.63 | up | putative stress-sensitive restriction system protein\ Context:(NC_002946)-[354395-356284]\ Notes:Best Blastp Hit: pir\|\|B55225 stress-sensitive restriction system protein 2 - Corynebacterium glutamicum (ATCC 13032) >gi\|549844\|gb\|AAC00044.1\| (U13922) This orf may encode a typeI or typeIII restriction endonuclease which is stress-sensitive and ATP-dependent. It contains a typical ATP binding region (Walker motif) [Corynebacterium glutamicum] |
| NGO0364 | 0.1664 | -4.90 | down | 0.0562 | -7.41 | down | 0.7878 | 1.20 | up | restriction endonuclease R.NgoVII\ Context:(NC_002946)-[356285-357322]\ Notes:Best Blastp Hit: pir\|\|T10166 restriction endonuclease (EC 3.1.21.-) NgoVII - Neisseria gonorrhoeae >gi\|1165246\|gb\|AAA86271.1\| (U43736) R.NgoVII [Neisseria gonorrhoeae] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0365 | 0.3342 | -4.48 | down | 0.0130 | -62.89 | down | 0.9117 | -1.08 | down | site-specific DNA-methyltransferase M.NgoVII\ Context:(NC_002946)-[357319-358443]\ Notes:Best Blastp Hit: pir\|\|T10165 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) NgoVII - Neisseria gonorrhoeae >gi\|1165245\|gb\|AAA86270.1\| (U43736) M.NgoVII [Neisseria gonorrhoeae] COG0270 Site-specific DNA methylase dcm |
| NGO0366 | 0.1637 | -2.73 | down | 0.0570 | -4.26 | down | 0.3780 | 1.97 | up | hypothetical protein\ Context:(NC_002946)+[358468-358725]\ Notes:Best Blastp Hit: possibly phase variable - 22 tandem repeats of AACGC in the coding sequence (ON) |
| NGO0367 | 0.5670 | -1.28 | down | 0.2234 | -2.03 | down | 0.0590 | -2.46 | down | DNA repair protein RadA\ Context:(NC_002946)+[358830-360209]\ Notes:Sms; stabilizes the strand-invasion intermediate during the DNA repair; involved in recombination of donor DNA and plays an important role in DNA damage repair after exposure to mutagenic agents |
| NGO0368 | 0.3940 | -1.98 | down | 0.5235 | 1.92 | up | 0.3161 | 2.42 | up | hypothetical protein\ Context:(NC_002946)-[360484-360864]\ Notes:Best Blastp Hit: pir\|\|D81158 conserved hypothetical protein NMB0783 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226015\|gb\|AAF41196.1\| (AE002432) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0369 | 0.4963 | 1.67 | up | 0.1854 | 1.55 | up | 0.2413 | 2.08 | up | hypothetical protein\ Context:(NC_002946)-[361088-361531]\ Notes:Best Blastp Hit: emb\|CAB84264.1\| (AL162754) putative periplasmic protein [Neisseria meningitidis] COG0607 Rhodanese-related sulfurtransferases |
| NGO0370 | 0.1909 | -3.10 | down | 0.2255 | -3.07 | down | 0.8161 | -1.15 | down | putative exodeoxyribonuclease\ Context:(NC_002946)-[361486-365088]\ Notes:Best Blastp Hit: pir\|\|F81158 exodeoxyribonuclease V 135 KD polypeptide NMB0785 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226017\|gb\|AAF41198.1\| (AE002432) exodeoxyribonuclease V 135 KD polypeptide [Neisseria meningitidis MC58] COG1074 ATP-dependent exo DNAse (exonuclease V) |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0371 | 0.0199 | -4.94 | down | 0.0871 | -2.43 | down | 0.1433 | -2.05 | down | hypothetical protein\ Context:(NC_002946)-[365165-366073]\ Notes:Best Blastp Hit: pir\|\|G81158 conserved hypothetical protein NMB0786 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226018\|gb\|AAF41199.1\| (AE002432) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0372 | 0.2896 | 1.79 | up | 0.4911 | 1.35 | up | 0.4910 | 1.24 | up | putative ABC transporter; periplasmic binding protein; amino acid\ Context:(NC_002946)+[366358-367185]\ Notes:Best Blastp Hit: pir\|\|H81158 amino acid ABC transporter; periplasmic amino acid-binding protein NMB0787 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226019\|gb\|AAF41200.1\| (AE002432) amino acid ABC transporter; periplasmic amino acid-binding protein [Neisseria meningitidis MC58] COG0834 Periplasmic amino acid binding proteins |
| NGO0373 | 0.5785 | 1.57 | up | 0.0747 | 2.93 | up | 0.3382 | -1.64 | down | putative ABC transporter; permease protein; amino acid\ Context:(NC_002946)+[367175-367891]\ Notes:Best Blastp Hit: pir\|\|E81947 probable amino acid permease integral membrane protein NMA0999 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379701\|emb\|CAB84268.1\| (AL162754) putative amino acid permease integral membrane protein [Neisseria meningitidis] COG0765 Amino acid ABC transporter permease |
| NGO0374 | 0.2672 | 2.05 | up | 0.0191 | 2.56 | up | 0.4749 | 1.26 | up | putative ABC transporter; ATP-binding protein; amino acid\ Context:(NC_002946)+[367901-368656]\ Notes:Best Blastp Hit: pir\|\|F81947 probable amino acid permease ATP-binding protein NMA1000 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379702\|emb\|CAB84269.1\| (AL162754) putative amino acid permease ATP-binding protein [Neisseria meningitidis] COG1126 ABC-type polar amino acid transport system |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0375 | 0.3588 | 1.69 | up | 0.2253 | 3.60 | up | 0.4799 | 1.38 | up | Pgm\ Context:(NC_002946)-[368712-370094]\ Notes:Best Blastp Hit: sp\|P40390\|PGMU_NEIGO phosphoglucomutase (glucose phosphomutase) (PGM) >gi\|1073189\|pir\|\|A53614 phosphoglucomutase (EC 5.4.2.2) - Neisseria gonorrhoeae (strain 1291) >gi\|414527\|gb\|AAA20588.1\| (U02489) phosphoglucomutase [Neisseria gonorrhoeae] >gi\|452116\|gb\|AAA20399.1\| (L23426) phosphoglucomutase [Neisseria gonorrhoeae] COG1109 Phosphomannomutase |
| NGO0376 | 0.1139 | 2.99 | up | 0.1042 | 1.88 | up | 0.2631 | 1.98 | up | putative peptidyl-prolyl cis-trans isomerase B\ Context:(NC_002946)-[370262-370771]\ Notes:Best Blastp Hit: pir\|\|F81156 peptidylprolyl isomerase (EC 5.2.1.8) B NMA1002 [similarity] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226024\|gb\|AAF41204.1\| (AE002433) peptidyl-prolyl cis-trans isomerase [Neisseria meningitidis MC58] >gi\|7379704\|emb\|CAB84271.1\| (AL162754) putative peptidyl-prolyl cis-trans isomerase B [Neisseria meningitidis] COG0652 Peptidyl-prolyl cis-trans isomerase |
| NGO0377 | 0.0002 | -33.96 | down | 0.0001 | -68.48 | down | 0.0328 | -12.48 | down | putative transport protein\ Context:(NC_002946)-[370891-372306]\ Notes:Best Blastp Hit: pir\|\|G81156 transporter; NadC family NMB0792 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226025\|gb\|AAF41205.1\| (AE002433) transporter; NadC family [Neisseria meningitidis MC58] COG0471 Cation transporters |
| NGO0378 | 0.8933 | -1.19 | down | 0.4428 | -3.60 | down | 0.8906 | 1.29 | up | hypothetical protein\ Context:(NC_002946)-[372535-372897]\ Notes:Best Blastp Hit: pir\|\|A81157 hypothetical protein NMB0794 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226027\|gb\|AAF41207.1\| (AE002433) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0379 | 0.7035 | 1.19 | up | 0.2542 | -1.55 | down | 0.8426 | -1.05 | down | peptidyl-tRNA hydrolase\ Context:(NC_002946)-[373161-373739]\ Notes:Enables the recycling of peptidyl-tRNAs produced at termination of translation |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0380 | 0.0587 | 3.90 | up | 0.9805 | -1.01 | down | 0.5130 | -1.20 | down | hypothetical protein\ Context:(NC_002946)-[373792-374070]\ Notes:Best Blastp Hit: sp\|Q9JRC2\|YA05_NEIMA hypothetical protein NMA1005/NMB0796 >gi\|7226029\|gb\|AAF41209.1\| (AE002433) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379707\|emb\|CAB84274.1\| (AL162754) hypothetical protein NMA1005 [Neisseria meningitidis] |
| NGO0381 | 0.9446 | -1.05 | down | 0.1612 | -1.97 | down | 0.1664 | -1.45 | down | hypothetical protein\ Context:(NC_002946)-[374063-374500]\ Notes:Best Blastp Hit: pir\|\|D81157 conserved hypothetical protein NMB0797 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226030\|gb\|AAF41210.1\| (AE002433) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0382 | 0.2729 | 1.79 | up | 0.5897 | 1.21 | up | 0.5565 | 1.23 | up | hypothetical protein\ Context:(NC_002946)-[374716-376683]\ Notes:Best Blastp Hit: pir\|\|E81157 cell division protein FtsH NMB0798 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226031\|gb\|AAF41211.1\| (AE002433) cell division protein FtsH [Neisseria meningitidis MC58] COG0465 ATP-dependent Zn proteases |
| NGO0383 | 0.1061 | -2.48 | down | 0.3251 | -1.73 | down | 0.2742 | -2.69 | down | hypothetical protein\ Context:(NC_002946)-[376747-377367]\ Notes:Best Blastp Hit: pir\|\|F81157 cell division protein FtsJ NMB0799 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226032\|gb\|AAF41212.1\| (AE002433) cell division protein FtsJ [Neisseria meningitidis MC58] >gi\|7379710\|emb\|CAB84277.1\| (AL162754) putative cell division protein [Neisseria meningitidis] COG0293 Methyltranferase FtsJ involved in cell |
| NGO0384 | 0.2159 | 2.15 | up | 0.0968 | 1.95 | up | 0.9860 | 1.00 | up | hypothetical protein\ Context:(NC_002946)+[377477-377761]\ Notes:Best Blastp Hit: emb\|CAB84278.1\| (AL162754) hypothetical protein NMA1009 [Neisseria meningitidis] COG1534 Predicted RNA-binding protein containing KH |
| NGO0385 | 0.8764 | 1.07 | up | 0.7850 | -1.14 | down | 0.2262 | -1.49 | down | delta-aminolevulinic acid dehydratase\ Context:(NC_002946)+[377930-378946]\ Notes:catalyzes the formation of porphobilinogen from 5-aminolevulinate |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0386 | 0.7797 | 1.15 | up | 0.6506 | -1.23 | down | 0.9651 | -1.01 | down | putative lyase\ Context:(NC_002946)-[379010-380167]\ Notes:Best Blastp Hit: pir\|\|A81158 cystathionine beta-lyase (EC 4.4.1.8) NMB0802 [similarity] - Neisseria meningitidis (group B strain MD58) >gi\|7226035\|gb\|AAF41215.1\| (AE002433) cystathionine gamma-synthase [Neisseria meningitidis MC58] COG0626 Cystathionine beta-lyases/cystathionine |
| NGO0387 | 0.0935 | 2.65 | up | 0.0675 | 5.84 | up | 0.1193 | 1.58 | up | putative GTP cyclohydrolase\ Context:(NC_002946)+[380370-381143]\ Notes:similar protein in Methanocaldococcus converts GTP to 7;8-dihydro-D-neopterin 2';3'-cyclic phosphate as the first step in methanopterin biosynthesis |
| NGO0388 | 0.3397 | 1.51 | up | 0.8842 | -1.09 | down | 0.1794 | 1.55 | up | putative oxidoreductase; NAD(P)H-flavin\ Context:(NC_002946)+[381340-382005]\ Notes:Best Blastp Hit: pir\|\|C81155 NAD(P)H nitroreductase; probable NMB0804 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226038\|gb\|AAF41217.1\| (AE002434) NAD(P)H nitroreductase; putative [Neisseria meningitidis MC58] COG0778 Nitroreductase family proteins |
| NGO0389 | 0.0065 | 9.91 | up | 0.1109 | 5.71 | up | 0.1842 | 2.09 | up | hypothetical protein\ Context:(NC_002946)-[382060-382818]\ Notes:Best Blastp Hit: pir\|\|E81155 conserved hypothetical protein NMB0806 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226040\|gb\|AAF41219.1\| (AE002434) conserved hypothetical protein [Neisseria meningitidis MC58] COG1187 Predicted pseudouridylate synthase family 1 |
| NGO0390 | 0.0603 | 3.56 | up | 0.1337 | 9.32 | up | 0.7127 | 1.21 | up | inorganic polyphosphate/ATP-NAD kinase\ Context:(NC_002946)-[382843-383733]\ Notes:catalyzes the phosphorylation of NAD to NADP |
| NGO0391 | 0.5566 | -1.28 | down | 0.5218 | -1.31 | down | 0.8057 | -1.07 | down | hypothetical protein\ Context:(NC_002946)-[383753-384319]\ Notes:Best Blastp Hit: pir\|\|G81155 hypothetical protein NMB0808 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226042\|gb\|AAF41221.1\| (AE002434) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0392 | 0.3873 | 1.55 | up | 0.4296 | 1.32 | up | 0.3782 | 1.33 | up | hypothetical protein\ Context:(NC_002946)-[384369-385145]\ Notes:Best Blastp Hit: pir\|\|A81950 hypothetical protein NMA1019 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379721\|emb\|CAB84288.1\| (AL162754) hypothetical protein NMA1019 [Neisseria meningitidis] COG0451 Nucleoside-diphosphate-sugar epimerases |
| NGO0393 | 0.8240 | 1.16 | up | 0.9489 | 1.02 | up | 0.9869 | 1.00 | up | TetR family transcriptional regulator\ Context:(NC_002946)-[385200-385850]\ Notes:Best Blastp Hit: gb\|AAF41223.1\| (AE002434) transcriptional regulator; TetR family [Neisseria meningitidis MC58] COG1309 Transcriptional regulators; AcrR family |
| NGO0394 | 0.7847 | -1.17 | down | 0.1603 | 1.94 | up | 0.9649 | 1.01 | up | putative UDP-N-acetylenolpyruvoylglucosamine reductase\ Context:(NC_002946)-[385862-386902]\ Notes:Best Blastp Hit: pir\|\|C81950 probable UDP-N-acetylmuramate dehydrogenase (EC 1.1.1.158) NMA1021 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379723\|emb\|CAB84290.1\| (AL162754) putative UDP-N-acetylenolpyruvoylglucosamine reductase [Neisseria meningitidis] COG0812 UDP-N-acetylmuramate dehydrogenase |
| NGO0395 | 0.5666 | -1.54 | down | 0.1920 | -3.75 | down | 0.5202 | -1.58 | down | multidrug efflux protein\ Context:(NC_002946)-[386946-388325]\ Notes:NorM; MdtK; functions as a Na(+)/drug antiporter; inactivation in Vibrio cholerae results in susceptibility to fluoroquinolones |
| NGO0396 | 0.0366 | 4.53 | up | 0.2390 | 1.56 | up | 0.6636 | -1.26 | down | hypothetical protein\ Context:(NC_002946)+[388382-388570]\ Notes:Best Blastp Hit: gb\|AAF41226.1\| (AE002434) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0397 | 0.2747 | 1.80 | up | 0.9027 | 1.06 | up | 0.8161 | 1.07 | up | ATP phosphoribosyltransferase regulatory subunit\ Context:(NC_002946)+[388662-389813]\ Notes:May allow the feedback regulation of ATP phosphoribosyltransferase activity by histidine |
| NGO0398 | 0.6431 | 1.26 | up | 0.8391 | 1.11 | up | 0.5486 | 1.19 | up | adenylosuccinate synthetase\ Context:(NC_002946)+[389912-391216]\ Notes:catalyzes the formation of N6-(1;2;-dicarboxyethyl)-AMP from L-aspartate; inosine monophosphate and GTP in AMP biosynthesis |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0399 | 0.7333 | 1.24 | up | 0.8441 | 1.07 | up | 0.9247 | -1.04 | down | heat shock protein HtpX\ Context:(NC_002946)-[391452-392291]\ Notes:putative metalloprotease |
| NGO0400 | 0.4589 | 1.47 | up | 0.7810 | 1.13 | up | 0.4733 | 1.23 | up | adenylate kinase\ Context:(NC_002946)+[392506-393153]\ Notes:essential enzyme that recycles AMP in active cells; converts ATP and AMP to two molecules of ADP |
| NGO0401 | 0.2094 | 2.08 | up | 0.6182 | 1.21 | up | 0.6001 | 1.16 | up | orotidine 5'-phosphate decarboxylase\ Context:(NC_002946)+[393677-394417]\ Notes:OMP decarboxylase; OMPDCase; OMPdecase; type 1 subfamily; involved in last step of pyrimidine biosynthesis; converts orotidine 5'-phosphate to UMP and carbon dioxide; OMP decarboxylase; OMPDCase; OMPdecase |
| NGO0402 | 0.3655 | 1.56 | up | 0.4043 | 1.33 | up | 0.7328 | 1.09 | up | putative sugar kinase / ADP-heptose synthase\ Context:(NC_002946)+[394473-395435]\ Notes:Best Blastp Hit: gb\|AAF41238.1\| (AE002435) ADP-heptose synthase; putative [Neisseria meningitidis MC58] COG0524 Sugar kinases; ribokinase family |
| NGO0403 | 0.1736 | 1.82 | up | 0.3332 | 2.05 | up | 0.4786 | -1.31 | down | ADP-L-glycero-D-mannoheptose epimerase\ Context:(NC_002946)+[395499-396503]\ Notes:Best Blastp Hit: gb\|AAA79173.1\| (L07845) ADP-L-glycero-D-mannoheptose epimerase [Neisseria gonorrhoeae] COG0451 Nucleoside-diphosphate-sugar epimerases |
| NGO0404 | 0.0034 | 6.60 | up | 0.1162 | 4.38 | up | 0.0243 | 3.98 | up | putative type I restriction-modification system methyltransferase protein\ Context:(NC_002946)+[396578-398122]\ Notes:Best Blastp Hit: pir\|\|F81152 type I restriction enzyme EcoR124II M protein NMB0829 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226064\|gb\|AAF41241.1\| (AE002436) type I restriction enzyme EcoR124II M protein [Neisseria meningitidis MC58] COG0286 Type I restriction-modification system |
| NGO0405 | 0.0172 | 5.82 | up | 0.0215 | 20.08 | up | 0.0694 | 7.25 | up | DNA-damage-inducible protein D\ Context:(NC_002946)+[398238-399089]\ Notes:Best Blastp Hit: pir\|\|G65165 DNA-damage-inducible protein d - Escherichia coli >gi\|290495\|gb\|AAA61998.1\| (L10328) o278 [Escherichia coli] >gi\|1790076\|gb\|AAC76669.1\| (AE000441) DNA-damage-inducible protein [Escherichia coli] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0407 | 0.8402 | -1.14 | down | 0.4268 | 1.63 | up | 0.2562 | 2.80 | up | putative type I site-specific deoxyribonuclease\ Context:(NC_002946)+[400709-403807]\ Notes:Best Blastp Hit: gb\|AAF41246.1\| (AE002436) type I restriction enzyme EcoR124II R protein; putative [Neisseria meningitidis MC58] COG0610 Restriction enzymes type I helicase subunits |
| NGO0408 | 0.8740 | -1.09 | down | 0.3537 | 1.40 | up | 0.0736 | 1.78 | up | hypothetical protein\ Context:(NC_002946)-[403847-406138]\ Notes:Best Blastp Hit: pir\|\|D81153 ATP-dependent Clp proteinase; ATP-binding chain ClpA NMB0836 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226070\|gb\|AAF41247.1\| (AE002436) ATP-dependent Clp protease; ATP-binding subunit ClpA [Neisseria meningitidis MC58] COG0542 ATPases with chaperone activity; ATP-binding |
| NGO0409 | 0.1828 | -2.07 | down | 0.2998 | -1.62 | down | 0.8607 | -1.06 | down | hypothetical protein\ Context:(NC_002946)-[406140-406442]\ Notes:Best Blastp Hit: pir\|\|E81153 conserved hypothetical protein NMB0837 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226071\|gb\|AAF41248.1\| (AE002436) conserved hypothetical protein [Neisseria meningitidis MC58] COG2127 Uncharacterized ACR |
| NGO0410 | 0.4165 | 1.59 | up | 0.9415 | -1.03 | down | 0.9027 | -1.05 | down | CspA\ Context:(NC_002946)+[406687-406890]\ Notes:Best Blastp Hit: pir\|\|C81151 cold-shock domain family protein NMB0838 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226073\|gb\|AAF41249.1\| (AE002437) cold-shock domain family protein [Neisseria meningitidis MC58] COG1278 Cold shock proteins; putative cold shock protein |
| NGO0411 | 0.9145 | -1.06 | down | 0.4260 | -1.44 | down | 0.8222 | -1.07 | down | hypothetical protein\ Context:(NC_002946)-[407189-408520]\ Notes:Best Blastp Hit: pir\|\|H81869 hypothetical protein NMA1048 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379746\|emb\|CAB84314.1\| (AL162755) hypothetical protein NMA1048 [Neisseria meningitidis] COG0312 Predicted Zn-dependent proteases and their |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0412 | 0.2800 | -1.81 | down | 0.2237 | -1.91 | down | 0.1231 | -1.75 | down | hypothetical protein\ Context:(NC_002946)+[408674-409180]\ Notes:Best Blastp Hit: pir\|\|A81870 hypothetical protein NMA1049 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379747\|emb\|CAB84315.1\| (AL162755) hypothetical protein NMA1049 [Neisseria meningitidis] |
| NGO0413 | 0.4108 | -1.67 | down | 0.5978 | 1.23 | up | 0.4518 | -1.23 | down | putative thiosulphate sulphur transferase\ Context:(NC_002946)+[409227-409940]\ Notes:Best Blastp Hit: gb\|AAF62913.1\| (AF234832) putative thiosulphate sulphur transferase [Neisseria gonorrhoeae] |
| NGO0414 | 0.6172 | 1.60 | up | 0.1232 | -2.11 | down | 0.5096 | -1.50 | down | hypothetical protein\ Context:(NC_002946)+[410009-411709]\ Notes:Best Blastp Hit: gb\|AAF62912.1\| (AF234832) RecJ [Neisseria gonorrhoeae] COG0608 Single-stranded DNA-specific exonuclease |
| NGO0415 | 0.9113 | 1.06 | up | 0.5878 | 1.18 | up | 0.4663 | -1.36 | down | hypothetical protein\ Context:(NC_002946)+[412067-413425]\ Notes:Best Blastp Hit: emb\|CAB84318.1\| (AL162755) putative poly(A) polymerase [Neisseria meningitidis] COG0617 tRNA nucleotidyltransferase/poly(A) |
| NGO0416 | 0.0437 | 3.32 | up | 0.0292 | 2.69 | up | 0.4411 | 1.23 | up | hypothetical protein\ Context:(NC_002946)+[413598-413921]\ Notes:Best Blastp Hit: pir\|\|A81152 hypothetical protein NMB0844 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226079\|gb\|AAF41255.1\| (AE002437) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0417 | 0.0919 | -2.54 | down | 0.9511 | -1.03 | down | 0.1596 | -3.17 | down | hypothetical protein\ Context:(NC_002946)-[414026-414979]\ Notes:Best Blastp Hit: pir\|\|F81870 hypothetical protein NMA1056 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379752\|emb\|CAB84320.1\| (AL162755) hypothetical protein NMA1056 [Neisseria meningitidis] COG1702 Phosphate starvation-inducible protein |
| NGO0418 | 0.0352 | 4.09 | up | 0.6044 | -1.58 | down | 0.8864 | 1.08 | up | putative glycosyl transferase\ Context:(NC_002946)-[415005-415490]\ Notes:Best Blastp Hit: emb\|CAB84321.1\| (AL162755) putative glycosyl transferase [Neisseria meningitidis] COG0438 Glycosyltransferases I |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0419 | 0.3755 | -2.11 | down | 0.4174 | -2.23 | down | 0.7349 | -1.39 | down | hypothetical protein\ Context:(NC_002946)-[415590-416177]\ Notes: |
| NGO0420 | 0.0214 | 3.47 | up | 0.0394 | 2.40 | up | 0.0230 | 2.01 | up | hypothetical protein\ Context:(NC_002946)+[416315-417049]\ Notes:Best Blastp Hit: pir\|\|A81871 probable periplasmic protein NMA1059 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379755\|emb\|CAB84323.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] |
| NGO0421 | 0.2650 | 2.65 | up | 0.1187 | 8.78 | up | 0.0715 | 5.37 | up | deoxycytidine triphosphate deaminase\ Context:(NC_002946)-[417115-417681]\ Notes:Catalyzes the formation of dUTP from dCTP in thymidylate biosynthesis |
| NGO0422 | 0.4294 | 1.58 | up | 0.1074 | 3.59 | up | 0.2736 | 1.61 | up | hypothetical protein\ Context:(NC_002946)-[417777-418166]\ Notes:Best Blastp Hit: pir\|\|C81871 probable periplasmic protein NMA1061 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379757\|emb\|CAB84325.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] |
| NGO0423 | 0.3847 | 1.55 | up | 0.0948 | 2.75 | up | 0.2176 | 2.07 | up | recombination associated protein\ Context:(NC_002946)-[418218-419117]\ Notes:Required for efficient pilin antigenic variation |
| NGO0424 | 0.3866 | 1.48 | up | 0.1537 | 3.30 | up | 0.2104 | 1.45 | up | GTP-binding protein EngA\ Context:(NC_002946)-[419148-420605]\ Notes:EngA; essential Neisserial GTPase; synchronizes cellular events by interacting with multiple targets with tandem G-domains; overexpression in Escherichia coli suppresses rrmJ mutation; structural analysis of the Thermotoga maritima ortholog shows different nucleotide binding affinities in the two binding domains |
| NGO0425 | 0.8381 | 1.11 | up | 0.4366 | 1.44 | up | 0.5380 | -1.71 | down | hypothetical protein\ Context:(NC_002946)-[420755-421384]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0426 | 0.6629 | -1.29 | down | 0.9819 | 1.01 | up | 0.0620 | -2.06 | down | histidyl-tRNA synthetase\ Context:(NC_002946)-[421385-422680]\ Notes:catalyzes a two-step reaction; first charging a histidine molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA; class II aminoacyl-tRNA synthetase; forms homodimers; some organisms have a paralogous gene; hisZ; that is similar to hisS and produces a protein that performs the first step in histidine biosynthesis along with HisG |
| NGO0427 | 0.5582 | -1.40 | down | 0.0041 | -11.22 | down | 0.2494 | -3.64 | down | hypothetical protein\ Context:(NC_002946)-[422808-423464]\ Notes:Best Blastp Hit: emb\|CAB84330.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] COG1101 ATPase components of various transport |
| NGO0428 | 0.2072 | -2.39 | down | 0.0002 | -16.80 | down | 0.3222 | -2.74 | down | hypothetical protein\ Context:(NC_002946)-[423520-423744]\ Notes:Best Blastp Hit: emb\|CAB84342.1\| (AL162755) hypothetical protein NMA1079 [Neisseria meningitidis] |
| NGO0429 | 0.1976 | -4.49 | down | 0.0209 | -25.47 | down | 0.5215 | -2.06 | down | hypothetical protein\ Context:(NC_002946)-[423973-424110]\ Notes:Best Blastp Hit: emb\|CAB84343.1\| (AL162755) hypothetical protein NMA1080 [Neisseria meningitidis] |
| NGO0430 | 0.0080 | -4.58 | down | 0.1128 | -5.42 | down | 0.3425 | 1.97 | up | hypothetical protein\ Context:(NC_002946)-[425228-425518]\ Notes:Best Blastp Hit: gb\|AAF41275.1\| (AE002439) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0432 | 0.9998 | 1.00 | up | 0.0310 | -5.30 | down | 0.6151 | -1.49 | down | hypothetical protein\ Context:(NC_002946)-[426078-426620]\ Notes:Best Blastp Hit: pir\|\|A81874 probable periplasmic protein NMA1084 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379779\|emb\|CAB84347.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] |
| NGO0433 | 0.1420 | -2.80 | down | 0.0046 | -8.84 | down | 0.5236 | -1.48 | down | hypothetical protein\ Context:(NC_002946)+[426786-427709]\ Notes:Best Blastp Hit: emb\|CAB84348.1\| (AL162755) hypothetical protein NMA1085 [Neisseria meningitidis] COG0564 Predicted pseudouridylate synthase family 2 |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0434 | 0.0119 | 5.84 | up | 0.3117 | 1.85 | up | 0.2310 | 1.67 | up | hypothetical protein\ Context:(NC_002946)-[427788-428429]\ Notes:Best Blastp Hit: pir\|\|C81874 hypothetical protein NMA1086 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379781\|emb\|CAB84349.1\|(AL162755) hypothetical protein NMA1086 [Neisseria meningitidis] |
| NGO0435 | 0.5845 | 1.49 | up | 0.7283 | -1.19 | down | 0.3559 | -1.35 | down | spermidine synthase\ Context:(NC_002946)-[428484-429275]\ Notes:catalyzes the formation of spermidine from putrescine and S-adenosylmethioninamine |
| NGO0436 | 0.7201 | 1.27 | up | 0.1892 | -1.96 | down | 0.2811 | -1.38 | down | 3-methyl-2-oxobutanoatehydroxymethyltransferase\ Context:(NC_002946)+[429658-430449]\ Notes:catalyzes the formation of tetrahydrofolate and 2-dehydropantoate from 5;10-methylenetetrahydrofolate and 3-methyl-2-oxobutanoate |
| NGO0437 | 0.7170 | 1.25 | up | 0.7789 | -1.14 | down | 0.0864 | -2.46 | down | pantoate--beta-alanine ligase\ Context:(NC_002946)+[430572-431408]\ Notes:catalyzes the formation of (R)-pantothenate from pantoate and beta-alanine |
| NGO0439 | 0.9283 | 1.04 | up | 0.4709 | -1.36 | down | 0.3871 | -1.29 | down | outer membrane lipoprotein LolB\ Context:(NC_002946)+[433712-434293]\ Notes:Incorporates lipoproteins in the outer membrane after they are released by the LolA protein |
| NGO0440 | 0.6148 | 1.26 | up | 0.4272 | -1.50 | down | 0.9233 | -1.03 | down | putative isopentenyl monophosphate kinase\ Context:(NC_002946)+[434303-435148]\ Notes:Best Blastp Hit: pir\|\|B81149 conserved hypothetical protein NMB0874 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226111\|gb\|AAF41285.1\| (AE002439) conserved hypothetical protein [Neisseria meningitidis MC58] COG1947 Uncharacterized ACR; YchB/YabH family |
| NGO0441 | 0.2774 | 1.80 | up | 0.5295 | 1.26 | up | 0.5033 | -1.21 | down | ribose-phosphate pyrophosphokinase\ Context:(NC_002946)+[435487-436470]\ Notes:catalyzes the formation of 5-phospho-alpha-D-ribose 1-phosphate from D-ribose 5-phosphate and ATP |

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| NGO0442 | 0.2620 | 2.02 | up | 0.3905 | 1.33 | up | 0.4523 | 1.28 | up | 50S ribosomal protein L25/general stress protein Ctc\ Context:(NC_002946)+[436537-437109]\ Notes:the Ctc family of proteins consists of two types; one that contains the N-terminal ribosomal protein L25 domain only which in Escherichia coli binds the 5S rRNA while a subset of proteins contain a C-terminal extension that is involved in the stress response |
| NGO0443 | 0.0035 | -5.30 | down | 0.0545 | -5.67 | down | 0.2999 | -2.22 | down | putative D-alanyl-D-alanine carboxypeptidase / penicillin binding protein\ Context:(NC_002946)-[437235-438404]\ Notes:Best Blastp Hit: pir\|\|H81146 penicillin-binding protein NMB0877 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226115\|gb\|AAF41288.1\| (AE002440) penicillin-binding protein [Neisseria meningitidis MC58] COG1686 D-alanyl-D-alanine carboxypeptidase |
| NGO0444 | 0.1835 | -1.92 | down | 0.4501 | -1.62 | down | 0.8010 | -1.15 | down | threonine dehydratase\ Context:(NC_002946)+[438553-440079]\ Notes:threonine deaminase; threonine dehydratase; in Escherichia coli; IlvA is part of the isoleucine biosynthetic pathway |
| NGO0445 | 0.0215 | -4.26 | down | 0.0580 | -7.63 | down | 0.7637 | 1.20 | up | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)-[440135-441211]\ Notes:Best Blastp Hit: pir\|\|F81875 sulfate ABC transporter; ATP-binding protein NMA1097 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379792\|emb\|CAB84360.1\| (AL162755) putative sulphate permease ATP-binding protein [Neisseria meningitidis] COG1118 ABC-type sulfate/molybdenum transport |
| NGO0446 | 0.3026 | -2.74 | down | 0.0259 | -10.04 | down | 0.0455 | 2.32 | up | putative ABC transporter\ Context:(NC_002946)-[441352-442173]\ Notes:Best Blastp Hit: pir\|\|C81147 sulfate ABC transporter; permease protein NMB0880 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226118\|gb\|AAF41291.1\| (AE002440) sulfate ABC transporter; permease protein [Neisseria meningitidis MC58] COG0555 ABC-type cysteine/molybdate transport |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0448 | 0.2010 | -2.21 | down | 0.0802 | -2.47 | down | 0.6709 | -1.30 | down | hypothetical protein\ Context:(NC_002946)+[443377-443709]\ Notes:Best Blastp Hit: pir\|\|B81876 hypothetical protein NMA1101 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379796\|emb\|CAB84364.1\| (AL162755) hypothetical protein NMA1101 [Neisseria meningitidis] |
| NGO0449 | 0.1720 | 2.30 | up | 0.4099 | 1.44 | up | 0.3683 | 1.41 | up | hypothetical protein\ Context:(NC_002946)+[444039-444548]\ Notes:Best Blastp Hit: gb\|AAF41294.1\| (AE002440) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379797\|emb\|CAB84365.1\| (AL162755) putative integral membrane protein [Neisseria meningitidis] COG1755 Uncharacterized BCR; YpbQ family |
| NGO0451 | 0.0774 | 4.63 | up | 0.0395 | 2.16 | up | 0.3976 | 1.30 | up | replicative DNA helicase\ Context:(NC_002946)+[445524-446930]\ Notes:unwinds double stranded DNA |
| NGO0452 | 0.4533 | 1.49 | up | 0.7038 | 1.20 | up | 0.9699 | -1.01 | down | hypothetical protein\ Context:(NC_002946)+[447238-447903]\ Notes:Best Blastp Hit: pir\|\|F81876 hypothetical protein NMA1106 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379800\|emb\|CAB84368.1\| (AL162755) hypothetical protein NMA1106 [Neisseria meningitidis] |
| NGO0453 | 0.4598 | 1.45 | up | 0.5081 | -1.54 | down | 0.6571 | -1.15 | down | hypothetical protein\ Context:(NC_002946)+[447935-448546]\ Notes:Best Blastp Hit: pir\|\|F81145 type IV pilus assembly protein PilV; probable NMB0887 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226125\|gb\|AAF41297.1\| (AE002441) type IV pilus assembly protein PilV; putative [Neisseria meningitidis MC58] |
| NGO0454 | 0.5060 | 1.46 | up | 0.8523 | 1.09 | up | 0.8281 | -1.08 | down | hypothetical protein\ Context:(NC_002946)+[448543-449523]\ Notes:Best Blastp Hit: pir\|\|H81876 probable membrane protein NMA1108 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379802\|emb\|CAB84370.1\| (AL162755) putative membrane protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0455 | 0.1675 | 2.24 | up | 0.3439 | 1.53 | up | 0.7674 | 1.11 | up | hypothetical protein\ Context:(NC_002946)+[449502-450113]\ Notes:Best Blastp Hit: pir\|\|H81145 hypothetical protein NMB0889 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226127\|gb\|AAF41299.1\| (AE002441) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0456 | 0.1842 | 2.19 | up | 0.3264 | 1.52 | up | 0.5407 | 1.24 | up | putative type IV pilin-like protein\ Context:(NC_002946)+[450100-450588]\ Notes:Best Blastp Hit: gb\|AAF62322.1\| (AE002441) type IV pilin-related protein [Neisseria meningitidis MC58] |
| NGO0457 | 0.0120 | 6.38 | up | 0.9980 | 1.00 | up | 0.8256 | 1.19 | up | hypothetical protein\ Context:(NC_002946)-[450658-450966]\ Notes: |
| NGO0459 | 0.5484 | -1.29 | down | 0.5389 | -1.33 | down | 0.6351 | -1.20 | down | deoxyuridine 5'-triphosphate nucleotidohydrolase\ Context:(NC_002946)+[451840-452292]\ Notes:catalyzes the formation of dUMP from dUTP |
| NGO0460 | 0.4330 | -1.45 | down | 0.6354 | -1.27 | down | 0.4433 | -1.32 | down | hypothetical protein\ Context:(NC_002946)+[452364-453551]\ Notes:Best Blastp Hit: gb\|AAF41303.1\| (AE002441) aminotransferase; class I [Neisseria meningitidis MC58] COG0436 PLP-dependent aminotransferases |
| NGO0461 | 0.1390 | 2.18 | up | 0.1158 | 1.84 | up | 0.3750 | 1.31 | up | hypothetical protein\ Context:(NC_002946)+[453863-454642]\ Notes:Best Blastp Hit: pir\|\|F81877 hypothetical protein NMA1114 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379808\|emb\|CAB84376.1\| (AL162755) hypothetical protein NMA1114 [Neisseria meningitidis] |
| NGO0462 | 0.0332 | -3.51 | down | 0.1550 | -2.16 | down | 0.6434 | -1.25 | down | putative phage integrase; putative phage associated protein\ Context:(NC_002946)+[455173-456369]\ Notes:Best Blastp Hit: pir\|\|B82272 integrase; phage family VC0847 [imported] - Vibrio cholerae (group O1 strain N16961) >gi\|498253\|gb\|AAC44230.1\| (U02372) integrase [Vibrio cholerae] >gi\|1100883\|gb\|AAA82714.1\| (U39068) integrase [Vibrio cholerae] >gi\|9655299\|gb\|AAF94009.1\| (AE004170) integrase; phage family [Vibrio cholerae] |
| NGO0463 | 0.8679 | 1.12 | up | 0.0602 | -5.72 | down | 0.3211 | -2.17 | down | putative phage associated protein\ Context:(NC_002946)-[456725-456994]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0464 | 0.9598 | 1.06 | up | 0.0932 | -8.60 | down | 0.1602 | -3.99 | down | putative phage associated protein\ Context:(NC_002946)-[457189-457872]\ Notes:Best Blastp Hit: gb\|AAF94355.1\|(AE004199) hypothetical protein [Vibrio cholerae] |
| NGO0465 | 0.0551 | -2.72 | down | 0.0051 | -5.66 | down | 0.6500 | -1.21 | down | putative phage associated protein\ Context:(NC_002946)-[457883-458419]\ Notes: |
| NGO0467 | 0.1375 | 2.20 | up | 0.4566 | 1.32 | up | 0.6611 | -1.33 | down | putative phage associated protein\ Context:(NC_002946)-[458797-459288]\ Notes:Best Blastp Hit: pir\|\|T13296 hypothetical protein 8 - Streptococcus phage phi-O1205 >gi\|2444088\|gb\|AAC79524.1\| (U88974) ORF8 [Streptococcus thermophilus temperate bacteriophage O1205] |
| NGO0471 | 0.3575 | -2.07 | down | 0.5102 | -1.30 | down | 0.5713 | -1.20 | down | putative phage associated protein\ Context:(NC_002946)-[460520-460735]\ Notes:Best Blastp Hit: gb\|AAF41312.1\|(AE002442) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0472 | 0.0611 | 2.82 | up | 0.1902 | 1.57 | up | 0.2702 | 1.44 | up | putative phage associated protein\ Context:(NC_002946)-[460949-461236]\ Notes: |
| NGO0475 | 0.3040 | 1.57 | up | 0.0497 | 3.32 | up | 0.9090 | -1.06 | down | putative phage associated protein\ Context:(NC_002946)-[462203-462403]\ Notes: |
| NGO0476 | 0.9421 | -1.04 | down | 0.4053 | -1.47 | down | 0.1750 | -1.59 | down | putative phage associated protein\ Context:(NC_002946)-[462601-463014]\ Notes:Best Blastp Hit: sp\|P41637\|CADH_PINTA cinnamyl-alcohol dehydrogenase (CAD) >gi\|1076238\|pir\|\|S49443 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) A - loblolly pine >gi\|558385\|emb\|CAA86072.1\| (Z37991) cinnamyl alcohol dehydrogenase [Pinus taeda] |
| NGO0477 | 0.9076 | -1.06 | down | 0.5973 | -1.27 | down | 0.2917 | -1.40 | down | putative phage associated protein\ Context:(NC_002946)-[463011-463448]\ Notes:Best Blastp Hit: sp\|P55409\|Y4DJ_RHISN hypothetical transcriptional regulator Y4DJ >gi\|7465604\|pir\|\|T02773 y4dJ protein - Rhizobium sp. plasmid pNGR234a >gi\|2182353\|gb\|AAB91639.1\| (AE000069) Y4dJ [Rhizobium sp. NGR234] |
| NGO0478 | 0.7193 | 1.20 | up | 0.8680 | -1.07 | down | 0.6544 | -1.15 | down | putative phage associated protein\ Context:(NC_002946)-[463489-463926]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0479 | 0.1228 | -2.26 | down | 0.5170 | 2.07 | up | 0.4560 | 1.53 | up | putative lambda repressor protein cI; putative phage associated protein\ Context:(NC_002946)-[464039-464755]\ Notes:Best Blastp Hit: gb\|AAF83310.1\|AE003899_2 (AE003899) phage-related repressor protein [Xylella fastidiosa] |
| NGO0482 | 0.2078 | -2.19 | down | 0.0108 | -10.37 | down | 0.9981 | 1.00 | up | putative phage associated protein\ Context:(NC_002946)-[465465-465827]\ Notes: |
| NGO0484 | 0.0397 | -8.67 | down | 0.0051 | -44.79 | down | 0.8421 | -1.29 | down | putative phage associated protein\ Context:(NC_002946)+[465978-467042]\ Notes:Best Blastp Hit: gi\|9634200 Gp54 [Bacteriophage HK97] >gi\|6901629\|gb\|AAF31132.1\| (AF069529) Gp54 [Bacteriophage HK97] |
| NGO0485 | 0.6250 | 1.59 | up | 0.0490 | -7.16 | down | 0.5044 | 1.77 | up | putative replicative DNA helicase; putative phage associated protein\ Context:(NC_002946)+[467039-468400]\ Notes:Best Blastp Hit: sp\|P37469\|DNAC_BACSU replicative DNA helicase >gi\|2127189\|pir\|\|S65970 replicative DNA helicase dnaC - Bacillus subtilis >gi\|467330\|dbj\|BAA05176.1\| (D26185) replicative DNA helicase [Bacillus subtilis] >gi\|2636591\|emb\|CAB16081.1\| (Z99124) replicative DNA helicase [Bacillus subtilis] COG0305 Replicative DNA helicase |
| NGO0487 | 0.1175 | 2.44 | up | 0.0652 | 2.42 | up | 0.4810 | 1.41 | up | putative phage associated protein\ Context:(NC_002946)+[468740-469234]\ Notes: |
| NGO0488 | 0.0761 | -3.49 | down | 0.1881 | -2.20 | down | 0.8544 | 1.09 | up | putative phage associated protein\ Context:(NC_002946)+[469411-469560]\ Notes: |
| NGO0489 | 0.8392 | 1.19 | up | 0.0716 | -3.29 | down | 0.6553 | -1.21 | down | putative phage associated protein\ Context:(NC_002946)+[469696-470241]\ Notes:Best Blastp Hit: sp\|Q37873\|RUSA_BP82 crossover junction endodeoxyribonuclease RusA (Holliday junction nuclease RusA) (Holliday juction resolvase) >gi\|2120247\|pir\|\|S66583 crossover junction endodeoxyribonuclease (EC 3.1.22.4) rusA - phage 82 >gi\|1051116\|emb\|CAA63330.1\| (X92588) Can suppress the phenotype of ruv mutants [Bacteriophage 82] |
| NGO0490 | 0.7139 | 1.34 | up | 0.3080 | -2.47 | down | 0.2413 | -2.16 | down | putative phage associated protein\ Context:(NC_002946)+[470231-470464]\ Notes: |
| NGO0491 | 0.0319 | -5.16 | down | 0.0005 | -37.07 | down | 0.0520 | -4.72 | down | putative phage associated protein\ Context:(NC_002946)+[470508-470915]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0492 | 0.4768 | -1.37 | down | 0.5048 | -1.37 | down | 0.1993 | -1.59 | down | putative phage associated protein\ Context:(NC_002946)+[471138-471644]\ Notes:Best Blastp Hit: pir\|\|F69137 hypothetical protein MTH296 - Methanobacterium thermoautotrophicum (strain Delta H) >gi\|2621349\|gb\|AAB84802.1\| (AE000815) unknown [Methanobacterium thermoautotrophicum] |
| NGO0493 | 0.5308 | -1.72 | down | 0.6003 | 1.70 | up | 0.8990 | -1.11 | down | putative phage associated protein\ Context:(NC_002946)+[471965-472186]\ Notes: |
| NGO0494 | 0.7293 | 1.39 | up | 0.1015 | -4.85 | down | 0.5900 | -1.31 | down | putative phage associated protein\ Context:(NC_002946)+[472479-472928]\ Notes:Best Blastp Hit: sp\|P76546\|YFFO_ECOLI hypothetical 15.7 KDA protein in EutB-EutH intergenic region >gi\|7466364\|pir\|\|E65019 hypothetical protein b2446 - Escherichia coli (strain K-12) >gi\|1788787\|gb\|AAC75499.1\| (AE000331) orf; hypothetical protein [Escherichia coli] |
| NGO0495 | 0.2413 | -1.78 | down | 0.2136 | -2.13 | down | 0.5664 | 1.40 | up | putative phage associated protein\ Context:(NC_002946)+[472990-474411]\ Notes:Best Blastp Hit: pir\|\|H82649 hypothetical protein XF1674 XF1569 [imported] - Xylella fastidiosa (strain 9a5c) >gi\|9106614\|gb\|AAF84378.1\|AE003986_8 (AE003986) hypothetical protein [Xylella fastidiosa] >gi\|9106736\|gb\|AAF84483.1\|AE003993_2 (AE003993) hypothetical protein [Xylella fastidiosa] |
| NGO0496 | 0.0626 | -4.38 | down | 0.0361 | -5.40 | down | 0.8859 | 1.06 | up | putative phage associated protein\ Context:(NC_002946)+[474408-476555]\ Notes:Best Blastp Hit: pir\|\|G81057 hypothetical protein NMB1656 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226908\|gb\|AAF42005.1\| (AE002516) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0497 | 0.2712 | -2.28 | down | 0.0971 | -3.75 | down | 0.2414 | -2.35 | down | putative phage associated protein\ Context:(NC_002946)+[476623-477780]\ Notes:Best Blastp Hit: pir\|\|B81819 hypothetical protein NMA1914 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380548\|emb\|CAB85135.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO0498 | 0.1126 | -3.82 | down | 0.0426 | -7.72 | down | 0.4108 | -1.84 | down | putative phage associated protein\ Context:(NC_002946)+[477821-479320]\ Notes:Best Blastp Hit: sp\|P23739\|SUIS_RAT sucrase-isomaltase; intestinal [contains: sucrase ; isomaltase ] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0499 | 0.3674 | -2.08 | down | 0.2443 | -4.70 | down | 0.9071 | 1.16 | up | putative phage associated protein\ Context:(NC_002946)+[479327-479689]\ Notes: |
| NGO0500 | 0.1051 | 2.67 | up | 0.9673 | -1.03 | down | 0.8949 | 1.07 | up | putative phage associated protein\ Context:(NC_002946)+[479692-480222]\ Notes: |
| NGO0501 | 0.3938 | -2.06 | down | 0.0251 | -10.08 | down | 0.0082 | -4.81 | down | putative phage associated protein\ Context:(NC_002946)+[480370-480702]\ Notes: |
| NGO0502 | 0.1907 | 2.32 | up | 0.2920 | -3.52 | down | 0.5113 | -1.98 | down | putative phage associated protein\ Context:(NC_002946)+[480699-481127]\ Notes: |
| NGO0503 | 0.7560 | 1.24 | up | 0.3363 | -2.32 | down | 0.5373 | -1.21 | down | putative phage associated protein\ Context:(NC_002946)+[481153-481926]\ Notes: |
| NGO0504 | 0.4724 | 2.42 | up | 0.1899 | -3.87 | down | 0.4443 | -1.90 | down | putative phage associated protein\ Context:(NC_002946)+[481987-482316]\ Notes: |
| NGO0505 | 0.4680 | -2.12 | down | 0.0043 | -18.89 | down | 0.5371 | -1.38 | down | putative phage associated protein\ Context:(NC_002946)+[482328-482594]\ Notes:Best Blastp Hit: gb\|AAD32742.1\| (AF127374) MmcR [Streptomyces lavendulae] |
| NGO0506 | 0.0901 | -3.16 | down | 0.1044 | -6.84 | down | 0.2176 | -2.23 | down | putative phage associated protein\ Context:(NC_002946)+[482594-483193]\ Notes: |
| NGO0507 | 0.0015 | -20.67 | down | 0.1267 | -7.24 | down | 0.0089 | -4.78 | down | putative phage associated protein\ Context:(NC_002946)+[483190-484044]\ Notes: |
| NGO0508 | 0.0488 | -5.68 | down | 0.0130 | -28.14 | down | 0.1535 | -2.97 | down | putative phage associated protein\ Context:(NC_002946)+[484046-484477]\ Notes:Best Blastp Hit: sp\|P77685\|SPR_ECOLI lipoprotein SPR precursor >gi\|7430106\|pir\|\|F64986 hypothetical protein b2175 - Escherichia coli (strain K-12) >gi\|1498150\|dbj\|BAA13140.1\| (D86610) Spr [Escherichia coli] >gi\|1736840\|dbj\|BAA15983.1\| (D90849) Probable lipoprotein NlpC homolog precursor. [Escherichia coli] >gi\|1788501\|gb\|AAC75236.1\| (AE000307) putative lipoprotein [Escherichia coli] |
| NGO0509 | 0.6482 | 1.23 | up | 0.6280 | 1.22 | up | 0.8221 | -1.07 | down | putative phage associated protein\ Context:(NC_002946)-[484505-484786]\ Notes:Best Blastp Hit: gb\|AAF84381.1\|AE003986_11 (AE003986) hypothetical protein [Xylella fastidiosa] >gi\|9106739\|gb\|AAF84486.1\|AE003993_5 (AE003993) hypothetical protein [Xylella fastidiosa] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0510 | 0.0571 | -16.53 | down | 0.0435 | -22.39 | down | 0.4706 | -2.57 | down | putative phage associated protein\ Context:(NC_002946)+[485026-489171]\ Notes:Best Blastp Hit: gi\|10955733 phage lambda host specific protein J [Yersinia pestis] >gi\|7467468\|pir\|\|T14652 protein J - Yersinia pestis plasmid pMT1 >gi\|2996342\|gb\|AAC13222.1\| (AF053947) phage lambda host specific protein J [Yersinia pestis] |
| NGO0511 | 0.0032 | -7.67 | down | 0.0117 | -10.90 | down | 0.1416 | -3.45 | down | hypothetical protein\ Context:(NC_002946)+[489283-489588]\ Notes: |
| NGO0512 | 0.0238 | -8.10 | down | 0.0057 | -53.52 | down | 0.2830 | 1.94 | up | putative phage associated protein\ Context:(NC_002946)-[489593-490528]\ Notes:Best Blastp Hit: gb\|AAB32262.1\|S75490_1 (S75490) orf2 [Neisseria gonorrhoeae] |
| NGO0513 | 0.2643 | -3.61 | down | 0.0082 | -24.63 | down | 0.7052 | 1.52 | up | putative phage associated protein\ Context:(NC_002946)+[489659-490129]\ Notes: |
| NGO0514 | 0.7176 | -1.74 | down | 0.8348 | 1.09 | up | 0.5730 | -1.48 | down | putative phage associated protein\ Context:(NC_002946)+[490130-490462]\ Notes: |
| NGO0515 | 0.4648 | -1.75 | down | 0.0261 | -4.01 | down | 0.2546 | 1.62 | up | putative phage associated protein\ Context:(NC_002946)-[490591-490824]\ Notes: |
| NGO0516 | 0.8638 | -1.08 | down | 0.5811 | -1.33 | down | 0.6644 | -1.14 | down | putative plasmid stable inheritance protein putative phage associated protein\ Context:(NC_002946)-[490832-491179]\ Notes:Best Blastp Hit: gb\|AAF41321.1\| (AE002443) pemK protein [Neisseria meningitidis MC58] |
| NGO0517 | 0.9058 | 1.06 | up | 0.6175 | -1.27 | down | 0.8912 | 1.04 | up | putative pemI-like protein (PemI); putative phage associated protein\ Context:(NC_002946)-[491179-491415]\ Notes:Best Blastp Hit: gb\|AAF41322.1\| (AE002443) pemI protein [Neisseria meningitidis MC58] |
| NGO0518 | 0.2576 | 2.45 | up | 0.0393 | -8.66 | down | 0.9321 | -1.07 | down | putative phage associated protein\ Context:(NC_002946)+[491622-492161]\ Notes: |
| NGO0520 | 0.0760 | -5.73 | down | 0.0034 | -18.03 | down | 0.2427 | -1.88 | down | putative phage associated protein\ Context:(NC_002946)+[492680-492991]\ Notes: |
| NGO0521 | 0.4250 | -2.02 | down | 0.0006 | -41.07 | down | 0.9933 | 1.01 | up | phage associated protein\ Context:(NC_002946)+[493004-493153]\ Notes:Best Blastp Hit: gb\|AAF41392.1\| (AE002449) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0522 | 0.0055 | -21.57 | down | 0.0440 | -32.67 | down | 0.5590 | 1.38 | up | putative tail length tape measure protein; putative phage associated protein\ Context:(NC_002946)+[493183-496230]\ Notes:Best Blastp Hit: gi\|9634160 tail length tape measure protein [Bacteriophage HK97] >gi\|6901589\|gb\|AAF31092.1\|AF069529_5 (AF069529) tail length tape measure protein [Bacteriophage HK97] |
| NGO0523 | 0.6458 | -1.28 | down | 0.4541 | 1.42 | up | 0.4291 | -1.40 | down | putative phage associated protein\ Context:(NC_002946)-[496290-496769]\ Notes:Best Blastp Hit: pir\|\|H81143 hypothetical protein NMB0899 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226136\|gb\|AAF41307.1\| (AE002442) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0524 | 0.8047 | -1.21 | down | 0.7152 | 1.17 | up | 0.9619 | 1.01 | up | putative integrase\ Context:(NC_002946)-[497111-498100]\ Notes:Best Blastp Hit: gb\|AAF68420.1\|AF237934_1 (AF237934) putative integrase/recombinase [Pasteurella multocida] COG0582 Integrase |
| NGO0525 | 0.4245 | 3.58 | up | 0.8957 | 1.18 | up | 0.2665 | 3.72 | up | hypothetical protein\ Context:(NC_002946)-[498360-498548]\ Notes:Best Blastp Hit: emb\|CAB84662.1\| (AL162755) hypothetical protein NMA1423 [Neisseria meningitidis] |
| NGO0526 | 0.3045 | -1.81 | down | 0.1018 | -2.21 | down | 0.0403 | -2.15 | down | phosphoribosylaminoimidazole synthetase\ Context:(NC_002946)+[498789-499823]\ Notes:catalyzes the formation of 1-(5-phosphoribosyl)-5-aminoimidazole from 2-(formamido)-N1-(5-phosphoribosyl)acetamidine and ATP in purine biosynthesis |
| NGO0527 | 0.0165 | -14.91 | down | 0.5816 | -2.21 | down | 0.7092 | -1.29 | down | hypothetical protein\ Context:(NC_002946)+[500439-500957]\ Notes:Best Blastp Hit: pir\|\|D81804 hypothetical protein NMA1789 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380430\|emb\|CAB85016.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0529 | 0.2403 | -2.26 | down | 0.0076 | -9.10 | down | 0.0872 | -2.18 | down | putative high-affinity choline transport protein\ Context:(NC_002946)+[501653-503635]\ Notes:Best Blastp Hit: pir\|\|E81839 probable transmembrane transport protein NMA1483 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380131\|emb\|CAB84716.1\| (AL162756) putative transmembrane transport protein [Neisseria meningitidis] COG1292 Choline-glycine betaine transporter |
| NGO0530 | 0.3637 | 1.83 | up | 0.2368 | 1.94 | up | 0.2508 | -1.59 | down | acyl-CoA synthetase\ Context:(NC_002946)-[503725-505278]\ Notes:activates fatty acids by binding to coenzyme A |
| NGO0531 | 0.7611 | -1.48 | down | 0.0780 | -4.71 | down | 0.7142 | -1.54 | down | hypothetical protein\ Context:(NC_002946)+[505291-505446]\ Notes:Best Blastp Hit: pir\|\|T30159 hypothetical protein C37A2.7 - Caenorhabditis elegans >gi\|1943794\|gb\|AAB52450.1\| (U97194) strong similarity to 60S acidic ribosomal protein P2 [Caenorhabditis elegans] |
| NGO0532 | 0.1212 | 5.67 | up | 0.3045 | 1.76 | up | 0.2908 | 1.77 | up | hypothetical protein\ Context:(NC_002946)-[505529-506722]\ Notes:Best Blastp Hit: emb\|CAB84713.1\| (AL162756) putative periplasmic protein [Neisseria meningitidis] |
| NGO0533 | 0.9854 | -1.02 | down | 0.0478 | -7.21 | down | 0.6229 | -1.26 | down | hypothetical protein\ Context:(NC_002946)-[506719-507702]\ Notes:Best Blastp Hit: pir\|\|A81839 probable periplasmic protein NMA1479 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380127\|emb\|CAB84712.1\| (AL162756) putative periplasmic protein [Neisseria meningitidis] |
| NGO0534 | 0.7457 | -1.28 | down | 0.0036 | -13.40 | down | 0.3016 | 1.78 | up | putative alginate O-acetylation - like protein\ Context:(NC_002946)-[507713-509149]\ Notes:Best Blastp Hit: pir\|\|C81103 alginate O-acetylation protein AlgI; probable NMB1273 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226512\|gb\|AAF41650.1\| (AE002475) alginate O-acetylation protein AlgI; putative [Neisseria meningitidis MC58] COG1696 Predicted membrane protein involved in |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0537 | 0.2058 | -2.30 | down | 0.1393 | -2.32 | down | 0.7901 | 1.08 | up | hypothetical protein\ Context:(NC_002946)+[510723-511097]\ Notes:Best Blastp Hit: emb\|CAB84710.1\|(AL162756) putative mercuric ion binding protein [Neisseria meningitidis] COG2217 Cation transport ATPases |
| NGO0539 | 0.4877 | 1.46 | up | 0.9080 | 1.05 | up | 0.7559 | 1.10 | up | hypothetical protein\ Context:(NC_002946)+[512905-514002]\ Notes:Best Blastp Hit: pir\|\|G81102 hypothetical protein NMB1269 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226508\|gb\|AAF41646.1\|(AE002475) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0541 | 0.1339 | 2.72 | up | 0.1440 | 2.91 | up | 0.5950 | -1.26 | down | putative low-molecular weight phosphotyrosine protein phosphatase\ Context:(NC_002946)+[515356-515811]\ Notes:Best Blastp Hit: pir\|\|E81102 low molecular weight protein tyrosine-phosphatase NMB1267 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226506\|gb\|AAF41644.1\| (AE002475) low molecular weight protein tyrosine-phosphatase [Neisseria meningitidis MC58] COG0394 protein-tyrosine-phosphatase |
| NGO0542 | 0.1394 | 2.13 | up | 0.3311 | -1.60 | down | 0.6754 | -1.12 | down | hypothetical protein\ Context:(NC_002946)+[515888-516364]\ Notes:Best Blastp Hit: pir\|\|B81838 probable cation uptake regulator NMA1471 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380120\|emb\|CAB84705.1\| (AL162756) putative cation uptake regulator [Neisseria meningitidis] COG0735 Ferric uptake regulation protein |
| NGO0543 | 0.3543 | 1.55 | up | 0.0430 | 2.12 | up | 0.7818 | 1.09 | up | hypothetical protein\ Context:(NC_002946)+[516352-517278]\ Notes:Best Blastp Hit: emb\|CAB84704.1\|(AL162756) hypothetical protein NMA1470 [Neisseria meningitidis] COG0523 Putative GTPases (G3E family) |
| NGO0544 | 0.0267 | 3.42 | up | 0.1634 | 1.65 | up | 0.9863 | 1.01 | up | putative peptidyl-prolyl cis-trans isomerase A\ Context:(NC_002946)+[517343-517900]\ Notes:Best Blastp Hit: pir\|\|H81837 probable peptidylprolyl isomerase (EC 5.2.1.8) A NMA1469 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380118\|emb\|CAB84703.1\|(AL162756) putative peptidyl-prolyl cis-trans isomerase A [Neisseria meningitidis] COG0652 Peptidyl-prolyl cis-trans isomerase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0545 | 0.2804 | -2.39 | down | 0.0177 | -4.95 | down | 0.4993 | -2.04 | down | putative type III restriction-modification system methyltransferase\ Context:(NC_002946)+[518016-520079]\ Notes:Best Blastp Hit: possibly phase variable - 13 tandem repeats of CCAAC in the coding sequence (ON) COG2189 Adenine specific DNA methylase Mod |
| NGO0546 | 0.2848 | 3.87 | up | 0.5169 | -2.09 | down | 0.0650 | -4.63 | down | putative type III restriction-modification system endonuclease protein\ Context:(NC_002946)+[520169-523108]\ Notes:Best Blastp Hit: gb\|AAF41638.1\|(AE002474) type III restriction-modification system EcoPI enzyme; subunit res [Neisseria meningitidis MC58] |
| NGO0547 | 0.7788 | -1.14 | down | 0.5025 | 1.43 | up | 0.7991 | 1.07 | up | hypothetical protein\ Context:(NC_002946)-[523202-524161]\ Notes:Best Blastp Hit: pir\|\|F81129 conserved hypothetical protein NMB1023 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226263\|gb\|AAF41423.1\| (AE002453) conserved hypothetical protein [Neisseria meningitidis MC58] COG0037 Predicted ATPases of the PP-loop superamily |
| NGO0548 | 0.9382 | -1.04 | down | 0.3985 | -1.56 | down | 0.4490 | -1.32 | down | hypothetical protein\ Context:(NC_002946)-[524253-525119]\ Notes:Best Blastp Hit: pir\|\|G81129 conserved hypothetical protein NMB1024 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226264\|gb\|AAF41424.1\| (AE002453) conserved hypothetical protein [Neisseria meningitidis MC58] COG0354 Predicted aminomethyltransferase related to |
| NGO0549 | 0.2618 | 1.71 | up | 0.5049 | -1.58 | down | 0.9344 | -1.02 | down | hypothetical protein\ Context:(NC_002946)-[525151-525513]\ Notes:Best Blastp Hit: gb\|AAF41425.1\|(AE002453) conserved hypothetical protein [Neisseria meningitidis MC58] COG0251 Putative translation initiation inhibitor |
| NGO0550 | 0.8195 | 1.12 | up | 0.7558 | 1.15 | up | 0.8569 | 1.05 | up | hypothetical protein\ Context:(NC_002946)+[525588-526067]\ Notes:Best Blastp Hit: pir\|\|B81837 hypothetical protein NMA1462 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380112\|emb\|CAB84696.1\|(AL162756) hypothetical protein NMA1462 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0551 | 0.5770 | 1.40 | up | 0.4653 | -1.36 | down | 0.9310 | 1.02 | up | putative dnaJ-family protein\ Context:(NC_002946)+[526089-526781]\ Notes:Best Blastp Hit: emb\|CAB84695.1\| (AL162756) putative dnaJ-family protein [Neisseria meningitidis] COG0484 Molecular chaperones; DnaJ family (contain |
| NGO0552 | 0.5637 | -1.54 | down | 0.6453 | -1.35 | down | 0.1456 | -2.45 | down | hypothetical protein\ Context:(NC_002946)+[526785-527660]\ Notes:Best Blastp Hit: pir\|\|B81130 conserved hypothetical protein NMB1028 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226267\|gb\|AAF41427.1\| (AE002453) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0553 | 0.0516 | 2.57 | up | 0.1926 | 2.19 | up | 0.0072 | 3.30 | up | putative TonB-dependent receptor\ Context:(NC_002946)+[527868-531488]\ Notes:Best Blastp Hit: gb\|AAG08282.1\|AE004902_10 (AE004902) hypothetical protein [Pseudomonas aeruginosa] COG1629 Outer membrane receptor proteins; mostly |
| NGO0554 | 0.0003 | 64.24 | up | 0.0008 | 52.81 | up | 0.0002 | 18.19 | up | hypothetical protein\ Context:(NC_002946)+[531770-532720]\ Notes:Best Blastp Hit: sp\|Q03155\|AIDA_ECOLI adhesin Aida-i precursor >gi\|281809\|pir\|\|S28634 adhesin AIDA-I precursor - Escherichia coli plasmid pIB6 >gi\|42255\|emb\|CAA46156.1\| (X65022) AIDA-I [Escherichia coli] |
| NGO0555 | 0.0004 | 68.62 | up | 0.2234 | 6.03 | up | 0.0054 | 18.38 | up | hypothetical protein\ Context:(NC_002946)+[532940-534433]\ Notes:Best Blastp Hit: gb\|AAF40758.1\| (AE002388) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0556 | 0.1712 | -2.05 | down | 0.5037 | -1.26 | down | 0.4404 | -1.34 | down | aspartate ammonia-lyase\ Context:(NC_002946)-[534501-535898]\ Notes:catalyzes the formation of fumarate from aspartate |
| NGO0557 | 0.2753 | -1.89 | down | 0.3143 | -1.48 | down | 0.6249 | -1.20 | down | hypothetical protein\ Context:(NC_002946)-[535924-536112]\ Notes: |
| NGO0558 | 0.2942 | -1.85 | down | 0.9232 | -1.05 | down | 0.3609 | -1.47 | down | hypothetical protein\ Context:(NC_002946)-[536176-536736]\ Notes:Best Blastp Hit: pir\|\|D81130 conserved hypothetical protein NMB1030 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226269\|gb\|AAF41429.1\| (AE002453) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0561 | 0.0480 | 4.31 | up | 0.0557 | 3.39 | up | 0.0530 | 1.80 | up | hypothetical protein\ Context:(NC_002946)+[540134-541684]\ Notes:Best Blastp Hit: gb\|AAF41720.1\| (AE002483) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0562 | 0.2075 | 2.15 | up | 0.1381 | 1.70 | up | 0.1705 | 1.80 | up | putative dihydrolipoamide dehydrogenase\ Context:(NC_002946)-[542108-543892]\ Notes:Best Blastp Hit: gb\|AAF41719.1\| (AE002482) pyruvate dehydrogenase; E3 component; lipoamide dehydrogenase [Neisseria meningitidis MC58] COG1249 Dihydrolipoamide dehydrogenase/glutathione |
| NGO0563 | 0.1371 | 2.69 | up | 0.0136 | 2.81 | up | 0.0264 | 2.81 | up | hypothetical protein\ Context:(NC_002946)-[543910-544200]\ Notes:Best Blastp Hit: pir\|\|G81094 hypothetical protein NMB1343 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226587\|gb\|AAF41718.1\| (AE002482) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0564 | 0.1871 | 2.65 | up | 0.1063 | 5.20 | up | 0.1423 | 2.06 | up | dihydrolipoamide acetyltransferase\ Context:(NC_002946)-[544445-546034]\ Notes:Catalyzes the transfer of acetyl from acetyldihydrolipoamide to coenzyme A to form acetyl CoA |
| NGO0565 | 0.2612 | 2.46 | up | 0.0435 | 2.11 | up | 0.0556 | 2.76 | up | pyruvate dehydrogenase subunit E1\ Context:(NC_002946)-[546184-548847]\ Notes:E1 component; part of pyruvate dehydrogenase; forms a complex with DlaT and LpdC |
| NGO0566 | 0.0907 | 2.25 | up | 0.1030 | 2.14 | up | 0.2983 | 1.35 | up | prolyl-tRNA synthetase\ Context:(NC_002946)+[549544-551256]\ Notes:catalyzes the formation of prolyl-tRNA(Pro) from proline and tRNA(Pro) |
| NGO0567 | 0.1326 | 2.95 | up | 0.0999 | 2.97 | up | 0.9052 | -1.06 | down | putative hydrolase\ Context:(NC_002946)+[551319-551975]\ Notes:Best Blastp Hit: pir\|\|B81094 isomerase; probable NMB1338 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226582\|gb\|AAF41713.1\| (AE002482) isomerase; putative [Neisseria meningitidis MC58] COG0179 2-keto-4-pentenoate |
| NGO0568 | 0.3792 | 1.99 | up | 0.1227 | -2.95 | down | 0.2222 | -1.78 | down | Holliday junction resolvase-like protein\ Context:(NC_002946)-[551985-552440]\ Notes:similar to RuvC resolvase with substantial differences; NMR structural information suggests this protein is monomeric; unknown cellular function |
| NGO0569 | 0.4235 | 1.68 | up | 0.7050 | 1.25 | up | 0.8963 | -1.06 | down | hypothetical protein\ Context:(NC_002946)-[552433-552981]\ Notes:Best Blastp Hit: gb\|AAF41711.1\| (AE002482) conserved hypothetical protein [Neisseria meningitidis MC58] COG1678 Uncharacterized ACR |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0570 | 0.1976 | 1.94 | up | 0.3497 | 1.97 | up | 0.3787 | 1.44 | up | hypothetical protein\ Context:(NC_002946)-[552983-553543]\ Notes:Best Blastp Hit: emb\|CAB84776.1\|(AL162756) hypothetical lipoprotein [Neisseria meningitidis] |
| NGO0571 | 0.9107 | -1.05 | down | 0.6887 | 1.17 | up | 0.9078 | -1.03 | down | hypothetical protein\ Context:(NC_002946)+[553869-555665]\ Notes:Best Blastp Hit: possibly phase variable - 9A residue homopolymer repeat in the coding sequence (ON) COG0739 Membrane proteins related to |
| NGO0572 | 0.0880 | 2.79 | up | 0.1922 | 1.67 | up | 0.9223 | 1.03 | up | putative carboxy-terminal processing protease\ Context:(NC_002946)+[555792-557267]\ Notes:Best Blastp Hit: pir\|\|E81846 probable carboxy-terminal processing proteinase NMA1546 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380187\|emb\|CAB84773.1\|(AL162756) putative carboxy-terminal processing protease [Neisseria meningitidis] COG0793 Periplasmic protease |
| NGO0573 | 0.0134 | 3.97 | up | 0.1074 | 3.69 | up | 0.0834 | 1.83 | up | excinuclease ABC subunit B\ Context:(NC_002946)+[557597-559624]\ Notes:The UvrABC repair system catalyzes the recognition and processing of DNA lesions. The beta-hairpin of the Uvr-B subunit is inserted between the strands; where it probes for the presence of a lesion |
| NGO0574 | 0.0897 | 3.33 | up | 0.0061 | 3.64 | up | 0.0295 | 3.45 | up | Cah\ Context:(NC_002946)-[559802-560560]\ Notes:Best Blastp Hit: sp\|Q50940\|CAH_NEIGO carbonic anhydrase precursor (carbonate dehydratase) >gi\|1841441\|emb\|CAA72038.1\| (Y11152) carbonic anhydrase [Neisseria gonorrhoeae] |
| NGO0575 | 0.0761 | 3.96 | up | 0.1904 | 6.42 | up | 0.9739 | -1.02 | down | tRNA (guanine-N(7))-methyltransferase\ Context:(NC_002946)-[561640-562356]\ Notes:tRNA (guanine-N(7)-)-methyltransferase; catalyzes the formation of N(7)-methylguanine at position 46 (m7G46) in tRNA by transferring the methyl residue from S-adenosyl-L-methionine |
| NGO0578 | 0.0558 | 3.36 | up | 0.5538 | -1.48 | down | 0.2974 | 1.75 | up | excinuclease ABC subunit C\ Context:(NC_002946)-[564000-565886]\ Notes:The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvrC both incises the 5' and 3' sides of the lesion. The N-terminal half is responsible for the 3' incision and the C-terminal half is responsible for the 5' incision |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0579 | 0.3283 | 2.12 | up | 0.7905 | -1.13 | down | 0.9508 | -1.03 | down | putative transport ATPase\ Context:(NC_002946)-[565941-568118]\ Notes:Best Blastp Hit: pir\|\|F81845 probable cation-transporting ATPase NMA1539 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380180\|emb\|CAB84766.1\| (AL162756) putative cation-transporting ATPase [Neisseria meningitidis] COG2217 Cation transport ATPases |
| NGO0580 | 0.1627 | 2.16 | up | 0.3162 | 1.47 | up | 0.3413 | 1.41 | up | putative thioredoxin reductase\ Context:(NC_002946)+[568257-569207]\ Notes:Best Blastp Hit: pir\|\|C81097 thioredoxin reductase NMB1324 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226566\|gb\|AAF41699.1\| (AE002480) thioredoxin reductase [Neisseria meningitidis MC58] COG0492 Thioredoxin reductase/alkyl |
| NGO0581 | 0.0482 | 2.93 | up | 0.1864 | 1.70 | up | 0.4145 | 1.34 | up | 30S ribosomal protein S6\ Context:(NC_002946)+[569363-569731]\ Notes:binds cooperatively with S18 to the S15-16S complex; allowing platform assembly to continue with S11 and S21 |
| NGO0582 | 0.0780 | 3.14 | up | 0.1436 | 1.75 | up | 0.2767 | 1.54 | up | PriB\ Context:(NC_002946)+[569732-570034]\ Notes:Best Blastp Hit: pir\|\|A81097 primosomal replication protein n; probable NMB1322 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226564\|gb\|AAF41697.1\| (AE002480) primosomal replication protein n; putative [Neisseria meningitidis MC58]; putative primosomal replication protein |
| NGO0583 | 0.1158 | 2.79 | up | 0.2107 | 1.65 | up | 0.3097 | 1.51 | up | 30S ribosomal protein S18\ Context:(NC_002946)+[570041-570271]\ Notes:binds as a heterodimer with protein S6 to the central domain of the 16S rRNA; helps stabilize the platform of the 30S subunit |
| NGO0584 | 0.0621 | 3.10 | up | 0.0974 | 1.87 | up | 0.2695 | 1.48 | up | 50S ribosomal protein L9\ Context:(NC_002946)+[570288-570740]\ Notes:in Escherichia coli this protein is wrapped around the base of the L1 stalk |
| NGO0585 | 0.8303 | -1.13 | down | 0.2486 | -1.94 | down | 0.8499 | 1.11 | up | hypothetical protein\ Context:(NC_002946)-[571363-572169]\ Notes:Best Blastp Hit: emb\|CAB84760.1\| (AL162756) conserved hypothetical integral membrane protein [Neisseria meningitidis] COG0730 Predicted permeases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0586 | 0.1596 | 2.02 | up | 0.8813 | -1.06 | down | 0.4732 | 1.20 | up | putative phosphatidylserine synthase\ Context:(NC_002946)-[572170-572916]\ Notes:Best Blastp Hit: pir\|\|E81096 CDPdiacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8) NMA1532 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226560\|gb\|AAF41693.1\| (AE002480) CDP-diacylglycerol--serine O-phosphatidyltransferse [Neisseria meningitidis MC58] >gi\|7380173\|emb\|CAB84759.1\| (AL162756) phosphatidylserine synthase [Neisseria meningitidis] COG1183 Phosphatidylserine synthase |
| NGO0587 | 0.9314 | -1.10 | down | 0.0556 | -9.57 | down | 0.9275 | 1.04 | up | hypothetical protein\ Context:(NC_002946)-[572971-573243]\ Notes:Best Blastp Hit: gb\|AAF41692.1\| (AE002480) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0588 | 0.0143 | -4.05 | down | 0.6776 | 1.16 | up | 0.0897 | -2.39 | down | hypothetical protein\ Context:(NC_002946)+[573500-573982]\ Notes:Best Blastp Hit: pir\|\|E81844 hypothetical protein NMA1529 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380171\|emb\|CAB84757.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0589 | 0.6143 | -1.40 | down | 0.1268 | -1.81 | down | 0.6248 | 1.33 | up | putative ABC transporter; permease protein\ Context:(NC_002946)-[574029-575240]\ Notes:Best Blastp Hit: pir\|\|B81096 uracil permease NMB1315 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226557\|gb\|AAF41690.1\| (AE002480) uracil permease [Neisseria meningitidis MC58] COG2233 Xanthine/uracil permeases |
| NGO0590 | 0.8261 | -1.10 | down | 0.4126 | 1.57 | up | 0.1001 | 1.66 | up | putative ftsK-like cell division/stress response protein\ Context:(NC_002946)+[575669-577900]\ Notes:Best Blastp Hit: pir\|\|A81096 cell division protein FtsK NMB1314 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226556\|gb\|AAF41689.1\| (AE002480) cell division protein FtsK [Neisseria meningitidis MC58] COG1674 DNA segregation ATPase FtsK/SpoIIIE and |
| NGO0592 | 0.6027 | 1.35 | up | 0.8364 | 1.08 | up | 0.9983 | -1.00 | down | trigger factor\ Context:(NC_002946)+[578772-580085]\ Notes:Tig; RopA; peptidyl-prolyl cis/trans isomerase; promotes folding of newly synthesized proteins; binds ribosomal 50S subunit; forms a homodimer |

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| NGO0593 | 0.4386 | 1.52 | up | 0.8236 | -1.10 | down | 0.8491 | 1.06 | up | putative endopeptidase\ Context:(NC_002946)+[580181-580795]\ Notes:Best Blastp Hit: pir\|\|A81844 endopeptidase (EC 3.4.21.92) NMA1525 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380167\|emb\|CAB84753.1\| (AL162756) endopeptidase [Neisseria meningitidis] COG0740 Protease subunits of ATP-dependent |
| NGO0594 | 0.6756 | 1.22 | up | 0.1991 | 1.59 | up | 0.3929 | 1.35 | up | 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase\ Context:(NC_002946)-[580849-582114]\ Notes:catalyzes the conversion of 2C-methyl-D-erythritol 2;4-cyclodiphosphate into 4-hydroxy-3-methyl-2-en-1-yl diphosphate; involved in isoprenoid synthesis |
| NGO0595 | 0.0121 | 3.93 | up | 0.0527 | 2.51 | up | 0.1611 | 1.56 | up | hypothetical protein\ Context:(NC_002946)-[582130-582891]\ Notes:Best Blastp Hit: gb\|AAF41684.1\| (AE002479) fimbrial biogenesis and twitching motility protein; putative [Neisseria meningitidis MC58] |
| NGO0596 | 0.2504 | 1.67 | up | 0.0373 | 2.28 | up | 0.3098 | 1.33 | up | hypothetical protein\ Context:(NC_002946)-[582894-583988]\ Notes:Best Blastp Hit: pir\|\|B81098 conserved hypothetical protein NMB1308 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226549\|gb\|AAF41683.1\| (AE002479) conserved hypothetical protein [Neisseria meningitidis MC58] COG0820 Predicted Fe-S-cluster redox enzyme |
| NGO0597 | 0.3018 | 1.70 | up | 0.5830 | 1.26 | up | 0.8449 | 1.06 | up | putative nucleoside diphosphate kinase\ Context:(NC_002946)-[584132-584443]\ Notes:Best Blastp Hit: pir\|\|A81098 nucleoside diphosphate kinase (EC 2.7.4.6) NMA1521 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226548\|gb\|AAF41682.1\| (AE002479) nucleoside diphosphate kinase [Neisseria meningitidis MC58] >gi\|7380163\|emb\|CAB84749.1\| (AL162756) nucleoside diphosphate kinase [Neisseria meningitidis] COG0105 Nucleoside diphosphate kinase |

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| NGO0598 | 0.3343 | 1.62 | up | 0.6764 | -1.24 | down | 0.5022 | 1.21 | up | hypothetical protein\ Context:(NC_002946)-[584616-585767]\ Notes:Best Blastp Hit: pir\|\|H81097 probable nucleotide-binding protein NMA1520 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226547\|gb\|AAF41681.1\| (AE002479) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380162\|emb\|CAB84748.1\| (AL162756) putative nucleotide-binding protein [Neisseria meningitidis] COG1485 Predicted ATPase |
| NGO0600 | 0.0024 | -16.84 | down | 0.0001 | -31.89 | down | 0.1268 | -6.75 | down | putative esterase D\ Context:(NC_002946)-[586297-587043]\ Notes:Best Blastp Hit: pir\|\|G81097 esterase; probable NMB1305 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226546\|gb\|AAF41680.1\| (AE002479) esterase; putative [Neisseria meningitidis MC58] COG0627 Predicted esterase |
| NGO0602 | 0.3168 | -3.09 | down | 0.0069 | -8.93 | down | 0.4126 | -1.57 | down | MerR family transcriptional regulator\ Context:(NC_002946)+[588393-588800]\ Notes:Best Blastp Hit: pir\|\|E81097 transcription regulator; MerR family NMB1303 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226544\|gb\|AAF41678.1\| (AE002479) transcriptional regulator; MerR family [Neisseria meningitidis MC58] >gi\|7380159\|emb\|CAB84745.1\| (AL162756) putative transcriptional regulator [Neisseria meningitidis] COG0789 Predicted transcriptional regulators |
| NGO0603 | 0.4820 | 1.42 | up | 0.3169 | 1.55 | up | 0.7958 | 1.11 | up | IhfB\ Context:(NC_002946)-[588996-589292]\ Notes:Best Blastp Hit: pir\|\|H81099 integration host factor; beta chain NMB1302 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226542\|gb\|AAF41677.1\| (AE002478) integration host factor; beta subunit [Neisseria meningitidis MC58] >gi\|7380158\|emb\|CAB84744.1\| (AL162756) integration host factor beta-subunit [Neisseria meningitidis] >gi\|9965584\|gb\|AAG10095.1\| (U90958) IfhA [Neisseria gonorrhoeae] COG0776 Histone-like DNA-binding protein; integration host factor beta subunit |

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| NGO0604 | 0.0908 | 2.86 | up | 0.2089 | 1.54 | up | 0.2028 | 1.66 | up | 30S ribosomal protein S1\ Context:(NC_002946)-[589321-591006]\ Notes:in Escherichia coli this protein is involved in binding to the leader sequence of mRNAs and is itself bound to the 30S subunit; autoregulates expression via a C-terminal domain; in most gram negative organisms this protein is composed of 6 repeats of the S1 domain while in gram positive there are 4 repeats; the S1 nucleic acid-binding domain is found associated with other proteins |
| NGO0605 | 0.8497 | 1.11 | up | 0.9084 | -1.05 | down | 0.9515 | -1.02 | down | putative cytidylate kinase\ Context:(NC_002946)-[591159-591815]\ Notes:Best Blastp Hit: sp\|P57065\|KCY_NEIMB cytidylate kinase (CK) (cytidine monophosphate kinase) (CMP KINASE) >gi\|11279481\|pir\|\|F81099 cytidylate kinase NMB1300 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226540\|gb\|AAF41675.1\| (AE002478) cytidylate kinase [Neisseria meningitidis MC58] COG0283 Cytidylate kinase |
| NGO0606 | 0.0608 | -5.30 | down | 0.0670 | -4.18 | down | 0.2874 | -1.74 | down | putative sodium-dependent transport protein\ Context:(NC_002946)-[592048-593418]\ Notes:Best Blastp Hit: sp\|P45320\|YG90_HAEIN hypothetical sodium-dependent transporter HI1690 >gi\|1075054\|pir\|\|H64136 neurotransmitter transport protein homolog - Haemophilus influenzae (strain Rd KW20) >gi\|1574543\|gb\|AAC23336.1\| (U32842) sodium-dependent transporter; putative [Haemophilus influenzae Rd] COG0733 Sodium-dependent transporters (SNF family) |
| NGO0607 | 0.0159 | 7.97 | up | 0.0320 | 7.38 | up | 0.0540 | 4.83 | up | hypothetical protein\ Context:(NC_002946)-[593892-594584]\ Notes:Best Blastp Hit: gb\|AAF41674.1\| (AE002478) ribosomal small subunit pseudouridine synthase A [Neisseria meningitidis MC58] >gi\|7380155\|emb\|CAB84740.1\| (AL162756) putative ribosomal small subunit pseudouridine synthase [Neisseria meningitidis] COG1187 Predicted pseudouridylate synthase family 1 |

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| NGO0608 | 0.0103 | 6.32 | up | 0.0251 | 23.31 | up | 0.0241 | 6.80 | up | putative murein transglycosylase / nitrite reductase transcriptional regulator\ Context:(NC_002946)-[594652-596628]\ Notes:Best Blastp Hit: pir\|\|D81842 probable membrane bound murein transglycosylase NMA1507 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380154\|emb\|CAB84739.1\| (AL162756) putative membrane bound murein transglycosylase [Neisseria meningitidis] COG0741 Soluble lytic murein transglycosylase and |
| NGO0609 | 0.6385 | -1.42 | down | 0.6023 | -1.19 | down | 0.1296 | -2.50 | down | hypothetical protein\ Context:(NC_002946)+[596807-597472]\ Notes:Best Blastp Hit: pir\|\|C81842 hypothetical protein NMA1506 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380153\|emb\|CAB84738.1\| (AL162756) hypothetical protein [Neisseria meningitidis] COG0500 SAM-dependent methyltransferases |
| NGO0610 | 0.4889 | -1.36 | down | 0.7982 | -1.14 | down | 0.5130 | -1.26 | down | formamidopyrimidine-DNA glycosylase\ Context:(NC_002946)+[597525-598352]\ Notes:Best Blastp Hit: sp\|P55044\|FPG_NEIMB formamidopyrimidine-DNA glycosylase (FapY-DNA glycosylase) >gi\|11264471\|pir\|\|B81099 formamidopyrimidine-DNA glycosylase NMB1295 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226536\|gb\|AAF41671.1\| (AE002478) formamidopyrimidine-DNA glycosylase [Neisseria meningitidis MC58] COG0266 Formamidopyrimidine-DNA glycosylase |
| NGO0611 | 0.5991 | 1.52 | up | 0.2558 | -1.96 | down | 0.3142 | -1.66 | down | 1-acyl-SN-glycerol-3-phosphate acyltransferase\ Context:(NC_002946)+[598440-599207]\ Notes:Best Blastp Hit: sp\|Q59601\|PLSC_NEIGO 1-acyl-SN-glycerol-3-phosphate acyltransferase (1-AGP acyltransferase) (1-AGPAT) (lysophosphatidic acid acyltransferase) (LPAAT) >gi\|2120869\|pir\|\|S70545 1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) - Neisseria gonorrhoeae >gi\|972976\|gb\|AAB40877.1\| (U21806) 1-acyl-sn-glycerol-3-phosphate acyltransferase [Neisseria gonorrhoeae] COG0204 1-acyl-sn-glycerol-3-phosphate |

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| NGO0613 | 0.0034 | -8.09 | down | 0.0020 | -8.69 | down | 0.2370 | -2.14 | down | hypothetical protein\ Context:(NC_002946)-[599470-599781]\ Notes:Best Blastp Hit: pir\|\|H81098 hypothetical protein NMB1293 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226534\|gb\|AAF41669.1\|(AE002478) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0614 | 0.2757 | 1.78 | up | 0.0479 | 2.17 | up | 0.2073 | 1.51 | up | ribonucleotide-diphosphate reductase subunit alpha\ Context:(NC_002946)+[600312-602591]\ Notes:Catalyzes the rate-limiting step in dNTP synthesis |
| NGO0615 | 0.2810 | 1.75 | up | 0.2621 | 1.46 | up | 0.3441 | 1.34 | up | ribonucleotide-diphosphate reductase subunit beta\ Context:(NC_002946)+[602904-604037]\ Notes:B2 or R2 protein; type 1a enzyme; catalyzes the rate-limiting step in dNTP synthesis; converts nucleotides to deoxynucleotides; forms a homodimer and then a multimeric complex with NrdA |
| NGO0616 | 0.0075 | 8.39 | up | 0.0268 | 6.49 | up | 0.1045 | 2.90 | up | hypothetical protein\ Context:(NC_002946)-[604489-604767]\ Notes:Best Blastp Hit: gb\|AAF41662.1\|(AE002477) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380144\|emb\|CAB84729.1\|(AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0617 | 0.0638 | 3.52 | up | 0.0205 | 2.63 | up | 0.0888 | 2.27 | up | phosphopyruvate hydratase\ Context:(NC_002946)-[604935-606221]\ Notes:enolase; catalyzes the formation of phosphoenolpyruvate from 2-phospho-D-glycerate in glycolysis |
| NGO0618 | 0.2189 | 1.78 | up | 0.4923 | 1.33 | up | 0.4744 | 1.21 | up | hypothetical protein\ Context:(NC_002946)-[606268-606708]\ Notes:Best Blastp Hit: pir\|\|C81100 hypothetical protein NMB1284 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226524\|gb\|AAF41660.1\|(AE002477) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0619 | 0.0966 | -2.61 | down | 0.1848 | -2.03 | down | 0.1319 | -1.99 | down | 2-dehydro-3-deoxyphosphooctonate aldolase\ Context:(NC_002946)-[606723-607565]\ Notes:catalyzes the formation of 2-dehydro-3-deoxy-D-octonate 8-phosphate from phosphoenolpyruvate and D-arabinose 5-phosphate in LPS biosynthesis |

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| NGO0620 | 0.7432 | 1.22 | up | 0.9731 | -1.01 | down | 0.6967 | 1.13 | up | aspartate alpha-decarboxylase\ Context:(NC_002946)-[607587-607970]\ Notes:Converts L-aspartate to beta-alanine and provides the major route of beta-alanine production in bacteria. Beta-alanine is essential for the biosynthesis of pantothenate (vitamin B5) |
| NGO0621 | 0.0974 | 2.51 | up | 0.8396 | -1.19 | down | 0.7021 | 1.44 | up | hypothetical protein\ Context:(NC_002946)-[608132-608434]\ Notes: |
| NGO0622 | 0.6930 | -1.44 | down | 0.9419 | 1.11 | up | 0.2554 | 4.04 | up | hypothetical protein\ Context:(NC_002946)-[608468-608587]\ Notes: |
| NGO0623 | 0.0102 | 5.58 | up | 0.4581 | 2.11 | up | 0.8057 | 1.21 | up | putative transcription-repair coupling factor\ Context:(NC_002946)-[608660-612364]\ Notes:Best Blastp Hit: pir\|\|A81102 transcription-repair coupling factor NMB1281 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226520\|gb\|AAF41657.1\| (AE002476) transcription-repair coupling factor [Neisseria meningitidis MC58] COG1197 Transcription-repair coupling factor - |
| NGO0624 | 0.8225 | 1.11 | up | 0.9308 | 1.06 | up | 0.5858 | 1.18 | up | putative oxidoreductase\ Context:(NC_002946)+[612423-613976]\ Notes:Best Blastp Hit: emb\|CAB84723.1\| (AL162756) putative oxidoreductase [Neisseria meningitidis] |
| NGO0625 | 0.2504 | 1.82 | up | 0.0904 | 5.01 | up | 0.0780 | 3.43 | up | hypothetical protein\ Context:(NC_002946)+[613967-614215]\ Notes:Best Blastp Hit: emb\|CAB84722.1\| (AL162756) hypothetical protein NMA1489 [Neisseria meningitidis] |
| NGO0626 | 0.9518 | -1.04 | down | 0.3248 | 2.15 | up | 0.5869 | -1.30 | down | putative murein hydrolase\ Context:(NC_002946)+[614124-615215]\ Notes:Best Blastp Hit: pir\|\|G81101 membrane-bound lytic murein transglycosylase B; probable NMB1279 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226518\|gb\|AAF41655.1\| (AE002476) membrane-bound lytic murein transglycosylase B; putative [Neisseria meningitidis MC58] |
| NGO0627 | 0.2592 | -1.83 | down | 0.7124 | 1.28 | up | 0.4161 | -1.64 | down | Gcr\ Context:(NC_002946)-[615338-617344]\ Notes:Best Blastp Hit: pir\|\|F81101 site-specific recombinase NMB1278 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226517\|gb\|AAF41654.1\| (AE002476) site-specific recombinase [Neisseria meningitidis MC58]; putative site-specific recombinase |

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| NGO0629 | 0.0753 | 2.57 | up | 0.0380 | 6.43 | up | 0.0627 | 2.26 | up | DNA gyrase subunit A\ Context:(NC_002946)-[618439-621189]\ Notes:Best Blastp Hit: sp\|P48371\|GYRA_NEIGO DNA gyrase subunit A >gi\|2120873\|pir\|\|S60779 DNA gyrase chain A - Neisseria gonorrhoeae >gi\|529408\|gb\|AAA82128.1\| (U08817) DNA gyrase subunit A [Neisseria gonorrhoeae] COG0188 DNA gyrase (topoisomerase II) A subunit |
| NGO0630 | 0.8980 | -1.11 | down | 0.3986 | -1.67 | down | 0.7267 | 1.22 | up | putative chaperone protein HscB\ Context:(NC_002946)-[621287-621640]\ Notes:Best Blastp Hit: gb\|AAF62332.1\| (AE002486) chaperone protein HscB [Neisseria meningitidis MC58] COG1076 DnaJ-domain-containing proteins 1 |
| NGO0631 | 0.4427 | -1.72 | down | 0.0064 | -37.39 | down | 0.4707 | -2.43 | down | hypothetical protein\ Context:(NC_002946)+[621689-621838]\ Notes: |
| NGO0632 | 0.2007 | 2.11 | up | 0.4108 | 1.65 | up | 0.1439 | 1.92 | up | hypothetical protein\ Context:(NC_002946)-[622050-622370]\ Notes:Best Blastp Hit: pir\|\|H81089 HesB/YadR/YfhF family protein NMB1381 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226622\|gb\|AAF41749.1\| (AE002486) HesB/YadR/YfhF family protein [Neisseria meningitidis MC58] COG0316 Uncharacterized ACR; HesB/YadR/YfhF family |
| NGO0633 | 0.6662 | 1.23 | up | 0.0874 | 1.83 | up | 0.1770 | 1.72 | up | scaffold protein\ Context:(NC_002946)-[622457-622843]\ Notes:Best Blastp Hit: pir\|\|G81852 NifU-like protein NMA1596 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380237\|emb\|CAB84823.1\| (AL162756) NifU-like protein [Neisseria meningitidis] COG0822 NifU homologs involved in Fe-S cluster |
| NGO0635 | 0.0443 | 3.66 | up | 0.0198 | 2.96 | up | 0.0076 | 3.31 | up | hypothetical protein\ Context:(NC_002946)-[623656-623946]\ Notes:Best Blastp Hit: pir\|\|I50969 MHC class II beta chain - Melanochromis auratus (fragment) >gi\|2147702\|pir\|\|I50985 MHC class II beta chain - Melanochromis auratus (fragment) >gi\|308982\|gb\|AAA49352.1\| (L17439) Mhc class II beta chain [Melanochromis auratus] >gi\|309016\|gb\|AAA49368.1\| (L17463) MHC class II beta chain [Melanochromis auratus] |

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| NGO0636 | 0.0771 | 2.81 | up | 0.0207 | 3.17 | up | 0.0369 | 2.16 | up | putative NifS-like aminotransferase\ Context:(NC_002946)-[623952-625166]\ Notes:Best Blastp Hit: pir\|\|E81852 NifS-like aminotranfserase NMA1594 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380235\|emb\|CAB84821.1\| (AL162756) NifS-like aminotranfserase [Neisseria meningitidis] COG1104 Cysteine sulfinate desulfinase/cysteine |
| NGO0637 | 0.1273 | 2.35 | up | 0.0660 | 2.00 | up | 0.1235 | 1.79 | up | hypothetical protein\ Context:(NC_002946)-[625195-625641]\ Notes:Best Blastp Hit: sp\|Q51134\|YF93_NEIMA hypothetical protein NMA1593/NMB1378 precursor >gi\|11278638\|pir\|\|D81852 conserved hypothetical DNA-binding protein NMA1593 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380234\|emb\|CAB84820.1\| (AL162756) conserved hypothetical DNA-binding protein [Neisseria meningitidis] >gi\|7413461\|gb\|AAF62328.1\| (AE002486) conserved hypothetical protein [Neisseria meningitidis MC58] COG1959 Uncharacterized BCR; YjeB/RRF2 family |
| NGO0638 | 0.0900 | -9.30 | down | 0.0138 | -27.09 | down | 0.2545 | -3.00 | down | hypothetical protein\ Context:(NC_002946)+[625640-625870]\ Notes: |
| NGO0639 | 0.0102 | 4.89 | up | 0.0196 | 2.91 | up | 0.0380 | 2.15 | up | putative L-lactate dehydrogenase\ Context:(NC_002946)+[625991-627163]\ Notes:Best Blastp Hit: pir\|\|C81852 L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) NMA1592 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380233\|emb\|CAB84819.1\| (AL162756) L-lactate dehydrogenase [Neisseria meningitidis] COG1304 L-lactate dehydrogenase (FMN-dependent) and |
| NGO0640 | 0.0299 | -3.11 | down | 0.3894 | 1.87 | up | 0.4841 | 1.34 | up | RmsR\ Context:(NC_002946)-[627312-630086]\ Notes:Best Blastp Hit: gb\|AAD02478.1\| (AF048762) hypothetical membrane lipoprotein [Neisseria meningitidis]; putative restriction modification system-R protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0641 | 0.0550 | 3.21 | up | 0.0685 | 6.26 | up | 0.1712 | 1.75 | up | putative type III restriction/modification system modification methylase\ Context:(NC_002946)-[630076-632346]\ Notes:Best Blastp Hit: possibly phase variable - 37 tandem repeats of CGGT in the coding sequence (ON) and an 8T residue homopolymer repeat in the coding sequence (ON) COG2189 Adenine specific DNA methylase Mod |
| NGO0642 | 0.4125 | -1.54 | down | 0.5062 | -1.58 | down | 0.5590 | -1.27 | down | putative tRNA pseudouridine synthase B\ Context:(NC_002946)-[632563-633483]\ Notes:Best Blastp Hit: pir\|\|G81851 pseudouridylate synthase (EC 4.2.1.70) B tRNA-specific NMA1588 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380229\|emb\|CAB84815.1\|(AL162756) tRNA pseudouridine synthase B [Neisseria meningitidis] COG0130 Pseudouridine synthase |
| NGO0643 | 0.6211 | 1.37 | up | 0.1727 | 1.73 | up | 0.8387 | 1.07 | up | hypothetical protein\ Context:(NC_002946)-[633541-634086]\ Notes:Best Blastp Hit: pir\|\|F81851 hypothetical protein NMA1587 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380228\|emb\|CAB84814.1\|(AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0644 | 0.5322 | 1.44 | up | 0.5054 | 1.26 | up | 0.9650 | 1.01 | up | ribosome-binding factor A\ Context:(NC_002946)-[634076-634447]\ Notes:associates with free 30S ribosomal subunits; essential for efficient processing of 16S rRNA; in Escherichia coli rbfA is induced by cold shock |
| NGO0645 | 0.0923 | -2.61 | down | 0.1558 | -1.95 | down | 0.0595 | -1.81 | down | ATP-dependent protease ATP-binding subunit\ Context:(NC_002946)+[634630-635874]\ Notes:binds and unfolds substrates as part of the ClpXP protease |
| NGO0646 | 0.0792 | -3.02 | down | 0.0890 | -2.07 | down | 0.2074 | -1.44 | down | bifunctionalN-succinyldiaminopimelate-aminotransferase/acetylornithine transaminase protein\ Context:(NC_002946)-[635981-637174]\ Notes:DapATase; bifunctional enzyme that functions in arginine and lysine biosynthetic pathways; catalyzes the formation of N-acetyl-L-glutamate 5-semialdehyde from 2-oxoglutarate and N(2)-acetyl-L-ornithine or N-succinyl-2-L-amino-6-oxoheptanedioate from 2-oxoglutarate and N-succinyl-L-2;6-diaminoheptanedioate |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0647 | 0.0006 | -13.09 | down | 0.0003 | -18.55 | down | 0.0017 | -14.86 | down | hypothetical protein\ Context:(NC_002946)+[637578-638078]\ Notes:Best Blastp Hit: pir\|\|G81090 hypothetical protein NMB1370 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226616\|gb\|AAF41744.1\| (AE002485) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0648 | 0.6514 | 1.28 | up | 0.7352 | -1.11 | down | 0.6751 | 1.15 | up | hypothetical protein\ Context:(NC_002946)+[638163-638717]\ Notes:Best Blastp Hit: pir\|\|F81090 hypothetical protein NMB1369 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226615\|gb\|AAF41743.1\| (AE002485) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0649 | 0.3869 | -2.12 | down | 0.3024 | -2.29 | down | 0.3599 | -1.68 | down | hypothetical protein\ Context:(NC_002946)+[638731-638931]\ Notes: |
| NGO0650 | 0.0421 | 3.71 | up | 0.0061 | 7.45 | up | 0.0466 | 2.24 | up | putative ATP-dependent RNA helicase\ Context:(NC_002946)-[639282-640670]\ Notes:Best Blastp Hit: gb\|AAF41742.1\| (AE002485) ATP-dependent RNA helicase; putative [Neisseria meningitidis MC58] COG0513 Superfamily II DNA and RNA helicases |
| NGO0651 | 0.4316 | 2.12 | up | 0.1954 | -3.25 | down | 0.3100 | -2.51 | down | hypothetical protein\ Context:(NC_002946)+[640881-641945]\ Notes:Best Blastp Hit: gb\|AAF41741.1\| (AE002485) conserved hypothetical protein [Neisseria meningitidis MC58] COG1092 Predicted SAM-dependent methyltransferases |
| NGO0652 | 0.1872 | 2.18 | up | 0.2214 | 1.58 | up | 0.3211 | 1.38 | up | putative thioredoxin I\ Context:(NC_002946)-[641997-642329]\ Notes:Best Blastp Hit: pir\|\|E81850 thioredoxin I NMA1578 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380219\|emb\|CAB84805.1\| (AL162756) thioredoxin I [Neisseria meningitidis] COG0526 Thiol-disulfide isomerase and thioredoxins |
| NGO0653 | 0.0007 | -14.27 | down | 0.0060 | -12.21 | down | 0.6988 | 1.28 | up | hypothetical protein\ Context:(NC_002946)+[642627-643100]\ Notes:Best Blastp Hit: pir\|\|D81850 hypothetical protein NMA1577 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380218\|emb\|CAB84804.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |

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| NGO0654 | 0.5503 | -1.35 | down | 0.2968 | -1.55 | down | 0.4548 | -1.27 | down | putative NH(3)-dependent NAD synthetase\ Context:(NC_002946)-[643171-643992]\ Notes:Best Blastp Hit: pir\|\|C81850 NAD+ synthase (glutamine-hydrolyzing) (EC 6.3.5.1) NMA1576 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7380217\|emb\|CAB84803.1\| (AL162756) NH(3)-dependent NAD synthetase [Neisseria meningitidis] COG0171 NAD synthase |
| NGO0655 | 0.0005 | -12.84 | down | 0.0002 | -57.57 | down | 0.0340 | -7.80 | down | exodeoxyribonuclease VII large subunit\ Context:(NC_002946)+[644189-645544]\ Notes:bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides |
| NGO0656 | 0.0486 | -7.65 | down | 0.0075 | -14.87 | down | 0.0270 | -6.94 | down | putative membrane transporter\ Context:(NC_002946)+[646046-647587]\ Notes:Best Blastp Hit: pir\|\|A81850 probable integral membrane transporter NMA1574 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380215\|emb\|CAB84801.1\| (AL162756) putative integral membrane transporter [Neisseria meningitidis] COG0477 Permeases |
| NGO0657 | 0.7812 | -1.13 | down | 0.8347 | 1.10 | up | 0.2521 | 1.53 | up | hypothetical protein\ Context:(NC_002946)-[647646-648698]\ Notes:Best Blastp Hit: pir\|\|B81092 conserved hypothetical protein NMB1361 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226606\|gb\|AAF41735.1\| (AE002484) conserved hypothetical protein [Neisseria meningitidis MC58] COG1187 Predicted pseudouridylate synthase family 1 |
| NGO0658 | 0.0039 | -6.10 | down | 0.0023 | -6.44 | down | 0.0723 | -2.73 | down | pyridoxamine 5'-phosphate oxidase\ Context:(NC_002946)+[648916-649548]\ Notes:catalyzes the formation of pyridoxal 5'-phosphate from pyridoxamine 5'-phosphate |
| NGO0659 | 0.3082 | -2.04 | down | 0.1041 | -2.74 | down | 0.9019 | -1.04 | down | putative iron/sulphur-binding oxidoreductase\ Context:(NC_002946)-[649678-650688]\ Notes:Best Blastp Hit: pir\|\|H81091 probable CDP-6-deoxy-Delta(3;4)-glucoseen reductase (EC 1.3.1.-) NMB1359 [similarity] - Neisseria meningitidis (group B strain MD58) >gi\|7226604\|gb\|AAF41733.1\| (AE002484) CDP-6-deoxy-delta-3;4-glucoseen reductase; putative [Neisseria meningitidis MC58] COG0543 2-Octaprenylphenol hydroxylase and related |

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| NGO0660 | 0.0789 | 2.68 | up | 0.0294 | 3.97 | up | 0.0909 | 1.82 | up | aspartyl/glutamyl-tRNA amidotransferase subunit B\ Context:(NC_002946)-[650780-652210]\ Notes:allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases; reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA |
| NGO0661 | 0.0051 | 5.55 | up | 0.0423 | 5.83 | up | 0.1166 | 1.77 | up | hypothetical protein\ Context:(NC_002946)-[652253-653185]\ Notes:Best Blastp Hit: pir\|\|F81091 conserved hypothetical protein NMB1357 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226602\|gb\|AAF41731.1\| (AE002484) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0662 | 0.4295 | 1.43 | up | 0.3598 | 1.42 | up | 0.2520 | 1.35 | up | putative Glu-tRNA(Gln) amidotransferase subunit\ Context:(NC_002946)-[653182-654627]\ Notes:Best Blastp Hit: pir\|\|C81849 Glu-tRNA(Gln) amidotransferase subunit A NMA1568 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380209\|emb\|CAB84795.1\| (AL162756) Glu-tRNA(Gln) amidotransferase subunit A [Neisseria meningitidis] COG0154 Glu-tRNAGln amidotransferase A subunit |
| NGO0663 | 0.8163 | 1.15 | up | 0.9758 | 1.01 | up | 0.4047 | 1.32 | up | aspartyl/glutamyl-tRNA amidotransferase subunit C\ Context:(NC_002946)-[654690-654980]\ Notes:allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases; reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA; some Mycoplasma proteins contain an N-terminal fusion to an unknown domain |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0664 | 0.5687 | -1.35 | down | 0.6239 | 1.21 | up | 0.9310 | -1.03 | down | hypothetical protein\ Context:(NC_002946)+[655130-655783]\ Notes:Best Blastp Hit: pir\|\|E81093 conserved hypothetical protein NMB1354 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226598\|gb\|AAF41728.1\| (AE002483) conserved hypothetical protein [Neisseria meningitidis MC58] COG2095 Integral membrane proteins of the MarC |
| NGO0665 | 0.1664 | 2.84 | up | 0.3422 | 1.45 | up | 0.8780 | 1.05 | up | putative aldehyde dehydrogenase\ Context:(NC_002946)+[655788-657131]\ Notes:Best Blastp Hit: pir\|\|D81093 aldehyde dehydrogenase family protein NMB1353 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226597\|gb\|AAF41727.1\| (AE002483) aldehyde dehydrogenase family protein [Neisseria meningitidis MC58] COG1012 NAD-dependent aldehyde dehydrogenases |
| NGO0666 | 0.5747 | 1.29 | up | 0.8419 | -1.10 | down | 0.4020 | 1.35 | up | hypothetical protein\ Context:(NC_002946)-[657180-657608]\ Notes:Best Blastp Hit: pir\|\|C81093 hypothetical protein NMB1352 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226596\|gb\|AAF41726.1\| (AE002483) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380205\|emb\|CAB84791.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0667 | 0.1424 | -2.75 | down | 0.0044 | -24.83 | down | 0.8308 | 1.13 | up | hypothetical protein\ Context:(NC_002946)-[657753-657938]\ Notes: |
| NGO0668 | 0.1105 | 2.55 | up | 0.2110 | 2.48 | up | 0.0592 | 2.72 | up | putative SUN-family protein\ Context:(NC_002946)-[657954-659210]\ Notes:Best Blastp Hit: emb\|CAB84790.1\| (AL162756) SUN-family protein [Neisseria meningitidis] COG0144 Predicted rRNA methylase |
| NGO0669 | 0.6397 | 1.23 | up | 0.2594 | 1.50 | up | 0.9435 | 1.02 | up | hypothetical protein\ Context:(NC_002946)-[659246-660115]\ Notes:Best Blastp Hit: pir\|\|D81848 hypothetical protein NMA1561 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380202\|emb\|CAB84788.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0670 | 0.6950 | -1.21 | down | 0.5406 | 1.25 | up | 0.4044 | -1.65 | down | putative methylase family protein\ Context:(NC_002946)-[660156-660971]\ Notes:Best Blastp Hit: pir\|\|G81092 RNA methylase; probable NMB1348 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226592\|gb\|AAF41722.1\| (AE002483) RNA methylase; putative [Neisseria meningitidis MC58] COG0565 rRNA methylase |
| NGO0671 | 0.1808 | 1.88 | up | 0.1381 | 3.09 | up | 0.7422 | -1.16 | down | hypothetical protein\ Context:(NC_002946)+[661215-662000]\ Notes:Best Blastp Hit: pir\|\|F81092 extragenic suppressor protein SuhB NMB1347 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226591\|gb\|AAF41721.1\| (AE002483) extragenic suppressor protein SuhB [Neisseria meningitidis MC58] COG0483 Inositol phosphatase family proteins |
| NGO0672 | 0.3928 | -2.79 | down | 0.0434 | -15.69 | down | 0.5245 | -1.99 | down | hypothetical protein\ Context:(NC_002946)+[662118-662309]\ Notes: |
| NGO0674 | 0.5229 | 1.45 | up | 0.1249 | 1.72 | up | 0.5150 | 1.28 | up | 3-isopropylmalate dehydrogenase\ Context:(NC_002946)-[662987-664057]\ Notes:catalyzes the oxidation of 3-isopropylmalate to 3-carboxy-4-methyl-2-oxopentanoate in leucine biosynthesis |
| NGO0675 | 0.3824 | 1.58 | up | 0.3655 | 1.42 | up | 0.8412 | 1.05 | up | putative type II restriction endonuclease NlaIV\ Context:(NC_002946)-[664091-664822]\ Notes:Best Blastp Hit: sp\|P50183\|T2N4_NEILA type II restriction enzyme NLAIV (endonuclease NLAIV) (R.NLAIV) >gi\|628599\|pir\|\|S43887 restriction endonuclease - Neisseria lactamica >gi\|476228\|gb\|AAA53238.1\| (U06074) R.NlaIV [Neisseria lactamica] |
| NGO0676 | 0.2180 | 1.83 | up | 0.2364 | 1.85 | up | 0.4993 | 1.27 | up | putative DNA modification methylase (N.MgoV)\ Context:(NC_002946)-[664838-666109]\ Notes:Best Blastp Hit: possibly phase variable - 9A residue homopolymer repeat in the coding sequence (ON) COG0270 Site-specific DNA methylase dcm |
| NGO0677 | 0.5080 | 1.47 | up | 0.6599 | 1.18 | up | 0.9703 | -1.01 | down | isopropylmalate isomerase small subunit\ Context:(NC_002946)-[666276-666917]\ Notes:catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate in leucine biosynthesis; forms a heterodimer of LeuC/D |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0678 | 0.2952 | 1.89 | up | 0.5702 | 1.23 | up | 0.4461 | 1.28 | up | hypothetical protein\ Context:(NC_002946)-[666979-667233]\ Notes:Best Blastp Hit: gb\|AAF41434.1\|(AE002454) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380104\|emb\|CAB84687.1\| (AL162756) putative lipoprotein [Neisseria meningitidis] |
| NGO0679 | 0.9044 | -1.06 | down | 0.6579 | -1.20 | down | 0.3943 | -1.29 | down | isopropylmalate isomerase large subunit\ Context:(NC_002946)-[667328-668737]\ Notes:dehydratase component; catalyzes the isomerization between 2-isopropylmalate and 3-isopropylmalate |
| NGO0680 | 0.0177 | 3.87 | up | 0.4711 | 1.26 | up | 0.4124 | 1.26 | up | hypothetical protein\ Context:(NC_002946)+[669169-670338]\ Notes:Best Blastp Hit: pir\|\|H81835 probable glutamate--cysteine ligase (EC 6.3.2.2) NMA1449 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380102\|emb\|CAB84685.1\| (AL162756) putative glutamate--cysteine ligase [Neisseria meningitidis] |
| NGO0681 | 0.0995 | -3.89 | down | 0.0333 | -9.55 | down | 0.4188 | -2.71 | down | DNA repair protein RadC\ Context:(NC_002946)+[670461-671138]\ Notes:Involved in DNA double-strand break repair and recombination. Promotes the annealing of complementary single-stranded DNA and by simulation of RAD51 recombinase |
| NGO0682 | 0.0671 | 3.62 | up | 0.7713 | 1.11 | up | 0.2878 | -2.48 | down | hypothetical protein\ Context:(NC_002946)+[671211-671936]\ Notes:Best Blastp Hit: pir\|\|B81129 conserved hypothetical protein NMB1039 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226279\|gb\|AAF41438.1\| (AE002454) conserved hypothetical protein [Neisseria meningitidis MC58] COG1636 Uncharacterized BCR |
| NGO0683 | 0.7088 | 1.21 | up | 0.8310 | 1.08 | up | 0.9562 | -1.02 | down | hypothetical protein\ Context:(NC_002946)+[672088-673368]\ Notes:Best Blastp Hit: pir\|\|E81835 probable periplasmic protein NMA1446 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380099\|emb\|CAB84682.1\| (AL162756) putative periplasmic protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0684 | 0.2102 | 2.57 | up | 0.3024 | 1.80 | up | 0.6837 | -1.30 | down | putative GTP binding protein\ Context:(NC_002946)+[673443-674552]\ Notes:Best Blastp Hit: emb\|CAB84681.1\| (AL162756) hypothetical protein NMA1445 [Neisseria meningitidis] COG1159 Predicted GTPases; Era/HflX family |
| NGO0685 | 0.7425 | 1.33 | up | 0.9993 | -1.00 | down | 0.2042 | 2.38 | up | putative P-type cation-transporting ATPase\ Context:(NC_002946)+[674549-677005]\ Notes:Best Blastp Hit: pir\|\|C81835 probable P-type cation-transporting ATPase NMA1444 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380097\|emb\|CAB84680.1\| (AL162756) putative P-type cation-transporting ATPase [Neisseria meningitidis] COG2217 Cation transport ATPases |
| NGO0686 | 0.0429 | 18.03 | up | 0.0572 | -4.52 | down | 0.9496 | 1.08 | up | hypothetical protein\ Context:(NC_002946)+[677179-677331]\ Notes:Best Blastp Hit: gb\|AAF41441.1\| (AE002455) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0687 | 0.6848 | -1.23 | down | 0.8391 | 1.09 | up | 0.2607 | 2.12 | up | putative ferredoxin-NADP reductase\ Context:(NC_002946)-[677673-678449]\ Notes:Best Blastp Hit: gb\|AAF41442.1\| (AE002455) ferredoxin--NADP reductase [Neisseria meningitidis MC58] >gi\|7380095\|emb\|CAB84678.1\| (AL162756) putative ferredoxin--NADP reductase [Neisseria meningitidis] COG1018 Flavodoxin reductases (ferredoxin-NADPH |
| NGO0688 | 0.3139 | 1.73 | up | 0.6413 | 1.17 | up | 0.1715 | -2.51 | down | hypothetical protein\ Context:(NC_002946)-[678637-679431]\ Notes:Best Blastp Hit: pir\|\|E81127 hypothetical protein NMB1045 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226285\|gb\|AAF41443.1\| (AE002455) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0689 | 0.9827 | -1.01 | down | 0.6346 | -1.23 | down | 0.8395 | -1.06 | down | threonine synthase\ Context:(NC_002946)-[679478-680887]\ Notes:catalyzes the formation of L-threonine from O-phospho-L-homoserine |
| NGO0690 | 0.9081 | 1.06 | up | 0.8237 | -1.09 | down | 0.4708 | -1.23 | down | hypothetical protein\ Context:(NC_002946)-[680960-681328]\ Notes:Best Blastp Hit: pir\|\|F81834 probable lipoprotein NMA1439 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380092\|emb\|CAB84675.1\| (AL162756) putative lipoprotein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0693 | 0.1059 | -3.18 | down | 0.1732 | -2.50 | down | 0.3477 | -1.79 | down | hypothetical protein\ Context:(NC_002946)-[684226-684741]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO0694 | 0.2883 | 1.87 | up | 0.3244 | 1.45 | up | 0.6910 | -1.13 | down | hypothetical protein\ Context:(NC_002946)-[684728-687346]\ Notes:Best Blastp Hit: sp\|P24328\|PERT_BORPA pertactin precursor (outer membrane protein P.70) (P.95) >gi\|95503\|pir\|\|S15204 pertactin - Bordetella parapertussis >gi\|39762\|emb\|CAA38419.1\| (X54547) pertactin [Bordetella parapertussis] |
| NGO0696 | 0.0652 | -2.79 | down | 0.0138 | -3.34 | down | 0.1245 | -2.44 | down | recombination factor protein RarA\ Context:(NC_002946)+[688651-689961]\ Notes:Best Blastp Hit: pir\|\|E81103 conserved hypothetical protein NMB1258 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226497\|gb\|AAF41636.1\| (AE002474) conserved hypothetical protein [Neisseria meningitidis MC58] COG2256 Uncharacterized ATPase related to the |
| NGO0697 | 0.0015 | 14.03 | up | 0.3595 | 2.72 | up | 0.6490 | 1.43 | up | putative type I restriction enzyme\ Context:(NC_002946)+[690060-693086]\ Notes:Best Blastp Hit: gb\|AAG22017.1\|AF288038_2 (AF288038) putative HsdR [Streptococcus thermophilus] COG0610 Restriction enzymes type I helicase subunits |
| NGO0698 | 0.0017 | 22.40 | up | 0.0500 | 8.03 | up | 0.0455 | 9.97 | up | hypothetical protein\ Context:(NC_002946)+[693136-693369]\ Notes:Best Blastp Hit: pir\|\|G81152 probable DNA-binding protein NMA1039 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226065\|gb\|AAF41242.1\| (AE002436) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379741\|emb\|CAB84308.1\| (AL162754) putative DNA-binding protein [Neisseria meningitidis] |
| NGO0699 | 0.3188 | 2.22 | up | 0.1000 | 6.56 | up | 0.1688 | 4.55 | up | hypothetical protein\ Context:(NC_002946)+[693416-694618]\ Notes:Best Blastp Hit: gb\|AAG22014.1\|AF288037_3 (AF288037) putative HsdS [Streptococcus thermophilus] COG0732 Restriction endonuclease S subunits |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0700 | 0.0064 | 8.50 | up | 0.0201 | 7.98 | up | 0.1414 | 5.38 | up | hypothetical protein\ Context:(NC_002946)+[694611-695171]\ Notes:Best Blastp Hit: pir\|\|G69096 hypothetical protein MTH1717 - Methanobacterium thermoautotrophicum (strain Delta H) >gi\|2622849\|gb\|AAB86189.1\| (AE000928) unknown [Methanobacterium thermoautotrophicum] |
| NGO0701 | 0.0629 | 3.85 | up | 0.1156 | 4.51 | up | 0.1117 | 7.27 | up | hypothetical protein\ Context:(NC_002946)+[695182-696024]\ Notes: |
| NGO0702 | 0.2561 | 1.77 | up | 0.0737 | 5.31 | up | 0.2097 | 2.76 | up | hypothetical protein\ Context:(NC_002946)+[696091-697692]\ Notes:Best Blastp Hit: gb\|AAG22013.1\|AF288037_2 (AF288037) putative HsdM [Streptococcus thermophilus] COG0286 Type I restriction-modification system |
| NGO0703 | 0.0943 | -4.04 | down | 0.2020 | -7.58 | down | 0.8706 | -1.18 | down | hypothetical protein\ Context:(NC_002946)-[697719-697988]\ Notes: |
| NGO0704 | 0.3152 | -2.10 | down | 0.8288 | 1.21 | up | 0.5618 | -1.39 | down | bifunctional 3;4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein\ Context:(NC_002946)-[698003-699094]\ Notes:bifunctional enzyme DHBP synthase/GTP cyclohydrolase II; functions in riboflavin synthesis; converts GTP to 2;5-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine; converts ribulose 5-phopshate to 3;4-dihydroxy-2-butanone 4-phosphate |
| NGO0709 | 0.2246 | -4.43 | down | 0.0119 | -35.36 | down | 0.8970 | 1.15 | up | hypothetical protein\ Context:(NC_002946)+[708430-708798]\ Notes: |
| NGO0710 | 0.2283 | 3.51 | up | 0.9300 | 1.09 | up | 0.1181 | -2.65 | down | putative adenine glycosylase\ Context:(NC_002946)-[709174-710223]\ Notes:Best Blastp Hit: gb\|AAF41760.1\|(AE002488) A/G-specific adenine glycosylase [Neisseria meningitidis MC58] COG1194 A/G-specific DNA glycosylase |
| NGO0711 | 0.1019 | -5.40 | down | 0.0089 | -19.44 | down | 0.3191 | 1.54 | up | putative alcohol dehydrogenase\ Context:(NC_002946)+[710377-711393]\ Notes:Best Blastp Hit: pir\|\|C81088 alcohol dehydrogenase; zinc-containing NMB1395 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226634\|gb\|AAF41759.1\| (AE002488) alcohol dehydrogenase; zinc-containing [Neisseria meningitidis MC58] COG1065 Zn-dependent oxidoreductases |
| NGO0712 | 0.7342 | 1.29 | up | 0.7435 | -1.41 | down | 0.3812 | -2.66 | down | hypothetical protein\ Context:(NC_002946)+[711637-711822]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0713 | 0.0216 | 5.83 | up | 0.0098 | 3.25 | up | 0.0235 | 4.10 | up | keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase\ Context:(NC_002946)-[712011-712649]\ Notes:catalyzes the formation of pyruvate and glyoxylate from 4-hydroxy-2-oxoglutarate; or pyruvate and D-glyceraldehyde 3-phosphate from 2-dehydro-3-deoxy-D-glyconate 6-phosphate |
| NGO0714 | 0.0024 | 8.11 | up | 0.1443 | 2.72 | up | 0.0478 | 2.29 | up | phosphogluconate dehydratase\ Context:(NC_002946)-[712859-714694]\ Notes:catalyzes the formation of 2-dehydro-3-deoxy-6-phospho-D-gluconate from 6-phospho-D-gluconate |
| NGO0715 | 0.2672 | 1.79 | up | 0.1780 | 1.71 | up | 0.1321 | 1.65 | up | glucose-6-phosphate 1-dehydrogenase\ Context:(NC_002946)+[715214-716659]\ Notes:catalyzes the formation of D-glucono-1;5-lactone 6-phosphate from D-glucose 6-phosphate |
| NGO0716 | 0.1554 | 2.19 | up | 0.3589 | 1.44 | up | 0.1486 | 1.61 | up | hypothetical protein\ Context:(NC_002946)+[716811-717506]\ Notes:Best Blastp Hit: gb\|AAF41755.1\|(AE002487) oxidoreductase; Sol/DevB family [Neisseria meningitidis MC58] >gi\|7380250\|emb\|CAB84836.1\|(AL162756) 6-phosphogluconolactonase [Neisseria meningitidis] COG0363 Glucosamine-6-phosphate deaminase |
| NGO0717 | 0.1143 | 2.24 | up | 0.2295 | 1.63 | up | 0.1788 | 1.51 | up | glucokinase\ Context:(NC_002946)+[717487-718473]\ Notes:catalyzes the conversion of ATP and D-glucose to ADP and D-glucose 6-phosphate |
| NGO0718 | 0.0309 | 3.76 | up | 0.0539 | 5.54 | up | 0.0337 | 2.26 | up | RpiR family transcriptional regulator\ Context:(NC_002946)+[718522-719370]\ Notes:Best Blastp Hit: pir\|\|D81089 RpiR/YebK/YfhH family protein NMB1389 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226627\|gb\|AAF41753.1\|(AE002487) RpiR/YebK/YfhH family protein [Neisseria meningitidis MC58] >gi\|7380248\|emb\|CAB84834.1\|(AL162756) putative transcriptional regulator [Neisseria meningitidis] COG1737 Transcriptional regulators; RpiR family |

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|---|---|---|---|---|---|---|---|---|---|
| NGO0719 | 0.0845 | 3.61 | up | 0.0375 | 2.77 | up | 0.0821 | 3.72 | up | glucose-6-phosphate isomerase\ Context:(NC_002946)+[719596-721242]\ Notes:functions in sugar metabolism in glycolysis and the Embden-Meyerhof pathways (EMP) and in gluconeogenesis; catalyzes reversible isomerization of glucose-6-phosphate to fructose-6-phosphate; member of PGI family |
| NGO0720 | 0.8001 | 1.25 | up | 0.2690 | -3.18 | down | 0.0337 | 3.14 | up | putative phage associated protein\ Context:(NC_002946)+[721256-721459]\ Notes:Best Blastp Hit: pir\|\|B81089 hypothetical protein NMB1387 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226625\|gb\|AAF41751.1\| (AE002487) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0721 | 0.7642 | 1.16 | up | 0.9404 | 1.06 | up | 0.7179 | -1.17 | down | putative phage associated protein\ Context:(NC_002946)+[721459-722472]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO0722 | 0.1066 | 3.51 | up | 0.5273 | 1.92 | up | 0.6574 | 1.51 | up | putative phage associated protein\ Context:(NC_002946)+[722517-722657]\ Notes:Best Blastp Hit: emb\|CAB84831.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0723 | 0.0027 | -7.34 | down | 0.0457 | -5.39 | down | 0.1035 | -3.09 | down | putative phage associated protein\ Context:(NC_002946)+[722896-723144]\ Notes:Best Blastp Hit: emb\|CAB84476.1\| (AL162755) hypothetical protein NMA1216 [Neisseria meningitidis] |
| NGO0724 | 0.3677 | -3.92 | down | 0.8600 | -1.10 | down | 0.5811 | 1.22 | up | putative phage associated protein\ Context:(NC_002946)+[723086-723208]\ Notes:Best Blastp Hit: emb\|CAB84476.1\| (AL162755) hypothetical protein NMA1216 [Neisseria meningitidis] |
| NGO0725 | 0.0869 | -3.78 | down | 0.7317 | -1.24 | down | 0.9857 | -1.02 | down | putative phage associated protein\ Context:(NC_002946)-[723158-723466]\ Notes:Best Blastp Hit: gb\|AAF41506.1\| (AE002461) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0727 | 0.1410 | -3.55 | down | 0.0312 | -4.35 | down | 0.8314 | -1.11 | down | putative baseplate protein; putative phage associated protein\ Context:(NC_002946)-[726767-727315]\ Notes:Best Blastp Hit: gi\|9634072 P2 J homolog; baseplate or base of tail fibre [Enterobacteria phage 186] >gi\|3522880\|gb\|AAC34162.1\| (U32222) P2 J homolog; baseplate or base of tail fibre [Enterobacteria phage 186] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0728 | 0.3517 | -1.57 | down | 0.0718 | -6.14 | down | 0.7761 | 1.27 | up | putative phage associated protein\ Context:(NC_002946)-[727336-728238]\ Notes:Best Blastp Hit: dbj\|BAA36244.1\|(AB008550) orf17; similar to W gene of P2:baseplate [Pseudomonas aeruginosa phage phi CTX] |
| NGO0729 | 0.3909 | -2.09 | down | 0.7836 | -1.28 | down | 0.6462 | -1.20 | down | putative phage associated protein\ Context:(NC_002946)-[728344-728556]\ Notes:Best Blastp Hit: emb\|CAB84478.1\| (AL162755) hypothetical protein NMA1218 [Neisseria meningitidis] |
| NGO0731 | 0.6507 | 1.23 | up | 0.9286 | -1.05 | down | 0.8772 | 1.06 | up | putative phage associated protein\ Context:(NC_002946)-[729286-729570]\ Notes:Best Blastp Hit: pir\|\|B81890 hypothetical protein NMA1219 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379908\|emb\|CAB84479.1\| (AL162755) hypothetical protein NMA1219 [Neisseria meningitidis] |
| NGO0732 | 0.4898 | 1.44 | up | 0.8125 | 1.12 | up | 0.7777 | -1.10 | down | putative phage associated protein\ Context:(NC_002946)-[729607-729870]\ Notes:Best Blastp Hit: emb\|CAB84480.1\| (AL162755) hypothetical protein NMA1220 [Neisseria meningitidis] |
| NGO0734 | 0.7605 | -1.16 | down | 0.3938 | -1.97 | down | 0.6953 | -1.25 | down | putative oxidoreductase\ Context:(NC_002946)-[731378-732157]\ Notes:Best Blastp Hit: gb\|AAF41809.1\|(AE002495) ferredoxin--NADP reductase [Neisseria meningitidis MC58] COG1018 Flavodoxin reductases (ferredoxin-NADPH |
| NGO0735 | 0.5146 | 2.73 | up | 0.9184 | 1.15 | up | 0.9612 | -1.10 | down | hypothetical protein\ Context:(NC_002946)+[732156-732314]\ Notes: |
| NGO0736 | 0.8895 | 1.07 | up | 0.8360 | 1.09 | up | 0.3266 | -2.22 | down | hypothetical protein\ Context:(NC_002946)-[732449-732745]\ Notes:Best Blastp Hit: gb\|AAF42108.1\|(AE002526) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0738 | 0.5548 | -1.66 | down | 0.0358 | -5.08 | down | 0.2242 | -2.49 | down | putative DNA-damage-inducibile protein\ Context:(NC_002946)+[733057-734115]\ Notes:Best Blastp Hit: emb\|CAB72023.1\| (AJ391259) putative DNA-damage inducible protein P [Neisseria meningitidis] >gi\|7380303\|emb\|CAB84889.1\| (AL162756) impB/mucB/samB family protein [Neisseria meningitidis] COG0389 Nucleotidyltransferase/DNA polymerase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0739 | 0.9892 | -1.01 | down | 0.8283 | 1.11 | up | 0.9773 | 1.01 | up | putative ATP-dependent DNA helicase\ Context:(NC_002946)-[734185-736200]\ Notes:Best Blastp Hit: possibly phase variable - two 8A residue homopolymer repeats in the coding sequence (ON) COG0210 Superfamily I DNA and RNA helicases |
| NGO0740 | 0.1595 | 3.23 | up | 0.6476 | -1.46 | down | 0.7255 | -1.31 | down | 3-dehydroquinate dehydratase\ Context:(NC_002946)-[736220-736984]\ Notes:catalyzes the dehydration of 3-dehydroquinate to form 3-dehydroshikimate in aromatic amino acid biosynthesis |
| NGO0741 | 0.6302 | 1.27 | up | 0.8339 | -1.09 | down | 0.9493 | -1.02 | down | recombinase A\ Context:(NC_002946)+[737184-738230]\ Notes:catalyzes the hydrolysis of ATP in the presence of single-stranded DNA; the ATP-dependent uptake of single-stranded DNA by duplex DNA; and the ATP-dependent hybridization of homologous single-stranded DNAs |
| NGO0742 | 0.0719 | 3.18 | up | 0.0535 | 5.84 | up | 0.1337 | 2.20 | up | hypothetical protein\ Context:(NC_002946)-[738883-739218]\ Notes:Best Blastp Hit: pir\|\|E81082 conserved hypothetical protein NMB1444 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226685\|gb\|AAF41804.1\| (AE002494) conserved hypothetical protein [Neisseria meningitidis MC58] COG0718 Uncharacterized BCR; YbaB family |
| NGO0743 | 0.9775 | -1.02 | down | 0.5225 | 1.50 | up | 0.4945 | -1.46 | down | DNA polymerase III subunits gamma and tau\ Context:(NC_002946)-[739299-741422]\ Notes:catalyzes the DNA-template-directed extension of the 3'-end of a DNA strand; the tau chain serves as a scaffold to help in the dimerizaton of the alpha;epsilon and theta core complex; the gamma chain seems to interact with the delta and delta' subunits to transfer the beta subunit on the DNA |
| NGO0744 | 0.7204 | -1.18 | down | 0.5604 | 1.79 | up | 0.5103 | 1.45 | up | DNA mismatch repair protein\ Context:(NC_002946)-[741517-743493]\ Notes:This protein is involved in the repair of mismatches in DNA. It is required for dam-dependent methyl-directed DNA mismatch repair. Promotes the formation of a stable complex between two or more DNA-binding proteins in an ATP-dependent manner without itself being part of a final effector complex |

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| NGO0745 | 0.6010 | 1.37 | up | 0.7112 | 1.15 | up | 0.6414 | 1.17 | up | hypothetical protein\ Context:(NC_002946)+[743637-743822]\ Notes:Best Blastp Hit: emb\|CAB84882.1\|(AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0746 | 0.7217 | -1.34 | down | 0.2878 | -1.64 | down | 0.5497 | -1.26 | down | putative O-methyltransferase\ Context:(NC_002946)+[743833-744501]\ Notes:Best Blastp Hit: pir\|\|A81860 probable methyltransferase NMA1653 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380295\|emb\|CAB84881.1\| (AL162756) putative methyltransferase [Neisseria meningitidis] COG0500 SAM-dependent methyltransferases |
| NGO0747 | 0.9334 | 1.06 | up | 0.2550 | 1.79 | up | 0.5929 | 1.24 | up | hypothetical protein\ Context:(NC_002946)+[744501-745214]\ Notes:Best Blastp Hit: pir\|\|H81083 hypothetical protein NMB1440 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226681\|gb\|AAF41801.1\|(AE002493) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0748 | 0.4459 | -1.62 | down | 0.1259 | -2.72 | down | 0.4262 | -2.33 | down | putative phosphoribosylaminoimidazole carboxylase catalytic subunit\ Context:(NC_002946)+[745262-745747]\ Notes:Best Blastp Hit: pir\|\|G81083 phosphoribosylaminoimidazole carboxylase; catalytic chain NMB1439 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226680\|gb\|AAF41800.1\| (AE002493) phosphoribosylaminoimidazole carboxylase; catalytic subunit [Neisseria meningitidis MC58] COG0041 Phosphoribosylcarboxyaminoimidazole (NCAIR) |
| NGO0751 | 0.0197 | -6.83 | down | 0.0328 | -4.22 | down | 0.4530 | -2.01 | down | hypothetical protein\ Context:(NC_002946)+[747669-748577]\ Notes:Best Blastp Hit: emb\|CAC03614.1\|(AJ272538) hypothetical protein [Kluyvera ascorbata] |

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| NGO0752 | 0.6878 | -1.27 | down | 0.1510 | 2.86 | up | 0.5144 | -1.58 | down | NarL/NarP\ Context:(NC_002946)-[748733-749389]\ Notes:Best Blastp Hit: pir\|\|C81104 transcription regulator; LuxR family NMB1250 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226490\|gb\|AAF41630.1\| (AE002473) transcriptional regulator; LuxR family [Neisseria meningitidis MC58] >gi\|7380078\|emb\|CAB84659.1\| (AL162755) putative two-component system response regulator [Neisseria meningitidis] COG2197 Response regulators consisting of a; putative nitrite/nitrate two-component system transcriptional response regulator |
| NGO0753 | 0.0985 | 2.43 | up | 0.5379 | 1.54 | up | 0.5476 | 1.25 | up | NarX/NarQ\ Context:(NC_002946)-[749386-751155]\ Notes:Best Blastp Hit: pir\|\|B81104 nitrate/nitrite sensor protein (EC 2.7.3.-) NMB1249 [similarity] - Neisseria meningitidis (group B strain MD58) >gi\|7226489\|gb\|AAF41629.1\| (AE002473) nitrate/nitrite sensory protein NarX; putative [Neisseria meningitidis MC58] COG0642 Sensory transduction histidine kinases; putative nitrite/nitrate two-component system sensor kinase |
| NGO0754 | 0.5471 | 1.80 | up | 0.0154 | -6.32 | down | 0.8806 | -1.14 | down | putative molybdopterin-guanine dinucleotide biosynthesis protein\ Context:(NC_002946)+[751362-751976]\ Notes:Best Blastp Hit: emb\|CAB84657.1\| (AL162755) putative molybdopterin-guanine dinucleotide biosynthesis protein A [Neisseria meningitidis] COG0746 Molybdopterin-guanine dinucleotide |
| NGO0755 | 0.4726 | 1.39 | up | 0.7707 | 1.11 | up | 0.6919 | 1.12 | up | riboflavin synthase subunit alpha\ Context:(NC_002946)+[752139-752756]\ Notes:catalyzes the formation of riboflavin from 6;7-dimethyl-8-(1-D-ribityl)lumazine |
| NGO0756 | 0.5499 | 1.46 | up | 0.5891 | -1.44 | down | 0.1855 | -2.02 | down | hypothetical protein\ Context:(NC_002946)+[752764-753627]\ Notes:Best Blastp Hit: pir\|\|H81910 hypothetical protein NMA1415 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380074\|emb\|CAB84655.1\| (AL162755) hypothetical protein NMA1415 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0757 | 0.0081 | 5.13 | up | 0.0048 | 6.09 | up | 0.0370 | 2.92 | up | hypothetical protein\ Context:(NC_002946)-[753640-754074]\ Notes:Best Blastp Hit: emb\|CAB84654.1\|(AL162755) putative periplasmic protein [Neisseria meningitidis] |
| NGO0758 | 0.3243 | -1.61 | down | 0.4475 | -1.56 | down | 0.2356 | -1.52 | down | putative ribulose-phosphate 3-epimerase\ Context:(NC_002946)+[754220-754912]\ Notes:Best Blastp Hit: pir\|\|A81106 ribulose-phosphate 3-epimerase NMB1244 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226484\|gb\|AAF41625.1\| (AE002472) ribulose-phosphate 3-epimerase [Neisseria meningitidis MC58] COG0036 Pentose-5-phosphate-3-epimerase |
| NGO0759 | 0.9116 | -1.10 | down | 0.8247 | -1.24 | down | 0.8419 | -1.20 | down | hypothetical protein\ Context:(NC_002946)-[755001-755147]\ Notes: |
| NGO0760 | 0.3315 | -2.10 | down | 0.0751 | -3.84 | down | 0.6872 | 1.14 | up | Holliday junction DNA helicase B\ Context:(NC_002946)-[755151-756182]\ Notes:promotes strand exchange during homologous recombination; RuvAB complex promotes branch migration; RuvABC complex scans the DNA duringbranch migration and resolves Holliday junctions at consensus sequences; forms hexameric rings around opposite DNA arms; requires ATP for branch migration and orientation of RuvAB complex determines direction of migration |
| NGO0761 | 0.0279 | -5.63 | down | 0.0265 | -5.45 | down | 0.0027 | -7.40 | down | hypothetical protein\ Context:(NC_002946)-[756266-756574]\ Notes:Best Blastp Hit: pir\|\|G81105 hypothetical protein NMB1242 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226482\|gb\|AAF41623.1\|(AE002472) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0762 | 0.3443 | -2.37 | down | 0.0445 | -3.11 | down | 0.4493 | -1.62 | down | hypothetical protein\ Context:(NC_002946)+[756606-756746]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0763 | 0.3092 | 1.73 | up | 0.1180 | 1.78 | up | 0.8859 | 1.05 | up | multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase\ Context:(NC_002946)-[756992-758224]\ Notes:catalyzes the addition and repair of the essential 3'-terminal CCA sequence in tRNAs without using a nucleic acid template; phosphohydrolase activities include hydrolysis of pyrophosphate; 5'-nucleoside tri- and diphosphates; NADP; and 2'-AMP with the production of Pi; metal-dependent phosphodiesterase activity for 2';3'-cAMP; 2';3'-cGMP; and 2';3'-cCMP; and hydrolysis 2';3'-cyclic substrates with the formation of 2'-nucleotides and 3'-nucleotides; these phosphohydrolase activities are probably involved in the repair of the tRNA 3'-CCA terminus degraded by intracellular RNases |
| NGO0764 | 0.2026 | 1.82 | up | 0.6159 | 1.25 | up | 0.7453 | 1.11 | up | putative ABC-transporter; ATP-binding protein\ Context:(NC_002946)-[758303-759931]\ Notes:Best Blastp Hit: gb\|AAF41621.1\| (AE002472) ABC transporter; ATP-binding protein [Neisseria meningitidis MC58] COG0488 ATPase components of ABC transporters with |
| NGO0765 | 0.4788 | -1.39 | down | 0.8861 | -1.06 | down | 0.5994 | -1.20 | down | hypothetical protein\ Context:(NC_002946)+[760081-760455]\ Notes:Best Blastp Hit: gb\|AAF41620.1\| (AE002472) conserved hypothetical protein [Neisseria meningitidis MC58] COG1393 Arsenate reductase; E.coli type |
| NGO0766 | 0.5517 | 1.30 | up | 0.9097 | 1.05 | up | 0.5951 | 1.16 | up | putative peptidyl-prolyl cis-trans isomerase\ Context:(NC_002946)+[760504-762042]\ Notes:Best Blastp Hit: gb\|AAF41619.1\| (AE002472) peptidyl-prolyl cis-trans isomerase-related protein [Neisseria meningitidis MC58] COG0760 Parvulin-like peptidyl-prolyl isomerase |
| NGO0767 | 0.0746 | 7.45 | up | 0.7107 | -1.24 | down | 0.3564 | -3.46 | down | putative recombination protein\ Context:(NC_002946)+[762109-762726]\ Notes:Best Blastp Hit: pir\|\|G81909 probable recombination protein NMA1406 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380065\|emb\|CAB84646.1\| (AL162755) putative recombination protein [Neisseria meningitidis] COG0353 Recombinational DNA repair protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0768 | 0.8637 | 1.08 | up | 0.9618 | -1.02 | down | 0.4981 | 1.30 | up | hypothetical protein\ Context:(NC_002946)-[762907-763158]\ Notes: |
| NGO0769 | 0.7564 | -1.15 | down | 0.5528 | -1.33 | down | 0.4715 | -1.41 | down | LolC\ Context:(NC_002946)+[763287-764534]\ Notes:Best Blastp Hit: sp\|P57062\|LOLC_NEIMB lipoprotein releasing system transmembrane protein LolC >gi\|11279734\|pir\|\|D81107 conserved hypothetical protein NMB1235 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226474\|gb\|AAF41616.1\| (AE002471) conserved hypothetical protein [Neisseria meningitidis MC58] COG0577 Predicted permease; putative lipoprotein releasing system transmembrane protein |
| NGO0770 | 0.4218 | 1.69 | up | 0.1807 | 1.78 | up | 0.5215 | 1.19 | up | hypothetical protein\ Context:(NC_002946)+[764527-765222]\ Notes:Best Blastp Hit: sp\|P57031\|LOLD_NEIMB lipoprotein releasing system ATP-binding protein LolD >gi\|11277321\|pir\|\|C81107 ABC transporter; ATP-binding protein NMB1234 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226473\|gb\|AAF41615.1\| (AE002471) ABC transporter; ATP-binding protein [Neisseria meningitidis MC58] COG1136 ABC-type (unclassified) transport system |
| NGO0771 | 0.1789 | 1.95 | up | 0.0438 | 2.79 | up | 0.6971 | 1.13 | up | putative exodeoxyribonuclease V alpha subunit\ Context:(NC_002946)+[765289-767034]\ Notes:Best Blastp Hit: gb\|AAC14132.1\| (AF058330) RecD [Neisseria gonorrhoeae] COG0507 ATP-dependent exoDNAse (exonuclease V) |
| NGO0773 | 0.0225 | 5.64 | up | 0.0320 | 2.27 | up | 0.3249 | 1.31 | up | Irg1\ Context:(NC_002946)+[767722-768723]\ Notes:Best Blastp Hit: gb\|AAC82509.1\| (U65994) pilin gene inverting protein homolog PivNG [Neisseria gonorrhoeae]; putative invertase related gene 1 |
| NGO0774 | 0.0692 | -4.11 | down | 0.1267 | -9.79 | down | 0.6051 | 1.26 | up | hypothetical protein\ Context:(NC_002946)+[768871-769440]\ Notes: |
| NGO0775 | 0.1248 | 3.10 | up | 0.0517 | 3.28 | up | 0.1191 | 3.82 | up | hypothetical protein\ Context:(NC_002946)+[769563-772025]\ Notes:Best Blastp Hit: pir\|\|H81106 ATP-dependent proteinase La NMB1231 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226470\|gb\|AAF41612.1\| (AE002471) ATP-dependent protease La [Neisseria meningitidis MC58] COG0466 ATP-dependent Lon protease; bacterial type |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0776 | 0.6344 | -1.34 | down | 0.7470 | -1.28 | down | 0.0346 | 2.52 | up | hypothetical protein\ Context:(NC_002946)-[772015-772605]\ Notes: |
| NGO0777 | 0.1531 | 2.62 | up | 0.2676 | 1.48 | up | 0.2588 | 1.65 | up | DbhA\ Context:(NC_002946)+[772207-772476]\ Notes:Best Blastp Hit: pir\|\|G81106 DNA-binding protein HU-beta NMB1230 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226469\|gb\|AAF41611.1\| (AE002471) DNA-binding protein HU-beta [Neisseria meningitidis MC58] >gi\|7380057\|emb\|CAB84638.1\| (AL162755) putative DNA-binding protein [Neisseria meningitidis] COG0776 Histone-like DNA-binding protein; putative DNA-binding protein Hu |
| NGO0778 | 0.1399 | 2.58 | up | 0.5191 | 1.78 | up | 0.5047 | 1.55 | up | hypothetical protein\ Context:(NC_002946)-[772652-773086]\ Notes:Best Blastp Hit: pir\|\|F81908 probable membrane protein NMA1396 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380056\|emb\|CAB84637.1\| (AL162755) putative membrane protein [Neisseria meningitidis] |
| NGO0779 | 0.0096 | 6.38 | up | 0.0847 | 3.32 | up | 0.1626 | 1.53 | up | homoserine dehydrogenase\ Context:(NC_002946)-[773079-774386]\ Notes:catalyzes the formation of L-aspartate 4-semialdehyde from L-homoserine |
| NGO0780 | 0.3004 | 1.76 | up | 0.8921 | 1.06 | up | 0.5830 | -1.38 | down | hypothetical protein\ Context:(NC_002946)+[774582-774953]\ Notes:Best Blastp Hit: pir\|\|D81108 conserved hypothetical protein NMB1227 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226465\|gb\|AAF41608.1\| (AE002470) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0781 | 0.0502 | 4.28 | up | 0.0970 | 7.01 | up | 0.1176 | 1.62 | up | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)+[775030-776952]\ Notes:Best Blastp Hit: gb\|AAF41607.1\| (AE002470) ABC transporter; ATP-binding protein [Neisseria meningitidis MC58] COG0488 ATPase components of ABC transporters with |
| NGO0782 | 0.1895 | 2.20 | up | 0.0917 | 1.97 | up | 0.3110 | 1.47 | up | hypothetical protein\ Context:(NC_002946)+[776978-777334]\ Notes:Best Blastp Hit: pir\|\|C81908 probable periplasmic protein NMA1391 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380053\|emb\|CAB84633.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0783 | 0.3774 | -1.49 | down | 0.9898 | 1.01 | up | 0.5414 | -1.18 | down | hypothetical protein\ Context:(NC_002946)+[777425-777937]\ Notes:Best Blastp Hit: pir\|\|B81108 hypothetical protein NMB1225 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226463\|gb\|AAF41606.1\|(AE002470) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0784 | 0.0086 | -5.05 | down | 0.8601 | -1.11 | down | 0.0254 | -5.24 | down | hypothetical protein\ Context:(NC_002946)+[777985-778161]\ Notes: |
| NGO0785 | 0.0032 | -30.06 | down | 0.1696 | -13.80 | down | 0.4439 | -3.58 | down | hypothetical protein\ Context:(NC_002946)+[778408-778830]\ Notes: |
| NGO0786 | 0.6540 | -1.31 | down | 0.0201 | -3.84 | down | 0.0457 | 2.25 | up | uracil-DNA glycosylase\ Context:(NC_002946)-[778867-779526]\ Notes:Excises uracil residues from the DNA which can arise as a result of misincorporation of dUMP residues by DNA polymerase or due to deamination of cytosine |
| NGO0787 | 0.2967 | 1.69 | up | 0.7180 | 1.17 | up | 0.3221 | 1.32 | up | hypothetical protein\ Context:(NC_002946)+[779607-780014]\ Notes:Best Blastp Hit: pir\|\|A81908 probable membrane protein NMA1383 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380051\|emb\|CAB84629.1\| (AL162755) putative membrane protein [Neisseria meningitidis] |
| NGO0788 | 0.1062 | 2.78 | up | 0.0687 | 2.02 | up | 0.1168 | 2.19 | up | GNA1220\ Context:(NC_002946)+[780029-780976]\ Notes:Best Blastp Hit: gb\|AAF44771.1\|AF235154_1 (AF235154) GNA1220 [Neisseria gonorrhoeae] >gi\|7274434\|gb\|AAF44772.1\|AF235155_1 (AF235155) GNA1220 [Neisseria gonorrhoeae] >gi\|7274436\|gb\|AAF44773.1\|AF235156_1 (AF235156) GNA1220 [Neisseria gonorrhoeae] COG0330 Membrane protease subunits; genome-derived Neisseria antigen 1220 |
| NGO0789 | 0.0293 | -4.41 | down | 0.0016 | -21.71 | down | 0.2386 | -2.76 | down | hypothetical protein\ Context:(NC_002946)-[781083-782153]\ Notes:Best Blastp Hit: gb\|AAF41601.1\|(AE002470) transporter; putative [Neisseria meningitidis MC58] COG0628 Predicted permease |
| NGO0790 | 0.3709 | 3.57 | up | 0.3367 | -5.06 | down | 0.7873 | 1.39 | up | hypothetical protein\ Context:(NC_002946)-[782211-782369]\ Notes: |

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| NGO0791 | 0.8101 | 1.14 | up | 0.7104 | -1.17 | down | 0.8689 | -1.05 | down | hypothetical protein\ Context:(NC_002946)+[782338-782613]\ Notes:Best Blastp Hit: gb\|AAF41600.1\|(AE002469) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380048\|emb\|CAB84626.1\|(AL162755) hypothetical protein NMA1380 [Neisseria meningitidis] |
| NGO0792 | 0.8497 | -1.09 | down | 0.7495 | -1.14 | down | 0.9573 | 1.02 | up | putative lipoate-protein ligase\ Context:(NC_002946)+[782666-783238]\ Notes:Best Blastp Hit: pir\|\|E81109 lipoate-protein ligase B NMB1217 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226455\|gb\|AAF41599.1\| (AE002469) lipoate-protein ligase B [Neisseria meningitidis MC58] COG0321 Lipoate-protein ligase B |
| NGO0793 | 0.2725 | 1.81 | up | 0.3703 | 1.89 | up | 0.9476 | 1.03 | up | lipoyl synthase\ Context:(NC_002946)+[783231-784214]\ Notes:catalyzes the radical-mediated insertion of two sulfur atoms into an acyl carrier protein (ACP) bound to an octanoyl group to produce a lipoyl group |
| NGO0794 | 0.5936 | 1.35 | up | 0.8772 | -1.05 | down | 0.8555 | 1.06 | up | BfrA\ Context:(NC_002946)+[784689-785153]\ Notes:Best Blastp Hit: sp\|P72080\|BFRA_NEIMB bacterioferritin A (Bfr A) >gi\|11277091\|pir\|\|F81110 bacterioferritin A NMB1207 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|1673579\|gb\|AAB18968.1\| (U76633) bacterioferritin [Neisseria gonorrhoeae] >gi\|7226444\|gb\|AAF41589.1\|(AE002468) bacterioferritin A [Neisseria meningitidis MC58] COG2193 Bacterioferritin (cytochrome b1) |
| NGO0795 | 0.8825 | 1.09 | up | 0.7736 | -1.10 | down | 0.6317 | 1.21 | up | BfrB\ Context:(NC_002946)+[785181-785654]\ Notes:Best Blastp Hit: sp\|P56999\|BFRB_NEIMA bacterioferritin B (Bfr B) >gi\|11277092\|pir\|\|E81110 bacterioferritin B NMB1206 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226443\|gb\|AAF41588.1\|(AE002468) bacterioferritin B [Neisseria meningitidis MC58] >gi\|7380044\|emb\|CAB84622.1\| (AL162755) putative bacterioferritin B [Neisseria meningitidis] COG2193 Bacterioferritin (cytochrome b1) |
| NGO0796 | 0.0680 | -3.44 | down | 0.0303 | -12.26 | down | 0.7412 | -1.44 | down | hypothetical protein\ Context:(NC_002946)-[785742-786314]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0797 | 0.2321 | -2.81 | down | 0.6924 | -1.30 | down | 0.4406 | -1.72 | down | putative transcriptional regulator\ Context:(NC_002946)+[785985-786302]\ Notes:Best Blastp Hit: pir\|\|C81110 transcription regulator NMB1204 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226441\|gb\|AAF41586.1\| (AE002468) transcriptional regulator [Neisseria meningitidis MC58] >gi\|7380043\|emb\|CAB84621.1\| (AL162755) putative transcriptional regulator [Neisseria meningitidis] COG1396 Predicted transcriptional regulators |
| NGO0798 | 0.4557 | -2.07 | down | 0.0370 | -19.51 | down | 0.2020 | 3.02 | up | putative uridylyltransferase\ Context:(NC_002946)+[786351-788909]\ Notes:Best Blastp Hit: pir\|\|B81110 protein-PII uridylyltransferase NMB1203 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226440\|gb\|AAF41585.1\| (AE002468) protein-PII uridylyltransferase [Neisseria meningitidis MC58] |
| NGO0799 | 0.8939 | -1.07 | down | 0.4313 | -1.37 | down | 0.9641 | 1.01 | up | inositol-5-monophosphate dehydrogenase\ Context:(NC_002946)+[789056-790519]\ Notes:catalyzes the synthesis of xanthosine monophosphate by the NAD+ dependent oxidation of inosine monophosphate |
| NGO0800 | 0.0528 | 3.96 | up | 0.5780 | 1.69 | up | 0.1948 | 1.85 | up | hypothetical protein\ Context:(NC_002946)-[790591-790839]\ Notes: |
| NGO0801 | 0.0345 | 2.76 | up | 0.2397 | 1.74 | up | 0.4543 | 1.43 | up | putative ribonuclease\ Context:(NC_002946)-[790855-793230]\ Notes:Best Blastp Hit: pir\|\|G81109 ribonuclease II family protein NMB1200 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226437\|gb\|AAF41582.1\| (AE002468) ribonuclease II family protein [Neisseria meningitidis MC58] COG0557 Exoribonucleases |
| NGO0802 | 0.0420 | -3.31 | down | 0.3719 | 1.45 | up | 0.8756 | -1.09 | down | hypothetical protein\ Context:(NC_002946)+[793665-793934]\ Notes:Best Blastp Hit: emb\|CAB84478.1\| (AL162755) hypothetical protein NMA1218 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0803 | 0.0448 | 3.13 | up | 0.0283 | 2.50 | up | 0.1026 | 1.65 | up | putative GTP-binding protein\ Context:(NC_002946)-[793931-795742]\ Notes:Best Blastp Hit: pir\|\|H81111 GTP-binding protein TypA NMB1199 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226435\|gb\|AAF41581.1\| (AE002467) GTP-binding protein TypA [Neisseria meningitidis MC58] COG1217 Membrane GTPase |
| NGO0804 | 0.0018 | -8.49 | down | 0.0063 | -9.61 | down | 0.0336 | -5.67 | down | hypothetical protein\ Context:(NC_002946)-[795859-796749]\ Notes:Best Blastp Hit: pir\|\|C81906 hypothetical protein NMA1369 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380037\|emb\|CAB84615.1\| (AL162755) hypothetical protein NMA1369 [Neisseria meningitidis] COG0063 Predicted sugar kinase |
| NGO0805 | 0.0210 | -6.84 | down | 0.0008 | -20.93 | down | 0.0528 | -5.48 | down | hypothetical protein\ Context:(NC_002946)+[796889-797470]\ Notes:Best Blastp Hit: pir\|\|F81111 nickel-dependent hydrogenase; b-type cytochrome chain NMB1196; NMB1158 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226395\|gb\|AAF41544.1\| (AE002464) nickel-dependent hydrogenase; b-type cytochrome subunit [Neisseria meningitidis MC58] >gi\|7226433\|gb\|AAF41579.1\| (AE002467) nickel-dependent hydrogenase; b-type cytochrome subunit [Neisseria meningitidis MC58] |
| NGO0806 | 0.6021 | 1.57 | up | 0.2805 | -4.42 | down | 0.7104 | -1.44 | down | hypothetical protein\ Context:(NC_002946)+[797898-798980]\ Notes:Best Blastp Hit: >gi\|11354227\|pir\|\|T46867 uroporphyrin-III C-methyltransferase (EC 2.1.1.107) [imported] - Neisseria meningitidis gi\|1752671\|emb\|CAA71251.1\| (Y10177) sirohaem synthase [Neisseria meningitidis] |
| NGO0809 | 0.5506 | 1.31 | up | 0.7360 | -1.11 | down | 0.9179 | -1.03 | down | dihydroxy-acid dehydratase\ Context:(NC_002946)+[802735-804594]\ Notes:catalyzes the dehydration of 2;3-dihydroxy-3-methylbutanoate to 3-methyl-2-oxobutanoate in valine and isoleucine biosynthesis |
| NGO0810 | 0.8494 | 1.22 | up | 0.2375 | -1.98 | down | 0.5300 | -1.34 | down | hypothetical protein\ Context:(NC_002946)+[804636-804938]\ Notes:Best Blastp Hit: gb\|AAA47469.1\| (M57505) ORF3 [Pseudorabies virus] |

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| NGO0811 | 0.0774 | -3.08 | down | 0.5501 | -1.52 | down | 0.4141 | -1.56 | down | hypothetical protein\ Context:(NC_002946)-[804781-805686]\ Notes:Best Blastp Hit: gb\|AAF41535.1\| (AE002463) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226423\|gb\|AAF41570.1\| (AE002466) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0812 | 0.1886 | -2.05 | down | 0.0038 | -5.36 | down | 0.0435 | -3.95 | down | hypothetical protein\ Context:(NC_002946)+[805132-805749]\ Notes:Best Blastp Hit: pir\|\|B81117 hypothetical protein NMB1147; NMB1185 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226384\|gb\|AAF41534.1\| (AE002463) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226422\|gb\|AAF41569.1\| (AE002466) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0813 | 0.0734 | 3.19 | up | 0.0526 | 2.22 | up | 0.3532 | 1.28 | up | putative biotin synthase\ Context:(NC_002946)-[805845-806897]\ Notes:Best Blastp Hit: pir\|\|A81117 biotin synthetase NMB1146; NMB1184 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226383\|gb\|AAF41533.1\| (AE002463) biotin synthetase [Neisseria meningitidis MC58] >gi\|7226421\|gb\|AAF41568.1\| (AE002466) biotin synthetase [Neisseria meningitidis MC58] COG0502 Biotin synthase and related enzymes |
| NGO0814 | 0.9561 | -1.04 | down | 0.9003 | 1.06 | up | 0.2480 | 1.48 | up | hypothetical protein\ Context:(NC_002946)-[806915-807067]\ Notes:Best Blastp Hit: emb\|CAB84603.1\| (AL162755) hypothetical protein NMA1357 [Neisseria meningitidis] |
| NGO0815 | 0.2544 | 1.69 | up | 0.2179 | 1.61 | up | 0.4560 | 1.22 | up | putative UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase\ Context:(NC_002946)-[807104-808480]\ Notes:Best Blastp Hit: pir\|\|F81904 probable UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase (EC 6.3.2.-) NMA1356 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380024\|emb\|CAB84602.1\| (AL162755) putative UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso- diaminopimelate ligase [Neisseria meningitidis] COG0773 UDP-N-acetylmuramate-alanine ligase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0816 | 0.5061 | 1.40 | up | 0.9248 | 1.04 | up | 0.8508 | 1.06 | up | hypothetical protein\ Context:(NC_002946)-[808542-808847]\ Notes:Best Blastp Hit: pir\|\|G81116 hypothetical protein NMB1144; NMB1182 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226381\|gb\|AAF41531.1\| (AE002463) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226419\|gb\|AAF41566.1\| (AE002466) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0818 | 0.1104 | 2.51 | up | 0.8693 | 1.06 | up | 0.6732 | 1.19 | up | hypothetical protein\ Context:(NC_002946)-[809472-809669]\ Notes:Best Blastp Hit: pir\|\|T26843 hypothetical protein Y43F4B.5 - Caenorhabditis elegans >gi\|3880930\|emb\|CAA16334.1\| (AL021481) contains similarity to Pfam domain: PF00408 (Phosphoglucomutase/phosphomannomutase); Score=3.3; E-value=4.3e-11; N=1 cDNA EST EMBL:M89080 comes from this gene cDNA EST EMBL:T00805 comes from this gene cDNA EST EMBL:T00831 comes from this gen> |
| NGO0819 | 0.5191 | -1.51 | down | 0.3633 | 1.42 | up | 0.9876 | 1.01 | up | putative RNA methyltransferase\ Context:(NC_002946)-[809679-810464]\ Notes:Best Blastp Hit: emb\|CAB84598.1\| (AL162755) putative RNA methyltransferase [Neisseria meningitidis] COG0566 rRNA methylases |
| NGO0820 | 0.8782 | -1.17 | down | 0.9825 | -1.01 | down | 0.2613 | -1.62 | down | hypothetical protein\ Context:(NC_002946)-[810538-811818]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0037 Predicted ATPases of the PP-loop superamily |
| NGO0821 | 0.6430 | 1.26 | up | 0.7803 | 1.13 | up | 0.2603 | -1.79 | down | acetyl-CoA carboxylase carboxyltransferase subunit alpha\ Context:(NC_002946)-[811916-812875]\ Notes:catalyzes the carboxylation of acetyl-CoA to malonyl-CoA; forms a tetramer composed of two alpha (AccA) and two beta (AccD) subunits; one of the two catalytic subunits that can form the acetyl CoA carboxylase enzyme together with a carrier protein |

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| NGO0822 | 0.2017 | 1.82 | up | 0.0306 | 2.37 | up | 0.9774 | 1.01 | up | hypothetical protein\ Context:(NC_002946)+[813087-813488]\ Notes:Best Blastp Hit: pir\|\|A81119 conserved hypothetical protein NMB1138; NMB1176; NMA1348 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226375\|gb\|AAF41526.1\| (AE002462) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7226413\|gb\|AAF41561.1\| (AE002465) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380017\|emb\|CAB84595.1\| (AL162755) hypothetical protein NMA1348 [Neisseria meningitidis] COG1188 Predicted small RNA-binding protein (S4 |
| NGO0823 | 0.5324 | 1.42 | up | 0.7905 | 1.12 | up | 0.1972 | 1.82 | up | hypothetical protein\ Context:(NC_002946)-[813556-813753]\ Notes:Best Blastp Hit: gb\|AAF41525.1\| (AE002462) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7226412\|gb\|AAF41560.1\| (AE002465) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380016\|emb\|CAB84594.1\| (AL162755) hypothetical protein NMA1347 [Neisseria meningitidis] |
| NGO0825 | 0.4089 | 1.46 | up | 0.0151 | 4.20 | up | 0.7007 | 1.22 | up | putative ferredoxin\ Context:(NC_002946)-[814566-814907]\ Notes:Best Blastp Hit: pir\|\|E81118 ferredoxin [2Fe-2S] NMB1134; NMB1172; NMA1344 [similarity] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226371\|gb\|AAF41522.1\| (AE002462) ferredoxin; 2Fe-2S type [Neisseria meningitidis MC58] >gi\|7226409\|gb\|AAF41557.1\| (AE002465) ferredoxin; 2Fe-2S type [Neisseria meningitidis MC58] >gi\|7380014\|emb\|CAB84592.1\| (AL162755) putative ferredoxin [Neisseria meningitidis] COG0633 Ferredoxin |
| NGO0826 | 0.1808 | 2.10 | up | 0.0115 | 3.40 | up | 0.0542 | 2.18 | up | hypothetical protein\ Context:(NC_002946)-[814963-815721]\ Notes:Best Blastp Hit: emb\|CAB84591.1\| (AL162755) hypothetical protein NMA1343 [Neisseria meningitidis] |
| NGO0827 | 0.1032 | 2.18 | up | 0.0818 | 1.99 | up | 0.2837 | 2.00 | up | hypothetical protein\ Context:(NC_002946)-[815760-816323]\ Notes:Best Blastp Hit: emb\|CAB84590.1\| (AL162755) hypothetical protein NMA1341 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0828 | 0.0182 | 6.70 | up | 0.0250 | 13.35 | up | 0.0456 | 3.58 | up | hypothetical protein\ Context:(NC_002946)-[816373-816519]\ Notes:Best Blastp Hit: gb\|AAF41523.1\| (AE002462) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226410\|gb\|AAF41558.1\| (AE002465) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0829 | 0.0144 | 3.93 | up | 0.0393 | 5.26 | up | 0.0509 | 1.99 | up | chaperone protein HscA\ Context:(NC_002946)-[816596-818458]\ Notes:involved in the maturation of iron-sulfur cluster-containing proteins |
| NGO0830 | 0.3433 | -1.59 | down | 0.0637 | -2.58 | down | 0.1006 | -1.95 | down | putative poly-isoprenyl transferase\ Context:(NC_002946)+[818629-819501]\ Notes:Best Blastp Hit: pir\|\|A81118 phytoene synthase; probable NMB1130; NMB1168 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226367\|gb\|AAF41518.1\| (AE002462) phytoene synthase; putative [Neisseria meningitidis MC58] >gi\|7226405\|gb\|AAF41553.1\| (AE002465) phytoene synthase; putative [Neisseria meningitidis MC58] COG1562 Phytoene/squalene synthetase |
| NGO0831 | 0.1088 | -2.95 | down | 0.1872 | -2.07 | down | 0.8788 | -1.08 | down | putative oxidoreductase\ Context:(NC_002946)+[819576-820949]\ Notes:Best Blastp Hit: gb\|AAF41516.1\| (AE002462) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7226403\|gb\|AAF41551.1\| (AE002465) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0832 | 0.8727 | 1.09 | up | 0.8639 | -1.08 | down | 0.8591 | 1.06 | up | short chain dehydrogenase\ Context:(NC_002946)+[820972-821691]\ Notes:Best Blastp Hit: emb\|CAB84586.1\| (AL162755) putative oxidoreductase [Neisseria meningitidis] COG1028 Dehydrogenases with different specificities |
| NGO0834 | 0.8852 | -1.08 | down | 0.7952 | -1.14 | down | 0.6618 | -1.18 | down | hypothetical protein\ Context:(NC_002946)+[821857-822528]\ Notes:Best Blastp Hit: gb\|AAF41514.1\| (AE002461) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226400\|gb\|AAF41549.1\| (AE002464) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380007\|emb\|CAB84585.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] COG1462 Uncharacterized protein CsgG involved |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0835 | 0.4859 | -1.48 | down | 0.5471 | -1.30 | down | 0.6939 | -1.12 | down | GNA1162\ Context:(NC_002946)+[822902-823549]\ Notes:Best Blastp Hit: gb\|AAF44774.1\|AF235157_1 (AF235157) GNA1162 [Neisseria gonorrhoeae] >gi\|7274440\|gb\|AAF44775.1\|AF235158_1 (AF235158) GNA1162 [Neisseria gonorrhoeae] >gi\|7274442\|gb\|AAF44776.1\|AF235159_1 (AF235159) GNA1162 [Neisseria gonorrhoeae]; genome-derived Neisseria antigen 1162 |
| NGO0836 | 0.0531 | -4.62 | down | 0.1861 | -6.48 | down | 0.2752 | 2.85 | up | hypothetical protein\ Context:(NC_002946)+[823589-823732]\ Notes:Best Blastp Hit: gb\|AAF41511.1\| (AE002461) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226397\|gb\|AAF41546.1\| (AE002464) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0841 | 0.5680 | -1.33 | down | 0.4118 | -1.46 | down | 0.7561 | -1.10 | down | hypothetical protein\ Context:(NC_002946)+[825812-826480]\ Notes:Best Blastp Hit: pir\|\|B81896 hypothetical protein NMA1279 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379956\|emb\|CAB84531.1\| (AL162755) hypothetical protein NMA1279 [Neisseria meningitidis] COG0593 ATPase involved in DNA replication |
| NGO0842 | 0.8490 | -1.15 | down | 0.8854 | 1.06 | up | 0.8973 | -1.05 | down | hypothetical protein\ Context:(NC_002946)+[826477-827145]\ Notes:Best Blastp Hit: emb\|CAB84530.1\| (AL162755) hypothetical protein NMA1278 [Neisseria meningitidis] COG0560 Phosphoserine phosphatase |
| NGO0843 | 0.0006 | -48.89 | down | 0.0001 | -165.28 | down | 0.0000 | -59.40 | down | hypothetical protein\ Context:(NC_002946)-[827290-827577]\ Notes: |
| NGO0844 | 0.0022 | -8.38 | down | 0.0052 | -6.57 | down | 0.0004 | -9.41 | down | acetylglutamate kinase\ Context:(NC_002946)-[827592-828488]\ Notes:catalyzes the phosphorylation of N-acetyl-L-glutamate to form N-acetyl-L-glutamate 5-phosphate |
| NGO0845 | 0.5066 | 1.38 | up | 0.6858 | -1.17 | down | 0.3180 | 1.30 | up | hypothetical protein\ Context:(NC_002946)+[828658-829788]\ Notes:Best Blastp Hit: pir\|\|F81895 hypothetical protein NMA1274 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379952\|emb\|CAB84527.1\| (AL162755) hypothetical protein NMA1274 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0846 | 0.0240 | 3.61 | up | 0.1538 | 2.25 | up | 0.8114 | 1.15 | up | prolipoprotein diacylglyceryl transferase\ Context:(NC_002946)+[829862-830713]\ Notes:transfers the N-acyl diglyceride moiety to the prospective N-terminal cysteine in prolipoprotein |
| NGO0847 | 0.5409 | 1.35 | up | 0.9778 | 1.01 | up | 0.7762 | -1.08 | down | hypothetical protein\ Context:(NC_002946)-[830798-831460]\ Notes:Best Blastp Hit: gb\|AAF41466.1\|(AE002457) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0848 | 0.7825 | -1.13 | down | 0.8756 | -1.07 | down | 0.2750 | -1.56 | down | 2-isopropylmalate synthase\ Context:(NC_002946)-[831659-833212]\ Notes:catalyzes the formation of 2-isopropylmalate from acetyl-CoA and 2-oxoisovalerate in leucine biosynthesis |
| NGO0850 | 0.0003 | -21.60 | down | 0.0015 | -21.58 | down | 0.0281 | -4.03 | down | gamma-glutamyl phosphate reductase\ Context:(NC_002946)+[834819-836081]\ Notes:Catalyzes the phosphorylation of L-glutamate during the proline biosynthesis pathway |
| NGO0851 | 0.8302 | -1.15 | down | 0.0369 | -3.21 | down | 0.7142 | -1.16 | down | putative cell-division protein\ Context:(NC_002946)-[836257-839301]\ Notes:Best Blastp Hit: pir\|\|E81125 cell division protein FtsK NMB1067 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226307\|gb\|AAF41463.1\| (AE002457) cell division protein FtsK [Neisseria meningitidis MC58] COG1674 DNA segregation ATPase FtsK/SpoIIIE and |
| NGO0852 | 0.5146 | -1.57 | down | 0.0063 | -5.27 | down | 0.2745 | -1.86 | down | hypothetical protein\ Context:(NC_002946)+[839467-840147]\ Notes:Best Blastp Hit: pir\|\|G81894 probable integral membrane protein NMA1265 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379945\|emb\|CAB84520.1\| (AL162755) putative integral membrane protein [Neisseria meningitidis] |
| NGO0853 | 0.7463 | 1.24 | up | 0.1578 | -3.58 | down | 0.4446 | 2.38 | up | hypothetical protein\ Context:(NC_002946)+[840176-840535]\ Notes:Best Blastp Hit: pir\|\|F81894 probable integral membrane protein NMA1264 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379944\|emb\|CAB84519.1\| (AL162755) putative integral membrane protein [Neisseria meningitidis] COG0239 Integral membrane protein possibly involved |
| NGO0854 | 0.0334 | -32.31 | down | 0.0644 | -13.67 | down | 0.0824 | -28.36 | down | hypothetical protein\ Context:(NC_002946)-[840823-840960]\ Notes: |

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| NGO0857 | 0.3054 | 1.77 | up | 0.9594 | -1.02 | down | 0.7658 | -1.09 | down | putative dihydroneopterin aldolase\ Context:(NC_002946)-[841711-842067]\ Notes:Best Blastp Hit: pir\|\|A81127 dihydroneopterin aldolase NMB1063 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226302\|gb\|AAF41459.1\| (AE002456) dihydroneopterin aldolase [Neisseria meningitidis MC58] COG1539 Dihydroneopterin aldolase |
| NGO0858 | 0.0067 | -13.37 | down | 0.0073 | -8.15 | down | 0.0656 | -2.08 | down | hypothetical protein\ Context:(NC_002946)+[842123-842725]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0344 Predicted membrane protein; YgiH/UPF0078 |
| NGO0859 | 0.0193 | -6.11 | down | 0.0020 | -26.41 | down | 0.3161 | -2.18 | down | hypothetical protein\ Context:(NC_002946)+[842817-843662]\ Notes:Best Blastp Hit: pir\|\|G81126 conserved hypothetical protein NMB1061 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226300\|gb\|AAF41457.1\| (AE002456) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0860 | 0.5176 | -1.33 | down | 0.0241 | -10.96 | down | 0.6862 | -1.24 | down | hypothetical protein\ Context:(NC_002946)+[843668-844126]\ Notes: |
| NGO0861 | 0.1400 | 2.34 | up | 0.2820 | 1.55 | up | 0.3316 | 1.36 | up | hypothetical protein\ Context:(NC_002946)-[844152-844400]\ Notes: |
| NGO0862 | 0.1635 | -2.02 | down | 0.8176 | 1.16 | up | 0.5034 | -1.20 | down | fructose-1;6-bisphosphatase\ Context:(NC_002946)+[844641-845615]\ Notes:catalyzes the formation of D-fructose 6-phosphate from fructose-1;6-bisphosphate |
| NGO0863 | 0.1716 | 2.38 | up | 0.2598 | 1.61 | up | 0.5140 | 1.32 | up | hypothetical protein\ Context:(NC_002946)-[845774-845992]\ Notes:Best Blastp Hit: gb\|AAF41455.1\| (AE002456) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379938\|emb\|CAB84513.1\| (AL162755) hypothetical protein NMA1258 [Neisseria meningitidis] |
| NGO0865 | 0.1619 | 2.09 | up | 0.2347 | 1.62 | up | 0.7588 | 1.09 | up | hypothetical protein\ Context:(NC_002946)+[848531-848773]\ Notes:Best Blastp Hit: gb\|AAF41453.1\| (AE002456) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0866 | 0.7343 | 1.18 | up | 0.8496 | 1.09 | up | 0.5696 | 1.18 | up | serine hydroxymethyltransferase\ Context:(NC_002946)+[848840-850090]\ Notes:catalyzes the reaction of glycine with 5;10-methylenetetrahydrofolate to form L-serine and tetrahydrofolate |

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| NGO0867 | 0.0181 | 4.38 | up | 0.7836 | 1.18 | up | 0.1308 | 1.71 | up | hypothetical protein\ Context:(NC_002946)-[850163-850552]\ Notes:Best Blastp Hit: pir\|\|F81234 conserved hypothetical protein NMB0121 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225338\|gb\|AAF40580.1\| (AE002371) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0868 | 0.1476 | -2.54 | down | 0.0174 | -10.27 | down | 0.5902 | -2.03 | down | OpcA\ Context:(NC_002946)+[851492-852283]\ Notes:Best Blastp Hit: emb\|CAB45007.1\| (AJ242839) OpcA protein [Neisseria gonorrhoeae]; class 5 outer membrane protein |
| NGO0869 | 0.0193 | -6.80 | down | 0.0501 | -4.79 | down | 0.4218 | -2.07 | down | hypothetical protein\ Context:(NC_002946)+[852434-853078]\ Notes:Best Blastp Hit: pir\|\|D81128 dedA protein NMB1052 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226292\|gb\|AAF41450.1\| (AE002455) dedA protein [Neisseria meningitidis MC58] >gi\|7379932\|emb\|CAB84505.1\| (AL162755) DedA protein ortholog [Neisseria meningitidis] COG0586 Uncharacterized membrane-associated protein |
| NGO0870 | 0.6561 | -1.22 | down | 0.5899 | -1.19 | down | 0.4889 | 1.25 | up | AbcZ\ Context:(NC_002946)+[853097-855007]\ Notes:Best Blastp Hit: emb\|CAB45011.1\| (AJ242839) putative ATP-binding protein [Neisseria gonorrhoeae] COG0488 ATPase components of ABC transporters with; putative ABC-type transporter; ATP-binding protein |
| NGO0871 | 0.0061 | -7.35 | down | 0.0018 | -12.05 | down | 0.3385 | -2.13 | down | hypothetical protein\ Context:(NC_002946)+[855029-855358]\ Notes:Best Blastp Hit: emb\|CAB45013.1\| (AJ242839) hypothetical protein [Neisseria gonorrhoeae] |
| NGO0872 | 0.2759 | 1.99 | up | 0.0891 | 6.09 | up | 0.0809 | 4.28 | up | anthranilate synthase component I\ Context:(NC_002946)+[855507-856982]\ Notes:with component II; the glutamine amidotransferase; catalyzes the formation of anthranilate from chorismate and glutamine |
| NGO0873 | 0.0419 | 4.14 | up | 0.0310 | 25.53 | up | 0.0648 | 10.36 | up | DNA modification methylase M.NGOI\ Context:(NC_002946)+[857066-858004]\ Notes:Best Blastp Hit: emb\|CAB44950.1\| (AJ242840) DNA modification methylase [Neisseria gonorrhoeae] >gi\|5262959\|emb\|CAB45015.2\| (AJ242839) DNA modification methylase [Neisseria gonorrhoeae] COG0270 Site-specific DNA methylase dcm; DcmD |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0874 | 0.2754 | 1.87 | up | 0.0345 | 6.22 | up | 0.1109 | 4.24 | up | type II DNA restriction endonuclease R.NGOI\ Context:(NC_002946)+[858005-858865]\ Notes:Best Blastp Hit: sp\|P31032\|T2NM_NEIGO type II restriction enzyme NgoI (endonuclease NgomI) (R.NGOMI) >gi\|281723\|pir\|\|B42709 DNA restriction endonuclease NgoMI - Neisseria gonorrhoeae >gi\|5051443\|emb\|CAB44951.1\| (AJ242840) putative DNA restriction endonuclease [Neisseria gonorrhoeae] >gi\|5262960\|emb\|CAB45874.1\| (AJ242839) putative DNA restriction endonuclease [Neisseria gonorrhoeae] |
| NGO0875 | 0.0019 | 15.61 | up | 0.1132 | 5.96 | up | 0.3816 | 1.79 | up | phosphoribosylaminoimidazole carboxylase ATPase subunit\ Context:(NC_002946)+[858882-860018]\ Notes:With PurE catalyzes the conversion of aminoimidazole ribonucleotide to carboxyaminoimidazole ribonucleotide in the de novo purine nucleotide biosynthetic pathway |
| NGO0876 | 0.5439 | -1.43 | down | 0.6920 | -1.35 | down | 0.2126 | -2.26 | down | hypothetical protein\ Context:(NC_002946)+[860065-860547]\ Notes:Best Blastp Hit: gb\|AAF41418.1\| (AE002452) conserved hypothetical protein [Neisseria meningitidis MC58] COG0454 Predicted acetyltransferases |
| NGO0878 | 0.5114 | 1.55 | up | 0.9595 | 1.05 | up | 0.3696 | -1.81 | down | hypothetical protein\ Context:(NC_002946)+[861698-861901]\ Notes:Best Blastp Hit: dbj\|BAA82522.1\| (AB030007) tunicate retinoic acid-inducible modular protease [Polyandrocarpa misakiensis] |
| NGO0879 | 0.6654 | -1.40 | down | 0.0274 | -3.39 | down | 0.6149 | -1.54 | down | hypothetical protein\ Context:(NC_002946)-[861993-862184]\ Notes: |
| NGO0880 | 0.0005 | -17.91 | down | 0.0028 | -5.24 | down | 0.3225 | -2.70 | down | hypothetical protein\ Context:(NC_002946)+[862282-862887]\ Notes:Best Blastp Hit: pir\|\|B81892 hypothetical protein NMA1237 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379924\|emb\|CAB84495.1\| (AL162755) hypothetical protein NMA1237 [Neisseria meningitidis] |
| NGO0883 | 0.0823 | 3.38 | up | 0.7612 | -1.72 | down | 0.6398 | -3.05 | down | hypothetical protein\ Context:(NC_002946)+[864823-865149]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0885 | 0.3050 | -1.72 | down | 0.1430 | -3.99 | down | 0.7288 | -1.43 | down | putative rubredoxin\ Context:(NC_002946)-[865554-865724]\ Notes:Best Blastp Hit: pir\|\|H81133 rubredoxin NMB0993 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226233\|gb\|AAF41396.1\| (AE002450) rubredoxin [Neisseria meningitidis MC58] >gi\|7379892\|emb\|CAB84462.1\| (AL162755) putative rubredoxin [Neisseria meningitidis] COG1773 Rubredoxin |
| NGO0886 | 0.0022 | -13.59 | down | 0.0092 | -32.72 | down | 0.4235 | -2.11 | down | putative acyl-CoA dehydrogenase\ Context:(NC_002946)-[865857-866939]\ Notes:Best Blastp Hit: emb\|CAB84463.1\| (AL162755) putative acyl-CoA dehydrogenase [Neisseria meningitidis] COG1960 Acyl-CoA dehydrogenases |
| NGO0887 | 0.5297 | 1.59 | up | 0.3639 | -2.43 | down | 0.2264 | -2.14 | down | hypothetical protein\ Context:(NC_002946)-[867077-867625]\ Notes:Best Blastp Hit: emb\|CAB84464.1\| (AL162755) hypothetical protein NMA1203 [Neisseria meningitidis] |
| NGO0888 | 0.0250 | -4.28 | down | 0.0029 | -5.62 | down | 0.3069 | -2.33 | down | hypothetical protein\ Context:(NC_002946)-[867765-868025]\ Notes:Best Blastp Hit: gb\|AAF41399.1\| (AE002450) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379895\|emb\|CAB84465.1\| (AL162755) hypothetical protein NMA1204 [Neisseria meningitidis] |
| NGO0889 | 0.0878 | 2.69 | up | 0.6614 | -1.64 | down | 0.3189 | 2.70 | up | hypothetical protein\ Context:(NC_002946)+[868110-868271]\ Notes: |
| NGO0890 | 0.9129 | 1.05 | up | 0.7252 | -1.17 | down | 0.9752 | -1.01 | down | D-lactate dehydrogenase\ Context:(NC_002946)-[868321-870012]\ Notes:component of the membrane-bound D-lactate oxidase; FAD-binding; NADH independent |
| NGO0891 | 0.3315 | -1.65 | down | 0.3136 | -1.80 | down | 0.1050 | -1.79 | down | hypothetical protein\ Context:(NC_002946)-[870109-870528]\ Notes:Best Blastp Hit: pir\|\|S52906 virion protein j13L - African swine fever virus >gi\|695432\|emb\|CAA59319.1\| (X84893) j13L [African swine fever virus] |
| NGO0892 | 0.1461 | -2.98 | down | 0.0002 | -53.52 | down | 0.3056 | -1.88 | down | hypothetical protein\ Context:(NC_002946)+[870645-870926]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0893 | 0.0158 | -5.17 | down | 0.0250 | -4.49 | down | 0.2013 | -2.00 | down | putative oxidoreductase\ Context:(NC_002946)+[871108-874941]\ Notes:Best Blastp Hit: emb\|CAB84467.1\| (AL162755) putative oxidoreductase [Neisseria meningitidis] COG0247 Fe-S oxidoreductases |
| NGO0894 | 0.6461 | -1.46 | down | 0.0426 | -11.95 | down | 0.0437 | -3.21 | down | hypothetical protein\ Context:(NC_002946)+[875018-876019]\ Notes:Best Blastp Hit: pir\|\|H81888 hypothetical protein NMA1207 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379898\|emb\|CAB84468.1\| (AL162755) hypothetical protein NMA1207 [Neisseria meningitidis] COG0042 Predicted TIM-barrel enzymes; possibly |
| NGO0895 | 0.2456 | 1.82 | up | 0.1300 | 1.97 | up | 0.0732 | 2.48 | up | hypothetical protein\ Context:(NC_002946)-[876080-876262]\ Notes:Best Blastp Hit: emb\|CAB84469.1\| (AL162755) hypothetical protein NMA1208 [Neisseria meningitidis] |
| NGO0896 | 0.1751 | -2.88 | down | 0.2579 | 3.35 | up | 0.5683 | 2.02 | up | hypothetical protein\ Context:(NC_002946)-[876435-876566]\ Notes: |
| NGO0897 | 0.0569 | -3.61 | down | 0.0988 | -4.65 | down | 0.6719 | -1.33 | down | hypothetical protein\ Context:(NC_002946)+[876614-876778]\ Notes: |
| NGO0899 | 0.5671 | -1.33 | down | 0.2245 | -2.06 | down | 0.8625 | -1.09 | down | hypothetical protein\ Context:(NC_002946)-[878296-878772]\ Notes:Best Blastp Hit: pir\|\|G81858 transcription elongation factor NMA1643 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380285\|emb\|CAB84871.1\| (AL162756) transcription elongation factor [Neisseria meningitidis] COG0782 Transcription elongation factor |
| NGO0900 | 0.6365 | 1.30 | up | 0.7196 | -1.23 | down | 0.4309 | 1.59 | up | 3-phosphoshikimate 1-carboxyvinyltransferase\ Context:(NC_002946)+[879163-880464]\ Notes:catalyzes the formation of 5-O-(1-carboxyvinyl)-3-phosphoshikimate from phosphoenolpyruvate and 3-phosphoshikimate in tryptophan biosynthesis |
| NGO0901 | 0.2165 | -2.23 | down | 0.0589 | -10.51 | down | 0.1491 | -2.69 | down | putative lipoprotein\ Context:(NC_002946)-[880542-881075]\ Notes:Best Blastp Hit: emb\|CAB84873.1\| (AL162756) putative lipoprotein [Neisseria meningitidis] COG0791 Cell wall-associated hydrolases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0902 | 0.2068 | 2.14 | up | 0.3757 | -2.42 | down | 0.7839 | -1.30 | down | putative phopholipase D-family protein\ Context:(NC_002946)-[881132-882709]\ Notes:Best Blastp Hit: emb\|CAB84874.1\| (AL162756) phopholipase D-family protein [Neisseria meningitidis] COG1502 Cardiolipin synthase; phoaphatidylserine |
| NGO0903 | 0.0113 | -10.47 | down | 0.0247 | -31.07 | down | 0.5253 | -1.41 | down | AgrA\ Context:(NC_002946)-[882770-884176]\ Notes:Best Blastp Hit: emb\|CAB84875.1\| (AL162756) putative integral membrane protein [Neisseria meningitidis] COG0477 Permeases; aminoglycoside resistance efflux transporter protein |
| NGO0904 | 0.4539 | -1.41 | down | 0.0740 | -2.36 | down | 0.0584 | -1.83 | down | hypothetical protein\ Context:(NC_002946)+[884459-885238]\ Notes:Best Blastp Hit: pir\|\|D81859 conserved hypothetical protein NMA1648 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380290\|emb\|CAB84876.1\| (AL162756) conserved hypothetical protein [Neisseria meningitidis] COG0247 Fe-S oxidoreductases |
| NGO0905 | 0.1584 | -2.00 | down | 0.0477 | -2.49 | down | 0.0800 | -1.82 | down | hypothetical protein\ Context:(NC_002946)+[885235-885936]\ Notes:Best Blastp Hit: emb\|CAB84877.1\| (AL162756) conserved hypothetical protein [Neisseria meningitidis] COG1556 Uncharacterized ACR; YkgG family |
| NGO0906 | 0.0852 | -2.63 | down | 0.0460 | -2.05 | down | 0.0799 | -2.28 | down | hypothetical protein\ Context:(NC_002946)+[885933-887387]\ Notes:Best Blastp Hit: pir\|\|F81859 conserved hypothetical iron-sulfur protein NMA1650 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7380292\|emb\|CAB84878.1\| (AL162756) conserved hypothetical iron-sulphur protein [Neisseria meningitidis] COG1139 Uncharacterized conserved protein containing |
| NGO0907 | 0.6598 | 1.85 | up | 0.8099 | -1.44 | down | 0.9812 | 1.03 | up | FitB\ Context:(NC_002946)-[887536-887955]\ Notes:Best Blastp Hit: gb\|AAF19189.1\|AF200716_2 (AF200716) trafficking protein B [Neisseria gonorrhoeae] |
| NGO0908 | 0.9576 | -1.03 | down | 0.7627 | 1.15 | up | 0.7666 | 1.19 | up | FitA\ Context:(NC_002946)-[887955-888191]\ Notes:Best Blastp Hit: gb\|AAF19188.1\|AF200716_1 (AF200716) trafficking protein A [Neisseria gonorrhoeae] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0912 | 0.9358 | -1.04 | down | 0.8325 | -1.08 | down | 0.8195 | 1.10 | up | succinyl-CoA synthetase subunit alpha\ Context:(NC_002946)-[890632-891522]\ Notes:Catalyzes the only substrate-level phosphorylation in the TCA cycle |
| NGO0913 | 0.4680 | 1.53 | up | 0.5766 | 1.20 | up | 0.5443 | 1.27 | up | succinyl-CoA synthetase subunit beta\ Context:(NC_002946)-[891533-892699]\ Notes:catalyzes the interconversion of succinyl-CoA and succinate |
| NGO0914 | 0.5677 | 1.35 | up | 0.8928 | 1.05 | up | 0.9837 | 1.01 | up | hypothetical protein\ Context:(NC_002946)-[892771-893058]\ Notes:Best Blastp Hit: gb\|AAF41364.1\| (AE002447) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379845\|emb\|CAB84414.1\| (AL162755) putative membrane protein [Neisseria meningitidis] |
| NGO0915 | 0.7294 | -1.20 | down | 0.5676 | -1.24 | down | 0.6211 | -1.17 | down | dihydrolipoamide dehydrogenase\ Context:(NC_002946)-[893178-894611]\ Notes:E3 component of 2-oxoglutarate dehydrogenase complex; catalyzes the oxidation of dihydrolipoamide to lipoamide |
| NGO0916 | 0.5010 | 1.62 | up | 0.1472 | 3.31 | up | 0.3041 | 1.73 | up | dihydrolipoamide acetyltransferase\ Context:(NC_002946)-[894872-896053]\ Notes:component of 2-oxoglutarate dehydrogenase complex; catalyzes the transfer of acetyl from acetyldihydrolipoamide to coenzyme A to form acetyl CoA as part of the conversion of 2-oxoglutarate to succinyl-CoA |
| NGO0917 | 0.7939 | 1.25 | up | 0.1785 | 5.60 | up | 0.3877 | 1.51 | up | alpha-ketoglutarate decarboxylase\ Context:(NC_002946)-[896153-898981]\ Notes:kgd; produces succinic semialdehyde; part of alternative pathway from alpha-ketoglutarate to succinate; essential for normal growth |
| NGO0918 | 0.7541 | -1.21 | down | 0.6410 | -1.19 | down | 0.3545 | -1.35 | down | type II citrate synthase\ Context:(NC_002946)-[899186-900469]\ Notes:type II enzyme; in Escherichia coli this enzyme forms a trimer of dimers which is allosterically inhibited by NADH and competitively inhibited by alpha-ketoglutarate; allosteric inhibition is lost when Cys206 is chemically modified which also affects hexamer formation; forms oxaloacetate and acetyl-CoA and water from citrate and coenzyme A; functions in TCA cycle; glyoxylate cycle and respiration; enzyme from Helicobacter pylori is not inhibited by NADH |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0919 | 0.9944 | 1.00 | up | 0.9549 | -1.02 | down | 0.1475 | -1.65 | down | hypothetical protein\ Context:(NC_002946)-[900581-900829]\ Notes:Best Blastp Hit: gb\|AAF41358.1\|(AE002446) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379840\|emb\|CAB84409.1\|(AL162755) hypothetical protein NMA1147 [Neisseria meningitidis] |
| NGO0920 | 0.2032 | -1.95 | down | 0.3359 | -1.50 | down | 0.0458 | -1.94 | down | succinate dehydrogenase iron-sulfur subunit\ Context:(NC_002946)-[900833-901561]\ Notes:part of four member succinate dehydrogenase enzyme complex that forms a trimeric complex (trimer of tetramers); SdhA/B are the catalytic subcomplex and can exhibit succinate dehydrogenase activity in the absence of SdhC/D which are the membrane components and form cytochrome b556; SdhC binds ubiquinone; oxidizes succinate to fumarate while reducing ubiquinone to ubiquinol; the catalytic subunits are similar to fumarate reductase |
| NGO0921 | 0.0221 | -4.01 | down | 0.2809 | -1.66 | down | 0.0104 | -2.75 | down | putative succinate dehydrogenase flavoprotein subunit\ Context:(NC_002946)-[901660-903423]\ Notes:Best Blastp Hit: pir\|\|D81881 probable succinate dehydrogenase (EC 1.3.99.1) flavoprotein NMA1145 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379838\|emb\|CAB84407.1\| (AL162755) putative succinate dehydrogenase flavoprotein subunit [Neisseria meningitidis] COG1053 Succinate dehydrogenase/fumarate reductase |
| NGO0922 | 0.1184 | -2.24 | down | 0.3994 | -1.46 | down | 0.0168 | -2.20 | down | putative succinate dehydrogenase hydrophobic membrane anchor protein\ Context:(NC_002946)-[903426-903767]\ Notes:Best Blastp Hit: pir\|\|E81138 succinate dehydrogenase; hydrophobic membrane anchor protein NMB0949 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226188\|gb\|AAF41355.1\| (AE002446) succinate dehydrogenase; hydrophobic membrane anchor protein [Neisseria meningitidis MC58] COG2142 Cytochrome b subunit of fumarate reductase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0923 | 0.0074 | -7.89 | down | 0.1842 | -1.96 | down | 0.0106 | -4.59 | down | putative fumarate reductase cytochrome b large subunit\ Context:(NC_002946)-[903761-904138]\ Notes:Best Blastp Hit: pir\|\|D81138 succinate dehydrogenase; cytochrome b556 chain NMB0948 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226187\|gb\|AAF41354.1\| (AE002446) succinate dehydrogenase; cytochrome b556 subunit [Neisseria meningitidis MC58] >gi\|7379836\|emb\|CAB84405.1\| (AL162755) putative succinate dehydrogenase cytochrome B subunit [Neisseria meningitidis] COG2009 Cytochrome b subunit of succinate |
| NGO0924 | 0.4139 | 2.14 | up | 0.0330 | -15.17 | down | 0.6165 | 1.69 | up | hypothetical protein\ Context:(NC_002946)-[904199-904408]\ Notes: |
| NGO0925 | 0.3629 | -1.50 | down | 0.3788 | -1.50 | down | 0.6889 | -1.13 | down | dihydrolipoamide dehydrogenase\ Context:(NC_002946)-[904425-905828]\ Notes:Catalyzes the oxidation of dihydrolipoamide to lipoamide |
| NGO0926 | 0.2161 | 2.30 | up | 0.2074 | 1.53 | up | 0.3266 | 1.58 | up | putative peroxiredoxin family protein/glutaredoxin\ Context:(NC_002946)-[906077-906814]\ Notes:Best Blastp Hit: gb\|AAF41352.1\| (AE002445) peroxiredoxin 2 family protein/glutaredoxin [Neisseria meningitidis MC58] >gi\|7379834\|emb\|CAB84403.1\| (AL162755) putative redoxin [Neisseria meningitidis] COG0678 Peroxiredoxin |
| NGO0927 | 0.3963 | 1.47 | up | 0.1113 | 2.27 | up | 0.5640 | 1.23 | up | hypothetical protein\ Context:(NC_002946)-[906917-907081]\ Notes:Best Blastp Hit: gb\|AAF41351.1\| (AE002445) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0928 | 0.4876 | 1.67 | up | 0.0971 | 3.65 | up | 0.1143 | 2.39 | up | 5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase\ Context:(NC_002946)-[907093-909369]\ Notes:catalyzes the transfer of a methyl group from 5-methyltetrahydrofolate to homocysteine to form methionine |
| NGO0929 | 0.2836 | -1.75 | down | 0.6118 | 1.19 | up | 0.7486 | -1.13 | down | 5;10-methylenetetrahydrofolate reductase\ Context:(NC_002946)-[909505-910383]\ Notes:MTHFR; catalyzes NADH-linked reduction of 5;10-methylenetetrahydrofolate to 5-methyltetrahydrofolate using FAD as a cofactor |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO0930 | 0.1405 | 2.71 | up | 0.2910 | 1.49 | up | 0.4061 | 1.42 | up | 50S ribosomal protein L31 type B\ Context:(NC_002946)+[910582-910857]\ Notes:RpmE2; there appears to be two types of ribosomal proteins L31 in bacterial genomes; some contain a CxxC motif while others do not; Bacillus subtilis has both types; the proteins in this cluster do not have the CXXC motif; RpmE is found in exponentially growing Bacilli while YtiA was found after exponential growth; expression of ytiA is controlled by a zinc-specific transcriptional repressor; RpmE contains one zinc ion and a CxxC motif is responsible for this binding; forms an RNP particle along with proteins L5; L18; and L25 and 5S rRNA; found crosslinked to L2 and L25 and EF-G; may be near the peptidyltransferase site of the 50S ribosome |
| NGO0931 | 0.1235 | 2.73 | up | 0.2453 | 1.56 | up | 0.3908 | 1.39 | up | 50S ribosomal protein L36\ Context:(NC_002946)+[910857-910982]\ Notes:smallest protein in the large subunit; similar to what is found with protein L31 and L33 several bacterial genomes contain paralogs which may be regulated by zinc; the protein from Thermus thermophilus has a zinc-binding motif and contains a bound zinc ion; the proteins in this group do not have the motif |
| NGO0932 | 0.9285 | -1.06 | down | 0.3803 | -1.58 | down | 0.3592 | -1.53 | down | hypothetical protein\ Context:(NC_002946)+[911041-911481]\ Notes:Best Blastp Hit: gb\|AAA53170.1\| (U00415) gp120 [Human immunodeficiency virus type 1] |
| NGO0933 | 0.4724 | 1.36 | up | 0.9825 | 1.01 | up | 0.7956 | 1.09 | up | homoserine O-acetyltransferase\ Context:(NC_002946)+[911429-912568]\ Notes:Catalyzes the conversion of acetyl-CoA and L-homoserine to CoA and O-acetyl-L-homoserine |
| NGO0934 | 0.6300 | 1.25 | up | 0.8609 | -1.09 | down | 0.5383 | -1.40 | down | hypothetical protein\ Context:(NC_002946)+[912565-913146]\ Notes:Best Blastp Hit: pir\|\|B81880 hypothetical protein NMA1135 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379828\|emb\|CAB84397.1\| (AL162755) hypothetical protein NMA1135 [Neisseria meningitidis] |
| NGO0936 | 0.0452 | 3.15 | up | 0.2299 | 1.61 | up | 0.2884 | 1.58 | up | elongation factor P\ Context:(NC_002946)-[914253-914813]\ Notes:Involved in peptide bond synthesis; alters the affinity of the ribosome for aminoacyl-tRNA |

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| NGO0937 | 0.5137 | 1.62 | up | 0.3623 | -2.12 | down | 0.4983 | -1.59 | down | hypothetical protein\ Context:(NC_002946)-[914856-916007]\ Notes:Best Blastp Hit: pir\|\|G81879 hypothetical protein NMA1132 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379825\|emb\|CAB84394.1\| (AL162755) hypothetical protein NMA1132 [Neisseria meningitidis] |
| NGO0938 | 0.5013 | -1.87 | down | 0.9609 | 1.02 | up | 0.8520 | 1.26 | up | hypothetical protein\ Context:(NC_002946)-[916026-916334]\ Notes:Best Blastp Hit: pir\|\|F81879 probable membrane protein NMA1131 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379824\|emb\|CAB84393.1\| (AL162755) putative membrane protein [Neisseria meningitidis] |
| NGO0939 | 0.0637 | -10.69 | down | 0.0866 | -21.65 | down | 0.1896 | 2.89 | up | hypothetical protein\ Context:(NC_002946)-[916342-916653]\ Notes: |
| NGO0940 | 0.9431 | 1.05 | up | 0.0479 | -4.03 | down | 0.6903 | -1.38 | down | putative tRNA delta transferase\ Context:(NC_002946)+[916655-917596]\ Notes:Best Blastp Hit: pir\|\|E81879 probable tRNA isopentenyltransferase (EC 2.5.1.8) NMA1130 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379823\|emb\|CAB84392.1\| (AL162755) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Neisseria meningitidis] COG0324 tRNA delta (2)-isopentenylpyrophosphate |
| NGO0941 | 0.3276 | 2.11 | up | 0.3421 | -3.48 | down | 0.6934 | -1.46 | down | putative cytosine deaminase\ Context:(NC_002946)+[917600-918319]\ Notes:Best Blastp Hit: gb\|AAF41340.1\| (AE002444) cytidine and deoxycytidylate deaminase family protein [Neisseria meningitidis MC58] COG0590 Cytosine deaminase-related enzymes |
| NGO0942 | 0.7490 | -1.32 | down | 0.0154 | -14.22 | down | 0.9001 | -1.13 | down | hypothetical protein\ Context:(NC_002946)+[918324-918812]\ Notes:Best Blastp Hit: gb\|AAF41339.1\| (AE002444) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0947 | 0.5976 | 1.37 | up | 0.6723 | 1.18 | up | 0.3774 | 1.32 | up | dihydrodipicolinate synthase\ Context:(NC_002946)+[921445-922320]\ Notes:catalyzes the formation of dihydrodipicolinate from L-aspartate 4-semialdehyde and pyruvate in lysine and diaminopimelate biosynthesis |

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| NGO0948 | 0.1168 | 2.33 | up | 0.0960 | 2.40 | up | 0.1523 | 1.77 | up | hypothetical protein\ Context:(NC_002946)+[922329-923525]\ Notes:Best Blastp Hit: pir\|\|C81141 hypothetical protein NMB0928 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226166\|gb\|AAF41335.1\|(AE002444) hypothetical protein [Neisseria meningitidis MC58] |
| NGO0949 | 0.4615 | 1.49 | up | 0.4933 | 1.39 | up | 0.8414 | -1.07 | down | proline iminopeptidase\ Context:(NC_002946)-[923582-924514]\ Notes:Best Blastp Hit: sp\|P42786\|PIP_NEIGO proline iminopeptidase (prolyl aminopeptidase) >gi\|1073191\|pir\|\|S39592 prolyl aminopeptidase (EC 3.4.11.5) - Neisseria gonorrhoeae >gi\|396840\|emb\|CAA80948.1\| (Z25461) proline iminopeptidase Pip [Neisseria gonorrhoeae] COG0596 Predicted hydrolases or acyltransferases |
| NGO0950 | 0.9474 | 1.05 | up | 0.0866 | -2.44 | down | 0.9414 | -1.03 | down | hypothetical protein\ Context:(NC_002946)-[924507-924803]\ Notes: |
| NGO0952 | 0.4778 | 1.36 | up | 0.0393 | 3.14 | up | 0.3112 | 1.74 | up | putative TonB-dependent receptor protein\ Context:(NC_002946)+[926135-928903]\ Notes:Best Blastp Hit: emb\|CAB84928.1\| (AL162756) putative outer membrane substrate binding protein [Neisseria meningitidis] COG1629 Outer membrane receptor proteins; mostly Fe |
| NGO0953 | 0.0764 | -3.69 | down | 0.0185 | -6.88 | down | 0.3077 | -1.98 | down | hypothetical protein\ Context:(NC_002946)+[928934-929149]\ Notes: |
| NGO0955 | 0.0500 | -8.36 | down | 0.1464 | -2.20 | down | 0.2112 | -2.29 | down | hypothetical protein\ Context:(NC_002946)-[929779-929928]\ Notes: |
| NGO0956 | 0.3783 | 1.56 | up | 0.9512 | -1.03 | down | 0.8009 | -1.09 | down | aspartate kinase\ Context:(NC_002946)-[929928-931145]\ Notes:catalyzes the formation of 4-phospho-L-aspartate from L-aspartate and ATP; in Bacillus; lysine sensitive; regulated by response to starvation. |
| NGO0957 | 0.8992 | 1.16 | up | 0.1771 | -10.92 | down | 0.6605 | -1.48 | down | hypothetical protein\ Context:(NC_002946)+[931182-931346]\ Notes: |
| NGO0958 | 0.4256 | -1.72 | down | 0.0594 | -3.50 | down | 0.2552 | -1.44 | down | putative ribonuclease PH\ Context:(NC_002946)-[931347-932075]\ Notes:Best Blastp Hit: pir\|\|A81866 tRNA nucleotidyltransferase (EC 2.7.7.56) - Neisseria meningitidis (group A strain Z2491) >gi\|7380343\|emb\|CAB84930.1\|(AL162756) ribonuclease PH [Neisseria meningitidis] COG0689 RNase PH |

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| NGO0959 | 0.6292 | -1.28 | down | 0.6038 | -1.33 | down | 0.3481 | -1.40 | down | hypothetical protein\ Context:(NC_002946)-[932157-932621]\ Notes:Best Blastp Hit: emb\|CAB84931.1\|(AL162756) conserved hypothetical protein [Neisseria meningitidis] COG0589 Universal stress protein UspA and related |
| NGO0960 | 0.1669 | -5.05 | down | 0.0005 | -35.26 | down | 0.0170 | -9.51 | down | hypothetical protein\ Context:(NC_002946)+[932839-933615]\ Notes:Best Blastp Hit: gb\|AAF41857.1\|(AE002499) HesA/MoeB/ThiF family protein [Neisseria meningitidis MC58] COG1179 Dinucleotide-utilizing enzymes involved in |
| NGO0961 | 0.0241 | -6.84 | down | 0.0613 | -4.70 | down | 0.1840 | -2.90 | down | hypothetical protein\ Context:(NC_002946)+[933860-934714]\ Notes:Best Blastp Hit: pir\|\|D81075 conserved hypothetical protein NMB1504 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226747\|gb\|AAF41860.1\| (AE002500) conserved hypothetical protein [Neisseria meningitidis MC58] COG1354 Uncharacterized ACR |
| NGO0962 | 0.0775 | -3.21 | down | 0.1985 | -2.37 | down | 0.1198 | -2.85 | down | nicotinate phosphoribosyltransferase\ Context:(NC_002946)+[934704-935963]\ Notes:catalyzes the formation of nictonate and 5-phospho-alpha-D-ribose 1-diphosphate from nicotinate D-ribonucleotide and diphosphate |
| NGO0963 | 0.9433 | 1.03 | up | 0.7204 | -1.21 | down | 0.7684 | 1.08 | up | arginyl-tRNA synthetase\ Context:(NC_002946)+[936055-937773]\ Notes:catalyzes a two-step reaction; first charging an arginine molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA; class-I aminoacyl-tRNA synthetase |
| NGO0967 | 0.9485 | -1.05 | down | 0.8242 | -1.18 | down | 0.5510 | 1.63 | up | hypothetical protein\ Context:(NC_002946)+[939735-939995]\ Notes:Best Blastp Hit: gb\|AAF41506.1\|(AE002461) hypothetical protein [Neisseria meningitidis MC58] |

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| NGO0968 | 0.1138 | -2.76 | down | 0.0299 | -3.33 | down | 0.1409 | -1.77 | down | putative ABC transporter; permease protein; amino acid\ Context:(NC_002946)-[940182-940928]\ Notes:Best Blastp Hit: pir\|\|A81076 amino acid ABC transporter; permease protein NMB1509 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226752\|gb\|AAF41865.1\| (AE002500) amino acid ABC transporter; permease protein [Neisseria meningitidis MC58] >gi\|7380350\|emb\|CAB84937.1\| (AL162756) putative binding-protein-dependent transport systems inner membrane protein [Neisseria meningitidis] COG0765 Amino acid ABC transporter permease |
| NGO0969 | 0.5563 | -1.61 | down | 0.0396 | -4.34 | down | 0.3250 | -2.09 | down | hypothetical protein\ Context:(NC_002946)-[941107-941808]\ Notes:Best Blastp Hit: gb\|AAF41866.1\| (AE002500) thermonuclease family protein [Neisseria meningitidis MC58] >gi\|7380351\|emb\|CAB84938.1\| (AL162756) putative nuclease [Neisseria meningitidis] COG1525 Micrococcal nuclease (thermonuclease) |
| NGO0970 | 0.8546 | 1.13 | up | 0.2872 | -1.72 | down | 0.1102 | -1.90 | down | ribose-5-phosphate isomerase A\ Context:(NC_002946)-[941847-942518]\ Notes:Catalyzes D-ribose 5-phosphate --> D-ribulose 5-phosphate in the nonoxidative branch of the pentose phosphate pathway |
| NGO0971 | 0.0811 | 3.48 | up | 0.3450 | 1.68 | up | 0.2943 | -1.59 | down | 2-C-methyl-D-erythritol 2;4-cyclodiphosphate synthase\ Context:(NC_002946)-[942595-943077]\ Notes:catalyzes the conversion of 4-diphosphocytidyl-2-C-methyl-D-erythritol 2-phosphate into 2-C-methyl-D-erythritol 2;4-cyclodiphosphate |
| NGO0972 | 0.3716 | 1.62 | up | 0.2746 | -1.83 | down | 0.7559 | -1.23 | down | hypothetical protein\ Context:(NC_002946)-[943109-943798]\ Notes:Best Blastp Hit: pir\|\|D81867 conserved hypothetical protein NMA1713 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380354\|emb\|CAB84941.1\| (AL162756) conserved hypothetical protein [Neisseria meningitidis] COG1211 4-diphosphocytidyl-2-methylerithritol |

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| NGO0973 | 0.9380 | 1.04 | up | 0.8400 | -1.09 | down | 0.5384 | 1.19 | up | putative DNA polymerase III; epsilon chain\ Context:(NC_002946)-[943795-944529]\ Notes:Best Blastp Hit: pir\|\|E81867 DNA-directed DNA polymerase (EC 2.7.7.7) III epsilon chain NMA1714 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380355\|emb\|CAB84942.1\| (AL162756) DNA polymerase III; epsilon chain [Neisseria meningitidis] COG0847 DNA polymerase III epsilon subunit |
| NGO0974 | 0.0088 | -8.62 | down | 0.0141 | -8.34 | down | 0.0938 | -3.27 | down | hypothetical protein\ Context:(NC_002946)-[944685-945995]\ Notes:Best Blastp Hit: pir\|\|B81074 transporter; probable NMB1515 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226759\|gb\|AAF41871.1\| (AE002501) transporter; putative [Neisseria meningitidis MC58] |
| NGO0975 | 0.7735 | -1.14 | down | 0.8410 | -1.09 | down | 0.4629 | -1.48 | down | FixS\ Context:(NC_002946)-[945985-946170]\ Notes:Best Blastp Hit: gb\|AAF41872.1\| (AE002501) fixS protein [Neisseria meningitidis MC58] >gi\|7380357\|emb\|CAB84944.1\| (AL162756) putative inner membrane protein [Neisseria meningitidis]; putative nitrogen fixation protein |
| NGO0976 | 0.4620 | 1.41 | up | 0.9502 | 1.03 | up | 0.8770 | -1.05 | down | hypothetical protein\ Context:(NC_002946)-[946170-946469]\ Notes:Best Blastp Hit: gb\|AAF41873.1\| (AE002501) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380358\|emb\|CAB84945.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0977 | 0.1132 | 2.55 | up | 0.0379 | 5.23 | up | 0.0667 | 2.60 | up | putative acetate kinase\ Context:(NC_002946)+[946790-948016]\ Notes:Best Blastp Hit: pir\|\|A81868 acetate kinase (EC 2.7.2.1) NMA1718 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380359\|emb\|CAB84946.1\| (AL162756) acetate kinase [Neisseria meningitidis] COG0282 Acetate kinase |
| NGO0978 | 0.0081 | 7.44 | up | 0.1023 | 6.72 | up | 0.1101 | 2.04 | up | thiol:disulfide interchange protein precursor\ Context:(NC_002946)-[948529-950370]\ Notes:two electrons are transferred from cytoplasmic NADPH to thioredoxin and then to the inner membrane protein DsbD which keeps the disulfide isomerase DsbC in a reduced state in the oxidizing periplasm; DsbC in turns rearranges incorrectly made disulfide bonds in the periplasm |

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| NGO0979 | 0.4328 | -1.49 | down | 0.8459 | -1.07 | down | 0.4859 | -1.88 | down | hypothetical protein\ Context:(NC_002946)+[950461-950931]\ Notes:Best Blastp Hit: pir\|\|C81868 hypothetical protein NMA1720 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380361\|emb\|CAB84948.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO0980 | 0.2078 | -2.25 | down | 0.0601 | -2.21 | down | 0.3245 | -1.54 | down | putative transferase\ Context:(NC_002946)-[951004-951831]\ Notes:Best Blastp Hit: emb\|CAB84949.1\| (AL162756) putative transferase [Neisseria meningitidis] COG1562 Phytoene/squalene synthetase |
| NGO0981 | 0.3627 | 1.68 | up | 0.4332 | 1.41 | up | 0.3530 | 1.43 | up | putative peptidyl-prolyl cis-trans isomerase\ Context:(NC_002946)-[951903-952385]\ Notes:Best Blastp Hit: gb\|AAF41878.1\| (AE002501) FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [Neisseria meningitidis MC58] >gi\|7380363\|emb\|CAB84950.1\| (AL162756) putative peptidyl-prolyl isomerase [Neisseria meningitidis] COG1047 FKBP-type peptidyl-prolyl cis-trans |
| NGO0982 | 0.3342 | 3.73 | up | 0.2811 | -3.84 | down | 0.4082 | 2.68 | up | hypothetical protein\ Context:(NC_002946)+[952514-952798]\ Notes: |
| NGO0983 | 0.5444 | 1.46 | up | 0.7563 | 1.13 | up | 0.5756 | 1.21 | up | Lip\ Context:(NC_002946)+[952858-953124]\ Notes:outer membrane protein H.8 |
| NGO0984 | 0.2237 | -2.92 | down | 0.0856 | -7.35 | down | 0.4317 | -1.31 | down | hypothetical protein\ Context:(NC_002946)+[953234-954601]\ Notes:Best Blastp Hit: pir\|\|G81868 hypothetical protein NMA1724 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380365\|emb\|CAB84952.1\| (AL162756) hypothetical protein [Neisseria meningitidis] COG0277 FAD/FMN-containing dehydrogenases |
| NGO0986 | 0.0690 | 3.04 | up | 0.9731 | 1.02 | up | 0.3099 | -1.45 | down | SsrA-binding protein\ Context:(NC_002946)-[957331-957783]\ Notes:binds to ssrA RNA (tmRNA) and is required for its successful binding to ribosomes; also appears to function in the trans-translation step by promoting accommodation of tmRNA into the ribosomal A site; SmpB protects the tmRNA from RNase R degradation in Caulobacter crescentus; both the tmRNA and SmpB are regulated in cell cycle-dependent manner; functions in release of stalled ribosomes from damaged mRNAs and targeting proteins for degradation |

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| NGO0987 | 0.8658 | -1.08 | down | 0.8098 | -1.15 | down | 0.0534 | -1.95 | down | ADP-heptose--LPS heptosyltransferase II\ Context:(NC_002946)-[957832-958842]\ Notes:Best Blastp Hit: pir\|\|S61299 lipopolysaccharide heptosyltransferase (EC 2.4.99.-) II rfaF [similarity] - Neisseria gonorrhoeae >gi\|599920\|emb\|CAA85504.1\| (Z37141) ADP-heptose:LPS heptosyltransferase II [Neisseria gonorrhoeae] COG0859 ADP-heptose: LPS heptosyltransferase; RfaF |
| NGO0988 | 0.3158 | -1.62 | down | 0.5406 | -1.34 | down | 0.8270 | -1.07 | down | putative methylated-DNA-protein-cysteine methyltransferase\ Context:(NC_002946)-[959239-960108]\ Notes:Best Blastp Hit: emb\|CAB84956.1\| (AL162756) putative methylated-DNA-protein-cysteine methyltransferase [Neisseria meningitidis] COG0350 Methylated DNA-protein cysteine |
| NGO0990 | 0.7060 | 1.41 | up | 0.4497 | -2.52 | down | 0.1133 | -5.89 | down | AraC family transcriptional regulator\ Context:(NC_002946)-[960876-961739]\ Notes:Best Blastp Hit: sp\|P77634\|YBCM_ECOLI hypothetical transcriptional regulator in EMRE-RUS intergenic region >gi\|7467042\|pir\|\|H64786 ybcM protein - Escherichia coli >gi\|1778460\|gb\|AAB40743.1\| (U82598) hypothetical protein [Escherichia coli] >gi\|1786758\|gb\|AAC73647.1\| (AE000160) putative ARAC-type regulatory protein [Escherichia coli] COG2207 AraC-type DNA-binding domain-containing |
| NGO0991 | 0.8540 | -1.09 | down | 0.3445 | -1.49 | down | 0.5398 | -1.28 | down | succinyl-diaminopimelate desuccinylase\ Context:(NC_002946)-[962111-963256]\ Notes:dapE-encoded N-succinyl-L;L-diaminopimelic acid desuccinylase (DapE); catalyzes the hydrolysis of N-succinyl-L;Ldiaminopimelate L;L-SDAP to L;L-diaminopimelate and succinate. It is a metalloprotease containing dinuclear active sites. Its structure is similar to the carboxypeptidase G2 from Pseudomonas sp. strain RS-16 and the aminopeptidase from Aeromonas proteolytica. |

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| NGO0992 | 0.1845 | -2.01 | down | 0.0449 | -2.69 | down | 0.1065 | -2.48 | down | hypothetical protein\ Context:(NC_002946)-[963369-963989]\ Notes:Best Blastp Hit: pir\|\|G81071 conserved hypothetical protein NMB1531 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226776\|gb\|AAF41886.1\| (AE002503) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380373\|emb\|CAB84959.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] |
| NGO0993 | 0.0108 | -6.12 | down | 0.1941 | -1.76 | down | 0.1249 | -3.82 | down | hypothetical protein\ Context:(NC_002946)-[964023-964532]\ Notes:Best Blastp Hit: pir\|\|H81071 conserved hypothetical protein NMB1532 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226777\|gb\|AAF41887.1\| (AE002503) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO0994 | 0.0330 | 4.48 | up | 0.0241 | 4.07 | up | 0.0889 | 2.83 | up | Laz\ Context:(NC_002946)-[964627-965178]\ Notes:Best Blastp Hit: sp\|P07212\|H8_NEIMC H.8 outer membrane protein precursor >gi\|279443\|pir\|\|AZNHM azurin precursor - Neisseria meningitidis >gi\|45042\|emb\|CAA68589.1\| (Y00530) outer membrane protein H.8 (AA 1-183) [Neisseria meningitidis]; lipid modified azurin protein |
| NGO0995 | 0.9393 | -1.03 | down | 0.7395 | 1.22 | up | 0.3859 | -1.31 | down | hypothetical protein\ Context:(NC_002946)-[965461-965883]\ Notes:Best Blastp Hit: pir\|\|F81797 hypothetical protein NMA1734 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380376\|emb\|CAB84962.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO0996 | 0.0764 | 2.85 | up | 0.0636 | 4.98 | up | 0.1133 | 2.11 | up | preprotein translocase subunit SecA\ Context:(NC_002946)+[966015-968765]\ Notes:functions in protein export; can interact with acidic membrane phospholipids and the SecYEG protein complex; binds to preproteins; binds to ATP and undergoes a conformational change to promote membrane insertion of SecA/bound preprotein |
| NGO0998 | 0.0035 | 10.24 | up | 0.1460 | 4.75 | up | 0.0110 | 4.86 | up | DNA primase\ Context:(NC_002946)+[968910-970682]\ Notes:synthesizes RNA primers at the replication forks |

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| NGO0999 | 0.1102 | 2.75 | up | 0.0643 | 2.35 | up | 0.1925 | 1.91 | up | RNA polymerase sigma factor RpoD\ Context:(NC_002946)+[970869-972797]\ Notes:sigma factors are initiation factors that promote the attachment of RNA polymerase to specific initiation sites and are then released; this is the primary sigma factor of bacteria |
| NGO1000 | 0.6969 | -1.28 | down | 0.3136 | -1.92 | down | 0.3597 | -1.44 | down | putative phage associated protein\ Context:(NC_002946)-[972837-973064]\ Notes:Best Blastp Hit: pir\|\|F72596 hypothetical protein APE1239 - Aeropyrum pernix (strain K1) >gi\|5104914\|dbj\|BAA80228.1\| (AP000061) 221aa long hypothetical protein [Aeropyrum pernix] |
| NGO1001 | 0.6214 | -1.53 | down | 0.2468 | -4.01 | down | 0.2632 | -2.49 | down | putative phage associated protein\ Context:(NC_002946)-[973188-973673]\ Notes:Best Blastp Hit: dbj\|BAB04059.1\| (AP001508) unknown [Bacillus halodurans] |
| NGO1002 | 0.6058 | -1.60 | down | 0.9808 | 1.03 | up | 0.6313 | 1.76 | up | putative phage associated protein\ Context:(NC_002946)-[973680-974048]\ Notes: |
| NGO1003 | 0.1940 | 2.69 | up | 0.4598 | -2.10 | down | 0.9593 | 1.04 | up | putative phage associated protein\ Context:(NC_002946)-[974075-974617]\ Notes:Best Blastp Hit: dbj\|BAB04058.1\| (AP001508) unknown conserved protein in others [Bacillus halodurans] |
| NGO1004 | 0.5988 | -1.41 | down | 0.2015 | -4.36 | down | 0.4130 | 1.63 | up | putative phage associated protein\ Context:(NC_002946)-[974783-975142]\ Notes: |
| NGO1005 | 0.9278 | -1.05 | down | 0.9345 | -1.05 | down | 0.2139 | -1.93 | down | putative phage associated protein\ Context:(NC_002946)-[975275-976141]\ Notes: |
| NGO1007 | 0.5504 | 1.34 | up | 0.3036 | 1.73 | up | 0.7081 | -1.30 | down | putative phage associated protein\ Context:(NC_002946)-[976976-977185]\ Notes:Best Blastp Hit: gi\|9633475 hypothetical protein [Bacteriophage VT2-Sa] >gi\|5881671\|dbj\|BAA84362.1\| (AP000363) hypothetical protein [Bacteriophage VT2-Sa] |
| NGO1008 | 0.1284 | 2.46 | up | 0.3214 | -1.47 | down | 0.9662 | 1.01 | up | putative phage associated protein\ Context:(NC_002946)-[977178-977468]\ Notes:Best Blastp Hit: pir\|\|A81123 hypothetical protein NMB1087 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226325\|gb\|AAF41479.1\| (AE002459) hypothetical protein [Neisseria meningitidis MC58] |

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| NGO1009 | 0.6135 | -1.38 | down | 0.0603 | -1.94 | down | 0.4809 | -1.31 | down | putative phage associated protein\ Context:(NC_002946)-[977473-977760]\ Notes:Best Blastp Hit: gb\|AAF41415.1\| (AE002452) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1010 | 0.9626 | -1.03 | down | 0.5200 | 1.43 | up | 0.8186 | -1.17 | down | putative phage associated protein\ Context:(NC_002946)-[977880-978314]\ Notes: |
| NGO1011 | 0.1009 | -3.15 | down | 0.1407 | -3.37 | down | 0.6415 | -1.50 | down | putative phage associated protein\ Context:(NC_002946)-[978515-978889]\ Notes:Best Blastp Hit: dbj\|BAB06568.1\| (AP001516) GTP pyrophosphokinase [Bacillus halodurans] |
| NGO1012 | 0.2657 | 1.72 | up | 0.0549 | 1.97 | up | 0.5536 | 1.19 | up | putative phage associated protein\ Context:(NC_002946)-[978886-979764]\ Notes: |
| NGO1013 | 0.0870 | -2.59 | down | 0.2776 | -1.76 | down | 0.8696 | -1.09 | down | putative phage repressor; putative phage associated protein\ Context:(NC_002946)-[980160-980540]\ Notes:Best Blastp Hit: pir\|\|H81130 transcription regulator NMB1007 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226247\|gb\|AAF41408.1\| (AE002452) transcriptional regulator [Neisseria meningitidis MC58] COG1396 Predicted transcriptional regulators |
| NGO1014 | 0.7903 | 1.18 | up | 0.1308 | -3.75 | down | 0.2167 | 1.78 | up | putative phage associated protein\ Context:(NC_002946)+[980749-981042]\ Notes:Best Blastp Hit: gb\|AAF41406.1\| (AE002451) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1015 | 0.0385 | -7.05 | down | 0.0728 | -12.54 | down | 0.6616 | 1.37 | up | putative phage associated protein\ Context:(NC_002946)+[981023-981313]\ Notes:Best Blastp Hit: gb\|AAF41404.1\| (AE002451) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1020 | 0.0424 | -6.40 | down | 0.0136 | -29.43 | down | 0.8544 | -1.13 | down | putative phage associated protein\ Context:(NC_002946)+[982212-984008]\ Notes: |
| NGO1024 | 0.0055 | -5.30 | down | 0.5336 | -1.60 | down | 0.0246 | -5.85 | down | hypothetical protein\ Context:(NC_002946)+[986456-987631]\ Notes:Best Blastp Hit: pir\|\|F81861 hypothetical protein NMA1666 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380308\|emb\|CAB84894.1\| (AL162756) hypothetical protein [Neisseria meningitidis] COG2070 Dioxygenases related to 2-nitropropane |

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| NGO1025 | 0.9700 | -1.02 | down | 0.9768 | -1.01 | down | 0.6679 | -1.12 | down | hypothetical protein\ Context:(NC_002946)-[987973-988521]\ Notes:Best Blastp Hit: pir\|\|G81861 probable inner membrane protein NMA1667 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380309\|emb\|CAB84895.1\| (AL162756) putative inner membrane protein [Neisseria meningitidis] |
| NGO1026 | 0.2225 | 2.41 | up | 0.6870 | 1.36 | up | 0.9506 | 1.02 | up | putative ferredoxin\ Context:(NC_002946)-[988524-990020]\ Notes:Best Blastp Hit: gb\|AAF41813.1\| (AE002495) ferredoxin; 4Fe-4S bacterial type [Neisseria meningitidis MC58] COG0348 Polyferredoxin |
| NGO1027 | 0.6041 | -1.72 | down | 0.0709 | -8.11 | down | 0.8188 | -1.18 | down | hypothetical protein\ Context:(NC_002946)-[990282-990482]\ Notes:Best Blastp Hit: gb\|AAF41815.1\| (AE002495) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1028 | 0.2743 | 1.82 | up | 0.2065 | 1.57 | up | 0.1888 | 1.50 | up | transketolase\ Context:(NC_002946)+[990554-992533]\ Notes:catalyzes the formation of ribose 5-phosphate and xylulose 5-phosphate from sedoheptulose 7-phosphate and glyceraldehyde 3-phosphate; can transfer ketol groups between several groups; in Escherichia coli there are two tkt genes; tktA expressed during exponential growth and the tktB during stationary phase |
| NGO1029 | 0.0955 | 2.61 | up | 0.0126 | 3.04 | up | 0.0116 | 2.81 | up | fumarate hydratase\ Context:(NC_002946)+[992677-994065]\ Notes:class II family (does not require metal); tetrameric enzyme; fumarase C; reversibly converts (S)-malate to fumarate and water; functions in the TCA cycle |
| NGO1030 | 0.4078 | 1.58 | up | 0.0100 | -3.25 | down | 0.5151 | -1.63 | down | hypothetical protein\ Context:(NC_002946)-[994130-995053]\ Notes:Best Blastp Hit: gb\|AAF41818.1\| (AE002495) conserved hypothetical protein [Neisseria meningitidis MC58] COG0697 Predicted permeases |
| NGO1031 | 0.2099 | 1.78 | up | 0.8063 | 1.12 | up | 0.8570 | -1.06 | down | putative single-stranded DNA binding protein\ Context:(NC_002946)-[995426-995950]\ Notes:Best Blastp Hit: pir\|\|A81080 single-strand binding protein NMB1460 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226702\|gb\|AAF41819.1\| (AE002496) single-strand binding protein [Neisseria meningitidis MC58] >gi\|7380314\|emb\|CAB84900.1\| (AL162756) single-stranded binding protein [Neisseria meningitidis] COG0629 Single-stranded DNA-binding protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1032 | 0.8398 | 1.11 | up | 0.1641 | -2.06 | down | 0.2675 | -1.66 | down | hypothetical protein\ Context:(NC_002946)-[995954-997336]\ Notes:Best Blastp Hit: pir\|\|B81080 drug resistance translocase family protein NMB1461 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226703\|gb\|AAF41820.1\| (AE002496) drug resistance translocase family protein [Neisseria meningitidis MC58] COG0477 Permeases |
| NGO1033 | 0.0102 | -9.97 | down | 0.0276 | -4.18 | down | 0.1197 | -2.58 | down | putative transglycosylase\ Context:(NC_002946)-[997448-998071]\ Notes:Best Blastp Hit: pir\|\|C81080 transglycosylase; probable NMB1462 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226704\|gb\|AAF41821.1\| (AE002496) transglycosylase; putative [Neisseria meningitidis MC58] COG0741 Soluble lytic murein transglycosylase and |
| NGO1034 | 0.1615 | -2.20 | down | 0.0342 | -8.49 | down | 0.6798 | -1.33 | down | hypothetical protein\ Context:(NC_002946)+[998126-998470]\ Notes:Best Blastp Hit: gb\|AAF42457.1\| (AE002563) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1037 | 0.0916 | -3.56 | down | 0.0255 | -6.02 | down | 0.6127 | -1.19 | down | hypothetical protein\ Context:(NC_002946)-[999363-999746]\ Notes: |
| NGO1040 | 0.6239 | 1.70 | up | 0.0791 | -10.45 | down | 0.9598 | -1.07 | down | hypothetical protein\ Context:(NC_002946)+[1000964-1001692]\ Notes:Best Blastp Hit: gb\|AAF41823.1\| (AE002496) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1041 | 0.5365 | 1.57 | up | 0.4876 | -1.67 | down | 0.6475 | 1.28 | up | putative exopolyphosphatase\ Context:(NC_002946)+[1001855-1003363]\ Notes:Best Blastp Hit: pir\|\|B81863 exopolyphosphatase (EC 3.6.1.-) NMA1679 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380320\|emb\|CAB84907.1\| (AL162756) exopolyphosphatase [Neisseria meningitidis] COG0248 Exopolyphosphatase |
| NGO1042 | 0.5045 | -1.92 | down | 0.0084 | -9.90 | down | 0.4928 | -1.60 | down | hypothetical protein\ Context:(NC_002946)+[1003525-1003908]\ Notes:Best Blastp Hit: pir\|\|C81863 probable membrane protein NMA1680 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380321\|emb\|CAB84908.1\| (AL162756) putative membrane protein [Neisseria meningitidis] |
| NGO1043 | 0.1001 | 2.50 | up | 0.2914 | 1.51 | up | 0.3762 | 1.63 | up | hypothetical protein\ Context:(NC_002946)-[1003573-1003917]\ Notes: |

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| NGO1044 | 0.6254 | 1.24 | up | 0.4380 | 1.37 | up | 0.4538 | 1.25 | up | hypothetical protein\ Context:(NC_002946)-[1004234-1004779]\ Notes:Best Blastp Hit: pir\|\|A81081 hypothetical protein NMB1470 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226710\|gb\|AAF41827.1\| (AE002496) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1045 | 0.3572 | 1.63 | up | 0.3622 | 1.43 | up | 0.3284 | 1.36 | up | tryptophanyl-tRNA synthetase\ Context:(NC_002946)-[1004860-1005870]\ Notes:catalyzes a two-step reaction; first charging a tryptophan molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA |
| NGO1046 | 0.0895 | 4.78 | up | 0.0745 | 12.57 | up | 0.0737 | 7.76 | up | putative ClpB protein\ Context:(NC_002946)+[1006130-1008709]\ Notes:Best Blastp Hit: pir\|\|F81863 ClpB protein NMA1683 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380324\|emb\|CAB84911.1\| (AL162756) ClpB protein [Neisseria meningitidis] COG0542 ATPases with chaperone activity; ATP-binding |
| NGO1047 | 0.9797 | -1.02 | down | 0.2212 | -1.69 | down | 0.0387 | -2.07 | down | aminotransferase AlaT\ Context:(NC_002946)-[1008781-1009995]\ Notes:broad specificity; family IV; in Corynebacterium glutamicum this protein can use glutamate; 2-aminobutyrate; and aspartate as amino donors and pyruvate as the acceptor |
| NGO1048 | 0.5450 | -1.32 | down | 0.4299 | -1.55 | down | 0.9178 | -1.03 | down | hypothetical protein\ Context:(NC_002946)-[1010084-1010293]\ Notes:Best Blastp Hit: pir\|\|H81078 4-oxalocrotonate tautomerase; probable NMB1474 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226715\|gb\|AAF41831.1\| (AE002497) 4-oxalocrotonate tautomerase; putative [Neisseria meningitidis MC58] >gi\|7380326\|emb\|CAB84913.1\| (AL162756) putative tautomerase [Neisseria meningitidis] COG1942 Uncharacterized protein |
| NGO1049 | 0.1643 | 2.36 | up | 0.5929 | 1.22 | up | 0.2950 | 1.38 | up | hypothetical protein\ Context:(NC_002946)+[1010485-1011291]\ Notes:Best Blastp Hit: pir\|\|A81079 conserved hypothetical protein NMB1475 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226716\|gb\|AAF41832.1\| (AE002497) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1051 | 0.8063 | -1.17 | down | 0.3904 | -2.19 | down | 0.1616 | 2.09 | up | hypothetical protein\ Context:(NC_002946)+[1012691-1012930]\ Notes: |

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| NGO1052 | 0.4299 | 1.48 | up | 0.7533 | 1.14 | up | 0.2606 | 1.40 | up | phosphoglycolate phosphatase\ Context:(NC_002946)+[1012965-1013675]\ Notes:catalyzes the dephosphorylation of 2-phosphoglycolate to form glycolate and phosphate |
| NGO1053 | 0.3754 | -1.65 | down | 0.4339 | -1.37 | down | 0.6686 | -1.23 | down | recombination regulator RecX\ Context:(NC_002946)+[1013748-1014209]\ Notes:binds RecA and inhibits RecA-mediated DNA strand exchange and ATP hydrolysis and coprotease activities |
| NGO1054 | 0.2110 | 3.51 | up | 0.1973 | 2.42 | up | 0.6386 | 1.27 | up | hypothetical protein\ Context:(NC_002946)+[1014283-1014444]\ Notes:Best Blastp Hit: emb\|CAB84918.1\| (AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO1055 | 0.0006 | -15.33 | down | 0.0009 | -8.61 | down | 0.0047 | -5.33 | down | putative acyl-CoA hydrolase\ Context:(NC_002946)+[1014597-1015079]\ Notes:Best Blastp Hit: pir\|\|G81079 acyl CoA thioester hydrolase family protein NMB1482 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226722\|gb\|AAF41838.1\| (AE002497) acyl CoA thioester hydrolase family protein [Neisseria meningitidis MC58] COG1607 Acyl-CoA hydrolase |
| NGO1056 | 0.9863 | -1.01 | down | 0.8171 | -1.11 | down | 0.5665 | -1.32 | down | hypothetical protein\ Context:(NC_002946)-[1015477-1016688]\ Notes:Best Blastp Hit: gb\|AAF41839.1\| (AE002497) lipoprotein NlpD; putative [Neisseria meningitidis MC58] COG0739 Membrane proteins related to |
| NGO1058 | 0.3412 | 1.83 | up | 0.6103 | -1.30 | down | 0.3528 | 1.34 | up | hypothetical protein\ Context:(NC_002946)-[1016592-1017338]\ Notes:Best Blastp Hit: pir\|\|B81077 stationary-phase survival protein SurE NMB1484 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226725\|gb\|AAF41840.1\| (AE002498) stationary-phase survival protein SurE [Neisseria meningitidis MC58] COG0496 Survival protein SurE; predicted acid |
| NGO1059 | 0.0571 | 3.30 | up | 0.1738 | 1.68 | up | 0.0415 | 2.50 | up | hypothetical protein\ Context:(NC_002946)-[1017355-1018911]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0861 Membrane protein TerC; possibly involved in |

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| NGO1060 | 0.0402 | 5.11 | up | 0.1503 | 1.85 | up | 0.3345 | 1.30 | up | FimB\ Context:(NC_002946)-[1019279-1020064]\ Notes:Best Blastp Hit: pir\|\|E81077 fimbrial assembly protein NMB1487 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226728\|gb\|AAF41843.1\| (AE002498) fimbrial assembly protein [Neisseria meningitidis MC58]; putative fimbrial assembly protein |
| NGO1061 | 0.3213 | 2.24 | up | 0.8374 | -1.13 | down | 0.8026 | -1.09 | down | putative succinate semialdehyde dehydrogenase\ Context:(NC_002946)-[1020175-1021608]\ Notes:Best Blastp Hit: pir\|\|C81865 succinate-semialdehyde dehydrogenase (NAD(P)+) (EC 1.2.1.16) NMA1696 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380337\|emb\|CAB84924.1\| (AL162756) succinate semialdehyde dehydrogenase [Neisseria meningitidis] COG1012 NAD-dependent aldehyde dehydrogenases |
| NGO1062 | 0.7252 | 1.16 | up | 0.9050 | -1.05 | down | 0.7438 | 1.09 | up | hypothetical protein\ Context:(NC_002946)+[1022009-1022803]\ Notes:Best Blastp Hit: pir\|\|D81193 hypothetical protein NMB0488 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225715\|gb\|AAF40923.1\| (AE002405) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1063 | 0.3051 | 1.73 | up | 0.0716 | 2.30 | up | 0.2572 | 1.56 | up | hypothetical protein\ Context:(NC_002946)-[1022564-1022944]\ Notes:Best Blastp Hit: emb\|CAB84925.1\| (AL162756) putative lipoprotein [Neisseria meningitidis] |
| NGO1064 | 0.1860 | -1.94 | down | 0.0296 | -3.13 | down | 0.0071 | -3.89 | down | hypothetical protein\ Context:(NC_002946)+[1023468-1025549]\ Notes:Best Blastp Hit: pir\|\|C81078 carbon starvation protein A homolog NMB1493 [similarity] - Neisseria meningitidis (group B strain MD58) >gi\|7226734\|gb\|AAF41849.1\| (AE002498) carbon starvation protein A [Neisseria meningitidis MC58] COG1966 Carbon starvation protein CstA; predicted |
| NGO1065 | 0.1310 | -2.34 | down | 0.0508 | -2.31 | down | 0.0120 | -2.74 | down | hypothetical protein\ Context:(NC_002946)+[1025539-1025733]\ Notes:Best Blastp Hit: gb\|AAF41850.1\| (AE002498) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380340\|emb\|CAB84927.1\| (AL162756) conserved hypothetical protein [Neisseria meningitidis] |
| NGO1066 | 0.3288 | 1.71 | up | 0.4568 | 1.36 | up | 0.8118 | 1.08 | up | MafI protein\ Context:(NC_002946)+[1025841-1026155]\ Notes:MafI1 |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1068 | 0.2933 | -1.57 | down | 0.4150 | -1.53 | down | 0.2730 | -1.88 | down | MafB2\ Context:(NC_002946)+[1027291-1028697]\ Notes:Best Blastp Hit: gb\|AAD31039.1\|AF142582_3 (AF142582) adhesin MafB [Neisseria gonorrhoeae]; putative MafB-like protein |
| NGO1069 | 0.1742 | 1.88 | up | 0.7613 | 1.16 | up | 0.2791 | 1.35 | up | hypothetical protein\ Context:(NC_002946)+[1028713-1029015]\ Notes:Best Blastp Hit: pir\|\|E81004 hypothetical protein NMB2113 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227373\|gb\|AAF42426.1\| (AE002560) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379072\|emb\|CAB83621.1\| (AL162752) hypothetical protein NMA0316 [Neisseria meningitidis] |
| NGO1070 | 0.3075 | 1.84 | up | 0.3382 | 1.67 | up | 0.4838 | 1.35 | up | hypothetical protein\ Context:(NC_002946)+[1029707-1030024]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO1072 | 0.0963 | 2.98 | up | 0.0451 | 2.16 | up | 0.8985 | 1.05 | up | hypothetical protein\ Context:(NC_002946)+[1030403-1030687]\ Notes: |
| NGO1073 | 0.1908 | 2.41 | up | 0.2879 | 1.50 | up | 0.6697 | 1.16 | up | hypothetical protein\ Context:(NC_002946)+[1030690-1031013]\ Notes:Best Blastp Hit: pir\|\|F81004 hypothetical protein NMB2115 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227374\|gb\|AAF42427.1\| (AE002560) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1074 | 0.4761 | 1.46 | up | 0.5657 | 1.30 | up | 0.8978 | -1.05 | down | MafI protein 2\ Context:(NC_002946)+[1031165-1031512]\ Notes:MafI2 |
| NGO1077 | 0.4669 | 1.70 | up | 0.4026 | 1.47 | up | 0.6676 | -1.23 | down | hypothetical protein\ Context:(NC_002946)-[1035986-1036333]\ Notes: |
| NGO1078 | 0.3800 | -1.52 | down | 0.4890 | -1.43 | down | 0.2205 | -2.06 | down | putative acyl-CoA hydrolase\ Context:(NC_002946)+[1036789-1037235]\ Notes:Best Blastp Hit: pir\|\|E81878 probable acyl-CoA hydrolase NMA1121 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379815\|emb\|CAB84383.1\| (AL162755) putative acyl-CoA hydrolase [Neisseria meningitidis] COG1607 Acyl-CoA hydrolase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1079 | 0.0184 | -4.11 | down | 0.1822 | -2.84 | down | 0.1409 | -1.73 | down | putative oxidoreductase\ Context:(NC_002946)-[1037286-1038107]\ Notes:Best Blastp Hit: pir\|\|D81878 probable oxidoreductase NMA1120 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379814\|emb\|CAB84382.1\| (AL162755) putative oxidoreductase [Neisseria meningitidis] COG0300 Short-chain dehydrogenases of various |
| NGO1080 | 0.0064 | -5.90 | down | 0.0489 | -4.92 | down | 0.1082 | -4.75 | down | putative C-type cytochrome\ Context:(NC_002946)+[1038226-1038684]\ Notes:Best Blastp Hit: emb\|CAB84381.1\| (AL162755) putative C-type cytochrome [Neisseria meningitidis] |
| NGO1081 | 0.0659 | 2.97 | up | 0.1358 | 1.89 | up | 0.2470 | 1.60 | up | alpha-2;3-sialyltransferase\ Context:(NC_002946)-[1038827-1039963]\ Notes:Best Blastp Hit: gb\|AAC44539.1\| (U60664) alpha-2;3-sialyltransferase [Neisseria gonorrhoeae] |
| NGO1082 | 0.8775 | 1.09 | up | 0.8572 | 1.07 | up | 0.2685 | 1.41 | up | putative isocitrate dehydrogenase\ Context:(NC_002946)+[1040336-1042561]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO1083 | 0.3494 | -1.78 | down | 0.0356 | -5.01 | down | 0.3755 | -1.78 | down | hypothetical protein\ Context:(NC_002946)+[1042858-1043178]\ Notes: |
| NGO1084 | 0.4321 | 1.68 | up | 0.2580 | 4.35 | up | 0.8863 | 1.22 | up | hypothetical protein\ Context:(NC_002946)+[1044120-1044287]\ Notes:Best Blastp Hit: emb\|CAB84549.1\| (AL162755) hypothetical protein NMA1297 [Neisseria meningitidis] |
| NGO1085 | 0.9171 | 1.08 | up | 0.0323 | -4.16 | down | 0.7061 | -1.31 | down | putative phage associated protein\ Context:(NC_002946)+[1044447-1045292]\ Notes:Best Blastp Hit: sp\|P44189\|YE18_HAEIN hypothetical protein HI1418 >gi\|1074769\|pir\|\|A64029 hypothetical protein HI1418 - Haemophilus influenzae (strain Rd KW20) >gi\|1574254\|gb\|AAC23068.1\| (U32821) H. influenzae predicted coding region HI1418 [Haemophilus influenzae Rd] |
| NGO1086 | 0.0244 | -6.62 | down | 0.0004 | -10.84 | down | 0.2120 | -1.86 | down | putative phage associated protein\ Context:(NC_002946)-[1045279-1045479]\ Notes:Best Blastp Hit: gb\|AAF41392.1\| (AE002449) hypothetical protein [Neisseria meningitidis MC58] |

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| NGO1087 | 0.5535 | -1.70 | down | 0.0528 | -10.47 | down | 0.9176 | -1.05 | down | putative phage associated protein\ Context:(NC_002946)+[1045494-1046174]\ Notes:Best Blastp Hit: pir\|\|T32944 hypothetical protein W01B11.5 - Caenorhabditis elegans >gi\|2804494\|gb\|AAB97600.1\| (AF043704) similar to S. cerevisiae SLA2 (GB:Z22811) [Caenorhabditis elegans] |
| NGO1088 | 0.3786 | -2.46 | down | 0.0005 | -9.02 | down | 0.7141 | -1.55 | down | putative phage associated protein\ Context:(NC_002946)-[1046153-1046638]\ Notes: |
| NGO1089 | 0.3385 | -2.24 | down | 0.0052 | -13.76 | down | 0.1721 | -3.62 | down | putative phage associated protein\ Context:(NC_002946)-[1046644-1047117]\ Notes: |
| NGO1090 | 0.6201 | 1.40 | up | 0.9884 | -1.01 | down | 0.9119 | -1.07 | down | putative phage associated protein\ Context:(NC_002946)-[1047173-1048468]\ Notes:Best Blastp Hit: gi\|9632520 hypothetical protein [Bacteriophage 933W] >gi\|9633449\|ref\|NP_050552.1\| hypothetical protein [Bacteriophage VT2-Sa] >gi\|4585431\|gb\|AAD25459.1\| |
| NGO1091 | 0.0086 | -5.84 | down | 0.0068 | -9.51 | down | 0.0251 | -3.80 | down | putative phage associated protein\ Context:(NC_002946)-[1048489-1048887]\ Notes:Best Blastp Hit: gb\|AAF79659.1\|AC025416_33 (AC025416) F5O11.3 [Arabidopsis thaliana] |
| NGO1092 | 0.9367 | 1.06 | up | 0.0906 | -4.03 | down | 0.2595 | -1.96 | down | putative phage associated protein\ Context:(NC_002946)-[1049094-1055027]\ Notes:Best Blastp Hit: pir\|\|A81819 hypothetical protein NMA1913 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380547\|emb\|CAB85134.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1093 | 0.0604 | 10.08 | up | 0.4301 | -2.21 | down | 0.2722 | -3.27 | down | putative phage associated protein\ Context:(NC_002946)-[1055027-1056445]\ Notes: |
| NGO1094 | 0.5909 | 1.34 | up | 0.3688 | -2.91 | down | 0.9395 | 1.08 | up | putative phage associated protein\ Context:(NC_002946)-[1056442-1057638]\ Notes:Best Blastp Hit: emb\|CAA42694.1\| (X60098) M protein [Streptococcus sp.] |
| NGO1095 | 0.0204 | 7.25 | up | 0.2066 | -6.51 | down | 0.5845 | -2.28 | down | putative phage associated protein\ Context:(NC_002946)-[1057849-1058322]\ Notes:Best Blastp Hit: pir\|\|H81143 hypothetical protein NMB0899 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226136\|gb\|AAF41307.1\| (AE002442) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1096 | 0.2695 | -3.36 | down | 0.0081 | -30.61 | down | 0.7850 | 1.18 | up | putative phage associated protein\ Context:(NC_002946)-[1058422-1058637]\ Notes: |

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| NGO1097 | 0.7580 | 1.19 | up | 0.0069 | -5.39 | down | 0.6968 | -1.36 | down | putative phage associated protein\ Context:(NC_002946)-[1058674-1060926]\ Notes:Best Blastp Hit: gi\|9632518 putative portal protein [Bacteriophage 933W] >gi\|9633447\|ref\|NP_050550.1\| hypothetical protein [Bacteriophage VT2-Sa] >gi\|4585429\|gb\|AAD25457.1\|AF125520_52 (AF125520) putative portal protein [Bacteriophage 933W] >gi\|5881643\|dbj\|BAA84334.1\| (AP000363) hypothetical protein [Bacteriophage VT2-Sa] >gi\|7649880\|dbj\|BAA94158.1\| (AP000422) portal protein [Escherichia coli O157:H7] |
| NGO1098 | 0.5066 | 2.11 | up | 0.2129 | -5.57 | down | 0.4024 | -1.98 | down | putative phage associated protein\ Context:(NC_002946)-[1060926-1062200]\ Notes:Best Blastp Hit: sp\|P44184\|YE10_HAEIN hypothetical protein HI1410 >gi\|1074763\|pir\|\|E64028 hypothetical protein HI1410 - Haemophilus influenzae (strain Rd KW20) >gi\|1574247\|gb\|AAC23058.1\| (U32820) H. influenzae predicted coding region HI1410 [Haemophilus influenzae Rd] COG1783 Phage terminase large subunit |
| NGO1099 | 0.7481 | 1.29 | up | 0.0230 | -4.68 | down | 0.5105 | -1.62 | down | putative phage associated protein\ Context:(NC_002946)-[1062181-1062423]\ Notes: |
| NGO1100 | 0.8479 | 1.20 | up | 0.2223 | -3.57 | down | 0.4473 | -3.37 | down | putative phage associated protein\ Context:(NC_002946)-[1062478-1062720]\ Notes: |
| NGO1101 | 0.1339 | -2.95 | down | 0.0366 | -6.15 | down | 0.4493 | -1.35 | down | putative phage associated protein\ Context:(NC_002946)-[1062720-1063034]\ Notes:Best Blastp Hit: gb\|AAF53095.1\| (AE003632) CG14926 gene product [Drosophila melanogaster] |
| NGO1102 | 0.0064 | -11.71 | down | 0.0397 | -8.52 | down | 0.0850 | -2.94 | down | putative phage associated protein\ Context:(NC_002946)-[1063207-1063725]\ Notes:Best Blastp Hit: gb\|AAF24756.1\| (AF148565) putative endonuclease [Streptococcus thermophilus bacteriophage ST3] |
| NGO1103 | 0.0171 | -6.15 | down | 0.0141 | -17.91 | down | 0.4444 | -2.28 | down | putative phage associated protein\ Context:(NC_002946)-[1063716-1064099]\ Notes:Best Blastp Hit: dbj\|BAA94132.1\| (AP000422) hypothetical protein [Escherichia coli O157:H7] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1104 | 0.7582 | -1.29 | down | 0.1054 | -6.96 | down | 0.7592 | -1.30 | down | putative phage associated protein\ Context:(NC_002946)-[1064096-1064401]\ Notes:Best Blastp Hit: sp\|Q47271\|YBCO_ECOLI hypothetical 10.3 KD protein IN EMRE-RUS INTERGENIC REGION >gi\|2120252\|pir\|\|S66582 hypothetical protein 96 - phage 82 >gi\|7467043\|pir\|\|C64787 ybcO protein |
| NGO1105 | 0.0942 | -3.59 | down | 0.0858 | -6.28 | down | 0.3731 | -2.05 | down | putative phage associated protein\ Context:(NC_002946)+[1064373-1064993]\ Notes: |
| NGO1106 | 0.2312 | 5.27 | up | 0.3150 | 1.58 | up | 0.8921 | -1.07 | down | putative phage associated protein\ Context:(NC_002946)-[1065119-1065268]\ Notes: |
| NGO1107 | 0.1842 | -3.30 | down | 0.1710 | -4.96 | down | 0.6776 | 1.51 | up | putative phage associated protein\ Context:(NC_002946)+[1065246-1065614]\ Notes:Best Blastp Hit: gb\|AAF41506.1\| (AE002461) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1108 | 0.2414 | 2.68 | up | 0.1197 | -3.62 | down | 0.0148 | -5.59 | down | putative phage associated protein\ Context:(NC_002946)-[1065652-1066146]\ Notes: |
| NGO1110 | 0.1921 | 2.32 | up | 0.0448 | -4.04 | down | 0.9959 | 1.00 | up | putative replicative DNA helicase; putative phage associated protein\ Context:(NC_002946)-[1066486-1067847]\ Notes:Best Blastp Hit: sp\|P37469\|DNAC_BACSU replicative DNA helicase >gi\|2127189\|pir\|\|S65970 replicative DNA helicase dnaC - Bacillus subtilis >gi\|467330\|dbj\|BAA05176.1\| (D26185) replicative DNA helicase [Bacillus subtilis] >gi\|2636591\|emb\|CAB16081.1\| (Z99124) replicative DNA helicase [Bacillus subtilis] COG0305 Replicative DNA helicase |
| NGO1111 | 0.0008 | -13.15 | down | 0.0263 | -15.77 | down | 0.6673 | -1.68 | down | putative phage associated protein\ Context:(NC_002946)-[1067844-1068974]\ Notes:Best Blastp Hit: gi\|9634200 Gp54 [Bacteriophage HK97] >gi\|6901629\|gb\|AAF31132.1\| (AF069529) Gp54 [Bacteriophage HK97] |
| NGO1115 | 0.0424 | 14.38 | up | 0.0182 | -18.27 | down | 0.5138 | -2.64 | down | putative phage associated protein\ Context:(NC_002946)-[1069893-1070081]\ Notes: |
| NGO1116 | 0.7611 | 1.18 | up | 0.5903 | -1.27 | down | 0.2700 | -1.42 | down | putative phage repressor protein; putative phage associated protein\ Context:(NC_002946)+[1070260-1070907]\ Notes:Best Blastp Hit: gb\|AAF41318.1\| (AE002442) transcriptional regulator [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1117 | 0.7928 | 1.14 | up | 0.8353 | 1.10 | up | 0.7474 | -1.09 | down | putative phage associated protein\ Context:(NC_002946)+[1071067-1071606]\ Notes:Best Blastp Hit: gb\|AAF30438.1\|AE002103_3 (AE002103) hypothetical [Ureaplasma urealyticum] |
| NGO1118 | 0.5192 | 1.40 | up | 0.7041 | 1.17 | up | 0.8966 | 1.04 | up | putative phage associated protein\ Context:(NC_002946)+[1071607-1071966]\ Notes: |
| NGO1119 | 0.1386 | -5.48 | down | 0.4268 | -2.57 | down | 0.4402 | -1.79 | down | putative phage associated protein\ Context:(NC_002946)-[1071983-1072201]\ Notes: |
| NGO1120 | 0.7126 | 1.30 | up | 0.0517 | 2.02 | up | 0.9561 | 1.02 | up | putative phage associated protein\ Context:(NC_002946)+[1072684-1072884]\ Notes: |
| NGO1123 | 0.3834 | 1.45 | up | 0.0670 | 2.70 | up | 0.5768 | 1.21 | up | putative phage associated protein\ Context:(NC_002946)+[1073806-1074138]\ Notes: |
| NGO1124 | 0.1775 | 1.94 | up | 0.1247 | 3.52 | up | 0.9730 | 1.01 | up | putative phage associated protein\ Context:(NC_002946)+[1074307-1074567]\ Notes:Best Blastp Hit: gb\|AAF41312.1\| (AE002442) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1128 | 0.3857 | 2.21 | up | 0.7898 | 1.28 | up | 0.6250 | -1.36 | down | putative phage associated protein\ Context:(NC_002946)+[1075799-1076290]\ Notes:Best Blastp Hit: pir\|\|T13296 hypothetical protein 8 - Streptococcus phage phi-O1205 >gi\|2444088\|gb\|AAC79524.1\| (U88974) ORF8 [Streptococcus thermophilus temperate bacteriophage O1205] |
| NGO1131 | 0.1198 | -2.57 | down | 0.0804 | -3.22 | down | 0.3203 | -2.00 | down | putative phage associated protein\ Context:(NC_002946)+[1077648-1078061]\ Notes: |
| NGO1132 | 0.6610 | -1.59 | down | 0.2005 | -2.88 | down | 0.2591 | 1.47 | up | putative phage associated protein\ Context:(NC_002946)+[1078087-1078281]\ Notes: |
| NGO1133 | 0.4332 | 1.47 | up | 0.9693 | -1.02 | down | 0.9320 | -1.03 | down | hypothetical protein\ Context:(NC_002946)+[1078572-1079246]\ Notes:Best Blastp Hit: pir\|\|F81104 hypothetical protein NMB1253 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226493\|gb\|AAF41633.1\| (AE002473) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1134 | 0.3297 | 1.65 | up | 0.9225 | -1.05 | down | 0.7450 | -1.13 | down | putative GTP cyclohydrolase II\ Context:(NC_002946)+[1079239-1079832]\ Notes:Best Blastp Hit: pir\|\|G81104 GTP cyclohydrolase II NMB1254 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226494\|gb\|AAF41634.1\| (AE002473) GTP cyclohydrolase II [Neisseria meningitidis MC58] COG0807 GTP cyclohydrolase II |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1135 | 0.0546 | -9.36 | down | 0.0655 | -28.76 | down | 0.9264 | -1.08 | down | hypothetical protein\ Context:(NC_002946)-[1079913-1080224]\ Notes: |
| NGO1136 | 0.0859 | 2.74 | up | 0.6963 | 1.17 | up | 0.7439 | 1.11 | up | hypothetical protein\ Context:(NC_002946)+[1079991-1080200]\ Notes:Best Blastp Hit: emb\|CAB87331.1\| (AL163672) putative glycosyl transferase [Streptomyces coelicolor A3(2)] COG0463 Glycosyltransferases involved in cell wall |
| NGO1137 | 0.0696 | 3.15 | up | 0.1104 | 1.92 | up | 0.3629 | 1.35 | up | Irg2\ Context:(NC_002946)+[1080185-1081147]\ Notes:Best Blastp Hit: gb\|AAC82509.1\| (U65994) pilin gene inverting protein homolog PivNG [Neisseria gonorrhoeae]; putative invertase related gene 2; putative phage associated protein |
| NGO1143 | 0.0375 | 3.84 | up | 0.0769 | 3.73 | up | 0.2054 | 1.47 | up | putative phage associated protein\ Context:(NC_002946)-[1085886-1086104]\ Notes:Best Blastp Hit: emb\|CAB84432.1\| (AL162755) putative integral membrane protein [Neisseria meningitidis] >gi\|7380631\|emb\|CAB85221.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1144 | 0.0906 | -7.64 | down | 0.0521 | -19.03 | down | 0.6785 | 1.51 | up | putative phage associated protein\ Context:(NC_002946)-[1086190-1086393]\ Notes:Best Blastp Hit: emb\|CAB84063.1\| (AL162754) hypothetical protein NMA0780 [Neisseria meningitidis] |
| NGO1145 | 0.1228 | 7.98 | up | 0.4395 | -3.80 | down | 0.6939 | -1.63 | down | putative phage associated protein\ Context:(NC_002946)-[1086407-1086718]\ Notes:Best Blastp Hit: pir\|\|F81922 hypothetical protein NMA0781 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379502\|emb\|CAB84064.1\| (AL162754) hypothetical protein NMA0781 [Neisseria meningitidis] |
| NGO1146 | 0.3123 | -2.80 | down | 0.0287 | -14.56 | down | 0.5292 | 1.52 | up | putative phage associated protein\ Context:(NC_002946)-[1086789-1088060]\ Notes:Best Blastp Hit: pir\|\|G81922 probable phage replication protein NMA0782 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379503\|emb\|CAB84065.1\| (AL162754) putative phage replication protein [Neisseria meningitidis] |
| NGO1147 | 0.6787 | 1.47 | up | 0.1493 | -9.31 | down | 0.5364 | 2.94 | up | hypothetical protein\ Context:(NC_002946)-[1088047-1088271]\ Notes:Best Blastp Hit: emb\|CAB84066.1\| (AL162754) hypothetical protein NMA0783 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1148 | 0.7112 | 1.38 | up | 0.2287 | 1.83 | up | 0.7400 | 1.17 | up | hypothetical protein\ Context:(NC_002946)-[1088667-1088873]\ Notes:Best Blastp Hit: emb\|CAB85032.1\|(AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1149 | 0.9610 | 1.03 | up | 0.2994 | 1.81 | up | 0.5543 | 1.17 | up | putative O-succinylhomoserine sulfhydrolase\ Context:(NC_002946)-[1088968-1090128]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0626 Cystathionine |
| NGO1150 | 0.1438 | 2.66 | up | 0.1275 | 2.91 | up | 0.7833 | 1.07 | up | hypothetical protein\ Context:(NC_002946)-[1090274-1091044]\ Notes:Best Blastp Hit: pir\|\|F81806 hypothetical protein NMA1809 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380448\|emb\|CAB85034.1\|(AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1151 | 0.3621 | -1.50 | down | 0.3160 | -1.59 | down | 0.8889 | 1.05 | up | hypothetical protein\ Context:(NC_002946)+[1091146-1091397]\ Notes:Best Blastp Hit: gb\|AAF41963.1\|(AE002511) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1152 | 0.6984 | 1.23 | up | 0.7364 | -1.16 | down | 0.8094 | -1.08 | down | ABC transporter; periplasmic histidine-binding protein precursor\ Context:(NC_002946)+[1091449-1092255]\ Notes:Best Blastp Hit: sp\|Q06758\|HISJ_NEIGO histidine-binding protein precursor (HBP) >gi\|95363\|pir\|\|S19184 hypothetical protein - Neisseria gonorrhoeae >gi\|49068\|emb\|CAA45768.1\| (X64421) gene homologous to hisJ (E.coli) and argT (S.typhimurium) [Neisseria gonorrhoeae] COG0834 Periplasmic amino acid binding proteins; Hbp |
| NGO1154 | 0.1023 | 2.89 | up | 0.4191 | 1.66 | up | 0.1109 | 1.62 | up | potassium transporter peripheral membrane component\ Context:(NC_002946)+[1094183-1095595]\ Notes:involved in potassium uptake; found to be peripherally associated with the inner membrane in Escherichia coli; contains an NAD-binding domain |
| NGO1155 | 0.0110 | -7.62 | down | 0.0228 | -7.72 | down | 0.0998 | -4.30 | down | hypothetical protein\ Context:(NC_002946)-[1096079-1096537]\ Notes:Best Blastp Hit: pir\|\|G64866 probable membrane protein b1202 - Escherichia coli >gi\|1787452\|gb\|AAC74286.1\| (AE000218) putative adhesion and penetration protein [Escherichia coli] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1156 | 0.8734 | 1.07 | up | 0.7177 | -1.20 | down | 0.8633 | 1.11 | up | hypothetical protein\ Context:(NC_002946)-[1096627-1097481]\ Notes:Best Blastp Hit: pir\|\|G64866 probable membrane protein b1202 - Escherichia coli >gi\|1787452\|gb\|AAC74286.1\| (AE000218) putative adhesion and penetration protein [Escherichia coli] |
| NGO1158 | 0.6503 | -1.23 | down | 0.7208 | 1.25 | up | 0.4749 | -1.37 | down | hypothetical protein\ Context:(NC_002946)-[1098435-1099703]\ Notes: |
| NGO1159 | 0.0324 | -3.16 | down | 0.3049 | -1.71 | down | 0.7721 | -1.19 | down | hypothetical protein\ Context:(NC_002946)-[1100191-1100343]\ Notes: |
| NGO1160 | 0.4449 | -1.43 | down | 0.0840 | -2.67 | down | 0.7374 | -1.11 | down | phosphomethylpyrimidine kinase\ Context:(NC_002946)+[1100403-1101209]\ Notes:catalyzes the formation of 4-amino-2-methyl-5-diphosphomethylpyrimidine |
| NGO1161 | 0.2318 | 1.93 | up | 0.9060 | 1.06 | up | 0.6185 | 1.21 | up | tellurite resistance protein TehB\ Context:(NC_002946)-[1101267-1102136]\ Notes:with TehA confers resistance to tellurite |
| NGO1162 | 0.8322 | 1.12 | up | 0.4022 | 2.24 | up | 0.1689 | -1.68 | down | ribonuclease H\ Context:(NC_002946)+[1102249-1102686]\ Notes:Best Blastp Hit: pir\|\|F81807 ribonuclease H (EC 3.1.26.4) I NMA1817 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380456\|emb\|CAB85042.1\| (AL162757) ribonuclease HI [Neisseria meningitidis] COG0328 Ribonuclease HI |
| NGO1163 | 0.8352 | 1.24 | up | 0.1104 | 2.21 | up | 0.9648 | -1.04 | down | hypothetical protein\ Context:(NC_002946)+[1102723-1102881]\ Notes: |
| NGO1173 | 0.0244 | -7.21 | down | 0.0436 | -11.28 | down | 0.3771 | -2.34 | down | putative DNA mismatch endonuclease; patch repair protein\ Context:(NC_002946)-[1110897-1111319]\ Notes:Best Blastp Hit: pir\|\|H81959 patch repair protein (EC 3.1.-.-) NMA0429 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379179\|emb\|CAB83728.1\| (AL162753) patch repair protein [Neisseria meningitidis] |
| NGO1176 | 0.0553 | -4.55 | down | 0.1931 | -5.70 | down | 0.4817 | 1.59 | up | hypothetical protein\ Context:(NC_002946)+[1114327-1114473]\ Notes: |
| NGO1177 | 0.3608 | 1.54 | up | 0.7006 | 1.18 | up | 0.5856 | 1.18 | up | hypothetical protein\ Context:(NC_002946)-[1114850-1115299]\ Notes:Best Blastp Hit: gb\|AAF62338.1\| (AE002551) type IV pilin-related protein [Neisseria meningitidis MC58] |
| NGO1178 | 0.4277 | 1.61 | up | 0.4689 | 1.35 | up | 0.4227 | 1.25 | up | ComE1\ Context:(NC_002946)-[1115387-1115686]\ Notes:COG1555 DNA uptake protein ComEA and related; DNA-binding competence protein 1 |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1179 | 0.7940 | -1.44 | down | 0.3001 | -3.78 | down | 0.3496 | 2.41 | up | hypothetical protein\ Context:(NC_002946)+[1121383-1121601]\ Notes:Best Blastp Hit: emb\|CAB85400.1\|(AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1182 | 0.0175 | -3.76 | down | 0.0131 | -3.46 | down | 0.0223 | -3.66 | down | putative nitrogen regulatory protein P-II\ Context:(NC_002946)-[1123800-1124138]\ Notes:Best Blastp Hit: pir\|\|B81019 nitrogen regulatory protein P-II NMB1995 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227257\|gb\|AAF42322.1\| (AE002548) nitrogen regulatory protein P-II [Neisseria meningitidis MC58] COG0347 Nitrogen regulatory protein PII |
| NGO1183 | 0.0055 | -6.42 | down | 0.0123 | -5.76 | down | 0.9647 | -1.04 | down | phosphoribosylformylglycinamidine synthase\ Context:(NC_002946)+[1124290-1128246]\ Notes:catalyzes the formation of 2-(formamido)-N1-(5-phospho-D-ribosyl)acetamidine from N2-formyl-N1-(5-phospho-D-ribosyl)glycinamide and L-glutamine in purine biosynthesis |
| NGO1184 | 0.0568 | -4.21 | down | 0.0088 | -8.04 | down | 0.0086 | -4.78 | down | hypothetical protein\ Context:(NC_002946)-[1128345-1129463]\ Notes:Best Blastp Hit: pir\|\|G75287 NADH oxidase-related protein - Deinococcus radiodurans (strain R1) >gi\|6460144\|gb\|AAF11879.1\|AE002064_10 (AE002064) NADH oxidase-related protein [Deinococcus radiodurans] COG1902 NADH:flavin oxidoreductases; Old Yellow |
| NGO1185 | 0.5803 | -1.40 | down | 0.0028 | -5.86 | down | 0.8086 | -1.26 | down | ArsR family transcriptional regulator\ Context:(NC_002946)-[1129602-1129913]\ Notes:Best Blastp Hit: pir\|\|D70029 transcription regulator ArsR family homolog yvbA - Bacillus subtilis >gi\|2635892\|emb\|CAB15384.1\| (Z99121) similar to transcriptional regulator (ArsR family) [Bacillus subtilis] COG0640 Predicted transcriptional regulators |
| NGO1186 | 0.0807 | -4.74 | down | 0.1856 | -4.85 | down | 0.4702 | -2.91 | down | hypothetical protein\ Context:(NC_002946)-[1129938-1130132]\ Notes: |
| NGO1187 | 0.5893 | 1.32 | up | 0.4719 | -1.35 | down | 0.6595 | 1.19 | up | hypothetical protein\ Context:(NC_002946)+[1130145-1130897]\ Notes:Best Blastp Hit: emb\|CAB83742.1\|(AL162753) putative hydroxyacylglutathione hydrolase [Neisseria meningitidis] COG0491 Zn-dependent hydrolases; including |
| NGO1188 | 0.1179 | -3.17 | down | 0.0995 | -2.39 | down | 0.0134 | -2.69 | down | MgtE\ Context:(NC_002946)+[1131131-1132585]\ Notes:putative magnesium transporter |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1189 | 0.2146 | -1.91 | down | 0.7345 | -1.41 | down | 0.4363 | -1.95 | down | Hsp33-like chaperonin\ Context:(NC_002946)-[1132671-1133579]\ Notes:becomes active under oxidative stress; four conserved cysteines bind a zinc atom when they are in the reduced state and the enzyme is inactive; oxidative stress results in oxidized cysteines; release of zinc; and binding of Hsp33 to aggregation-prone proteins; forms dimers and higher order oligomers |
| NGO1190 | 0.3993 | 1.64 | up | 0.8626 | -1.07 | down | 0.5380 | 1.21 | up | GNA2001\ Context:(NC_002946)+[1133860-1134492]\ Notes:Best Blastp Hit: gb\|AAF44765.1\|AF235148_1 (AF235148) GNA2001 [Neisseria gonorrhoeae] >gi\|7274424\|gb\|AAF44767.1\|AF235150_1 (AF235150) GNA2001 [Neisseria gonorrhoeae] COG0791 Cell wall-associated hydrolases; genome-derived Neisseria antigen 2001 |
| NGO1191 | 0.0792 | 4.96 | up | 0.3966 | -1.79 | down | 0.9933 | -1.00 | down | hypothetical protein\ Context:(NC_002946)+[1134511-1134729]\ Notes:Best Blastp Hit: gb\|AAF42329.1\| (AE002550) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379189\|emb\|CAB83738.1\| (AL162753) hypothetical protein [Neisseria meningitidis] |
| NGO1192 | 0.6778 | -1.37 | down | 0.0234 | -3.58 | down | 0.5666 | -1.33 | down | hypothetical protein\ Context:(NC_002946)+[1134874-1135218]\ Notes:Best Blastp Hit: pir\|\|H81960 hypothetical inner membrane protein NMA0437 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379187\|emb\|CAB83736.1\| (AL162753) hypothetical inner membrane protein [Neisseria meningitidis] COG1380 Predicted membrane protein; YohJ family |
| NGO1193 | 0.0288 | -4.87 | down | 0.0295 | -6.85 | down | 0.0093 | -5.67 | down | hypothetical protein\ Context:(NC_002946)+[1135218-1135910]\ Notes:Best Blastp Hit: pir\|\|B81017 conserved hypothetical protein NMB2004 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227268\|gb\|AAF42331.1\| (AE002550) conserved hypothetical protein [Neisseria meningitidis MC58] COG1346 Predicted membrane protein; YohK family |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1194 | 0.5845 | 1.41 | up | 0.7657 | 1.13 | up | 0.6382 | 1.25 | up | bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein\ Context:(NC_002946)+[1135977-1137197]\ Notes:bifunctional arginine biosynthesis protein ArgJ; functions at the 1st and 5th steps in arginine biosynthesis; involved in synthesis of acetylglutamate from glutamate and acetyl-CoA and ornithine by transacetylation between acetylornithine and glutmate |
| NGO1195 | 0.0756 | 3.73 | up | 0.8512 | -1.21 | down | 0.3745 | 2.36 | up | hypothetical protein\ Context:(NC_002946)+[1137257-1138666]\ Notes:Best Blastp Hit: >pir\|\|D81017 chloride channel protein-related protein NMB2006 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) gb\|AAF42333.1\| (AE002550) chloride channel protein-related protein [Neisseria meningitidis MC58] emb\|CAB83733.1\| (AL162753) hypothetical inner membrane protein [Neisseria meningitidis Z2491] |
| NGO1196 | 0.5819 | 1.53 | up | 0.6049 | -1.52 | down | 0.1285 | 1.63 | up | putative ATP-dependent DNA helicase related protein\ Context:(NC_002946)+[1138854-1140245]\ Notes:Best Blastp Hit: 0e+00 2213 95%/97% 501/463aa gi\|7379183\|emb\|CAB83732.1\| (AL162753) ATP-dependent DNA helicase [Neisseria meningitidis] COG1643 HrpA-like helicases |
| NGO1197 | 0.0078 | 9.07 | up | 0.1084 | 5.00 | up | 0.4222 | 1.83 | up | hypothetical protein\ Context:(NC_002946)+[1140196-1141815]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO1198 | 0.0035 | -5.81 | down | 0.0322 | -5.53 | down | 0.1913 | -2.58 | down | hypothetical protein\ Context:(NC_002946)+[1142045-1143619]\ Notes:Best Blastp Hit: gb\|AAF42335.1\| (AE002550) YhbX/YhjW/YijP/YjdB family protein [Neisseria meningitidis MC58] COG2194 Predicted membrane-associated |
| NGO1199 | 0.4407 | -2.16 | down | 0.4482 | -2.12 | down | 0.1616 | 3.19 | up | HrpA\ Context:(NC_002946)+[1143685-1146915]\ Notes:Best Blastp Hit: emb\|CAB83729.1\| (AL162753) putative DNA helicase [Neisseria meningitidis] COG1643 HrpA-like helicases; putative ATP dependent DNA helicase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1201 | 0.0090 | -25.30 | down | 0.0908 | -5.99 | down | 0.0846 | -10.14 | down | hypothetical protein\ Context:(NC_002946)-[1148343-1148453]\ Notes:Best Blastp Hit: emb\|CAB84427.1\|(AL162755) hypothetical protein NMA1165 [Neisseria meningitidis] |
| NGO1203 | 0.4222 | -1.51 | down | 0.4981 | -1.36 | down | 0.3778 | -1.30 | down | anthranilate phosphoribosyltransferase\ Context:(NC_002946)-[1149327-1150355]\ Notes:Catalyzes the conversion of N-(5-phospho-D-ribosyl)-anthranilate and diphosphate to anthranilate and 5-phospho-alpha-D-ribose 1-diphosphate |
| NGO1204 | 0.1293 | -2.06 | down | 0.0317 | -4.57 | down | 0.0421 | -3.37 | down | anthranilate synthase component II\ Context:(NC_002946)-[1150419-1151009]\ Notes:TrpG; with TrpE catalyzes the formation of anthranilate and glutamate from chorismate and glutamine; TrpG provides the glutamine amidotransferase activity |
| NGO1205 | 0.0756 | 2.80 | up | 0.0687 | 3.44 | up | 0.0923 | 1.71 | up | putative TonB-dependent receptor protein\ Context:(NC_002946)+[1151402-1153696]\ Notes:Best Blastp Hit: emb\|CAB84423.1\| (AL162755) putative outer-membrane receptor protein [Neisseria meningitidis] COG1629 Outer membrane receptor proteins; mostly Fe |
| NGO1206 | 0.2603 | -2.01 | down | 0.8507 | 1.12 | up | 0.8902 | -1.08 | down | phosphatidylserine decarboxylase\ Context:(NC_002946)-[1154088-1154867]\ Notes:catalyzes the decarboxylaton of phospatidyl-L-sering to phosphatidylethanolamine |
| NGO1207 | 0.0459 | 2.68 | up | 0.9448 | 1.08 | up | 0.4199 | 3.27 | up | excinuclease ABC subunit A\ Context:(NC_002946)+[1155021-1157870]\ Notes:The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvrA is an ATPase and a DNA-binding protein. A damage recognition complex composed of 2 uvrA and 2 uvrB subunits scans DNA for abnormalities. When the presence of a lesion has been verified by uvrB; the uvrA molecules dissociate |
| NGO1208 | 0.6137 | -1.46 | down | 0.7162 | -1.32 | down | 0.7570 | -1.29 | down | NgoMIIIM\ Context:(NC_002946)+[1157888-1158529]\ Notes:Best Blastp Hit: gb\|AAG17897.1\|AF297971_1 (AF297971) restriction endonuclease R.NgoMIII [Neisseria gonorrhoeae] |
| NGO1209 | 0.8784 | -1.09 | down | 0.2904 | 1.62 | up | 0.4828 | -1.25 | down | DNA cytosine methyltransferase M.NgoMIII\ Context:(NC_002946)+[1158533-1159666]\ Notes:Best Blastp Hit: possibly phase variable - two 8A residue homopolymer repeats in the the coding sequence (ON) COG0270 Site-specific DNA methylase dcm |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1212 | 0.2493 | 1.73 | up | 0.5448 | 1.24 | up | 0.3965 | 1.24 | up | CTP synthetase\ Context:(NC_002946)-[1160954-1162588]\ Notes:CTP synthase; CTP synthase; cytidine triphosphate synthetase; catalyzes the ATP-dependent amination of UTP to CTP with either L-glutamine or ammonia as the source of nitrogen; in Escherichia coli this enzyme forms a homotetramer |
| NGO1213 | 0.3446 | -1.76 | down | 0.4124 | -1.67 | down | 0.6330 | -1.43 | down | putative long-chain-fatty-acid--CoA-ligase\ Context:(NC_002946)-[1162700-1164370]\ Notes:Best Blastp Hit: pir\|\|H81068 long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) NMB1555 [similarity] - Neisseria meningitidis (group B strain MD58) >gi\|7226802\|gb\|AAF41909.1\|(AE002506) long-chain-fatty-acid--CoA ligase [Neisseria meningitidis MC58] COG0318 Acyl-CoA synthetases (AMP-forming)/AMP-acid |
| NGO1214 | 0.0778 | -2.55 | down | 0.0257 | -3.57 | down | 0.1135 | -1.70 | down | tRNA(5-methylaminomethyl-2-thiouridylate)-methyltransferase\ Context:(NC_002946)-[1164441-1165592]\ Notes:Enables the biosynthesis of the modified nucleoside 5-methylaminomethyl-2-thiouridine present in the wobble position of some tRNAs |
| NGO1215 | 0.3129 | -1.65 | down | 0.4251 | -1.43 | down | 0.2289 | -2.11 | down | hypothetical protein\ Context:(NC_002946)-[1165669-1166142]\ Notes:Best Blastp Hit: pir\|\|A81799 hypothetical protein NMA1745 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380387\|emb\|CAB84973.1\|(AL162757) hypothetical protein NMA1745 [Neisseria meningitidis] |
| NGO1216 | 0.2092 | -1.88 | down | 0.2472 | 1.72 | up | 0.3153 | -1.91 | down | diacylglycerol kinase\ Context:(NC_002946)-[1166274-1166657]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0818 Diacylglycerol kinase |
| NGO1217 | 0.0313 | 3.16 | up | 0.0218 | 2.46 | up | 0.2444 | 1.56 | up | glutathione synthetase\ Context:(NC_002946)-[1166816-1167775]\ Notes:The second step in the glutathione biosynthesis pathway; where it synthesizes ATP + gamma-L-glutamyl-L-cysteine + glycine = ADP + phosphate + glutathione |

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| NGO1218 | 0.6766 | 1.23 | up | 0.3141 | 1.41 | up | 0.7123 | 1.11 | up | glutaminyl-tRNA synthetase\ Context:(NC_002946)-[1167864-1169585]\ Notes:catalyzes a two-step reaction; first charging a glutamine molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA |
| NGO1219 | 0.4413 | -1.53 | down | 0.0399 | -3.25 | down | 0.0324 | -3.61 | down | DeoR family transcriptional regulator\ Context:(NC_002946)-[1169664-1170437]\ Notes:Best Blastp Hit: gb\|AAF41915.1\| (AE002506) transcriptional regulator; DeoR family [Neisseria meningitidis MC58] COG1349 Transcriptional regulators of sugar |
| NGO1220 | 0.9974 | -1.00 | down | 0.0134 | -5.62 | down | 0.2194 | -2.30 | down | hypothetical protein\ Context:(NC_002946)-[1170480-1171382]\ Notes:Best Blastp Hit: pir\|\|G81069 conserved hypothetical protein NMB1562 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226809\|gb\|AAF41916.1\| (AE002506) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1221 | 0.1577 | 2.15 | up | 0.1539 | 1.91 | up | 0.6157 | -1.25 | down | GntR family transcriptional regulator\ Context:(NC_002946)-[1171531-1172247]\ Notes:Best Blastp Hit: gb\|AAF41917.1\| (AE002506) transcriptional regulator; GntR family [Neisseria meningitidis MC58] >gi\|7380393\|emb\|CAB84979.1\| (AL162757) putative gntR-family transcriptional regulator [Neisseria meningitidis] COG1802 Transcriptional regulators; GntR family |
| NGO1222 | 0.0658 | 2.47 | up | 0.0776 | 1.99 | up | 0.5951 | 1.18 | up | hypothetical protein\ Context:(NC_002946)-[1172769-1173119]\ Notes:Best Blastp Hit: pir\|\|A81800 hypothetical protein NMA1753 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380395\|emb\|CAB84981.1\| (AL162757) hypothetical protein [Neisseria meningitidis] COG1765 Uncharacterized ACR |
| NGO1223 | 0.0660 | 2.95 | up | 0.2637 | 3.00 | up | 0.6636 | 1.13 | up | hypothetical protein\ Context:(NC_002946)-[1173309-1173980]\ Notes:Best Blastp Hit: pir\|\|A81068 hypothetical protein NMB1565 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226813\|gb\|AAF41919.1\| (AE002507) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380396\|emb\|CAB84982.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |

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| NGO1224 | 0.1477 | 2.27 | up | 0.5937 | 1.31 | up | 0.4800 | 1.40 | up | putativephosphoribosylglycinamidetransformylase\ Context:(NC_002946)-[1173996-1174622]\ Notes:Best Blastp Hit: pir\|\|C81800 phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) NMA1755 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380397\|emb\|CAB84983.1\| (AL162757) phosphoribosylglycinamide transformylase [Neisseria meningitidis] COG0299 Folate-dependent |
| NGO1225 | 0.0792 | 2.98 | up | 0.1714 | 1.82 | up | 0.1613 | 1.78 | up | putative peptidyl-prolylisomerase\ Context:(NC_002946)-[1174729-1175547]\ Notes:Best Blastp Hit: gb\|AAF41921.1\| (AE002507) macrophage infectivity potentiator [Neisseria meningitidis MC58] COG0545 FKBP-type peptidyl-prolyl cis-trans |
| NGO1226 | 0.7727 | -1.19 | down | 0.7925 | 1.20 | up | 0.7066 | 1.26 | up | HolC\ Context:(NC_002946)-[1175807-1176247]\ Notes:Best Blastp Hit: pir\|\|E81800 DNA-directed DNA polymerase (EC 2.7.7.7) III chi chain NMA1757 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380399\|emb\|CAB84985.1\| (AL162757) DNA polymerase III chi subunit [Neisseria meningitidis]; putative DNA polymerase III chi subunit |
| NGO1227 | 0.6523 | 1.28 | up | 0.7342 | 1.13 | up | 0.7509 | 1.12 | up | AmpA\ Context:(NC_002946)-[1176310-1177716]\ Notes:Best Blastp Hit: pir\|\|F81800 leucyl aminopeptidase (EC 3.4.11.1) NMA1758 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380400\|emb\|CAB84986.1\| (AL162757) aminopeptidase A [Neisseria meningitidis] COG0260 Leucyl aminopeptidase; putative aminopeptidase A |
| NGO1228 | 0.0018 | -11.46 | down | 0.0128 | -12.99 | down | 0.4615 | -1.39 | down | hypothetical protein\ Context:(NC_002946)+[1177890-1179005]\ Notes:Best Blastp Hit: emb\|CAB84987.1\| (AL162757) conserved integral membrane hypothetical protein [Neisseria meningitidis] COG0795 Predicted permeases |
| NGO1229 | 0.5850 | 1.39 | up | 0.6821 | -1.46 | down | 0.0898 | 3.65 | up | hypothetical protein\ Context:(NC_002946)+[1179002-1180072]\ Notes:Best Blastp Hit: emb\|CAB84988.1\| (AL162757) conserved hypothetical integral membrane protein [Neisseria meningitidis] COG0795 Predicted permeases |
| NGO1230 | 0.5670 | -1.59 | down | 0.1514 | -11.30 | down | 0.7746 | 1.24 | up | hypothetical protein\ Context:(NC_002946)+[1180077-1180238]\ Notes:Best Blastp Hit: gb\|AAF42247.1\| (AE002540) conserved hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1231 | 0.7214 | -1.22 | down | 0.7751 | -1.10 | down | 0.7805 | 1.13 | up | bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase\ Context:(NC_002946)+[1180387-1182972]\ Notes:catalyzes the conversion of citrate to isocitrate and the conversion of 2-methylaconitate to 2-methylisocitrate |
| NGO1232 | 0.0053 | -8.67 | down | 0.0028 | -5.42 | down | 0.3209 | -2.40 | down | ornithine carbamoyltransferase\ Context:(NC_002946)+[1183114-1184109]\ Notes:catalyzes the formation of ornithine and carbamylphosphate from citrulline in the arginine catabolic pathway |
| NGO1233 | 0.0972 | 2.84 | up | 0.1010 | 1.81 | up | 0.1476 | 2.10 | up | ketol-acid reductoisomerase\ Context:(NC_002946)-[1184228-1185241]\ Notes:catalyzes the formation of (R)-2;3-dihydroxy-3-methylbutanoate from (S)-2-hydroxy-2-methyl-3-oxobutanoate in valine and isoleucine biosynthesis |
| NGO1234 | 0.1450 | 2.29 | up | 0.4266 | 1.42 | up | 0.4327 | 1.27 | up | hypothetical protein\ Context:(NC_002946)-[1185321-1185614]\ Notes:Best Blastp Hit: emb\|CAB84992.1\|(AL162757) conserved hypothetical protein [Neisseria meningitidis] COG1359 Uncharacterized ACR; YneC family |
| NGO1235 | 0.0965 | 2.65 | up | 0.4744 | 1.34 | up | 0.4428 | 1.23 | up | acetolactate synthase 3 regulatory subunit\ Context:(NC_002946)-[1185681-1186172]\ Notes:with IlvI catalyzes the formation of 2-acetolactate from pyruvate; the small subunit is required for full activity and valine sensitivity; E.coli produces 3 isoenzymes of acetolactate synthase which differ in specificity to substrates; valine sensitivity and affinity for cofactors; also known as acetolactate synthase 3 small subunit |
| NGO1236 | 0.6600 | 1.27 | up | 0.7432 | 1.16 | up | 0.7001 | 1.11 | up | IlvI\ Context:(NC_002946)-[1186183-1187910]\ Notes:Best Blastp Hit: pir\|\|F81801 acetolactate synthase (EC 4.1.3.18) III large chain NMA1766 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380408\|emb\|CAB84994.1\|(AL162757) acetolactate synthase isozyme III large subunit [Neisseria meningitidis] COG0028 Thiamine pyrophosphate-requiring enzymes; putative acetolactate synthase isozyme III large subunit |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1237 | 0.2432 | 1.87 | up | 0.6282 | 1.26 | up | 0.4344 | 1.29 | up | hypothetical protein\ Context:(NC_002946)+[1188975-1189628]\ Notes:Best Blastp Hit: gb\|AAF41931.1\|(AE002508) conserved hypothetical protein [Neisseria meningitidis MC58] COG1999 Uncharacterized protein SCO1/SenC/PrrC |
| NGO1238 | 0.1649 | 1.93 | up | 0.5528 | 1.31 | up | 0.3867 | 1.32 | up | ATP phosphoribosyltransferase catalytic subunit\ Context:(NC_002946)+[1189707-1190372]\ Notes:short form of enzyme; requires HisZ for function; catalyzes the formation of N'-5'-phosphoribosyl-ATP from phosphoribosyl pyrophosphate; crucial role in histidine biosynthesis; forms heteromultimer of HisG and HisZ |
| NGO1239 | 0.0465 | 3.41 | up | 0.0951 | 1.89 | up | 0.3383 | 1.37 | up | hypothetical protein\ Context:(NC_002946)+[1190464-1191351]\ Notes:Best Blastp Hit: pir\|\|D81067 hypothetical protein NMB1580; NMA1769 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226828\|gb\|AAF41933.1\| (AE002508) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380411\|emb\|CAB84997.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1240 | 0.0568 | 2.64 | up | 0.0243 | 2.51 | up | 0.0842 | 1.72 | up | histidinol dehydrogenase\ Context:(NC_002946)+[1191348-1192637]\ Notes:catalyzes the oxidation of L-histidinol to L-histidinaldehyde and then to L-histidine in histidine biosynthesis; functions as a dimer |
| NGO1241 | 0.0465 | 2.81 | up | 0.0393 | 4.15 | up | 0.0237 | 3.29 | up | histidinol-phosphate aminotransferase\ Context:(NC_002946)+[1192683-1193762]\ Notes:catalyzes the formation of L-histidinol phosphate from imidazole-acetol phosphate and glutamate in histidine biosynthesis |
| NGO1242 | 0.3404 | 1.75 | up | 0.5403 | 1.25 | up | 0.1391 | 1.60 | up | imidazoleglycerol-phosphate dehydratase\ Context:(NC_002946)+[1193956-1194690]\ Notes:catalyzes the dehydration of D-erythro-1-(imidazol-4-yl)glycerol 3-phosphate to 3-(imidazol-4-yl)-2-oxopropyl phosphate in histidine biosynthesis |
| NGO1243 | 0.4245 | -1.71 | down | 0.3006 | -1.57 | down | 0.9754 | 1.01 | up | hypothetical protein\ Context:(NC_002946)+[1194766-1195635]\ Notes:Best Blastp Hit: emb\|CAB85001.1\|(AL162757) hypothetical protein [Neisseria meningitidis] COG2084 3-hydroxyisobutyrate dehydrogenase and |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1244 | 0.0087 | 27.03 | up | 0.4222 | -2.26 | down | 0.6310 | 1.78 | up | MarR family transcriptional regulator\ Context:(NC_002946)+[1195870-1196301]\ Notes:Best Blastp Hit: gb\|AAF41938.1\| (AE002509) transcriptional regulator; MarR family [Neisseria meningitidis MC58] COG1846 Transcriptional regulators; MarR/EmrR |
| NGO1245 | 0.5391 | -1.44 | down | 0.0056 | -11.26 | down | 0.1673 | -3.09 | down | hypothetical protein\ Context:(NC_002946)+[1196312-1197178]\ Notes:Best Blastp Hit: pir\|\|D81065 hypothetical protein NMB1586 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226835\|gb\|AAF41939.1\| (AE002509) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1246 | 0.6151 | 1.36 | up | 0.0037 | -5.84 | down | 0.7040 | -1.28 | down | putative periplasmic protease\ Context:(NC_002946)-[1197229-1198281]\ Notes:SohB; periplasmic protein; member of the peptidase S49 family |
| NGO1247 | 0.0008 | -20.65 | down | 0.0168 | -6.94 | down | 0.1475 | -10.81 | down | hypothetical protein\ Context:(NC_002946)-[1199032-1199595]\ Notes:Best Blastp Hit: pir\|\|C81803 CDPdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) NMA1779 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380421\|emb\|CAB85007.1\| (AL162757) CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Neisseria meningitidis] COG0558 Phosphatidylglycerophosphate synthase |
| NGO1248 | 0.1287 | -2.37 | down | 0.0056 | -14.09 | down | 0.1169 | -2.99 | down | hypothetical protein\ Context:(NC_002946)-[1199701-1200123]\ Notes:Best Blastp Hit: pir\|\|E81803 hypothetical protein NMA1781 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380423\|emb\|CAB85009.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1249 | 0.0621 | -4.10 | down | 0.4699 | -1.45 | down | 0.1179 | -2.50 | down | hypothetical protein\ Context:(NC_002946)-[1200302-1200637]\ Notes:Best Blastp Hit: pir\|\|H81065 conserved hypothetical protein NMB1590 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226839\|gb\|AAF41943.1\| (AE002509) conserved hypothetical protein [Neisseria meningitidis MC58] COG0599 Uncharacterized ACR; homolog |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1250 | 0.7055 | -1.18 | down | 0.4082 | -1.49 | down | 0.5590 | -1.31 | down | mtrCDE transcriptional regulator; activator\ Context:(NC_002946)+[1200818-1201660]\ Notes:Best Blastp Hit: gb\|AAD44696.1\|AF128630_1 (AF128630) MtrA [Neisseria gonorrhoeae] >gi\|7228474\|gb\|AAF42471.1\|AF133676_1 (AF133676) MtrA [Neisseria gonorrhoeae] COG2207 AraC-type DNA-binding domain-containing |
| NGO1251 | 0.3106 | 1.78 | up | 0.4584 | 1.37 | up | 0.9898 | -1.00 | down | hypothetical protein\ Context:(NC_002946)-[1201722-1202300]\ Notes:Best Blastp Hit: pir\|\|H81803 hypothetical protein NMA1784 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380426\|emb\|CAB85012.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1252 | 0.4143 | -1.80 | down | 0.0211 | -10.51 | down | 0.0677 | -4.41 | down | hypothetical protein\ Context:(NC_002946)+[1202358-1203260]\ Notes:Best Blastp Hit: emb\|CAB85013.1\| (AL162757) conserved hypothetical integral membrane protein [Neisseria meningitidis] COG0697 Predicted permeases |
| NGO1253 | 0.0917 | 2.55 | up | 0.0874 | 1.82 | up | 0.2122 | 1.64 | up | putative ABC transporter; periplasmic binding protein; polyamine\ Context:(NC_002946)-[1203301-1204431]\ Notes:Best Blastp Hit: pir\|\|D81066 spermidine/putrescine ABC transporter; periplasmic spermidine/putrescine-binding protein NMB1594 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226843\|gb\|AAF41947.1\| (AE002509) spermidine/putrescine ABC transporter; periplasmic spermidine/putrescine-binding protein |
| NGO1254 | 0.1561 | 1.90 | up | 0.7065 | 1.35 | up | 0.2816 | 2.56 | up | hypothetical protein\ Context:(NC_002946)+[1204635-1207259]\ Notes:Best Blastp Hit: pir\|\|C81804 alanine--tRNA ligase (EC 6.1.1.7) NMA1788 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380429\|emb\|CAB85015.1\| (AL162757) alanyl-tRNA synthetase [Neisseria meningitidis] COG0013 Alanyl-tRNA synthetase |
| NGO1255 | 0.3150 | -5.44 | down | 0.3997 | -7.08 | down | 0.8508 | -1.39 | down | hypothetical protein\ Context:(NC_002946)+[1207321-1207662]\ Notes:Best Blastp Hit: pir\|\|D81804 hypothetical protein NMA1789 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380430\|emb\|CAB85016.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1257 | 0.0037 | -12.88 | down | 0.0018 | -14.27 | down | 0.0902 | -4.80 | down | hypothetical protein\ Context:(NC_002946)-[1209532-1209675]\ Notes: |
| NGO1258 | 0.5536 | 1.39 | up | 0.8535 | 1.08 | up | 0.5219 | 1.26 | up | phosphoglyceromutase\ Context:(NC_002946)-[1209692-1210375]\ Notes:catalyzes the interconversion of 2-phosphoglycerate to 3-phosphoglycerate |
| NGO1259 | 0.1039 | -2.72 | down | 0.0009 | -7.52 | down | 0.0083 | -4.26 | down | DNA topoisomerase IV subunit A\ Context:(NC_002946)+[1210524-1212827]\ Notes:decatenates newly replicated chromosomal DNA and relaxes positive and negative DNA supercoiling |
| NGO1260 | 0.1827 | 2.33 | up | 0.9976 | 1.00 | up | 0.8637 | 1.07 | up | Rsp\ Context:(NC_002946)+[1212847-1214571]\ Notes:Best Blastp Hit: gb\|AAC82507.1\| (U65994) Rsp [Neisseria gonorrhoeae] COG2204 AAA superfamily ATPases with N-terminal; putative transcriptional regulator |
| NGO1261 | 0.5749 | 1.40 | up | 0.4138 | -2.31 | down | 0.9529 | 1.02 | up | hypothetical protein\ Context:(NC_002946)+[1214671-1215423]\ Notes:Best Blastp Hit: sp\|P72077\|YHIQ_NEIGO hypothetical 27.3 KD protein >gi\|3851182\|gb\|AAC82508.1\| (U65994) unknown [Neisseria gonorrhoeae] COG0500 SAM-dependent methyltransferases |
| NGO1273 | 0.0351 | -4.34 | down | 0.0080 | -4.98 | down | 0.0186 | -2.71 | down | hypothetical protein\ Context:(NC_002946)+[1224369-1224773]\ Notes:Best Blastp Hit: emb\|CAB85043.1\| (AL162757) hypothetical protein [Neisseria meningitidis] COG0537 Diadenosine tetraphosphate (Ap4A) |
| NGO1274 | 0.0049 | -6.02 | down | 0.0433 | -4.38 | down | 0.6989 | -1.35 | down | hypothetical protein\ Context:(NC_002946)+[1224813-1225994]\ Notes:Best Blastp Hit: pir\|\|H81807 conserved hypothetical protein NMA1819 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|6900400\|emb\|CAB72012.1\| (AJ391256) hypothetical protein [Neisseria meningitidis] >gi\|7380458\|emb\|CAB85044.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] COG1619 Uncharacterized proteins; homologs of |
| NGO1275 | 0.1525 | -2.59 | down | 0.0900 | -4.67 | down | 0.9163 | 1.04 | up | NorB\ Context:(NC_002946)-[1226096-1228207]\ Notes:Best Blastp Hit: emb\|CAB85109.1\| (AL162757) nitric oxide reductase [Neisseria meningitidis]; putative nitric oxide reductase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1276 | 0.1020 | -2.75 | down | 0.1060 | -7.85 | down | 0.3057 | -3.47 | down | AniA\ Context:(NC_002946)+[1228725-1229903]\ Notes:Best Blastp Hit: sp\|Q02219\|ANIA_NEIGO major outer membrane protein PAN 1 precursor >gi\|477564\|pir\|\|A49208 outer membrane protein Pan 1 - Neisseria gonorrhoeae >gi\|150277\|gb\|AAA25462.1\| (M97926) major anaerobically induced outer membrane protein [Neisseria gonorrhoeae] >gi\|258387\|gb\|AAB23836.1\| Pan 1=outer membrane protein [Neisseria gonorrhoeae; Peptide; 392 aa]; nitrite reductase |
| NGO1277 | 0.0105 | -7.76 | down | 0.3273 | -1.62 | down | 0.7206 | -1.23 | down | hypothetical protein\ Context:(NC_002946)+[1230081-1230836]\ Notes:Best Blastp Hit: gb\|AAF62335.1\| (AE002513) hypothetical protein [Neisseria meningitidis MC58] COG1262 Uncharacterized BCR |
| NGO1279 | 0.6485 | 1.22 | up | 0.5555 | 1.35 | up | 0.2368 | 1.52 | up | hypothetical protein\ Context:(NC_002946)-[1232381-1232938]\ Notes:Best Blastp Hit: pir\|\|E81059 conserved hypothetical protein NMB1637 NMA1891 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|2253229\|gb\|AAC32673.1\| (AF004820) hypthetical proteinNitroreductase family proteins |
| NGO1282 | 0.0317 | -3.32 | down | 0.0055 | -7.54 | down | 0.0661 | -3.10 | down | hypothetical protein\ Context:(NC_002946)-[1234709-1235023]\ Notes:Best Blastp Hit: pir\|\|G81059 hypothetical protein NMB1639 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226889\|gb\|AAF41988.1\| (AE002514) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1283 | 0.2170 | -2.83 | down | 0.1656 | -2.36 | down | 0.3459 | -1.31 | down | phosphoserine aminotransferase\ Context:(NC_002946)-[1235044-1236150]\ Notes:catalyzes the formation of 3-phosphonooxypyruvate and glutamate from O-phospho-L-serine and 2-oxoglutarate; required both in major phosphorylated pathway of serine biosynthesis and in the biosynthesis of pyridoxine |
| NGO1284 | 0.7444 | -1.23 | down | 0.7052 | 1.21 | up | 0.5723 | 1.24 | up | hypothetical protein\ Context:(NC_002946)+[1236499-1236948]\ Notes:in Streptococcus pneumoniae this gene was found to be essential; structure determination of the Streptococcus protein shows that it is similar to a number of other proteins |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1285 | 0.7578 | -1.16 | down | 0.9871 | -1.01 | down | 0.9533 | -1.04 | down | transcription elongation factor NusA\ Context:(NC_002946)+[1236976-1238478]\ Notes:modifies transcription through interactions with RNA polymerase affecting elongation; readthrough; termination; and antitermination |
| NGO1286 | 0.0186 | 6.47 | up | 0.0793 | 4.78 | up | 0.0650 | 1.91 | up | translation initiation factor IF-2\ Context:(NC_002946)+[1238490-1241321]\ Notes:Protects formylmethionyl-tRNA from spontaneous hydrolysis and promotes its binding to the 30S ribosomal subunits during initiation of protein synthesis. Also involved in the hydrolysis of GTP during the formation of the 70S ribosomal complex |
| NGO1287 | 0.0421 | -6.16 | down | 0.0030 | -9.50 | down | 0.4044 | -2.83 | down | hypothetical protein\ Context:(NC_002946)-[1241481-1242821]\ Notes:Best Blastp Hit: pir\|\|C81058 hypothetical protein NMB1644 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226895\|gb\|AAF41993.1\|(AE002515) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1288 | 0.0350 | -4.38 | down | 0.0005 | -42.59 | down | 0.3147 | -2.34 | down | hypothetical protein\ Context:(NC_002946)-[1242895-1244235]\ Notes:Best Blastp Hit: pir\|\|D81058 hypothetical protein NMB1645 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226896\|gb\|AAF41994.1\|(AE002515) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1289 | 0.0127 | -3.98 | down | 0.0207 | -5.66 | down | 0.9573 | -1.04 | down | hypothetical protein\ Context:(NC_002946)+[1244378-1245004]\ Notes:Best Blastp Hit: pir\|\|D81817 probable hemeolysin NMA1900 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380534\|emb\|CAB85121.1\|(AL162757) putative haemolysin [Neisseria meningitidis] COG1272 Predicted membrane proteins; hemolysin |
| NGO1290 | 0.0001 | -101.04 | down | 0.0000 | -209.10 | down | 0.0052 | -20.49 | down | putative amino-acid transporter; sodium/alanine symporter\ Context:(NC_002946)-[1245069-1246487]\ Notes:Best Blastp Hit: pir\|\|F81058 amino acid symporter; probable NMB1647 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226898\|gb\|AAF41996.1\|(AE002515) amino acid symporter; putative [Neisseria meningitidis MC58] COG1115 Sodium-alanine symporters |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1291 | 0.2686 | 1.79 | up | 0.0945 | 1.76 | up | 0.3763 | 1.43 | up | hypothetical protein\ Context:(NC_002946)+[1246814-1247542]\ Notes:Best Blastp Hit: pir\|\|F81817 conserved hypothetical protein NMA1902 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380536\|emb\|CAB85123.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] COG0217 Uncharacterized ACR; YebC family |
| NGO1292 | 0.0455 | -2.87 | down | 0.0326 | -7.80 | down | 0.2013 | -1.69 | down | Dsb\ Context:(NC_002946)-[1247601-1248089]\ Notes:Best Blastp Hit: gb\|AAF41998.1\| (AE002515) disulfide bond formation protein B [Neisseria meningitidis MC58] COG1495 Disulfide bond formation protein DsbB; putative disulfide bond formation protein |
| NGO1293 | 0.1412 | 2.84 | up | 0.0377 | -7.71 | down | 0.6717 | 1.57 | up | hypothetical protein\ Context:(NC_002946)-[1248518-1248802]\ Notes: |
| NGO1294 | 0.0454 | -5.12 | down | 0.0008 | -22.04 | down | 0.0533 | -6.15 | down | AsnC family transcriptional regulator\ Context:(NC_002946)-[1249111-1249575]\ Notes:Best Blastp Hit: pir\|\|A81059 leucine-responsive regulatory protein NMB1650 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226901\|gb\|AAF41999.1\| (AE002515) leucine-responsive regulatory protein [Neisseria meningitidis MC58] COG1522 Transcriptional regulators; Lrp family |
| NGO1295 | 0.7967 | 1.19 | up | 0.4587 | 1.37 | up | 0.5366 | 1.21 | up | hypothetical protein\ Context:(NC_002946)+[1249797-1250855]\ Notes:Best Blastp Hit: pir\|\|B81818 alanine racemase (EC 5.1.1.1) NMA1906 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380540\|emb\|CAB85127.1\| (AL162757) alanine racemase [Neisseria meningitidis] COG0787 Alanine racemase |
| NGO1296 | 0.0591 | -6.02 | down | 0.3076 | -5.46 | down | 0.7256 | -1.51 | down | hypothetical protein\ Context:(NC_002946)-[1251143-1251325]\ Notes: |
| NGO1297 | 0.2883 | -1.78 | down | 0.0499 | -2.88 | down | 0.2466 | -1.38 | down | hypothetical protein\ Context:(NC_002946)-[1251397-1252752]\ Notes:Best Blastp Hit: pir\|\|E81818 conserved hypothetical protein NMA1908 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380543\|emb\|CAB85130.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] |
| NGO1298 | 0.4458 | 1.49 | up | 0.1505 | 2.10 | up | 0.8675 | 1.07 | up | hypothetical protein\ Context:(NC_002946)-[1252767-1253039]\ Notes:ACT domain-containing protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1299 | 0.1718 | 2.40 | up | 0.1851 | 1.97 | up | 0.9481 | -1.02 | down | hypothetical protein\ Context:(NC_002946)-[1253164-1253901]\ Notes:Best Blastp Hit: pir\|\|E81057 conserved hypothetical protein NMB1654 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226906\|gb\|AAF42003.1\| (AE002516) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1300 | 0.5252 | -1.44 | down | 0.1874 | -2.04 | down | 0.1915 | -1.88 | down | N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase\ Context:(NC_002946)-[1254039-1254950]\ Notes:involved in methylation of ribosomal protein L3 |
| NGO1301 | 0.7016 | 1.38 | up | 0.0932 | -12.80 | down | 0.5223 | 1.53 | up | hypothetical protein\ Context:(NC_002946)+[1255045-1255755]\ Notes:Best Blastp Hit: pir\|\|A81819 hypothetical protein NMA1913 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380547\|emb\|CAB85134.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1306 | 0.3691 | 1.49 | up | 0.6250 | 1.18 | up | 0.6776 | -1.13 | down | hypothetical protein\ Context:(NC_002946)-[1263560-1263847]\ Notes:Best Blastp Hit: possibly phase variable - 8G residue homopolymer repeat in the coding sequence (ON) |
| NGO1307 | 0.1072 | 2.92 | up | 0.0655 | 1.96 | up | 0.4963 | 1.24 | up | putative flavoprotein\ Context:(NC_002946)+[1263920-1265104]\ Notes:Best Blastp Hit: pir\|\|D81819 hypothetical protein NMA1916 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380550\|emb\|CAB85137.1\| (AL162757) hypothetical protein [Neisseria meningitidis] COG0452 Flavoprotein involved in panthothenate |
| NGO1308 | 0.0105 | 6.79 | up | 0.0329 | 9.45 | up | 0.2911 | 2.04 | up | putativeguanosine-3';5'-bis(diphosphate)3'-pyrophosphohydrolase\ Context:(NC_002946)-[1265171-1267327]\ Notes:Best Blastp Hit: pir\|\|B81058 guanosine-3';5'-bis(diphosphate) 3'-pyrophosphohydrolase NMB1659 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226911\|gb\|AAF42008.1\| (AE002516) guanosine-3`;5`-bis(diphosphate) 3`-pyrophosphohydrolase [Neisseria meningitidis MC58] COG0317 Guanosine polyphosphate |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1309 | 0.3487 | 1.71 | up | 0.5931 | 1.24 | up | 0.3476 | 1.42 | up | hypothetical protein\ Context:(NC_002946)-[1267420-1267626]\ Notes:Best Blastp Hit: gb\|AAF42009.1\|(AE002517) DNA-directed RNA polymerase; omega subunit [Neisseria meningitidis MC58] >gi\|7380552\|emb\|CAB85139.1\| (AL162757) DNA-directed RNA polymerase omega chain [Neisseria meningitidis] COG1758 RNA polymerase-associated protein RpoZ |
| NGO1310 | 0.7962 | 1.14 | up | 0.9974 | 1.00 | up | 0.7361 | -1.10 | down | KguA\ Context:(NC_002946)-[1267684-1268301]\ Notes:Best Blastp Hit: pir\|\|G81819 guanylate kinase (EC 2.7.4.8) NMA1919 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380553\|emb\|CAB85140.1\|(AL162757) guanylate kinase [Neisseria meningitidis] COG0194 Guanylate kinase; putative guanylate kinase |
| NGO1311 | 0.3499 | 1.81 | up | 0.1075 | 2.51 | up | 0.6767 | 1.13 | up | adenine phosphoribosyltransferase\ Context:(NC_002946)+[1268429-1269028]\ Notes:catalyzes a salvage reaction resulting in the formation of AMP which is metabolically less costly than a de novo synthesis |
| NGO1312 | 0.0357 | 3.48 | up | 0.4243 | 1.61 | up | 0.4020 | -1.48 | down | hypothetical protein\ Context:(NC_002946)-[1269074-1269883]\ Notes:Best Blastp Hit: emb\|CAB85142.1\|(AL162757) conserved hypothetical protein [Neisseria meningitidis] COG0561 Predicted hydrolases of the HAD superfamily |
| NGO1313 | 0.0129 | -14.23 | down | 0.1499 | -27.47 | down | 0.7497 | -1.70 | down | hypothetical protein\ Context:(NC_002946)+[1269916-1270026]\ Notes:Best Blastp Hit: emb\|CAB85143.1\|(AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1314 | 0.4387 | -1.62 | down | 0.6588 | -1.30 | down | 0.6081 | 1.37 | up | putative protease\ Context:(NC_002946)+[1270187-1271542]\ Notes:Best Blastp Hit: pir\|\|B81056 proteinase; probable NMB1664 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226917\|gb\|AAF42013.1\|(AE002517) protease; putative [Neisseria meningitidis MC58] COG0826 Protease related to collagenase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1315 | 0.3159 | -1.71 | down | 0.6492 | 1.22 | up | 0.6267 | -1.29 | down | hypothetical protein\ Context:(NC_002946)+[1271673-1272146]\ Notes:Best Blastp Hit: pir\|\|D81820 hypothetical protein NMA1924 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380558\|emb\|CAB85145.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1318 | 0.1800 | 2.20 | up | 0.1381 | 2.12 | up | 0.0599 | 2.22 | up | hypothetical protein\ Context:(NC_002946)-[1275619-1276311]\ Notes:Best Blastp Hit: pir\|\|E81820 heme utilisation protein NMA1927 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|6692578\|gb\|AAF24745.1\|AF133695_1 (AF133695) HemO [Neisseria meningitidis] >gi\|7380559\|emb\|CAB85147.1\| (AL162757) haem utilisation protein [Neisseria meningitidis] |
| NGO1319 | 0.0009 | -12.25 | down | 0.0178 | -11.41 | down | 0.4998 | -1.49 | down | PqiA\ Context:(NC_002946)+[1276589-1277893]\ Notes:Best Blastp Hit: pir\|\|F81820 hypothetical integral membrane protein NMA1928 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380560\|emb\|CAB85148.1\| (AL162757) hypothetical integral membrane protein [Neisseria meningitidis]; putative paraquot-inducible protein A |
| NGO1320 | 0.0017 | 10.63 | up | 0.2735 | 2.72 | up | 0.2232 | 3.26 | up | PqiB\ Context:(NC_002946)+[1277886-1279547]\ Notes:Best Blastp Hit: pir\|\|A81057 hypothetical integral membrane protein pqiB NMA1929 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226924\|gb\|AAF42020.1\| (AE002517) pqiB protein [Neisseria meningitidis MC58] >gi\|7380561\|emb\|CAB85149.1\| (AL162757) hypothetical integral membrane protein [Neisseria meningitidis]; putative paraquat-inducible protein B |
| NGO1321 | 0.0206 | 4.89 | up | 0.0225 | 16.27 | up | 0.0413 | 4.42 | up | hypothetical protein\ Context:(NC_002946)+[1279547-1280065]\ Notes:Best Blastp Hit: pir\|\|H81820 probable lipoprotein NMA1930 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380562\|emb\|CAB85150.1\| (AL162757) putative lipoprotein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1322 | 0.2221 | 2.28 | up | 0.1639 | 8.27 | up | 0.0991 | 14.06 | up | putative DNA-3-methyladenineglycosylase I\ Context:(NC_002946)+[1280069-1280620]\ Notes:Best Blastp Hit: pir\|\|A81821 DNA-3-methyladenine glycosidase I (EC 3.2.2.20) NMA1931 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380563\|emb\|CAB85151.1\| (AL162757) DNA-3-methyladenine glycosylase I [Neisseria meningitidis] |
| NGO1323 | 0.0144 | 6.21 | up | 0.0747 | 6.06 | up | 0.0642 | 6.12 | up | hypothetical protein\ Context:(NC_002946)+[1280610-1281251]\ Notes:Best Blastp Hit: gb\|AAF42023.1\| (AE002517) GDSL lipase family protein [Neisseria meningitidis MC58] >gi\|7380564\|emb\|CAB85152.1\| (AL162757) putative lipase [Neisseria meningitidis] |
| NGO1324 | 0.0535 | 3.99 | up | 0.3958 | 2.34 | up | 0.6143 | 1.16 | up | hypothetical protein\ Context:(NC_002946)+[1281422-1281781]\ Notes:Best Blastp Hit: pir\|\|C81821 probable integral membrane protein NMA1933 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380565\|emb\|CAB85153.1\| (AL162757) putative integral membrane protein [Neisseria meningitidis] |
| NGO1325 | 0.9925 | -1.01 | down | 0.0281 | -3.91 | down | 0.5376 | 1.59 | up | glycine dehydrogenase\ Context:(NC_002946)+[1281812-1284664]\ Notes:acts in conjunction with GvcH to form H-protein-S-aminomethyldihydrolipoyllysine from glycine |
| NGO1327 | 0.1411 | 8.82 | up | 0.9825 | 1.03 | up | 0.8012 | -1.39 | down | hypothetical protein\ Context:(NC_002946)+[1285805-1285942]\ Notes:Best Blastp Hit: emb\|CAB85155.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1328 | 0.0091 | -4.77 | down | 0.0263 | -4.26 | down | 0.0027 | -3.61 | down | putative cytochrome\ Context:(NC_002946)-[1286026-1286865]\ Notes:Best Blastp Hit: gb\|AAF42025.1\| (AE002518) cytochrome c5 [Neisseria meningitidis MC58] |
| NGO1329 | 0.6497 | -1.42 | down | 0.5130 | 1.43 | up | 0.7524 | -1.17 | down | aromatic amino acid aminotransferase\ Context:(NC_002946)-[1287290-1288483]\ Notes:catalyzes the formation of L-glutamate and an aromatic oxo acid from an aromatic amino acid and 2-oxoglutarate |
| NGO1330 | 0.4425 | 1.55 | up | 0.8343 | 1.19 | up | 0.1649 | -1.75 | down | tRNA (uracil-5-)-methyltransferase\ Context:(NC_002946)-[1288503-1289591]\ Notes:catalyzes the formation of 5-methyl-uridine at position 54 in all tRNAs |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1331 | 0.0790 | -3.24 | down | 0.0063 | -4.23 | down | 0.4090 | -1.67 | down | chorismate synthase\ Context:(NC_002946)+[1289738-1290838]\ Notes:catalyzes the formation of chorismate from 5-O-(1-carboxyvinyl)-3-phosphoshikimate in aromatic amino acid biosynthesis |
| NGO1332 | 0.7306 | -1.18 | down | 0.5685 | -1.30 | down | 0.8478 | -1.06 | down | hypothetical protein\ Context:(NC_002946)+[1290929-1291354]\ Notes:Best Blastp Hit: pir\|\|C81055 hypothetical protein NMB1681 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226934\|gb\|AAF42029.1\|(AE002518) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1333 | 0.7617 | 1.18 | up | 0.7371 | -1.41 | down | 0.4472 | 1.63 | up | DNA topoisomerase IV subunit B\ Context:(NC_002946)-[1291428-1293413]\ Notes:decatenates newly replicated chromosomal DNA and relaxes positive and negative DNA supercoiling |
| NGO1334 | 0.6169 | -1.40 | down | 0.1514 | -2.56 | down | 0.1633 | -2.27 | down | dinucleoside polyphosphate hydrolase\ Context:(NC_002946)-[1293480-1294088]\ Notes:Hydrolyzes diadenosine polyphosphate |
| NGO1335 | 0.3658 | 1.61 | up | 0.9076 | 1.05 | up | 0.6615 | 1.14 | up | seryl-tRNA synthetase\ Context:(NC_002946)+[1294170-1295465]\ Notes:catalyzes a two-step reaction; first charging a serine molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA |
| NGO1336 | 0.9003 | 1.06 | up | 0.6706 | 1.20 | up | 0.8827 | 1.04 | up | D-lactate dehydrogenase\ Context:(NC_002946)-[1295538-1296536]\ Notes:Catalyzes the reduction of sulfopyruvate to (R)-sulfolactate much more efficiently than the reverse reaction. Also catalyzes the reduction of oxaloacetate; alpha-ketoglutarate; and to a much lower extent; KHTCA; but not pyruvate. Involved in the biosynthes |
| NGO1337 | 0.5758 | 1.51 | up | 0.1576 | -2.03 | down | 0.6445 | -1.33 | down | peptide chain release factor 1\ Context:(NC_002946)-[1296661-1297737]\ Notes:recognizes the termination signals UAG and UAA during protein translation a specificity which is dependent on amino acid residues residing in loops of the L-shaped tRNA-like molecule of RF1; this protein is similar to release factor 2 |
| NGO1338 | 0.1834 | 4.71 | up | 0.8709 | 1.11 | up | 0.6586 | 1.21 | up | hypothetical protein\ Context:(NC_002946)-[1297827-1298597]\ Notes:Best Blastp Hit: gb\|AAF42035.1\|(AE002519) conserved hypothetical protein [Neisseria meningitidis MC58] COG0084 Predicted hydrolases of PHP superfamily |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1339 | 0.1808 | 2.69 | up | 0.3880 | -1.62 | down | 0.1372 | 1.66 | up | AnsA\ Context:(NC_002946)-[1298600-1299592]\ Notes:Best Blastp Hit: emb\|CAB85167.1\| (AL162757) L-asparaginase [Neisseria meningitidis] COG0252 L-asparaginase; putative L-asparaginase |
| NGO1340 | 0.3793 | -1.62 | down | 0.2837 | -1.72 | down | 0.7770 | -1.10 | down | hypothetical protein\ Context:(NC_002946)-[1299659-1300342]\ Notes:Best Blastp Hit: pir\|\|B81823 DedA-family integral membrane protein NMA1948 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380580\|emb\|CAB85168.1\| (AL162757) DedA-family integral membrane protein [Neisseria meningitidis] COG0586 Uncharacterized membrane-associated |
| NGO1341 | 0.2564 | -1.83 | down | 0.2137 | -2.16 | down | 0.2196 | -1.59 | down | MrsA\ Context:(NC_002946)-[1300531-1301868]\ Notes:Best Blastp Hit: pir\|\|C81054 phosphoglucomutase/phosphomannomutase family protein NMB1690 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226944\|gb\|AAF42038.1\| (AE002519) phosphoglucomutase/phosphomannomutase family protein [Neisseria meningitidis MC58] COG1109 Phosphomannomutase; putative phosphoglucomutase protein |
| NGO1342 | 0.1555 | -2.37 | down | 0.4502 | -1.40 | down | 0.0461 | -4.02 | down | DHPS\ Context:(NC_002946)-[1301995-1302849]\ Notes:Best Blastp Hit: sp\|Q51161\|DHPS_NEIME dihydropteroate synthase (DHPS) (dihydropteroate pyrophosphorylase) >GI\|95427\|pir\|\|S25614 dihydropteroate synthase (EC 2.5.1.15) - Neisseria meningitidis (strain 952/68) >gi\|2120887\|pir\|\|S65839 dihydropteroate synthase (EC 2.5.1.15) - Neisseria meningitidis (strain 952/68) >gi\|45036\|emb\|CAA48206.1\| (X68069) dihydropteroate synthase [Neisseria meningitidis] COG0294 Dihydropteroate synthase; putative dihydropteroate synthase |
| NGO1343 | 0.8504 | -1.19 | down | 0.8193 | -1.10 | down | 0.3060 | -1.35 | down | hypothetical protein\ Context:(NC_002946)-[1302989-1303882]\ Notes:Best Blastp Hit: gb\|AAF42040.1\| (AE002519) chorismate mutase-related protein [Neisseria meningitidis MC58] COG0722 DAHP synthase/3-Deoxy-D-manno-octulosonic |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1344 | 0.1998 | -5.90 | down | 0.1302 | -15.37 | down | 0.8507 | 1.24 | up | hypothetical protein\ Context:(NC_002946)+[1303973-1306075]\ Notes:Best Blastp Hit: pir\|\|G81051 hypothetical protein NMB1693 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226948\|gb\|AAF42041.1\| (AE002520) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1345 | 0.7202 | -1.17 | down | 0.5124 | -1.28 | down | 0.7843 | -1.08 | down | hypothetical protein\ Context:(NC_002946)-[1306139-1307617]\ Notes:Best Blastp Hit: pir\|\|H81051 conserved hypothetical protein NMB1694 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226949\|gb\|AAF42042.1\| (AE002520) conserved hypothetical protein [Neisseria meningitidis MC58] COG0043 Uncharacterized ACR; YigC family |
| NGO1346 | 0.2534 | -1.76 | down | 0.6218 | -1.23 | down | 0.9696 | -1.01 | down | hypothetical protein\ Context:(NC_002946)-[1307637-1308152]\ Notes:Best Blastp Hit: pir\|\|G81823 hypothetical protein NMA1953 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380585\|emb\|CAB85173.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1347 | 0.4593 | 1.40 | up | 0.9084 | -1.05 | down | 0.7623 | 1.10 | up | hypothetical protein\ Context:(NC_002946)-[1308159-1308500]\ Notes:Best Blastp Hit: pir\|\|H81823 probable integral membrane protein NMA1954 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380586\|emb\|CAB85174.1\| (AL162757) putative integral membrane protein [Neisseria meningitidis] |
| NGO1348 | 0.0179 | -8.48 | down | 0.1396 | -7.43 | down | 0.6336 | -1.39 | down | hypothetical protein\ Context:(NC_002946)-[1308544-1308711]\ Notes:Best Blastp Hit: pir\|\|B81171 hypothetical protein NMB0676 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225903\|gb\|AAF41094.1\| (AE002422) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1349 | 0.2057 | 2.75 | up | 0.4574 | -1.85 | down | 0.1081 | -2.14 | down | hypothetical protein\ Context:(NC_002946)-[1308789-1309538]\ Notes:Best Blastp Hit: emb\|CAB85175.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1350 | 0.0448 | -5.30 | down | 0.0003 | -13.15 | down | 0.5326 | -1.26 | down | hypothetical protein\ Context:(NC_002946)+[1309781-1310347]\ Notes:Best Blastp Hit: pir\|\|G81052 hypothetical protein NMB1701 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226956\|gb\|AAF42049.1\| (AE002520) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1352 | 0.0258 | -4.21 | down | 0.0146 | -6.97 | down | 0.0624 | -2.06 | down | putative 3-oxoacyl-(acyl-carrier-protein) synthase\ Context:(NC_002946)+[1311101-1312243]\ Notes:Best Blastp Hit: pir\|\|A81053 3-oxoacyl-(acyl-carrier-protein) synthase II NMB1703 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226958\|gb\|AAF42051.1\|(AE002520) 3-oxoacyl-(acyl-carrier-protein) synthase II [Neisseria meningitidis MC58] COG0304 3-oxoacyl-(acyl-carrier-protein) synthase I |
| NGO1353 | 0.1825 | -2.26 | down | 0.3101 | -1.70 | down | 0.7603 | 1.13 | up | hypothetical protein\ Context:(NC_002946)+[1312530-1313294]\ Notes:Best Blastp Hit: emb\|CAB85178.1\|(AL162757) beta-1;4-glucosyltransferase [Neisseria meningitidis] COG0463 Glycosyltransferases involved in cell |
| NGO1354 | 0.8848 | -1.08 | down | 0.4820 | -1.24 | down | 0.3149 | -1.37 | down | RfaK\ Context:(NC_002946)+[1313295-1314359]\ Notes:Best Blastp Hit: gb\|AAF42053.1\| (AE002520) alpha-1;2-N-acetylglucosamine transferase [Neisseria meningitidis MC58] COG0438 Glycosyltransferases I; putative alpha-1;2-N-acetylglucosamine transferase |
| NGO1355 | 0.0341 | -4.64 | down | 0.0007 | -21.61 | down | 0.6420 | -1.17 | down | putative sodium dependent ion transport protein\ Context:(NC_002946)+[1314593-1315930]\ Notes:Best Blastp Hit: pir\|\|F81050 sodium- and chloride-dependent transporter NMB1707 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226963\|gb\|AAF42055.1\|(AE002521) sodium- and chloride-dependent transporter [Neisseria meningitidis MC58] COG0733 Sodium-dependent transporters (SNF family) |
| NGO1357 | 0.6841 | -1.26 | down | 0.7376 | 1.33 | up | 0.6473 | 1.15 | up | thymidylate synthase\ Context:(NC_002946)-[1317126-1317920]\ Notes:ThyA; catalyzes formation of dTMP and 7;8-dihydrofolate from 5;10-methylenetetrahydrofolate and dUMP; involved in deoxyribonucleotide biosynthesis; there are 2 copies in some Bacilli; one of which appears to be phage-derived |
| NGO1358 | 0.3086 | -1.82 | down | 0.1956 | -1.77 | down | 0.0783 | -1.76 | down | glutamate dehydrogenase\ Context:(NC_002946)+[1318344-1319678]\ Notes:converts 2-oxoglutarate to glutamate; in Escherichia coli this enzyme plays a role in glutamate synthesis when the cell is under energy restriction; uses NADPH; forms a homohexamer |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1359 | 0.1725 | -4.93 | down | 0.0250 | -5.50 | down | 0.2378 | -2.84 | down | hypothetical protein\ Context:(NC_002946)-[1319675-1319929]\ Notes:Best Blastp Hit: gb\|AAF41523.1\| (AE002462) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226410\|gb\|AAF41558.1\| (AE002465) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1360 | 0.0020 | -12.50 | down | 0.0017 | -13.43 | down | 0.0665 | -3.67 | down | GntR family transcriptional regulator\ Context:(NC_002946)-[1319917-1320696]\ Notes:Best Blastp Hit: emb\|CAB85185.1\| (AL162757) GntR-family transcriptional regulator [Neisseria meningitidis] COG2186 Transcriptional regulators; FadR family |
| NGO1361 | 0.0001 | -46.05 | down | 0.0048 | -36.06 | down | 0.0010 | -29.77 | down | hypothetical protein\ Context:(NC_002946)+[1320974-1321261]\ Notes:Best Blastp Hit: gb\|AAF42059.1\| (AE002521) L-lactate permease-related protein [Neisseria meningitidis MC58] COG1620 L-lactate permease |
| NGO1362 | 0.0001 | -19.33 | down | 0.0316 | -14.34 | down | 0.2267 | -4.30 | down | hypothetical protein\ Context:(NC_002946)+[1321289-1321438]\ Notes:Best Blastp Hit: emb\|CAB85187.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1363 | 0.3134 | 1.66 | up | 0.4198 | 1.55 | up | 0.0440 | 3.33 | up | hypothetical protein\ Context:(NC_002946)-[1321639-1323042]\ Notes:Best Blastp Hit: gb\|AAF42061.1\| (AE002521) multidrug efflux pump channel protein [Neisseria meningitidis MC58] |
| NGO1364 | 0.4277 | 1.52 | up | 0.4878 | 1.46 | up | 0.3910 | -1.31 | down | antibiotic resistance efflux pump component\ Context:(NC_002946)-[1323095-1326298]\ Notes:Best Blastp Hit: gb\|AAC45560.1\| (U60099) RND protein [Neisseria gonorrhoeae] COG0841 Cation efflux system protein |
| NGO1365 | 0.1761 | 2.32 | up | 0.1047 | -1.73 | down | 0.9954 | 1.00 | up | antibiotic resistance efflux pump component\ Context:(NC_002946)-[1326310-1327548]\ Notes:Best Blastp Hit: sp\|P43505\|MTRC_NEIGO membrane fusion protein MtrC precursor >gi\|550460\|gb\|AAA80193.1\| (U14993) membrane fusion protein [Neisseria gonorrhoeae] COG0845 Membrane permeases; predicted cation efflux |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1366 | 0.5148 | -1.47 | down | 0.0977 | -4.85 | down | 0.7110 | -1.17 | down | mtrCDE transcriptional regulator; repressor\ Context:(NC_002946)+[1327798-1328430]\ Notes:Best Blastp Hit: sp\|P39897\|MTRR_NEIGO regulatory protein MtrR >gi\|541020\|pir\|\|S40250 MtrR protein - Neisseria gonorrhoeae >gi\|7449616\|pir\|\|S42419 probable transcription repressor mtrR - Neisseria gonorrhoeae (strain FA19) >gi\|438189\|emb\|CAA81047.1\| (Z25797) MtrR protein [Neisseria gonorrhoeae] COG1309 Transcriptional regulators; AcrR family |
| NGO1367 | 0.6062 | 1.67 | up | 0.4606 | -2.58 | down | 0.4246 | -2.17 | down | hypothetical protein\ Context:(NC_002946)-[1328523-1328780]\ Notes:Best Blastp Hit: emb\|CAB85192.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1368 | 0.0048 | -6.18 | down | 0.8017 | -1.11 | down | 0.2440 | -2.68 | down | antibiotic resistance efflux pump component\ Context:(NC_002946)+[1329067-1330635]\ Notes:Best Blastp Hit: gb\|AAD51362.2\|AF176820_1 (AF176820) putative efflux pump component MtrF [Neisseria gonorrhoeae] |
| NGO1369 | 0.4126 | 2.89 | up | 0.0552 | -9.92 | down | 0.8063 | 1.21 | up | putative exodeoxyribonuclease V\ Context:(NC_002946)-[1330703-1333909]\ Notes:Best Blastp Hit: pir\|\|D81826 exodeoxyribonuclease V (EC 3.1.11.5) NMA1974 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380606\|emb\|CAB85194.1\| (AL162757) exodeoxyribonuclease V [Neisseria meningitidis] COG1330 Exonuclease V gamma subunit; RecC |
| NGO1370 | 0.0083 | -11.15 | down | 0.0007 | -11.75 | down | 0.0198 | -13.83 | down | hypothetical protein\ Context:(NC_002946)-[1334010-1335419]\ Notes:Best Blastp Hit: pir\|\|E81826 probable integral membrane protein NMA1975 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380607\|emb\|CAB85195.1\| (AL162757) putative integral membrane protein [Neisseria meningitidis] |
| NGO1371 | 0.0325 | -3.01 | down | 0.0823 | -3.00 | down | 0.2398 | -1.91 | down | CcoP\ Context:(NC_002946)-[1335763-1337082]\ Notes:Best Blastp Hit: gb\|AAF42068.1\| (AE002522) cytochrome c oxidase; subunit III [Neisseria meningitidis MC58] COG2010 Cytochrome c; mono- and diheme variants; putative cytochrome c oxidase subunit |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1372 | 0.8827 | -1.09 | down | 0.3466 | -1.46 | down | 0.4849 | -1.34 | down | hypothetical protein\ Context:(NC_002946)-[1337106-1337276]\ Notes:Best Blastp Hit: emb\|CAB85198.1\|(AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1373 | 0.4495 | -1.44 | down | 0.1731 | -1.79 | down | 0.1911 | -1.58 | down | CcoO\ Context:(NC_002946)-[1337281-1337892]\ Notes:Best Blastp Hit: pir\|\|D81050 cytochrome c oxidase; chain II NMB1724 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226978\|gb\|AAF42069.1\|(AE002522) cytochrome c oxidase; subunit II [Neisseria meningitidis MC58]; putative cytochrome c oxidase subunit |
| NGO1374 | 0.9533 | 1.03 | up | 0.3657 | -1.43 | down | 0.3315 | -1.39 | down | CcoN\ Context:(NC_002946)-[1337919-1339364]\ Notes:Best Blastp Hit: pir\|\|E81050 cytochrome-c oxidase (EC 1.9.3.1) fixN chain NMB1725 [similarity] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226979\|gb\|AAF42070.1\| (AE002522) cytochrome c oxidase; subunit I [Neisseria meningitidis MC58] >gi\|7380611\|emb\|CAB85200.1\| (AL162757) cytochrome c oxidase subunit [Neisseria meningitidis] COG0843 Cytochrome c oxidase; heme b and; putative cytochrome c oxidase subunit |
| NGO1375 | 0.1588 | 2.51 | up | 0.0804 | 2.56 | up | 0.0091 | 4.40 | up | hypothetical protein\ Context:(NC_002946)+[1339678-1341426]\ Notes:Best Blastp Hit: pir\|\|E81048 conserved hypothetical protein NMB1726 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226981\|gb\|AAF42071.1\| (AE002523) conserved hypothetical protein [Neisseria meningitidis MC58] COG0265 Trypsin-like serine proteases; typically |
| NGO1376 | 0.4011 | 1.74 | up | 0.6539 | 1.18 | up | 0.2707 | 1.68 | up | hypothetical protein\ Context:(NC_002946)+[1341452-1341919]\ Notes:Best Blastp Hit: pir\|\|C81827 hypothetical protein NMA1982 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380613\|emb\|CAB85202.1\|(AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1377 | 0.0068 | 8.28 | up | 0.0303 | 3.54 | up | 0.0068 | 4.26 | up | hypothetical protein\ Context:(NC_002946)-[1342420-1342854]\ Notes:Best Blastp Hit: sp\|O06434\|EXBD_NEIGO biopolymer transport ExbD protein >gi\|2098623\|gb\|AAC45288.1\| (U79563) ExbD [Neisseria gonorrhoeae] COG0848 biopolymer transport protein ExbD |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1378 | 0.0021 | 8.71 | up | 0.0315 | 3.54 | up | 0.0096 | 3.68 | up | ExbB\ Context:(NC_002946)-[1342857-1343567]\ Notes:Best Blastp Hit: sp\|O06433\|EXBB_NEIGO biopolymer transport ExbB protein >gi\|2098622\|gb\|AAC45287.1\| (U79563) ExbB [Neisseria gonorrhoeae] COG0811 biopolymer transport proteins |
| NGO1379 | 0.0415 | 3.48 | up | 0.0755 | 2.84 | up | 0.0236 | 3.09 | up | TonB\ Context:(NC_002946)-[1343585-1344436]\ Notes:Best Blastp Hit: sp\|O06432\|TONB_NEIGO TonB protein >gi\|2098621\|gb\|AAC45286.1\| (U79563) TonB [Neisseria gonorrhoeae] |
| NGO1380 | 0.8195 | -1.12 | down | 0.5648 | -1.46 | down | 0.3080 | -1.66 | down | hypothetical protein\ Context:(NC_002946)+[1344692-1345330]\ Notes:Best Blastp Hit: pir\|\|B81049 conserved hypothetical protein NMB1731 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226986\|gb\|AAF42076.1\| (AE002523) conserved hypothetical protein [Neisseria meningitidis MC58] COG1994 Zn-dependent proteases |
| NGO1381 | 0.6198 | -1.27 | down | 0.3535 | -1.57 | down | 0.4168 | -1.26 | down | glutaredoxin 2\ Context:(NC_002946)-[1345402-1346043]\ Notes:cofactor involved in the reduction of disulfides |
| NGO1382 | 0.5106 | 1.54 | up | 0.5357 | 1.49 | up | 0.2518 | 1.94 | up | putative GTP pyrophosphokinase\ Context:(NC_002946)+[1346186-1348399]\ Notes:Best Blastp Hit: pir\|\|F81049 GTP pyrophosphokinase NMB1735 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226990\|gb\|AAF42080.1\| (AE002523) GTP pyrophosphokinase [Neisseria meningitidis MC58] COG0317 Guanosine |
| NGO1383 | 0.5906 | 1.33 | up | 0.4987 | 1.27 | up | 0.8423 | -1.08 | down | hypothetical protein\ Context:(NC_002946)-[1348463-1348840]\ Notes:Best Blastp Hit: pir\|\|E81783 hypothetical protein NMA2118 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380741\|emb\|CAB85332.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1384 | 0.0219 | -4.45 | down | 0.3223 | -1.57 | down | 0.0297 | -2.78 | down | hypothetical protein\ Context:(NC_002946)-[1348909-1349394]\ Notes:Best Blastp Hit: pir\|\|D81783 hypothetical protein NMA2117 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380740\|emb\|CAB85331.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1385 | 0.1448 | 2.15 | up | 0.2064 | 2.46 | up | 0.6465 | -1.20 | down | hypothetical protein\ Context:(NC_002946)-[1349345-1349974]\ Notes:Best Blastp Hit: possibly an alternative C terminus for MafB |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1386 | 0.5901 | 1.27 | up | 0.2591 | 1.52 | up | 0.5293 | 1.24 | up | hypothetical protein\ Context:(NC_002946)-[1350801-1351505]\ Notes:Best Blastp Hit: possibly an alternative C terminus for MafB |
| NGO1387 | 0.6080 | 1.33 | up | 0.3033 | 1.42 | up | 0.6676 | -1.15 | down | hypothetical protein\ Context:(NC_002946)-[1351641-1352183]\ Notes:Best Blastp Hit: sp\|P45941\|YQCF_BACSU hypothetical 21.5 KD protein in CWLA-CISA intergenic region >gi\|7475297\|pir\|\|E69949 hypothetical protein yqcF - Bacillus subtilis >gi\|1217878\|dbj\|BAA06963.1\| (D32216) ORF95 [Bacillus subtilis] >gi\|1303771\|dbj\|BAA12427.1\| (D84432) YqcF [Bacillus subtilis] >gi\|2635032\|emb\|CAB14528.1\| (Z99117) yqcF [Bacillus subtilis] |
| NGO1388 | 0.3121 | 1.72 | up | 0.3973 | 1.47 | up | 0.9278 | 1.04 | up | hypothetical protein\ Context:(NC_002946)-[1352310-1352537]\ Notes:Best Blastp Hit: pir\|\|S24525 Ig heavy chain V region - mouse >gi\|51255\|emb\|CAA47230.1\| (X66668) immunoglobulin heavy chain [Mus musculus] |
| NGO1389 | 0.1155 | 5.05 | up | 0.0541 | 3.46 | up | 0.7521 | -1.11 | down | hypothetical protein\ Context:(NC_002946)-[1352596-1352919]\ Notes: |
| NGO1390 | 0.0915 | -2.79 | down | 0.0653 | -4.58 | down | 0.0446 | -4.14 | down | hypothetical protein\ Context:(NC_002946)-[1352909-1353262]\ Notes: |
| NGO1391 | 0.6278 | 1.29 | up | 0.6114 | 1.21 | up | 0.8210 | -1.06 | down | hypothetical protein\ Context:(NC_002946)-[1353559-1354107]\ Notes:Best Blastp Hit: emb\|CAC01359.1\| (AL390975) hypothetical protein SCP8.21 [Streptomyces coelicolor A3(2)] |
| NGO1392 | 0.7596 | 1.14 | up | 0.9733 | 1.02 | up | 0.6578 | -1.23 | down | MafB3\ Context:(NC_002946)-[1354097-1355914]\ Notes:Best Blastp Hit: pir\|\|H81782 adhesin MafB2 NMA2113 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380736\|emb\|CAB85327.1\| (AL162758) adhesin MafB2 [Neisseria meningitidis]; putative MafB-like protein |
| NGO1395 | 0.4404 | -1.93 | down | 0.1417 | -8.10 | down | 0.1953 | -4.24 | down | hypothetical protein\ Context:(NC_002946)+[1357719-1358300]\ Notes:Best Blastp Hit: emb\|CAB84330.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] COG1101 ATPase components of various transport |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1396 | 0.5628 | -1.38 | down | 0.3540 | -1.98 | down | 0.0740 | -2.61 | down | putative electron transfer flavoprotein-ubiquinone oxidoreductase\ Context:(NC_002946)+[1358282-1360090]\ Notes:Best Blastp Hit: emb\|CAB84049.1\|(AL162754) putative electron transfer flavoprotein-ubiquinone oxidoreductase [Neisseria meningitidis] COG0644 Dehydrogenases (flavoproteins) |
| NGO1397 | 0.0298 | -3.20 | down | 0.1049 | -2.58 | down | 0.5321 | -1.45 | down | NosL\ Context:(NC_002946)-[1360224-1360718]\ Notes:Best Blastp Hit: pir\|\|G81183 protein disulfide isomerase NosL; probable NMB0580 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225808\|gb\|AAF41008.1\| (AE002413) protein disulfide isomerase NosL; putative [Neisseria meningitidis MC58] >gi\|7379486\|emb\|CAB84048.1\| (AL162754) putative lipoprotein [Neisseria meningitidis]; putative dissimilatory nitrous oxide reduction protein; lipoprotein |
| NGO1398 | 0.0052 | -9.95 | down | 0.0004 | -20.07 | down | 0.9536 | -1.07 | down | hypothetical protein\ Context:(NC_002946)-[1360715-1361545]\ Notes:Best Blastp Hit: pir\|\|T44663 nosY protein [imported] - Bradyrhizobium japonicum >gi\|3850617\|emb\|CAA05522.1\| (AJ002531) nosY [Bradyrhizobium japonicum] COG1277 Predicted membrane protein |
| NGO1399 | 0.1627 | 2.74 | up | 0.1427 | -5.24 | down | 0.3190 | -2.38 | down | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)-[1361542-1362468]\ Notes:Best Blastp Hit: pir\|\|D81920 probable ABC-transporter ATP-binding protein NMA0763 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379484\|emb\|CAB84046.1\| (AL162754) putative ABC-transporter ATP-binding protein [Neisseria meningitidis] COG1131 ABC-type multidrug transport system; ATPase |
| NGO1403 | 0.3272 | -1.83 | down | 0.0180 | -6.43 | down | 0.0790 | -2.18 | down | glutamyl-tRNA reductase\ Context:(NC_002946)-[1368673-1369920]\ Notes:catalyzes the formation of glutamate-1-semialdehyde from glutamyl-tRNA(Glu) and NADPH; the second step of the pathway is catalyzed by glutamate-1-semialdehyde aminomutase which results in the formation of 5-aminolevulinic acid; functions in porphyrin (tetrapyrroles) biosynthesis; the crystal structure showed a C-terminal dimerization domain that appears to be absent in Chlamydial proteins |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1404 | 0.5252 | -1.42 | down | 0.4152 | -1.57 | down | 0.2002 | -1.48 | down | glycine cleavage system protein H\ Context:(NC_002946)-[1370073-1370459]\ Notes:part of multienzyme complex composed of H; L; P; and T proteins which catalyzes oxidation of glycine to yield carbon dioxide; ammonia; 5;10-CH2-H4folate and a reduced pyridine nucleotide; protein H is involved in transfer of methylamine group from the P to T protein; covalently bound to a lipoyl cofactor |
| NGO1405 | 0.8768 | 1.13 | up | 0.2009 | -2.38 | down | 0.2117 | -1.83 | down | hypothetical protein\ Context:(NC_002946)-[1370511-1371050]\ Notes: |
| NGO1406 | 0.1371 | -2.61 | down | 0.0308 | -8.61 | down | 0.0963 | -3.41 | down | glycine cleavage system aminomethyltransferase T\ Context:(NC_002946)-[1371197-1372297]\ Notes:catalyzes the transfer of a methylene carbon from the methylamine-loaded GcvH protein to tetrahydrofolate; causing the release of ammonia and the generation of reduced GcvH protein |
| NGO1407 | 0.4293 | 1.50 | up | 0.1634 | 1.87 | up | 0.8704 | 1.05 | up | AsnC family transcriptional regulator\ Context:(NC_002946)+[1372809-1373291]\ Notes:Best Blastp Hit: gb\|AAF41001.1\| (AE002413) transcriptional regulator; AsnC family [Neisseria meningitidis MC58] COG1522 Transcriptional regulators; Lrp family |
| NGO1408 | 0.4907 | 1.49 | up | 0.5265 | 1.27 | up | 0.6094 | 1.18 | up | hypothetical protein\ Context:(NC_002946)+[1373338-1373943]\ Notes:Best Blastp Hit: pir\|\|D81919 hypothetical protein NMA0755 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379476\|emb\|CAB84038.1\| (AL162754) hypothetical protein NMA0755 [Neisseria meningitidis] |
| NGO1410 | 0.0847 | -3.00 | down | 0.7908 | -1.27 | down | 0.9882 | 1.01 | up | hypothetical protein\ Context:(NC_002946)+[1373940-1374299]\ Notes:Best Blastp Hit: pir\|\|C81919 probable membrane protein NMA0754 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379475\|emb\|CAB84037.1\| (AL162754) putative membrane protein [Neisseria meningitidis] |
| NGO1411 | 0.1645 | 2.37 | up | 0.0279 | 3.16 | up | 0.1293 | 2.46 | up | hypothetical protein\ Context:(NC_002946)+[1374586-1376079]\ Notes:Best Blastp Hit: gb\|AAF40998.1\| (AE002413) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1413 | 0.6655 | -1.25 | down | 0.0895 | -1.96 | down | 0.1468 | -1.77 | down | Na(+)-translocating NADH-quinone reductase subunit A\ Context:(NC_002946)+[1377044-1378387]\ Notes:uses the energy from reduction of ubiquinone-1 to ubiquinol to move Na(+) ions from the cytoplasm to the periplasm |
| NGO1414 | 0.4317 | -1.54 | down | 0.6403 | -1.50 | down | 0.2691 | -1.55 | down | Na(+)-translocating NADH-quinone reductase subunit B\ Context:(NC_002946)+[1378390-1379622]\ Notes:uses the energy from reduction of ubiquinone-1 to ubiquinol to move Na(+) ions from the cytoplasm to the periplasm |
| NGO1415 | 0.8794 | 1.08 | up | 0.4329 | 1.34 | up | 0.5678 | 1.16 | up | Na(+)-translocating NADH-quinone reductase subunit C\ Context:(NC_002946)+[1379615-1380391]\ Notes:uses the energy from reduction of ubiquinone-1 to ubiquinol to move Na(+) ions from the cytoplasm to the periplasm |
| NGO1416 | 0.8076 | 1.13 | up | 0.7720 | 1.37 | up | 0.5105 | 1.74 | up | Na(+)-translocating NADH-quinone reductase subunit D\ Context:(NC_002946)+[1380391-1381017]\ Notes:Part of the NQR complex which catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions; coupled with the transport of Na(+) ions from the cytoplasm to the periplasm |
| NGO1417 | 0.8707 | -1.07 | down | 0.3474 | 3.76 | up | 0.2128 | 2.58 | up | Na(+)-translocating NADH-quinone reductase subunit E\ Context:(NC_002946)+[1381021-1381614]\ Notes:Part of the NQR complex which consists of NqrA; NqrB; NqrC; NqrD; NqrE and NqrF; NQR complex catalyzes the reduction of ubiquinone-1 to ubiquinol by two successive reactions; coupled with the transport of Na(+) ions from the cytoplasm to the periplasm; NqrE is probably involved in the second step; the conversion of ubisemiquinone to ubiquinol. |
| NGO1418 | 0.6069 | -1.33 | down | 0.9706 | -1.03 | down | 0.7228 | 1.29 | up | Na(+)-translocating NADH-quinone reductase subunit F\ Context:(NC_002946)+[1381628-1382845]\ Notes:uses the energy from reduction of ubiquinone-1 to ubiquinol to move Na(+) ions from the cytoplasm to the periplasm |
| NGO1419 | 0.0024 | -18.79 | down | 0.1894 | -8.10 | down | 0.7539 | 1.48 | up | hypothetical protein\ Context:(NC_002946)+[1383027-1383194]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1420 | 0.6219 | -1.29 | down | 0.3169 | -1.92 | down | 0.2677 | 1.75 | up | hypothetical protein\ Context:(NC_002946)+[1383362-1384417]\ Notes:Best Blastp Hit: pir\|\|F81184 thiamin biosynthesis lipoprotein ApbE NMB0563 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225790\|gb\|AAF40991.1\| (AE002412) thiamine biosynthesis lipoprotein ApbE [Neisseria meningitidis MC58] COG1477 Membrane-associated lipoprotein ApbE |
| NGO1421 | 0.3031 | 2.05 | up | 0.2823 | 1.45 | up | 0.3160 | -1.79 | down | hypothetical protein\ Context:(NC_002946)+[1384443-1384658]\ Notes:Best Blastp Hit: gb\|AAF40990.1\| (AE002412) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379466\|emb\|CAB84028.1\| (AL162754) putative periplasmic protein [Neisseria meningitidis] |
| NGO1422 | 0.0916 | 3.07 | up | 0.0403 | 2.17 | up | 0.2328 | 1.94 | up | putative heat shock protein\ Context:(NC_002946)-[1384782-1385360]\ Notes:Best Blastp Hit: pir\|\|D81184 probable heat shock protein grpE NMA0744 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225788\|gb\|AAF40989.1\| (AE002412) grpE protein [Neisseria meningitidis MC58] >gi\|7379465\|emb\|CAB84027.1\| (AL162754) probable heat shock protein [Neisseria meningitidis] COG0576 Molecular chaperone GrpE (heat shock |
| NGO1423 | 0.0331 | -3.36 | down | 0.0453 | -4.83 | down | 0.0766 | -2.20 | down | hypothetical protein\ Context:(NC_002946)+[1385543-1386361]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG1045 Serine acetyltransferase |
| NGO1424 | 0.9403 | 1.04 | up | 0.7148 | 1.12 | up | 0.3533 | 1.39 | up | putative ubiquinone biosynthesis protein UbiB\ Context:(NC_002946)-[1386565-1388076]\ Notes:an Escherichia coli mutant results in accumulation of octaprenylphenol and no ubiquinone; functions in the formation of 2-octaprenyl-6-hydroxy-phenol from 2-octaprenylphenol in ubiquinone (coenzyme Q) biosynthesis; similar to eukaryotic proteins that exhibit kinase functions |
| NGO1426 | 0.7209 | -1.21 | down | 0.5339 | -1.28 | down | 0.0174 | -3.13 | down | iron-sulfur cluster insertion protein ErpA\ Context:(NC_002946)-[1388728-1389066]\ Notes:essential respiratory protein A; may be involved in the transfer of iron-sulfur clusters; essential for growth using oxygen or alternate electron acceptors |

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| NGO1427 | 0.9556 | -1.03 | down | 0.7651 | -1.11 | down | 0.2025 | -1.58 | down | putative transcriptional regulator; repressor\ Context:(NC_002946)-[1389199-1389909]\ Notes:Best Blastp Hit: gb\|AAF40984.1\| (AE002411) repressor protein; putative [Neisseria meningitidis MC58] |
| NGO1428 | 0.1282 | -2.23 | down | 0.4343 | -1.46 | down | 0.2483 | -2.33 | down | hypothetical protein\ Context:(NC_002946)+[1390072-1390344]\ Notes:Best Blastp Hit: gb\|AAF40983.1\| (AE002411) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1429 | 0.1064 | 3.70 | up | 0.0211 | 3.09 | up | 0.1060 | 3.23 | up | molecular chaperone DnaK\ Context:(NC_002946)+[1390552-1392480]\ Notes:heat shock protein 70; assists in folding of nascent polypeptide chains; refolding of misfolded proteins; utilizes ATPase activity to help fold; co-chaperones are DnaJ and GrpE; multiple copies in some bacteria |
| NGO1430 | 0.0198 | -18.33 | down | 0.0451 | -34.28 | down | 0.5453 | 1.95 | up | hypothetical protein\ Context:(NC_002946)+[1392703-1393950]\ Notes:Best Blastp Hit: gb\|AAA25906.1\| (M60717) nosA [Pseudomonas stutzeri] |
| NGO1431 | 0.2737 | -2.94 | down | 0.0746 | -8.29 | down | 0.2292 | 2.17 | up | hypothetical protein\ Context:(NC_002946)+[1393922-1394623]\ Notes:Best Blastp Hit: dbj\|BAA05664.1\| (D28119) outer membrane protein C [Pseudomonas aeruginosa] >gi\|9949962\|gb\|AAG07177.1\|AE004797_12 (AE004797) outer membrane protein OprC [Pseudomonas aeruginosa] |
| NGO1432 | 0.0801 | -5.84 | down | 0.0872 | -7.12 | down | 0.5420 | 1.50 | up | hypothetical protein\ Context:(NC_002946)+[1394680-1395657]\ Notes:Best Blastp Hit: pir\|\|D72405 hypothetical protein - Thermotoga maritima (strain MSB8) >gi\|4980699\|gb\|AAD35294.1\|AE001705_5 (AE001705) hypothetical protein [Thermotoga maritima] COG0715 Putative taurine-binding periplasmic |
| NGO1433 | 0.8788 | 1.14 | up | 0.1434 | -5.92 | down | 0.7295 | -1.52 | down | putative ABC transporter; permease protein\ Context:(NC_002946)+[1396210-1396911]\ Notes:Best Blastp Hit: gb\|AAG07323.1\|AE004811_6 (AE004811) probable permease of ABC taurine transporter [Pseudomonas aeruginosa] COG0600 Uncharacterized permeases |
| NGO1434 | 0.9658 | -1.02 | down | 0.6023 | -1.29 | down | 0.4318 | -1.28 | down | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)+[1397102-1397710]\ Notes:Best Blastp Hit: gb\|AAD31787.1\|AF126201_5 (AF126201) AtsC [Pseudomonas putida] COG1116 ABC-type nitrate transport system; ATPase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1435 | 0.5436 | 1.45 | up | 0.8601 | 1.09 | up | 0.7996 | 1.10 | up | CadB\ Context:(NC_002946)+[1397890-1398516]\ Notes:Best Blastp Hit: gb\|AAB51227.1\| (AF134905) CadD [Staphylococcus aureus]; putative cadmium resistance protein |
| NGO1437 | 0.3343 | -1.98 | down | 0.0006 | -33.03 | down | 0.2961 | -2.09 | down | primosome assembly protein PriA\ Context:(NC_002946)-[1399954-1402143]\ Notes:binding of PriA to forked DNA starts the assembly of the primosome; also possesses 3'-5' helicase activity |
| NGO1438 | 0.6293 | 1.25 | up | 0.9149 | -1.05 | down | 0.9794 | 1.01 | up | hypothetical protein\ Context:(NC_002946)+[1402283-1403068]\ Notes:Best Blastp Hit: gb\|AAF40979.1\| (AE002411) thiol:disulfide interchange protein DsbC [Neisseria meningitidis MC58] >gi\|7379452\|emb\|CAB84014.1\| (AL162754) putative thiol:disulphide interchange protein [Neisseria meningitidis] COG1651 protein-disulfide isomerases DsbC/DsbG |
| NGO1439 | 0.2776 | -1.94 | down | 0.4096 | -2.35 | down | 0.3204 | 1.91 | up | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)-[1403167-1405101]\ Notes:Best Blastp Hit: pir\|\|C81187 ABC transporter; ATP-binding protein NMB0549 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225775\|gb\|AAF40978.1\| (AE002410) ABC transporter; ATP-binding protein [Neisseria meningitidis MC58] COG0577 Predicted permease |
| NGO1440 | 0.0214 | 3.54 | up | 0.0356 | 2.29 | up | 0.1945 | 1.48 | up | putative ABC transporter; periplasmic protein\ Context:(NC_002946)-[1405167-1406345]\ Notes:Best Blastp Hit: emb\|CAB84012.1\| (AL162754) putative periplasmic protein [Neisseria meningitidis] COG0845 Membrane permeases; predicted cation efflux |
| NGO1441 | 0.7399 | 1.17 | up | 0.5516 | 1.23 | up | 0.5644 | -1.25 | down | putative type IV pilin protein\ Context:(NC_002946)+[1406571-1406960]\ Notes:Best Blastp Hit: emb\|CAB84011.1\| (AL162754) putative pilin [Neisseria meningitidis] |
| NGO1442 | 0.5717 | 1.33 | up | 0.9528 | 1.03 | up | 0.7687 | 1.09 | up | alcohol dehydrogenase\ Context:(NC_002946)+[1407240-1408280]\ Notes:similar to zinc-dependent eukaryotic ADH enzymes and distinct from fermentative ADHs |

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| NGO1443 | 0.1915 | 2.00 | up | 0.2139 | 2.91 | up | 0.8859 | -1.09 | down | hypothetical protein\ Context:(NC_002946)-[1408581-1412066]\ Notes:Best Blastp Hit: gb\|AAF40974.1\|(AE002410) conserved hypothetical protein [Neisseria meningitidis MC58] COG1196 Chromosome segregation ATPases |
| NGO1444 | 0.9236 | -1.06 | down | 0.0076 | -16.26 | down | 0.9267 | -1.08 | down | hypothetical protein\ Context:(NC_002946)+[1412050-1412229]\ Notes: |
| NGO1445 | 0.7532 | -1.17 | down | 0.9513 | 1.03 | up | 0.2116 | -1.45 | down | hypothetical protein\ Context:(NC_002946)+[1412494-1413162]\ Notes:Best Blastp Hit: gb\|AAG01335.1\|AF288222_1 (AF288222) putative outer membrane protein XadA [Xanthomonas oryzae pv. oryzae] |
| NGO1446 | 0.0074 | -10.41 | down | 0.0807 | -3.06 | down | 0.1979 | -3.05 | down | hypothetical protein\ Context:(NC_002946)+[1413134-1413619]\ Notes:Best Blastp Hit: sp\|P31489\|YADA_YEREN invasin precursor (outer membrane adhesin) >gi\|96987\|pir\|\|S04912 yopA protein - Yersinia enterocolitica plasmid pYV6471/76 >gi\|48607\|emb\|CAA32086.1\| (X13882) YadA [Yersinia enterocolitica] |
| NGO1447 | 0.0284 | -25.37 | down | 0.5193 | -1.65 | down | 0.8768 | 1.37 | up | hypothetical protein\ Context:(NC_002946)+[1413742-1413864]\ Notes: |
| NGO1448 | 0.1815 | -2.14 | down | 0.2144 | -2.64 | down | 0.6476 | -1.55 | down | UDP-2;3-diacylglucosamine hydrolase\ Context:(NC_002946)+[1413828-1414550]\ Notes:catalyzes the formation of 2;3=diacylglucosamine 1-phosphate from UDP-2;3=diacylglucosamine |
| NGO1449 | 0.9691 | 1.02 | up | 0.3799 | -1.37 | down | 0.6769 | -1.15 | down | LctP\ Context:(NC_002946)+[1414819-1416405]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG1620 L-lactate permease; putative L-lactate permease |
| NGO1450 | 0.7245 | 1.20 | up | 0.9557 | -1.02 | down | 0.4821 | -1.24 | down | hypothetical protein\ Context:(NC_002946)-[1416571-1416774]\ Notes:Best Blastp Hit: gb\|AAF40971.1\|(AE002410) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1451 | 0.4017 | -1.83 | down | 0.0319 | -8.64 | down | 0.7116 | -1.51 | down | hypothetical protein\ Context:(NC_002946)+[1416890-1417387]\ Notes:Best Blastp Hit: pir\|\|C81186 hypothetical protein NMB0541 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225767\|gb\|AAF40970.1\|(AE002410) hypothetical protein [Neisseria meningitidis MC58] |

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| NGO1452 | 0.3833 | 1.60 | up | 0.3224 | 1.39 | up | 0.5551 | 1.15 | up | aromatic amino acid aminotransferase\ Context:(NC_002946)+[1417469-1418659]\ Notes:catalyzes the formation of L-glutamate and an aromatic oxo acid from an aromatic amino acid and 2-oxoglutarate |
| NGO1454 | 0.1055 | 2.23 | up | 0.0694 | 2.17 | up | 0.1320 | 1.54 | up | lysyl-tRNA synthetase\ Context:(NC_002946)-[1419715-1421226]\ Notes:class II; LysRS2; catalyzes a two-step reaction; first charging a lysine molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA; in Methanosarcina barkeri; LysRS2 charges both tRNA molecules for lysine that exist in this organism and in addition can charge the tRNAPyl with lysine in the presence of LysRS1 |
| NGO1455 | 0.4761 | 1.62 | up | 0.2024 | -2.94 | down | 0.7305 | 1.31 | up | hypothetical protein\ Context:(NC_002946)-[1421381-1422634]\ Notes:Best Blastp Hit: gb\|AAF41787.1\| (AE002492) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380281\|emb\|CAB84867.1\| (AL162756) putative integral membrane protein [Neisseria meningitidis] |
| NGO1456 | 0.1996 | 2.15 | up | 0.2398 | 1.52 | up | 0.0328 | 2.21 | up | putative aminopeptidase\ Context:(NC_002946)+[1423093-1424889]\ Notes:Best Blastp Hit: pir\|\|D81858 probable aminopeptidase NMA1640 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380282\|emb\|CAB84868.1\| (AL162756) putative aminopeptidase [Neisseria meningitidis] COG0006 Xaa-Pro aminopeptidase |
| NGO1457 | 0.2173 | 1.86 | up | 0.3555 | 1.83 | up | 0.0894 | 2.14 | up | hypothetical protein\ Context:(NC_002946)+[1425019-1425291]\ Notes:Best Blastp Hit: gb\|AAF41506.1\| (AE002461) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1458 | 0.3544 | 1.73 | up | 0.8431 | -1.19 | down | 0.4079 | 2.62 | up | hypothetical protein\ Context:(NC_002946)+[1425288-1425692]\ Notes:Best Blastp Hit: emb\|CAB83729.1\| (AL162753) putative DNA helicase [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1459 | 0.0135 | -22.80 | down | 0.2670 | -1.82 | down | 0.2344 | 3.22 | up | hypothetical protein\ Context:(NC_002946)+[1425714-1425971]\ Notes:Best Blastp Hit: pir\|\|A81102 transcription-repair coupling factor NMB1281 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226520\|gb\|AAF41657.1\| (AE002476) transcription-repair coupling factor [Neisseria meningitidis MC58] |
| NGO1460 | 0.0714 | -4.20 | down | 0.6731 | -1.70 | down | 0.5780 | 1.52 | up | hypothetical protein\ Context:(NC_002946)+[1425993-1426172]\ Notes: |
| NGO1461 | 0.0504 | -4.76 | down | 0.0615 | -8.44 | down | 0.4841 | -1.48 | down | hypothetical protein\ Context:(NC_002946)-[1426490-1427032]\ Notes:Best Blastp Hit: gb\|AAF41506.1\| (AE002461) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1463 | 0.3992 | 2.26 | up | 0.6338 | -2.74 | down | 0.3804 | -4.25 | down | hypothetical protein\ Context:(NC_002946)+[1427461-1427640]\ Notes: |
| NGO1465 | 0.0014 | -25.54 | down | 0.0100 | -24.59 | down | 0.2565 | -1.81 | down | hypothetical protein\ Context:(NC_002946)-[1428738-1429151]\ Notes:Best Blastp Hit: gb\|AAD38303.1\|AF036242_3 (AF036242) unknown [Neisseria meningitidis] |
| NGO1466 | 0.2422 | -2.22 | down | 0.5789 | 1.59 | up | 0.3506 | -1.62 | down | bifunctionalphosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase\ Context:(NC_002946)-[1429169-1430749]\ Notes:involved in de novo purine biosynthesis |
| NGO1467 | 0.1993 | -2.19 | down | 0.0675 | -3.27 | down | 0.3862 | -1.34 | down | hypothetical protein\ Context:(NC_002946)-[1430910-1432052]\ Notes:Best Blastp Hit: gb\|AAF41386.1\| (AE002449) chloride channel protein-related protein [Neisseria meningitidis MC58] COG0038 Permease; putative chloride channel |
| NGO1468 | 0.1292 | 2.37 | up | 0.1057 | 1.82 | up | 0.7214 | -1.12 | down | hypothetical protein\ Context:(NC_002946)-[1432197-1433030]\ Notes:Best Blastp Hit: gb\|AAF41385.1\| (AE002449) phosphoserine phosphatase [Neisseria meningitidis MC58] COG0560 Phosphoserine phosphatase |
| NGO1469 | 0.5743 | -1.90 | down | 0.0261 | -8.28 | down | 0.8244 | -1.17 | down | hypothetical protein\ Context:(NC_002946)+[1433076-1433204]\ Notes:Best Blastp Hit: emb\|CAB84440.1\| (AL162755) hypothetical protein NMA1178 [Neisseria meningitidis] |

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| NGO1470 | 0.0140 | 3.99 | up | 0.1104 | 2.01 | up | 0.0431 | 2.04 | up | NAD(P) transhydrogenase subunit alpha\ Context:(NC_002946)+[1433319-1434857]\ Notes:forms a tetramer composed of 2 alpha subunits and 2 beta subunits in the inner membrane; involved in catalyzing transfer of hydride ion equivalents between NAD and NADP; stereospecific (AB-specific); functions as a proton pump by translocating protons from cytoplasm to periplasm |
| NGO1471 | 0.2435 | 1.76 | up | 0.0490 | 2.08 | up | 0.0987 | 2.05 | up | hypothetical protein\ Context:(NC_002946)+[1434861-1435244]\ Notes:Best Blastp Hit: pir\|\|E81134 hypothetical protein NMB0979 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226219\|gb\|AAF41383.1\| (AE002449) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1472 | 0.0089 | 4.64 | up | 0.0238 | 2.62 | up | 0.0295 | 2.69 | up | pyridine nucleotide transhydrogenase\ Context:(NC_002946)+[1435324-1436709]\ Notes:catalyzes reversible transfer of hydride ion equivalent between NAD and NADP; membrane-bound proton pump that translocates protons from cytosolic to periplasmic side of the inner membrane; forms a tetramer composed of two alpha and 2 beta subunits; AB-stereospecific enzyme |
| NGO1473 | 0.7675 | 1.15 | up | 0.7698 | 1.13 | up | 0.9227 | 1.03 | up | MdaB\ Context:(NC_002946)-[1436917-1437495]\ Notes:Best Blastp Hit: pir\|\|D81979 hypothetical protein NMA0600 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379335\|emb\|CAB83890.1\| (AL162753) hypothetical protein NMA0600 [Neisseria meningitidis] COG2249 Putative NADPH-quinone reductase; YabF; putative modulator of drug activity |
| NGO1474 | 0.0048 | -5.86 | down | 0.0767 | -6.55 | down | 0.2489 | -2.02 | down | LysR family transcriptional regulator\ Context:(NC_002946)+[1437734-1438645]\ Notes:Best Blastp Hit: pir\|\|E81979 probable lysR-family transcription regulator NMA0601 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379336\|emb\|CAB83891.1\| (AL162753) putative lysR-family transcriptional regulator [Neisseria meningitidis] COG0583 Transcriptional regulators; LysR family |

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| NGO1475 | 0.9247 | -1.06 | down | 0.0752 | -2.10 | down | 0.1187 | -1.92 | down | hypothetical protein\ Context:(NC_002946)-[1439310-1439669]\ Notes:Best Blastp Hit: pir\|\|B81195 conserved hypothetical protein NMB0479 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225707\|gb\|AAF40916.1\| (AE002404) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380635\|emb\|CAB85225.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] COG2018 Uncharacterized ACR; distantly related |
| NGO1476 | 0.0918 | -2.65 | down | 0.2851 | -1.83 | down | 0.4969 | -1.36 | down | hypothetical protein\ Context:(NC_002946)-[1439690-1440205]\ Notes:Best Blastp Hit: pir\|\|A81195 hypothetical protein NMB0478 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225706\|gb\|AAF40915.1\| (AE002404) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380636\|emb\|CAB85226.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1478 | 0.0305 | -4.56 | down | 0.8940 | -1.05 | down | 0.1473 | -3.36 | down | hypothetical protein\ Context:(NC_002946)-[1440881-1441126]\ Notes:Best Blastp Hit: pir\|\|G81194 hypothetical protein NMB0476 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225704\|gb\|AAF40913.1\| (AE002404) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380638\|emb\|CAB85228.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1479 | 0.0659 | -2.70 | down | 0.0600 | -2.76 | down | 0.0148 | -6.48 | down | hypothetical protein\ Context:(NC_002946)-[1441350-1441979]\ Notes:Best Blastp Hit: pir\|\|G81194 hypothetical protein NMB0476 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225704\|gb\|AAF40913.1\| (AE002404) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380638\|emb\|CAB85228.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1481 | 0.5491 | -1.61 | down | 0.2978 | 1.41 | up | 0.4599 | -1.80 | down | hypothetical protein\ Context:(NC_002946)-[1443640-1444422]\ Notes:Best Blastp Hit: emb\|CAB85230.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] COG0500 SAM-dependent methyltransferases |

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| NGO1482 | 0.8101 | -1.11 | down | 0.0982 | 2.27 | up | 0.4318 | -1.49 | down | hypothetical protein\ Context:(NC_002946)-[1444410-1445057]\ Notes:Best Blastp Hit: pir\|\|G81830 conserved hypothetical protein NMA2012 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380641\|emb\|CAB85231.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] |
| NGO1483 | 0.8391 | -1.11 | down | 0.4870 | -1.29 | down | 0.3830 | -1.60 | down | 8-amino-7-oxononanoate synthase\ Context:(NC_002946)-[1445067-1446209]\ Notes:catalyzes the formation of 8-amino-7-oxononanoate from 6-carboxyhexanoyl-CoA and L-alanine |
| NGO1484 | 0.0721 | -2.61 | down | 0.0767 | -2.62 | down | 0.1696 | -1.53 | down | hypothetical protein\ Context:(NC_002946)+[1446432-1447508]\ Notes:Best Blastp Hit: emb\|CAB85233.1\| (AL162757) hypothetical protein [Neisseria meningitidis] COG1376 Uncharacterized ACR; ErfK family |
| NGO1485 | 0.0161 | 4.25 | up | 0.0334 | 3.28 | up | 0.0830 | 2.13 | up | hypothetical protein\ Context:(NC_002946)-[1447712-1449178]\ Notes:Best Blastp Hit: pir\|\|A81194 C4-dicarboxylate transporter NMB0470 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225698\|gb\|AAF40907.1\| (AE002404) C4-dicarboxylate transporter [Neisseria meningitidis MC58] COG0471 Cation transporters |
| NGO1486 | 0.2563 | 1.89 | up | 0.0817 | 2.07 | up | 0.0782 | 2.18 | up | agmatinase\ Context:(NC_002946)-[1449376-1450299]\ Notes:catalyzes the formation of putrescine from agmatine |
| NGO1487 | 0.0384 | 3.24 | up | 0.0149 | 2.91 | up | 0.0598 | 1.98 | up | arginine decarboxylase\ Context:(NC_002946)-[1450398-1452290]\ Notes:catalyzes the formation of agmatine from arginine in putrescine and spermidine biosynthesis |
| NGO1488 | 0.7389 | -1.28 | down | 0.7535 | -1.15 | down | 0.5499 | -1.73 | down | hypothetical protein\ Context:(NC_002946)-[1452457-1452741]\ Notes:Best Blastp Hit: gb\|AAF40904.1\| (AE002403) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1489 | 0.1381 | 2.14 | up | 0.0610 | 3.63 | up | 0.2186 | 1.69 | up | aspartyl-tRNA synthetase\ Context:(NC_002946)-[1452891-1454441]\ Notes:Catalyzes a two-step reaction; first charging an aspartate molecule by linking its carboxyl group to the alpha-phosphate of ATP; followed by transfer of the aminoacyl-adenylate to its tRNA |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1490 | 0.4077 | 1.43 | up | 0.8498 | -1.08 | down | 0.9217 | -1.03 | down | putative aspartyl-tRNA synthetase\ Context:(NC_002946)-[1454443-1454697]\ Notes:Best Blastp Hit: pir\|\|F81831 aspartate--tRNA ligase (EC 6.1.1.12) NMA2019 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380648\|emb\|CAB85238.1\| (AL162757) |
| NGO1491 | 0.4249 | 1.54 | up | 0.3620 | 1.48 | up | 0.9473 | -1.02 | down | hypothetical protein\ Context:(NC_002946)-[1454755-1455492]\ Notes:Best Blastp Hit: pir\|\|G81831 probable integral membrane protein NMA2020 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380649\|emb\|CAB85239.1\| (AL162757) putative integral membrane protein [Neisseria meningitidis] |
| NGO1492 | 0.9737 | -1.02 | down | 0.3459 | -1.47 | down | 0.3620 | -1.33 | down | putative phospholipase\ Context:(NC_002946)-[1455598-1456746]\ Notes:Best Blastp Hit: emb\|CAB85240.1\| (AL162757) putative phopholipase [Neisseria meningitidis] |
| NGO1493 | 0.0749 | 3.10 | up | 0.2084 | 1.75 | up | 0.2008 | 1.50 | up | 30S ribosomal protein S20\ Context:(NC_002946)-[1456906-1457169]\ Notes:binds directly to the 16S rRNA and is involved in post-translational inhibition of arginine and ornithine decarboxylase |
| NGO1494 | 0.1401 | 2.35 | up | 0.3173 | 1.43 | up | 0.2787 | 1.61 | up | putative ABC transporter; periplasmic binding protein; polyamine\ Context:(NC_002946)+[1457473-1458615]\ Notes:Best Blastp Hit: pir\|\|C81195 spermidine/putrescine ABC transporter; periplasmic spermidine/putrescine-binding protein NMB0462 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225689\|gb\|AAF40899.1\| (AE002403) spermidine/putrescine ABC transporter; periplasmic spermidine/putrescine-binding protein [Neisseria meningitidis MC58] COG0687 Spermidine/putrescine-binding periplasmic |
| NGO1495 | 0.0007 | 12.12 | up | 0.0013 | 7.11 | up | 0.0011 | 7.36 | up | TbpA\ Context:(NC_002946)-[1460228-1462966]\ Notes:Best Blastp Hit: gb\|AAF74987.1\| (AF124339) transferrin-binding protein A [Neisseria gonorrhoeae] COG1629 Outer membrane receptor proteins; mostly |
| NGO1496 | 0.0005 | 13.85 | up | 0.0005 | 10.24 | up | 0.0014 | 8.79 | up | TbpB\ Context:(NC_002946)-[1463053-1465164]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON); transferrin-binding protein B |
| NGO1497 | 0.5650 | -2.34 | down | 0.5911 | -1.33 | down | 0.4151 | -2.60 | down | hypothetical protein\ Context:(NC_002946)-[1465247-1465390]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1498 | 0.0131 | 12.95 | up | 0.1154 | 3.74 | up | 0.1111 | 1.84 | up | hypothetical protein\ Context:(NC_002946)-[1465500-1465661]\ Notes:Best Blastp Hit: emb\|CAB83896.1\|(AL162753) hypothetical protein NMA0606 [Neisseria meningitidis] |
| NGO1499 | 0.9722 | 1.02 | up | 0.2582 | -2.05 | down | 0.8543 | -1.09 | down | hypothetical protein\ Context:(NC_002946)+[1467069-1468178]\ Notes:Best Blastp Hit: emb\|CAB84863.1\|(AL162756) hypothetical protein [Neisseria meningitidis] |
| NGO1500 | 0.1493 | -2.24 | down | 0.0208 | -4.37 | down | 0.1058 | -2.19 | down | glutamate racemase\ Context:(NC_002946)-[1468907-1469719]\ Notes:converts L-glutamate to D-glutamate; a component of peptidoglycan |
| NGO1501 | 0.8727 | -1.09 | down | 0.6295 | -1.27 | down | 0.0843 | -2.17 | down | hypothetical protein\ Context:(NC_002946)+[1469908-1470369]\ Notes:Best Blastp Hit: pir\|\|F81832 conserved hypothetical protein NMA2027 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380656\|emb\|CAB85246.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] COG0802 Predicted nucleotide-binding protein; YjeE |
| NGO1502 | 0.2448 | -2.07 | down | 0.2060 | -1.94 | down | 0.1439 | -1.61 | down | putative amidase\ Context:(NC_002946)+[1470318-1471616]\ Notes:Best Blastp Hit: gb\|AAF06680.1\|AF163663_5 (AF058689) putative N-acetylmuramoyl-L-alanine amidase-precursor AmiC [Neisseria meningitidis] COG0860 N-acetylmuramoyl-L-alanine amidase |
| NGO1503 | 0.4852 | 1.46 | up | 0.4260 | 1.30 | up | 0.8088 | -1.09 | down | hypothetical protein\ Context:(NC_002946)+[1471644-1472516]\ Notes:Best Blastp Hit: emb\|CAB85248.1\|(AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1504 | 0.3348 | 1.53 | up | 0.4639 | 1.26 | up | 0.4330 | 1.23 | up | hypothetical protein\ Context:(NC_002946)-[1472562-1473704]\ Notes:Best Blastp Hit: gb\|AAF40892.1\|(AE002401) conserved hypothetical protein [Neisseria meningitidis MC58] COG0116 Predicted N6-adenine-specific DNA |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1505 | 0.9996 | -1.00 | down | 0.6673 | -1.16 | down | 0.8187 | -1.11 | down | hypothetical protein\ Context:(NC_002946)-[1473753-1474175]\ Notes:Best Blastp Hit: pir\|\|H81197 probable secreted protein NMA2031; NMB0454 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|6274535\|gb\|AAF06683.1\|AF163663_8 (AF058689) Tou4 [Neisseria meningitidis] >gi\|6449089\|gb\|AAF08818.1\|AF194079_5 (AF194079) Tou4 putative secreted protein [Neisseria meningitidis] |
| NGO1506 | 0.7761 | 1.13 | up | 0.3459 | 1.38 | up | 0.9516 | -1.02 | down | putative NTP pyrophosphohydrolase\ Context:(NC_002946)-[1474168-1474977]\ Notes:Best Blastp Hit: gb\|AAF40890.1\| (AE002401) mutT protein [Neisseria meningitidis MC58] COG0494 NTP pyrophosphohydrolases (MutT family) |
| NGO1507 | 0.2157 | 1.91 | up | 0.7955 | 1.15 | up | 0.4273 | 1.27 | up | putative acyl-carrier protein synthase\ Context:(NC_002946)-[1475059-1475436]\ Notes:Best Blastp Hit: pir\|\|F81197 holo-(acyl-carrier protein) synthase NMB0452 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|6449091\|gb\|AAF08820.1\|AF194079_7 (AF194079) Dpj [Neisseria meningitidis] >gi\|7225677\|gb\|AAF40889.1\| (AE002401) holo-(acyl-carrier protein) synthase [Neisseria meningitidis MC58] COG0736 Acyl-carrier protein synthase |
| NGO1508 | 0.8768 | 1.07 | up | 0.1858 | 1.71 | up | 0.8209 | 1.06 | up | pyridoxal phosphate biosynthetic protein PdxJ\ Context:(NC_002946)-[1475486-1476214]\ Notes:involved in the de novo synthesis of pyridoxine (Vitamin B6) |
| NGO1509 | 0.1394 | 2.78 | up | 0.4106 | 1.45 | up | 0.4411 | -1.23 | down | hypothetical protein\ Context:(NC_002946)-[1476267-1477010]\ Notes:Best Blastp Hit: sp\|Q9ZHY2\|RECO_NEIGO DNA repair protein RECO (recombination protein O) >gi\|4105531\|gb\|AAD05426.1\| (AF047375) RecO [Neisseria gonorrhoeae] COG1381 Recombination protein RecO |
| NGO1510 | 0.6834 | 1.22 | up | 0.9438 | -1.03 | down | 0.6471 | -1.14 | down | putative chorismate mutase\ Context:(NC_002946)-[1477047-1478174]\ Notes:Best Blastp Hit: gb\|AAD05425.1\| (AF047375) PheA [Neisseria gonorrhoeae] COG0077 Prephenate dehydratase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1511 | 0.0224 | -3.57 | down | 0.0200 | -3.69 | down | 0.0591 | -2.06 | down | putative drug resistance protein\ Context:(NC_002946)-[1477747-1479249]\ Notes:Best Blastp Hit: gb\|AAF08825.1\|AF194079_12 (AF194079) Bcr [Neisseria meningitidis] COG0477 Permeases |
| NGO1512 | 0.3679 | -1.94 | down | 0.0905 | -2.77 | down | 0.1475 | -3.06 | down | hypothetical protein\ Context:(NC_002946)-[1479533-1480408]\ Notes:Best Blastp Hit: gb\|AAF40881.1\|(AE002400) conserved hypothetical protein [Neisseria meningitidis MC58] COG0697 Predicted permeases |
| NGO1513 | 0.1085 | 3.05 | up | 0.1086 | 2.03 | up | 0.2274 | 1.77 | up | OpaD\ Context:(NC_002946)+[1481445-1482281]\ Notes:Best Blastp Hit: phase variable - 13 tandem repeats of CTCTT in the coding sequence (ON); outer membrane opacity protein D |
| NGO1514 | 0.0605 | -2.69 | down | 0.0869 | -1.87 | down | 0.0055 | -2.64 | down | hypothetical protein\ Context:(NC_002946)-[1482948-1483862]\ Notes:Best Blastp Hit: pir\|\|B81199 nitrilase NMB0441 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225666\|gb\|AAF40879.1\| (AE002400) nitrilase [Neisseria meningitidis MC58] COG0388 Predicted amidohydrolase |
| NGO1515 | 0.2406 | 1.96 | up | 0.1101 | -2.13 | down | 0.7056 | -1.24 | down | putative oxidoreductase\ Context:(NC_002946)+[1483845-1484717]\ Notes:Best Blastp Hit: pir\|\|A81775 probable oxidoreductase NMA2045 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380673\|emb\|CAB85263.1\| (AL162758) putative oxidoreductase [Neisseria meningitidis] COG0287 Prephenate dehydrogenase |
| NGO1516 | 0.0008 | -22.21 | down | 0.0006 | -28.07 | down | 0.0079 | -7.59 | down | hypothetical protein\ Context:(NC_002946)-[1484775-1485977]\ Notes:Best Blastp Hit: emb\|CAB85264.1\|(AL162758) hypothetical integral membrane protein [Neisseria meningitidis] |
| NGO1517 | 0.7362 | -1.19 | down | 0.2565 | -1.77 | down | 0.2974 | -1.48 | down | hypothetical protein\ Context:(NC_002946)-[1485974-1486342]\ Notes:Best Blastp Hit: pir\|\|C81775 hypothetical protein NMA2047 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380675\|emb\|CAB85265.1\|(AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1518 | 0.0041 | -7.57 | down | 0.0518 | -5.08 | down | 0.7923 | -1.31 | down | hypothetical protein\ Context:(NC_002946)-[1486339-1487112]\ Notes:Best Blastp Hit: emb\|CAB63177.1\|(AL133469) hypothetical protein SCM10.16c [Streptomyces coelicolor A3(2)] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1519 | 0.7430 | -1.22 | down | 0.3750 | -1.38 | down | 0.1503 | -1.66 | down | hypothetical protein\ Context:(NC_002946)+[1486516-1486959]\ Notes:Best Blastp Hit: pir\|\|D81775 conserved hypothetical protein NMA2048 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380676\|emb\|CAB85266.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] COG1959 Uncharacterized BCR; YjeB/RRF2 family |
| NGO1520 | 0.5583 | -1.31 | down | 0.2223 | -1.77 | down | 0.1191 | -2.20 | down | hypothetical protein\ Context:(NC_002946)-[1487121-1487825]\ Notes:Best Blastp Hit: pir\|\|E81198 conserved hypothetical protein NMB0436 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225661\|gb\|AAF40874.1\| (AE002400) conserved hypothetical protein [Neisseria meningitidis MC58] COG0009 Putative translation factor (SUA5) |
| NGO1521 | 0.1642 | -2.81 | down | 0.0016 | -14.09 | down | 0.5842 | -1.56 | down | putative acetate kinase\ Context:(NC_002946)-[1487852-1489051]\ Notes:Best Blastp Hit: pir\|\|D81198 acetate kinase NMB0435 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225660\|gb\|AAF40873.1\| (AE002400) acetate kinase [Neisseria meningitidis MC58] COG0282 Acetate kinase |
| NGO1524 | 0.0183 | -6.09 | down | 0.0987 | -4.08 | down | 0.8279 | -1.11 | down | hypothetical protein\ Context:(NC_002946)-[1493757-1494545]\ Notes:Best Blastp Hit: gb\|AAF40870.1\| (AE002399) conserved hypothetical protein [Neisseria meningitidis MC58] COG0730 Predicted permeases |
| NGO1525 | 0.7051 | 1.46 | up | 0.0607 | -14.73 | down | 0.7891 | -1.47 | down | methylcitrate synthase\ Context:(NC_002946)-[1494697-1495845]\ Notes:catalyzes the synthesis of 2-methylcitrate from propionyl-CoA and oxaloacetate; also catalyzes the condensation of oxaloacetate with acetyl-CoA but with a lower specificity |
| NGO1526 | 0.0500 | -4.57 | down | 0.0093 | -18.43 | down | 0.7756 | -1.23 | down | 2-methylisocitrate lyase\ Context:(NC_002946)-[1495930-1496808]\ Notes:catalyzes the formation of pyruvate and succinate from 2-methylisocitrate |
| NGO1527 | 0.4690 | 1.51 | up | 0.9025 | -1.08 | down | 0.8319 | 1.07 | up | hypothetical protein\ Context:(NC_002946)-[1497426-1498736]\ Notes:Best Blastp Hit: pir\|\|D81776 conserved hypothetical protein NMA2056 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380684\|emb\|CAB85274.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] COG2252 Permeases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1528 | 0.1606 | 2.12 | up | 0.6315 | -1.30 | down | 0.6616 | 1.13 | up | cell division protein FtsZ\ Context:(NC_002946)-[1498872-1500050]\ Notes:GTPase; similar structure to tubulin; forms ring-shaped polymers at the site of cell division; other proteins such as FtsA; ZipA; and ZapA; interact with and regulate FtsZ function |
| NGO1529 | 0.3311 | 1.63 | up | 0.1156 | -2.35 | down | 0.8611 | 1.05 | up | hypothetical protein\ Context:(NC_002946)-[1500169-1501413]\ Notes:Best Blastp Hit: pir\|\|E81201 cell division protein FtsA NMB0426 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225649\|gb\|AAF40864.1\|(AE002398) cell division protein FtsA [Neisseria meningitidis MC58] COG0849 Predicted ATPases of the HSP70 class |
| NGO1530 | 0.8858 | -1.08 | down | 0.8186 | -1.14 | down | 0.3891 | -1.41 | down | hypothetical protein\ Context:(NC_002946)-[1501499-1502227]\ Notes:Best Blastp Hit: pir\|\|G81776 cell division protein NMA2059 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380687\|emb\|CAB85277.1\|(AL162758) cell division protein [Neisseria meningitidis] COG1589 Cell division septal protein FtsQ |
| NGO1531 | 0.3167 | 2.23 | up | 0.3498 | -1.64 | down | 0.4848 | -1.38 | down | D-alanine--D-alanine ligase\ Context:(NC_002946)-[1502217-1503131]\ Notes:D-alanine--D-alanine ligase; DdlA; DdlB; cytoplasmic; catalyzes the formation of D-alanyl-D-alanine from two D-alanines in peptidoglycan synthesis; there are two forms of this enzyme in Escherichia coli |
| NGO1532 | 0.7000 | 1.24 | up | 0.9800 | -1.01 | down | 0.6314 | 1.15 | up | UDP-N-acetylmuramate--L-alanine ligase\ Context:(NC_002946)-[1503243-1504652]\ Notes:Catalyzes the formation of UDP-N-acetylmuramoyl-L-alanine from UDP-N-acetylmuramate and L-alanine in peptidoglycan synthesis |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1533 | 0.3779 | 1.49 | up | 0.2722 | -1.74 | down | 0.5767 | 1.17 | up | hypothetical protein\ Context:(NC_002946)-[1504807-1505874]\ Notes:Best Blastp Hit: pir\|\|A81201 UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase NMB0422 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225645\|gb\|AAF40860.1\|(AE002398) UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Neisseria meningitidis MC58] COG0707 UDP-glucuronosyltransferases |
| NGO1534 | 0.2274 | -2.39 | down | 0.2441 | -1.82 | down | 0.6096 | -1.24 | down | hypothetical protein\ Context:(NC_002946)-[1505878-1507176]\ Notes:Best Blastp Hit: pir\|\|C81777 cell division protein NMA2063 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380691\|emb\|CAB85281.1\|(AL162758) cell division protein [Neisseria meningitidis] COG0772 Bacterial cell division membrane protein |
| NGO1535 | 0.1013 | 3.33 | up | 0.0429 | 3.11 | up | 0.1356 | 2.32 | up | UDP-N-acetylmuramoyl-L-alanyl-D-glutamatesynthetase\ Context:(NC_002946)-[1507328-1508665]\ Notes:UDP-N-acetylmuramoylalanine--D-glutamate ligase; involved in peptidoglycan biosynthesis; cytoplasmic; catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine during cell wall formation |
| NGO1536 | 0.0362 | 4.08 | up | 0.0720 | 4.95 | up | 0.0715 | 4.51 | up | hypothetical protein\ Context:(NC_002946)-[1508750-1509130]\ Notes:Best Blastp Hit: gb\|AAF40857.1\|(AE002398) conserved hypothetical protein [Neisseria meningitidis MC58] COG0790 TPR repeat proteins |
| NGO1537 | 0.7849 | 1.18 | up | 0.2096 | 2.00 | up | 0.0667 | 4.87 | up | phospho-N-acetylmuramoyl-pentapeptide-transferase\ Context:(NC_002946)-[1509255-1510337]\ Notes:First step of the lipid cycle reactions in the biosynthesis of the cell wall peptidoglycan |
| NGO1538 | 0.0344 | 3.07 | up | 0.0248 | 3.75 | up | 0.1049 | 2.14 | up | hypothetical protein\ Context:(NC_002946)-[1510582-1510764]\ Notes:Best Blastp Hit: emb\|CAB85285.1\|(AL162758) putative periplasmic protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1539 | 0.0889 | 2.24 | up | 0.0152 | 2.63 | up | 0.0552 | 2.00 | up | putative UDP-MurNAc-pentapeptide synthetase\ Context:(NC_002946)-[1510761-1512119]\ Notes:Best Blastp Hit: emb\|CAB85286.1\| (AL162758) UDP-MurNAc-pentapeptide synthetase [Neisseria meningitidis] COG0770 UDP-N-acetylmuramyl pentapeptide synthase |
| NGO1540 | 0.0051 | 7.85 | up | 0.0157 | 4.58 | up | 0.2637 | 1.85 | up | Dca\ Context:(NC_002946)-[1512244-1513890]\ Notes:Best Blastp Hit: gb\|AAF12796.1\|AF195057_1 (AF195057) DcaA [Neisseria gonorrhoeae] COG2194 Predicted membrane-associated; division cell wall protein |
| NGO1541 | 0.0086 | 4.31 | up | 0.0175 | 7.26 | up | 0.0323 | 2.63 | up | UDP-N-acetylmuramoylalanyl-D-glutamate--2; 6-diaminopimelate ligase\ Context:(NC_002946)-[1513913-1515391]\ Notes:involved in cell wall formation; peptidoglycan synthesis; cytoplasmic enzyme; catalyzes the addition of meso-diaminopimelic acid to the nucleotide precursor UDP-N-aceylmuramoyl-l-alanyl-d-glutamate |
| NGO1542 | 0.1269 | 2.06 | up | 0.9548 | -1.03 | down | 0.3742 | 1.28 | up | Pbp2\ Context:(NC_002946)-[1515416-1517164]\ Notes:Best Blastp Hit: pir\|\|S49090 penicillin-binding protein 2 - Neisseria gonorrhoeae >gi\|509155\|emb\|CAA42191.1\| (X59632) penicillin-binding protein 2 [Neisseria gonorrhoeae] COG0768 Cell division protein |
| NGO1543 | 0.1240 | 2.39 | up | 0.1483 | 1.82 | up | 0.2794 | 1.39 | up | hypothetical protein\ Context:(NC_002946)-[1517225-1517488]\ Notes:Best Blastp Hit: gb\|AAF40851.1\| (AE002397) cell division protein FtsL-related protein [Neisseria meningitidis MC58] >gi\|7380699\|emb\|CAB85290.1\| (AL162758) putative small periplasmic protein [Neisseria meningitidis] |
| NGO1544 | 0.1536 | 1.96 | up | 0.4385 | 1.40 | up | 0.2747 | 1.38 | up | S-adenosyl-methyltransferase MraW\ Context:(NC_002946)-[1517515-1518471]\ Notes:Best Blastp Hit: pir\|\|D81778 conserved hypothetical protein NMA2074 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380700\|emb\|CAB85291.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] COG0275 Predicted S-adenosylmethionine-dependent |
| NGO1545 | 0.2109 | 2.00 | up | 0.2814 | 1.56 | up | 0.3380 | 1.43 | up | cell division protein MraZ\ Context:(NC_002946)-[1518468-1518923]\ Notes:MraZ; UPF0040; crystal structure shows similarity to AbrB |

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| NGO1546 | 0.8241 | 1.25 | up | 0.8407 | 1.25 | up | 0.6712 | -1.64 | down | hypothetical protein\ Context:(NC_002946)+[1519202-1520449]\ Notes:Best Blastp Hit: pir\|\|F81778 conserved hypothetical protein NMA2076 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380702\|emb\|CAB85293.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] COG1565 Uncharacterized ACR |
| NGO1547 | 0.5775 | 1.81 | up | 0.1329 | -2.78 | down | 0.9090 | 1.08 | up | hypothetical protein\ Context:(NC_002946)-[1520890-1521711]\ Notes:Best Blastp Hit: pir\|\|E81203 bacitracin resistance protein NMB0408 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225630\|gb\|AAF40847.1\| (AE002396) bacitracin resistance protein [Neisseria meningitidis MC58] COG1968 Uncharacterized ACR; bacitracin resistance |
| NGO1548 | 0.9784 | 1.01 | up | 0.9081 | 1.05 | up | 0.9179 | 1.03 | up | DsbA\ Context:(NC_002946)-[1521744-1522388]\ Notes:Best Blastp Hit: gb\|AAF40846.1\| (AE002396) thiol:disulfide interchange protein DsbA [Neisseria meningitidis MC58] COG0526 Thiol-disulfide isomerase and thioredoxins; putative thiol-disulfide isomerase |
| NGO1549 | 0.6036 | -1.27 | down | 0.9191 | -1.05 | down | 0.6388 | 1.15 | up | hypothetical protein\ Context:(NC_002946)-[1522391-1523260]\ Notes:Best Blastp Hit: pir\|\|C81203 conserved hypothetical protein NMB0406 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225628\|gb\|AAF40845.1\| (AE002396) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1550 | 0.7861 | 1.16 | up | 0.7115 | 1.18 | up | 0.3098 | 1.37 | up | hypothetical protein\ Context:(NC_002946)-[1523360-1524856]\ Notes:Best Blastp Hit: pir\|\|B81779 probable chelatase NMA2080 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380706\|emb\|CAB85297.1\| (AL162758) putative chelatase [Neisseria meningitidis] COG0606 Predicted ATPases |
| NGO1551 | 0.6656 | -1.38 | down | 0.6530 | -1.25 | down | 0.3770 | -1.42 | down | hypothetical protein\ Context:(NC_002946)-[1524870-1525526]\ Notes:Best Blastp Hit: emb\|CAB85298.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1552 | 0.0061 | -6.40 | down | 0.0131 | -7.50 | down | 0.0150 | -7.51 | down | putative sodium/proline symporter; proline permease\ Context:(NC_002946)+[1525688-1527205]\ Notes:Best Blastp Hit: pir\|\|G81202 sodium/proline symporter NMB0402 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225624\|gb\|AAF40841.1\| (AE002396) |
| NGO1557 | 0.0730 | -5.62 | down | 0.1277 | -3.98 | down | 0.1401 | -2.95 | down | hypothetical protein\ Context:(NC_002946)+[1532654-1532992]\ Notes: |
| NGO1558 | 0.2022 | -2.87 | down | 0.0036 | -15.55 | down | 0.0776 | -4.75 | down | hypothetical protein\ Context:(NC_002946)-[1533130-1533348]\ Notes: |
| NGO1559 | 0.0333 | 4.07 | up | 0.0789 | 3.01 | up | 0.0097 | 3.95 | up | hypothetical protein\ Context:(NC_002946)+[1533468-1534145]\ Notes:Best Blastp Hit: gb\|AAC33455.1\| (AF067083) outer membrane protein homolog [Vitreoscilla sp.] COG1360 Flagellar motor protein MotB |
| NGO1560 | 0.0918 | 6.55 | up | 0.2753 | -6.06 | down | 0.5017 | 3.65 | up | hypothetical protein\ Context:(NC_002946)+[1534233-1534379]\ Notes: |
| NGO1561 | 0.0314 | -2.98 | down | 0.7226 | 1.12 | up | 0.4858 | -1.46 | down | putative exodeoxyribonuclease III\ Context:(NC_002946)-[1534419-1535189]\ Notes:Best Blastp Hit: pir\|\|G81204 exodeoxyribonuclease III NMB0399 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225621\|gb\|AAF40839.1\| (AE002395) exodeoxyribonuclease III [Neisseria meningitidis MC58] COG0708 Exonuclease III |
| NGO1562 | 0.8586 | 1.14 | up | 0.7227 | 1.24 | up | 0.3649 | -1.45 | down | ArsR family transcriptional regulator\ Context:(NC_002946)-[1535249-1535530]\ Notes:Best Blastp Hit: gb\|AAF40838.1\| (AE002395) transcriptional regulator; ArsR family [Neisseria meningitidis MC58] COG0640 Predicted transcriptional regulators |
| NGO1563 | 0.0343 | -3.68 | down | 0.0073 | -5.54 | down | 0.1930 | 1.94 | up | hypothetical protein\ Context:(NC_002946)+[1535587-1535772]\ Notes: |
| NGO1564 | 0.4837 | 1.66 | up | 0.1381 | -5.10 | down | 0.3042 | 1.73 | up | hypothetical protein\ Context:(NC_002946)+[1535783-1536034]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1565 | 0.0490 | 3.10 | up | 0.0452 | 3.21 | up | 0.1369 | 1.66 | up | putative nicotinate-nucleotide pyrophosphorylase\ Context:(NC_002946)-[1536265-1537146]\ Notes:Best Blastp Hit: pir\|\|A81780 nicotinate-nucleotide pyrophosphorylase (carboxylating) (EC 2.4.2.19) NMA2088 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380713\|emb\|CAB85304.1\| (AL162758) nicotinate-nucleotide pyrophosphorylase [Neisseria meningitidis] COG0157 Nicotinate-nucleotide pyrophosphorylase |
| NGO1566 | 0.7770 | 1.12 | up | 0.6166 | 1.21 | up | 0.7396 | 1.12 | up | hypothetical protein\ Context:(NC_002946)-[1537222-1538160]\ Notes:Best Blastp Hit: pir\|\|C81204 conserved hypothetical protein NMB0395 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225617\|gb\|AAF40835.1\| (AE002395) conserved hypothetical protein [Neisseria meningitidis MC58] COG1051 ADP-ribose pyrophosphatase |
| NGO1567 | 0.3752 | 1.52 | up | 0.3110 | -1.69 | down | 0.8306 | -1.05 | down | quinolinate synthetase\ Context:(NC_002946)+[1538362-1539474]\ Notes:3 different subfamilies; catalyzes the formation of quinolinate from iminoaspartate and dihydroxyacetone phosphate |
| NGO1568 | 0.0954 | 2.39 | up | 0.2429 | 1.85 | up | 0.0735 | 1.82 | up | hypothetical protein\ Context:(NC_002946)+[1539526-1541034]\ Notes:Best Blastp Hit: pir\|\|H81203 l-aspartate oxidase NMB0392 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225614\|gb\|AAF40832.1\| (AE002395) l-aspartate oxidase [Neisseria meningitidis MC58] COG0029 Aspartate oxidase |
| NGO1573 | 0.0731 | 2.69 | up | 0.0913 | 7.93 | up | 0.1588 | 1.71 | up | putative ABC transporter ATP-binding protein\ Context:(NC_002946)+[1547577-1549253]\ Notes:ChvD; in Agrobacterium tumefaciens; mutations in both Walker boxes were found to affect virulence |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1574 | 0.7320 | 1.34 | up | 0.3316 | 1.67 | up | 0.6564 | -1.19 | down | hypothetical protein\ Context:(NC_002946)-[1549313-1549798]\ Notes:Best Blastp Hit: pir\|\|G81205 phosphatidylglycerophosphatase (EC 3.1.3.27) A NMA2102 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225607\|gb\|AAF40826.1\| (AE002394) phosphatidylglycerophosphatase A [Neisseria meningitidis MC58] >gi\|7380727\|emb\|CAB85318.1\| (AL162758) phosphatidylglycerophosphatase A [Neisseria meningitidis] COG1267 Phosphatidylglycerophosphatase A |
| NGO1575 | 0.8907 | -1.07 | down | 0.1846 | -1.90 | down | 0.5109 | -1.23 | down | thiamine monophosphate kinase\ Context:(NC_002946)-[1549791-1550747]\ Notes:catalyzes the formation of thiamine diphosphate from thiamine phosphate ant ATP |
| NGO1576 | 0.0006 | -33.69 | down | 0.0026 | -19.49 | down | 0.0956 | -2.62 | down | hypothetical protein\ Context:(NC_002946)+[1551327-1551491]\ Notes: |
| NGO1577 | 0.2256 | 2.06 | up | 0.5320 | 1.28 | up | 0.6748 | 1.17 | up | Omp3\ Context:(NC_002946)-[1551522-1552232]\ Notes:Best Blastp Hit: sp\|P07050\|OMP3_NEIGO outer membrane protein P.III precursor (gonococcal protein III) (PIII) >gi\|78109\|pir\|\|A27894 outer membrane protein PIII precursor - Neisseria gonorrhoeae >gi\|44890\|emb\|CAA28752.1\| (X05105) PIII (AA 1-236) [Neisseria gonorrhoeae] COG1360 Flagellar motor protein MotB |
| NGO1578 | 0.0391 | -2.98 | down | 0.2009 | -1.91 | down | 0.7461 | -1.20 | down | transcriptional regulator CysB-like protein\ Context:(NC_002946)+[1552596-1553546]\ Notes:Best Blastp Hit: pir\|\|B81782 transcription regulator NMA2106 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380730\|emb\|CAB85321.1\| (AL162758) transcriptional regulator [Neisseria meningitidis] COG0583 Transcriptional regulators; LysR family |
| NGO1579 | 0.8333 | 1.12 | up | 0.9480 | -1.03 | down | 0.9633 | -1.01 | down | putative anaerobic transcriptional regulator\ Context:(NC_002946)-[1553659-1554393]\ Notes:Best Blastp Hit: gb\|AAF40820.1\| (AE002394) transcriptional regulator; Crp/Fnr family [Neisseria meningitidis MC58] >gi\|7380731\|emb\|CAB85322.1\| (AL162758) putative anaerobic transcriptional regulatory protein [Neisseria meningitidis] COG0664 cAMP-binding domains - Catabolite gene |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1580 | 0.6879 | 1.31 | up | 0.3262 | 1.94 | up | 0.2294 | 1.62 | up | coproporphyrinogen III oxidase\ Context:(NC_002946)+[1554528-1555949]\ Notes:catalyzes the oxygen-independent formation of protoporphyrinogen-IX from coproporphyrinogen-III |
| NGO1581 | 0.7213 | -1.25 | down | 0.7082 | -1.16 | down | 0.5348 | -1.35 | down | putative transport protein\ Context:(NC_002946)-[1556189-1557763]\ Notes:Best Blastp Hit: gb\|AAF40818.1\|(AE002393) phosphate permease; putative [Neisseria meningitidis MC58] >gi\|7380733\|emb\|CAB85324.1\|(AL162758) putative phosphate permease [Neisseria meningitidis] COG0306 Phosphate permease |
| NGO1582 | 0.4881 | -1.87 | down | 0.1006 | -4.09 | down | 0.7715 | 1.23 | up | hypothetical protein\ Context:(NC_002946)+[1557793-1557990]\ Notes: |
| NGO1583 | 0.6438 | -1.25 | down | 0.0166 | -4.94 | down | 0.1212 | -2.55 | down | anhydro-N-acetylmuramic acid kinase\ Context:(NC_002946)+[1558058-1559188]\ Notes:catalyzes hydrolysis of 1;6-anhydro bond of anyhydro-N-acetylmuramic acid (anhMurNAc) and phosphorylates anhMurNAc to produce N-acetyl-muramate-6-phosphate; involved in murein recycling |
| NGO1585 | 0.9733 | -1.02 | down | 0.1044 | 3.08 | up | 0.4332 | 1.78 | up | MafB4\ Context:(NC_002946)+[1560252-1561982]\ Notes:Best Blastp Hit: pir\|\|H81782 adhesin MafB2 NMA2113 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380736\|emb\|CAB85327.1\| (AL162758) adhesin MafB2 [Neisseria meningitidis]; putative MafB-like adhesin |
| NGO1586 | 0.2452 | 1.99 | up | 0.1266 | 9.25 | up | 0.4041 | 2.70 | up | hypothetical protein\ Context:(NC_002946)+[1561960-1562241]\ Notes:Best Blastp Hit: emb\|CAB85330.1\|(AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1588 | 0.7378 | 1.24 | up | 0.1340 | 1.74 | up | 0.5773 | 1.40 | up | hypothetical protein\ Context:(NC_002946)+[1562941-1563357]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO1589 | 0.5596 | -1.43 | down | 0.4529 | 1.40 | up | 0.7507 | 1.12 | up | hypothetical protein\ Context:(NC_002946)+[1563493-1564170]\ Notes:Best Blastp Hit: possibly an alternative C terminus for MafB |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1590 | 0.2830 | 1.94 | up | 0.0755 | 6.24 | up | 0.4607 | 1.57 | up | hypothetical protein\ Context:(NC_002946)+[1564176-1564574]\ Notes:Best Blastp Hit: pir\|\|A81207 hypothetical protein NMB0371 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225593\|gb\|AAF40813.1\| (AE002393) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1591 | 0.2526 | 2.01 | up | 0.0746 | 1.87 | up | 0.5921 | 1.31 | up | hypothetical protein\ Context:(NC_002946)+[1564605-1564982]\ Notes:Best Blastp Hit: pir\|\|H81206 hypothetical protein NMB0370 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225592\|gb\|AAF40812.1\| (AE002393) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1592 | 0.8487 | -1.09 | down | 0.4962 | 1.44 | up | 0.5793 | 1.39 | up | hypothetical protein\ Context:(NC_002946)+[1565113-1565850]\ Notes:Best Blastp Hit: possibly an alternative C terminus for MafB |
| NGO1593 | 0.7823 | -1.19 | down | 0.1487 | 1.69 | up | 0.7452 | 1.39 | up | hypothetical protein\ Context:(NC_002946)+[1565922-1566266]\ Notes:Best Blastp Hit: pir\|\|T29187 hypothetical protein C55C3.3 - Caenorhabditis elegans >gi\|1255819\|gb\|AAA96170.1\| (U53335) weak similarity in one exon to C. reinhardtii kinesin-like protein 1 (PIR:A53953) and in another exon to Drosophila 150 kDa dynein-associated polypeptide (GLUED protein) (PIR:A53953) [Caenorhabditis elegans] |
| NGO1594 | 0.0976 | -2.93 | down | 0.0201 | -3.67 | down | 0.0607 | -2.81 | down | hypothetical protein\ Context:(NC_002946)+[1566514-1566786]\ Notes: |
| NGO1595 | 0.3967 | 1.93 | up | 0.4623 | 1.37 | up | 0.4139 | -1.44 | down | hypothetical protein\ Context:(NC_002946)+[1566907-1567452]\ Notes:Best Blastp Hit: sp\|P45941\|YQCF_BACSU hypothetical 21.5 KD protein in CWLA-CISA intergenic region >gi\|7475297\|pir\|\|E69949 hypothetical protein yqcF - Bacillus subtilis >gi\|1217878\|dbj\|BAA06963.1\| (D32216) ORF95 [Bacillus subtilis] >gi\|1303771\|dbj\|BAA12427.1\| (D84432) YqcF [Bacillus subtilis] >gi\|2635032\|emb\|CAB14528.1\| (Z99117) yqcF [Bacillus subtilis] |
| NGO1596 | 0.5728 | 1.57 | up | 0.6051 | 1.32 | up | 0.1816 | -2.81 | down | hypothetical protein\ Context:(NC_002946)+[1567856-1568257]\ Notes:Best Blastp Hit: pir\|\|D81174 hypothetical protein NMB0659 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225885\|gb\|AAF41078.1\| (AE002420) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1597 | 0.6259 | -1.56 | down | 0.0550 | -7.92 | down | 0.7977 | -1.18 | down | hypothetical protein\ Context:(NC_002946)-[1568599-1570263]\ Notes: |
| NGO1598 | 0.3730 | 1.84 | up | 0.5316 | -1.37 | down | 0.1544 | -1.98 | down | hypothetical protein\ Context:(NC_002946)-[1570369-1570644]\ Notes:Best Blastp Hit: gb\|AAC44904.1\| (U82701) [Neisseria gonorrhoeae] |
| NGO1599 | 0.0290 | -4.66 | down | 0.0090 | -8.00 | down | 0.2351 | -3.79 | down | AmpG\ Context:(NC_002946)-[1570641-1571924]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) COG0477 Permeases; putative signal transducer protein |
| NGO1600 | 0.3902 | -1.54 | down | 0.1776 | -1.85 | down | 0.4508 | -1.29 | down | hypothetical protein\ Context:(NC_002946)-[1572073-1573491]\ Notes:Best Blastp Hit: gb\|AAC44901.1\| (U82700) glutamine synthetase [Neisseria gonorrhoeae] COG0174 Glutamine synthase |
| NGO1601 | 0.6296 | -1.37 | down | 0.0050 | -23.64 | down | 0.3542 | -2.23 | down | hypothetical protein\ Context:(NC_002946)+[1572106-1573584]\ Notes:Best Blastp Hit: gb\|AAB61771.1\| (M84113) ORF1 [Neisseria gonorrhoeae] |
| NGO1602 | 0.1986 | -2.34 | down | 0.0032 | -4.82 | down | 0.5716 | -1.30 | down | putative shikimate dehydrogenase\ Context:(NC_002946)+[1573802-1574611]\ Notes:Best Blastp Hit: gb\|AAC44913.1\| (U82842) shikimate dehydrogenase [Neisseria gonorrhoeae] COG0169 Shikimate 5-dehydrogenase |
| NGO1603 | 0.0310 | -5.00 | down | 0.0044 | -7.05 | down | 0.8925 | 1.09 | up | monofunctional peptidoglycan transglycosylase\ Context:(NC_002946)+[1574614-1575315]\ Notes:Best Blastp Hit: sp\|Q51005\|MTGA_NEIGO monofunctional biosynthetic peptidoglycan transglycosylase (monofunctional TGASE) >gi\|1196663\|gb\|AAB37748.1\| (L47159) peptidoglycan transglycosylase [Neisseria gonorrhoeae] >gi\|1778807\|gb\|AAC44899.1\| (U82700) monofunctional peptidoglycan transglycosylase [Neisseria gonorrhoeae] COG0744 Membrane carboxypeptidase |
| NGO1604 | 0.7427 | 1.27 | up | 0.0004 | -13.89 | down | 0.9076 | -1.11 | down | hypothetical protein\ Context:(NC_002946)+[1575327-1575569]\ Notes:Best Blastp Hit: pir\|\|G81933 hypothetical protein NMA0876 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379591\|emb\|CAB84156.1\| (AL162754) hypothetical protein NMA0876 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1605 | 0.2722 | 2.07 | up | 0.9873 | 1.01 | up | 0.7844 | -1.09 | down | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)-[1575855-1576589]\ Notes:Best Blastp Hit: emb\|CAB85343.1\| (AL162758) putative ABC transporter ATP-binding protein [Neisseria meningitidis] COG1137 ABC-type (unclassified) transport system |
| NGO1606 | 0.2173 | 1.92 | up | 0.6902 | 1.15 | up | 0.3524 | 1.27 | up | hypothetical protein\ Context:(NC_002946)-[1576660-1577190]\ Notes:Best Blastp Hit: pir\|\|B81208 conserved hypothetical protein NMB0355 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225577\|gb\|AAF40798.1\| (AE002392) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380753\|emb\|CAB85344.1\| (AL162758) putative outer membrane hypothetical protein [Neisseria meningitidis] COG1934 Uncharacterized BCR |
| NGO1607 | 0.4442 | 1.45 | up | 0.9631 | -1.02 | down | 0.4847 | -1.22 | down | hypothetical protein\ Context:(NC_002946)-[1577171-1577752]\ Notes:Best Blastp Hit: pir\|\|A81208 hypothetical protein NMB0354 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225576\|gb\|AAF40797.1\| (AE002392) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1608 | 0.5150 | 1.39 | up | 0.1374 | 1.90 | up | 0.5949 | 1.16 | up | hypothetical protein\ Context:(NC_002946)-[1577749-1578312]\ Notes:Best Blastp Hit: pir\|\|C81785 conserved hypothetical protein NMA2134 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380755\|emb\|CAB85346.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] COG1778 Uncharacterized proteins of HAD |
| NGO1609 | 0.4010 | 1.44 | up | 0.0735 | -2.04 | down | 0.7536 | -1.11 | down | KpsF\ Context:(NC_002946)-[1578351-1579406]\ Notes:Best Blastp Hit: pir\|\|D81785 conserved hypothetical protein NMA2135 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380756\|emb\|CAB85347.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] COG0794 Predicted sugar phosphate aminotransferases; putative polysialic acid capsule expression protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1610 | 0.3427 | 1.68 | up | 0.7630 | 1.13 | up | 0.2849 | 1.40 | up | transaldolase\ Context:(NC_002946)+[1579422-1580477]\ Notes:catalyzes the reversible formation of D-erythrose 4-phosphate and D-fructose 6-phosphate from sedoheptulose 7-phosphate and D-glyceraldehyde 3-phosphate |
| NGO1611 | 0.5647 | -1.33 | down | 0.0942 | -2.12 | down | 0.3378 | -1.58 | down | glutamyl-Q tRNA(Asp) synthetase\ Context:(NC_002946)+[1580935-1581822]\ Notes:this tRNA synthetase lacks the tRNA anticodon interaction domain; instead this enzyme modifies tRNA(Asp) with glutamate by esterifying glutamate to the 2-amino-5-(4;5-dihydroxy-2-cyclopenten-1-yl) moiety of queosine generating a modified nucleoside at the first anticodon position of tRNAAsp; the modified tRNA does not bind elongation factor Tu |
| NGO1612 | 0.0762 | -2.38 | down | 0.0986 | -2.60 | down | 0.1545 | -1.77 | down | tRNA-dihydrouridine synthase A\ Context:(NC_002946)-[1581892-1582938]\ Notes:Best Blastp Hit: pir\|\|H81785 conserved hypothetical protein NMA2139 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380760\|emb\|CAB85351.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] COG0042 Predicted TIM-barrel enzymes; possibly |
| NGO1613 | 0.3444 | -1.53 | down | 0.0551 | -2.88 | down | 0.0713 | -2.04 | down | putative integrase/recombinase; putative phage associated protein\ Context:(NC_002946)+[1583028-1584182]\ Notes:Best Blastp Hit: emb\|CAB96965.1\| (AJ251482) hypothetical protein [Pseudomonas syringae pv. pisi] |
| NGO1614 | 0.5554 | 1.53 | up | 0.1012 | -7.24 | down | 0.6888 | -1.22 | down | putative phage associated protein\ Context:(NC_002946)-[1584232-1584498]\ Notes: |
| NGO1615 | 0.0355 | -3.47 | down | 0.0191 | -8.77 | down | 0.2521 | -1.91 | down | putative phage associated protein\ Context:(NC_002946)-[1584606-1585754]\ Notes:Best Blastp Hit: pir\|\|I41051 hsdM protein - Escherichia coli >gi\|450688\|emb\|CAA53205.1\| (X75452) hsdM gene of EcoprrI [Escherichia coli] |
| NGO1620 | 0.7528 | 1.14 | up | 0.6143 | 1.22 | up | 0.6867 | -1.37 | down | putative phage associated protein\ Context:(NC_002946)-[1587922-1588425]\ Notes:Best Blastp Hit: emb\|CAB63672.1\| (AJ251789) hypothetical protein [Lactobacillus casei bacteriophage A2] |
| NGO1622 | 0.2594 | -2.17 | down | 0.3089 | -1.84 | down | 0.4779 | -1.58 | down | putative phage associated protein\ Context:(NC_002946)-[1588835-1589110]\ Notes:Best Blastp Hit: gb\|AAF41312.1\| (AE002442) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1623 | 0.8993 | -1.07 | down | 0.9972 | -1.00 | down | 0.8043 | -1.49 | down | putative phage associated protein\ Context:(NC_002946)-[1589263-1589550]\ Notes: |
| NGO1624 | 0.7336 | 1.26 | up | 0.8061 | 1.30 | up | 0.2655 | -2.19 | down | putative phage associated protein\ Context:(NC_002946)-[1589736-1589936]\ Notes: |
| NGO1625 | 0.8454 | 1.13 | up | 0.9121 | 1.06 | up | 0.7772 | -1.15 | down | putative phage associated protein\ Context:(NC_002946)-[1590177-1590593]\ Notes: |
| NGO1626 | 0.3147 | 1.75 | up | 0.4384 | 1.37 | up | 0.6203 | 1.19 | up | putative phage associated protein\ Context:(NC_002946)-[1590602-1591249]\ Notes:Best Blastp Hit: gb\|AAF30438.1\|AE002103_3 (AE002103) hypothetical [Ureaplasma urealyticum] |
| NGO1627 | 0.6815 | 1.27 | up | 0.7271 | -1.18 | down | 0.4739 | -1.33 | down | putative phage associated protein\ Context:(NC_002946)-[1591369-1591770]\ Notes:Best Blastp Hit: gi\|9628618 orf14 [Bacteriophage HP1] >gi\|1730858\|sp\|P51716\|YO14_BPHP1 hypothetical 14.9 KD protein in REP-HOL intergenic region (ORF14) >gi\|2120197\|pir\|\|S69520 hypothetical protein 14 - phage HP1 >gi\|1046241\|gb\|AAB09199.1\| (U24159) orf14 [Bacteriophage HP1] |
| NGO1628 | 0.4279 | 1.63 | up | 0.8316 | 1.09 | up | 0.7828 | -1.12 | down | putative phage associated protein\ Context:(NC_002946)-[1591873-1592055]\ Notes:Best Blastp Hit: pir\|\|S75025 hypothetical protein slr1999 - Synechocystis sp. (strain PCC 6803) >gi\|1652970\|dbj\|BAA17887.1\| (D90910) hypothetical protein [Synechocystis sp.] COG1598 Uncharacterized ACR |
| NGO1629 | 0.0405 | -8.29 | down | 0.0501 | -3.91 | down | 0.1614 | -4.06 | down | putative phage associated protein\ Context:(NC_002946)-[1592225-1593043]\ Notes: |
| NGO1630 | 0.0866 | -4.27 | down | 0.0357 | -5.97 | down | 0.0128 | -7.46 | down | putative phage repressor protein; putative phage associated protein\ Context:(NC_002946)-[1593316-1594071]\ Notes:Best Blastp Hit: pdb\|1LLI\|B Chain B; Lambda Repressor Mutant With Val 36 Replaced By Leu; Met 40 Replaced By Leu; And Val 47 Replaced By Ile (V36l;M40l;V47i) Complexed With Dna Operator >gi\|640244\|pdb\|1LLI\|A Chain A; Lambda Repressor Mutant With Val 36 Replaced By Leu; Met 40 Replaced By Leu; And Val 47 Replaced By Ile (V36l;M40l;V47i) Complexed With Dna Operator |
| NGO1632 | 0.2661 | 1.76 | up | 0.4228 | 1.40 | up | 0.4556 | 1.23 | up | putative phage associated protein\ Context:(NC_002946)-[1594614-1594802]\ Notes: |
| NGO1633 | 0.6766 | 1.54 | up | 0.5794 | -1.59 | down | 0.0476 | -5.20 | down | putative phage associated protein\ Context:(NC_002946)+[1594975-1595202]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1634 | 0.0908 | -3.58 | down | 0.0096 | -17.88 | down | 0.5415 | -2.00 | down | putative phage associated protein\ Context:(NC_002946)+[1595199-1595750]\ Notes:Best Blastp Hit: pir\|\|S30432 hypothetical protein - Streptomyces clavuligerus plasmid pSCL |
| NGO1635 | 0.0644 | -15.78 | down | 0.0225 | -13.90 | down | 0.3927 | -2.71 | down | putative phage associated protein\ Context:(NC_002946)+[1596026-1596241]\ Notes: |
| NGO1636 | 0.1274 | -2.81 | down | 0.0265 | -5.21 | down | 0.3036 | -1.67 | down | putative DNA replication protein; putative phage associated protein\ Context:(NC_002946)+[1596419-1597036]\ Notes:Best Blastp Hit: pir\|\|T03011 dnaC protein homolog - Salmonella typhimurium >gi\|3294483\|gb\|AAC26072.1\| (AF001386) unknown [Salmonella typhimurium] COG1484 DNA replication protein DnaC |
| NGO1637 | 0.0086 | 153.59 | up | 0.7522 | -2.00 | down | 0.8858 | -1.09 | down | putative phage associated protein\ Context:(NC_002946)+[1597106-1597261]\ Notes: |
| NGO1638 | 0.4481 | 1.55 | up | 0.3622 | -2.67 | down | 0.4499 | -1.87 | down | putative phage associated protein\ Context:(NC_002946)+[1597352-1597846]\ Notes: |
| NGO1639 | 0.3021 | 2.76 | up | 0.4765 | -2.28 | down | 0.7714 | 1.21 | up | putative phage associated protein\ Context:(NC_002946)-[1597884-1598387]\ Notes:Best Blastp Hit: gb\|AAF41506.1\| (AE002461) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1640 | 0.2875 | 2.54 | up | 0.0461 | -4.90 | down | 0.2975 | -1.50 | down | putative phage associated protein\ Context:(NC_002946)+[1598474-1599049]\ Notes:Best Blastp Hit: sp\|Q37873\|RUSA_BP82 crossover junction endodeoxyribonuclease RusA (Holliday junction nuclease RuSA) (Holliday juction resolvase) >gi\|2120247\|pir\|\|S66583 crossover junction endodeoxyribonuclease (EC 3.1.22.4) rusA - phage 82 >gi\|1051116\|emb\|CAA63330.1\| (X92588) Can suppress the phenotype of ruv mutants [Bacteriophage 82] |
| NGO1641 | 0.3560 | 1.59 | up | 0.3132 | 1.55 | up | 0.3607 | 1.29 | up | putative invertase related gene 6 (Irg6); putative phage associated protein\ Context:(NC_002946)-[1599378-1600340]\ Notes:Best Blastp Hit: gb\|AAC82509.1\| (U65994) pilin gene inverting protein homolog PivNG [Neisseria gonorrhoeae] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1642 | 0.1125 | -2.77 | down | 0.2738 | -1.59 | down | 0.0334 | -5.09 | down | putative phage associated protein\ Context:(NC_002946)-[1600891-1601214]\ Notes:Best Blastp Hit: sp\|Q09256\|YQB3_CAEEL hypothetical 16.6 KD protein C30G12.3 in chromosome II >gi\|7496734\|pir\|\|T15714 hypothetical protein C30G12.3 - Caenorhabditis elegans >gi\|687835\|gb\|AAC46672.1\| (U21319) C30G12.3 gene product [Caenorhabditis elegans] |
| NGO1646 | 0.6573 | 1.34 | up | 0.1089 | -5.92 | down | 0.2459 | 2.45 | up | putative phage associated protein\ Context:(NC_002946)+[1603894-1604178]\ Notes:Best Blastp Hit: emb\|CAB85024.1\| (AL162757) putative integral membrane protein [Neisseria meningitidis] |
| NGO1647 | 0.0528 | -4.01 | down | 0.1458 | -4.59 | down | 0.5717 | -1.45 | down | putative phage associated protein\ Context:(NC_002946)+[1604179-1605366]\ Notes:Best Blastp Hit: emb\|CAB85025.1\| (AL162757) hypothetical protein [Neisseria meningitidis] |
| NGO1648 | 0.0195 | -6.06 | down | 0.0099 | -17.25 | down | 0.2021 | -3.49 | down | Irg7\ Context:(NC_002946)+[1605581-1606537]\ Notes:Best Blastp Hit: pir\|\|E81070 pilin gene inverting protein PivNM-1A NMB1552;NMB1625 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226799\|gb\|AAF41907.1\| (AE002505) pilin gene inverting protein PivNM-1A [Neisseria meningitidis MC58] >gi\|7226876\|gb\|AAF41976.1\| (AE002513) pilin gene inverting protein PivNM-1B [Neisseria meningitidis MC58]; putative invertase related gene 7; putative phage associated protein |
| NGO1649 | 0.0803 | -2.34 | down | 0.0716 | -4.86 | down | 0.5481 | -1.34 | down | putative phage associated protein\ Context:(NC_002946)+[1606828-1607367]\ Notes: |
| NGO1651 | 0.1579 | 2.15 | up | 0.0962 | 3.44 | up | 0.5653 | 1.18 | up | putative phage associated protein\ Context:(NC_002946)+[1608229-1608609]\ Notes:Best Blastp Hit: gb\|AAF41305.1\| (AE002442) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1652 | 0.8229 | 1.11 | up | 0.6198 | -1.25 | down | 0.3067 | -2.26 | down | putative phage associated protein\ Context:(NC_002946)-[1608810-1609808]\ Notes:Best Blastp Hit: pir\|\|A81144 hypothetical protein NMB0900 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226137\|gb\|AAF41308.1\| (AE002442) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1653 | 0.0146 | -15.54 | down | 0.2437 | -4.38 | down | 0.2740 | -5.58 | down | hypothetical protein\ Context:(NC_002946)-[1610151-1610327]\ Notes:Best Blastp Hit: emb\|CAB84546.1\|(AL162755) hypothetical protein NMA1294 [Neisseria meningitidis] |
| NGO1654 | 0.7668 | 1.16 | up | 0.8012 | -1.14 | down | 0.8487 | -1.06 | down | D-tyrosyl-tRNA deacylase\ Context:(NC_002946)-[1610655-1611146]\ Notes:Hydrolyzes D-tyrosyl-tRNA(Tyr) into D-tyrosine and free tRNA(Tyr). Could be a defense mechanism against a harmful effect of D-tyrosine |
| NGO1655 | 0.1087 | 2.52 | up | 0.2005 | 1.73 | up | 0.2783 | 1.43 | up | hypothetical protein\ Context:(NC_002946)-[1611220-1611978]\ Notes:Best Blastp Hit: pir\|\|B81786 hypothetical protein NMA2141 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380762\|emb\|CAB85353.1\|(AL162758) hypothetical protein [Neisseria meningitidis] COG0760 Parvulin-like peptidyl-prolyl isomerase |
| NGO1656 | 0.1807 | 2.23 | up | 0.2086 | 1.56 | up | 0.3160 | 1.51 | up | hypothetical protein\ Context:(NC_002946)-[1612048-1612914]\ Notes:Best Blastp Hit: gb\|AAF40788.1\|(AE002391) cell-binding factor; putative [Neisseria meningitidis MC58] >gi\|7380763\|emb\|CAB85354.1\|(AL162758) putative periplasmi hypothetical protein [Neisseria meningitidis] COG0760 Parvulin-like peptidyl-prolyl isomerase |
| NGO1657 | 0.2198 | 2.05 | up | 0.2439 | 1.49 | up | 0.5417 | 1.23 | up | hypothetical protein\ Context:(NC_002946)-[1612963-1613241]\ Notes:Best Blastp Hit: gb\|AAF40787.1\|(AE002391) BolA/YrbA family protein [Neisseria meningitidis MC58] COG0271 Stress-induced morphogen BolA (activity |
| NGO1658 | 0.3798 | 1.59 | up | 0.5335 | 1.27 | up | 0.7726 | 1.10 | up | YciI-like protein\ Context:(NC_002946)-[1613241-1613531]\ Notes:unknown function; YciI from Haemophilus influenzae presents crystal structure similarity to a muconolactone isomerase; but does not seem to catalyze any of the predicted reactions based on sequence and structure similarity |

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| NGO1659 | 0.3681 | 1.57 | up | 0.8695 | 1.07 | up | 0.9436 | -1.02 | down | hypothetical protein\ Context:(NC_002946)-[1613534-1614064]\ Notes:Best Blastp Hit: pir\|\|D81209 intracellular septation protein A NMB0342 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225563\|gb\|AAF40785.1\| (AE002391) intracellular septation protein A [Neisseria meningitidis MC58] >gi\|7380766\|emb\|CAB85357.1\| (AL162758) putative morphogene [Neisseria meningitidis] |
| NGO1662 | 0.7673 | -1.15 | down | 0.5834 | -1.29 | down | 0.6630 | -1.14 | down | hypothetical protein\ Context:(NC_002946)-[1617306-1618475]\ Notes:Best Blastp Hit: gb\|AAF40782.1\| (AE002390) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1663 | 0.7959 | -1.14 | down | 0.3003 | -1.61 | down | 0.5127 | -1.20 | down | hypothetical protein\ Context:(NC_002946)-[1618486-1618800]\ Notes:Best Blastp Hit: emb\|CAB85361.1\| (AL162758) putative inner membrane hypothetical protein [Neisseria meningitidis] |
| NGO1664 | 0.0633 | -4.05 | down | 0.0102 | -14.60 | down | 0.1968 | -1.58 | down | hypothetical protein\ Context:(NC_002946)+[1618903-1619079]\ Notes:Best Blastp Hit: emb\|CAB85362.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1665 | 0.6572 | -1.27 | down | 0.1812 | -1.78 | down | 0.0800 | -1.65 | down | branched-chain amino acid aminotransferase\ Context:(NC_002946)+[1619110-1620108]\ Notes:catalyzes the transamination of the branched-chain amino acids to their respective alpha-keto acids |
| NGO1666 | 0.1305 | 2.22 | up | 0.0982 | 2.10 | up | 0.3569 | 1.30 | up | enoyl-(acyl carrier protein) reductase\ Context:(NC_002946)-[1620353-1621138]\ Notes:Catalyzes a key regulatory step in fatty acid biosynthesis |
| NGO1667 | 0.0677 | 2.70 | up | 0.0700 | 1.94 | up | 0.1560 | 1.66 | up | 2;3;4;5-tetrahydropyridine-2-carboxylateN-succinyltransferase\ Context:(NC_002946)-[1621293-1622114]\ Notes:catalyzes the formation of N-succinyl-2-amino-6-ketopimelate from succinyl-CoA and tetrahydrodipicolinate in the lysine biosynthetic pathway |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1668 | 0.3156 | -2.35 | down | 0.0165 | -18.01 | down | 0.3507 | -2.91 | down | glucose-6-phosphate isomerase\ Context:(NC_002946)-[1622324-1623967]\ Notes:Best Blastp Hit: pir\|\|G81787 glucose-6-phosphate isomerase (EC 5.3.1.9) 2 NMA2154 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380775\|emb\|CAB85366.1\| (AL162758) glucose-6-phosphate isomerase 2 [Neisseria meningitidis] COG0166 Glucose-6-phosphate isomerase |
| NGO1669 | 0.5777 | 1.36 | up | 0.8359 | 1.08 | up | 0.5935 | 1.19 | up | PilG\ Context:(NC_002946)+[1624476-1625708]\ Notes:Best Blastp Hit: pir\|\|S77585 pilus assembly protein pilG - Neisseria gonorrhoeae >gi\|639480\|gb\|AAC43469.1\| (U32588) PilG [Neisseria gonorrhoeae] COG1459 General secretion pathway protein F |
| NGO1670 | 0.2587 | 2.21 | up | 0.2787 | 2.19 | up | 0.7022 | 1.14 | up | PilD\ Context:(NC_002946)+[1625782-1626642]\ Notes:Best Blastp Hit: sp\|P33566\|LEP4_NEIGO type 4 prepilin-like proteins leader peptide processing enzyme [includes: leader peptidase (prepilin peptidase); N-methyltransferase ] >gi\|996088\|gb\|AAC43468.1\| (U32588) PilD [Neisseria gonorrhoeae] COG1989 Signal peptidase HopD; cleaves; type IV prepilin peptidase |
| NGO1671 | 0.3861 | -1.99 | down | 0.5482 | -1.36 | down | 0.7157 | -1.34 | down | hypothetical protein\ Context:(NC_002946)+[1626600-1627271]\ Notes:Best Blastp Hit: pir\|\|S77586 hypothetical protein X - Neisseria gonorrhoeae >gi\|996087\|gb\|AAC43467.1\| (U32588) OrfX [Neisseria gonorrhoeae] COG0237 Predicted ATPase |
| NGO1672 | 0.0348 | -9.42 | down | 0.0194 | -24.20 | down | 0.8285 | -1.53 | down | hypothetical protein\ Context:(NC_002946)+[1627156-1627473]\ Notes:Best Blastp Hit: pir\|\|S77587 hypothetical protein Y - Neisseria gonorrhoeae >gi\|996086\|gb\|AAC43466.1\| (U32588) ORFY; non-essential for pilus assembly; [Neisseria gonorrhoeae] |
| NGO1673 | 0.1765 | 2.08 | up | 0.5176 | 1.28 | up | 0.7575 | 1.11 | up | PilF\ Context:(NC_002946)-[1627559-1629235]\ Notes:Best Blastp Hit: sp\|P37094\|PILF_NEIGO type IV pilus assembly protein PilF >gi\|420911\|pir\|\|S32914 pilF protein - Neisseria gonorrhoeae >gi\|996085\|gb\|AAC43465.1\| (U32588) PilF [Neisseria gonorrhoeae] COG0630 Predicted ATPases involved in pili |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1674 | 0.1581 | -1.92 | down | 0.1806 | -1.96 | down | 0.2436 | -1.39 | down | hypothetical protein\ Context:(NC_002946)-[1629573-1630019]\ Notes:Best Blastp Hit: pir\|\|E81788 conserved hypothetical protein NMA2160 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380781\|emb\|CAB85372.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] |
| NGO1675 | 0.2289 | 1.99 | up | 0.5953 | 1.19 | up | 0.2980 | -1.32 | down | IspB\ Context:(NC_002946)-[1630023-1630997]\ Notes:Best Blastp Hit: pir\|\|A81213 octaprenyl-diphosphate synthase (EC 2.5.1.-) NMA2161 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225547\|gb\|AAF40771.1\| (AE002389) octaprenyl-diphosphate synthase [Neisseria meningitidis MC58] >gi\|7380782\|emb\|CAB85373.1\| (AL162758) octaprenyl-diphosphate synthase |
| NGO1676 | 0.1252 | 2.81 | up | 0.4998 | 1.29 | up | 0.4868 | 1.32 | up | 50S ribosomal protein L21\ Context:(NC_002946)+[1631221-1631529]\ Notes:Best Blastp Hit: pir\|\|H81212 50S ribosomal protein L21 NMB0325 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225546\|gb\|AAF40770.1\| (AE002389) 50S ribosomal protein L21 [Neisseria meningitidis MC58] >gi\|7380783\|emb\|CAB85374.1\| (AL162758) 50S ribosomal protein L21 [Neisseria meningitidis] COG0261 Ribosomal protein L21 |
| NGO1677 | 0.1359 | 2.52 | up | 0.4016 | 1.40 | up | 0.5413 | 1.21 | up | 50S ribosomal protein L27\ Context:(NC_002946)+[1631554-1631826]\ Notes:involved in the peptidyltransferase reaction during translation |
| NGO1678 | 0.0583 | 3.35 | up | 0.0228 | 3.13 | up | 0.1128 | 2.11 | up | hypothetical protein\ Context:(NC_002946)+[1632061-1633245]\ Notes:Best Blastp Hit: emb\|CAB85376.1\| (AL162758) putative monooxygenase [Neisseria meningitidis] COG0654 2-Octaprenyl-6-metoxyphenol hydroxylase |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1679 | 0.3825 | 1.72 | up | 0.8906 | 1.06 | up | 0.8211 | -1.06 | down | 50S ribosomal protein L33\ Context:(NC_002946)-[1633434-1633589]\ Notes:in Escherichia coli BM108; a mutation that results in lack of L33 synthesis had no effect on ribosome synthesis or function; there are paralogous genes in several bacterial genomes; and a CXXC motif for zinc binding and an upstream regulation region of the paralog lacking this motif that are regulated by zinc similar to other ribosomal proteins like L31; the proteins in this group lack the CXXC motif |
| NGO1680 | 0.1080 | 2.71 | up | 0.3620 | 1.42 | up | 0.4646 | 1.30 | up | 50S ribosomal protein L28\ Context:(NC_002946)-[1633621-1633854]\ Notes:required for 70S ribosome assembly |
| NGO1681 | 0.6953 | -1.41 | down | 0.0656 | -8.35 | down | 0.9674 | -1.05 | down | hypothetical protein\ Context:(NC_002946)-[1633926-1634114]\ Notes:Best Blastp Hit: emb\|CAB85379.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1682 | 0.2074 | -2.96 | down | 0.0348 | -5.73 | down | 0.6309 | 1.23 | up | efflux pump protein; fatty acid resistance\ Context:(NC_002946)-[1634104-1635627]\ Notes:Best Blastp Hit: gb\|AAD54074.1\| (AF132910) efflux pump protein FarB [Neisseria gonorrhoeae] COG0477 Permeases |
| NGO1683 | 0.5011 | 1.66 | up | 0.5053 | -1.59 | down | 0.4445 | -1.33 | down | efflux pump protein; fatty acid resistance\ Context:(NC_002946)-[1635651-1636835]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) COG1566 Multidrug resistance efflux pump |
| NGO1684 | 0.2367 | 2.07 | up | 0.2228 | 1.59 | up | 0.2164 | 1.53 | up | 7-cyano-7-deazaguanine reductase\ Context:(NC_002946)+[1637094-1637567]\ Notes:NADPH-dependent; catalyzes the reduction of 7-cyano-7-deazaguanine to 7-aminomethyl-7-deazaguanine in queuosine biosynthesis |
| NGO1685 | 0.4128 | 1.53 | up | 0.4337 | 1.84 | up | 0.0553 | 3.27 | up | hypothetical protein\ Context:(NC_002946)+[1637642-1638328]\ Notes:Best Blastp Hit: pir\|\|B81214 conserved hypothetical protein NMB0316 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225536\|gb\|AAF40761.1\| (AE002388) conserved hypothetical protein [Neisseria meningitidis MC58] COG1738 Uncharacterized ACR; YhhQ family |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1686 | 0.2103 | -1.79 | down | 0.0224 | -3.75 | down | 0.2756 | -1.58 | down | hypothetical protein\ Context:(NC_002946)-[1638678-1639970]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0739 Membrane proteins related to |
| NGO1687 | 0.8590 | -1.13 | down | 0.0557 | -4.05 | down | 0.8076 | -1.22 | down | hypothetical protein\ Context:(NC_002946)+[1639882-1641015]\ Notes:Best Blastp Hit: pir\|\|B81790 hypothetical protein NMA2173 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380794\|emb\|CAB85385.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1688 | 0.0083 | 6.47 | up | 0.0098 | 10.32 | up | 0.0138 | 4.76 | up | putative outer membrane protein OmpU\ Context:(NC_002946)-[1641216-1642685]\ Notes:Best Blastp Hit: emb\|CAB85386.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] |
| NGO1690 | 0.1721 | -2.22 | down | 0.4111 | 1.36 | up | 0.6145 | -1.20 | down | hypothetical protein\ Context:(NC_002946)-[1644374-1644619]\ Notes:Best Blastp Hit: gb\|AAF40757.1\| (AE002388) hypothetical protein [Neisseria meningitidis MC58] >gi\|7380797\|emb\|CAB85388.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1691 | 0.0983 | -5.95 | down | 0.0108 | -23.72 | down | 0.3596 | 1.47 | up | hypothetical protein\ Context:(NC_002946)+[1644588-1644734]\ Notes: |
| NGO1692 | 0.0492 | -2.71 | down | 0.0073 | -4.89 | down | 0.0482 | -2.20 | down | hypothetical protein\ Context:(NC_002946)+[1644722-1645159]\ Notes:Best Blastp Hit: pir\|\|F81790 conserved hypothetical inner membrane protein NMA2177 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380798\|emb\|CAB85389.1\| (AL162758) conserved hypothetical inner membrane protein [Neisseria meningitidis] COG1981 Predicted membrane protein |
| NGO1693 | 0.3263 | -1.62 | down | 0.2545 | -1.98 | down | 0.1778 | -1.94 | down | hypothetical protein\ Context:(NC_002946)+[1645171-1645647]\ Notes:Best Blastp Hit: pir\|\|D81213 conserved hypothetical protein NMB0309 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225530\|gb\|AAF40755.1\| (AE002388) conserved hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1694 | 0.0084 | -6.21 | down | 0.1400 | -2.50 | down | 0.1801 | -2.29 | down | hypothetical protein\ Context:(NC_002946)-[1645677-1646165]\ Notes:Best Blastp Hit: sp\|P04174\|DYR_NEIGO dihydrofolate reductase >gi\|66103\|pir\|\|RDNHD dihydrofolate reductase (EC 1.5.1.3) - Neisseria gonorrhoeae COG0262 Dihydrofolate reductase |
| NGO1695 | 0.7144 | -1.19 | down | 0.5028 | -1.30 | down | 0.3971 | -1.29 | down | phospho-2-dehydro-3-deoxyheptonate aldolase\ Context:(NC_002946)-[1646233-1647288]\ Notes:catalyzes the formation of 3-deoxy-D-arabino-hept-2-ulosonate 7 phosphate from phosphoenolpyruvate and D-erythrose 4-phosphate; phenylalanine sensitive |
| NGO1699 | 0.8659 | 1.10 | up | 0.9992 | -1.00 | down | 0.5412 | -1.19 | down | hypothetical protein\ Context:(NC_002946)-[1655425-1656231]\ Notes:Best Blastp Hit: gb\|AAF40747.1\|(AE002386) CcsA-related protein [Neisseria meningitidis MC58] |
| NGO1700 | 0.9940 | 1.00 | up | 0.4230 | -1.42 | down | 0.4177 | -1.26 | down | putative signal recognition particle protein\ Context:(NC_002946)+[1656451-1657821]\ Notes:Best Blastp Hit: pir\|\|F81215 signal recognition particle protein NMB0295 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225519\|gb\|AAF40746.1\| (AE002386) signal recognition particle protein [Neisseria meningitidis MC58] COG0541 Signal recognition particle GTPase Ffh |
| NGO1701 | 0.4327 | -1.47 | down | 0.6234 | -1.27 | down | 0.5932 | -1.17 | down | hypothetical protein\ Context:(NC_002946)+[1658077-1658532]\ Notes:Best Blastp Hit: gb\|AAC98737.1\|(AF052749) unknown [Pseudomonas putida] COG1145 Ferredoxin 2 |
| NGO1702 | 0.9924 | -1.01 | down | 0.0396 | -4.44 | down | 0.2450 | -2.14 | down | hypothetical protein\ Context:(NC_002946)-[1658587-1659111]\ Notes:Best Blastp Hit: pir\|\|F81792 hypothetical protein NMA2195 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|6900420\|emb\|CAB72030.1\|(AJ391261) hypothetical protein [Neisseria meningitidis] >gi\|7380814\|emb\|CAB85406.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1704 | 0.4065 | -1.61 | down | 0.0930 | -2.41 | down | 0.3854 | -1.61 | down | hypothetical protein\ Context:(NC_002946)-[1660138-1660335]\ Notes:Best Blastp Hit: pir\|\|F81792 hypothetical protein NMA2195 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|6900420\|emb\|CAB72030.1\| (AJ391261) hypothetical protein [Neisseria meningitidis] >gi\|7380814\|emb\|CAB85406.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1705 | 0.3784 | -1.91 | down | 0.1766 | -3.18 | down | 0.8264 | 1.16 | up | hypothetical protein\ Context:(NC_002946)-[1660384-1660782]\ Notes:Best Blastp Hit: gb\|AAF40742.1\| (AE002386) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380815\|emb\|CAB85407.1\| (AL162758) conserved hypothetical inner membrane protein [Neisseria meningitidis] |
| NGO1706 | 0.5755 | -1.28 | down | 0.7319 | 1.13 | up | 0.7728 | -1.10 | down | LysR family transcriptional regulator\ Context:(NC_002946)+[1660890-1661801]\ Notes:Best Blastp Hit: gb\|AAF40741.1\| (AE002386) transcriptional regulator; putative [Neisseria meningitidis MC58] COG0583 Transcriptional regulators; LysR family |
| NGO1707 | 0.3906 | 1.59 | up | 0.7774 | 1.13 | up | 0.9184 | -1.05 | down | putative deoxyribodopyrimidine photolyase\ Context:(NC_002946)+[1661791-1663089]\ Notes:Best Blastp Hit: emb\|CAB85409.1\| (AL162758) deoxyribodopyrimidine photolyase [Neisseria meningitidis] COG0415 Deoxypyrimidine photolyase |
| NGO1708 | 0.3652 | 1.82 | up | 0.0654 | -3.82 | down | 0.6217 | -1.61 | down | ATP-dependent DNA helicase DinG\ Context:(NC_002946)+[1663270-1665420]\ Notes:helicase involved in DNA repair and perhaps also replication |
| NGO1709 | 0.1748 | 2.42 | up | 0.0464 | 4.11 | up | 0.0754 | 4.95 | up | hypothetical protein\ Context:(NC_002946)+[1665456-1666070]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO1710 | 0.0367 | -4.53 | down | 0.0633 | -8.39 | down | 0.4521 | -2.10 | down | putative trans-acylase protein\ Context:(NC_002946)-[1666206-1668074]\ Notes:Best Blastp Hit: emb\|CAB85413.1\| (AL162758) putative inner membrane trans-acylase protein [Neisseria meningitidis] COG1835 Predicted acyltransferases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1711 | 0.6815 | -1.29 | down | 0.2427 | 1.56 | up | 0.5464 | 1.20 | up | adenylosuccinate lyase\ Context:(NC_002946)-[1668154-1669524]\ Notes:Catalyzes two discrete reactions in the de novo synthesis of purines: the cleavage of adenylosuccinate and succinylaminoimidazole carboxamide ribotide |
| NGO1712 | 0.1697 | -2.46 | down | 0.0139 | -5.62 | down | 0.0057 | -5.59 | down | hypothetical protein\ Context:(NC_002946)-[1669596-1670228]\ Notes:Best Blastp Hit: emb\|CAB85415.1\| (AL162758) hypothetical protein [Neisseria meningitidis] COG1611 Predicted Rossmann fold nucleotide-binding |
| NGO1713 | 0.5098 | 1.37 | up | 0.6132 | -1.22 | down | 0.9495 | 1.03 | up | hypothetical protein\ Context:(NC_002946)+[1670357-1672264]\ Notes:Best Blastp Hit: emb\|CAB85416.1\| (AL162758) hypothetical protein [Neisseria meningitidis] COG0557 Exoribonucleases |
| NGO1714 | 0.6927 | 1.37 | up | 0.0469 | 2.15 | up | 0.2994 | 1.76 | up | putative cis-trans isomerase\ Context:(NC_002946)-[1672744-1673745]\ Notes:Best Blastp Hit: >pir\|\|B81216 peptidyl-prolyl cis-trans isomerase NMB0281 [imported] - Neisseria meningitidis (group B strain MD58) gb\|AAF40735.1\| (AE002385) peptidyl-prolyl cis-trans isomerase [Neisseria meningitidis MC58] COG0760 Parvulin-like peptidyl-prolyl isomerase |
| NGO1715 | 0.8369 | 1.10 | up | 0.7744 | -1.12 | down | 0.2631 | 1.34 | up | OstA\ Context:(NC_002946)-[1673847-1676252]\ Notes:Best Blastp Hit: emb\|CAB85418.1\| (AL162758) putative solvent tolerance protein [Neisseria meningitidis] COG1452 Organic solvent tolerance protein OstA |
| NGO1716 | 0.8590 | -1.09 | down | 0.5925 | -1.29 | down | 0.3135 | -1.34 | down | hypothetical protein\ Context:(NC_002946)+[1676322-1677326]\ Notes:Best Blastp Hit: pir\|\|C81794 hypothetical protein NMA2208 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380827\|emb\|CAB85419.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1717 | 0.3563 | 1.67 | up | 0.5720 | 1.27 | up | 0.6386 | 1.17 | up | putative thiol:disulphide interchange protein\ Context:(NC_002946)-[1677383-1678087]\ Notes:Best Blastp Hit: gb\|AAF40732.1\| (AE002384) thiol:disulfide interchange protein DsbA [Neisseria meningitidis MC58] COG0526 Thiol-disulfide isomerase and thioredoxins |

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| NGO1718 | 0.0004 | -25.19 | down | 0.0003 | -16.75 | down | 0.0080 | -11.14 | down | hypothetical protein\ Context:(NC_002946)+[1678525-1680063]\ Notes:Best Blastp Hit: pir\|\|B81217 virulence factor MviN NMB0277 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225502\|gb\|AAF40731.1\| (AE002384) virulence factor MviN [Neisseria meningitidis MC58] COG0728 Uncharacterized membrane protein; putative |
| NGO1719 | 0.2329 | -2.67 | down | 0.0043 | -10.55 | down | 0.8877 | 1.15 | up | hypothetical protein\ Context:(NC_002946)+[1680196-1681155]\ Notes:Best Blastp Hit: gb\|AAF40730.1\| (AE002384) conserved hypothetical protein [Neisseria meningitidis MC58] COG0429 Predicted hydrolase of the |
| NGO1720 | 0.1699 | 3.80 | up | 0.0209 | -9.17 | down | 0.1809 | -7.53 | down | hypothetical protein\ Context:(NC_002946)-[1681152-1681262]\ Notes: |
| NGO1721 | 0.9559 | 1.03 | up | 0.2650 | -1.44 | down | 0.2435 | -2.41 | down | indole-3-glycerol-phosphate synthase\ Context:(NC_002946)+[1681206-1681988]\ Notes:involved in tryptophan biosynthesis; amino acid biosynthesis; converts 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate to C(1)-(3-indolyl)-glycerol 3-phosphate and carbon dioxide and water |
| NGO1722 | 0.0661 | 4.39 | up | 0.1362 | -3.20 | down | 0.5523 | 1.63 | up | RecQ\ Context:(NC_002946)+[1682051-1684354]\ Notes:Best Blastp Hit: gb\|AAD05424.1\| (AF047374) RecQ [Neisseria gonorrhoeae] COG0514 Superfamily II DNA helicases; RecQ family; putative ATP-dependent DNA helicase |
| NGO1723 | 0.4672 | -1.64 | down | 0.2279 | -2.83 | down | 0.4097 | 2.05 | up | hypothetical protein\ Context:(NC_002946)-[1684391-1685692]\ Notes:Best Blastp Hit: emb\|CAB85425.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1724 | 0.3287 | 1.76 | up | 0.2669 | 3.09 | up | 0.3703 | -1.39 | down | hypothetical protein\ Context:(NC_002946)-[1686074-1686862]\ Notes:Best Blastp Hit: gb\|AAF40725.1\| (AE002383) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1725 | 0.0451 | -3.32 | down | 0.0187 | -3.66 | down | 0.0321 | -2.63 | down | putative bioH - biotin biosynthesis protein\ Context:(NC_002946)-[1686859-1687635]\ Notes:Best Blastp Hit: emb\|CAB85427.1\| (AL162758) putative hydrolase [Neisseria meningitidis] COG0570 BioH; catalyzes some early step in biotin |

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| NGO1726 | 0.1775 | -1.93 | down | 0.0253 | -3.19 | down | 0.8660 | -1.07 | down | hypothetical protein\ Context:(NC_002946)+[1687607-1688332]\ Notes:Best Blastp Hit: emb\|CAB85428.1\| (AL162758) hypothetical protein [Neisseria meningitidis] COG1040 Predicted amidophosphoribosyl transferases |
| NGO1727 | 0.0259 | 8.25 | up | 0.1803 | 3.63 | up | 0.2738 | 1.36 | up | hypothetical protein\ Context:(NC_002946)+[1688397-1688861]\ Notes:Best Blastp Hit: gb\|AAF40722.1\| (AE002383) RNA methyltransferase; TrmH family [Neisseria meningitidis MC58] COG0219 Predicted rRNA methylase (SpoU class) |
| NGO1728 | 0.9870 | 1.01 | up | 0.6399 | -1.24 | down | 0.5125 | 1.20 | up | hypothetical protein\ Context:(NC_002946)+[1688989-1689675]\ Notes:Best Blastp Hit: gb\|AAF40721.1\| (AE002383) conserved hypothetical protein [Neisseria meningitidis MC58] COG0797 Lipoproteins |
| NGO1729 | 0.4549 | -1.43 | down | 0.1477 | -2.18 | down | 0.1250 | -2.16 | down | hypothetical protein\ Context:(NC_002946)+[1689736-1690062]\ Notes:Best Blastp Hit: pir\|\|C81218 conserved hypothetical protein NMB0266 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225490\|gb\|AAF40720.1\| (AE002383) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1730 | 0.6343 | 1.34 | up | 0.1441 | -2.82 | down | 0.2730 | -1.76 | down | Holliday junction DNA helicase motor protein\ Context:(NC_002946)+[1690144-1690728]\ Notes:plays an essential role in ATP-dependent branch migration of the Holliday junction |
| NGO1731 | 0.6627 | -2.02 | down | 0.8943 | 1.31 | up | 0.7517 | -1.37 | down | hypothetical protein\ Context:(NC_002946)+[1690728-1690865]\ Notes:Best Blastp Hit: emb\|CAB85433.1\| (AL162758) hypothetical protein [Neisseria meningitidis] |
| NGO1732 | 0.9218 | 1.07 | up | 0.6268 | 1.27 | up | 0.9460 | -1.05 | down | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)+[1690892-1692748]\ Notes:Best Blastp Hit: emb\|CAB85434.1\| (AL162758) putative ABC transporter [Neisseria meningitidis] COG1132 ABC-type multidrug/protein/lipid |
| NGO1733 | 0.0314 | -3.41 | down | 0.5179 | -1.45 | down | 0.8659 | 1.07 | up | ribosome-associated GTPase\ Context:(NC_002946)+[1692753-1693676]\ Notes:EngC; RsgA; CpgA; circularly permuted GTPase; ribosome small subunit-dependent GTPase A; has the pattern G4-G1-G3 as opposed to other GTPases; interacts strongly with 30S ribosome which stimulates GTPase activity |

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| NGO1734 | 0.6314 | -1.26 | down | 0.1267 | -3.05 | down | 0.4516 | -1.30 | down | putative exodeoxyribonuclease VII small subunit\ Context:(NC_002946)+[1693789-1694013]\ Notes:Best Blastp Hit: gb\|AAF40716.1\| (AE002383) exodeoxyribonuclease; small subunit [Neisseria meningitidis MC58] COG1722 Exonuclease VII small subunit |
| NGO1735 | 0.3462 | 1.89 | up | 0.5147 | 1.23 | up | 0.7152 | 1.09 | up | hypothetical protein\ Context:(NC_002946)+[1693997-1694893]\ Notes:Best Blastp Hit: pir\|\|E81796 geranyltranstransferase (EC 2.5.1.10) NMA2226 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380845\|emb\|CAB85437.1\| (AL162758) geranyltranstransferase [Neisseria meningitidis] COG0142 Geranylgeranyl pyrophosphate synthase |
| NGO1736 | 0.3409 | -1.88 | down | 0.1629 | -2.25 | down | 0.2487 | -2.02 | down | hypothetical protein\ Context:(NC_002946)-[1695010-1695360]\ Notes:Best Blastp Hit: pir\|\|F81796 hypothetical inner membrane protein NMA2227 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380846\|emb\|CAB85438.1\| (AL162758) hypothetical inner membrane protei [Neisseria meningitidis] |
| NGO1737 | 0.0307 | -6.24 | down | 0.0080 | -6.02 | down | 0.1062 | -2.56 | down | NADH dehydrogenase subunit N\ Context:(NC_002946)-[1695421-1696866]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1738 | 0.1846 | -2.18 | down | 0.0136 | -4.87 | down | 0.1145 | -3.39 | down | NADH dehydrogenase subunit M\ Context:(NC_002946)-[1696876-1698372]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1739 | 0.1933 | -2.30 | down | 0.1722 | -3.35 | down | 0.7784 | 1.60 | up | hypothetical protein\ Context:(NC_002946)-[1698486-1699649]\ Notes:Best Blastp Hit: pir\|\|A71813 hypothetical protein jhp1392 - Helicobacter pylori (strain J99) >gi\|4156012\|gb\|AAD06973.1\| (AE001561) putative [Helicobacter pylori J99] |
| NGO1740 | 0.0731 | -3.61 | down | 0.0691 | -8.95 | down | 0.1337 | -5.10 | down | NADH dehydrogenase subunit L\ Context:(NC_002946)-[1699833-1701857]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1741 | 0.2149 | -2.48 | down | 0.0010 | -17.77 | down | 0.3741 | -2.74 | down | NADH dehydrogenase subunit K\ Context:(NC_002946)-[1701860-1702165]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1742 | 0.0019 | -13.74 | down | 0.0005 | -54.37 | down | 0.6016 | -1.86 | down | hypothetical protein\ Context:(NC_002946)-[1702162-1702833]\ Notes:Best Blastp Hit: gb\|AAF40707.1\| (AE002382) NADH dehydrogenase I; J subunit [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1743 | 0.8343 | -1.12 | down | 0.6893 | -1.33 | down | 0.0379 | -2.60 | down | NADH dehydrogenase subunit I\ Context:(NC_002946)-[1702845-1703324]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1744 | 0.0041 | -5.24 | down | 0.0352 | -12.94 | down | 0.0822 | -3.22 | down | hypothetical protein\ Context:(NC_002946)-[1703405-1704481]\ Notes:Best Blastp Hit: pir\|\|E81219 NADH dehydrogenase I; H chain NMB0250 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225473\|gb\|AAF40704.1\| (AE002382) NADH dehydrogenase I; H subunit [Neisseria meningitidis MC58] COG1005 NADH-ubiquinone oxidoreductase subunit 1 |
| NGO1745 | 0.0092 | -5.91 | down | 0.0006 | -5.87 | down | 0.0158 | -2.69 | down | NADH dehydrogenase subunit G\ Context:(NC_002946)-[1704484-1706745]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1746 | 0.0010 | -10.14 | down | 0.0480 | -3.77 | down | 0.0152 | -15.89 | down | hypothetical protein\ Context:(NC_002946)-[1707458-1708759]\ Notes:Best Blastp Hit: pir\|\|D81222 NADH dehydrogenase I; F chain NMB0246 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225468\|gb\|AAF40700.1\| (AE002381) NADH dehydrogenase I; F subunit [Neisseria meningitidis MC58] COG1894 NADH-ubiquinone oxidoreductase; NADH-binding |
| NGO1747 | 0.0006 | -31.46 | down | 0.0018 | -27.64 | down | 0.0010 | -10.46 | down | NADH dehydrogenase subunit E\ Context:(NC_002946)-[1709149-1709622]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1748 | 0.0015 | -39.09 | down | 0.0006 | -18.61 | down | 0.0036 | -16.06 | down | NADH dehydrogenase subunit D\ Context:(NC_002946)-[1709622-1710878]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1749 | 0.0001 | -24.96 | down | 0.0007 | -39.62 | down | 0.0073 | -20.47 | down | NADH dehydrogenase subunit C\ Context:(NC_002946)-[1710868-1711461]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone |
| NGO1750 | 0.0008 | -27.33 | down | 0.0000 | -393.27 | down | 0.0330 | -17.23 | down | NADH dehydrogenase subunit B\ Context:(NC_002946)-[1711474-1711956]\ Notes:The point of entry for the majority of electrons that traverse the respiratory chain eventually resulting in the reduction of oxygen |

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| NGO1751 | 0.0041 | -11.74 | down | 0.0000 | -53.97 | down | 0.0147 | -13.92 | down | hypothetical protein\ Context:(NC_002946)-[1711947-1712303]\ Notes:Best Blastp Hit: pir\|\|G81992 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain A NMA0019 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378797\|emb\|CAB83339.1\| (AL162752) NADH dehydrogenase I chain A [Neisseria meningitidis] COG0838 NADH-ubiquinone oxidoreductase subunit 3 |
| NGO1752 | 0.3902 | 1.58 | up | 0.6692 | 1.22 | up | 0.6533 | 1.16 | up | hypothetical protein\ Context:(NC_002946)-[1712796-1714283]\ Notes:Best Blastp Hit: pir\|\|H81992 probable integral membrane protein NMA0020 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378798\|emb\|CAB83340.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] COG0421 Spermidine synthase |
| NGO1753 | 0.9160 | 1.06 | up | 0.7748 | -1.15 | down | 0.7911 | -1.09 | down | hypothetical protein\ Context:(NC_002946)-[1714270-1714890]\ Notes:Best Blastp Hit: pir\|\|E81221 probable integral membrane protein NMA0021 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225461\|gb\|AAF40693.1\| (AE002381) hypothetical protein [Neisseria meningitidis MC58] >gi\|7378799\|emb\|CAB83341.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] |
| NGO1754 | 0.3484 | 1.72 | up | 0.3787 | 1.41 | up | 0.8928 | 1.05 | up | MafI protein\ Context:(NC_002946)-[1715118-1715465]\ Notes:MafI3 |
| NGO1755 | 0.1022 | -5.91 | down | 0.2327 | -6.02 | down | 0.4670 | 2.41 | up | hypothetical protein\ Context:(NC_002946)-[1715638-1715838]\ Notes:Best Blastp Hit: emb\|CAB83579.1\| (AL162752) truncated pilin [Neisseria meningitidis] |
| NGO1756 | 0.9426 | 1.05 | up | 0.1874 | -2.77 | down | 0.4042 | 1.35 | up | hypothetical protein\ Context:(NC_002946)-[1716172-1716486]\ Notes: |
| NGO1757 | 0.3575 | 1.67 | up | 0.7562 | 1.34 | up | 0.7336 | 1.26 | up | hypothetical protein\ Context:(NC_002946)-[1716628-1718835]\ Notes:Best Blastp Hit: pir\|\|F81993 DNA helicase II (EC 3.6.1.-) NMA0027 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|6900436\|emb\|CAB72035.1\| (AJ391262) DNA helicase II [Neisseria meningitidis] >gi\|7378804\|emb\|CAB83346.1\| (AL162752) DNA helicase II [Neisseria meningitidis] COG0210 Superfamily I DNA and RNA helicases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1758 | 0.1217 | -2.57 | down | 0.0058 | -9.50 | down | 0.0861 | 1.67 | up | GlnE\ Context:(NC_002946)-[1719259-1721949]\ Notes:Best Blastp Hit: pir\|\|E81994 probable [glutamate--ammonia-ligase] adenylyltransferase (EC 2.7.7.42) NMA0035 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378811\|emb\|CAB83353.1\| (AL162752) putative glutamate-ammonia-ligase adenylyltransferase [Neisseria meningitidis] COG1391 Glutamine synthetase adenylyltransferase |
| NGO1759 | 0.2730 | -2.41 | down | 0.0259 | -9.18 | down | 0.5683 | -1.94 | down | hypothetical protein\ Context:(NC_002946)-[1722143-1722478]\ Notes:Best Blastp Hit: gb\|AAF40679.1\| (AE002380) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1760 | 0.0158 | -5.99 | down | 0.0304 | -16.48 | down | 0.4272 | -2.98 | down | hypothetical protein\ Context:(NC_002946)-[1722492-1722965]\ Notes:Best Blastp Hit: pir\|\|H81222 hypothetical protein NMB0222 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225445\|gb\|AAF40678.1\| (AE002380) hypothetical protein [Neisseria meningitidis MC58] >gi\|7378813\|emb\|CAB83355.1\| (AL162752) hypothetical protein NMA0037 [Neisseria meningitidis] |
| NGO1761 | 0.2079 | 2.30 | up | 0.8885 | 1.09 | up | 0.6449 | 1.25 | up | dihydroorotate dehydrogenase 2\ Context:(NC_002946)-[1723162-1724169]\ Notes:catalyzes the conversion of dihydroorotate to orotate in the pyrimidine biosynthesis pathway; uses a flavin nucleotide as an essential cofactor; class 2 enzymes are monomeric and compared to the class 1 class 2 possess an extended N terminus; which plays a role in the membrane association of the enzyme and provides the binding site for the respiratory quinones that serve as physiological electron acceptors |
| NGO1762 | 0.1338 | 2.55 | up | 0.1717 | 1.61 | up | 0.2472 | 1.71 | up | hypothetical protein\ Context:(NC_002946)+[1724401-1724637]\ Notes:Best Blastp Hit: pir\|\|F81222 acyl carrier protein NMB0220 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225443\|gb\|AAF40676.1\| (AE002380) acyl carrier protein [Neisseria meningitidis MC58] >gi\|7378819\|emb\|CAB83361.1\| (AL162752) acyl carrier protein [Neisseria meningitidis] COG0236 Acyl carrier protein |

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| NGO1763 | 0.1354 | 2.54 | up | 0.0542 | 2.04 | up | 0.2874 | 1.55 | up | 3-oxoacyl-(acyl carrier protein) synthase II\ Context:(NC_002946)+[1724794-1726041]\ Notes:FabF; beta-ketoacyl-ACP synthase II; KASII; catalyzes a condensation reaction in fatty acid biosynthesis: addition of an acyl acceptor of two carbons from malonyl-ACP; required for the elongation of short-chain unsaturated acyl-ACP |
| NGO1765 | 0.0287 | -4.35 | down | 0.0502 | -2.87 | down | 0.9116 | 1.06 | up | PglA\ Context:(NC_002946)+[1728025-1729155]\ Notes:Best Blastp Hit: possibly phase variable - 10G residue homopolymer repeat in the coding sequence (ON) COG0438 Glycosyltransferases I; putative glycosyltransferase |
| NGO1767 | 0.7052 | -1.24 | down | 0.2111 | -1.54 | down | 0.6270 | -1.17 | down | KatA\ Context:(NC_002946)+[1730757-1732271]\ Notes:Best Blastp Hit: pir\|\|D81224 catalase (EC 1.11.1.6) NMA0050 [similarity] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225438\|gb\|AAF40672.1\| (AE002379) catalase [Neisseria meningitidis MC58] >gi\|7378825\|emb\|CAB83367.1\| (AL162752) catalase [Neisseria meningitidis] COG0753 Catalase; putative catalase |
| NGO1768 | 0.0374 | -7.21 | down | 0.0009 | -36.42 | down | 0.0173 | -6.90 | down | hypothetical protein\ Context:(NC_002946)+[1732787-1733353]\ Notes:Best Blastp Hit: pir\|\|C81224 conserved hypothetical protein NMB0215 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225437\|gb\|AAF40671.1\| (AE002379) conserved hypothetical protein [Neisseria meningitidis MC58] COG1971 Predicted membrane protein |
| NGO1769 | 0.0457 | -4.38 | down | 0.0160 | -22.14 | down | 0.0262 | -8.01 | down | CcpR\ Context:(NC_002946)+[1733575-1734738]\ Notes:Best Blastp Hit: pir\|\|B70313 cytochrome-c peroxidase (EC 1.11.1.5) - Aquifex aeolicus >gi\|2982865\|gb\|AAC06485.1\| (AE000675) cytochrome c peroxidase [Aquifex aeolicus] COG1858 Cytochrome c peroxidase; putative cytochrome-c peroxidase |
| NGO1770 | 0.9668 | -1.03 | down | 0.0846 | 2.78 | up | 0.1531 | 2.84 | up | PrlC\ Context:(NC_002946)-[1735319-1737355]\ Notes:Best Blastp Hit: pir\|\|G81996 oligopeptidase A (EC 3.4.24.70) NMA0054 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378829\|emb\|CAB83371.1\| (AL162752) oligopeptidase A [Neisseria meningitidis] COG0339 Zn-dependent oligopeptidases; putative oligopeptidase A |

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| NGO1771 | 0.1584 | -2.75 | down | 0.0004 | -14.39 | down | 0.0801 | -4.11 | down | hypothetical protein\ Context:(NC_002946)-[1737443-1738435]\ Notes:Best Blastp Hit: pir\|\|E81225 hypothetical protein NMB0213 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225434\|gb\|AAF40669.1\|(AE002378) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1772 | 0.7799 | 1.14 | up | 0.4257 | -1.63 | down | 0.5703 | 1.18 | up | DNA gyrase subunit B\ Context:(NC_002946)+[1738581-1740971]\ Notes:negatively supercoils closed circular double-stranded DNA |
| NGO1773 | 0.3377 | -1.66 | down | 0.1699 | -2.60 | down | 0.1050 | -2.60 | down | hypothetical protein\ Context:(NC_002946)+[1741070-1742455]\ Notes:Best Blastp Hit: pir\|\|C81225 L-serine dehydratase NMB0211 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225432\|gb\|AAF40667.1\|(AE002378) L-serine dehydratase [Neisseria meningitidis MC58] COG1760 L-serine deaminase |
| NGO1774 | 0.5141 | -1.95 | down | 0.1823 | -3.31 | down | 0.1151 | -2.94 | down | putative potassium-efflux system protein\ Context:(NC_002946)-[1743699-1745651]\ Notes:Best Blastp Hit: gb\|AAF40666.1\| (AE002378) glutathione-regulated potassium-efflux system protein [Neisseria meningitidis MC58] COG0475 K efflux system; membrane domain |
| NGO1775 | 0.3046 | -2.37 | down | 0.0030 | -10.27 | down | 0.0630 | -3.99 | down | putative ferredoxin\ Context:(NC_002946)+[1745797-1746636]\ Notes:Best Blastp Hit: emb\|CAB83377.1\|(AL162752) putative ferredoxin [Neisseria meningitidis] COG1145 Ferredoxin 2 |
| NGO1776 | 0.0057 | -4.91 | down | 0.0035 | -30.48 | down | 0.2003 | -5.19 | down | glyceraldehyde-3-phosphate dehydrogenase\ Context:(NC_002946)+[1746835-1747866]\ Notes:catalyzes the formation of 3-phospho-D-glyceroyl phosphate from D-glyceraldehyde 3-phosphate |
| NGO1777 | 0.8525 | -1.29 | down | 0.0024 | -45.25 | down | 0.1642 | -4.27 | down | hypothetical protein\ Context:(NC_002946)+[1747904-1748062]\ Notes:Best Blastp Hit: gb\|AAF42457.1\|(AE002563) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1778 | 0.1935 | -2.77 | down | 0.0010 | -5.69 | down | 0.0525 | -3.24 | down | leucyl/phenylalanyl-tRNA--protein transferase\ Context:(NC_002946)-[1748121-1748846]\ Notes:leucyltransferase; phenylalanyltransferse; functions in the N-end rule pathway; transfers Leu; Phe; Met; from aminoacyl-tRNAs to N-terminal of proteins with Arg or Lys |

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| NGO1779 | 0.0968 | 2.72 | up | 0.2495 | 1.64 | up | 0.2776 | 1.49 | up | hypothetical protein\ Context:(NC_002946)-[1748916-1749350]\ Notes:Best Blastp Hit: sp\|Q51008\|FUR_NEIGO ferric uptake regulation protein (ferric uptake regulator) >gi\|349012\|gb\|AAA72351.1\| (L11361) [Neisseria gonorrheae fur gene homologue; complete cds.]; gene product [Neisseria gonorrhoeae] COG0735 Ferric uptake regulation protein |
| NGO1780 | 0.4595 | 1.53 | up | 0.7894 | 1.13 | up | 0.2403 | 1.42 | up | hypothetical protein\ Context:(NC_002946)+[1749577-1749954]\ Notes:Best Blastp Hit: pir\|\|H81997 probable lipoprotein NMA0065 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378838\|emb\|CAB83381.1\| (AL162752) putative lipoprotein [Neisseria meningitidis] |
| NGO1781 | 0.0886 | 2.50 | up | 0.0451 | 2.21 | up | 0.0539 | 1.74 | up | dihydrodipicolinate reductase\ Context:(NC_002946)+[1749964-1750773]\ Notes:catalyzes the reduction of 2;3-dihydrodipicolinate to 2;3;4;5-tetrahydrodipicolinate in lysine and diaminopimelate biosynthesis |
| NGO1782 | 0.0397 | -3.04 | down | 0.0082 | -7.53 | down | 0.0804 | -2.96 | down | LpxB\ Context:(NC_002946)-[1751413-1752585]\ Notes:Best Blastp Hit: pir\|\|A81226 lipid-A-disaccharide synthase NMB0199 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225420\|gb\|AAF40656.1\| (AE002377) lipid-A-disaccharide synthase [Neisseria meningitidis MC58] COG0763 Lipid A disaccharide synthetase; putative lipid-A-disaccharide synthase |
| NGO1783 | 0.0784 | 2.86 | up | 0.5355 | -1.28 | down | 0.1529 | -1.87 | down | RluC\ Context:(NC_002946)-[1752736-1753728]\ Notes:Best Blastp Hit: pir\|\|E81998 pseudouridylate synthase (EC 4.2.1.70) C rRNA-specific NMA0070 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378843\|emb\|CAB83386.1\| (AL162752) ribosomal large subunit pseudouridine synthase C [Neisseria meningitidis] COG0564 Predicted pseudouridylate synthase family 2; putative ribosomal large subunit pseudouridine synthase C |
| NGO1784 | 0.0324 | -5.50 | down | 0.0350 | -7.88 | down | 0.8428 | -1.14 | down | hypothetical protein\ Context:(NC_002946)-[1753810-1754115]\ Notes:Best Blastp Hit: gb\|AAF40654.1\| (AE002377) hypothetical protein [Neisseria meningitidis MC58] |

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| NGO1785 | 0.8604 | 1.08 | up | 0.1731 | 2.15 | up | 0.3808 | 1.72 | up | Rne\ Context:(NC_002946)+[1754221-1756980]\ Notes:Best Blastp Hit: gb\|AAF40653.1\| (AE002377) ribonuclease E [Neisseria meningitidis MC58] COG1530 Ribonucleases G and E; putative ribonuclease E |
| NGO1786 | 0.1278 | 3.12 | up | 0.8284 | 1.17 | up | 0.6961 | -1.28 | down | PdxA\ Context:(NC_002946)-[1757210-1758202]\ Notes:Best Blastp Hit: pir\|\|H81227 pyridoxal phosphate biosynthetic protein PdxA NMB0195 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225415\|gb\|AAF40652.1\| (AE002376) pyridoxal phosphate biosynthetic protein PdxA [Neisseria meningitidis MC58] COG1995 Pyridoxin biosynthesis protein of unknown; putative pyridoxal phosphate biosynthetic protein |
| NGO1787 | 0.9749 | -1.02 | down | 0.3130 | -1.59 | down | 0.4244 | -1.25 | down | putative amino-acid transport protein\ Context:(NC_002946)+[1758361-1759788]\ Notes:Best Blastp Hit: pir\|\|G81227 probable amino-acid transport protein NMA0073 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225414\|gb\|AAF40651.1\| (AE002376) amino acid symporter; putative [Neisseria meningitidis MC58] >gi\|7378846\|emb\|CAB83389.1\| (AL162752) putative amino-acid transport protein [Neisseria meningitidis] COG1115 Sodium-alanine symporters |
| NGO1788 | 0.3143 | -1.88 | down | 0.1792 | -2.25 | down | 0.9295 | 1.04 | up | tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA\ Context:(NC_002946)+[1759970-1761856]\ Notes:GidA; glucose-inhibited cell division protein A; involved in the 5-carboxymethylaminomethyl modification (mnm(5)s(2)U) of the wobble uridine base in some tRNAs |
| NGO1789 | 0.7804 | -1.18 | down | 0.0378 | -4.68 | down | 0.0856 | 3.42 | up | hypothetical protein\ Context:(NC_002946)+[1761924-1762508]\ Notes:Best Blastp Hit: pir\|\|B81999 ribonuclease H (EC 3.1.26.4) II NMA0075 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378848\|emb\|CAB83391.1\| (AL162752) ribonuclease HII [Neisseria meningitidis] COG0164 Ribonuclease HII |

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| NGO1790 | 0.3733 | -1.47 | down | 0.4369 | -1.48 | down | 0.2440 | -2.01 | down | putative parA family protein - putative ATPase\ Context:(NC_002946)-[1763256-1764029]\ Notes:Best Blastp Hit: pir\|\|C81999 parA family protein NMA0076 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378849\|emb\|CAB83392.1\| (AL162752) parA family protein [Neisseria meningitidis] COG1192 ATPases involved in chromosome partitioning |
| NGO1791 | 0.0116 | -4.96 | down | 0.0194 | -4.20 | down | 0.0568 | -2.20 | down | glucose-inhibited division protein B\ Context:(NC_002946)-[1764129-1764752]\ Notes:probable SAM-dependent methyltransferase |
| NGO1792 | 0.1886 | -2.52 | down | 0.0070 | -9.56 | down | 0.1353 | -2.75 | down | hypothetical protein\ Context:(NC_002946)-[1764847-1765422]\ Notes:Best Blastp Hit: emb\|CAB83394.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] |
| NGO1793 | 0.0266 | -10.18 | down | 0.0917 | -16.66 | down | 0.4263 | -2.89 | down | hypothetical protein\ Context:(NC_002946)+[1765476-1766705]\ Notes:Best Blastp Hit: gb\|AAF40645.1\| (AE002376) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1795 | 0.3548 | 1.53 | up | 0.4088 | -1.63 | down | 0.9420 | 1.02 | up | DcmB\ Context:(NC_002946)+[1767623-1768648]\ Notes:Best Blastp Hit: pir\|\|CTNHP2 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) NgoPII - Neisseria gonorrhoeae >gi\|44873\|emb\|CAA30038.1\| (X06965) NgoPII methylase (AA 1-341) [Neisseria gonorrhoeae] >gi\|44888\|emb\|CAA36888.1\| (X52661) NgoPII restriction and modification [Neisseria gonorrhoeae] >gi\|293960\|gb\|AAA17019.1\| (L14564) cytosine methylase [Neisseria gonorrhoeae] >gi\|227054\|prf\|\|1613419B NgoPII methylase [Neisseria gonorrhoeae] COG0270 Site-specific DNA methylase dcm; site-specific DNA-methyltransferase M. NgoPII |

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| NGO1796 | 0.4846 | 1.53 | up | 0.6768 | 1.18 | up | 0.3822 | 1.33 | up | Rrf\ Context:(NC_002946)+[1768790-1769347]\ Notes:Best Blastp Hit: pir\|\|D81229 ribosome recycling factor NMB0187 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225406\|gb\|AAF40644.1\| (AE002375) ribosome recycling factor [Neisseria meningitidis MC58] >gi\|7378853\|emb\|CAB83396.1\| (AL162752) ribosome recycling factor [Neisseria meningitidis] COG0233 Ribosome recycling factor; putative ribosome recycling factor |
| NGO1797 | 0.4013 | 1.53 | up | 0.8014 | 1.12 | up | 0.8778 | 1.04 | up | putative undecaprenyl diphosphate synthase\ Context:(NC_002946)+[1769403-1770149]\ Notes:Best Blastp Hit: pir\|\|C81229 undecaprenyl pyrophosphate synthetase NMB0186 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225405\|gb\|AAF40643.1\| (AE002375) undecaprenyl pyrophosphate synthetase [Neisseria meningitidis MC58] COG0020 Undecaprenyl pyrophosphate synthase |
| NGO1798 | 0.7661 | 1.16 | up | 0.8797 | -1.07 | down | 0.9404 | 1.02 | up | putative phosphatidate cytidylyltransferase\ Context:(NC_002946)+[1770152-1770949]\ Notes:Best Blastp Hit: pir\|\|A82000 phosphatidate cytidylyltransferase (EC 2.7.7.41) NMA0082 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378855\|emb\|CAB83398.1\| (AL162752) phosphatidate cytidylyltransferase [Neisseria meningitidis] COG0575 CDP-diglyceride synthetase |
| NGO1799 | 0.4083 | 1.43 | up | 0.9639 | 1.02 | up | 0.8108 | 1.07 | up | 1-deoxy-D-xylulose 5-phosphate reductoisomerase\ Context:(NC_002946)+[1771005-1772189]\ Notes:catalyzes the NADP-dependent rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol 4-phosphate |
| NGO1800 | 0.2928 | 1.72 | up | 0.0605 | 2.10 | up | 0.2069 | 1.52 | up | hypothetical protein\ Context:(NC_002946)+[1772224-1773564]\ Notes:Best Blastp Hit: emb\|CAB83400.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] COG0750 Predicted membrane-associated Zn-dependent |

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| NGO1801 | 0.2120 | 2.18 | up | 0.1070 | 1.81 | up | 0.1078 | 2.12 | up | hypothetical protein\ Context:(NC_002946)+[1773621-1775999]\ Notes:Best Blastp Hit: gb\|AAC17600.1\|(U81959) outer membrane protein [Neisseria gonorrhoeae] COG0729 Predicted outer membrane protein |
| NGO1802 | 0.0365 | 2.97 | up | 0.0233 | 2.59 | up | 0.0511 | 2.61 | up | hypothetical protein\ Context:(NC_002946)+[1776008-1776565]\ Notes:Best Blastp Hit: gb\|AAF40638.1\|(AE002375) outer membrane protein OmpH; putative [Neisseria meningitidis MC58] |
| NGO1803 | 0.0382 | 3.11 | up | 0.0395 | 3.30 | up | 0.0557 | 2.53 | up | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase\ Context:(NC_002946)+[1776598-1777641]\ Notes:adds the O-linked and N-linked 3(R)-hydroxy fatty acids to the glucosamine disaccharide during lipid A biosynthesis |
| NGO1804 | 0.1170 | 2.46 | up | 0.0685 | 3.94 | up | 0.1531 | 1.96 | up | (3R)-hydroxymyristoyl-ACP dehydratase\ Context:(NC_002946)+[1777677-1778126]\ Notes:in Pseudomonas aeruginosa this enzyme is a trimer of dimers; essential for membrane formation; performs third step of type II fatty acid biosynthesis; catalyzes dehydration of (3R)-hydroxyacyl-ACP to trans-2-acyl-ACP |
| NGO1805 | 0.1499 | 2.31 | up | 0.5650 | 1.48 | up | 0.4428 | 1.60 | up | hypothetical protein\ Context:(NC_002946)+[1778333-1779019]\ Notes:Best Blastp Hit: pir\|\|H82000 hypothetical protein NMA0089 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378862\|emb\|CAB83405.1\|(AL162752) hypothetical protein NMA0089 [Neisseria meningitidis] |
| NGO1806 | 0.2283 | 1.83 | up | 0.1850 | 2.64 | up | 0.0886 | 1.83 | up | UDP-N-acetylglucosamine acyltransferase\ Context:(NC_002946)+[1779062-1779838]\ Notes:catalyzes the addition of (R)-3-hydroxytetradecanoyl to the glucosamine disaccharide in lipid A biosynthesis |
| NGO1807 | 0.0051 | -6.60 | down | 0.0251 | -5.93 | down | 0.0054 | -4.20 | down | putative amino-acid transporter\ Context:(NC_002946)+[1780301-1781692]\ Notes:Best Blastp Hit: pir\|\|B81228 sodium/alanine symporter; probable NMB0177 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225396\|gb\|AAF40634.1\|(AE002375) sodium/alanine symporter; putative [Neisseria meningitidis MC58] COG1115 Sodium-alanine symporters |

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| NGO1808 | 0.0088 | -8.19 | down | 0.0016 | -24.23 | down | 0.0778 | -5.66 | down | D-amino acid dehydrogenase small subunit\ Context:(NC_002946)+[1781771-1783030]\ Notes:catalyzes the oxidative deamination of D-amino acids |
| NGO1809 | 0.5473 | 1.39 | up | 0.6152 | 1.21 | up | 0.1031 | 1.89 | up | valyl-tRNA synthetase\ Context:(NC_002946)+[1783135-1785972]\ Notes:valine--tRNA ligase; ValRS; converts valine ATP and tRNA(Val) to AMP PPi and valyl-tRNA(Val); class-I aminoacyl-tRNA synthetase type 1 subfamily; has a posttransfer editing process to hydrolyze mischarged Thr-tRNA(Val) which is done by the editing domain |
| NGO1810 | 0.2103 | 2.46 | up | 0.7188 | 1.24 | up | 0.4870 | 1.20 | up | hypothetical protein\ Context:(NC_002946)+[1786049-1786513]\ Notes: |
| NGO1811 | 0.9238 | -1.05 | down | 0.0276 | -2.77 | down | 0.8988 | -1.07 | down | tRNA pseudouridine synthase A\ Context:(NC_002946)+[1787384-1788181]\ Notes:mediates pseudouridylation (positions 38; 39; 40) at the tRNA anticodon region which contributes to the structural stability |
| NGO1812 | 0.1549 | 2.54 | up | 0.3736 | 1.34 | up | 0.3485 | 1.49 | up | major outer membrane protein porin P.IB\ Context:(NC_002946)+[1788698-1789744]\ Notes:Best Blastp Hit: gb\|AAC79472.1\| (AF090803) outer membrane protein I precursor [Neisseria gonorrhoeae]; por |
| NGO1813 | 0.1747 | 2.29 | up | 0.1573 | 1.63 | up | 0.9952 | 1.00 | up | LysR family transcriptional regulator\ Context:(NC_002946)-[1790265-1791185]\ Notes:Best Blastp Hit: pir\|\|H82001 probable hydrogen peroxide-inducible genes activator NMA0098 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378870\|emb\|CAB83413.1\| (AL162752) putative hydrogen peroxide-inducible genes activator [Neisseria meningitidis] COG0583 Transcriptional regulators; LysR family |
| NGO1814 | 0.3805 | 1.68 | up | 0.8092 | 1.09 | up | 0.5239 | 1.28 | up | hypothetical protein\ Context:(NC_002946)-[1791189-1791452]\ Notes:Best Blastp Hit: emb\|CAB83414.1\| (AL162752) putative cell division topological specificity factor [Neisseria meningitidis] COG0851 Bacterial cell division topological |
| NGO1816 | 0.9561 | 1.03 | up | 0.6394 | -1.22 | down | 0.5326 | -1.21 | down | septum formation inhibitor\ Context:(NC_002946)-[1792300-1793013]\ Notes:blocks the formation of polar Z-ring septums |

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| NGO1817 | 0.2768 | 1.93 | up | 0.4270 | 1.30 | up | 0.4411 | 1.24 | up | 50S ribosomal protein L17\ Context:(NC_002946)-[1793160-1793528]\ Notes:is a component of the macrolide binding site in the peptidyl transferase center |
| NGO1818 | 0.1296 | 2.42 | up | 0.2757 | 1.44 | up | 0.2972 | 1.39 | up | DNA-directed RNA polymerase subunit alpha\ Context:(NC_002946)-[1793552-1794538]\ Notes:catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. Dimerization of the alpha subunit is the first step in the sequential assembly of subunits to form the holoenzyme |
| NGO1819 | 0.1631 | 2.52 | up | 0.3555 | 1.41 | up | 0.1910 | 1.63 | up | 30S ribosomal protein S4\ Context:(NC_002946)-[1794564-1795184]\ Notes:primary rRNA binding protein; nucleates 30S assembly; involved in translational accuracy with proteins S5 and S12; interacts with protein S5; involved in autogeneously regulating ribosomal proteins by binding to pseudoknot structures in the polycistronic mRNA; interacts with transcription complex and functions similar to protein NusA in antitermination |
| NGO1820 | 0.0866 | 3.07 | up | 0.1974 | 1.58 | up | 0.2033 | 1.61 | up | 30S ribosomal protein S11\ Context:(NC_002946)-[1795204-1795599]\ Notes:located on the platform of the 30S subunit; it bridges several disparate RNA helices of the 16S rRNA; forms part of the Shine-Dalgarno cleft in the 70S ribosome; interacts with S7 and S18 and IF-3 |
| NGO1821 | 0.1005 | 2.96 | up | 0.2158 | 1.56 | up | 0.2163 | 1.57 | up | 30S ribosomal protein S13\ Context:(NC_002946)-[1795619-1795981]\ Notes:located at the top of the head of the 30S subunit; it contacts several helices of the 16S rRNA; makes contact with the large subunit via RNA-protein interactions and via protein-protein interactions with L5; contacts P-site tRNA |
| NGO18211 | 0.0921 | 2.59 | up | 0.2016 | 1.61 | up | 0.3547 | 1.34 | up | translation initiation factor IF-1\ Context:(NC_002946)-[1796181-1796399]\ Notes:stimulates the activities of the other two initiation factors; IF-2 and IF-3 |

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| NGO1822 | 0.2411 | 2.08 | up | 0.3337 | 1.47 | up | 0.4299 | 1.28 | up | preprotein translocase subunit SecY\ Context:(NC_002946)-[1796404-1797714]\ Notes:forms heterotrimeric complex in the membrane; in bacteria the complex consists of SecY which forms the channel pore and SecE and SecG; the SecG subunit is not essential; in bacteria translocation is driven via the SecA ATPase |
| NGO1823 | 0.1326 | 2.64 | up | 0.3960 | 1.37 | up | 0.3309 | 1.39 | up | 50S ribosomal protein L15\ Context:(NC_002946)-[1797726-1798160]\ Notes:late assembly protein |
| NGO18231 | 0.0872 | 2.91 | up | 0.3189 | 1.44 | up | 0.3385 | 1.36 | up | 50S ribosomal protein L30\ Context:(NC_002946)-[1798162-1798347]\ Notes:L30 binds domain II of the 23S rRNA and the 5S rRNA; similar to eukaryotic protein L7 |
| NGO1824 | 0.0927 | 2.78 | up | 0.3263 | 1.45 | up | 0.4242 | 1.30 | up | 30S ribosomal protein S5\ Context:(NC_002946)-[1798340-1798858]\ Notes:located at the back of the 30S subunit body where it stabilizes the conformation of the head with respect to the body; contacts S4 and S8; with S4 and S12 plays a role in translational accuracy; mutations in this gene result in spectinomycin resistance |
| NGO18241 | 0.0887 | 3.08 | up | 0.2855 | 1.49 | up | 0.2568 | 1.52 | up | 50S ribosomal protein L18\ Context:(NC_002946)-[1798877-1799230]\ Notes:binds 5S rRNA along with protein L5 and L25 |
| NGO1825 | 0.0805 | 3.15 | up | 0.2419 | 1.57 | up | 0.2614 | 1.47 | up | 50S ribosomal protein L6\ Context:(NC_002946)-[1799244-1799777]\ Notes:ribosomal protein L6 appears to have arisen as a result of an ancient gene duplication as based on structural comparison of the Bacillus stearothermophilus protein; RNA-binding appears to be in the C-terminal domain; mutations in the L6 gene confer resistance to aminoglycoside antibiotics such as gentamicin and these occur in truncations of the C-terminal domain; it has been localized to a region between the base of the L7/L12 stalk and the central protuberance |
| NGO1826 | 0.0846 | 3.11 | up | 0.3259 | 1.45 | up | 0.1658 | 1.65 | up | 30S ribosomal protein S8\ Context:(NC_002946)-[1799791-1800183]\ Notes:binds directly to 16S rRNA central domain where it helps coordinate assembly of the platform of the 30S subunit |

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| NGO18261 | 0.0945 | 3.02 | up | 0.3458 | 1.40 | up | 0.2914 | 1.42 | up | 30S ribosomal protein S14\ Context:(NC_002946)-[1800199-1800504]\ Notes:located in the peptidyl transferase center and involved in assembly of 30S ribosome subunit; similar to what is observed with proteins L31 and L33; some proteins in this family contain CXXC motifs that are involved in zinc binding; if two copies are present in a genome; then the duplicated copy appears to have lost the zinc-binding motif and is instead regulated by zinc; the proteins in this group do not appear to have the zinc-binding motif |
| NGO1827 | 0.1440 | 2.70 | up | 0.2727 | 1.49 | up | 0.3091 | 1.43 | up | 50S ribosomal protein L5\ Context:(NC_002946)-[1800507-1801046]\ Notes:part of 50S and 5S/L5/L18/L25 subcomplex; contacts 5S rRNA and P site tRNA; forms a bridge to the 30S subunit in the ribosome by binding to S13 |
| NGO1828 | 0.1390 | 2.69 | up | 0.3216 | 1.45 | up | 0.2768 | 1.47 | up | 50S ribosomal protein L24\ Context:(NC_002946)-[1801056-1801379]\ Notes:assembly initiator protein; binds to 5' end of 23S rRNA and nucleates assembly of the 50S; surrounds polypeptide exit tunnel |
| NGO1829 | 0.1216 | 2.85 | up | 0.2794 | 1.49 | up | 0.3011 | 1.42 | up | 50S ribosomal protein L14\ Context:(NC_002946)-[1801391-1801759]\ Notes:binds to the 23S rRNA between the centers for peptidyl transferase and GTPase |
| NGO1830 | 0.1146 | 2.95 | up | 0.3036 | 1.46 | up | 0.0874 | 1.91 | up | 30S ribosomal protein S17\ Context:(NC_002946)-[1801981-1802244]\ Notes:primary binding protein; helps mediate assembly; involved in translation fidelity |
| NGO1831 | 0.0824 | 3.25 | up | 0.1744 | 1.62 | up | 0.1359 | 1.70 | up | 50S ribosomal protein L29\ Context:(NC_002946)-[1802244-1802435]\ Notes:one of the stabilizing components for the large ribosomal subunit |
| NGO18311 | 0.0790 | 3.02 | up | 0.2552 | 1.48 | up | 0.1022 | 1.86 | up | 50S ribosomal protein L16\ Context:(NC_002946)-[1802435-1802851]\ Notes:located in the peptidyl transferase center and may be involved in peptidyl transferase activity; similar to archaeal L10e |
| NGO1832 | 0.0698 | 3.17 | up | 0.1844 | 1.62 | up | 0.1436 | 1.69 | up | 30S ribosomal protein S3\ Context:(NC_002946)-[1802835-1803527]\ Notes:forms a complex with S10 and S14; binds the lower part of the 30S subunit head and the mRNA in the complete ribosome to position it for translation |

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| NGO1833 | 0.0322 | 4.00 | up | 0.5081 | 1.36 | up | 0.1017 | 1.71 | up | 50S ribosomal protein L22\ Context:(NC_002946)-[1803537-1803866]\ Notes:binds specifically to 23S rRNA during the early stages of 50S assembly; makes contact with all 6 domains of the 23S rRNA in the assembled 50S subunit and ribosome; mutations in this gene result in erythromycin resistance; located near peptidyl-transferase center |
| NGO1834 | 0.0718 | 3.27 | up | 0.1557 | 1.74 | up | 0.1898 | 1.56 | up | 30S ribosomal protein S19\ Context:(NC_002946)-[1803875-1804153]\ Notes:protein S19 forms a complex with S13 that binds strongly to the 16S ribosomal RNA |
| NGO1835 | 0.0788 | 3.23 | up | 0.2097 | 1.59 | up | 0.1138 | 1.81 | up | 50S ribosomal protein L2\ Context:(NC_002946)-[1804159-1804992]\ Notes:one of the primary rRNA-binding proteins; required for association of the 30S and 50S subunits to form the 70S ribosome; for tRNA binding and peptide bond formation |
| NGO1836 | 0.0842 | 2.96 | up | 0.1769 | 1.69 | up | 0.1722 | 1.60 | up | 50S ribosomal protein L23\ Context:(NC_002946)-[1804998-1805318]\ Notes:binds third domain of 23S rRNA and protein L29; part of exit tunnel |
| NGO1837 | 0.0766 | 2.97 | up | 0.1807 | 1.70 | up | 0.2132 | 1.50 | up | 50S ribosomal protein L4\ Context:(NC_002946)-[1805309-1805929]\ Notes:L4 is important during the early stages of 50S assembly; it initially binds near the 5' end of the 23S rRNA |
| NGO1838 | 0.1290 | 2.80 | up | 0.1672 | 1.66 | up | 0.1060 | 1.98 | up | 50S ribosomal protein L3\ Context:(NC_002946)-[1805929-1806573]\ Notes:binds directly near the 3' end of the 23S rRNA; where it nucleates assembly of the 50S subunit; essential for peptidyltransferase activity; mutations in this gene confer resistance to tiamulin |
| NGO1839 | 0.6487 | 1.41 | up | 0.4473 | -1.95 | down | 0.9290 | -1.06 | down | hypothetical protein\ Context:(NC_002946)-[1806791-1806982]\ Notes:Best Blastp Hit: emb\|CAB83446.1\|(AL162752) hypothetical protein NMA0132 [Neisseria meningitidis] |

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| NGO1841 | 0.1097 | 3.03 | up | 0.0842 | 1.96 | up | 0.0729 | 2.17 | up | 30S ribosomal protein S10\ Context:(NC_002946)-[1807359-1807670]\ Notes:NusE; involved in assembly of the 30S subunit; in the ribosome; this protein is involved in the binding of tRNA; in Escherichia coli this protein was also found to be involved in transcription antitermination; NusB/S10 heterodimers bind boxA sequences in the leader RNA of rrn operons which is required for antitermination; binding of NusB/S10 to boxA nucleates assembly of the antitermination complex |
| NGO1843 | 0.1149 | 2.65 | up | 0.1298 | 1.96 | up | 0.0751 | 1.94 | up | elongation factor G\ Context:(NC_002946)-[1808960-1811065]\ Notes:EF-G; promotes GTP-dependent translocation of the ribosome during translation; many organisms have multiple copies of this gene |
| NGO1844 | 0.0789 | 3.12 | up | 0.3846 | 1.36 | up | 0.2423 | 1.49 | up | 30S ribosomal protein S7\ Context:(NC_002946)-[1811084-1811554]\ Notes:binds directly to 16S rRNA where it nucleates assembly of the head domain of the 30S subunit |
| NGO1845 | 0.0903 | 2.95 | up | 0.3400 | 1.41 | up | 0.3548 | 1.38 | up | 30S ribosomal protein S12\ Context:(NC_002946)-[1811672-1812043]\ Notes:interacts with and stabilizes bases of the 16S rRNA that are involved in tRNA selection in the A site and with the mRNA backbone; located at the interface of the 30S and 50S subunits; it traverses the body of the 30S subunit contacting proteins on the other side; mutations in the S12 gene confer streptomycin resistance |
| NGO1846 | 0.0115 | -12.77 | down | 0.0008 | -31.40 | down | 0.0691 | -6.14 | down | hypothetical protein\ Context:(NC_002946)-[1812222-1812371]\ Notes:Best Blastp Hit: emb\|CAB83453.1\|(AL162752) hypothetical protein NMA0138 [Neisseria meningitidis] |
| NGO1847 | 0.2672 | -2.23 | down | 0.0046 | -16.84 | down | 0.2159 | -3.43 | down | hypothetical protein\ Context:(NC_002946)-[1812378-1813307]\ Notes:Best Blastp Hit: gb\|AAF41823.1\|(AE002496) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1848 | 0.5314 | -1.38 | down | 0.0945 | -5.91 | down | 0.6454 | -1.54 | down | hypothetical protein\ Context:(NC_002946)-[1813279-1813521]\ Notes:Best Blastp Hit: gb\|AAF40593.1\|(AE002372) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1849 | 0.0013 | -15.59 | down | 0.0011 | -13.64 | down | 0.0039 | -13.67 | down | hypothetical protein\ Context:(NC_002946)-[1813761-1814822]\ Notes:Best Blastp Hit: possibly phase variable - 8G residue homopolymer repeat in the coding sequence (ON) |
| NGO1850 | 0.0264 | 3.88 | up | 0.0308 | 4.23 | up | 0.0747 | 2.36 | up | DNA-directed RNA polymerase subunit beta'\ Context:(NC_002946)-[1815110-1819285]\ Notes:DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. Subunit beta' binds to sigma factor allowing it to bind to the -10 region of the promoter |
| NGO1851 | 0.0496 | 2.99 | up | 0.0205 | 3.15 | up | 0.0701 | 2.03 | up | DNA-directed RNA polymerase subunit beta\ Context:(NC_002946)-[1819438-1823616]\ Notes:DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates; beta subunit is part of the catalytic core which binds with a sigma factor to produce the holoenzyme |
| NGO1852 | 0.1350 | 2.50 | up | 0.4554 | 1.30 | up | 0.3596 | 1.49 | up | 50S ribosomal protein L7/L12\ Context:(NC_002946)-[1823807-1824178]\ Notes:present in two forms; L12 is normal; while L7 is aminoacylated at the N-terminal serine; the only multicopy ribosomal protein; 4:1 ratio of L7/L12 per ribosome; two L12 dimers bind L10; critically important for translation efficiency and fidelity; stimulates GTPase activity of translation factors |
| NGO1853 | 0.1397 | 2.52 | up | 0.4756 | 1.29 | up | 0.4447 | 1.32 | up | 50S ribosomal protein L10\ Context:(NC_002946)-[1824236-1824736]\ Notes:binds the two ribosomal protein L7/L12 dimers and anchors them to the large ribosomal subunit |
| NGO1854 | 0.2334 | 2.02 | up | 0.6453 | 1.17 | up | 0.6818 | 1.14 | up | 50S ribosomal protein L1\ Context:(NC_002946)-[1824964-1825659]\ Notes:in Escherichia coli and Methanococcus; this protein autoregulates expression; the binding site in the mRNA mimics the binding site in the 23S rRNA |
| NGO1855 | 0.2727 | 2.00 | up | 0.6165 | 1.19 | up | 0.5398 | 1.26 | up | 50S ribosomal protein L11\ Context:(NC_002946)-[1825659-1826093]\ Notes:binds directly to 23S ribosomal RNA |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1856 | 0.0882 | 2.87 | up | 0.1612 | 1.68 | up | 0.2799 | 1.39 | up | transcription antitermination protein NusG\ Context:(NC_002946)-[1826194-1826730]\ Notes:Modulates Rho-dependent transcription termination |
| NGO1857 | 0.0802 | 3.85 | up | 0.0805 | 1.94 | up | 0.2099 | 1.45 | up | preprotein translocase subunit SecE\ Context:(NC_002946)-[1826732-1827010]\ Notes:forms a complex with SecY and SecG; SecYEG forms a putative protein-conducting channel to which secA binds and translocates targeted polypeptides across the cytoplasmic membrane; a process driven by ATP and a proton-motive force |
| NGO1859 | 0.9639 | 1.02 | up | 0.2575 | -2.04 | down | 0.1780 | -2.08 | down | putative ferredoxin\ Context:(NC_002946)-[1828808-1829059]\ Notes:Best Blastp Hit: pir\|\|H81234 ferredoxin; 4Fe-4S bacterial type NMB0123 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225340\|gb\|AAF40582.1\| (AE002371) ferredoxin; 4Fe-4S bacterial type [Neisseria meningitidis MC58] COG1145 Ferredoxin 2 |
| NGO1860 | 0.7606 | 1.18 | up | 0.9929 | -1.00 | down | 0.8235 | -1.07 | down | putative DNA methylase\ Context:(NC_002946)-[1829182-1829751]\ Notes:Best Blastp Hit: emb\|CAB83466.1\| (AL162752) possible DNA methylase [Neisseria meningitidis] COG0742 N6-adenine-specific methylase |
| NGO1861 | 0.0033 | -7.70 | down | 0.7545 | -1.21 | down | 0.7009 | 1.37 | up | hypothetical protein\ Context:(NC_002946)-[1829854-1830192]\ Notes:Best Blastp Hit: pir\|\|F82008 hypothetical protein NMA0153 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378924\|emb\|CAB83467.1\| (AL162752) hypothetical protein NMA0153 [Neisseria meningitidis] |
| NGO1863 | 0.3573 | 1.57 | up | 0.0846 | 2.06 | up | 0.0601 | 1.89 | up | DNA topoisomerase I\ Context:(NC_002946)-[1832027-1834333]\ Notes:catalyzes the ATP-dependent breakage of single-stranded DNA followed by passage and rejoining; maintains net negative superhelicity |
| NGO1864 | 0.4737 | -1.39 | down | 0.4224 | -1.47 | down | 0.4186 | -1.29 | down | hypothetical protein\ Context:(NC_002946)-[1834411-1834872]\ Notes:Best Blastp Hit: gb\|AAF40576.1\| (AE002370) smg protein; putative [Neisseria meningitidis MC58] >gi\|7378928\|emb\|CAB83471.1\| (AL162752) hypothetical protein NMA0157 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1865 | 0.7091 | 1.20 | up | 0.8693 | -1.08 | down | 0.8096 | -1.07 | down | hypothetical protein\ Context:(NC_002946)-[1834898-1836085]\ Notes:Best Blastp Hit: pir\|\|C82009 DprA homolog NMA0158 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378929\|emb\|CAB83472.1\| (AL162752) DprA homolog [Neisseria meningitidis] COG0758 protein involved in DNA uptake |
| NGO1866 | 0.4259 | 1.44 | up | 0.8807 | 1.07 | up | 0.9140 | -1.04 | down | putative two-component system transcriptional response regulator\ Context:(NC_002946)-[1836176-1837453]\ Notes:Best Blastp Hit: gb\|AAF40574.1\| (AE002370) nitrogen assimilation regulatory protein NtrX [Neisseria meningitidis MC58] COG2204 AAA superfamily ATPases with N-terminal |
| NGO1867 | 0.3836 | 1.65 | up | 0.3918 | 1.66 | up | 0.3328 | 1.32 | up | putative two-component system sensor kinase\ Context:(NC_002946)-[1837446-1839566]\ Notes:Best Blastp Hit: emb\|CAB83474.1\| (AL162752) putative two-component sensor [Neisseria meningitidis] COG0642 Sensory transduction histidine kinases |
| NGO1868 | 0.3382 | 1.65 | up | 0.4623 | 1.36 | up | 0.3416 | 1.32 | up | hypothetical protein\ Context:(NC_002946)-[1839566-1840165]\ Notes:Best Blastp Hit: pir\|\|F82009 hypothetical protein NMA0161 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378932\|emb\|CAB83475.1\| (AL162752) hypothetical protein NMA0161 [Neisseria meningitidis] |
| NGO1869 | 0.0821 | 2.27 | up | 0.6920 | 1.19 | up | 0.1919 | 1.44 | up | putative 16S RNA methyltransferase\ Context:(NC_002946)-[1840131-1841390]\ Notes:Best Blastp Hit: emb\|CAB83476.1\| (AL162752) SUN homolog [Neisseria meningitidis] COG0144 Predicted rRNA methylase |
| NGO1870 | 0.0999 | 2.13 | up | 0.6446 | 1.28 | up | 0.5736 | 1.17 | up | hypothetical protein\ Context:(NC_002946)-[1841469-1842395]\ Notes:Best Blastp Hit: pir\|\|F81238 methionyl-tRNA formyltransferase NMB0111 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225326\|gb\|AAF40570.1\| (AE002369) methionyl-tRNA formyltransferase [Neisseria meningitidis MC58] COG0223 Methionyl-tRNA formyltransferase |
| NGO1871 | 0.1973 | 2.18 | up | 0.3137 | 1.45 | up | 0.3929 | 1.43 | up | peptide deformylase\ Context:(NC_002946)-[1842483-1842986]\ Notes:cleaves off formyl group from N-terminal methionine residues of newly synthesized proteins; binds iron(2+) |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1872 | 0.1440 | 2.53 | up | 0.1674 | 1.67 | up | 0.0822 | 2.03 | up | hypothetical protein\ Context:(NC_002946)-[1843059-1843256]\ Notes: |
| NGO1873 | 0.2318 | 2.13 | up | 0.0801 | 1.93 | up | 0.2559 | 1.65 | up | hypothetical protein\ Context:(NC_002946)+[1843284-1844621]\ Notes:Best Blastp Hit: pir\|\|D81238 hypothetical protein NMB0109 - Neisseria meningitidis (group B strain MD58) >gi\|7225324\|gb\|AAF40568.1\| (AE002369) conserved hypothetical protein [Neisseria meningitidis MC58] COG1652 Uncharacterized BCR |
| NGO1874 | 0.0612 | -4.17 | down | 0.0074 | -52.58 | down | 0.4482 | 1.51 | up | hypothetical protein\ Context:(NC_002946)+[1844694-1844858]\ Notes:Best Blastp Hit: gb\|AAA96487.1\| (L36381) putative [Neisseria gonorrhoeae] |
| NGO1875 | 0.4075 | 1.49 | up | 0.1128 | 1.99 | up | 0.8568 | 1.06 | up | hypothetical protein\ Context:(NC_002946)-[1845042-1845692]\ Notes:Best Blastp Hit: pir\|\|C82010 probable integral membrane protein NMA0166 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378937\|emb\|CAB83480.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] |
| NGO1876 | 0.1921 | 1.92 | up | 0.4593 | 1.32 | up | 0.9395 | -1.02 | down | aspartate carbamoyltransferase regulatory subunit\ Context:(NC_002946)-[1845754-1846212]\ Notes:involved in the allosteric regulation of aspartate carbamoyltransferase |
| NGO1877 | 0.6707 | 1.21 | up | 0.8739 | -1.08 | down | 0.4624 | -1.44 | down | aspartate carbamoyltransferase catalytic subunit\ Context:(NC_002946)-[1846222-1847142]\ Notes:catalyzes the transfer of the carbamoyl moiety from carbamoyl phosphate to L- aspartate in pyrimidine biosynthesis |
| NGO1878 | 0.1575 | -2.15 | down | 0.5849 | -1.27 | down | 0.1068 | -1.73 | down | hypothetical protein\ Context:(NC_002946)+[1847378-1848220]\ Notes:Best Blastp Hit: pir\|\|F82010 hypothetical protein NMA0169 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378940\|emb\|CAB83483.1\| (AL162752) hypothetical protein NMA0169 [Neisseria meningitidis] COG0454 Predicted acetyltransferases |
| NGO18781 | 0.5895 | -2.58 | down | 0.3350 | 6.58 | up | 0.6964 | 2.52 | up | hypothetical protein\ Context:(NC_002946)+[1848738-1848974]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1879 | 0.1089 | 5.62 | up | 0.7348 | 1.56 | up | 0.8984 | -1.10 | down | hypothetical protein\ Context:(NC_002946)+[1849022-1849612]\ Notes:Best Blastp Hit: gb\|AAF40562.1\|(AE002369) bacteriocin resistance protein; putative [Neisseria meningitidis MC58] >gi\|7378945\|emb\|CAB83488.1\| (AL162752) hypothetical protein NMA0173 [Neisseria meningitidis] COG1101 ATPase components of various transport |
| NGO1880 | 0.6307 | 1.28 | up | 0.9291 | -1.04 | down | 0.9911 | -1.00 | down | hypothetical protein\ Context:(NC_002946)-[1849888-1850439]\ Notes:Best Blastp Hit: pir\|\|D82011 probable integral membrane protein NMA0174 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378946\|emb\|CAB83489.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] |
| NGO1881 | 0.0033 | 6.18 | up | 0.0312 | 3.86 | up | 0.0224 | 2.55 | up | PykA\ Context:(NC_002946)+[1851528-1853000]\ Notes:Best Blastp Hit: pir\|\|B81239 pyruvate kinase II NMB0089 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225307\|gb\|AAF40552.1\| (AE002368) pyruvate kinase II [Neisseria meningitidis MC58] COG0469 Pyruvate kinase; putative pyruvate kinase |
| NGO1886 | 0.2748 | -3.10 | down | 0.0010 | -32.15 | down | 0.6057 | -1.72 | down | hypothetical protein\ Context:(NC_002946)-[1854669-1855091]\ Notes:Best Blastp Hit: emb\|CAB83494.1\|(AL162752) hypothetical protein NMA0179 [Neisseria meningitidis] |
| NGO1887 | 0.0032 | -7.65 | down | 0.2289 | -3.64 | down | 0.9723 | -1.02 | down | hypothetical protein\ Context:(NC_002946)-[1855269-1855418]\ Notes:Best Blastp Hit: pir\|\|G81075 hypothetical protein NMB1507 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|4582968\|gb\|AAD24874.1\|AF073777_2 (AF073777) unknown [Neisseria meningitidis] >gi\|7226750\|gb\|AAF41863.1\| (AE002500) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1888 | 0.1307 | -4.26 | down | 0.0796 | -3.38 | down | 0.1996 | -2.12 | down | hypothetical protein\ Context:(NC_002946)-[1855436-1855633]\ Notes:Best Blastp Hit: gb\|AAF40550.1\|(AE002368) hypothetical protein [Neisseria meningitidis MC58] >gi\|7378953\|emb\|CAB83496.1\| (AL162752) hypothetical protein NMA0181 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1889 | 0.6236 | -1.36 | down | 0.0622 | -2.75 | down | 0.0688 | -2.40 | down | hypothetical protein\ Context:(NC_002946)-[1855643-1856659]\ Notes:Best Blastp Hit: pir\|\|G81238 hypothetical protein NMB0086 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225304\|gb\|AAF40549.1\|(AE002368) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1890 | 0.9515 | -1.04 | down | 0.3843 | 1.58 | up | 0.7956 | 1.11 | up | GltS\ Context:(NC_002946)-[1856758-1857972]\ Notes:Best Blastp Hit: pir\|\|F81240 sodium/glutamate symporter NMB0085 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225302\|gb\|AAF40548.1\|(AE002367) sodium/glutamate symporter [Neisseria meningitidis MC58] COG0786 Glutamate permease; putative glutamate permease |
| NGO1891 | 0.8692 | 1.12 | up | 0.2247 | -2.59 | down | 0.6309 | -1.41 | down | hypothetical protein\ Context:(NC_002946)-[1858225-1858506]\ Notes:Best Blastp Hit: gb\|AAC45837.1\|(AF001598) similar to Bordetella pertussis toxin accessory protein encoded by GenBank Accession Number X95386 [Neisseria gonorrhoeae] COG2183 Predicted RNA binding protein; contains S1 |
| NGO1893 | 0.6943 | -1.23 | down | 0.2777 | 1.64 | up | 0.7680 | -1.21 | down | DamH\ Context:(NC_002946)-[1859711-1860718]\ Notes:Best Blastp Hit: gb\|AAC45839.1\| (AF001598) N6-methyladenine methyltransferase [Neisseria gonorrhoeae] |
| NGO1894 | 0.5575 | -1.34 | down | 0.3967 | -1.37 | down | 0.1932 | -1.56 | down | putative 5-methylcytosine methyltransferase\ Context:(NC_002946)-[1860711-1861712]\ Notes:Best Blastp Hit: gb\|AAC45838.1\| (AF001598) 5-methylcytosine methyltransferase [Neisseria gonorrhoeae] COG0270 Site-specific DNA methylase dcm |
| NGO1895 | 0.5550 | 1.52 | up | 0.1900 | -1.83 | down | 0.5823 | -1.46 | down | hypothetical protein\ Context:(NC_002946)-[1861743-1864016]\ Notes:Best Blastp Hit: sp\|P57072\|YHGF_NEIMA hypothetical protein NMA0194 >gi\|11278680\|pir\|\|E82013 probable transcription accessory protein NMA0194 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378963\|emb\|CAB83508.1\| (AL162752) putative transcriptional accessory protein [Neisseria meningitidis] COG2183 Predicted RNA binding protein; contains S1 |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1896 | 0.0922 | -2.60 | down | 0.2135 | -2.02 | down | 0.1110 | -2.29 | down | hypothetical protein\ Context:(NC_002946)+[1864135-1865151]\ Notes:Best Blastp Hit: sp\|Q05026\|GALE_NEIGO UDP-glucose 4-epimerase (galactowaldenase) (UDP-galactose 4-epimerase) >gi\|486715\|pir\|\|S34984 UDPglucose 4-epimerase (EC 5.1.3.2) - Neisseria gonorrhoeae >gi\|1051296\|emb\|CAA79721.1\| (Z21508) UDP-glucose 4-epimerase [Neisseria gonorrhoeae] COG1087 UDP-glucose 4-epimerase |
| NGO1897 | 0.0809 | 3.91 | up | 0.3519 | 2.04 | up | 0.2236 | 1.78 | up | hypothetical protein\ Context:(NC_002946)+[1865152-1866192]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG1088 dTDP-D-glucose 4;6-dehydratase |
| NGO1898 | 0.3062 | -2.32 | down | 0.0337 | -3.86 | down | 0.9819 | -1.02 | down | glucose-1-phosphate thymidylyltransferase\ Context:(NC_002946)+[1866297-1867163]\ Notes:Best Blastp Hit: sp\|P37762\|RFBA_NEIGO glucose-1-phosphate thymidylyltransferase (DTDP-glucose synthase) (DTDP-glucose pyrophosphorylase) >gi\|628591\|pir\|\|S47046 glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) - Neisseria gonorrhoeae >gi\|520897\|emb\|CAA83653.1\| (Z32742) Glucose-1-phosphate thymidylyltransferase [Neisseria gonorrhoeae] >gi\|1333794\|emb\|CAA79719.1\| (Z21508) glucose-1-phosphate thymid transferase [Neisseria gonorrhoeae] COG1209 dTDP-glucose pyrophosphorylase |
| NGO1900 | 0.8934 | 1.06 | up | 0.6604 | -1.25 | down | 0.9363 | -1.02 | down | hypothetical protein\ Context:(NC_002946)-[1867902-1869920]\ Notes:Best Blastp Hit: pir\|\|B82015 probable integral membrane protein NMA0207 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378976\|emb\|CAB83521.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] COG1297 Uncharacterized membrane protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1901 | 0.1580 | 2.13 | up | 0.1518 | 1.77 | up | 0.2545 | 1.58 | up | putative heat shock protein/chaperone DnaJ\ Context:(NC_002946)-[1870115-1871236]\ Notes:Best Blastp Hit: sp\|P57107\|DNAJ_NEIMA chaperone protein DNAJ >gi\|11277169\|pir\|\|D81242 DnaJ protein NMA0209 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225280\|gb\|AAF40528.1\| (AE002365) dnaJ protein [Neisseria meningitidis MC58] >gi\|7378977\|emb\|CAB83522.1\| (AL162752) DnaJ protein [Neisseria meningitidis] COG0484 Molecular chaperones; DnaJ family (contain |
| NGO1904 | 0.3386 | 1.55 | up | 0.2719 | 1.47 | up | 0.6486 | 1.13 | up | DskA\ Context:(NC_002946)-[1878578-1878994]\ Notes:Best Blastp Hit: gb\|AAF40525.1\| (AE002364) DnaK suppressor protein [Neisseria meningitidis MC58] COG1734 DnaK suppressor protein DskA; putative dosage-dependent DnaK suppressor protein |
| NGO1905 | 0.9756 | -1.02 | down | 0.1768 | -1.69 | down | 0.2309 | -1.49 | down | putative pyrroline-5-carboxylate reductase\ Context:(NC_002946)-[1879145-1879936]\ Notes:Best Blastp Hit: pir\|\|H82015 probable pyrroline-5-carboxylate reductase (EC 1.5.1.2) NMA0215 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378982\|emb\|CAB83527.1\| (AL162752) putative pyrroline-5-carboxylate reductase [Neisseria meningitidis] COG0345 Pyrroline-5-carboxylate reductase |
| NGO1906 | 0.0884 | -2.59 | down | 0.1776 | -1.97 | down | 0.1969 | -2.15 | down | hypothetical protein\ Context:(NC_002946)-[1879985-1880392]\ Notes:Best Blastp Hit: pir\|\|A82016 probable lipoprotein NMA0216 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378983\|emb\|CAB83528.1\| (AL162752) putative lipoprotein [Neisseria meningitidis] |
| NGO1907 | 0.3817 | 1.77 | up | 0.9377 | 1.06 | up | 0.3533 | -2.05 | down | hypothetical protein\ Context:(NC_002946)-[1880392-1881078]\ Notes:Best Blastp Hit: pir\|\|C81243 conserved hypothetical protein NMB0053 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225273\|gb\|AAF40522.1\| (AE002364) conserved hypothetical protein [Neisseria meningitidis MC58] COG0325 Predicted enzyme with a TIM-barrel fold |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1908 | 0.4734 | 1.53 | up | 0.6266 | 1.20 | up | 0.5965 | 1.20 | up | twitching motility/pilus retraction protein\ Context:(NC_002946)+[1881198-1882241]\ Notes:Best Blastp Hit: gb\|AAB30824.1\| (S72391) PilT=ATP binding casette protein homolog [Neisseria gonorrhoeae; MS11; Peptide; 347 aa] COG0630 Predicted ATPases involved in pili |
| NGO1909 | 0.2233 | 2.37 | up | 0.0587 | 2.59 | up | 0.0795 | 2.58 | up | putative twitching motility - like protein\ Context:(NC_002946)+[1882405-1883631]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0630 Predicted ATPases involved in pili |
| NGO1910 | 0.0491 | -4.28 | down | 0.0086 | -11.15 | down | 0.4587 | 1.46 | up | hypothetical protein\ Context:(NC_002946)+[1883748-1885898]\ Notes:Best Blastp Hit: pir\|\|H81242 conserved hypothetical protein NMB0050 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225270\|gb\|AAF40519.1\| (AE002364) conserved hypothetical protein [Neisseria meningitidis MC58] COG1289 Uncharacterized membrane protein; YhfK |
| NGO1911 | 0.2534 | 2.46 | up | 0.6414 | 1.20 | up | 0.3702 | -1.35 | down | hypothetical protein\ Context:(NC_002946)-[1886380-1886664]\ Notes:Best Blastp Hit: emb\|CAA05407.1\| (AJ002423) hypothetical protein [Neisseria gonorrhoeae] |
| NGO1913 | 0.0448 | -4.13 | down | 0.0463 | -13.54 | down | 0.8388 | -1.20 | down | hypothetical protein\ Context:(NC_002946)+[1891120-1891512]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) |
| NGO1914 | 0.0034 | -5.74 | down | 0.1626 | -2.91 | down | 0.0774 | -1.93 | down | 6-phosphogluconate dehydrogenase\ Context:(NC_002946)+[1891592-1893040]\ Notes:catalyzes the formation of D-ribulose 5-phosphate from 6-phospho-D-gluconate |
| NGO1915 | 0.1214 | -2.61 | down | 0.0691 | -3.90 | down | 0.2079 | -3.49 | down | 3-deoxy-D-manno-octulosonic-acid transferase\ Context:(NC_002946)+[1893103-1894374]\ Notes:catalyzes the transfer of 2-keto-3-deoxy-D-manno-octulosonic acid to lipid A |
| NGO1916 | 0.8723 | -1.12 | down | 0.0600 | -3.16 | down | 0.1505 | -2.91 | down | hypothetical protein\ Context:(NC_002946)+[1894415-1894864]\ Notes:Best Blastp Hit: pir\|\|C81248 conserved hypothetical protein NMB0013 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225238\|gb\|AAF40492.1\| (AE002359) conserved hypothetical protein [Neisseria meningitidis MC58] |

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| NGO1917 | 0.2533 | -2.08 | down | 0.5940 | -1.28 | down | 0.1311 | -3.33 | down | hypothetical protein\ Context:(NC_002946)+[1894897-1895871]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) COG0861 Membrane protein TerC; possibly involved in |
| NGO1918 | 0.9172 | -1.05 | down | 0.7528 | -1.14 | down | 0.6727 | -1.12 | down | UDP-N-acetylglucosamine1-carboxyvinyltransferase\ Context:(NC_002946)+[1896236-1897489]\ Notes:adds enolpyruvyl to UDP-N-acetylglucosamine as a component of cell wall formation; gram-positive bacteria have 2 copies of MurA which are active |
| NGO1919 | 0.3991 | -1.54 | down | 0.5325 | 1.26 | up | 0.4576 | 1.37 | up | phosphoglycerate kinase\ Context:(NC_002946)+[1897570-1898763]\ Notes:Converts 3-phospho-D-glycerate to 3-phospho-D-glyceroyl phosphate during the glycolysis pathway |
| NGO1920 | 0.1472 | 2.30 | up | 0.7337 | 1.15 | up | 0.3585 | 1.35 | up | hypothetical protein\ Context:(NC_002946)-[1898815-1899063]\ Notes:Best Blastp Hit: emb\|CAB83564.1\| (AL162752) hypothetical protein NMA0256 [Neisseria meningitidis] COG0271 Stress-induced morphogen BolA (activity |
| NGO1921 | 0.4791 | 1.49 | up | 0.9157 | -1.04 | down | 0.4575 | 1.21 | up | hypothetical protein\ Context:(NC_002946)-[1899156-1900073]\ Notes:Best Blastp Hit: sp\|P95357\|FTSX_NEIGO cell division protein FtsX homolog >gi\|1684782\|gb\|AAB36525.1\| (U76418) FtsX-like protein [Neisseria gonorrhoeae] COG2177 Cell division protein FtsX |
| NGO1922 | 0.7909 | -1.18 | down | 0.3014 | -1.45 | down | 0.6348 | -1.14 | down | hypothetical protein\ Context:(NC_002946)-[1900070-1900720]\ Notes:Best Blastp Hit: pir\|\|E81247 cell division ATP-binding protein FtsE NMB0007 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225232\|gb\|AAF40486.1\| (AE002359) cell division ATP-binding protein FtsE [Neisseria meningitidis MC58] COG1135 Uncharacterized ABC-type transport system |
| NGO1923 | 0.3644 | -1.55 | down | 0.2008 | -2.22 | down | 0.5544 | -1.19 | down | putative thioredoxin\ Context:(NC_002946)-[1900914-1901396]\ Notes:Best Blastp Hit: gb\|AAB36523.1\| (U76418) thioredoxin-like protein [Neisseria gonorrhoeae] COG0526 Thiol-disulfide isomerase and thioredoxins |

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| NGO1924 | 0.1818 | -2.05 | down | 0.0664 | -2.90 | down | 0.1553 | -1.86 | down | ArsC\ Context:(NC_002946)+[1901520-1901873]\ Notes:Best Blastp Hit: pir\|\|C81247 arsenate reductase NMB0005 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225230\|gb\|AAF40484.1\| (AE002359) arsenate reductase [Neisseria meningitidis MC58] >gi\|7379014\|emb\|CAB83560.1\| (AL162752) putative oxidoreductase [Neisseria meningitidis]; putative arsenate reductase |
| NGO1925 | 0.2190 | 2.21 | up | 0.9662 | -1.02 | down | 0.9870 | 1.00 | up | hypothetical protein\ Context:(NC_002946)+[1901870-1902526]\ Notes:Best Blastp Hit: emb\|CAB83559.1\| (AL162752) putative periplasmic protein [Neisseria meningitidis] COG1434 Uncharacterized ACR |
| NGO1926 | 0.3538 | 1.50 | up | 0.4751 | 1.32 | up | 0.1524 | 1.49 | up | glutamyl-tRNA synthetase\ Context:(NC_002946)+[1902642-1904036]\ Notes:Charges one glutamine molecule and pairs it to its corresponding RNA trinucleotide during protein translation |
| NGO1927 | 0.9496 | 1.04 | up | 0.7732 | 1.13 | up | 0.7125 | -1.18 | down | hypothetical protein\ Context:(NC_002946)+[1904057-1904452]\ Notes:Best Blastp Hit: pir\|\|H81246 hypothetical protein NMB0002 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225227\|gb\|AAF40481.1\| (AE002359) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1928 | 0.1664 | 3.04 | up | 0.2002 | 2.00 | up | 0.4300 | 1.59 | up | putative acetyltransferase\ Context:(NC_002946)+[1904456-1904947]\ Notes:Best Blastp Hit: pir\|\|D82019 probable acetyltransferase NMA0248 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379010\|emb\|CAB83556.1\| (AL162752) putative acetyltransferase [Neisseria meningitidis] COG0456 Acetyltransferases |
| NGO1929 | 0.5404 | -2.78 | down | 0.1018 | -6.96 | down | 0.3952 | 1.45 | up | hypothetical protein\ Context:(NC_002946)+[1904953-1905081]\ Notes:Best Blastp Hit: gb\|AAA96487.1\| (L36381) putative [Neisseria gonorrhoeae] |
| NGO1930 | 0.9653 | -1.02 | down | 0.4648 | -1.76 | down | 0.0230 | -3.77 | down | DNA mismatch repair protein\ Context:(NC_002946)-[1905223-1907817]\ Notes:This protein performs the mismatch recognition step during the DNA repair process |

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| NGO1931 | 0.0686 | 3.38 | up | 0.0216 | 2.59 | up | 0.0779 | 2.34 | up | GapC\ Context:(NC_002946)+[1908251-1909255]\ Notes:Best Blastp Hit: pir\|\|B82019 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C NMA0246 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379008\|emb\|CAB83554.1\| (AL162752) glyceraldehyde 3-phosphate dehydrogenase C [Neisseria meningitidis] COG0057 Glyceraldehyde-3-phosphate dehydrogenase; putative glyceraldehyde 3-phosphate dehydrogenase C |
| NGO1932 | 0.8055 | -1.18 | down | 0.3481 | 1.69 | up | 0.6075 | -1.29 | down | hypothetical protein\ Context:(NC_002946)-[1909407-1910087]\ Notes:Best Blastp Hit: gb\|AAF42466.1\| (AE002563) conserved hypothetical protein [Neisseria meningitidis MC58] COG1720 Uncharacterized ACR; YaeB/UPF0066 family |
| NGO1933 | 0.2479 | 1.84 | up | 0.6157 | 1.21 | up | 0.5482 | 1.20 | up | hypothetical protein\ Context:(NC_002946)+[1910547-1911182]\ Notes:Best Blastp Hit: gb\|AAF42465.1\| (AE002563) pyrazinamidase/nicotinamidase PncA; putative [Neisseria meningitidis MC58] COG1335 Amidases related to nicotinamidase |
| NGO1934 | 0.1869 | 1.94 | up | 0.0592 | 2.15 | up | 0.8946 | 1.03 | up | RfaC\ Context:(NC_002946)+[1911219-1912187]\ Notes:Best Blastp Hit: pir\|\|S60783 lipopolysaccharide heptosyltransferase (EC 2.4.99.-) I rfaC [similarity] - Neisseria gonorrhoeae >gi\|606855\|gb\|AAA93059.1\| (U10385) lipooligosaccharide heptosyltransferase-1 [Neisseria gonorrhoeae] COG0859 ADP-heptose:LPS heptosyltransferase; lipopolysaccharide heptosyltransferase I |
| NGO1935 | 0.2219 | 2.06 | up | 0.0611 | 2.53 | up | 0.4087 | 1.30 | up | EtfB\ Context:(NC_002946)+[1912413-1913162]\ Notes:Best Blastp Hit: pir\|\|A81001 electron transfer flavoprotein; beta chain NMB2155 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227413\|gb\|AAF42463.1\| (AE002563) electron transfer flavoprotein; beta subunit [Neisseria meningitidis MC58] COG2086 Electron transfer flavoprotein beta-subunit; putative electron transfer flavoprotein beta-subunit |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1936 | 0.2145 | 1.93 | up | 0.4182 | 1.35 | up | 0.5578 | 1.16 | up | EtfA\ Context:(NC_002946)+[1913173-1914108]\ Notes:Best Blastp Hit: pir\|\|H81000 electron transfer flavoprotein; alpha chain NMB2154 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227412\|gb\|AAF42462.1\| (AE002563) electron transfer flavoprotein; alpha subunit [Neisseria meningitidis MC58] COG2025 Electron transfer flavoprotein; putative electron transfer flavoprotein alpha-subunit |
| NGO1938 | 0.0004 | -27.26 | down | 0.0437 | -17.46 | down | 0.1674 | -2.87 | down | hypothetical protein\ Context:(NC_002946)-[1914832-1915035]\ Notes:Best Blastp Hit: pir\|\|F81000 hypothetical protein NMB2152 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227410\|gb\|AAF42460.1\| (AE002563) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1939 | 0.5419 | 1.32 | up | 0.3943 | 1.35 | up | 0.7807 | -1.08 | down | phosphoribosylamine--glycine ligase\ Context:(NC_002946)+[1915307-1916578]\ Notes:catalyzes the formation of N(1)-(5-phospho-D-ribosyl)glycinamide from 5-phospho-D-ribosylamine and glycine in purine biosynthesis |
| NGO1940 | 0.0304 | -4.45 | down | 0.0146 | -6.82 | down | 0.0008 | -6.57 | down | hypothetical protein\ Context:(NC_002946)+[1916612-1917214]\ Notes:Best Blastp Hit: emb\|CAB83545.1\| (AL162752) hypothetical protein NMA0237 [Neisseria meningitidis] COG0009 Putative translation factor (SUA5) |
| NGO1941 | 0.4033 | 2.51 | up | 0.8766 | 1.14 | up | 0.5854 | -1.60 | down | hypothetical protein\ Context:(NC_002946)+[1917229-1917744]\ Notes:Best Blastp Hit: emb\|CAB83544.1\| (AL162752) NMA0236; unknonwn; len: 77 aa [Neisseria meningitidis] |
| NGO1942 | 0.1911 | 2.45 | up | 0.3405 | 1.48 | up | 0.9519 | 1.02 | up | hypothetical protein\ Context:(NC_002946)-[1917896-1918318]\ Notes:Best Blastp Hit: pir\|\|A81003 probable lipoprotein NMA0233 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227404\|gb\|AAF42455.1\| (AE002562) hypothetical protein [Neisseria meningitidis MC58] >gi\|7378997\|emb\|CAB83542.1\| (AL162752) putative lipoprotein [Neisseria meningitidis] |
| NGO1943 | 0.3055 | -2.39 | down | 0.8157 | -1.33 | down | 0.3954 | -1.98 | down | hypothetical protein\ Context:(NC_002946)-[1918568-1918747]\ Notes:Best Blastp Hit: gb\|AAF42453.1\| (AE002562) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1944 | 0.2074 | 2.22 | up | 0.1409 | 1.83 | up | 0.6299 | -1.17 | down | RNA polymerase sigma factor\ Context:(NC_002946)-[1918753-1919340]\ Notes:Bacteria have multiple sigma factors which are active under specific conditions; the sigma factor binds with the catalytic core of RNA polymerase to produce the holoenzyme and directs bacterial core RNA polymerase to specific promoter elements to initiate transcription |
| NGO1945 | 0.3943 | 2.02 | up | 0.4562 | 2.73 | up | 0.0584 | -3.99 | down | hypothetical protein\ Context:(NC_002946)-[1919362-1920108]\ Notes:Best Blastp Hit: pir\|\|E82017 hypothetical protein NMA0229 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378995\|emb\|CAB83540.1\| (AL162752) hypothetical protein NMA0229 [Neisseria meningitidis] |
| NGO1946 | 0.8819 | -1.09 | down | 0.9388 | -1.05 | down | 0.0062 | -4.70 | down | hypothetical protein\ Context:(NC_002946)-[1920098-1920940]\ Notes:Best Blastp Hit: pir\|\|D82017 hypothetical protein NMA0228 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378994\|emb\|CAB83539.1\| (AL162752) hypothetical protein NMA0228 [Neisseria meningitidis] |
| NGO1947 | 0.2628 | 2.08 | up | 0.4431 | 1.35 | up | 0.3270 | 1.64 | up | hypothetical protein\ Context:(NC_002946)-[1921058-1921396]\ Notes:Best Blastp Hit: pir\|\|C81002 probable periplasmic protein NMA0227 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227398\|gb\|AAF42449.1\| (AE002562) hypothetical protein [Neisseria meningitidis MC58] >gi\|7378993\|emb\|CAB83538.1\| (AL162752) putative periplasmic protein [Neisseria meningitidis] |
| NGO1948 | 0.0046 | -7.85 | down | 0.0076 | -8.61 | down | 0.0006 | -7.92 | down | hypothetical protein\ Context:(NC_002946)-[1921470-1921919]\ Notes:Best Blastp Hit: pir\|\|B81002 conserved hypothetical protein NMB2140 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227397\|gb\|AAF42448.1\| (AE002562) conserved hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1949 | 0.3332 | -1.56 | down | 0.1522 | -1.94 | down | 0.2432 | -1.51 | down | hypothetical protein\ Context:(NC_002946)+[1922250-1923152]\ Notes:Best Blastp Hit: pir\|\|A82017 probable lipoprotein NMA0225 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378991\|emb\|CAB83536.1\|(AL162752) possible lipoprotein [Neisseria meningitidis] COG1752 Putative phosphoesterases; homologs of |
| NGO1951 | 0.8308 | -1.09 | down | 0.4486 | -1.51 | down | 0.2335 | -1.61 | down | peptide chain release factor 2\ Context:(NC_002946)+[1923255-1924358]\ Notes:recognizes the termination signals UGA and UAA during protein translation a specificity which is dependent on amino acid residues residing in loops of the L-shaped tRNA-like molecule of RF2; in some organisms control of PrfB protein levels is maintained through a +1 ribosomal frameshifting mechanism; this protein is similar to release factor 1 |
| NGO1952 | 0.7032 | -1.37 | down | 0.0023 | -20.01 | down | 0.1498 | 2.15 | up | hypothetical protein\ Context:(NC_002946)-[1924516-1924728]\ Notes:Best Blastp Hit: gb\|AAF42445.1\|(AE002562) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1953 | 0.7718 | 1.19 | up | 0.8425 | -1.12 | down | 0.4344 | -1.35 | down | hypothetical protein\ Context:(NC_002946)-[1924854-1925114]\ Notes:Best Blastp Hit: possibly phase variable - 8C residue homopolymer repeat in the coding sequence (ON) |
| NGO1954 | 0.1641 | -2.14 | down | 0.8644 | -1.14 | down | 0.9901 | -1.01 | down | putative peptide transporter\ Context:(NC_002946)-[1925126-1926583]\ Notes:Best Blastp Hit: gb\|AAF42444.1\| (AE002562) peptide transporter [Neisseria meningitidis MC58] COG0477 Permeases |
| NGO1955 | 0.6472 | 1.30 | up | 0.4188 | 2.10 | up | 0.1026 | 6.00 | up | hypothetical protein\ Context:(NC_002946)-[1927364-1931533]\ Notes:Best Blastp Hit: gb\|AAF42443.1\|(AE002561) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO1956 | 0.9310 | 1.08 | up | 0.0803 | -3.30 | down | 0.4461 | -1.62 | down | hypothetical protein\ Context:(NC_002946)-[1931588-1933495]\ Notes:Best Blastp Hit: pir\|\|G81003 conserved hypothetical protein NMB2134 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227390\|gb\|AAF42442.1\| (AE002561) conserved hypothetical protein [Neisseria meningitidis MC58] COG0729 Predicted outer membrane protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1957 | 0.7991 | 1.14 | up | 0.1597 | -2.09 | down | 0.9099 | -1.03 | down | serine/threonine transporter SstT\ Context:(NC_002946)+[1933806-1935035]\ Notes:involved in the import of serine and threonine coupled with the import of sodium |
| NGO1958 | 0.5114 | -1.52 | down | 0.8835 | 1.06 | up | 0.0421 | -3.15 | down | hypothetical protein\ Context:(NC_002946)+[1935186-1936475]\ Notes:Best Blastp Hit: gb\|AAF44763.1\|AF235146_1 (AF235146) GNA2132 [Neisseria gonorrhoeae] >gi\|7274418\|gb\|AAF44764.1\|AF235147_1 (AF235147) GNA2132 [Neisseria gonorrhoeae] |
| NGO1959 | 0.3476 | 1.67 | up | 0.9817 | 1.01 | up | 0.6118 | 1.20 | up | hypothetical protein\ Context:(NC_002946)+[1936475-1936678]\ Notes:Best Blastp Hit: pir\|\|B82029 probable malate dehydrogenase (acceptor) (EC 1.1.99.16) NMA0333 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379088\|emb\|CAB83637.1\| (AL162752) probable malate:quinone oxidoreductase [Neisseria meningitidis] |
| NGO1960 | 0.1871 | -2.37 | down | 0.0395 | -14.04 | down | 0.6529 | -1.25 | down | hypothetical protein\ Context:(NC_002946)+[1936946-1937212]\ Notes: |
| NGO1961 | 0.4746 | 1.41 | up | 0.7729 | 1.11 | up | 0.6466 | 1.17 | up | argininosuccinate synthase\ Context:(NC_002946)-[1937605-1938948]\ Notes:catalyzes the formation of arginosuccinate from citrulline and aspartate in arginine biosynthesis |
| NGO1962 | 0.8477 | 1.10 | up | 0.4118 | -1.52 | down | 0.7319 | 1.17 | up | hypothetical protein\ Context:(NC_002946)+[1939073-1939873]\ Notes:Best Blastp Hit: gb\|AAF42436.1\|(AE002560) CinA-related protein [Neisseria meningitidis MC58] COG1058 Uncharacterized ACR |
| NGO1963 | 0.4504 | 1.42 | up | 0.5344 | -1.32 | down | 0.3919 | -1.38 | down | putative protease\ Context:(NC_002946)+[1939913-1940899]\ Notes:Best Blastp Hit: emb\|CAB83609.1\|(AL162752) putative protease [Neisseria meningitidis] COG0616 Periplasmic serine proteases |
| NGO1965 | 0.9091 | -1.06 | down | 0.9079 | 1.06 | up | 0.1610 | -1.86 | down | hypothetical protein\ Context:(NC_002946)-[1942504-1942878]\ Notes:Best Blastp Hit: pir\|\|A82026 hypothetical protein NMA0307 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379063\|emb\|CAB83612.1\|(AL162752) hypothetical protein NMA0307 [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1966 | 0.9490 | -1.04 | down | 0.7677 | -1.15 | down | 0.3358 | -1.43 | down | hypothetical protein\ Context:(NC_002946)-[1943052-1943408]\ Notes:Best Blastp Hit: pir\|\|A81007 hypothetical protein NMB2106 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227367\|gb\|AAF42421.1\| (AE002559) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1967 | 0.7241 | -1.33 | down | 0.1771 | 3.13 | up | 0.8211 | -1.28 | down | hypothetical protein\ Context:(NC_002946)-[1944697-1945056]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) |
| NGO1969 | 0.2413 | 1.90 | up | 0.5546 | 1.30 | up | 0.5968 | -1.21 | down | hypothetical protein\ Context:(NC_002946)-[1947207-1947416]\ Notes:Best Blastp Hit: emb\|CAB83344.1\| (AL162752) hypothetical protein NMA0024 [Neisseria meningitidis] |
| NGO1970 | 0.0490 | 3.93 | up | 0.1125 | 2.01 | up | 0.7692 | -1.16 | down | hypothetical protein\ Context:(NC_002946)-[1947493-1947852]\ Notes:Best Blastp Hit: gb\|AAF40793.1\| (AE002391) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1971 | 0.3764 | 1.55 | up | 0.9954 | 1.00 | up | 0.5965 | -1.15 | down | MafB5\ Context:(NC_002946)-[1947857-1949353]\ Notes:Best Blastp Hit: possibly phase variable - two 8A residue homopolymer repeats in the coding sequence (ON); putative mafB-like adhesin |
| NGO1973 | 0.0047 | -8.15 | down | 0.2907 | -2.19 | down | 0.6145 | -1.48 | down | uridylate kinase\ Context:(NC_002946)-[1950486-1951205]\ Notes:Catalyzes the phosphorylation of UMP to UDP |
| NGO1974 | 0.1661 | 2.37 | up | 0.1906 | 1.58 | up | 0.3243 | 1.57 | up | elongation factor Ts\ Context:(NC_002946)-[1951422-1952276]\ Notes:EF-Ts; functions during elongation stage of protein translation; forms a dimer; associates with EF-Tu-GDP complex and promotes exchange of GDP to GTP resulting in regeneration of the active form of EF-Tu |
| NGO1975 | 0.1027 | 2.74 | up | 0.2749 | 1.45 | up | 0.1793 | 1.66 | up | 30S ribosomal protein S2\ Context:(NC_002946)-[1952405-1953133]\ Notes:one of the last subunits in the assembly of the 30S subunit; absence of S2 does not inhibit assembly but results in an inactive subunit |
| NGO1976 | 0.0290 | -6.88 | down | 0.0162 | -5.89 | down | 0.7557 | -1.22 | down | hypothetical protein\ Context:(NC_002946)-[1953306-1953539]\ Notes:Best Blastp Hit: gb\|AAF42417.1\| (AE002559) hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1977 | 0.0207 | -4.13 | down | 0.0249 | -5.83 | down | 0.8961 | -1.09 | down | hypothetical protein\ Context:(NC_002946)+[1953539-1954198]\ Notes:Best Blastp Hit: emb\|CAB83635.1\|(AL162752) hypothetical protein NMA0330 [Neisseria meningitidis] COG0212 5-formyltetrahydrofolate cyclo-ligase |
| NGO1978 | 0.4236 | 1.83 | up | 0.4887 | -1.91 | down | 0.0347 | -2.96 | down | hypothetical protein\ Context:(NC_002946)+[1954259-1954849]\ Notes:Best Blastp Hit: emb\|CAB83636.1\|(AL162752) hypothetical protein NMA0331 [Neisseria meningitidis] COG1670 Acetyltransferases; including N-acetylases |
| NGO1980 | 0.0168 | -4.29 | down | 0.0669 | -3.02 | down | 0.0144 | -3.85 | down | malate:quinone oxidoreductase\ Context:(NC_002946)+[1955233-1956699]\ Notes:malate dehydrogenase; catalyzes the oxidation of malate to oxaloacetate |
| NGO1981 | 0.7872 | 1.16 | up | 0.9544 | -1.04 | down | 0.8063 | 1.14 | up | hypothetical protein\ Context:(NC_002946)-[1956886-1957446]\ Notes:Best Blastp Hit: emb\|CAB83638.1\|(AL162752) putative adhesin component [Neisseria meningitidis] |
| NGO1982 | 0.1280 | 2.68 | up | 0.0560 | 3.03 | up | 0.2366 | 1.69 | up | hypothetical protein\ Context:(NC_002946)-[1957498-1957797]\ Notes:Best Blastp Hit: gb\|AAF42411.1\|(AE002558) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379090\|emb\|CAB83639.1\| (AL162752) hypothetical protein NMA0336 [Neisseria meningitidis] |
| NGO1983 | 0.4653 | 1.47 | up | 0.0499 | 3.36 | up | 0.1246 | 1.67 | up | hypothetical protein\ Context:(NC_002946)-[1957896-1958675]\ Notes:Best Blastp Hit: pir\|\|C81008 methionine aminopeptidase NMB2093 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227355\|gb\|AAF42410.1\| (AE002558) methionine aminopeptidase [Neisseria meningitidis MC58] COG0024 Methionine aminopeptidase |
| NGO1984 | 0.8633 | -1.08 | down | 0.9914 | 1.00 | up | 0.8430 | -1.14 | down | hypothetical protein\ Context:(NC_002946)-[1958715-1959365]\ Notes:Best Blastp Hit: gb\|AAF42409.1\|(AE002558) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1985 | 0.7611 | 1.18 | up | 0.8481 | -1.09 | down | 0.9947 | -1.00 | down | hypothetical protein\ Context:(NC_002946)-[1959373-1959981]\ Notes:Best Blastp Hit: pir\|\|G82029 probable lipoprotein NMA0339 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379093\|emb\|CAB83642.1\|(AL162752) putative lipoprotein [Neisseria meningitidis] |

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| NGO1986 | 0.9855 | -1.01 | down | 0.7006 | -1.20 | down | 0.6524 | -1.15 | down | phosphoheptose isomerase\ Context:(NC_002946)-[1960045-1960638]\ Notes:catalyzes the isomerization of sedoheptulose 7-phosphate to D-glycero-D-manno-heptose 7-phosphate |
| NGO1987 | 0.4749 | -1.38 | down | 0.7543 | -1.16 | down | 0.5167 | -1.25 | down | hypothetical protein\ Context:(NC_002946)-[1960643-1960990]\ Notes:Best Blastp Hit: pir\|\|A82030 hypothetical protein NMA0341 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379095\|emb\|CAB83644.1\| (AL162752) hypothetical protein NMA0341 [Neisseria meningitidis] COG0792 Predicted endonuclease distantly related to |
| NGO1988 | 0.1436 | 5.23 | up | 0.5464 | -2.31 | down | 0.4359 | -1.51 | down | hypothetical protein\ Context:(NC_002946)+[1961037-1961912]\ Notes:Best Blastp Hit: pir\|\|B82030 hypothetical protein NMA0342 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379096\|emb\|CAB83645.1\| (AL162752) hypothetical protein NMA0342 [Neisseria meningitidis] COG0313 Predicted methyltransferases |
| NGO1989 | 0.4194 | -1.89 | down | 0.0929 | -6.08 | down | 0.3459 | -2.66 | down | hypothetical protein\ Context:(NC_002946)+[1961935-1962756]\ Notes:Best Blastp Hit: pir\|\|E81007 hypothetical protein NMB2087 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227349\|gb\|AAF42404.1\| (AE002558) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1990 | 0.7842 | 1.14 | up | 0.5366 | -1.31 | down | 0.6663 | 1.12 | up | GTPase ObgE\ Context:(NC_002946)+[1962756-1963910]\ Notes:essential GTPase; exhibits high exchange rate for GTP/GDP; associates with 50S ribosomal subunit; involved in regulation of chromosomal replication |
| NGO1991 | 0.7933 | 1.13 | up | 0.1918 | 1.56 | up | 0.4499 | 1.21 | up | NgoIM\ Context:(NC_002946)+[1963964-1964911]\ Notes:Best Blastp Hit: gb\|AAB03206.2\| (U42459) cytosine DNA methylase M.NgoI [Neisseria gonorrhoeae] COG0270 Site-specific DNA methylase dcm |
| NGO1992 | 0.2331 | 2.17 | up | 0.0437 | 2.25 | up | 0.8418 | 1.06 | up | putative NgoI restriction endonuclease\ Context:(NC_002946)+[1964908-1965960]\ Notes:Best Blastp Hit: gb\|AAB03207.2\| (U42459) NgoI restriction endonuclease R.NgoI [Neisseria gonorrhoeae] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1993 | 0.1903 | 2.08 | up | 0.6483 | 1.27 | up | 0.2444 | 1.46 | up | hypothetical protein\ Context:(NC_002946)+[1965976-1967397]\ Notes:Best Blastp Hit: emb\|CAB83651.1\| (AL162752) cysteinyl-tRNA synthetase [Neisseria meningitidis] COG0215 Cysteinyl-tRNA synthetase |
| NGO1994 | 0.0266 | 5.58 | up | 0.0866 | 2.95 | up | 0.8729 | 1.06 | up | putative exodeoxyribonuclease\ Context:(NC_002946)+[1967568-1968347]\ Notes:Best Blastp Hit: pir\|\|H81009 exodeoxyribonuclease NMB2082 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227344\|gb\|AAF42400.1\| (AE002557) exodeoxyribonuclease [Neisseria meningitidis MC58] >gi\|7379103\|emb\|CAB83652.1\| (AL162752) putative nuclease [Neisseria meningitidis] COG0708 Exonuclease III |
| NGO1995 | 0.1389 | 2.87 | up | 0.9889 | -1.01 | down | 0.9751 | -1.02 | down | hypothetical protein\ Context:(NC_002946)+[1968334-1968678]\ Notes:Best Blastp Hit: pir\|\|G81009 hypothetical protein NMB2081 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227343\|gb\|AAF42399.1\| (AE002557) hypothetical protein [Neisseria meningitidis MC58] |
| NGO1996 | 0.0618 | 3.67 | up | 0.1930 | 3.12 | up | 0.3999 | -1.36 | down | hypothetical protein\ Context:(NC_002946)+[1968688-1969218]\ Notes:Best Blastp Hit: pir\|\|C82031 hypothetical protein NMA0350 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379105\|emb\|CAB83654.1\| (AL162752) hypothetical protein NMA0350 [Neisseria meningitidis] |
| NGO1997 | 0.4408 | 1.49 | up | 0.8022 | -1.13 | down | 0.9595 | -1.02 | down | aspartate-semialdehyde dehydrogenase\ Context:(NC_002946)-[1969311-1970426]\ Notes:catalyzes the formation of 4-aspartyl phosphate from aspartate 4-semialdehyde |
| NGO1998 | 0.5469 | 1.34 | up | 0.8820 | -1.07 | down | 0.7102 | -1.11 | down | hypothetical protein\ Context:(NC_002946)+[1970601-1971182]\ Notes:Best Blastp Hit: pir\|\|D81009 conserved hypothetical protein NMB2078 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227340\|gb\|AAF42396.1\| (AE002557) conserved hypothetical protein [Neisseria meningitidis MC58] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO1999 | 0.0819 | -2.69 | down | 0.3772 | -1.55 | down | 0.1927 | -2.91 | down | hypothetical protein\ Context:(NC_002946)-[1971244-1972098]\ Notes:Best Blastp Hit: pir\|\|F82031 methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) NMA0354 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379108\|emb\|CAB83657.1\| (AL162752) methylenetetrahydrofolate dehydrogenase/cyclohydrolase [Neisseria meningitidis] COG0190 5;10-methylene-tetrahydrofolate |
| NGO2000 | 0.5408 | -1.34 | down | 0.2803 | -1.77 | down | 0.3752 | -1.33 | down | putative transferase\ Context:(NC_002946)+[1972738-1973244]\ Notes:Best Blastp Hit: pir\|\|G82031 probable transferase NMA0356 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379109\|emb\|CAB83658.1\| (AL162752) putative transferase [Neisseria meningitidis] COG0615 Predicted cytidylyltransferases |
| NGO2001 | 0.3254 | 1.84 | up | 0.3922 | 1.45 | up | 0.7544 | 1.09 | up | bifunctional biotin--[acetyl-CoA-carboxylase] ligase/pantothenate kinase\ Context:(NC_002946)+[1973241-1975019]\ Notes:activates biotin to form biotinyl-5'-adenylate and transfers the biotin moiety to biotin-accepting proteins and catalyzes the formation of (R)-4'-phosphopantothenate from (R)-pantothenate in coenzyme A biosynthesis; type III; type III pantothenate kinases are not subject to feedback inhibition from coenzyme A and have a high Km for ATP |
| NGO2002 | 0.7511 | 1.16 | up | 0.2512 | 1.47 | up | 0.4942 | 1.20 | up | hypothetical protein\ Context:(NC_002946)+[1975132-1975956]\ Notes:Best Blastp Hit: pir\|\|A82032 probable periplasmic protein NMA0358 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379111\|emb\|CAB83660.1\| (AL162752) putative periplasmic protein [Neisseria meningitidis] |
| NGO2003 | 0.1030 | 5.33 | up | 0.1445 | -4.70 | down | 0.2183 | -6.89 | down | hypothetical protein\ Context:(NC_002946)-[1976165-1976287]\ Notes:Best Blastp Hit: gb\|AAF42392.1\| (AE002557) hypothetical protein [Neisseria meningitidis MC58] |
| NGO2004 | 0.2717 | -3.52 | down | 0.0248 | -15.46 | down | 0.7364 | 1.85 | up | hypothetical protein\ Context:(NC_002946)+[1976422-1976658]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2005 | 0.5135 | 1.51 | up | 0.2663 | -2.81 | down | 0.2893 | -2.75 | down | thiazole synthase\ Context:(NC_002946)-[1976689-1977477]\ Notes:functions in thiamine (vitamin B1) biosynthesis; in Bacillus subtilis this enzyme catalyzes the formation of thiazole from dehydroxyglycine and 1-deoxy-D-xylulose-5-phosphate and ThiS-thiocarboxylate |
| NGO2006 | 0.0762 | -6.04 | down | 0.0270 | -23.18 | down | 0.7746 | -1.64 | down | hypothetical protein\ Context:(NC_002946)-[1977556-1977750]\ Notes:Best Blastp Hit: emb\|CAB83663.1\| (AL162752) hypothetical protein NMA0362 [Neisseria meningitidis] |
| NGO2007 | 0.6671 | -1.37 | down | 0.1165 | -3.73 | down | 0.7165 | 1.36 | up | putative thiamin-phosphate pyrophosphorylase\ Context:(NC_002946)-[1978172-1978789]\ Notes:Best Blastp Hit: gb\|AAF42388.1\| (AE002556) thiamin-phosphate pyrophosphorylase [Neisseria meningitidis MC58] COG0352 Thiamine monophosphate synthase |
| NGO2008 | 0.5807 | 1.64 | up | 0.1416 | -5.49 | down | 0.8298 | -1.28 | down | putative oxidoreductase\ Context:(NC_002946)-[1978811-1979911]\ Notes:Best Blastp Hit: gb\|AAF42387.1\| (AE002556) D-amino acid oxidase flavoprotein; putative [Neisseria meningitidis MC58] COG0665 Predicted oxidoreductases |
| NGO2009 | 0.0029 | -7.72 | down | 0.0212 | -9.65 | down | 0.2298 | -2.24 | down | putative permease protein\ Context:(NC_002946)-[1979908-1981134]\ Notes:Best Blastp Hit: gb\|AAF42386.1\| (AE002556) conserved hypothetical protein [Neisseria meningitidis MC58] COG1457 Purine-cytosine permease and related |
| NGO2010 | 0.4183 | -1.43 | down | 0.5675 | -1.30 | down | 0.8500 | -1.14 | down | hypothetical protein\ Context:(NC_002946)+[1981421-1982863]\ Notes:Best Blastp Hit: pir\|\|A82033 TLDD protein homolog NMA0367 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379119\|emb\|CAB83668.1\| (AL162752) TLDD protein homolog [Neisseria meningitidis] COG0312 Predicted Zn-dependent proteases and their |
| NGO2011 | 0.0027 | -20.20 | down | 0.0013 | -29.62 | down | 0.0110 | -23.99 | down | putative ABC transporter; permease protein; amino acid\ Context:(NC_002946)+[1983007-1983666]\ Notes:Best Blastp Hit: pir\|\|F81391 amino-acid ABC transporter integral membrane protein Cj0467 [imported] - Campylobacter jejuni (strain NCTC 11168) >gi\|6967938\|emb\|CAB75105.1\| (AL139075) amino-acid ABC transporter integral membrane protein [Campylobacter jejuni] COG0765 Amino acid ABC transporter permease |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2012 | 0.0015 | -16.71 | down | 0.0030 | -59.64 | down | 0.1105 | -8.73 | down | putative ABC transporter; permease protein; amino acid\ Context:(NC_002946)+[1983656-1984324]\ Notes:Best Blastp Hit: pir\|\|B64666 glutamine ABC transporter; permease protein - Helicobacter pylori (strain 26695) >gi\|2314329\|gb\|AAD08216.1\| (AE000623) glutamine ABC transporter; permease protein (glnP) [Helicobacter pylori 26695] COG0765 Amino acid ABC transporter permease |
| NGO2013 | 0.0309 | -4.47 | down | 0.0584 | -3.84 | down | 0.0478 | -6.28 | down | putative ABC transporter; ATP-binding protein; amino acid\ Context:(NC_002946)+[1984326-1985057]\ Notes:Best Blastp Hit: pir\|\|H81391 amino-acid ABC transporter ATP-binding protein Cj0469 [imported] - Campylobacter jejuni (strain NCTC 11168) >gi\|6967940\|emb\|CAB75107.1\| (AL139075) amino-acid ABC transporter ATP-binding protein [Campylobacter jejuni] COG1126 ABC-type polar amino acid transport system |
| NGO2014 | 0.7049 | -1.21 | down | 0.4680 | -1.39 | down | 0.5831 | -1.17 | down | putative ABC transporter; periplasmic binding protein; amino acid\ Context:(NC_002946)+[1985170-1986024]\ Notes:Best Blastp Hit: gb\|AAD26123.1\| (AF109148) antigenic protein [Actinobacillus pleuropneumoniae] COG0834 Periplasmic amino acid binding proteins |
| NGO2015 | 0.0006 | -13.80 | down | 0.0421 | -6.71 | down | 0.0501 | -7.76 | down | hypothetical protein\ Context:(NC_002946)+[1986403-1987260]\ Notes:Best Blastp Hit: gb\|AAF42384.1\| (AE002556) hemK protein [Neisseria meningitidis MC58] COG0500 SAM-dependent methyltransferases |
| NGO2016 | 0.0156 | -4.24 | down | 0.0239 | -5.42 | down | 0.0149 | -5.76 | down | hypothetical protein\ Context:(NC_002946)+[1987346-1988734]\ Notes:Best Blastp Hit: pir\|\|D81010 conserved hypothetical protein NMB2064 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227326\|gb\|AAF42383.1\| (AE002556) conserved hypothetical protein [Neisseria meningitidis MC58] COG2056 Predicted permease |
| NGO2017 | 0.5679 | -1.45 | down | 0.1351 | -1.87 | down | 0.0853 | -1.63 | down | hypothetical protein\ Context:(NC_002946)+[1988735-1988959]\ Notes:Best Blastp Hit: gb\|AAF42382.1\| (AE002556) slyX protein; putative [Neisseria meningitidis MC58] |
| NGO2018 | 0.9553 | 1.03 | up | 0.5617 | -1.28 | down | 0.2691 | -1.44 | down | hypothetical protein\ Context:(NC_002946)+[1989067-1989261]\ Notes: |

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| NGO2019 | 0.0151 | -3.98 | down | 0.0421 | -3.86 | down | 0.0670 | -2.57 | down | hypothetical protein\ Context:(NC_002946)-[1989359-1990129]\ Notes:Best Blastp Hit: pir\|\|B81010 thiF protein NMB2062 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227324\|gb\|AAF42381.1\| (AE002556) thiF protein [Neisseria meningitidis MC58] COG0476 Dinucleotide-utilizing enzymes involved in |
| NGO2020 | 0.1073 | 2.90 | up | 0.0741 | 6.10 | up | 0.0357 | 2.49 | up | phosphoenolpyruvate carboxylase\ Context:(NC_002946)+[1990296-1992998]\ Notes:catalyzes the formation of oxaloacetate from phosphoenolpyruvate |
| NGO2021 | 0.7081 | 1.20 | up | 0.9507 | -1.03 | down | 0.9062 | 1.04 | up | putative glycerol-3-phosphate dehydrogenase\ Context:(NC_002946)+[1993121-1994110]\ Notes:Best Blastp Hit: gb\|AAF62339.1\| (AE002555) glycerol-3-phosphate dehydrogenase (NAD+) [Neisseria meningitidis MC58] COG0240 Glycerol 3-phosphate dehydrogenase |
| NGO2022 | 0.6224 | 1.31 | up | 0.7020 | 1.17 | up | 0.2554 | 1.42 | up | hypothetical protein\ Context:(NC_002946)+[1994164-1994493]\ Notes:Best Blastp Hit: pir\|\|F81953 hypothetical protein NMA0376 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379129\|emb\|CAB83677.1\| (AL162753) hypothetical protein NMA0376 [Neisseria meningitidis] |
| NGO2023 | 0.5367 | 1.32 | up | 0.7006 | 1.16 | up | 0.7880 | 1.07 | up | hypothetical protein\ Context:(NC_002946)+[1994504-1994809]\ Notes:Best Blastp Hit: gb\|AAF42378.1\| (AE002555) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379130\|emb\|CAB83678.1\| (AL162753) hypothetical protein NMA0377 [Neisseria meningitidis] |
| NGO2024 | 0.0756 | 3.13 | up | 0.3374 | 1.47 | up | 0.4640 | 1.30 | up | 50S ribosomal protein L13\ Context:(NC_002946)+[1995172-1995603]\ Notes:in Escherichia coli this protein is one of the earliest assembly proteins in the large subunit |
| NGO2025 | 0.1923 | 2.18 | up | 0.4182 | 1.44 | up | 0.5219 | 1.25 | up | 30S ribosomal protein S9\ Context:(NC_002946)+[1995616-1996008]\ Notes:forms a direct contact with the tRNA during translation |
| NGO2026 | 0.1732 | -9.16 | down | 0.3588 | -6.73 | down | 0.3735 | 4.91 | up | hypothetical protein\ Context:(NC_002946)-[1996389-1996883]\ Notes: |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2027 | 0.4545 | 1.57 | up | 0.1065 | -2.94 | down | 0.4724 | -1.58 | down | MetR\ Context:(NC_002946)-[1997076-1998005]\ Notes:Best Blastp Hit: pir\|\|H81011 transcription regulator; LysR family NMB2055 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227317\|gb\|AAF42375.1\| (AE002555) transcriptional regulator; LysR family [Neisseria meningitidis MC58] COG0583 Transcriptional regulators; LysR family; putative methionine biosynthesis transcriptional regulator |
| NGO2028 | 0.0715 | 5.28 | up | 0.3115 | 1.77 | up | 0.4695 | -1.43 | down | hypothetical protein\ Context:(NC_002946)+[1998134-1998883]\ Notes:Best Blastp Hit: pir\|\|D81954 hypothetical protein NMA0382 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379135\|emb\|CAB83683.1\| (AL162753) hypothetical protein NMA0382 [Neisseria meningitidis] COG0327 Uncharacterized ACR; YbgI/Acr family |
| NGO2029 | 0.5016 | -1.43 | down | 0.3915 | -1.50 | down | 0.1797 | -1.60 | down | PetA\ Context:(NC_002946)+[1999006-1999587]\ Notes:Best Blastp Hit: gb\|AAF42373.1\| (AE002555) ubiquinol--cytochrome c reductase; iron-sulfur subunit [Neisseria meningitidis MC58] >gi\|7379136\|emb\|CAB83684.1\| (AL162753) ubiquinol-cytochrome c reductase iron-sulfur subunit [Neisseria meningitidis] COG0723 Rieske Fe-S protein; putative ubiquinol--cytochrome c reductase iron-sulfur subunit |
| NGO2030 | 0.1633 | -2.02 | down | 0.3601 | -1.46 | down | 0.1707 | -1.63 | down | PetB\ Context:(NC_002946)+[1999606-2000955]\ Notes:Best Blastp Hit: pir\|\|F81954 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b NMA0384 [similarity] Neisseria meningitidis (group A strain Z2491) >gi\|7379137\|emb\|CAB83685.1\| (AL162753) cytochrome B [Neisseria meningitidis] COG1290 Cytochrome b (b6-like); putative cytochrome B |
| NGO2031 | 0.5306 | -1.43 | down | 0.8580 | -1.08 | down | 0.1433 | -2.08 | down | PetC\ Context:(NC_002946)+[2000970-2001758]\ Notes:Best Blastp Hit: emb\|CAB83686.1\| (AL162753) cytochrome C1 precursor [Neisseria meningitidis]; putative cytochrome C1 precursor |

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| NGO2032 | 0.0964 | -4.17 | down | 0.0922 | -2.53 | down | 0.0405 | -2.90 | down | hypothetical protein\ Context:(NC_002946)+[2002090-2003880]\ Notes:Best Blastp Hit: gb\|AAF42370.1\|(AE002555) conserved hypothetical protein [Neisseria meningitidis MC58] COG1322 Uncharacterized BCR; YigN family |
| NGO2033 | 0.0496 | -4.24 | down | 0.0024 | -4.89 | down | 0.0711 | -2.55 | down | putative hydrolase\ Context:(NC_002946)-[2003947-2004579]\ Notes:Best Blastp Hit: pir\|\|A81955 probable hydrolase NMA0387 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379140\|emb\|CAB83688.1\|(AL162753) putative hydrolase [Neisseria meningitidis] COG0491 Zn-dependent hydrolases |
| NGO2034 | 0.5368 | -1.91 | down | 0.0202 | -8.96 | down | 0.5434 | -1.83 | down | DNA ligase\ Context:(NC_002946)+[2004672-2005496]\ Notes:catalyzes the formation of a phosphodiester at the site of a single-strand break in duplex DNA |
| NGO2035 | 0.4143 | 1.49 | up | 0.4725 | -1.36 | down | 0.7380 | -1.10 | down | hypoxanthine-guanine phosphoribosyltransferase\ Context:(NC_002946)+[2005565-2006128]\ Notes:Catalyzes the salvage synthesis of inosine-5'-monophosphate (IMP) and guanosine-5'-monophosphate (GMP) from the purine bases hypoxanthine and guanine; respectively |
| NGO2036 | 0.3002 | 1.77 | up | 0.1495 | -2.12 | down | 0.4525 | -1.61 | down | putative sugar transport PTS system IIA protein\ Context:(NC_002946)+[2006212-2006649]\ Notes:Best Blastp Hit: emb\|CAB83691.1\| (AL162753) sugar transport PTS system IIA component [Neisseria meningitidis] |
| NGO2037 | 0.4171 | 1.45 | up | 0.9125 | 1.03 | up | 0.1726 | -1.88 | down | PtsH\ Context:(NC_002946)+[2006870-2007139]\ Notes:Best Blastp Hit: pir\|\|A81013 sugar transport PTS system phosphocarrier protein HPR NMA0391 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227306\|gb\|AAF42365.1\| (AE002554) phosphocarrier protein HPr [Neisseria meningitidis MC58] >gi\|7379144\|emb\|CAB83692.1\| (AL162753) sugar transport PTS system phosphocarrier protein HPR |

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| NGO2038 | 0.8866 | -1.07 | down | 0.6039 | 1.18 | up | 0.2819 | 1.35 | up | PtsI\ Context:(NC_002946)+[2007139-2008914]\ Notes:Best Blastp Hit: pir\|\|H81012 phosphoenolpyruvate-protein phosphotransferase NMB2044 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227305\|gb\|AAF42364.1\| (AE002554) phosphoenolpyruvate-protein phosphotransferase [Neisseria meningitidis MC58] COG1080 Phosphoenolpyruvate-protein kinase (PTS; putative phosphoenolpyruvate-protein phosphotransferase |
| NGO2039 | 0.9845 | 1.01 | up | 0.5214 | -1.32 | down | 0.8977 | 1.04 | up | putative ABC transporter; ATP-binding protein; amino acid\ Context:(NC_002946)-[2009041-2009982]\ Notes:Best Blastp Hit: emb\|CAB83694.1\| (AL162753) ABC-transport system ATP-binding protein [Neisseria meningitidis] COG1128 ABC-type spermidine/putrescine transport |
| NGO2040 | 0.5945 | 1.28 | up | 0.4176 | 1.35 | up | 0.9972 | 1.00 | up | hypothetical protein\ Context:(NC_002946)-[2009991-2010866]\ Notes:Best Blastp Hit: pir\|\|F81012 thiamin pyrophosphokinase-related protein NMB2041 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227303\|gb\|AAF42362.1\| (AE002554) thiamin pyrophosphokinase-related protein [Neisseria meningitidis MC58] |
| NGO2041 | 0.1130 | -3.21 | down | 0.0132 | -16.45 | down | 0.5864 | -1.35 | down | thiamine biosynthesis protein ThiC\ Context:(NC_002946)+[2011464-2013365]\ Notes:required for the synthesis of the hydromethylpyrimidine moiety of thiamine |
| NGO2042 | 0.9203 | 1.05 | up | 0.8703 | -1.08 | down | 0.9412 | -1.02 | down | hypothetical protein\ Context:(NC_002946)+[2015247-2015468]\ Notes: |
| NGO2043 | 0.5427 | 1.44 | up | 0.0200 | -2.71 | down | 0.8329 | -1.20 | down | putative dehydrogenase related protein\ Context:(NC_002946)+[2017051-2017365]\ Notes:Best Blastp Hit: pir\|\|F82022 probable glycerate dehydrogenase (EC 1.1.1.29) NMA0274 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379036\|emb\|CAB83582.1\| (AL162752) putative glycerate dehydrogenase [Neisseria meningitidis] COG1052 Lactate dehydrogenase and related |

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| NGO2044 | 0.0046 | 5.68 | up | 0.0616 | 9.31 | up | 0.1040 | 3.05 | up | methionyl-tRNA synthetase\ Context:(NC_002946)-[2017440-2019494]\ Notes:methionine--tRNA ligase; MetRS; adds methionine to tRNA(Met) with cleavage of ATP to AMP and diphosphate; some MetRS enzymes form dimers depending on a C-terminal domain that is also found in other proteins such as Trbp111 in Aquifex aeolicus and the cold-shock protein CsaA from Bacillus subtilis while others do not |
| NGO2045 | 0.6100 | 1.27 | up | 0.6729 | -1.19 | down | 0.4742 | 1.30 | up | D-fructose-6-phosphate amidotransferase\ Context:(NC_002946)-[2019610-2021448]\ Notes:Catalyzes the first step in hexosamine metabolism; converting fructose-6P into glucosamine-6Pusing glutamine as a nitrogen source |
| NGO2046 | 0.4030 | 2.05 | up | 0.2327 | -2.97 | down | 0.4588 | 1.69 | up | hypothetical protein\ Context:(NC_002946)+[2021482-2021670]\ Notes: |
| NGO2047 | 0.1043 | 4.37 | up | 0.8665 | 1.16 | up | 0.8350 | -1.25 | down | hypothetical protein\ Context:(NC_002946)+[2021721-2022242]\ Notes:Best Blastp Hit: possibly phase variable - 9A residue homopolymer repeat in the coding sequence (ON) |
| NGO2048 | 0.2183 | -2.17 | down | 0.0896 | -2.25 | down | 0.0352 | -2.61 | down | GNA33)\ Context:(NC_002946)-[2022525-2023850]\ Notes:Best Blastp Hit: gb\|AAF44779.1\|AF235145_1 (AF235145) GNA33 [Neisseria gonorrhoeae]; genome-derived Neisserial antigen 33 |
| NGO2050 | 0.8046 | 1.25 | up | 0.7628 | 1.10 | up | 0.4234 | 1.58 | up | hypothetical protein\ Context:(NC_002946)+[2024900-2026066]\ Notes:Best Blastp Hit: pir\|\|E81244 conserved hypothetical protein NMB0035 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225255\|gb\|AAF40506.1\| (AE002362) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO2051 | 0.9724 | -1.03 | down | 0.1339 | -2.21 | down | 0.7647 | -1.17 | down | hypothetical protein\ Context:(NC_002946)+[2026373-2027638]\ Notes:Best Blastp Hit: pir\|\|F81244 conserved hypothetical protein NMB0036 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225256\|gb\|AAF40507.1\| (AE002362) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO2052 | 0.6043 | 1.28 | up | 0.6389 | 1.37 | up | 0.6843 | 1.34 | up | PhnA\ Context:(NC_002946)-[2027710-2028039]\ Notes:Best Blastp Hit: pir\|\|G81244 phnA protein NMB0037 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225257\|gb\|AAF40508.1\| (AE002362) phnA protein [Neisseria meningitidis MC58]; alkylphosphonate uptake protein |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2053 | 0.2969 | 1.76 | up | 0.1284 | 2.50 | up | 0.4418 | 1.52 | up | UDP-N-acetylglucosamine pyrophosphorylase\ Context:(NC_002946)-[2028114-2029484]\ Notes:Best Blastp Hit: sp\|Q50986\|GLMU_NEIGO UDP-N-acetylglucosamine pyrophosphorylase (N-acetylglucosamine-1-phosphate uridyltransferase) >gi\|975206\|emb\|CAA90326.1\| (Z50023) uridyltransferase [Neisseria gonorrhoeae] COG1207 |
| NGO2054 | 0.2549 | -1.74 | down | 0.6535 | -1.24 | down | 0.9521 | -1.02 | down | hypothetical protein\ Context:(NC_002946)-[2029539-2029811]\ Notes:Best Blastp Hit: gb\|AAF40510.1\| (AE002362) hypothetical protein [Neisseria meningitidis MC58] |
| NGO2055 | 0.1259 | -3.95 | down | 0.0163 | -14.50 | down | 0.0101 | -9.62 | down | putative hydrolase\ Context:(NC_002946)-[2029787-2030515]\ Notes:Best Blastp Hit: emb\|CAB83593.1\| (AL162752) possible hydrolase [Neisseria meningitidis] COG1011 Predicted hydrolases of the HAD superfamily |
| NGO2056 | 0.2861 | 1.67 | up | 0.8787 | 1.08 | up | 0.4173 | 1.26 | up | putative ABC transporter; thiamine-binding periplasmic protein\ Context:(NC_002946)+[2030574-2031575]\ Notes:Best Blastp Hit: emb\|CAB83594.1\| (AL162752) putative thiamin-binding periplasmic protein [Neisseria meningitidis] COG1840 Thiamine-binding periplasmic proteins |
| NGO2057 | 0.4330 | 1.49 | up | 0.5827 | -1.29 | down | 0.9555 | 1.02 | up | hypothetical protein\ Context:(NC_002946)+[2031669-2032517]\ Notes:Best Blastp Hit: pir\|\|D81245 conserved hypothetical protein NMB0042 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225262\|gb\|AAF40513.1\| (AE002362) conserved hypothetical protein [Neisseria meningitidis MC58] COG0668 Uncharacterized ACR; integral membrane |
| NGO2058 | 0.0124 | -4.34 | down | 0.0033 | -17.53 | down | 0.1203 | -2.95 | down | hypothetical protein\ Context:(NC_002946)+[2032543-2033025]\ Notes:Best Blastp Hit: pir\|\|E81245 conserved hypothetical protein NMB0043 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225263\|gb\|AAF40514.1\| (AE002362) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379050\|emb\|CAB83596.1\| (AL162752) hypothetical protein NMA0289 [Neisseria meningitidis] COG1546 Uncharacterized protein CinA/YgaD |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2059 | 0.2672 | -1.94 | down | 0.0050 | -13.07 | down | 0.0611 | -3.33 | down | trifunctional thioredoxin/methionine sulfoxide reductase A/B protein\ Context:(NC_002946)-[2033109-2034677]\ Notes:this is a fusion of 3 domains; an N-termianl thioredoxin domain; and 2 domains at the C-terminus that are methionine sulfoxide reductases; MsrA and MsrB; methionine is modified to form methionine sulfoxide during normal cellular processes and due to oxidat |
| NGO2060 | 0.6771 | 1.20 | up | 0.4917 | 1.31 | up | 0.9905 | 1.00 | up | putative signal recognition particle protein\ Context:(NC_002946)+[2034823-2036088]\ Notes:Best Blastp Hit: sp\|P14929\|PILA_NEIGO probably signal recognition particle protein (DOCKING protein) COG0552 Signal recognition particle GTPase FtsY |
| NGO2065 | 0.7987 | -1.17 | down | 0.9713 | 1.02 | up | 0.2369 | 1.42 | up | UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase\ Context:(NC_002946)-[2039365-2040288]\ Notes:zinc-dependent; catalyzes the deacetylation of UDP-(3-O-acyl)-N-acetylglucosamine to UDP-3-O-(3-hydroxytetradecanoyl)-glucosamine in the second step of lipid A biosynthesis |
| NGO2068 | 0.4038 | -1.86 | down | 0.0952 | -4.39 | down | 0.3782 | -1.45 | down | hypothetical protein\ Context:(NC_002946)-[2046714-2047403]\ Notes:Best Blastp Hit: gb\|AAF42356.1\|(AE002553) conserved hypothetical protein [Neisseria meningitidis MC58] COG1451 Predicted metal-dependent hydrolase |
| NGO2069 | 0.9395 | 1.05 | up | 0.3129 | -2.14 | down | 0.5421 | -1.35 | down | NlaB\ Context:(NC_002946)-[2047400-2048143]\ Notes:Best Blastp Hit: pir\|\|G81013 1-acyl-sn-glycerol-3-phosphate acyltransferase; probable NMB2034 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227295\|gb\|AAF42355.1\| (AE002553) 1-acyl-sn-glycerol-3-phosphate acyltransferase; putative [Neisseria meningitidis MC58] COG0204 1-acyl-sn-glycerol-3-phosphate; putative 1-acyl-SN-glycerol-3-phosphate acyltransferase |
| NGO2070 | 0.5753 | 1.35 | up | 0.8813 | -1.06 | down | 0.9675 | -1.01 | down | D;D-heptose 1;7-bisphosphate phosphatase\ Context:(NC_002946)-[2048173-2048736]\ Notes:Converts the D-glycero-beta-D-manno-heptose 1;7-bisphosphate intermediate into D-glycero-beta-D-manno-heptose 1-phosphate |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2071 | 0.8033 | 1.27 | up | 0.7651 | -1.12 | down | 0.8896 | 1.05 | up | hypothetical protein\ Context:(NC_002946)+[2048879-2050531]\ Notes:Best Blastp Hit: pir\|\|C81957 probable integral membrane protein NMA0408 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379158\|emb\|CAB83707.1\| (AL162753) putative integral membrane protein [Neisseria meningitidis] COG1368 Phosphoglycerol transferase MdoB and related |
| NGO2072 | 0.3031 | -2.09 | down | 0.5044 | -1.32 | down | 0.6419 | -1.36 | down | lipooligosaccharide glycosyl transferase G\ Context:(NC_002946)-[2050598-2051653]\ Notes:Best Blastp Hit: possibly phase variable - 11C residue homopolymer repeat in the coding sequence (ON) COG0438 Glycosyltransferases I |
| NGO2073 | 0.2254 | -1.97 | down | 0.0048 | -4.59 | down | 0.7763 | -1.13 | down | TnaB\ Context:(NC_002946)-[2051805-2053046]\ Notes:Best Blastp Hit: pir\|\|E81013 tryptophan transporter NMB2031 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227293\|gb\|AAF42353.1\| (AE002553) tryptophan transporter [Neisseria meningitidis MC58] COG0814 Amino acid permeases; putative tryptophan transport protein; tryptophan permease |
| NGO2074 | 0.0214 | -4.70 | down | 0.2650 | -1.49 | down | 0.1128 | -2.19 | down | 3-demethylubiquinone-9 3-methyltransferase\ Context:(NC_002946)+[2053194-2053922]\ Notes:Involved in ubiquinone biosynthesis |
| NGO2075 | 0.0087 | -4.94 | down | 0.0682 | -2.68 | down | 0.0730 | -2.64 | down | homoserine kinase\ Context:(NC_002946)+[2053959-2054876]\ Notes:catalyzes the formation of O-phospho-L-homoserine from L-homoserine |
| NGO2076 | 0.6165 | -1.31 | down | 0.1159 | -4.00 | down | 0.3521 | -1.50 | down | putative glucokinase\ Context:(NC_002946)-[2055062-2055580]\ Notes:Best Blastp Hit: pir\|\|G81015 probable gluconokinase (EC 2.7.1.12) NMA0412 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227290\|gb\|AAF42351.1\| (AE002552) thermoresistant gluconokinase [Neisseria meningitidis MC58] >gi\|7379162\|emb\|CAB83711.1\| (AL162753) putative glucokinase [Neisseria meningitidis] COG0529 Adenylylsulfate kinase and related kinases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2077 | 0.0269 | -8.87 | down | 0.0012 | -40.39 | down | 0.0601 | -4.91 | down | GntP\ Context:(NC_002946)-[2055600-2056985]\ Notes:Best Blastp Hit: pir\|\|H81957 probable gluconate permease NMA0413 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379163\|emb\|CAB83712.1\| (AL162753) putative gluconate permease [Neisseria meningitidis] |
| NGO2078 | 0.0269 | -5.66 | down | 0.0008 | -31.01 | down | 0.0608 | -6.09 | down | putative ABC transporter; permease protein\ Context:(NC_002946)+[2057326-2058918]\ Notes:Best Blastp Hit: gb\|AAF42349.1\| (AE002552) ABC transporter; permease protein [Neisseria meningitidis MC58] COG1178 Uncharacterized transport system; permease |
| NGO2079 | 0.0044 | -9.02 | down | 0.0014 | -13.70 | down | 0.0101 | -6.57 | down | putative carbonic anhydrase\ Context:(NC_002946)+[2058947-2059546]\ Notes:Best Blastp Hit: pir\|\|D81015 conserved hypothetical protein NMB2025 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227287\|gb\|AAF42348.1\| (AE002552) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379165\|emb\|CAB83714.1\| (AL162753) hypothetical protein NMA0415 [Neisseria meningitidis] COG0288 Carbonic anhydrase |
| NGO2080 | 0.0547 | -2.67 | down | 0.0520 | -3.22 | down | 0.0730 | -3.49 | down | hypothetical protein\ Context:(NC_002946)+[2059543-2060148]\ Notes:Best Blastp Hit: sp\|P57090\|NADD_NEIMB probable nicotinate-nucleotide adenylyltransferase (deamido-NAD(+) pyrophosphorylase)(deamido-NAD(+) diphosphorylase) (nicotinate mononucleotide adenylyltransferase) (NAMN adenylyltransferase) >gi\|11278845\|pir\|\|C81015 conserved hypothetical protein NMB2024 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227286\|gb\|AAF42347.1\| (AE002552) conserved hypothetical protein [Neisseria meningitidis MC58] COG1057 Predicted nucleotidyltransferases |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2081 | 0.3090 | -2.23 | down | 0.7259 | -1.15 | down | 0.3755 | -1.32 | down | hypothetical protein\ Context:(NC_002946)+[2060207-2060593]\ Notes:Best Blastp Hit: gb\|AAF42346.1\|(AE002552) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379167\|emb\|CAB83716.1\|(AL162753) hypothetical protein NMA0417 [Neisseria meningitidis] COG0799 Uncharacterized ACR (homolog of plant |
| NGO2082 | 0.5692 | -1.33 | down | 0.0652 | -1.98 | down | 0.4554 | -1.40 | down | SPOUT methyltransferase superfamily protein\ Context:(NC_002946)+[2060646-2061116]\ Notes:enzyme from Escherichia coli has not been shown to exhibit methyltransferase activity; crystal structure shows homodimer |
| NGO2083 | 0.2733 | 1.85 | up | 0.3484 | 1.40 | up | 0.4895 | 1.30 | up | hypothetical protein\ Context:(NC_002946)+[2061190-2061456]\ Notes:Best Blastp Hit: gb\|AAF42344.1\|(AE002552) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379169\|emb\|CAB83718.1\|(AL162753) hypothetical protein NMA0419 [Neisseria meningitidis] |
| NGO2084 | 0.1292 | 2.43 | up | 0.1070 | 1.78 | up | 0.2182 | 1.89 | up | hypothetical protein\ Context:(NC_002946)+[2061613-2062296]\ Notes:Best Blastp Hit: pir\|\|G81014 conserved hypothetical protein NMB2020 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227282\|gb\|AAF42343.1\| (AE002552) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379170\|emb\|CAB83719.1\| (AL162753) putative integral membrane protein [Neisseria meningitidis] COG0670 Integral membrane protein YccA; interacts |
| NGO2085 | 0.3354 | -2.37 | down | 0.9145 | 1.13 | up | 0.2660 | -2.80 | down | phosphopantetheine adenylyltransferase\ Context:(NC_002946)+[2062426-2062941]\ Notes:Catalyzes the conversion of ATP and pantetheine 4'-phosphate to diphosphate and 3'-dephospho-coA |
| NGO2086 | 0.0743 | -2.88 | down | 0.2794 | -1.90 | down | 0.0132 | -4.41 | down | hypothetical protein\ Context:(NC_002946)-[2063080-2064387]\ Notes:Best Blastp Hit: emb\|CAC14203.1\|(AJ277636) MapB protein [Pasteurella multocida] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2088 | 0.0769 | -2.93 | down | 0.2513 | -4.31 | down | 0.2279 | 1.64 | up | putative ABC transporter; ATP-binding protein; enterobactin\ Context:(NC_002946)-[2065061-2065819]\ Notes:Best Blastp Hit: pir\|\|A81962 probable ABC transporter ATP-binding subunit NMA0448 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379196\|emb\|CAB83745.1\| (AL162753) putative ABC transporter ATP-binding subunit [Neisseria meningitidis] COG1120 ABC-type iron (III) transport system; ATPase |
| NGO2089 | 0.2660 | 2.51 | up | 0.8829 | 1.09 | up | 0.3906 | 1.85 | up | hypothetical protein\ Context:(NC_002946)-[2065903-2066529]\ Notes:Best Blastp Hit: pir\|\|G81018 hypothetical protein NMB1992 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227254\|gb\|AAF42319.1\| (AE002548) hypothetical protein [Neisseria meningitidis MC58] |
| NGO2090 | 0.6394 | -1.47 | down | 0.0353 | -11.76 | down | 0.3757 | 2.07 | up | putative ABC transporter; permease protein; enterobactin\ Context:(NC_002946)-[2066574-2067548]\ Notes:Best Blastp Hit: gb\|AAF42318.1\| (AE002548) iron(III) ABC transporter; permease protein [Neisseria meningitidis MC58] COG0609 Iron; hemin; cobalamine permeases |
| NGO2091 | 0.1190 | -3.31 | down | 0.2533 | -2.59 | down | 0.6541 | 1.36 | up | putative ABC transporter; permease protein; enterobactin\ Context:(NC_002946)-[2067538-2068506]\ Notes:Best Blastp Hit: pir\|\|E81018 iron(III) ABC transporter; permease protein NMB1990 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227252\|gb\|AAF42317.1\| (AE002548) iron(III) ABC transporter; permease protein [Neisseria meningitidis MC58] COG0609 Iron; hemin; cobalamine permeases |
| NGO2092 | 0.0048 | 7.42 | up | 0.0348 | 5.19 | up | 0.0001 | 9.10 | up | ferric enterobactin periplasmic binding protein\ Context:(NC_002946)-[2068734-2069705]\ Notes:Best Blastp Hit: gb\|AAD29611.1\|AF115385_1 (AF115385) putative ferric enterobactin periplasmic binding protein [Neisseria gonorrhoeae] COG0614 Ferrichrome-binding periplasmic proteins |
| NGO2093 | 0.0000 | 47.12 | up | 0.0048 | 20.11 | up | 0.0474 | 3.77 | up | FetA\ Context:(NC_002946)-[2069857-2071998]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) COG1629 Outer membrane receptor proteins; mostly Fe; ferric enterobactin receptor |

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| NGO2094 | 0.0710 | 4.26 | up | 0.0500 | 2.17 | up | 0.1133 | 3.06 | up | co-chaperonin GroES\ Context:(NC_002946)+[2072506-2072796]\ Notes:10 kDa chaperonin; Cpn10; GroES; forms homoheptameric ring; binds to one or both ends of the GroEL double barrel in the presence of adenine nucleotides capping it; folding of unfolded substrates initiates in a GroEL-substrate bound and capped by GroES; release of the folded substrate is dependent on ATP binding and hydrolysis in the trans ring |
| NGO2095 | 0.0831 | 4.36 | up | 0.0301 | 2.72 | up | 0.0920 | 3.61 | up | chaperonin GroEL\ Context:(NC_002946)+[2072888-2074522]\ Notes:60 kDa chaperone family; promotes refolding of misfolded polypeptides especially under stressful conditions; forms two stacked rings of heptamers to form a barrel-shaped 14mer; ends can be capped by GroES |
| NGO2096 | 0.3838 | -1.49 | down | 0.1970 | -2.02 | down | 0.1205 | -1.62 | down | putative sodium-dependent transporter\ Context:(NC_002946)+[2075176-2076762]\ Notes:Best Blastp Hit: pir\|\|E81964 probable sodium-dependent inner membrane transport protein NMA0470 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379216\|emb\|CAB83765.1\| (AL162753) putative sodium-dependent inner membrane transport protein [Neisseria meningitidis] COG0733 Sodium-dependent transporters (SNF family) |
| NGO2097 | 0.1056 | 4.14 | up | 0.6028 | 1.90 | up | 0.3722 | 2.11 | up | hypothetical protein\ Context:(NC_002946)-[2076903-2077325]\ Notes: |
| NGO2098 | 0.0584 | 9.98 | up | 0.3640 | 3.13 | up | 0.4126 | 1.56 | up | hypothetical protein\ Context:(NC_002946)-[2077519-2078739]\ Notes:Best Blastp Hit: pir\|\|D81964 diaminopimelate decarboxylase (EC 4.1.1.20) NMA0468 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379215\|emb\|CAB83764.1\| (AL162753) diaminopimelate decarboxylase [Neisseria meningitidis] COG0019 Diaminopimelate decarboxylase |
| NGO2099 | 0.7209 | -1.20 | down | 0.8037 | -1.11 | down | 0.7845 | 1.10 | up | hypothetical protein\ Context:(NC_002946)-[2078750-2078920]\ Notes:Best Blastp Hit: emb\|CAB83763.1\| (AL162753) putative lipoprotein [Neisseria meningitidis] |

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| NGO2100 | 0.0914 | 2.40 | up | 0.5161 | -1.46 | down | 0.3780 | 1.28 | up | frataxin-like protein\ Context:(NC_002946)+[2078991-2079314]\ Notes:defects in the mitochondrial frataxin protein cause Friedreich ataxis which is an autosomal recessive neurodegenerative disease; based on phylogenomic distribution this protein may have a role in iron-sulfur cluster protein assembly |
| NGO2101 | 0.9502 | 1.03 | up | 0.5390 | -1.29 | down | 0.4132 | -1.29 | down | hypothetical protein\ Context:(NC_002946)+[2079347-2079766]\ Notes:Best Blastp Hit: gb\|AAF42308.1\| (AE002546) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO2102 | 0.2492 | -1.77 | down | 0.5234 | -1.36 | down | 0.3042 | -1.96 | down | S-ribosylhomocysteinase\ Context:(NC_002946)+[2079788-2080294]\ Notes:catalyzes the hydrolysis of S-ribosylhomocysteine to homocysteine and autoinducer-2 |
| NGO2103 | 0.0143 | 6.41 | up | 0.0465 | 5.81 | up | 0.0775 | 2.42 | up | hypothetical protein\ Context:(NC_002946)+[2080439-2083231]\ Notes:Best Blastp Hit: pir\|\|F81963 DNA-directed DNA polymerase (EC 2.7.7.7) I NMA0462 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379209\|emb\|CAB83758.1\| (AL162753) DNA polymerase I [Neisseria meningitidis] COG0749 DNA polymerase I - 3'-5' exonuclease and |
| NGO2104 | 0.8554 | 1.09 | up | 0.5080 | 1.24 | up | 0.6993 | 1.11 | up | hypothetical protein\ Context:(NC_002946)+[2083793-2084488]\ Notes:Best Blastp Hit: pir\|\|C81019 hypothetical protein NMB1983 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227245\|gb\|AAF42311.1\| (AE002547) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379207\|emb\|CAB83756.1\| (AL162753) hypothetical protein [Neisseria meningitidis] |
| NGO2105 | 0.8578 | -1.11 | down | 0.2566 | 1.83 | up | 0.3714 | 1.76 | up | adhesion and penetration protein\ Context:(NC_002946)-[2084728-2089134]\ Notes:Best Blastp Hit: pir\|\|D81019 adhesion and penetration protein NMB1985 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227246\|gb\|AAF42312.1\| (AE002547) adhesion and penetration protein [Neisseria meningitidis MC58] |
| NGO2106 | 0.0008 | -11.76 | down | 0.0195 | -11.85 | down | 0.3959 | -2.06 | down | hypothetical protein\ Context:(NC_002946)+[2089206-2089541]\ Notes: |

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| NGO2107 | 0.1594 | 2.21 | up | 0.9948 | -1.00 | down | 0.0750 | -1.75 | down | tRNA modification GTPase TrmE\ Context:(NC_002946)+[2089572-2090918]\ Notes:in Escherichia coli this protein is involved in the biosynthesis of the hypermodified nucleoside 5-methylaminomethyl-2-thiouridine; which is found in the wobble position of some tRNAs and affects ribosomal frameshifting; shows potassium-dependent dimerization and GTP hydrolysis; also involved in regulation of glutamate-dependent acid resistance and activation of gadE |
| NGO2108 | 0.0102 | -62.56 | down | 0.0075 | -61.02 | down | 0.5976 | -2.77 | down | hypothetical protein\ Context:(NC_002946)-[2090831-2091019]\ Notes: |
| NGO2109 | 0.2644 | -2.69 | down | 0.0588 | -8.58 | down | 0.6587 | 1.20 | up | hemoglobin-haptoglobin utilization protein B\ Context:(NC_002946)-[2091811-2094240]\ Notes:Best Blastp Hit: emb\|CAB83769.1\| (AL162753) haemoglobin-haptoglobin-utilization protein [Neisseria meningitidis] COG1629 Outer membrane receptor proteins; mostly Fe |
| NGO2111 | 0.0140 | 10.62 | up | 0.0170 | 6.36 | up | 0.0034 | 5.17 | up | hypothetical protein\ Context:(NC_002946)+[2095595-2097208]\ Notes:Best Blastp Hit: pir\|\|B81021 conserved hypothetical protein NMB1971 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227232\|gb\|AAF42300.1\| (AE002545) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO2112 | 0.0013 | 8.07 | up | 0.0824 | 2.85 | up | 0.1523 | 1.73 | up | putative para-aminobenzoate synthase component\ Context:(NC_002946)-[2097269-2099158]\ Notes:Best Blastp Hit: emb\|CAB83772.1\| (AL162753) putative para-aminobenzoate synthase component I [Neisseria meningitidis] COG0147 Anthranilate/para-aminobenzoate synthases |
| NGO2113 | 0.0079 | -9.83 | down | 0.0001 | -51.17 | down | 0.0006 | -29.58 | down | hypothetical protein\ Context:(NC_002946)+[2099285-2100214]\ Notes:Best Blastp Hit: gb\|AAG03531.1\|AE004452_3 (AE004452) conserved hypothetical protein [Pseudomonas aeruginosa] |
| NGO2116 | 0.5570 | 1.44 | up | 0.3278 | 1.38 | up | 0.7363 | -1.10 | down | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)+[2102863-2103723]\ Notes:Best Blastp Hit: emb\|CAB83778.1\| (AL162753) putative ABC transport ATP-binding protein [Neisseria meningitidis] COG1127 Uncharacterized ABC-type transport system |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2117 | 0.9325 | 1.06 | up | 0.3669 | -1.36 | down | 0.2712 | -1.47 | down | ABC transporter inner membrane protein\ Context:(NC_002946)+[2103771-2104547]\ Notes:Best Blastp Hit: pir\|\|F81022 probable ABC transport inner membrane subunit NMA0486 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227225\|gb\|AAF42294.1\| (AE002544) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379230\|emb\|CAB83779.1\| (AL162753) |
| NGO2118 | 0.4215 | 1.49 | up | 0.8643 | -1.07 | down | 0.4624 | -1.21 | down | hypothetical protein\ Context:(NC_002946)+[2104529-2105092]\ Notes:Best Blastp Hit: pir\|\|E81022 probable outer membrane transport protein NMA0487 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227224\|gb\|AAF42293.1\| (AE002544) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379231\|emb\|CAB83780.1\| (AL162753 |
| NGO2119 | 0.9462 | -1.03 | down | 0.4434 | 1.33 | up | 0.1795 | -1.56 | down | hypothetical protein\ Context:(NC_002946)+[2105123-2105713]\ Notes:Best Blastp Hit: gb\|AAF42292.1\| (AE002544) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO2120 | 0.8943 | -1.06 | down | 0.4929 | 1.24 | up | 0.4950 | -1.30 | down | hypothetical protein\ Context:(NC_002946)+[2105764-2106042]\ Notes:Best Blastp Hit: pir\|\|C81022 hypothetical protein NMB1962 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227222\|gb\|AAF42291.1\| (AE002544) hypothetical protein [Neisseria meningitidis MC58] |
| NGO2121 | 0.7323 | -1.17 | down | 0.2150 | -1.68 | down | 0.1302 | -1.69 | down | hypothetical protein\ Context:(NC_002946)+[2106039-2106872]\ Notes:Best Blastp Hit: gb\|AAF42290.1\| (AE002544) VacJ-related protein [Neisseria meningitidis MC58] |
| NGO2122 | 0.3687 | 1.66 | up | 0.7507 | 1.11 | up | 0.4397 | 1.26 | up | hypothetical protein\ Context:(NC_002946)+[2106877-2107359]\ Notes:Best Blastp Hit: pir\|\|A81022 hypothetical protein NMB1960 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227220\|gb\|AAF42289.1\| (AE002544) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379235\|emb\|CAB83784.1\| (AL162753) hypothetical protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2123 | 0.8856 | 1.06 | up | 0.7622 | 1.12 | up | 0.2390 | -1.62 | down | hypothetical protein\ Context:(NC_002946)+[2107359-2107742]\ Notes:Best Blastp Hit: gb\|AAF42288.1\|(AE002544) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379236\|emb\|CAB83785.1\|(AL162753) conserved hypothetical protein [Neisseria meningitidis] COG0824 Predicted esterase |
| NGO2124 | 0.1155 | -2.31 | down | 0.3748 | -2.64 | down | 0.6192 | -1.67 | down | putative thioredoxin\ Context:(NC_002946)+[2107739-2108227]\ Notes:Best Blastp Hit: emb\|CAB83786.1\|(AL162753) putative periplasmic protein [Neisseria meningitidis] COG0526 Thiol-disulfide isomerase and thioredoxins |
| NGO2125 | 0.0173 | -8.58 | down | 0.0055 | -10.98 | down | 0.1744 | -3.08 | down | putative acetyltransferase\ Context:(NC_002946)-[2108308-2108826]\ Notes:Best Blastp Hit: emb\|CAB83787.1\|(AL162753) putative acetyltransferase [Neisseria meningitidis] COG2171 Tetrahydrodipicolinate |
| NGO2126 | 0.0060 | 20.33 | up | 0.0092 | 11.59 | up | 0.0377 | 7.69 | up | 50S ribosomal protein L31\ Context:(NC_002946)+[2108958-2109173]\ Notes:RpmE; there appears to be two types of ribosomal proteins L31 in bacterial genomes; some contain a CxxC motif while others do not; Bacillus subtilis has both types; the proteins in this cluster have the CXXC motif; RpmE is found in exponentially growing Bacilli while YtiA was found after exponential growth |
| NGO2127 | 0.6356 | 1.27 | up | 0.9954 | 1.00 | up | 0.3571 | -1.67 | down | CadD\ Context:(NC_002946)+[2109425-2110066]\ Notes:Best Blastp Hit: possibly phase variable - 9A residue homopolymer repeat in the coding sequence (ON); putative cadmium resistance protein |
| NGO2128 | 0.1054 | 2.31 | up | 0.2234 | -2.63 | down | 0.2635 | 1.34 | up | hypothetical protein\ Context:(NC_002946)+[2110212-2111888]\ Notes:Best Blastp Hit: pir\|\|F81967 probable inner membrane protein NMA0497 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379241\|emb\|CAB83790.1\| (AL162753) putative inner membrane protein [Neisseria meningitidis] |
| NGO2130 | 0.7839 | 1.16 | up | 0.6391 | -1.22 | down | 0.9030 | -1.05 | down | RegF\ Context:(NC_002946)+[2112095-2112700]\ Notes:Best Blastp Hit: emb\|CAA68006.1\| (X99693) regF [Neisseria gonorrhoeae] COG0625 Glutathione-S-transferases; putative regulator of pilE expression |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2131 | 0.1190 | 2.27 | up | 0.1336 | 3.92 | up | 0.1982 | 2.81 | up | ClpXP protease specificity-enhancing factor\ Context:(NC_002946)+[2112772-2113164]\ Notes:Best Blastp Hit: gb\|AAF42281.1\| (AE002543) stringent starvation protein B [Neisseria meningitidis MC58] |
| NGO2132 | 0.5520 | 1.49 | up | 0.6700 | -1.81 | down | 0.6052 | 1.85 | up | hypothetical protein\ Context:(NC_002946)+[2113212-2113397]\ Notes: |
| NGO2133 | 0.3602 | 1.59 | up | 0.4870 | -1.33 | down | 0.9701 | -1.01 | down | hypothetical protein\ Context:(NC_002946)-[2113363-2113905]\ Notes:Best Blastp Hit: gb\|AAF42280.1\| (AE002543) conserved hypothetical protein [Neisseria meningitidis MC58] COG1610 Uncharacterized protein; YqeY family |
| NGO2134 | 0.1684 | 2.40 | up | 0.7730 | 1.12 | up | 0.4300 | 1.36 | up | 30S ribosomal protein S21\ Context:(NC_002946)-[2113941-2114153]\ Notes:a small basic protein that is one of the last in the subunit assembly; omission does not prevent assembly but the subunit is inactive; binds central domain of 16S rRNA |
| NGO2135 | 0.6645 | 1.20 | up | 0.8826 | 1.06 | up | 0.2577 | 1.77 | up | putative transglycosylase\ Context:(NC_002946)-[2114442-2116292]\ Notes:Best Blastp Hit: emb\|CAB83796.1\| (AL162753) putative transglycosylase [Neisseria meningitidis] COG0741 Soluble lytic murein transglycosylase and |
| NGO2136 | 0.5848 | -1.39 | down | 0.0169 | -8.68 | down | 0.5253 | -1.89 | down | hypothetical protein\ Context:(NC_002946)+[2116331-2116516]\ Notes: |
| NGO2137 | 0.2922 | -1.73 | down | 0.4716 | -1.34 | down | 0.4304 | -1.49 | down | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)+[2116669-2117406]\ Notes:Best Blastp Hit: emb\|CAB83797.1\| (AL162753) putative ABC transport ATP-binding subunit [Neisseria meningitidis] COG1135 Uncharacterized ABC-type transport system |
| NGO2138 | 0.0472 | -3.37 | down | 0.0107 | -5.67 | down | 0.4488 | -1.38 | down | putative ABC transporter; permease protein\ Context:(NC_002946)+[2117408-2118094]\ Notes:Best Blastp Hit: pir\|\|D81023 ABC transporter; permease protein NMB1947 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227206\|gb\|AAF42276.1\| (AE002543) ABC transporter; permease protein [Neisseria meningitidis MC58] COG2011 Permease component of an uncharacterized ABC |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2139 | 0.4147 | 1.64 | up | 0.6806 | 1.16 | up | 0.5667 | 1.31 | up | hypothetical protein\ Context:(NC_002946)+[2118253-2119119]\ Notes:Best Blastp Hit: gb\|AAF44768.1\|AF235151_1 (AF235151) GNA1946 [Neisseria gonorrhoeae] >gi\|7274428\|gb\|AAF44769.1\|AF235152_1 (AF235152) GNA1946 [Neisseria gonorrhoeae] >gi\|7274430\|gb\|AAF44770.1\|AF235153_1 (AF235153) GNA1946 |
| NGO2140 | 0.0303 | -4.04 | down | 0.0937 | -5.95 | down | 0.1735 | -2.15 | down | aromatic acid decarboxylase\ Context:(NC_002946)-[2119182-2119754]\ Notes:catalyzes the formation of 2-octaprenylphenol from 3-octaprenyl-4-hydroxybenzoate |
| NGO2141 | 0.6879 | 1.21 | up | 0.6508 | -1.22 | down | 0.8068 | 1.07 | up | putative chromosome segregation protein\ Context:(NC_002946)+[2119909-2120769]\ Notes:Best Blastp Hit: pir\|\|A81969 probable chromosome segregation proteins NMA0508 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379252\|emb\|CAB83801.1\| (AL162753) putative chromosome segregation proteins [Neisseria meningitidis] COG1475 Predicted transcriptional regulators |
| NGO2142 | 0.0609 | -5.46 | down | 0.0581 | -9.25 | down | 0.5908 | 1.36 | up | hypothetical protein\ Context:(NC_002946)-[2120817-2121239]\ Notes:Best Blastp Hit: sp\|P44726\|YICC_HAEIN hypothetical protein HI0467 >gi\|1074414\|pir\|\|C64153 hypothetical protein HI0467 - Haemophilus influenzae (strain Rd KW20) >gi\|1573445\|gb\|AAC22126.1\| (U32729) conserved hypothetical protein [Haemophilus influenzae Rd] |
| NGO2143 | 0.7255 | 1.22 | up | 0.6712 | 1.33 | up | 0.7138 | -1.19 | down | AtpI\ Context:(NC_002946)+[2121443-2121796]\ Notes:Best Blastp Hit: pir\|\|F81025 hypothetical protein NMB1941 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227199\|gb\|AAF42270.1\| (AE002542) hypothetical protein [Neisseria meningitidis MC58]; putative ATP synthase I |
| NGO2144 | 0.7308 | 1.19 | up | 0.9427 | 1.03 | up | 0.6505 | -1.12 | down | F0F1 ATP synthase subunit A\ Context:(NC_002946)+[2121786-2122652]\ Notes:Produces ATP from ADP in the presence of a proton gradient across the membrane. Subunit A is part of the membrane proton channel F0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2145 | 0.1596 | 2.58 | up | 0.1327 | 1.69 | up | 0.2175 | 1.86 | up | F0F1 ATP synthase subunit C\ Context:(NC_002946)+[2122709-2122945]\ Notes:Produces ATP from ADP in the presence of a proton gradient across the membrane. Subunit C is part of the membrane proton channel F0 |
| NGO2146 | 0.1773 | 2.27 | up | 0.1907 | 1.57 | up | 0.3654 | 1.46 | up | F0F1 ATP synthase subunit B\ Context:(NC_002946)+[2123015-2123485]\ Notes:Produces ATP from ADP in the presence of a proton gradient across the membrane. Subunit B is part of the membrane proton channel. |
| NGO2147 | 0.1483 | 2.49 | up | 0.1277 | 1.68 | up | 0.3114 | 1.50 | up | F0F1 ATP synthase subunit delta\ Context:(NC_002946)+[2123490-2124023]\ Notes:produces ATP from ADP in the presence of a proton gradient across the membrane; the delta subunit is part of the catalytic core of the ATP synthase complex |
| NGO2148 | 0.1203 | 2.54 | up | 0.1691 | 1.58 | up | 0.2271 | 1.58 | up | F0F1 ATP synthase subunit alpha\ Context:(NC_002946)+[2124034-2125581]\ Notes:produces ATP from ADP in the presence of a proton gradient across the membrane; the alpha chain is a catalytic subunit |
| NGO2149 | 0.1391 | 2.44 | up | 0.1249 | 1.71 | up | 0.2477 | 1.59 | up | F0F1 ATP synthase subunit gamma\ Context:(NC_002946)+[2125606-2126481]\ Notes:Produces ATP from ADP in the presence of a proton gradient across the membrane. The gamma chain is a regulatory subunit |
| NGO2150 | 0.1765 | 2.19 | up | 0.0962 | 1.78 | up | 0.2762 | 1.60 | up | F0F1 ATP synthase subunit beta\ Context:(NC_002946)+[2126519-2127916]\ Notes:Produces ATP from ADP in the presence of a proton gradient across the membrane. The beta chain is a regulatory subunit |
| NGO2151 | 0.3142 | 1.89 | up | 0.2440 | 1.47 | up | 0.2095 | 1.74 | up | F0F1 ATP synthase subunit epsilon\ Context:(NC_002946)+[2127927-2128349]\ Notes:part of catalytic core of ATP synthase; alpha(3)beta(3)gamma(1)delta(1)epsilon(1); involved in producing ATP from ADP in the presence of the proton motive force across the membrane |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2153 | 0.2955 | 1.76 | up | 0.7222 | -1.18 | down | 0.8554 | 1.07 | up | glycyl-tRNA synthetase subunit alpha\ Context:(NC_002946)+[2128521-2129417]\ Notes:glycine--tRNA ligase alpha chain; GlyRS; class II aminoacyl tRNA synthetase; tetramer of alpha(2)beta(2); catalyzes a two-step reaction; first charging a glycine molecule by linking its carboxyl group to the alpha-phosphate of ATP; second by transfer of the aminoacyl-adenylate to its tRNA |
| NGO2154 | 0.0075 | 5.33 | up | 0.0455 | 3.10 | up | 0.1089 | 1.74 | up | glycyl-tRNA synthetase subunit beta\ Context:(NC_002946)+[2129534-2131597]\ Notes:glycine--tRNA ligase beta chain; glyS; class II aminoacyl tRNA synthetase; tetramer of alpha(2)beta(2); catalyzes a two-step reaction; first charging a glycine molecule by linking the carboxyl group to the alpha-phosphate of ATP; second by transfer of the aminoacyl-adenylate to its tRNA |
| NGO2156 | 0.4264 | 1.47 | up | 0.9458 | 1.03 | up | 0.9185 | -1.03 | down | LgtB\ Context:(NC_002946)+[2132700-2133539]\ Notes:Best Blastp Hit: sp\|Q50947\|LGTB_NEIGO lacto-N-neotetraose biosynthesis glycosyl transferase LgtB >gi\|595811\|gb\|AAA68010.1\| (U14554) glycosyl transferase [Neisseria gonorrhoeae]; lacto-N-neotetraose biosynthesis glycosyl tranferase |
| NGO2158 | 0.2245 | 1.97 | up | 0.3901 | 1.31 | up | 0.5226 | 1.18 | up | LgtD\ Context:(NC_002946)+[2134535-2135551]\ Notes:Best Blastp Hit: gb\|AAA68012.1\| (U14554) glycosyl transferase [Neisseria gonorrhoeae] COG0463 Glycosyltransferases involved in cell wall |
| NGO2159 | 0.4236 | 1.45 | up | 0.9803 | 1.01 | up | 0.5702 | -1.15 | down | LgtE\ Context:(NC_002946)+[2135570-2136412]\ Notes:Best Blastp Hit: sp\|Q50950\|LGTE_NEIGO lacto-N-neotetraose biosynthesis glycosyl transferase LgtE >gi\|595814\|gb\|AAA68013.1\| (U14554) glycosyl transferase [Neisseria gonorrhoeae] |
| NGO2160 | 0.1871 | 3.36 | up | 0.8654 | -1.23 | down | 0.3364 | 2.40 | up | hypothetical protein\ Context:(NC_002946)-[2136608-2137333]\ Notes:Best Blastp Hit: pir\|\|H81026 conserved hypothetical protein NMB1925 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227182\|gb\|AAF42254.1\| (AE002541) conserved hypothetical protein [Neisseria meningitidis MC58] COG1385 Uncharacterized BCR |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2161 | 0.5206 | 1.35 | up | 0.6160 | -1.22 | down | 0.8163 | -1.06 | down | hypothetical protein\ Context:(NC_002946)+[2137437-2138231]\ Notes:Best Blastp Hit: emb\|CAB83821.1\| (AL162753) hypothetical protein NMA0529 [Neisseria meningitidis] COG0483 Inositol phosphatase family proteins |
| NGO2162 | 0.6383 | 1.46 | up | 0.0090 | -9.00 | down | 0.5295 | -1.60 | down | hypothetical protein\ Context:(NC_002946)-[2138449-2138934]\ Notes:Best Blastp Hit: gb\|AAF42252.1\| (AE002541) conserved hypothetical protein [Neisseria meningitidis MC58] |
| NGO2163 | 0.1230 | 2.61 | up | 0.1437 | 1.65 | up | 0.3071 | 1.64 | up | 3-ketoacyl-(acyl-carrier-protein) reductase\ Context:(NC_002946)-[2138999-2139745]\ Notes:catalyzes the first of the two reduction steps in the elongation cycle of fatty acid synthesis |
| NGO2164 | 0.5201 | 1.41 | up | 0.5137 | 1.24 | up | 0.7605 | 1.12 | up | bifunctional GMP synthase/glutamine amidotransferase protein\ Context:(NC_002946)-[2139807-2141372]\ Notes:contains glutamine-hydrolyzing domain and glutamine amidotransferase; GMP-binding domain; functions to produce GMP from XMP in the IMP pathway |
| NGO2165 | 0.0777 | -3.36 | down | 0.7417 | -1.46 | down | 0.6941 | 1.34 | up | putative ABC transporter; ATP-binding protein\ Context:(NC_002946)-[2141472-2143340]\ Notes:Best Blastp Hit: gb\|AAF42249.1\| (AE002541) ABC transporter; ATP-binding protein [Neisseria meningitidis MC58] COG1132 ABC-type multidrug/protein/lipid transport |
| NGO2166 | 0.3450 | 1.61 | up | 0.4786 | 1.28 | up | 0.5728 | 1.20 | up | acyl-carrier-protein S-malonyltransferase\ Context:(NC_002946)-[2143479-2144405]\ Notes:Best Blastp Hit: pir\|\|B81026 malonyl CoA-acyl carrier protein transacylase NMB1918 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227176\|gb\|AAF42248.1\| (AE002541) malonyl CoA-acyl carrier protein transacylase [Neisseria meningitidis MC58] COG0331 (acyl-carrier-protein) S-malonyltransferase |
| NGO2167 | 0.4605 | -1.55 | down | 0.8081 | 1.10 | up | 0.7638 | -1.10 | down | hypothetical protein\ Context:(NC_002946)-[2144431-2144802]\ Notes:Best Blastp Hit: emb\|CAB83831.1\| (AL162753) putative integral membrane protein [Neisseria meningitidis] |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2168 | 0.6406 | 1.24 | up | 0.3249 | -1.81 | down | 0.7308 | -1.11 | down | 3-oxoacyl-(acyl carrier protein) synthase III\ Context:(NC_002946)-[2144849-2145811]\ Notes:FabH; beta-ketoacyl-acyl carrier protein synthase III; catalyzes the condensation of acetyl-CoA with malonyl-ACP to initiate cycles of fatty acid elongation; differs from 3-oxoacyl-(acyl carrier protein) synthase I and II in that it utilizes CoA thioesters as primers rather than acyl-ACPs |
| NGO2170 | 0.1622 | 3.66 | up | 0.4779 | 1.86 | up | 0.3870 | 2.10 | up | hypothetical protein\ Context:(NC_002946)-[2146659-2146910]\ Notes:Best Blastp Hit: gb\|AAF42244.1\| (AE002540) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379280\|emb\|CAB83834.1\| (AL162753) hypothetical protein NMA0541 [Neisseria meningitidis] |
| NGO2171 | 0.0612 | 3.09 | up | 0.4363 | 1.81 | up | 0.0972 | 1.67 | up | putative glycerol-3-phosphate acyltransferase PlsX\ Context:(NC_002946)-[2147048-2148094]\ Notes:involved in acylation of glycerol-3-phosphate to form 1-acyl-glycerol-3 phosphate for use in phospholipid biosynthesis; functions with PlsY |
| NGO2172 | 0.2510 | 1.86 | up | 0.1124 | 1.82 | up | 0.3249 | 1.36 | up | hypothetical protein\ Context:(NC_002946)-[2148184-2148711]\ Notes:Best Blastp Hit: pir\|\|G81028 conserved hypothetical protein NMB1912 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227169\|gb\|AAF42242.1\| (AE002540) conserved hypothetical protein [Neisseria meningitidis MC58] COG2236 Predicted phosphoribosyltransferases |
| NGO2173 | 0.0175 | 13.51 | up | 0.0694 | 4.93 | up | 0.9264 | 1.03 | up | 50S ribosomal protein L32\ Context:(NC_002946)-[2148886-2149065]\ Notes:some L32 proteins have zinc finger motifs consisting of CXXC while others do not |
| NGO2174 | 0.0642 | 3.09 | up | 0.2871 | 1.55 | up | 0.4991 | 1.25 | up | hypothetical protein\ Context:(NC_002946)-[2149099-2149599]\ Notes:Best Blastp Hit: pir\|\|A81973 hypothetical protein NMA0545 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379284\|emb\|CAB83838.1\| (AL162753) hypothetical protein NMA0545 [Neisseria meningitidis] |
| NGO2175 | 0.0875 | -2.75 | down | 0.2770 | -1.55 | down | 0.0372 | -3.05 | down | Maf-like protein\ Context:(NC_002946)+[2149747-2150337]\ Notes:Maf; overexpression in Bacillus subtilis inhibits septation in the dividing cell |

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|---|---|---|---|---|---|---|---|---|---|---|
| NGO2176 | 0.5967 | -1.85 | down | 0.0060 | -41.18 | down | 0.7378 | -1.43 | down | hypothetical protein\ Context:(NC_002946)-[2150090-2151172]\ Notes:Best Blastp Hit: sp\|P45610\|TONB_KLEPN TonB protein >gi\|484474\|pir\|\|JN0788 tonB protein - Klebsiella pneumoniae >gi\|405758\|emb\|CAA48498.1\|(X68478) TonB [Klebsiella pneumoniae] |
| NGO2177 | 0.1006 | -2.37 | down | 0.1441 | -2.37 | down | 0.0027 | -3.41 | down | hypothetical protein\ Context:(NC_002946)+[2150384-2151109]\ Notes:Best Blastp Hit: gb\|AAF42238.1\|(AE002540) conserved hypothetical protein [Neisseria meningitidis MC58] COG0313 Predicted methyltransferases |
| NGO2178 | 0.1964 | 1.98 | up | 0.0753 | 2.46 | up | 0.4033 | 1.32 | up | putative inner membrane protein translocase component YidC\ Context:(NC_002946)-[2151190-2152827]\ Notes:functions to insert inner membrane proteins into the IM in Escherichia coli; interacts with transmembrane segments; functions in both Sec-dependent and -independent membrane insertion; similar to Oxa1p in mitochondria |
| NGO2179 | 0.0007 | -20.69 | down | 0.0052 | -28.75 | down | 0.0915 | -3.68 | down | hypothetical protein\ Context:(NC_002946)+[2152852-2152986]\ Notes: |
| NGO2180 | 0.4335 | -2.28 | down | 0.2393 | -2.19 | down | 0.1013 | -3.55 | down | hypothetical protein\ Context:(NC_002946)-[2153000-2153221]\ Notes:Best Blastp Hit: pir\|\|E81973 hypothetical protein NMA0549 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379288\|emb\|CAB83842.1\|(AL162753) hypothetical protein NMA0549 [Neisseria meningitidis] COG0759 Uncharacterized ACR; YidD family |
| NGO2181 | 0.4656 | -1.45 | down | 0.9271 | -1.05 | down | 0.2728 | -1.86 | down | ribonuclease P\ Context:(NC_002946)-[2153286-2153651]\ Notes:protein component of RNaseP which catalyzes the removal of the 5'-leader sequence from pre-tRNA to produce the mature 5'terminus; this enzyme also cleaves other RNA substrates |
| NGO2182 | 0.3157 | 2.01 | up | 0.5446 | 1.33 | up | 0.5132 | 1.26 | up | 50S ribosomal protein L34\ Context:(NC_002946)-[2153654-2153788]\ Notes:in Escherichia coli transcription of this gene is enhanced by polyamines |
| NGO6151 | 0.5080 | 2.12 | up | 0.7058 | -1.52 | down | 0.4136 | -2.45 | down | hypothetical protein\ Context:(NC_002946)+[604158-604448]\ Notes: |

### Table S3_*nrrF* mutant strain_array fold changes_3hr

| Locus Tag | p value | *nrrF* mutant Fe-/Fe+ Fold Change | Regulation | Probe Comment | Biological Category |
|---|---|---|---|---|---|
| NGO0106 | 0.0009 | 6.43 | up | S-adenosylmethionine synthetase\ Context:(NC_002946)+[118517-119686]\ Notes:methionine adenosyltransferase; catalyzes the formation of S-adenosylmethionine from methionine and ATP; methionine adenosyltransferase | Amino Acid Biosynthesis and Metabolism |
| NGO0873 | 0.0310 | 25.53 | up | DNA modification methylase M.NGOI\ Context:(NC_002946)+[857066-858004]\ Notes:Best Blastp Hit: emb\|CAB44950.1\| (AJ242840) DNA modification methylase [Neisseria gonorrhoeae] >gi\|5262959\|emb\|CAB45015.2\| (AJ242839) DNA modification methylase [Neisseria gonorrhoeae] COG0270 Site-specific DNA methylase dcm; DcmD | Amino Acid Biosynthesis and Metabolism |
| NGO1217 | 0.0218 | 2.46 | up | glutathione synthetase\ Context:(NC_002946)-[1166816-1167775]\ Notes:The second step in the glutathione biosynthesis pathway; where it synthesizes ATP + gamma-L-glutamyl-L-cysteine + glycine = ADP + phosphate + glutathione | Amino Acid Biosynthesis and Metabolism |
| NGO1240 | 0.0243 | 2.51 | up | histidinol dehydrogenase\ Context:(NC_002946)+[1191348-1192637]\ Notes:catalyzes the oxidation of L-histidinol to L-histidinaldehyde and then to L-histidine in histidine biosynthesis; functions as a dimer | Amino Acid Biosynthesis and Metabolism |
| NGO1241 | 0.0393 | 4.15 | up | histidinol-phosphate aminotransferase\ Context:(NC_002946)+[1192683-1193762]\ Notes:catalyzes the formation of L-histidinol phosphate from imidazole-acetol phosphate and glutamate in histidine biosynthesis | Amino Acid Biosynthesis and Metabolism |
| NGO1487 | 0.0149 | 2.91 | up | arginine decarboxylase\ Context:(NC_002946)-[1450398-1452290]\ Notes:catalyzes the formation of agmatine from arginine in putrescine and spermidine biosynthesis | Amino Acid Biosynthesis and Metabolism |
| NGO1535 | 0.0429 | 3.11 | up | UDP-N-acetylmuramoyl-L-alanyl-D-glutamatesynthetase\ Context:(NC_002946)-[1507328-1508665]\ Notes:UDP-N-acetylmuramoylalanine--D-glutamate ligase; involved in peptidoglycan biosynthesis; cytoplasmic; catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine during cell wall formation | Amino Acid Biosynthesis and Metabolism |
| NGO1539 | 0.0152 | 2.63 | up | putative UDP-MurNAc-pentapeptide synthetase\ Context:(NC_002946)-[1510761-1512119]\ Notes:Best Blastp Hit: emb\|CAB85286.1\| (AL162758) UDP-MurNAc-pentapeptide synthetase [Neisseria meningitidis] COG0770 UDP-N-acetylmuramyl pentapeptide synthase | Amino Acid Biosynthesis and Metabolism |
| NGO1541 | 0.0175 | 7.26 | up | UDP-N-acetylmuramoylalanyl-D-glutamate--2; 6-diaminopimelate ligase\ Context:(NC_002946)-[1513913-1515391]\ Notes:involved in cell wall formation; peptidoglycan synthesis; cytoplasmic enzyme; catalyzes the addition of meso-diaminopimelic acid to the nucleotide precursor UDP-N-aceylmuramoyl-l-alanyl-d-glutamate | Amino Acid Biosynthesis and Metabolism |
| NGO1781 | 0.0451 | 2.21 | up | dihydrodipicolinate reductase\ Context:(NC_002946)+[1749964-1750773]\ Notes:catalyzes the reduction of 2;3-dihydrodipicolinate to 2;3;4;5-tetrahydrodipicolinate in lysine and diaminopimelate biosynthesis | Amino Acid Biosynthesis and Metabolism |
| NGO0803 | 0.0283 | 2.50 | up | putative GTP-binding protein\ Context:(NC_002946)-[793931-795742]\ Notes:Best Blastp Hit: pir\|\|H81111 GTP-binding protein TypA NMB1199 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226435\|gb\|AAF41581.1\| (AE002467) GTP-binding protein TypA [Neisseria meningitidis MC58] COG1217 Membrane GTPase | Cell Communication and Outer Membrane Proteins |
| NGO1688 | 0.0098 | 10.32 | up | putative outer membrane protein OmpU\ Context:(NC_002946)-[1641216-1642685]\ Notes:Best Blastp Hit: emb\|CAB85386.1\| (AL162758) conserved hypothetical protein [Neisseria meningitidis] | Cell Communication and Outer Membrane Proteins |
| NGO1802 | 0.0233 | 2.59 | up | hypothetical protein\ Context:(NC_002946)+[1776008-1776565]\ Notes:Best Blastp Hit: gb\|AAF40638.1\| (AE002375) outer membrane protein OmpH; putative [Neisseria meningitidis MC58] | Cell Communication and Outer Membrane Proteins |

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|---|---|---|---|---|---|
| NGO0264 | 0.0404 | 12.25 | up | putative bacteriocin production protein\ Context:(NC_002946)-[263603-264100]\ Notes:Best Blastp Hit: gb\|AAF62316.1\| (AE002423) colicin V production protein; putative [Neisseria meningitidis MC58] COG1286 Uncharacterized membrane protein; required | Cellular Processes |
| NGO0265 | 0.0419 | 2.33 | up | tetrapac protein\ Context:(NC_002946)-[264093-265133]\ Notes:Best Blastp Hit: emb\|CAA92429.1\| (Z68205) tpc [Neisseria gonorrhoeae] | Cellular Processes |
| NGO0554 | 0.0008 | 52.81 | up | hypothetical protein\ Context:(NC_002946)+[531770-532720]\ Notes:Best Blastp Hit: sp\|Q03155\|AIDA_ECOLI adhesin Aida-i precursor >gi\|281809\|pir\|\|S28634 adhesin AIDA-I precursor - Escherichia coli plasmid pIB6 >gi\|42255\|emb\|CAA46156.1\| (X65022) AIDA-I [Escherichia coli] | Cellular Processes |
| NGO0595 | 0.0527 | 2.51 | up | hypothetical protein\ Context:(NC_002946)-[582130-582891]\ Notes:Best Blastp Hit: gb\|AAF41684.1\| (AE002479) fimbrial biogenesis and twitching motility protein; putative [Neisseria meningitidis MC58] | Cellular Processes |
| NGO0771 | 0.0438 | 2.79 | up | putative exodeoxyribonuclease V alpha subunit\ Context:(NC_002946)+[765289-767034]\ Notes:Best Blastp Hit: gb\|AAC14132.1\| (AF058330) RecD [Neisseria gonorrhoeae] COG0507 ATP-dependent exoDNAse (exonuclease V) | Cellular Processes |
| NGO0773 | 0.0320 | 2.27 | up | Irg1\ Context:(NC_002946)+[767722-768723]\ Notes:Best Blastp Hit: gb\|AAC82509.1\| (U65994) pilin gene inverting protein homolog PivNG [Neisseria gonorrhoeae]; putative invertase related gene 1 | Cellular Processes |
| NGO0775 | 0.0517 | 3.28 | up | hypothetical protein\ Context:(NC_002946)+[769563-772025]\ Notes:Best Blastp Hit: pir\|\|H81106 ATP-dependent proteinase La NMB1231 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226470\|gb\|AAF41612.1\| (AE002471) ATP-dependent protease La [Neisseria meningitidis MC58] COG0466 ATP-dependent Lon protease; bacterial type | Cellular Processes |
| NGO0813 | 0.0526 | 2.22 | up | putative biotin synthase\ Context:(NC_002946)-[805845-806897]\ Notes:Best Blastp Hit: pir\|\|A81117 biotin synthetase NMB1146; NMB1184 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226383\|gb\|AAF41533.1\| (AE002463) biotin synthetase [Neisseria meningitidis MC58] >gi\|7226421\|gb\|AAF41568.1\| (AE002466) biotin synthetase [Neisseria meningitidis MC58] COG0502 Biotin synthase and related enzymes | Cellular Processes |
| NGO0874 | 0.0345 | 6.22 | up | type II DNA restriction endonuclease R.NGOI\ Context:(NC_002946)+[858005-858865]\ Notes:Best Blastp Hit: sp\|P31032\|T2NM_NEIGO type II restriction enzyme NgoI (endonuclease NgomI) (R.NGOMI) >gi\|281723\|pir\|\|B42709 DNA restriction endonuclease NgoMI - Neisseria gonorrhoeae >gi\|5051443\|emb\|CAB44951.1\| (AJ242840) putative DNA restriction endonuclease [Neisseria gonorrhoeae] >gi\|5262960\|emb\|CAB45874.1\| (AJ242839) putative DNA restriction endonuclease [Neisseria gonorrhoeae] | Cellular Processes |
| NGO1472 | 0.0238 | 2.62 | up | pyridine nucleotide transhydrogenase\ Context:(NC_002946)+[1435324-1436709]\ Notes:catalyzes reversible transfer of hydride ion equivalent between NAD and NADP; membrane-bound proton pump that translocates protons from cytosolic to periplasmic side of the inner membrane; forms a tetramer composed of two alpha and 2 beta subunits; AB-stereospecific enzyme | Cellular Processes |
| NGO1565 | 0.0452 | 3.21 | up | putative nicotinate-nucleotide pyrophosphorylase\ Context:(NC_002946)-[1536265-1537146]\ Notes:Best Blastp Hit: pir\|\|A81780 nicotinate-nucleotide pyrophosphorylase (carboxylating) (EC 2.4.2.19) NMA2088 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380713\|emb\|CAB85304.1\| (AL162758) nicotinate-nucleotide pyrophosphorylase [Neisseria meningitidis] COG0157 Nicotinate-nucleotide pyrophosphorylase | Cellular Processes |
| NGO1678 | 0.0228 | 3.13 | up | hypothetical protein\ Context:(NC_002946)+[1632061-1633245]\ Notes:Best Blastp Hit: emb\|CAB85376.1\| (AL162758) putative monooxygenase [Neisseria meningitidis] COG0654 2-Octaprenyl-6-metoxyphenol hydroxylase | Cellular Processes |

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|---|---|---|---|---|---|
| NGO1714 | 0.0469 | 2.15 | up | putative cis-trans isomerase\ Context:(NC_002946)-[1672744-1673745]\ Notes:Best Blastp Hit: >pir\|\|B81216 peptidyl-prolyl cis-trans isomerase NMB0281 [imported] - Neisseria meningitidis (group B strain MD58) gb\|AAF40735.1\| (AE002385) peptidyl-prolyl cis-trans isomerase [Neisseria meningitidis MC58] COG0760 Parvulin-like peptidyl-prolyl isomerase | Cellular Processes |
| NGO1983 | 0.0499 | 3.36 | up | hypothetical protein\ Context:(NC_002946)-[1957896-1958675]\ Notes:Best Blastp Hit: pir\|\|C81008 methionine aminopeptidase NMB2093 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227355\|gb\|AAF42410.1\| (AE002558) methionine aminopeptidase [Neisseria meningitidis MC58] COG0024 Methionine aminopeptidase | Cellular Processes |
| NGO1992 | 0.0437 | 2.25 | up | putative NgoI restriction endonuclease\ Context:(NC_002946)+[1964908-1965960]\ Notes:Best Blastp Hit: gb\|AAB03207.2\| (U42459) NgoI restriction endonuclease R.NgoI [Neisseria gonorrhoeae] | Cellular Processes |
| NGO0186 | 0.0358 | 2.33 | up | putative zinc-binding alcohol dehydrogenas\ Context:(NC_002946)-[186327-187391]\ Notes:Best Blastp Hit: pir\|\|H81925 probable alcohol dehydrogenase (EC 1.1.1.-) NMA0808 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379528\|emb\|CAB84091.1\| (AL162754) putative zinc-binding alcohol dehydrogenase [Neisseria meningitidis] COG1065 Zn-dependent oxidoreductases | Central Intermediary Metabolism |
| NGO0565 | 0.0435 | 2.11 | up | pyruvate dehydrogenase subunit E1\ Context:(NC_002946)-[546184-548847]\ Notes:E1 component; part of pyruvate dehydrogenase; forms a complex with DlaT and LpdC | Central Intermediary Metabolism |
| NGO0617 | 0.0205 | 2.63 | up | phosphopyruvate hydratase\ Context:(NC_002946)-[604935-606221]\ Notes:enolase; catalyzes the formation of phosphoenolpyruvate from 2-phospho-D-glycerate in glycolysis | Central Intermediary Metabolism |
| NGO0639 | 0.0196 | 2.91 | up | putative L-lactate dehydrogenase\ Context:(NC_002946)+[625991-627163]\ Notes:Best Blastp Hit: pir\|\|C81852 L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) NMA1592 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380233\|emb\|CAB84819.1\| (AL162756) L-lactate dehydrogenase [Neisseria meningitidis] COG1304 L-lactate dehydrogenase (FMN-dependent) and | Central Intermediary Metabolism |
| NGO0713 | 0.0098 | 3.25 | up | keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase\ Context:(NC_002946)-[712011-712649]\ Notes:catalyzes the formation of pyruvate and glyoxylate from 4-hydroxy-2-oxoglutarate; or pyruvate and D-glyceraldehyde 3-phosphate from 2-dehydro-3-deoxy-D-glyconate 6-phosphate | Central Intermediary Metabolism |
| NGO0719 | 0.0375 | 2.77 | up | glucose-6-phosphate isomerase\ Context:(NC_002946)+[719596-721242]\ Notes:functions in sugar metabolism in glycolysis and the Embden-Meyerhof pathways (EMP) and in gluconeogenesis; catalyzes reversible isomerization of glucose-6-phosphate to fructose-6-phosphate; member of PGI family | Central Intermediary Metabolism |
| NGO0977 | 0.0379 | 5.23 | up | putative acetate kinase\ Context:(NC_002946)+[946790-948016]\ Notes:Best Blastp Hit: pir\|\|A81868 acetate kinase (EC 2.7.2.1) NMA1718 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380359\|emb\|CAB84946.1\| (AL162756) acetate kinase [Neisseria meningitidis] COG0282 Acetate kinase | Central Intermediary Metabolism |
| NGO1881 | 0.0312 | 3.86 | up | PykA\ Context:(NC_002946)+[1851528-1853000]\ Notes:Best Blastp Hit: pir\|\|B81239 pyruvate kinase II NMB0089 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225307\|gb\|AAF40552.1\| (AE002368) pyruvate kinase II [Neisseria meningitidis MC58] COG0469 Pyruvate kinase; putative pyruvate kinase | Central Intermediary Metabolism |
| NGO1931 | 0.0216 | 2.59 | up | GapC\ Context:(NC_002946)+[1908251-1909255]\ Notes:Best Blastp Hit: pir\|\|B82019 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C NMA0246 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379008\|emb\|CAB83554.1\| (AL162752) glyceraldehyde 3-phosphate dehydrogenase C [Neisseria meningitidis] COG0057 Glyceraldehyde-3-phosphate dehydrogenase; putative glyceraldehyde 3-phosphate dehydrogenase C | Central Intermediary Metabolism |

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| NGO0829 | 0.0393 | 5.26 | up | chaperone protein HscA\ Context:(NC_002946)-[816596-818458]\ Notes:involved in the maturation of iron-sulfur cluster-containing proteins | Chaperone |
| NGO1422 | 0.0403 | 2.17 | up | putative heat shock protein\ Context:(NC_002946)-[1384782-1385360]\ Notes:Best Blastp Hit: pir\|\|D81184 probable heat shock protein grpE NMA0744 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225788\|gb\|AAF40989.1\| (AE002412) grpE protein [Neisseria meningitidis MC58] >gi\|7379465\|emb\|CAB84027.1\| (AL162754) probable heat shock protein [Neisseria meningitidis] COG0576 Molecular chaperone GrpE (heat shock | Chaperone |
| NGO1429 | 0.0211 | 3.09 | up | molecular chaperone DnaK\ Context:(NC_002946)+[1390552-1392480]\ Notes:heat shock protein 70; assists in folding of nascent polypeptide chains; refolding of misfolded proteins; utilizes ATPase activity to help fold; co-chaperones are DnaJ and GrpE; multiple copies in some bacteria | Chaperone |
| NGO2094 | 0.0500 | 2.17 | up | co-chaperonin GroES\ Context:(NC_002946)+[2072506-2072796]\ Notes:10 kDa chaperonin; Cpn10; GroES; forms homoheptameric ring; binds to one or both ends of the GroEL double barrel in the presence of adenine nucleotides capping it; folding of unfolded substrates initiates in a GroEL-substrate bound and capped by GroES; release of the folded substrate is dependent on ATP binding and hydrolysis in the trans ring | Chaperone |
| NGO2095 | 0.0301 | 2.72 | up | chaperonin GroEL\ Context:(NC_002946)+[2072888-2074522]\ Notes:60 kDa chaperone family; promotes refolding of misfolded polypeptides especially under stressful conditions; forms two stacked rings of heptamers to form a barrel-shaped 14mer; ends can be capped by GroES; misfolded proteins enter the barrel where they are refolded when GroES binds; many bacteria have multiple copies of the groEL gene which are active under different environmental conditions; the B.japonicum protein in this cluster is expressed constitutively; in Rhodobacter; Corynebacterium and Rhizobium this protein is essential for growth | Chaperone |
| NGO0636 | 0.0207 | 3.17 | up | putative NifS-like aminotransferase\ Context:(NC_002946)-[623952-625166]\ Notes:Best Blastp Hit: pir\|\|E81852 NifS-like aminotranfserase NMA1594 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380235\|emb\|CAB84821.1\| (AL162756) NifS-like aminotranfserase [Neisseria meningitidis] COG1104 Cysteine sulfinate desulfinase/cysteine | Co-Factor Metabolism |
| NGO0405 | 0.0215 | 20.08 | up | DNA-damage-inducible protein D\ Context:(NC_002946)+[398238-399089]\ Notes:Best Blastp Hit: pir\|\|G65165 DNA-damage-inducible protein d - Escherichia coli >gi\|290495\|gb\|AAA61998.1\| (L10328) o278 [Escherichia coli] >gi\|1790076\|gb\|AAC76669.1\| (AE000441) DNA-damage-inducible protein [Escherichia coli] | DNA Repair |
| NGO0451 | 0.0395 | 2.16 | up | replicative DNA helicase\ Context:(NC_002946)+[445524-446930]\ Notes:unwinds double stranded DNA | DNA Replication |
| NGO0629 | 0.0380 | 6.43 | up | DNA gyrase subunit A\ Context:(NC_002946)-[618439-621189]\ Notes:Best Blastp Hit: sp\|P48371\|GYRA_NEIGO DNA gyrase subunit A >gi\|2120873\|pir\|\|S60779 DNA gyrase chain A - Neisseria gonorrhoeae >gi\|529408\|gb\|AAA82128.1\| (U08817) DNA gyrase subunit A [Neisseria gonorrhoeae] COG0188 DNA gyrase (topoisomerase II) A subunit | DNA Replication |
| NGO2103 | 0.0465 | 5.81 | up | hypothetical protein\ Context:(NC_002946)+[2080439-2083231]\ Notes:Best Blastp Hit: pir\|\|F81963 DNA-directed DNA polymerase (EC 2.7.7.7) I NMA0462 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379209\|emb\|CAB83758.1\| (AL162753) DNA polymerase I [Neisseria meningitidis] COG0749 DNA polymerase I - 3'-5' exonuclease and | DNA Replication |
| NGO0574 | 0.0061 | 3.64 | up | Cah\ Context:(NC_002946)-[559802-560560]\ Notes:Best Blastp Hit: sp\|Q50940\|CAH_NEIGO carbonic anhydrase precursor (carbonate dehydratase) >gi\|1841441\|emb\|CAA72038.1\| (Y11152) carbonic anhydrase [Neisseria gonorrhoeae] | Energy Metabolism |
| NGO1029 | 0.0126 | 3.04 | up | fumarate hydratase\ Context:(NC_002946)+[992677-994065]\ Notes:class II family (does not require metal); tetrameric enzyme; fumarase C; reversibly converts (S)-malate to fumarate and water; functions in the TCA cycle | Energy Metabolism |

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| NGO0049 | 0.0101 | 4.24 | up | hypothetical protein\ Context:(NC_002946)-[47441-47974]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) | Hypothetical Protein |
| NGO0236 | 0.0195 | 4.53 | up | hypothetical protein\ Context:(NC_002946)-[239206-240492]\ Notes:Best Blastp Hit: pir\|\|G81172 hypothetical protein NMB0667 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225893\|gb\|AAF41085.1\| (AE002421) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0322 | 0.0199 | 4.67 | up | hypothetical protein\ Context:(NC_002946)+[321265-321744]\ Notes:Best Blastp Hit: pir\|\|G81162 hypothetical protein NMB0744 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225973\|gb\|AAF41157.1\| (AE002429) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0416 | 0.0292 | 2.69 | up | hypothetical protein\ Context:(NC_002946)+[413598-413921]\ Notes:Best Blastp Hit: pir\|\|A81152 hypothetical protein NMB0844 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226079\|gb\|AAF41255.1\| (AE002437) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0420 | 0.0394 | 2.40 | up | hypothetical protein\ Context:(NC_002946)+[416315-417049]\ Notes:Best Blastp Hit: pir\|\|A81871 probable periplasmic protein NMA1059 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379755\|emb\|CAB84323.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0543 | 0.0430 | 2.12 | up | hypothetical protein\ Context:(NC_002946)+[516352-517278]\ Notes:Best Blastp Hit: emb\|CAB84704.1\| (AL162756) hypothetical protein NMA1470 [Neisseria meningitidis] COG0523 Putative GTPases (G3E family) | Hypothetical Protein |
| NGO0563 | 0.0136 | 2.81 | up | hypothetical protein\ Context:(NC_002946)-[543910-544200]\ Notes:Best Blastp Hit: pir\|\|G81094 hypothetical protein NMB1343 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226587\|gb\|AAF41718.1\| (AE002482) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0616 | 0.0268 | 6.49 | up | hypothetical protein\ Context:(NC_002946)-[604489-604767]\ Notes:Best Blastp Hit: gb\|AAF41662.1\| (AE002477) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380144\|emb\|CAB84729.1\| (AL162756) hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0635 | 0.0198 | 2.96 | up | hypothetical protein\ Context:(NC_002946)-[623656-623946]\ Notes:Best Blastp Hit: pir\|\|I50969 MHC class II beta chain - Melanochromis auratus (fragment) >gi\|2147702\|pir\|\|I50985 MHC class II beta chain - Melanochromis auratus (fragment) >gi\|308982\|gb\|AAA49352.1\| (L17439) Mhc class II beta chain [Melanochromis auratus] >gi\|309016\|gb\|AAA49368.1\| (L17463) MHC class II beta chain [Melanochromis auratus] | Hypothetical Protein |
| NGO0661 | 0.0423 | 5.83 | up | hypothetical protein\ Context:(NC_002946)-[652253-653185]\ Notes:Best Blastp Hit: pir\|\|F81091 conserved hypothetical protein NMB1357 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226602\|gb\|AAF41731.1\| (AE002484) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0698 | 0.0500 | 8.03 | up | hypothetical protein\ Context:(NC_002946)+[693136-693369]\ Notes:Best Blastp Hit: pir\|\|G81152 probable DNA-binding protein NMA1039 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226065\|gb\|AAF41242.1\| (AE002436) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379741\|emb\|CAB84308.1\| (AL162754) putative DNA-binding protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0700 | 0.0201 | 7.98 | up | hypothetical protein\ Context:(NC_002946)+[694611-695171]\ Notes:Best Blastp Hit: pir\|\|G69096 hypothetical protein MTH1717 - Methanobacterium thermoautotrophicum (strain Delta H) >gi\|2622849\|gb\|AAB86189.1\| (AE000928) unknown [Methanobacterium thermoautotrophicum] | Hypothetical Protein |

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| NGO0742 | 0.0535 | 5.84 | up | hypothetical protein\ Context:(NC_002946)-[738883-739218]\ Notes:Best Blastp Hit: pir\|\|E81082 conserved hypothetical protein NMB1444 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226685\|gb\|AAF41804.1\| (AE002494) conserved hypothetical protein [Neisseria meningitidis MC58] COG0718 Uncharacterized BCR; YbaB family | Hypothetical Protein |
| NGO0757 | 0.0048 | 6.09 | up | hypothetical protein\ Context:(NC_002946)-[753640-754074]\ Notes:Best Blastp Hit: emb\|CAB84654.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0822 | 0.0306 | 2.37 | up | hypothetical protein\ Context:(NC_002946)+[813087-813488]\ Notes:Best Blastp Hit: pir\|\|A81119 conserved hypothetical protein NMB1138; NMB1176; NMA1348 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226375\|gb\|AAF41526.1\| (AE002462) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7226413\|gb\|AAF41561.1\| (AE002465) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380017\|emb\|CAB84595.1\| (AL162755) hypothetical protein NMA1348 [Neisseria meningitidis] COG1188 Predicted small RNA-binding protein (S4 | Hypothetical Protein |
| NGO0826 | 0.0115 | 3.40 | up | hypothetical protein\ Context:(NC_002946)-[814963-815721]\ Notes:Best Blastp Hit: emb\|CAB84591.1\| (AL162755) hypothetical protein NMA1343 [Neisseria meningitidis] | Hypothetical Protein |
| NGO0828 | 0.0250 | 13.35 | up | hypothetical protein\ Context:(NC_002946)-[816373-816519]\ Notes:Best Blastp Hit: gb\|AAF41523.1\| (AE002462) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226410\|gb\|AAF41558.1\| (AE002465) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0994 | 0.0241 | 4.07 | up | Laz\ Context:(NC_002946)-[964627-965178]\ Notes:Best Blastp Hit: sp\|P07212\|H8_NEIMC H.8 outer membrane protein precursor >gi\|279443\|pir\|\|AZNHM azurin precursor - Neisseria meningitidis >gi\|45042\|emb\|CAA68589.1\| (Y00530) outer membrane protein H.8 (AA 1-183) [Neisseria meningitidis]; lipid modified azurin protein | Hypothetical Protein |
| NGO1072 | 0.0451 | 2.16 | up | hypothetical protein\ Context:(NC_002946)+[1030403-1030687]\ Notes: | Hypothetical Protein |
| NGO1321 | 0.0225 | 16.27 | up | hypothetical protein\ Context:(NC_002946)+[1279547-1280065]\ Notes:Best Blastp Hit: pir\|\|H81820 probable lipoprotein NMA1930 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380562\|emb\|CAB85150.1\| (AL162757) putative lipoprotein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1411 | 0.0279 | 3.16 | up | hypothetical protein\ Context:(NC_002946)+[1374586-1376079]\ Notes:Best Blastp Hit: gb\|AAF40998.1\| (AE002413) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1471 | 0.0490 | 2.08 | up | hypothetical protein\ Context:(NC_002946)+[1434861-1435244]\ Notes:Best Blastp Hit: pir\|\|E81134 hypothetical protein NMB0979 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226219\|gb\|AAF41383.1\| (AE002449) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1538 | 0.0248 | 3.75 | up | hypothetical protein\ Context:(NC_002946)-[1510582-1510764]\ Notes:Best Blastp Hit: emb\|CAB85285.1\| (AL162758) putative periplasmic protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1709 | 0.0464 | 4.11 | up | hypothetical protein\ Context:(NC_002946)+[1665456-1666070]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) | Hypothetical Protein |
| NGO2111 | 0.0170 | 6.36 | up | hypothetical protein\ Context:(NC_002946)+[2095595-2097208]\ Notes:Best Blastp Hit: pir\|\|B81021 conserved hypothetical protein NMB1971 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227232\|gb\|AAF42300.1\| (AE002545) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0217 | 0.0077 | 3.41 | up | ABC transporter; periplasmic binding protein; iron related\ Context:(NC_002946)-[220733-221728]\ Notes:Best Blastp Hit: gb\|AAB63559.1\| (U33937) binds iron in a manner similar to transferrin; periplasmic iron-binding protein; Method: conceptual translation supplied by author [Neisseria gonorrhoeae] >gi\|1588872\|prf\|\|2209379A fbpA gene [Neisseria gonorrhoeae] COG1840 Thiamine-binding periplasmic proteins; FbpA | Iron Storage and Acquisition |

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|---|---|---|---|---|---|
| NGO0596 | 0.0373 | 2.28 | up | hypothetical protein\ Context:(NC_002946)-[582894-583988]\ Notes:Best Blastp Hit: pir\|\|B81098 conserved hypothetical protein NMB1308 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226549\|gb\|AAF41683.1\| (AE002479) conserved hypothetical protein [Neisseria meningitidis MC58] COG0820 Predicted Fe-S-cluster redox enzyme | Iron Storage and Acquisition |
| NGO0825 | 0.0151 | 4.20 | up | putative ferredoxin\ Context:(NC_002946)-[814566-814907]\ Notes:Best Blastp Hit: pir\|\|E81118 ferredoxin [2Fe-2S] NMB1134; NMB1172; NMA1344 [similarity] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226371\|gb\|AAF41522.1\| (AE002462) ferredoxin; 2Fe-2S type [Neisseria meningitidis MC58] >gi\|7226409\|gb\|AAF41557.1\| (AE002465) ferredoxin; 2Fe-2S type [Neisseria meningitidis MC58] >gi\|7380014\|emb\|CAB84592.1\| (AL162755) putative ferredoxin [Neisseria meningitidis] COG0633 Ferredoxin | Iron Storage and Acquisition |
| NGO0952 | 0.0393 | 3.14 | up | putative TonB-dependent receptor protein\ Context:(NC_002946)+[926135-928903]\ Notes:Best Blastp Hit: emb\|CAB84928.1\| (AL162756) putative outer membrane substrate binding protein [Neisseria meningitidis] COG1629 Outer membrane receptor proteins; mostly Fe | Iron Storage and Acquisition |
| NGO1377 | 0.0303 | 3.54 | up | hypothetical protein\ Context:(NC_002946)-[1342420-1342854]\ Notes:Best Blastp Hit: sp\|O06434\|EXBD_NEIGO biopolymer transport ExbD protein >gi\|2098623\|gb\|AAC45288.1\| (U79563) ExbD [Neisseria gonorrhoeae] COG0848 biopolymer transport protein ExbD | Iron Storage and Acquisition |
| NGO1378 | 0.0315 | 3.54 | up | ExbB\ Context:(NC_002946)-[1342857-1343567]\ Notes:Best Blastp Hit: sp\|O06433\|EXBB_NEIGO biopolymer transport ExbB protein >gi\|2098622\|gb\|AAC45287.1\| (U79563) ExbB [Neisseria gonorrhoeae] COG0811 biopolymer transport proteins | Iron Storage and Acquisition |
| NGO1495 | 0.0013 | 7.11 | up | TbpA\ Context:(NC_002946)-[1460228-1462966]\ Notes:Best Blastp Hit: gb\|AAF74987.1\| (AF124339) transferrin-binding protein A [Neisseria gonorrhoeae] COG1629 Outer membrane receptor proteins; mostly | Iron Storage and Acquisition |
| NGO1496 | 0.0005 | 10.24 | up | TbpB\ Context:(NC_002946)-[1463053-1465164]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON); transferrin-binding protein B | Iron Storage and Acquisition |
| NGO2092 | 0.0348 | 5.19 | up | ferric enterobactin periplasmic binding protein\ Context:(NC_002946)-[2068734-2069705]\ Notes:Best Blastp Hit: gb\|AAD29611.1\|AF115385_1 (AF115385) putative ferric enterobactin periplasmic binding protein [Neisseria gonorrhoeae] COG0614 Ferrichrome-binding periplasmic proteins | Iron Storage and Acquisition |
| NGO2093 | 0.0048 | 20.11 | up | FetA\ Context:(NC_002946)-[2069857-2071998]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) COG1629 Outer membrane receptor proteins; mostly Fe; ferric enterobactin receptor | Iron Storage and Acquisition |
| NGO1803 | 0.0395 | 3.30 | up | UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase\ Context:(NC_002946)+[1776598-1777641]\ Notes:adds the O-linked and N-linked 3(R)-hydroxy fatty acids to the glucosamine disaccharide during lipid A biosynthesis | Lipid/LPS Biosynthesis |
| NGO0475 | 0.0497 | 3.32 | up | putative phage associated protein\ Context:(NC_002946)-[462203-462403]\ Notes: | Phage Associated Protein |
| NGO1120 | 0.0517 | 2.02 | up | putative phage associated protein\ Context:(NC_002946)+[1072684-1072884]\ Notes: | Phage Associated Protein |
| NGO0344 | 0.0532 | 2.32 | up | GTP-binding protein LepA\ Context:(NC_002946)-[338704-340497]\ Notes:binds to the ribosome on the universally-conserved alpha-sarcin loop | Protein Synthesis |
| NGO0607 | 0.0320 | 7.38 | up | hypothetical protein\ Context:(NC_002946)-[593892-594584]\ Notes:Best Blastp Hit: gb\|AAF41674.1\| (AE002478) ribosomal small subunit pseudouridine synthase A [Neisseria meningitidis MC58] >gi\|7380155\|emb\|CAB84740.1\| (AL162756) putative ribosomal small subunit pseudouridine synthase [Neisseria meningitidis] COG1187 Predicted pseudouridylate synthase family 1 | Protein Synthesis |

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| NGO0660 | 0.0294 | 3.97 | up | aspartyl/glutamyl-tRNA amidotransferase subunit B\ Context:(NC_002946)-[650780-652210]\ Notes:allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases; reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA | Protein Synthesis |
| NGO2126 | 0.0092 | 11.59 | up | 50S ribosomal protein L31\ Context:(NC_002946)+[2108958-2109173]\ Notes:RpmE; there appears to be two types of ribosomal proteins L31 in bacterial genomes; some contain a CxxC motif while others do not; Bacillus subtilis has both types; the proteins in this cluster have the CXXC motif; RpmE is found in exponentially growing Bacilli while YtiA was found after exponential growth; expression of ytiA is controlled by a zinc-specific transcriptional repressor; RpmE contains one zinc ion and a CxxC motif is responsible for this binding; forms an RNP particle along with proteins L5; L18; and L25 and 5S rRNA; found crosslinked to L2 and L25 and EF-G; may be near the peptidyltransferase site of the 50S ribosome | Protein Synthesis |
| NGO2154 | 0.0455 | 3.10 | up | glycyl-tRNA synthetase subunit beta\ Context:(NC_002946)+[2129534-2131597]\ Notes:glycine--tRNA ligase beta chain; glyS; class II aminoacyl tRNA synthetase; tetramer of alpha(2)beta(2); catalyzes a two-step reaction; first charging a glycine molecule by linking the carboxyl group to the alpha-phosphate of ATP; second by transfer of the aminoacyl-adenylate to its tRNA | Protein Synthesis |
| NGO0048 | 0.0276 | 2.83 | up | carbamoyl phosphate synthase large subunit\ Context:(NC_002946)-[44215-47430]\ Notes:four CarB-CarA dimers form the carbamoyl phosphate synthetase holoenzyme that catalyzes the production of carbamoyl phosphate; CarB is responsible for the amidotransferase activity | Purine and Pyrimidine Metabolism |
| NGO0614 | 0.0479 | 2.17 | up | ribonucleotide-diphosphate reductase subunit alpha\ Context:(NC_002946)+[600312-602591]\ Notes:Catalyzes the rate-limiting step in dNTP synthesis | Purine and Pyrimidine Metabolism |
| NGO1308 | 0.0329 | 9.45 | up | putativeguanosine-3';5'-bis(diphosphate)3'-pyrophosphohydrolase\ Context:(NC_002946)-[1265171-1267327]\ Notes:Best Blastp Hit: pir\|\|B81058 guanosine-3';5'-bis(diphosphate) 3'-pyrophosphohydrolase NMB1659 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226911\|gb\|AAF42008.1\| (AE002516) guanosine-3`;5`-bis(diphosphate) 3`-pyrophosphohydrolase [Neisseria meningitidis MC58] COG0317 Guanosine polyphosphate | Purine and Pyrimidine Metabolism |
| NGO1540 | 0.0157 | 4.58 | up | Dca\ Context:(NC_002946)-[1512244-1513890]\ Notes:Best Blastp Hit: gb\|AAF12796.1\|AF195057_1 (AF195057) DcaA [Neisseria gonorrhoeae] COG2194 Predicted membrane-associated; division cell wall protein | Replication |
| NGO0650 | 0.0061 | 7.45 | up | putative ATP-dependent RNA helicase\ Context:(NC_002946)-[639282-640670]\ Notes:Best Blastp Hit: gb\|AAF41742.1\| (AE002485) ATP-dependent RNA helicase; putative [Neisseria meningitidis MC58] COG0513 Superfamily II DNA and RNA helicases | Transcription |
| NGO1850 | 0.0308 | 4.23 | up | DNA-directed RNA polymerase subunit beta'\ Context:(NC_002946)-[1815110-1819285]\ Notes:DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. Subunit beta' binds to sigma factor allowing it to bind to the -10 region of the promoter | Transcription |
| NGO1851 | 0.0205 | 3.15 | up | DNA-directed RNA polymerase subunit beta\ Context:(NC_002946)-[1819438-1823616]\ Notes:DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates; beta subunit is part of the catalytic core which binds with a sigma factor to produce the holoenzyme | Transcription |
| NGO0025 | 0.0443 | 3.77 | up | AraC family transcriptional regulator\ Context:(NC_002946)+[21326-22282]\ Notes:Best Blastp Hit: emb\|CAB83869.1\| (AL162753) putative araC-family transcriptional regulator [Neisseria meningitidis] COG2207 AraC-type DNA-binding domain-containing | Transcriptional Regulator |

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| NGO0608 | 0.0251 | 23.31 | up | putative murein transglycosylase / nitrite reductase transcriptional regulator\ Context:(NC_002946)-[594652-596628]\ Notes:Best Blastp Hit: pir\|\|D81842 probable membrane bound murein transglycosylase NMA1507 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380154\|emb\|CAB84739.1\| (AL162756) putative membrane bound murein transglycosylase [Neisseria meningitidis] COG0741 Soluble lytic murein transglycosylase and | Transcriptional Regulator |
| NGO0718 | 0.0539 | 5.54 | up | RpiR family transcriptional regulator\ Context:(NC_002946)+[718522-719370]\ Notes:Best Blastp Hit: pir\|\|D81089 RpiR/YebK/YfhH family protein NMB1389 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226627\|gb\|AAF41753.1\| (AE002487) RpiR/YebK/YfhH family protein [Neisseria meningitidis MC58] >gi\|7380248\|emb\|CAB84834.1\| (AL162756) putative transcriptional regulator [Neisseria meningitidis] COG1737 Transcriptional regulators; RpiR family | Transcriptional Regulator |
| NGO0094 | 0.0218 | 7.26 | up | hypothetical protein\ Context:(NC_002946)-[103398-105569]\ Notes:Best Blastp Hit: pir\|\|S70838 pilQ protein - Neisseria gonorrhoeae >gi\|1173875\|gb\|AAC43603.1\| (U40596) PilQ [Neisseria gonorrhoeae] >gi\|1589217\|prf\|\|2210365A pilQ gene [Neisseria gonorrhoeae] COG1450 General secretion pathway protein D | Transportation |
| NGO0189 | 0.0349 | 2.24 | up | preprotein translocase subunit SecD\ Context:(NC_002946)+[189979-191835]\ Notes:part of the preprotein secretory system; when complexed with proteins SecF and YajC; SecDFyajC stimulates the proton motive force-driven protein translocation; and appears to be required for the release of mature proteins from the extracytoplasmic side of the membrane | Transportation |
| NGO0374 | 0.0191 | 2.56 | up | putative ABC transporter; ATP-binding protein; amino acid\ Context:(NC_002946)+[367901-368656]\ Notes:Best Blastp Hit: pir\|\|F81947 probable amino acid permease ATP-binding protein NMA1000 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379702\|emb\|CAB84269.1\| (AL162754) putative amino acid permease ATP-binding protein [Neisseria meningitidis] COG1126 ABC-type polar amino acid transport system | Transportation |
| NGO1440 | 0.0356 | 2.29 | up | putative ABC transporter; periplasmic protein\ Context:(NC_002946)-[1405167-1406345]\ Notes:Best Blastp Hit: emb\|CAB84012.1\| (AL162754) putative periplasmic protein [Neisseria meningitidis] COG0845 Membrane permeases; predicted cation efflux | Transportation |
| NGO1485 | 0.0334 | 3.28 | up | hypothetical protein\ Context:(NC_002946)-[1447712-1449178]\ Notes:Best Blastp Hit: pir\|\|A81194 C4-dicarboxylate transporter NMB0470 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225698\|gb\|AAF40907.1\| (AE002404) C4-dicarboxylate transporter [Neisseria meningitidis MC58] COG0471 Cation transporters | Transportation |
| **Locus Tag** | **p value** | ***nrrF* mutant Fe-/Fe+ Fold Change** | **Regulation** | **Probe Comment** | **Biological Category** |
| NGO0082 | 0.0289 | -5.37 | down | valine--pyruvate transaminase\ Context:(NC_002946)-[87553-88845]\ Notes:transaminase C; catalyzes transamination of alanine; valine; and 2-aminobutyrate with their respective 2-keto acids; also catalyzes terminal step in valine biosynthesis | Amino Acid Biosynthesis and Metabolism |
| NGO0118 | 0.0236 | -3.33 | down | N-acetyl-gamma-glutamyl-phosphate reductase\ Context:(NC_002946)-[130990-132033]\ Notes:catalyzes the reduction of N-acetyl-5-glutamyl phosphate to N-acetyl-L-glutamate 5-semialdehyde in arginine biosynthesis and the reduction of N-acetyl-gamma-aminoadipyl-phosphate to N-acetyl-L-aminoadipate-semialdehyde in lysine biosynthesis; involved in both the arginine and lysine biosynthetic pathways; lysine is produced via the AAA pathway; lysine from alpha-aminoadipate | Amino Acid Biosynthesis and Metabolism |
| NGO0261 | 0.0001 | -36.92 | down | N-(5'-phosphoribosyl)anthranilate isomerase\ Context:(NC_002946)-[260589-261215]\ Notes:catalyzes the formation of 1-(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate from N-(5-phospho-beta-D-ribosyl)-anthranilate in tryptophan biosynthesis | Amino Acid Biosynthesis and Metabolism |

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| NGO0333 | 0.0381 | -3.38 | down | phosphoribosylaminoimidazole-succinocarboxamidesynthase\ Context:(NC_002946)+[328606-329565]\ Notes:catalyzes the formation of (S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido)succinate from 5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate and L-aspartate in purine biosynthesis; SAICAR synthase | Amino Acid Biosynthesis and Metabolism |
| NGO0844 | 0.0052 | -6.57 | down | acetylglutamate kinase\ Context:(NC_002946)-[827592-828488]\ Notes:catalyzes the phosphorylation of N-acetyl-L-glutamate to form N-acetyl-L-glutamate 5-phosphate | Amino Acid Biosynthesis and Metabolism |
| NGO0850 | 0.0015 | -21.58 | down | gamma-glutamyl phosphate reductase\ Context:(NC_002946)+[834819-836081]\ Notes:Catalyzes the phosphorylation of L-glutamate during the proline biosynthesis pathway | Amino Acid Biosynthesis and Metabolism |
| NGO1183 | 0.0123 | -5.76 | down | phosphoribosylformylglycinamidine synthase\ Context:(NC_002946)+[1124290-1128246]\ Notes:catalyzes the formation of 2-(formamido)-N1-(5-phospho-D-ribosyl)acetamidine from N2-formyl-N1-(5-phospho-D-ribosyl)glycinamide and L-glutamine in purine biosynthesis | Amino Acid Biosynthesis and Metabolism |
| NGO1204 | 0.0317 | -4.57 | down | anthranilate synthase component II\ Context:(NC_002946)-[1150419-1151009]\ Notes:TrpG; with TrpE catalyzes the formation of anthranilate and glutamate from chorismate and glutamine; TrpG provides the glutamine amidotransferase activity | Amino Acid Biosynthesis and Metabolism |
| NGO1232 | 0.0028 | -5.42 | down | ornithine carbamoyltransferase\ Context:(NC_002946)+[1183114-1184109]\ Notes:catalyzes the formation of ornithine and carbamylphosphate from citrulline in the arginine catabolic pathway | Amino Acid Biosynthesis and Metabolism |
| NGO1325 | 0.0281 | -3.91 | down | glycine dehydrogenase\ Context:(NC_002946)+[1281812-1284664]\ Notes:acts in conjunction with GvcH to form H-protein-S-aminomethyldihydrolipoyllysine from glycine | Amino Acid Biosynthesis and Metabolism |
| NGO1331 | 0.0063 | -4.23 | down | chorismate synthase\ Context:(NC_002946)+[1289738-1290838]\ Notes:catalyzes the formation of chorismate from 5-O-(1-carboxyvinyl)-3-phosphoshikimate in aromatic amino acid biosynthesis | Amino Acid Biosynthesis and Metabolism |
| NGO1406 | 0.0308 | -8.61 | down | glycine cleavage system aminomethyltransferase T\ Context:(NC_002946)-[1371197-1372297]\ Notes:catalyzes the transfer of a methylene carbon from the methylamine-loaded GcvH protein to tetrahydrofolate; causing the release of ammonia and the generation of reduced GcvH protein | Amino Acid Biosynthesis and Metabolism |
| NGO1423 | 0.0453 | -4.83 | down | hypothetical protein\ Context:(NC_002946)+[1385543-1386361]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG1045 Serine acetyltransferase | Amino Acid Biosynthesis and Metabolism |
| NGO1521 | 0.0016 | -14.09 | down | putative acetate kinase\ Context:(NC_002946)-[1487852-1489051]\ Notes:Best Blastp Hit: pir\|\|D81198 acetate kinase NMB0435 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225660\|gb\|AAF40873.1\| (AE002400) acetate kinase [Neisseria meningitidis MC58] COG0282 Acetate kinase | Amino Acid Biosynthesis and Metabolism |
| NGO1602 | 0.0032 | -4.82 | down | putative shikimate dehydrogenase\ Context:(NC_002946)+[1573802-1574611]\ Notes:Best Blastp Hit: gb\|AAC44913.1\| (U82842) shikimate dehydrogenase [Neisseria gonorrhoeae] COG0169 Shikimate 5-dehydrogenase | Amino Acid Biosynthesis and Metabolism |
| NGO1778 | 0.0010 | -5.69 | down | leucyl/phenylalanyl-tRNA--protein transferase\ Context:(NC_002946)-[1748121-1748846]\ Notes:leucyltransferase; phenylalanyltransferse; functions in the N-end rule pathway; transfers Leu; Phe; Met; from aminoacyl-tRNAs to N-terminal of proteins with Arg or Lys | Amino Acid Biosynthesis and Metabolism |
| NGO1808 | 0.0016 | -24.23 | down | D-amino acid dehydrogenase small subunit\ Context:(NC_002946)+[1781771-1783030]\ Notes:catalyzes the oxidative deamination of D-amino acids | Amino Acid Biosynthesis and Metabolism |
| NGO2041 | 0.0132 | -16.45 | down | thiamine biosynthesis protein ThiC\ Context:(NC_002946)+[2011464-2013365]\ Notes:required for the synthesis of the hydromethylpyrimidine moiety of thiamine | Amino Acid Biosynthesis and Metabolism |
| NGO0112 | 0.0053 | -12.40 | down | putative two-component system sensor kinase\ Context:(NC_002946)+[124550-125800]\ Notes:Best Blastp Hit: gb\|AAG24266.1\|AF139612_3 (AF139612) BasS [Neisseria gonorrhoeae] COG0642 Sensory transduction histidine kinases | Cell Communication and Outer Membrane Proteins |

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| NGO0140 | 0.0120 | -24.19 | down | hypothetical protein\ Context:(NC_002946)-[148156-148692]\ Notes:Best Blastp Hit: pir\|\|D81914 probable membrane protein NMA0712 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379436\|emb\|CAB83998.1\| (AL162754) putative membrane protein [Neisseria meningitidis] COG1238 Uncharacterized membrane protein | Cell Communication and Outer Membrane Proteins |
| NGO0237 | 0.0083 | -16.59 | down | N-acetyl-anhydromuranmyl-L-alanine amidase\ Context:(NC_002946)-[240686-241258]\ Notes:Best Blastp Hit: pir\|\|F81932 probable anhydro-N-acetylmuramyl-tripeptide amidase NMA0867 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379582\|emb\|CAB84147.1\| (AL162754) putative anhydro-N-acetylmuramyl-tripeptide amidase [Neisseria meningitidis] | Cell Communication and Outer Membrane Proteins |
| NGO0534 | 0.0036 | -13.40 | down | putative alginate O-acetylation - like protein\ Context:(NC_002946)-[507713-509149]\ Notes:Best Blastp Hit: pir\|\|C81103 alginate O-acetylation protein AlgI; probable NMB1273 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226512\|gb\|AAF41650.1\| (AE002475) alginate O-acetylation protein AlgI; putative [Neisseria meningitidis MC58] COG1696 Predicted membrane protein involved in | Cell Communication and Outer Membrane Proteins |
| NGO0798 | 0.0370 | -19.51 | down | putative uridylyltransferase\ Context:(NC_002946)+[786351-788909]\ Notes:Best Blastp Hit: pir\|\|B81110 protein-PII uridylyltransferase NMB1203 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226440\|gb\|AAF41585.1\| (AE002468) protein-PII uridylyltransferase [Neisseria meningitidis MC58] | Cell Communication and Outer Membrane Proteins |
| NGO0868 | 0.0174 | -10.27 | down | OpcA\ Context:(NC_002946)+[851492-852283]\ Notes:Best Blastp Hit: emb\|CAB45007.1\| (AJ242839) OpcA protein [Neisseria gonorrhoeae]; class 5 outer membrane protein | Cell Communication and Outer Membrane Proteins |
| NGO0869 | 0.0501 | -4.79 | down | hypothetical protein\ Context:(NC_002946)+[852434-853078]\ Notes:Best Blastp Hit: pir\|\|D81128 dedA protein NMB1052 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226292\|gb\|AAF41450.1\| (AE002455) dedA protein [Neisseria meningitidis MC58] >gi\|7379932\|emb\|CAB84505.1\| (AL162755) DedA protein ortholog [Neisseria meningitidis] COG0586 Uncharacterized membrane-associated protein | Cell Communication and Outer Membrane Proteins |
| NGO1042 | 0.0084 | -9.90 | down | hypothetical protein\ Context:(NC_002946)+[1003525-1003908]\ Notes:Best Blastp Hit: pir\|\|C81863 probable membrane protein NMA1680 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380321\|emb\|CAB84908.1\| (AL162756) putative membrane protein [Neisseria meningitidis] | Cell Communication and Outer Membrane Proteins |
| NGO1155 | 0.0228 | -7.72 | down | hypothetical protein\ Context:(NC_002946)-[1096079-1096537]\ Notes:Best Blastp Hit: pir\|\|G64866 probable membrane protein b1202 - Escherichia coli >gi\|1787452\|gb\|AAC74286.1\| (AE000218) putative adhesion and penetration protein [Escherichia coli] | Cell Communication and Outer Membrane Proteins |
| NGO1193 | 0.0295 | -6.85 | down | hypothetical protein\ Context:(NC_002946)+[1135218-1135910]\ Notes:Best Blastp Hit: pir\|\|B81017 conserved hypothetical protein NMB2004 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227268\|gb\|AAF42331.1\| (AE002550) conserved hypothetical protein [Neisseria meningitidis MC58] COG1346 Predicted membrane protein; YohK family | Cell Communication and Outer Membrane Proteins |
| NGO1398 | 0.0004 | -20.07 | down | hypothetical protein\ Context:(NC_002946)-[1360715-1361545]\ Notes:Best Blastp Hit: pir\|\|T44663 nosY protein [imported] - Bradyrhizobium japonicum >gi\|3850617\|emb\|CAA05522.1\| (AJ002531) nosY [Bradyrhizobium japonicum] COG1277 Predicted membrane protein | Cell Communication and Outer Membrane Proteins |
| NGO1500 | 0.0208 | -4.37 | down | glutamate racemase\ Context:(NC_002946)-[1468907-1469719]\ Notes:converts L-glutamate to D-glutamate; a component of peptidoglycan | Cell Communication and Outer Membrane Proteins |
| NGO1599 | 0.0090 | -8.00 | down | AmpG\ Context:(NC_002946)-[1570641-1571924]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) COG0477 Permeases; putative signal transducer protein | Cell Communication and Outer Membrane Proteins |

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| NGO1692 | 0.0073 | -4.89 | down | hypothetical protein\ Context:(NC_002946)+[1644722-1645159]\ Notes:Best Blastp Hit: pir\|\|F81790 conserved hypothetical inner membrane protein NMA2177 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380798\|emb\|CAB85389.1\| (AL162758) conserved hypothetical inner membrane protein [Neisseria meningitidis] COG1981 Predicted membrane protein | Cell Communication and Outer Membrane Proteins |
| NGO1718 | 0.0003 | -16.75 | down | hypothetical protein\ Context:(NC_002946)+[1678525-1680063]\ Notes:Best Blastp Hit: pir\|\|B81217 virulence factor MviN NMB0277 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225502\|gb\|AAF40731.1\| (AE002384) virulence factor MviN [Neisseria meningitidis MC58] COG0728 Uncharacterized membrane protein; putative | Cell Communication and Outer Membrane Proteins |
| NGO1768 | 0.0009 | -36.42 | down | hypothetical protein\ Context:(NC_002946)+[1732787-1733353]\ Notes:Best Blastp Hit: pir\|\|C81224 conserved hypothetical protein NMB0215 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225437\|gb\|AAF40671.1\| (AE002379) conserved hypothetical protein [Neisseria meningitidis MC58] COG1971 Predicted membrane protein | Cell Communication and Outer Membrane Proteins |
| NGO1910 | 0.0086 | -11.15 | down | hypothetical protein\ Context:(NC_002946)+[1883748-1885898]\ Notes:Best Blastp Hit: pir\|\|H81242 conserved hypothetical protein NMB0050 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225270\|gb\|AAF40519.1\| (AE002364) conserved hypothetical protein [Neisseria meningitidis MC58] COG1289 Uncharacterized membrane protein; YhfK | Cell Communication and Outer Membrane Proteins |
| NGO0032 | 0.0025 | -8.44 | down | hypothetical protein\ Context:(NC_002946)-[28180-28857]\ Notes:Best Blastp Hit: pir\|\|F81977 hypothetical protein NMA0585 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379321\|emb\|CAB83876.1\| (AL162753) hypothetical protein NMA0585 [Neisseria meningitidis] COG1214 Inactive homologs of metal-dependent | Cellular Processes |
| NGO0057 | 0.0008 | -13.27 | down | putative thioredoxin\ Context:(NC_002946)+[58575-59084]\ Notes:Best Blastp Hit: emb\|CAB83902.1\| (AL162753) putative periplasmic thioredoxin [Neisseria meningitidis] COG0526 Thiol-disulfide isomerase and thioredoxins | Cellular Processes |
| NGO0084 | 0.0127 | -5.14 | down | PglC\ Context:(NC_002946)-[90859-92034]\ Notes:Best Blastp Hit: pir\|\|H81983 pilin glycosylation protein NMA0638 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379371\|emb\|CAB83928.1\| (AL162753) pilin glycosylation protein [Neisseria meningitidis] COG0399 Predicted pyridoxal phosphate-dependent | Cellular Processes |
| NGO0104 | 0.0048 | -6.22 | down | O-sialoglycoprotein endopeptidase\ Context:(NC_002946)+[116169-117233]\ Notes:in most organisms; only the N-terminal domain is present in a single polypeptide; in some archaea this domain is fused to a kinase domain; this gene is essential for growth in Escherichia coli and Bacillus subtilis; the secreted glycoprotease from Pasteurella haemolytica showed specificity for O-sialoglycosylated proteins | Cellular Processes |
| NGO0139 | 0.0060 | -13.41 | down | putative endonuclease III\ Context:(NC_002946)-[147480-148109]\ Notes:Best Blastp Hit: pir\|\|D81187 endonuclease III NMB0533 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225758\|gb\|AAF40962.1\| (AE002409) endonuclease III [Neisseria meningitidis MC58] COG0177 Predicted EndoIII-related endonuclease | Cellular Processes |
| NGO0365 | 0.0130 | -62.89 | down | site-specific DNA-methyltransferase M.NgoVII\ Context:(NC_002946)-[357319-358443]\ Notes:Best Blastp Hit: pir\|\|T10165 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) NgoVII - Neisseria gonorrhoeae >gi\|1165245\|gb\|AAA86270.1\| (U43736) M.NgoVII [Neisseria gonorrhoeae] COG0270 Site-specific DNA methylase dcm | Cellular Processes |
| NGO0545 | 0.0177 | -4.95 | down | putative type III restriction-modification system methyltransferase\ Context:(NC_002946)+[518016-520079]\ Notes:Best Blastp Hit: possibly phase variable - 13 tandem repeats of CCAAC in the coding sequence (ON) COG2189 Adenine specific DNA methylase Mod | Cellular Processes |
| NGO0655 | 0.0002 | -57.57 | down | exodeoxyribonuclease VII large subunit\ Context:(NC_002946)+[644189-645544]\ Notes:bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides | Cellular Processes |

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| NGO0711 | 0.0089 | -19.44 | down | putative alcohol dehydrogenase\ Context:(NC_002946)+[710377-711393]\ Notes:Best Blastp Hit: pir\|\|C81088 alcohol dehydrogenase; zinc-containing NMB1395 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226634\|gb\|AAF41759.1\| (AE002488) alcohol dehydrogenase; zinc-containing [Neisseria meningitidis MC58] COG1065 Zn-dependent oxidoreductases | Cellular Processes |
| NGO0804 | 0.0063 | -9.61 | down | hypothetical protein\ Context:(NC_002946)-[795859-796749]\ Notes:Best Blastp Hit: pir\|\|C81906 hypothetical protein NMA1369 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380037\|emb\|CAB84615.1\| (AL162755) hypothetical protein NMA1369 [Neisseria meningitidis] COG0063 Predicted sugar kinase | Cellular Processes |
| NGO0886 | 0.0092 | -32.72 | down | putative acyl-CoA dehydrogenase\ Context:(NC_002946)-[865857-866939]\ Notes:Best Blastp Hit: emb\|CAB84463.1\| (AL162755) putative acyl-CoA dehydrogenase [Neisseria meningitidis] COG1960 Acyl-CoA dehydrogenases | Cellular Processes |
| NGO0893 | 0.0250 | -4.49 | down | putative oxidoreductase\ Context:(NC_002946)+[871108-874941]\ Notes:Best Blastp Hit: emb\|CAB84467.1\| (AL162755) putative oxidoreductase [Neisseria meningitidis] COG0247 Fe-S oxidoreductases | Cellular Processes |
| NGO0960 | 0.0005 | -35.26 | down | hypothetical protein\ Context:(NC_002946)+[932839-933615]\ Notes:Best Blastp Hit: gb\|AAF41857.1\| (AE002499) HesA/MoeB/ThiF family protein [Neisseria meningitidis MC58] COG1179 Dinucleotide-utilizing enzymes involved in | Cellular Processes |
| NGO1030 | 0.0100 | -3.25 | down | hypothetical protein\ Context:(NC_002946)-[994130-995053]\ Notes:Best Blastp Hit: gb\|AAF41818.1\| (AE002495) conserved hypothetical protein [Neisseria meningitidis MC58] COG0697 Predicted permeases | Cellular Processes |
| NGO1064 | 0.0296 | -3.13 | down | hypothetical protein\ Context:(NC_002946)+[1023468-1025549]\ Notes:Best Blastp Hit: pir\|\|C81078 carbon starvation protein A homolog NMB1493 [similarity] - Neisseria meningitidis (group B strain MD58) >gi\|7226734\|gb\|AAF41849.1\| (AE002498) carbon starvation protein A [Neisseria meningitidis MC58] COG1966 Carbon starvation protein CstA; predicted | Cellular Processes |
| NGO1246 | 0.0037 | -5.84 | down | putative periplasmic protease\ Context:(NC_002946)-[1197229-1198281]\ Notes:SohB; periplasmic protein; member of the peptidase S49 family | Cellular Processes |
| NGO1292 | 0.0326 | -7.80 | down | Dsb\ Context:(NC_002946)-[1247601-1248089]\ Notes:Best Blastp Hit: gb\|AAF41998.1\| (AE002515) disulfide bond formation protein B [Neisseria meningitidis MC58] COG1495 Disulfide bond formation protein DsbB; putative disulfide bond formation protein | Cellular Processes |
| NGO1403 | 0.0180 | -6.43 | down | glutamyl-tRNA reductase\ Context:(NC_002946)-[1368673-1369920]\ Notes:catalyzes the formation of glutamate-1-semialdehyde from glutamyl-tRNA(Glu) and NADPH; the second step of the pathway is catalyzed by glutamate-1-semialdehyde aminomutase which results in the formation of 5-aminolevulinic acid; functions in porphyrin (tetrapyrroles) biosynthesis; the crystal structure showed a C-terminal dimerization domain that appears to be absent in Chlamydial proteins | Cellular Processes |
| NGO1526 | 0.0093 | -18.43 | down | 2-methylisocitrate lyase\ Context:(NC_002946)-[1495930-1496808]\ Notes:catalyzes the formation of pyruvate and succinate from 2-methylisocitrate | Cellular Processes |
| NGO1583 | 0.0166 | -4.94 | down | anhydro-N-acetylmuramic acid kinase\ Context:(NC_002946)+[1558058-1559188]\ Notes:catalyzes hydrolysis of 1;6-anhydro bond of anyhydro-N-acetylmuramic acid (anhMurNAc) and phosphorylates anhMurNAc to produce N-acetyl-muramate-6-phosphate; involved in murein recycling | Cellular Processes |

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| NGO1603 | 0.0044 | -7.05 | down | monofunctional peptidoglycan transglycosylase\ Context:(NC_002946)+[1574614-1575315]\ Notes:Best Blastp Hit: sp\|Q51005\|MTGA_NEIGO monofunctional biosynthetic peptidoglycan transglycosylase (monofunctional TGASE) >gi\|1196663\|gb\|AAB37748.1\| (L47159) peptidoglycan transglycosylase [Neisseria gonorrhoeae] >gi\|1778807\|gb\|AAC44899.1\| (U82700) monofunctional peptidoglycan transglycosylase [Neisseria gonorrhoeae] COG0744 Membrane carboxypeptidase | Cellular Processes |
| NGO1682 | 0.0348 | -5.73 | down | efflux pump protein; fatty acid resistance\ Context:(NC_002946)-[1634104-1635627]\ Notes:Best Blastp Hit: gb\|AAD54074.1\| (AF132910) efflux pump protein FarB [Neisseria gonorrhoeae] COG0477 Permeases | Cellular Processes |
| NGO1726 | 0.0253 | -3.19 | down | hypothetical protein\ Context:(NC_002946)+[1687607-1688332]\ Notes:Best Blastp Hit: emb\|CAB85428.1\| (AL162758) hypothetical protein [Neisseria meningitidis] COG1040 Predicted amidophosphoribosyl transferases | Cellular Processes |
| NGO1758 | 0.0058 | -9.50 | down | GlnE\ Context:(NC_002946)-[1719259-1721949]\ Notes:Best Blastp Hit: pir\|\|E81994 probable [glutamate--ammonia-ligase] adenylyltransferase (EC 2.7.7.42) NMA0035 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378811\|emb\|CAB83353.1\| (AL162752) putative glutamate-ammonia-ligase adenylyltransferase [Neisseria meningitidis] COG1391 Glutamine synthetase adenylyltransferase | Cellular Processes |
| NGO1765 | 0.0502 | -2.87 | down | PglA\ Context:(NC_002946)+[1728025-1729155]\ Notes:Best Blastp Hit: possibly phase variable - 10G residue homopolymer repeat in the coding sequence (ON) COG0438 Glycosyltransferases I; putative glycosyltransferase | Cellular Processes |
| NGO1898 | 0.0337 | -3.86 | down | glucose-1-phosphate thymidylyltransferase\ Context:(NC_002946)+[1866297-1867163]\ Notes:Best Blastp Hit: sp\|P37762\|RFBA_NEIGO glucose-1-phosphate thymidylyltransferase (DTDP-glucose synthase) (DTDP-glucose pyrophosphorylase) >gi\|628591\|pir\|\|S47046 glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24) - Neisseria gonorrhoeae >gi\|520897\|emb\|CAA83653.1\| (Z32742) Glucose-1-phosphate thymidylyltransferase [Neisseria gonorrhoeae] >gi\|1333794\|emb\|CAA79719.1\| (Z21508) glucose-1-phosphate thymid transferase [Neisseria gonorrhoeae] COG1209 dTDP-glucose pyrophosphorylase | Cellular Processes |
| NGO2009 | 0.0212 | -9.65 | down | putative permease protein\ Context:(NC_002946)-[1979908-1981134]\ Notes:Best Blastp Hit: gb\|AAF42386.1\| (AE002556) conserved hypothetical protein [Neisseria meningitidis MC58] COG1457 Purine-cytosine permease and related | Cellular Processes |
| NGO2016 | 0.0239 | -5.42 | down | hypothetical protein\ Context:(NC_002946)+[1987346-1988734]\ Notes:Best Blastp Hit: pir\|\|D81010 conserved hypothetical protein NMB2064 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227326\|gb\|AAF42383.1\| (AE002556) conserved hypothetical protein [Neisseria meningitidis MC58] COG2056 Predicted permease | Cellular Processes |
| NGO2055 | 0.0163 | -14.50 | down | putative hydrolase\ Context:(NC_002946)-[2029787-2030515]\ Notes:Best Blastp Hit: emb\|CAB83593.1\| (AL162752) possible hydrolase [Neisseria meningitidis] COG1011 Predicted hydrolases of the HAD superfamily | Cellular Processes |
| NGO2059 | 0.0050 | -13.07 | down | trifunctional thioredoxin/methionine sulfoxide reductase A/B protein\ Context:(NC_002946)-[2033109-2034677]\ Notes:this is a fusion of 3 domains; an N-termianl thioredoxin domain; and 2 domains at the C-terminus that are methionine sulfoxide reductases; MsrA and MsrB; methionine is modified to form methionine sulfoxide during normal cellular processes and due to oxidat | Cellular Processes |
| NGO2125 | 0.0055 | -10.98 | down | putative acetyltransferase\ Context:(NC_002946)-[2108308-2108826]\ Notes:Best Blastp Hit: emb\|CAB83787.1\| (AL162753) putative acetyltransferase [Neisseria meningitidis] COG2171 Tetrahydrodipicolinate | Cellular Processes |

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| NGO0203 | 0.0223 | -2.74 | down | putative phosphatase\ Context:(NC_002946)-[206177-206887]\ Notes:Best Blastp Hit: gb\|AAF41046.1\| (AE002417) phosphoglycolate phosphatase [Neisseria meningitidis MC58] COG0546 Predicted phosphatases | Central Intermediary Metabolism |
| NGO1668 | 0.0165 | -18.01 | down | glucose-6-phosphate isomerase\ Context:(NC_002946)-[1622324-1623967]\ Notes:Best Blastp Hit: pir\|\|G81787 glucose-6-phosphate isomerase (EC 5.3.1.9) 2 NMA2154 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380775\|emb\|CAB85366.1\| (AL162758) glucose-6-phosphate isomerase 2 [Neisseria meningitidis] COG0166 Glucose-6-phosphate isomerase | Central Intermediary Metabolism |
| NGO1776 | 0.0035 | -30.48 | down | glyceraldehyde-3-phosphate dehydrogenase\ Context:(NC_002946)+[1746835-1747866]\ Notes:catalyzes the formation of 3-phospho-D-glyceroyl phosphate from D-glyceraldehyde 3-phosphate | Central Intermediary Metabolism |
| NGO2043 | 0.0200 | -2.71 | down | putative dehydrogenase related protein\ Context:(NC_002946)+[2017051-2017365]\ Notes:Best Blastp Hit: pir\|\|F82022 probable glycerate dehydrogenase (EC 1.1.1.29) NMA0274 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379036\|emb\|CAB83582.1\| (AL162752) putative glycerate dehydrogenase [Neisseria meningitidis] COG1052 Lactate dehydrogenase and related | Central Intermediary Metabolism |
| NGO0308 | 0.0025 | -20.60 | down | putative adenosylmethionine-8-amino-7-oxononanoate aminotranferase\ Context:(NC_002946)+[307549-308850]\ Notes:Best Blastp Hit: pir\|\|D81164 adenosylmethionine-8-amino-7-oxononanoate aminotransferase NMB0732 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225960\|gb\|AAF41145.1\| (AE002428) adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Neisseria meningitidis MC58] COG0161 Adenosylmethionine-8-amino-7-oxononanoate | Co-Factor Metabolism |
| NGO0309 | 0.0039 | -11.97 | down | dithiobiotin synthetase\ Context:(NC_002946)+[308847-309494]\ Notes:DTB synthetase; dethiobiotin synthase; involved in production of dethiobiotin from ATP and 7;8-diaminononanoate and carbon dioxide; contains magnesium | Co-Factor Metabolism |
| NGO0323 | 0.0125 | -6.67 | down | 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine-pyrophosphokinase\ Context:(NC_002946)-[321872-322366]\ Notes:Best Blastp Hit: H]COG08017; 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase | Co-Factor Metabolism |
| NGO0658 | 0.0023 | -6.44 | down | pyridoxamine 5'-phosphate oxidase\ Context:(NC_002946)+[648916-649548]\ Notes:catalyzes the formation of pyridoxal 5'-phosphate from pyridoxamine 5'-phosphate | Co-Factor Metabolism |
| NGO0754 | 0.0154 | -6.32 | down | putative molybdopterin-guanine dinucleotide biosynthesis protein\ Context:(NC_002946)+[751362-751976]\ Notes:Best Blastp Hit: emb\|CAB84657.1\| (AL162755) putative molybdopterin-guanine dinucleotide biosynthesis protein A [Neisseria meningitidis] COG0746 Molybdopterin-guanine dinucleotide | Co-Factor Metabolism |
| NGO1725 | 0.0187 | -3.66 | down | putative bioH - biotin biosynthesis protein\ Context:(NC_002946)-[1686859-1687635]\ Notes:Best Blastp Hit: emb\|CAB85427.1\| (AL162758) putative hydrolase [Neisseria meningitidis] COG0570 BioH; catalyzes some early step in biotin | Co-Factor Metabolism |
| NGO0318 | 0.0194 | -2.59 | down | hypothetical protein\ Context:(NC_002946)+[315740-317413]\ Notes:Best Blastp Hit: pir\|\|D81165 DNA repair protein RecN NMB0740 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225968\|gb\|AAF41153.1\| (AE002428) DNA repair protein RecN [Neisseria meningitidis MC58] COG0497 ATPases involved in DNA repair | DNA Repair |
| NGO0681 | 0.0333 | -9.55 | down | DNA repair protein RadC\ Context:(NC_002946)+[670461-671138]\ Notes:Involved in DNA double-strand break repair and recombination. Promotes the annealing of complementary single-stranded DNA and by simulation of RAD51 recombinase | DNA Repair |

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| NGO0738 | 0.0358 | -5.08 | down | putative DNA-damage-inducibile protein\ Context:(NC_002946)+[733057-734115]\ Notes:Best Blastp Hit: emb\|CAB72023.1\| (AJ391259) putative DNA-damage inducible protein P [Neisseria meningitidis] >gi\|7380303\|emb\|CAB84889.1\| (AL162756) impB/mucB/samB family protein [Neisseria meningitidis] COG0389 Nucleotidyltransferase/DNA polymerase | DNA Repair |
| NGO0786 | 0.0201 | -3.84 | down | uracil-DNA glycosylase\ Context:(NC_002946)-[778867-779526]\ Notes:Excises uracil residues from the DNA which can arise as a result of misincorporation of dUMP residues by DNA polymerase or due to deamination of cytosine | DNA Repair |
| NGO1173 | 0.0436 | -11.28 | down | putative DNA mismatch endonuclease; patch repair protein\ Context:(NC_002946)-[1110897-1111319]\ Notes:Best Blastp Hit: pir\|\|H81959 patch repair protein (EC 3.1.-.-) NMA0429 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379179\|emb\|CAB83728.1\| (AL162753) patch repair protein [Neisseria meningitidis] | DNA Repair |
| NGO0485 | 0.0490 | -7.16 | down | putative replicative DNA helicase; putative phage associated protein\ Context:(NC_002946)+[467039-468400]\ Notes:Best Blastp Hit: sp\|P37469\|DNAC_BACSU replicative DNA helicase >gi\|2127189\|pir\|\|S65970 replicative DNA helicase dnaC - Bacillus subtilis >gi\|467330\|dbj\|BAA05176.1\| (D26185) replicative DNA helicase [Bacillus subtilis] >gi\|2636591\|emb\|CAB16081.1\| (Z99124) replicative DNA helicase [Bacillus subtilis] COG0305 Replicative DNA helicase | DNA Replication |
| NGO0696 | 0.0138 | -3.34 | down | recombination factor protein RarA\ Context:(NC_002946)+[688651-689961]\ Notes:Best Blastp Hit: pir\|\|E81103 conserved hypothetical protein NMB1258 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226497\|gb\|AAF41636.1\| (AE002474) conserved hypothetical protein [Neisseria meningitidis MC58] COG2256 Uncharacterized ATPase related to the | DNA Replication |
| NGO1259 | 0.0009 | -7.52 | down | DNA topoisomerase IV subunit A\ Context:(NC_002946)+[1210524-1212827]\ Notes:decatenates newly replicated chromosomal DNA and relaxes positive and negative DNA supercoiling | DNA Replication |
| NGO1437 | 0.0006 | -33.03 | down | primosome assembly protein PriA\ Context:(NC_002946)-[1399954-1402143]\ Notes:binding of PriA to forked DNA starts the assembly of the primosome; also possesses 3'-5' helicase activity | DNA Replication |
| NGO2034 | 0.0202 | -8.96 | down | DNA ligase\ Context:(NC_002946)+[2004672-2005496]\ Notes:catalyzes the formation of a phosphodiester at the site of a single-strand break in duplex DNA | DNA Replication |
| NGO0059 | 0.0006 | -6.19 | down | putative flavoprotein oxidoreductase\ Context:(NC_002946)+[59981-60481]\ Notes:Best Blastp Hit: pir\|\|B81981 probable 4-hydroxyphenylacetate 3-monooxygenase (EC 1.14.13.3) small chain NMA0614 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7379349\|emb\|CAB83904.1\| (AL162753) putative NADH:FMN oxidoreductase [Neisseria meningitidis] COG1853 Conserved protein/domain typically | Energy Metabolism |
| NGO0102 | 0.0081 | -3.11 | down | putative cytochrome biogenesis protein\ Context:(NC_002946)+[112858-114873]\ Notes:Best Blastp Hit: pir\|\|E81040 cytochrome c-type biogenesis protein; probable NMB1804 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227058\|gb\|AAF42141.1\| (AE002530) cytochrome c-type biogenesis protein; putative [Neisseria meningitidis MC58] COG1333 ResB protein required for cytochrome c | Energy Metabolism |
| NGO0103 | 0.0345 | -7.32 | down | putative cytochrome synthesis protein\ Context:(NC_002946)+[114866-116053]\ Notes:Best Blastp Hit: emb\|CAB83947.1\| (AL162753) putative membrane protein [Neisseria meningitidis] COG0755 Cytochrome c biogenesis factors; CcmC | Energy Metabolism |
| NGO0600 | 0.0001 | -31.89 | down | putative esterase D\ Context:(NC_002946)-[586297-587043]\ Notes:Best Blastp Hit: pir\|\|G81097 esterase; probable NMB1305 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226546\|gb\|AAF41680.1\| (AE002479) esterase; putative [Neisseria meningitidis MC58] COG0627 Predicted esterase | Energy Metabolism |
| NGO1080 | 0.0489 | -4.92 | down | putative C-type cytochrome\ Context:(NC_002946)+[1038226-1038684]\ Notes:Best Blastp Hit: emb\|CAB84381.1\| (AL162755) putative C-type cytochrome [Neisseria meningitidis] | Energy Metabolism |

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|---|---|---|---|---|---|
| NGO1184 | 0.0088 | -8.04 | down | hypothetical protein\ Context:(NC_002946)-[1128345-1129463]\ Notes:Best Blastp Hit: pir\|\|G75287 NADH oxidase-related protein - Deinococcus radiodurans (strain R1) >gi\|6460144\|gb\|AAF11879.1\|AE002064_10 (AE002064) NADH oxidase-related protein [Deinococcus radiodurans] COG1902 NADH:flavin oxidoreductases; Old Yellow | Energy Metabolism |
| NGO1328 | 0.0263 | -4.26 | down | putative cytochrome\ Context:(NC_002946)-[1286026-1286865]\ Notes:Best Blastp Hit: gb\|AAF42025.1\| (AE002518) cytochrome c5 [Neisseria meningitidis MC58] | Energy Metabolism |
| NGO1737 | 0.0080 | -6.02 | down | NADH dehydrogenase subunit N\ Context:(NC_002946)-[1695421-1696866]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone | Energy Metabolism |
| NGO1738 | 0.0136 | -4.87 | down | NADH dehydrogenase subunit M\ Context:(NC_002946)-[1696876-1698372]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone | Energy Metabolism |
| NGO1741 | 0.0010 | -17.77 | down | NADH dehydrogenase subunit K\ Context:(NC_002946)-[1701860-1702165]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone | Energy Metabolism |
| NGO1742 | 0.0005 | -54.37 | down | hypothetical protein\ Context:(NC_002946)-[1702162-1702833]\ Notes:Best Blastp Hit: gb\|AAF40707.1\| (AE002382) NADH dehydrogenase I; J subunit [Neisseria meningitidis MC58] | Energy Metabolism |
| NGO1744 | 0.0352 | -12.94 | down | hypothetical protein\ Context:(NC_002946)-[1703405-1704481]\ Notes:Best Blastp Hit: pir\|\|E81219 NADH dehydrogenase I; H chain NMB0250 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225473\|gb\|AAF40704.1\| (AE002382) NADH dehydrogenase I; H subunit [Neisseria meningitidis MC58] COG1005 NADH-ubiquinone oxidoreductase subunit 1 | Energy Metabolism |
| NGO1745 | 0.0006 | -5.87 | down | NADH dehydrogenase subunit G\ Context:(NC_002946)-[1704484-1706745]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone | Energy Metabolism |
| NGO1746 | 0.0480 | -3.77 | down | hypothetical protein\ Context:(NC_002946)-[1707458-1708759]\ Notes:Best Blastp Hit: pir\|\|D81222 NADH dehydrogenase I; F chain NMB0246 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225468\|gb\|AAF40700.1\| (AE002381) NADH dehydrogenase I; F subunit [Neisseria meningitidis MC58] COG1894 NADH-ubiquinone oxidoreductase; NADH-binding | Energy Metabolism |
| NGO1747 | 0.0018 | -27.64 | down | NADH dehydrogenase subunit E\ Context:(NC_002946)-[1709149-1709622]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone | Energy Metabolism |
| NGO1748 | 0.0006 | -18.61 | down | NADH dehydrogenase subunit D\ Context:(NC_002946)-[1709622-1710878]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone | Energy Metabolism |
| NGO1749 | 0.0007 | -39.62 | down | NADH dehydrogenase subunit C\ Context:(NC_002946)-[1710868-1711461]\ Notes:Catalyzes the transfer of electrons from NADH to ubiquinone | Energy Metabolism |
| NGO1750 | 0.0000 | -393.27 | down | NADH dehydrogenase subunit B\ Context:(NC_002946)-[1711474-1711956]\ Notes:The point of entry for the majority of electrons that traverse the respiratory chain eventually resulting in the reduction of oxygen | Energy Metabolism |
| NGO1751 | 0.0000 | -53.97 | down | hypothetical protein\ Context:(NC_002946)-[1711947-1712303]\ Notes:Best Blastp Hit: pir\|\|G81992 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain A NMA0019 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378797\|emb\|CAB83339.1\| (AL162752) NADH dehydrogenase I chain A [Neisseria meningitidis] COG0838 NADH-ubiquinone oxidoreductase subunit 3 | Energy Metabolism |
| NGO1769 | 0.0160 | -22.14 | down | CcpR\ Context:(NC_002946)+[1733575-1734738]\ Notes:Best Blastp Hit: pir\|\|B70313 cytochrome-c peroxidase (EC 1.11.1.5) - Aquifex aeolicus >gi\|2982865\|gb\|AAC06485.1\| (AE000675) cytochrome c peroxidase [Aquifex aeolicus] COG1858 Cytochrome c peroxidase; putative cytochrome-c peroxidase | Energy Metabolism |

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| NGO2079 | 0.0014 | -13.70 | down | putative carbonic anhydrase\ Context:(NC_002946)+[2058947-2059546]\ Notes:Best Blastp Hit: pir\|\|D81015 conserved hypothetical protein NMB2025 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7227287\|gb\|AAF42348.1\| (AE002552) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379165\|emb\|CAB83714.1\| (AL162753) hypothetical protein NMA0415 [Neisseria meningitidis] COG0288 Carbonic anhydrase | Energy Metabolism |
| NGO0009 | 0.0476 | -4.50 | down | hypothetical protein\ Context:(NC_002946)+[11091-11546]\ Notes:Best Blastp Hit: sp\|P54298\|LUXM_VIBHA LUXM protein >gi\|487037\|pir\|\|S37349 luxM protein - Vibrio harveyi >gi\|295433\|gb\|AAC36807.1\| (L13940) Lux M [Vibrio harveyi] | Hypothetical Protein |
| NGO0010 | 0.0273 | -3.09 | down | hypothetical protein\ Context:(NC_002946)-[12107-12307]\ Notes:Best Blastp Hit: gb\|AAF42226.1\| (AE002539) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0033 | 0.0201 | -15.38 | down | hypothetical protein\ Context:(NC_002946)-[28996-29853]\ Notes:Best Blastp Hit: pir\|\|D81032 hypothetical protein NMB1870 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227128\|gb\|AAF42204.1\| (AE002537) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0076 | 0.0240 | -14.83 | down | hypothetical protein\ Context:(NC_002946)+[80406-80726]\ Notes:Best Blastp Hit: gb\|AAF42163.1\| (AE002532) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0109 | 0.0427 | -9.37 | down | hypothetical protein\ Context:(NC_002946)+[121880-122068]\ Notes: | Hypothetical Protein |
| NGO0115 | 0.0532 | -12.69 | down | hypothetical protein\ Context:(NC_002946)-[127801-128310]\ Notes:Best Blastp Hit: sp\|P15041\|YZSB_ECOLI very hypothetical 17.7 kD protein in SecB region>gi\|76221\|pir\|\|QQEC17 hypothetical 17.7K protein (secB region) - Escherichia coli >gi\|1128972\|gb\|AAA83908.1\| (M24489) ORF; putative [Escherichia coli] | Hypothetical Protein |
| NGO0120 | 0.0115 | -20.23 | down | hypothetical protein\ Context:(NC_002946)+[132347-132475]\ Notes: | Hypothetical Protein |
| NGO0121 | 0.0003 | -50.71 | down | hypothetical protein\ Context:(NC_002946)+[132575-133729]\ Notes:Best Blastp Hit: gb\|AAF42125.1\| (AE002528) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0141 | 0.0007 | -80.65 | down | hypothetical protein\ Context:(NC_002946)+[148719-148865]\ Notes: | Hypothetical Protein |
| NGO0166 | 0.0031 | -23.40 | down | hypothetical protein\ Context:(NC_002946)-[170109-170975]\ Notes:Best Blastp Hit: pir\|\|A81874 probable periplasmic protein NMA1084 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379779\|emb\|CAB84347.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0204 | 0.0307 | -16.97 | down | hypothetical protein\ Context:(NC_002946)-[206877-207704]\ Notes:Best Blastp Hit: pir\|\|B81178 conserved hypothetical protein NMB0621 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225851\|gb\|AAF41047.1\| (AE002417) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0247 | 0.0055 | -3.36 | down | hypothetical protein\ Context:(NC_002946)+[248228-248392]\ Notes:Best Blastp Hit: emb\|CAB84157.1\| (AL162754) hypothetical protein NMA0877 [Neisseria meningitidis] | Hypothetical Protein |
| NGO0285 | 0.0061 | -6.53 | down | hypothetical protein\ Context:(NC_002946)+[286106-286672]\ Notes:Best Blastp Hit: gb\|AAF62318.1\| (AE002425) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0324 | 0.0050 | -6.08 | down | hypothetical protein\ Context:(NC_002946)-[322376-322750]\ Notes:Best Blastp Hit: pir\|\|A81163 conserved hypothetical protein NMB0746 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225975\|gb\|AAF41159.1\| (AE002429) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0336 | 0.0252 | -2.92 | down | hypothetical protein\ Context:(NC_002946)-[331995-332663]\ Notes:Best Blastp Hit: pir\|\|D81161 conserved hypothetical protein NMB0759 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225989\|gb\|AAF41172.1\| (AE002430) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0339 | 0.0341 | -2.48 | down | hypothetical protein\ Context:(NC_002946)+[333959-334564]\ Notes:Best Blastp Hit: possibly phase variable - 8T residue homopolymer repeat in the coding sequence (ON) | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO0428 | 0.0002 | -16.80 | down | hypothetical protein\ Context:(NC_002946)-[423520-423744]\ Notes:Best Blastp Hit: emb\|CAB84342.1\| (AL162755) hypothetical protein NMA1079 [Neisseria meningitidis] | Hypothetical Protein |
| NGO0429 | 0.0209 | -25.47 | down | hypothetical protein\ Context:(NC_002946)-[423973-424110]\ Notes:Best Blastp Hit: emb\|CAB84343.1\| (AL162755) hypothetical protein NMA1080 [Neisseria meningitidis] | Hypothetical Protein |
| NGO0432 | 0.0310 | -5.30 | down | hypothetical protein\ Context:(NC_002946)-[426078-426620]\ Notes:Best Blastp Hit: pir\|\|A81874 probable periplasmic protein NMA1084 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379779\|emb\|CAB84347.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0511 | 0.0117 | -10.90 | down | hypothetical protein\ Context:(NC_002946)+[489283-489588]\ Notes: | Hypothetical Protein |
| NGO0533 | 0.0478 | -7.21 | down | hypothetical protein\ Context:(NC_002946)-[506719-507702]\ Notes:Best Blastp Hit: pir\|\|A81839 probable periplasmic protein NMA1479 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380127\|emb\|CAB84712.1\| (AL162756) putative periplasmic protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0613 | 0.0020 | -8.69 | down | hypothetical protein\ Context:(NC_002946)-[599470-599781]\ Notes:Best Blastp Hit: pir\|\|H81098 hypothetical protein NMB1293 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226534\|gb\|AAF41669.1\| (AE002478) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0631 | 0.0064 | -37.39 | down | hypothetical protein\ Context:(NC_002946)+[621689-621838]\ Notes: | Hypothetical Protein |
| NGO0638 | 0.0138 | -27.09 | down | hypothetical protein\ Context:(NC_002946)+[625640-625870]\ Notes: | Hypothetical Protein |
| NGO0647 | 0.0003 | -18.55 | down | hypothetical protein\ Context:(NC_002946)+[637578-638078]\ Notes:Best Blastp Hit: pir\|\|G81090 hypothetical protein NMB1370 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226616\|gb\|AAF41744.1\| (AE002485) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0653 | 0.0060 | -12.21 | down | hypothetical protein\ Context:(NC_002946)+[642627-643100]\ Notes:Best Blastp Hit: pir\|\|D81850 hypothetical protein NMA1577 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380218\|emb\|CAB84804.1\| (AL162756) hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0667 | 0.0044 | -24.83 | down | hypothetical protein\ Context:(NC_002946)-[657753-657938]\ Notes: | Hypothetical Protein |
| NGO0672 | 0.0434 | -15.69 | down | hypothetical protein\ Context:(NC_002946)+[662118-662309]\ Notes: | Hypothetical Protein |
| NGO0709 | 0.0119 | -35.36 | down | hypothetical protein\ Context:(NC_002946)+[708430-708798]\ Notes: | Hypothetical Protein |
| NGO0751 | 0.0328 | -4.22 | down | hypothetical protein\ Context:(NC_002946)+[747669-748577]\ Notes:Best Blastp Hit: emb\|CAC03614.1\| (AJ272538) hypothetical protein [Kluyvera ascorbata] | Hypothetical Protein |
| NGO0761 | 0.0265 | -5.45 | down | hypothetical protein\ Context:(NC_002946)-[756266-756574]\ Notes:Best Blastp Hit: pir\|\|G81105 hypothetical protein NMB1242 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226482\|gb\|AAF41623.1\| (AE002472) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0762 | 0.0445 | -3.11 | down | hypothetical protein\ Context:(NC_002946)+[756606-756746]\ Notes: | Hypothetical Protein |
| NGO0789 | 0.0016 | -21.71 | down | hypothetical protein\ Context:(NC_002946)-[781083-782153]\ Notes:Best Blastp Hit: gb\|AAF41601.1\| (AE002470) transporter; putative [Neisseria meningitidis MC58] COG0628 Predicted permease | Hypothetical Protein |
| NGO0796 | 0.0303 | -12.26 | down | hypothetical protein\ Context:(NC_002946)-[785742-786314]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO0805 | 0.0008 | -20.93 | down | hypothetical protein\ Context:(NC_002946)+[796889-797470]\ Notes:Best Blastp Hit: pir\|\|F81111 nickel-dependent hydrogenase; b-type cytochrome chain NMB1196; NMB1158 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226395\|gb\|AAF41544.1\| (AE002464) nickel-dependent hydrogenase; b-type cytochrome subunit [Neisseria meningitidis MC58] >gi\|7226433\|gb\|AAF41579.1\| (AE002467) nickel-dependent hydrogenase; b-type cytochrome subunit [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0812 | 0.0038 | -5.36 | down | hypothetical protein\ Context:(NC_002946)+[805132-805749]\ Notes:Best Blastp Hit: pir\|\|B81117 hypothetical protein NMB1147; NMB1185 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226384\|gb\|AAF41534.1\| (AE002463) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226422\|gb\|AAF41569.1\| (AE002466) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0843 | 0.0001 | -165.28 | down | hypothetical protein\ Context:(NC_002946)-[827290-827577]\ Notes: | Hypothetical Protein |
| NGO0852 | 0.0063 | -5.27 | down | hypothetical protein\ Context:(NC_002946)+[839467-840147]\ Notes:Best Blastp Hit: pir\|\|G81894 probable integral membrane protein NMA1265 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379945\|emb\|CAB84520.1\| (AL162755) putative integral membrane protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO0858 | 0.0073 | -8.15 | down | hypothetical protein\ Context:(NC_002946)+[842123-842725]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0344 Predicted membrane protein; YgiH/UPF0078 | Hypothetical Protein |
| NGO0859 | 0.0020 | -26.41 | down | hypothetical protein\ Context:(NC_002946)+[842817-843662]\ Notes:Best Blastp Hit: pir\|\|G81126 conserved hypothetical protein NMB1061 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226300\|gb\|AAF41457.1\| (AE002456) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0860 | 0.0241 | -10.96 | down | hypothetical protein\ Context:(NC_002946)+[843668-844126]\ Notes: | Hypothetical Protein |
| NGO0871 | 0.0018 | -12.05 | down | hypothetical protein\ Context:(NC_002946)+[855029-855358]\ Notes:Best Blastp Hit: emb\|CAB45013.1\| (AJ242839) hypothetical protein [Neisseria gonorrhoeae] | Hypothetical Protein |
| NGO0879 | 0.0274 | -3.39 | down | hypothetical protein\ Context:(NC_002946)-[861993-862184]\ Notes: | Hypothetical Protein |
| NGO0880 | 0.0028 | -5.24 | down | hypothetical protein\ Context:(NC_002946)+[862282-862887]\ Notes:Best Blastp Hit: pir\|\|B81892 hypothetical protein NMA1237 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379924\|emb\|CAB84495.1\| (AL162755) hypothetical protein NMA1237 [Neisseria meningitidis] | Hypothetical Protein |
| NGO0888 | 0.0029 | -5.62 | down | hypothetical protein\ Context:(NC_002946)-[867765-868025]\ Notes:Best Blastp Hit: gb\|AAF41399.1\| (AE002450) hypothetical protein [Neisseria meningitidis MC58] >gi\|7379895\|emb\|CAB84465.1\| (AL162755) hypothetical protein NMA1204 [Neisseria meningitidis] | Hypothetical Protein |
| NGO0892 | 0.0002 | -53.52 | down | hypothetical protein\ Context:(NC_002946)+[870645-870926]\ Notes: | Hypothetical Protein |
| NGO0894 | 0.0426 | -11.95 | down | hypothetical protein\ Context:(NC_002946)+[875018-876019]\ Notes:Best Blastp Hit: pir\|\|H81888 hypothetical protein NMA1207 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379898\|emb\|CAB84468.1\| (AL162755) hypothetical protein NMA1207 [Neisseria meningitidis] COG0042 Predicted TIM-barrel enzymes; possibly | Hypothetical Protein |
| NGO0905 | 0.0477 | -2.49 | down | hypothetical protein\ Context:(NC_002946)+[885235-885936]\ Notes:Best Blastp Hit: emb\|CAB84877.1\| (AL162756) conserved hypothetical protein [Neisseria meningitidis] COG1556 Uncharacterized ACR; YkgG family | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO0906 | 0.0460 | -2.05 | down | hypothetical protein\ Context:(NC_002946)+[885933-887387]\ Notes:Best Blastp Hit: pir\|\|F81859 conserved hypothetical iron-sulfur protein NMA1650 [similarity] - Neisseria meningitidis (group A strain Z2491) >gi\|7380292\|emb\|CAB84878.1\| (AL162756) conserved hypothetical iron-sulphur protein [Neisseria meningitidis] COG1139 Uncharacterized conserved protein containing | Hypothetical Protein |
| NGO0924 | 0.0330 | -15.17 | down | hypothetical protein\ Context:(NC_002946)-[904199-904408]\ Notes: | Hypothetical Protein |
| NGO0942 | 0.0154 | -14.22 | down | hypothetical protein\ Context:(NC_002946)+[918324-918812]\ Notes:Best Blastp Hit: gb\|AAF41339.1\| (AE002444) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO0953 | 0.0185 | -6.88 | down | hypothetical protein\ Context:(NC_002946)+[928934-929149]\ Notes: | Hypothetical Protein |
| NGO0969 | 0.0396 | -4.34 | down | hypothetical protein\ Context:(NC_002946)-[941107-941808]\ Notes:Best Blastp Hit: gb\|AAF41866.1\| (AE002500) thermonuclease family protein [Neisseria meningitidis MC58] >gi\|7380351\|emb\|CAB84938.1\| (AL162756) putative nuclease [Neisseria meningitidis] COG1525 Micrococcal nuclease (thermonuclease) | Hypothetical Protein |
| NGO0992 | 0.0449 | -2.69 | down | hypothetical protein\ Context:(NC_002946)-[963369-963989]\ Notes:Best Blastp Hit: pir\|\|G81071 conserved hypothetical protein NMB1531 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226776\|gb\|AAF41886.1\| (AE002503) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380373\|emb\|CAB84959.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1033 | 0.0276 | -4.18 | down | putative transglycosylase\ Context:(NC_002946)-[997448-998071]\ Notes:Best Blastp Hit: pir\|\|C81080 transglycosylase; probable NMB1462 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226704\|gb\|AAF41821.1\| (AE002496) transglycosylase; putative [Neisseria meningitidis MC58] COG0741 Soluble lytic murein transglycosylase and | Hypothetical Protein |
| NGO1034 | 0.0342 | -8.49 | down | hypothetical protein\ Context:(NC_002946)+[998126-998470]\ Notes:Best Blastp Hit: gb\|AAF42457.1\| (AE002563) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1037 | 0.0255 | -6.02 | down | hypothetical protein\ Context:(NC_002946)-[999363-999746]\ Notes: | Hypothetical Protein |
| NGO1065 | 0.0508 | -2.31 | down | hypothetical protein\ Context:(NC_002946)+[1025539-1025733]\ Notes:Best Blastp Hit: gb\|AAF41850.1\| (AE002498) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7380340\|emb\|CAB84927.1\| (AL162756) conserved hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1083 | 0.0356 | -5.01 | down | hypothetical protein\ Context:(NC_002946)+[1042858-1043178]\ Notes: | Hypothetical Protein |
| NGO1192 | 0.0234 | -3.58 | down | hypothetical protein\ Context:(NC_002946)+[1134874-1135218]\ Notes:Best Blastp Hit: pir\|\|H81960 hypothetical inner membrane protein NMA0437 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379187\|emb\|CAB83736.1\| (AL162753) hypothetical inner membrane protein [Neisseria meningitidis] COG1380 Predicted membrane protein; YohJ family | Hypothetical Protein |
| NGO1198 | 0.0322 | -5.53 | down | hypothetical protein\ Context:(NC_002946)+[1142045-1143619]\ Notes:Best Blastp Hit: gb\|AAF42335.1\| (AE002550) YhbX/YhjW/YijP/YjdB family protein [Neisseria meningitidis MC58] COG2194 Predicted membrane-associated | Hypothetical Protein |
| NGO1220 | 0.0134 | -5.62 | down | hypothetical protein\ Context:(NC_002946)-[1170480-1171382]\ Notes:Best Blastp Hit: pir\|\|G81069 conserved hypothetical protein NMB1562 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226809\|gb\|AAF41916.1\| (AE002506) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1228 | 0.0128 | -12.99 | down | hypothetical protein\ Context:(NC_002946)+[1177890-1179005]\ Notes:Best Blastp Hit: emb\|CAB84987.1\| (AL162757) conserved integral membrane hypothetical protein [Neisseria meningitidis] COG0795 Predicted permeases | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO1245 | 0.0056 | -11.26 | down | hypothetical protein\ Context:(NC_002946)+[1196312-1197178]\ Notes:Best Blastp Hit: pir\|\|D81065 hypothetical protein NMB1586 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226835\|gb\|AAF41939.1\| (AE002509) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1248 | 0.0056 | -14.09 | down | hypothetical protein\ Context:(NC_002946)-[1199701-1200123]\ Notes:Best Blastp Hit: pir\|\|E81803 hypothetical protein NMA1781 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380423\|emb\|CAB85009.1\| (AL162757) hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1252 | 0.0211 | -10.51 | down | hypothetical protein\ Context:(NC_002946)+[1202358-1203260]\ Notes:Best Blastp Hit: emb\|CAB85013.1\| (AL162757) conserved hypothetical integral membrane protein [Neisseria meningitidis] COG0697 Predicted permeases | Hypothetical Protein |
| NGO1257 | 0.0018 | -14.27 | down | hypothetical protein\ Context:(NC_002946)-[1209532-1209675]\ Notes: | Hypothetical Protein |
| NGO1273 | 0.0080 | -4.98 | down | hypothetical protein\ Context:(NC_002946)+[1224369-1224773]\ Notes:Best Blastp Hit: emb\|CAB85043.1\| (AL162757) hypothetical protein [Neisseria meningitidis] COG0537 Diadenosine tetraphosphate (Ap4A) | Hypothetical Protein |
| NGO1274 | 0.0433 | -4.38 | down | hypothetical protein\ Context:(NC_002946)+[1224813-1225994]\ Notes:Best Blastp Hit: pir\|\|H81807 conserved hypothetical protein NMA1819 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|6900400\|emb\|CAB72012.1\| (AJ391256) hypothetical protein [Neisseria meningitidis] >gi\|7380458\|emb\|CAB85044.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] COG1619 Uncharacterized proteins; homologs of | Hypothetical Protein |
| NGO1282 | 0.0055 | -7.54 | down | hypothetical protein\ Context:(NC_002946)-[1234709-1235023]\ Notes:Best Blastp Hit: pir\|\|G81059 hypothetical protein NMB1639 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226889\|gb\|AAF41988.1\| (AE002514) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1287 | 0.0030 | -9.50 | down | hypothetical protein\ Context:(NC_002946)-[1241481-1242821]\ Notes:Best Blastp Hit: pir\|\|C81058 hypothetical protein NMB1644 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226895\|gb\|AAF41993.1\| (AE002515) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1288 | 0.0005 | -42.59 | down | hypothetical protein\ Context:(NC_002946)-[1242895-1244235]\ Notes:Best Blastp Hit: pir\|\|D81058 hypothetical protein NMB1645 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226896\|gb\|AAF41994.1\| (AE002515) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1289 | 0.0207 | -5.66 | down | hypothetical protein\ Context:(NC_002946)+[1244378-1245004]\ Notes:Best Blastp Hit: pir\|\|D81817 probable hemeolysin NMA1900 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380534\|emb\|CAB85121.1\| (AL162757) putative haemolysin [Neisseria meningitidis] COG1272 Predicted membrane proteins; hemolysin | Hypothetical Protein |
| NGO1293 | 0.0377 | -7.71 | down | hypothetical protein\ Context:(NC_002946)-[1248518-1248802]\ Notes: | Hypothetical Protein |
| NGO1297 | 0.0499 | -2.88 | down | hypothetical protein\ Context:(NC_002946)-[1251397-1252752]\ Notes:Best Blastp Hit: pir\|\|E81818 conserved hypothetical protein NMA1908 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380543\|emb\|CAB85130.1\| (AL162757) conserved hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1319 | 0.0178 | -11.41 | down | PqiA\ Context:(NC_002946)+[1276589-1277893]\ Notes:Best Blastp Hit: pir\|\|F81820 hypothetical integral membrane protein NMA1928 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380560\|emb\|CAB85148.1\| (AL162757) hypothetical integral membrane protein [Neisseria meningitidis]; putative paraquot-inducible protein A | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO1350 | 0.0003 | -13.15 | down | hypothetical protein\ Context:(NC_002946)+[1309781-1310347]\ Notes:Best Blastp Hit: pir\|\|G81052 hypothetical protein NMB1701 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226956\|gb\|AAF42049.1\| (AE002520) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1359 | 0.0250 | -5.50 | down | hypothetical protein\ Context:(NC_002946)-[1319675-1319929]\ Notes:Best Blastp Hit: gb\|AAF41523.1\| (AE002462) hypothetical protein [Neisseria meningitidis MC58] >gi\|7226410\|gb\|AAF41558.1\| (AE002465) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1361 | 0.0048 | -36.06 | down | hypothetical protein\ Context:(NC_002946)+[1320974-1321261]\ Notes:Best Blastp Hit: gb\|AAF42059.1\| (AE002521) L-lactate permease-related protein [Neisseria meningitidis MC58] COG1620 L-lactate permease | Hypothetical Protein |
| NGO1362 | 0.0316 | -14.34 | down | hypothetical protein\ Context:(NC_002946)+[1321289-1321438]\ Notes:Best Blastp Hit: emb\|CAB85187.1\| (AL162757) hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1370 | 0.0007 | -11.75 | down | hypothetical protein\ Context:(NC_002946)-[1334010-1335419]\ Notes:Best Blastp Hit: pir\|\|E81826 probable integral membrane protein NMA1975 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380607\|emb\|CAB85195.1\| (AL162757) putative integral membrane protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1430 | 0.0451 | -34.28 | down | hypothetical protein\ Context:(NC_002946)+[1392703-1393950]\ Notes:Best Blastp Hit: gb\|AAA25906.1\| (M60717) nosA [Pseudomonas stutzeri] | Hypothetical Protein |
| NGO1444 | 0.0076 | -16.26 | down | hypothetical protein\ Context:(NC_002946)+[1412050-1412229]\ Notes: | Hypothetical Protein |
| NGO1451 | 0.0319 | -8.64 | down | hypothetical protein\ Context:(NC_002946)+[1416890-1417387]\ Notes:Best Blastp Hit: pir\|\|C81186 hypothetical protein NMB0541 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225767\|gb\|AAF40970.1\| (AE002410) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1465 | 0.0100 | -24.59 | down | hypothetical protein\ Context:(NC_002946)-[1428738-1429151]\ Notes:Best Blastp Hit: gb\|AAD38303.1\|AF036242_3 (AF036242) unknown [Neisseria meningitidis] | Hypothetical Protein |
| NGO1469 | 0.0261 | -8.28 | down | hypothetical protein\ Context:(NC_002946)+[1433076-1433204]\ Notes:Best Blastp Hit: emb\|CAB84440.1\| (AL162755) hypothetical protein NMA1178 [Neisseria meningitidis] | Hypothetical Protein |
| NGO1516 | 0.0006 | -28.07 | down | hypothetical protein\ Context:(NC_002946)-[1484775-1485977]\ Notes:Best Blastp Hit: emb\|CAB85264.1\| (AL162758) hypothetical integral membrane protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1518 | 0.0518 | -5.08 | down | hypothetical protein\ Context:(NC_002946)-[1486339-1487112]\ Notes:Best Blastp Hit: emb\|CAB63177.1\| (AL133469) hypothetical protein SCM10.16c [Streptomyces coelicolor A3(2)] | Hypothetical Protein |
| NGO1558 | 0.0036 | -15.55 | down | hypothetical protein\ Context:(NC_002946)-[1533130-1533348]\ Notes: | Hypothetical Protein |
| NGO1563 | 0.0073 | -5.54 | down | hypothetical protein\ Context:(NC_002946)+[1535587-1535772]\ Notes: | Hypothetical Protein |
| NGO1576 | 0.0026 | -19.49 | down | hypothetical protein\ Context:(NC_002946)+[1551327-1551491]\ Notes: | Hypothetical Protein |
| NGO1594 | 0.0201 | -3.67 | down | hypothetical protein\ Context:(NC_002946)+[1566514-1566786]\ Notes: | Hypothetical Protein |
| NGO1601 | 0.0050 | -23.64 | down | hypothetical protein\ Context:(NC_002946)+[1572106-1573584]\ Notes:Best Blastp Hit: gb\|AAB61771.1\| (M84113) ORF1 [Neisseria gonorrhoeae] | Hypothetical Protein |
| NGO1604 | 0.0004 | -13.89 | down | hypothetical protein\ Context:(NC_002946)+[1575327-1575569]\ Notes:Best Blastp Hit: pir\|\|G81933 hypothetical protein NMA0876 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379591\|emb\|CAB84156.1\| (AL162754) hypothetical protein NMA0876 [Neisseria meningitidis] | Hypothetical Protein |
| NGO1664 | 0.0102 | -14.60 | down | hypothetical protein\ Context:(NC_002946)+[1618903-1619079]\ Notes:Best Blastp Hit: emb\|CAB85362.1\| (AL162758) hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO1672 | 0.0194 | -24.20 | down | hypothetical protein\ Context:(NC_002946)+[1627156-1627473]\ Notes:Best Blastp Hit: pir\|\|S77587 hypothetical protein Y - Neisseria gonorrhoeae >gi\|996086\|gb\|AAC43466.1\| (U32588) ORFY; non-essential for pilus assembly; [Neisseria gonorrhoeae] | Hypothetical Protein |
| NGO1686 | 0.0224 | -3.75 | down | hypothetical protein\ Context:(NC_002946)-[1638678-1639970]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0739 Membrane proteins related to | Hypothetical Protein |
| NGO1691 | 0.0108 | -23.72 | down | hypothetical protein\ Context:(NC_002946)+[1644588-1644734]\ Notes: | Hypothetical Protein |
| NGO1702 | 0.0396 | -4.44 | down | hypothetical protein\ Context:(NC_002946)-[1658587-1659111]\ Notes:Best Blastp Hit: pir\|\|F81792 hypothetical protein NMA2195 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|6900420\|emb\|CAB72030.1\| (AJ391261) hypothetical protein [Neisseria meningitidis] >gi\|7380814\|emb\|CAB85406.1\| (AL162758) hypothetical protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1712 | 0.0139 | -5.62 | down | hypothetical protein\ Context:(NC_002946)-[1669596-1670228]\ Notes:Best Blastp Hit: emb\|CAB85415.1\| (AL162758) hypothetical protein [Neisseria meningitidis] COG1611 Predicted Rossmann fold nucleotide-binding | Hypothetical Protein |
| NGO1719 | 0.0043 | -10.55 | down | hypothetical protein\ Context:(NC_002946)+[1680196-1681155]\ Notes:Best Blastp Hit: gb\|AAF40730.1\| (AE002384) conserved hypothetical protein [Neisseria meningitidis MC58] COG0429 Predicted hydrolase of the | Hypothetical Protein |
| NGO1720 | 0.0209 | -9.17 | down | hypothetical protein\ Context:(NC_002946)-[1681152-1681262]\ Notes: | Hypothetical Protein |
| NGO1759 | 0.0259 | -9.18 | down | hypothetical protein\ Context:(NC_002946)-[1722143-1722478]\ Notes:Best Blastp Hit: gb\|AAF40679.1\| (AE002380) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1760 | 0.0304 | -16.48 | down | hypothetical protein\ Context:(NC_002946)-[1722492-1722965]\ Notes:Best Blastp Hit: pir\|\|H81222 hypothetical protein NMB0222 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225445\|gb\|AAF40678.1\| (AE002380) hypothetical protein [Neisseria meningitidis MC58] >gi\|7378813\|emb\|CAB83355.1\| (AL162752) hypothetical protein NMA0037 [Neisseria meningitidis] | Hypothetical Protein |
| NGO1771 | 0.0004 | -14.39 | down | hypothetical protein\ Context:(NC_002946)-[1737443-1738435]\ Notes:Best Blastp Hit: pir\|\|E81225 hypothetical protein NMB0213 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225434\|gb\|AAF40669.1\| (AE002378) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1777 | 0.0024 | -45.25 | down | hypothetical protein\ Context:(NC_002946)+[1747904-1748062]\ Notes:Best Blastp Hit: gb\|AAF42457.1\| (AE002563) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1784 | 0.0350 | -7.88 | down | hypothetical protein\ Context:(NC_002946)-[1753810-1754115]\ Notes:Best Blastp Hit: gb\|AAF40654.1\| (AE002377) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1789 | 0.0378 | -4.68 | down | hypothetical protein\ Context:(NC_002946)+[1761924-1762508]\ Notes:Best Blastp Hit: pir\|\|B81999 ribonuclease H (EC 3.1.26.4) II NMA0075 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7378848\|emb\|CAB83391.1\| (AL162752) ribonuclease HII [Neisseria meningitidis] COG0164 Ribonuclease HII | Hypothetical Protein |
| NGO1792 | 0.0070 | -9.56 | down | hypothetical protein\ Context:(NC_002946)-[1764847-1765422]\ Notes:Best Blastp Hit: emb\|CAB83394.1\| (AL162752) putative integral membrane protein [Neisseria meningitidis] | Hypothetical Protein |
| NGO1846 | 0.0008 | -31.40 | down | hypothetical protein\ Context:(NC_002946)-[1812222-1812371]\ Notes:Best Blastp Hit: emb\|CAB83453.1\| (AL162752) hypothetical protein NMA0138 [Neisseria meningitidis] | Hypothetical Protein |
| NGO1847 | 0.0046 | -16.84 | down | hypothetical protein\ Context:(NC_002946)-[1812378-1813307]\ Notes:Best Blastp Hit: gb\|AAF41823.1\| (AE002496) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1849 | 0.0011 | -13.64 | down | hypothetical protein\ Context:(NC_002946)-[1813761-1814822]\ Notes:Best Blastp Hit: possibly phase variable - 8G residue homopolymer repeat in the coding sequence (ON) | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO1874 | 0.0074 | -52.58 | down | hypothetical protein\ Context:(NC_002946)+[1844694-1844858]\ Notes:Best Blastp Hit: gb\|AAA96487.1\| (L36381) putative [Neisseria gonorrhoeae] | Hypothetical Protein |
| NGO1886 | 0.0010 | -32.15 | down | hypothetical protein\ Context:(NC_002946)-[1854669-1855091]\ Notes:Best Blastp Hit: emb\|CAB83494.1\| (AL162752) hypothetical protein NMA0179 [Neisseria meningitidis] | Hypothetical Protein |
| NGO1913 | 0.0463 | -13.54 | down | hypothetical protein\ Context:(NC_002946)+[1891120-1891512]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) | Hypothetical Protein |
| NGO1938 | 0.0437 | -17.46 | down | hypothetical protein\ Context:(NC_002946)-[1914832-1915035]\ Notes:Best Blastp Hit: pir\|\|F81000 hypothetical protein NMB2152 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227410\|gb\|AAF42460.1\| (AE002563) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1948 | 0.0076 | -8.61 | down | hypothetical protein\ Context:(NC_002946)-[1921470-1921919]\ Notes:Best Blastp Hit: pir\|\|B81002 conserved hypothetical protein NMB2140 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227397\|gb\|AAF42448.1\| (AE002562) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1952 | 0.0023 | -20.01 | down | hypothetical protein\ Context:(NC_002946)-[1924516-1924728]\ Notes:Best Blastp Hit: gb\|AAF42445.1\| (AE002562) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1960 | 0.0395 | -14.04 | down | hypothetical protein\ Context:(NC_002946)+[1936946-1937212]\ Notes: | Hypothetical Protein |
| NGO1976 | 0.0162 | -5.89 | down | hypothetical protein\ Context:(NC_002946)-[1953306-1953539]\ Notes:Best Blastp Hit: gb\|AAF42417.1\| (AE002559) hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO1977 | 0.0249 | -5.83 | down | hypothetical protein\ Context:(NC_002946)+[1953539-1954198]\ Notes:Best Blastp Hit: emb\|CAB83635.1\| (AL162752) hypothetical protein NMA0330 [Neisseria meningitidis] COG0212 5-formyltetrahydrofolate cyclo-ligase | Hypothetical Protein |
| NGO2004 | 0.0248 | -15.46 | down | hypothetical protein\ Context:(NC_002946)+[1976422-1976658]\ Notes: | Hypothetical Protein |
| NGO2006 | 0.0270 | -23.18 | down | hypothetical protein\ Context:(NC_002946)-[1977556-1977750]\ Notes:Best Blastp Hit: emb\|CAB83663.1\| (AL162752) hypothetical protein NMA0362 [Neisseria meningitidis] | Hypothetical Protein |
| NGO2019 | 0.0421 | -3.86 | down | hypothetical protein\ Context:(NC_002946)-[1989359-1990129]\ Notes:Best Blastp Hit: pir\|\|B81010 thiF protein NMB2062 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227324\|gb\|AAF42381.1\| (AE002556) thiF protein [Neisseria meningitidis MC58] COG0476 Dinucleotide-utilizing enzymes involved in | Hypothetical Protein |
| NGO2033 | 0.0024 | -4.89 | down | putative hydrolase\ Context:(NC_002946)-[2003947-2004579]\ Notes:Best Blastp Hit: pir\|\|A81955 probable hydrolase NMA0387 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379140\|emb\|CAB83688.1\| (AL162753) putative hydrolase [Neisseria meningitidis] COG0491 Zn-dependent hydrolases | Hypothetical Protein |
| NGO2058 | 0.0033 | -17.53 | down | hypothetical protein\ Context:(NC_002946)+[2032543-2033025]\ Notes:Best Blastp Hit: pir\|\|E81245 conserved hypothetical protein NMB0043 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225263\|gb\|AAF40514.1\| (AE002362) conserved hypothetical protein [Neisseria meningitidis MC58] >gi\|7379050\|emb\|CAB83596.1\| (AL162752) hypothetical protein NMA0289 [Neisseria meningitidis] COG1546 Uncharacterized protein CinA/YgaD | Hypothetical Protein |
| NGO2106 | 0.0195 | -11.85 | down | hypothetical protein\ Context:(NC_002946)+[2089206-2089541]\ Notes: | Hypothetical Protein |
| NGO2108 | 0.0075 | -61.02 | down | hypothetical protein\ Context:(NC_002946)-[2090831-2091019]\ Notes: | Hypothetical Protein |
| NGO2113 | 0.0001 | -51.17 | down | hypothetical protein\ Context:(NC_002946)+[2099285-2100214]\ Notes:Best Blastp Hit: gb\|AAG03531.1\|AE004452_3 (AE004452) conserved hypothetical protein [Pseudomonas aeruginosa] | Hypothetical Protein |
| NGO2136 | 0.0169 | -8.68 | down | hypothetical protein\ Context:(NC_002946)+[2116331-2116516]\ Notes: | Hypothetical Protein |

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|---|---|---|---|---|---|
| NGO2138 | 0.0107 | -5.67 | down | putative ABC transporter; permease protein\ Context:(NC_002946)+[2117408-2118094]\ Notes:Best Blastp Hit: pir\|\|D81023 ABC transporter; permease protein NMB1947 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227206\|gb\|AAF42276.1\| (AE002543) ABC transporter; permease protein [Neisseria meningitidis MC58] COG2011 Permease component of an uncharacterized ABC | Hypothetical Protein |
| NGO2162 | 0.0090 | -9.00 | down | hypothetical protein\ Context:(NC_002946)-[2138449-2138934]\ Notes:Best Blastp Hit: gb\|AAF42252.1\| (AE002541) conserved hypothetical protein [Neisseria meningitidis MC58] | Hypothetical Protein |
| NGO2179 | 0.0052 | -28.75 | down | hypothetical protein\ Context:(NC_002946)+[2152852-2152986]\ Notes: | Hypothetical Protein |
| NGO0021 | 0.0135 | -11.85 | down | putative TonB-dependent receptor protein; iron related\ Context:(NC_002946)-[17323-19500]\ Notes:Best Blastp Hit: pir\|\|D81976 probable ferric siderophore receptor protein NMA0575 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379311\|emb\|CAB83866.1\| (AL162753) putative ferric siderophore receptor protein [Neisseria meningitidis] COG1629 Outer membrane receptor proteins; mostly Fe | Iron Storage and Acquisition |
| NGO0023 | 0.0307 | -10.58 | down | putative ABC transporter; periplasmic binding protein;iron related\ Context:(NC_002946)-[20119-21090]\ Notes:Best Blastp Hit: gb\|AAF42214.1\| (AE002538) ABC transporter; periplasmic solute-binding protein; putative [Neisseria meningitidis MC58] COG0614 Ferrichrome-binding periplasmic proteins | Iron Storage and Acquisition |
| NGO1775 | 0.0030 | -10.27 | down | putative ferredoxin\ Context:(NC_002946)+[1745797-1746636]\ Notes:Best Blastp Hit: emb\|CAB83377.1\| (AL162752) putative ferredoxin [Neisseria meningitidis] COG1145 Ferredoxin 2 | Iron Storage and Acquisition |
| NGO2090 | 0.0353 | -11.76 | down | putative ABC transporter; permease protein; enterobactin\ Context:(NC_002946)-[2066574-2067548]\ Notes:Best Blastp Hit: gb\|AAF42318.1\| (AE002548) iron(III) ABC transporter; permease protein [Neisseria meningitidis MC58] COG0609 Iron; hemin; cobalamine permeases | Iron Storage and Acquisition |
| NGO2176 | 0.0060 | -41.18 | down | hypothetical protein\ Context:(NC_002946)-[2150090-2151172]\ Notes:Best Blastp Hit: sp\|P45610\|TONB_KLEPN TonB protein >gi\|484474\|pir\|\|JN0788 tonB protein - Klebsiella pneumoniae >gi\|405758\|emb\|CAA48498.1\| (X68478) TonB [Klebsiella pneumoniae] | Iron Storage and Acquisition |
| NGO0065 | 0.0425 | -6.12 | down | putative lipo-oligosaccharide acyltransferase\ Context:(NC_002946)+[64986-66860]\ Notes:Best Blastp Hit: gb\|AAF42171.1\| (AE002533) lipopolysaccharide biosynthesis protein WbpC; putative [Neisseria meningitidis MC58] COG1835 Predicted acyltransferases | Lipid/LPS Biosynthesis |
| NGO0205 | 0.0013 | -15.18 | down | LolA\ Context:(NC_002946)+[208087-208710]\ Notes:Best Blastp Hit: sp\|P57068\|LOLA_NEIMB outer-membrane lipoproteins carrier protein precursor >gi\|11281795\|pir\|\|C81178 outer membrane lipoprotein carrier protein NMB0622 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225852\|gb\|AAF41048.1\| (AE002417) outer membrane lipoprotein carrier protein [Neisseria meningitidis MC58]; putative lipoprotein carrier precursor; periplasmic binding | Lipid/LPS Biosynthesis |
| NGO0242 | 0.0067 | -9.40 | down | tetraacyldisaccharide 4'-kinase\ Context:(NC_002946)+[244922-245953]\ Notes:transfers the gamma-phosphate of ATP to the 4' position of a tetraacyldisaccharide 1-phosphate intermediate to form tetraacyldisaccharide 1;4'-bis-phosphate | Lipid/LPS Biosynthesis |
| NGO1055 | 0.0009 | -8.61 | down | putative acyl-CoA hydrolase\ Context:(NC_002946)+[1014597-1015079]\ Notes:Best Blastp Hit: pir\|\|G81079 acyl CoA thioester hydrolase family protein NMB1482 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226722\|gb\|AAF41838.1\| (AE002497) acyl CoA thioester hydrolase family protein [Neisseria meningitidis MC58] COG1607 Acyl-CoA hydrolase | Lipid/LPS Biosynthesis |

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|---|---|---|---|---|---|
| NGO1247 | 0.0168 | -6.94 | down | hypothetical protein\ Context:(NC_002946)-[1199032-1199595]\ Notes:Best Blastp Hit: pir\|\|C81803 CDPdiacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) NMA1779 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380421\|emb\|CAB85007.1\| (AL162757) CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Neisseria meningitidis] COG0558 Phosphatidylglycerophosphate synthase | Lipid/LPS Biosynthesis |
| NGO1352 | 0.0146 | -6.97 | down | putative 3-oxoacyl-(acyl-carrier-protein) synthase\ Context:(NC_002946)+[1311101-1312243]\ Notes:Best Blastp Hit: pir\|\|A81053 3-oxoacyl-(acyl-carrier-protein) synthase II NMB1703 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226958\|gb\|AAF42051.1\| (AE002520) 3-oxoacyl-(acyl-carrier-protein) synthase II [Neisseria meningitidis MC58] COG0304 3-oxoacyl-(acyl-carrier-protein) synthase I | Lipid/LPS Biosynthesis |
| NGO1782 | 0.0082 | -7.53 | down | LpxB\ Context:(NC_002946)-[1751413-1752585]\ Notes:Best Blastp Hit: pir\|\|A81226 lipid-A-disaccharide synthase NMB0199 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225420\|gb\|AAF40656.1\| (AE002377) lipid-A-disaccharide synthase [Neisseria meningitidis MC58] COG0763 Lipid A disaccharide synthetase; putative lipid-A-disaccharide synthase | Lipid/LPS Biosynthesis |
| NGO0465 | 0.0051 | -5.66 | down | putative phage associated protein\ Context:(NC_002946)-[457883-458419]\ Notes: | Phage Associated Protein |
| NGO0482 | 0.0108 | -10.37 | down | putative phage associated protein\ Context:(NC_002946)-[465465-465827]\ Notes: | Phage Associated Protein |
| NGO0484 | 0.0051 | -44.79 | down | putative phage associated protein\ Context:(NC_002946)+[465978-467042]\ Notes:Best Blastp Hit: gi\|9634200 Gp54 [Bacteriophage HK97] >gi\|6901629\|gb\|AAF31132.1\| (AF069529) Gp54 [Bacteriophage HK97] | Phage Associated Protein |
| NGO0491 | 0.0005 | -37.07 | down | putative phage associated protein\ Context:(NC_002946)+[470508-470915]\ Notes: | Phage Associated Protein |
| NGO0496 | 0.0361 | -5.40 | down | putative phage associated protein\ Context:(NC_002946)+[474408-476555]\ Notes:Best Blastp Hit: pir\|\|G81057 hypothetical protein NMB1656 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226908\|gb\|AAF42005.1\| (AE002516) hypothetical protein [Neisseria meningitidis MC58] | Phage Associated Protein |
| NGO0498 | 0.0426 | -7.72 | down | putative phage associated protein\ Context:(NC_002946)+[477821-479320]\ Notes:Best Blastp Hit: sp\|P23739\|SUIS_RAT sucrase-isomaltase; intestinal [contains: sucrase ; isomaltase ] | Phage Associated Protein |
| NGO0501 | 0.0251 | -10.08 | down | putative phage associated protein\ Context:(NC_002946)+[480370-480702]\ Notes: | Phage Associated Protein |
| NGO0505 | 0.0043 | -18.89 | down | putative phage associated protein\ Context:(NC_002946)+[482328-482594]\ Notes:Best Blastp Hit: gb\|AAD32742.1\| (AF127374) MmcR [Streptomyces lavendulae] | Phage Associated Protein |
| NGO0508 | 0.0130 | -28.14 | down | putative phage associated protein\ Context:(NC_002946)+[484046-484477]\ Notes:Best Blastp Hit: sp\|P77685\|SPR_ECOLI lipoprotein SPR precursor >gi\|7430106\|pir\|\|F64986 hypothetical protein b2175 - Escherichia coli (strain K-12) >gi\|1498150\|dbj\|BAA13140.1\| (D86610) Spr [Escherichia coli] >gi\|1736840\|dbj\|BAA15983.1\| (D90849) Probable lipoprotein NlpC homolog precursor. [Escherichia coli] >gi\|1788501\|gb\|AAC75236.1\| (AE000307) putative lipoprotein [Escherichia coli] | Phage Associated Protein |
| NGO0510 | 0.0435 | -22.39 | down | putative phage associated protein\ Context:(NC_002946)+[485026-489171]\ Notes:Best Blastp Hit: gi\|10955733 phage lambda host specific protein J [Yersinia pestis] >gi\|7467468\|pir\|\|T14652 protein J - Yersinia pestis plasmid pMT1 >gi\|2996342\|gb\|AAC13222.1\| (AF053947) phage lambda host specific protein J [Yersinia pestis] | Phage Associated Protein |
| NGO0512 | 0.0057 | -53.52 | down | putative phage associated protein\ Context:(NC_002946)-[489593-490528]\ Notes:Best Blastp Hit: gb\|AAB32262.1\|S75490_1 (S75490) orf2 [Neisseria gonorrhoeae] | Phage Associated Protein |
| NGO0513 | 0.0082 | -24.63 | down | putative phage associated protein\ Context:(NC_002946)+[489659-490129]\ Notes: | Phage Associated Protein |
| NGO0515 | 0.0261 | -4.01 | down | putative phage associated protein\ Context:(NC_002946)-[490591-490824]\ Notes: | Phage Associated Protein |
| NGO0518 | 0.0393 | -8.66 | down | putative phage associated protein\ Context:(NC_002946)+[491622-492161]\ Notes: | Phage Associated Protein |

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|---|---|---|---|---|---|
| NGO0520 | 0.0034 | -18.03 | down | putative phage associated protein\ Context:(NC_002946)+[492680-492991]\ Notes: | Phage Associated Protein |
| NGO0521 | 0.0006 | -41.07 | down | phage associated protein\ Context:(NC_002946)+[493004-493153]\ Notes:Best Blastp Hit: gb\|AAF41392.1\| (AE002449) hypothetical protein [Neisseria meningitidis MC58] | Phage Associated Protein |
| NGO0522 | 0.0440 | -32.67 | down | putative tail length tape measure protein; putative phage associated protein\ Context:(NC_002946)+[493183-496230]\ Notes:Best Blastp Hit: gi\|9634160 tail length tape measure protein [Bacteriophage HK97] >gi\|6901589\|gb\|AAF31092.1\|AF069529_5 (AF069529) tail length tape measure protein [Bacteriophage HK97] | Phage Associated Protein |
| NGO0723 | 0.0457 | -5.39 | down | putative phage associated protein\ Context:(NC_002946)+[722896-723144]\ Notes:Best Blastp Hit: emb\|CAB84476.1\| (AL162755) hypothetical protein NMA1216 [Neisseria meningitidis] | Phage Associated Protein |
| NGO0727 | 0.0312 | -4.35 | down | putative baseplate protein; putative phage associated protein\ Context:(NC_002946)-[726767-727315]\ Notes:Best Blastp Hit: gi\|9634072 P2 J homolog; baseplate or base of tail fibre [Enterobacteria phage 186] >gi\|3522880\|gb\|AAC34162.1\| (U32222) P2 J homolog; baseplate or base of tail fibre [Enterobacteria phage 186] | Phage Associated Protein |
| NGO1020 | 0.0136 | -29.43 | down | putative phage associated protein\ Context:(NC_002946)+[982212-984008]\ Notes: | Phage Associated Protein |
| NGO1085 | 0.0323 | -4.16 | down | putative phage associated protein\ Context:(NC_002946)+[1044447-1045292]\ Notes:Best Blastp Hit: sp\|P44189\|YE18_HAEIN hypothetical protein HI1418 >gi\|1074769\|pir\|\|A64029 hypothetical protein HI1418 - Haemophilus influenzae (strain Rd KW20) >gi\|1574254\|gb\|AAC23068.1\| (U32821) H. influenzae predicted coding region HI1418 [Haemophilus influenzae Rd] | Phage Associated Protein |
| NGO1086 | 0.0004 | -10.84 | down | putative phage associated protein\ Context:(NC_002946)-[1045279-1045479]\ Notes:Best Blastp Hit: gb\|AAF41392.1\| (AE002449) hypothetical protein [Neisseria meningitidis MC58] | Phage Associated Protein |
| NGO1087 | 0.0528 | -10.47 | down | putative phage associated protein\ Context:(NC_002946)+[1045494-1046174]\ Notes:Best Blastp Hit: pir\|\|T32944 hypothetical protein W01B11.5 - Caenorhabditis elegans >gi\|2804494\|gb\|AAB97600.1\| (AF043704) similar to S. cerevisiae SLA2 (GB:Z22811) [Caenorhabditis elegans] | Phage Associated Protein |
| NGO1088 | 0.0005 | -9.02 | down | putative phage associated protein\ Context:(NC_002946)-[1046153-1046638]\ Notes: | Phage Associated Protein |
| NGO1089 | 0.0052 | -13.76 | down | putative phage associated protein\ Context:(NC_002946)-[1046644-1047117]\ Notes: | Phage Associated Protein |
| NGO1091 | 0.0068 | -9.51 | down | putative phage associated protein\ Context:(NC_002946)-[1048489-1048887]\ Notes:Best Blastp Hit: gb\|AAF79659.1\|AC025416_33 (AC025416) F5O11.3 [Arabidopsis thaliana] | Phage Associated Protein |
| NGO1096 | 0.0081 | -30.61 | down | putative phage associated protein\ Context:(NC_002946)-[1058422-1058637]\ Notes: | Phage Associated Protein |
| NGO1097 | 0.0069 | -5.39 | down | putative phage associated protein\ Context:(NC_002946)-[1058674-1060926]\ Notes:Best Blastp Hit: gi\|9632518 putative portal protein [Bacteriophage 933W] >gi\|9633447\|ref\|NP_050550.1\| hypothetical protein [Bacteriophage VT2-Sa] >gi\|4585429\|gb\|AAD25457.1\|AF125520_52 (AF125520) putative portal protein [Bacteriophage 933W] >gi\|5881643\|dbj\|BAA84334.1\| (AP000363) hypothetical protein [Bacteriophage VT2-Sa] >gi\|7649880\|dbj\|BAA94158.1\| (AP000422) portal protein [Escherichia coli O157:H7] | Phage Associated Protein |
| NGO1099 | 0.0230 | -4.68 | down | putative phage associated protein\ Context:(NC_002946)-[1062181-1062423]\ Notes: | Phage Associated Protein |
| NGO1101 | 0.0366 | -6.15 | down | putative phage associated protein\ Context:(NC_002946)-[1062720-1063034]\ Notes:Best Blastp Hit: gb\|AAF53095.1\| (AE003632) CG14926 gene product [Drosophila melanogaster] | Phage Associated Protein |
| NGO1102 | 0.0397 | -8.52 | down | putative phage associated protein\ Context:(NC_002946)-[1063207-1063725]\ Notes:Best Blastp Hit: gb\|AAF24756.1\| (AF148565) putative endonuclease [Streptococcus thermophilus bacteriophage ST3] | Phage Associated Protein |
| NGO1103 | 0.0141 | -17.91 | down | putative phage associated protein\ Context:(NC_002946)-[1063716-1064099]\ Notes:Best Blastp Hit: dbj\|BAA94132.1\| (AP000422) hypothetical protein [Escherichia coli O157:H7] | Phage Associated Protein |

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|---|---|---|---|---|---|
| NGO1110 | 0.0448 | -4.04 | down | putative replicative DNA helicase; putative phage associated protein\ Context:(NC_002946)-[1066486-1067847]\ Notes:Best Blastp Hit: sp\|P37469\|DNAC_BACSU replicative DNA helicase >gi\|2127189\|pir\|\|S65970 replicative DNA helicase dnaC - Bacillus subtilis >gi\|467330\|dbj\|BAA05176.1\| (D26185) replicative DNA helicase [Bacillus subtilis] >gi\|2636591\|emb\|CAB16081.1\| (Z99124) replicative DNA helicase [Bacillus subtilis] COG0305 Replicative DNA helicase | Phage Associated Protein |
| NGO1111 | 0.0263 | -15.77 | down | putative phage associated protein\ Context:(NC_002946)-[1067844-1068974]\ Notes:Best Blastp Hit: gi\|9634200 Gp54 [Bacteriophage HK97] >gi\|6901629\|gb\|AAF31132.1\| (AF069529) Gp54 [Bacteriophage HK97] | Phage Associated Protein |
| NGO1115 | 0.0182 | -18.27 | down | putative phage associated protein\ Context:(NC_002946)-[1069893-1070081]\ Notes: | Phage Associated Protein |
| NGO1144 | 0.0521 | -19.03 | down | putative phage associated protein\ Context:(NC_002946)-[1086190-1086393]\ Notes:Best Blastp Hit: emb\|CAB84063.1\| (AL162754) hypothetical protein NMA0780 [Neisseria meningitidis] | Phage Associated Protein |
| NGO1146 | 0.0287 | -14.56 | down | putative phage associated protein\ Context:(NC_002946)-[1086789-1088060]\ Notes:Best Blastp Hit: pir\|\|G81922 probable phage replication protein NMA0782 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379503\|emb\|CAB84065.1\| (AL162754) putative phage replication protein [Neisseria meningitidis] | Phage Associated Protein |
| NGO1615 | 0.0191 | -8.77 | down | putative phage associated protein\ Context:(NC_002946)-[1584606-1585754]\ Notes:Best Blastp Hit: pir\|\|I41051 hsdM protein - Escherichia coli >gi\|450688\|emb\|CAA53205.1\| (X75452) hsdM gene of EcoprrI [Escherichia coli] | Phage Associated Protein |
| NGO1629 | 0.0501 | -3.91 | down | putative phage associated protein\ Context:(NC_002946)-[1592225-1593043]\ Notes: | Phage Associated Protein |
| NGO1630 | 0.0357 | -5.97 | down | putative phage repressor protein; putative phage associated protein\ Context:(NC_002946)-[1593316-1594071]\ Notes:Best Blastp Hit: pdb\|1LLI\|B Chain B; Lambda Repressor Mutant With Val 36 Replaced By Leu; Met 40 Replaced By Leu; And Val 47 Replaced By Ile (V36l;M40l;V47i) Complexed With Dna Operator >gi\|640244\|pdb\|1LLI\|A Chain A; Lambda Repressor Mutant With Val 36 Replaced By Leu; Met 40 Replaced By Leu; And Val 47 Replaced By Ile (V36l;M40l;V47i) Complexed With Dna Operator | Phage Associated Protein |
| NGO1634 | 0.0096 | -17.88 | down | putative phage associated protein\ Context:(NC_002946)+[1595199-1595750]\ Notes:Best Blastp Hit: pir\|\|S30432 hypothetical protein - Streptomyces clavuligerus plasmid pSCL | Phage Associated Protein |
| NGO1635 | 0.0225 | -13.90 | down | putative phage associated protein\ Context:(NC_002946)+[1596026-1596241]\ Notes: | Phage Associated Protein |
| NGO1636 | 0.0265 | -5.21 | down | putative DNA replication protein; putative phage associated protein\ Context:(NC_002946)+[1596419-1597036]\ Notes:Best Blastp Hit: pir\|\|T03011 dnaC protein homolog - Salmonella typhimurium >gi\|3294483\|gb\|AAC26072.1\| (AF001386) unknown [Salmonella typhimurium] COG1484 DNA replication protein DnaC | Phage Associated Protein |
| NGO1640 | 0.0461 | -4.90 | down | putative phage associated protein\ Context:(NC_002946)+[1598474-1599049]\ Notes:Best Blastp Hit: sp\|Q37873\|RUSA_BP82 crossover junction endodeoxyribonuclease RusA (Holliday junction nuclease RuSA) (Holliday juction resolvase) >gi\|2120247\|pir\|\|S66583 crossover junction endodeoxyribonuclease (EC 3.1.22.4) rusA - phage 82 >gi\|1051116\|emb\|CAA63330.1\| (X92588) Can suppress the phenotype of ruv mutants [Bacteriophage 82] | Phage Associated Protein |
| NGO1648 | 0.0099 | -17.25 | down | Irg7\ Context:(NC_002946)+[1605581-1606537]\ Notes:Best Blastp Hit: pir\|\|E81070 pilin gene inverting protein PivNM-1A NMB1552;NMB1625 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226799\|gb\|AAF41907.1\| (AE002505) pilin gene inverting protein PivNM-1A [Neisseria meningitidis MC58] >gi\|7226876\|gb\|AAF41976.1\| (AE002513) pilin gene inverting protein PivNM-1B [Neisseria meningitidis MC58]; putative invertase related gene 7; putative phage associated protein | Phage Associated Protein |
| NGO0256 | 0.0189 | -4.07 | down | transcription antitermination protein NusB\ Context:(NC_002946)-[254447-254872]\ Notes:Regulates rRNA biosynthesis by transcriptional antitermination | Protein Synthesis |

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|---|---|---|---|---|---|
| NGO0262 | 0.0251 | -2.98 | down | transcription elongation factor GreB\ Context:(NC_002946)-[261274-261765]\ Notes:necessary for efficient RNA polymerase transcription elongation past template-encoded arresting sites; arresting sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that pass through; resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as GreA or GreB allows the resumption of elongation from the new 3'terminus | Protein Synthesis |
| NGO0433 | 0.0046 | -8.84 | down | hypothetical protein\ Context:(NC_002946)+[426786-427709]\ Notes:Best Blastp Hit: emb\|CAB84348.1\| (AL162755) hypothetical protein NMA1085 [Neisseria meningitidis] COG0564 Predicted pseudouridylate synthase family 2 | Protein Synthesis |
| NGO0940 | 0.0479 | -4.03 | down | putative tRNA delta transferase\ Context:(NC_002946)+[916655-917596]\ Notes:Best Blastp Hit: pir\|\|E81879 probable tRNA isopentenyltransferase (EC 2.5.1.8) NMA1130 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379823\|emb\|CAB84392.1\| (AL162755) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Neisseria meningitidis] COG0324 tRNA delta (2)-isopentenylpyrophosphate | Protein Synthesis |
| NGO1214 | 0.0257 | -3.57 | down | tRNA(5-methylaminomethyl-2-thiouridylate)-methyltransferase\ Context:(NC_002946)-[1164441-1165592]\ Notes:Enables the biosynthesis of the modified nucleoside 5-methylaminomethyl-2-thiouridine present in the wobble position of some tRNAs | Protein Synthesis |
| NGO1791 | 0.0194 | -4.20 | down | glucose-inhibited division protein B\ Context:(NC_002946)-[1764129-1764752]\ Notes:probable SAM-dependent methyltransferase | Protein Synthesis |
| NGO1811 | 0.0276 | -2.77 | down | tRNA pseudouridine synthase A\ Context:(NC_002946)+[1787384-1788181]\ Notes:mediates pseudouridylation (positions 38; 39; 40) at the tRNA anticodon region which contributes to the structural stability | Protein Synthesis |
| NGO1940 | 0.0146 | -6.82 | down | hypothetical protein\ Context:(NC_002946)+[1916612-1917214]\ Notes:Best Blastp Hit: emb\|CAB83545.1\| (AL162752) hypothetical protein NMA0237 [Neisseria meningitidis] COG0009 Putative translation factor (SUA5) | Protein Synthesis |
| NGO2015 | 0.0421 | -6.71 | down | hypothetical protein\ Context:(NC_002946)+[1986403-1987260]\ Notes:Best Blastp Hit: gb\|AAF42384.1\| (AE002556) hemK protein [Neisseria meningitidis MC58] COG0500 SAM-dependent methyltransferases | Protein Synthesis |
| NGO0060 | 0.0445 | -4.04 | down | putative sugar-phosphate transferase\ Context:(NC_002946)+[60497-61192]\ Notes:Best Blastp Hit: gb\|AAF42176.1\| (AE002534) mannose-1-phosphate guanyltransferase-related protein [Neisseria meningitidis MC58] COG1208 Nucleoside-diphosphate-sugar | Purine and Pyrimidine Metabolism |
| NGO0263 | 0.0299 | -3.57 | down | amidophosphoribosyltransferase\ Context:(NC_002946)-[261865-263409]\ Notes:Catalyzes first step of the de novo purine nucleotide biosynthetic pathway | Purine and Pyrimidine Metabolism |
| NGO2080 | 0.0520 | -3.22 | down | hypothetical protein\ Context:(NC_002946)+[2059543-2060148]\ Notes:Best Blastp Hit: sp\|P57090\|NADD_NEIMB probable nicotinate-nucleotide adenyltransferase (deamido-NAD(+) pyrophosphorylase)(deamido-NAD(+) diphosphorylase) (nicotinate mononucleotide adenylyltransferase) (NAMN adenylyltransferase) >gi\|11278845\|pir\|\|C81015 conserved hypothetical protein NMB2024 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227286\|gb\|AAF42347.1\| (AE002552) conserved hypothetical protein [Neisseria meningitidis MC58] COG1057 Predicted nucleotidyltransferases | Purine and Pyrimidine Metabolism |
| NGO0187 | 0.0428 | -7.92 | down | hypothetical protein\ Context:(NC_002946)-[188256-189374]\ Notes:Best Blastp Hit: gb\|AAF41032.1\| (AE002416) histone deacetylase family protein [Neisseria meningitidis MC58] COG0123 Deacetylases; including yeast histone | Replication |
| NGO0851 | 0.0369 | -3.21 | down | putative cell-division protein\ Context:(NC_002946)-[836257-839301]\ Notes:Best Blastp Hit: pir\|\|E81125 cell division protein FtsK NMB1067 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226307\|gb\|AAF41463.1\| (AE002457) cell division protein FtsK [Neisseria meningitidis MC58] COG1674 DNA segregation ATPase FtsK/SpoIIIE and | Replication |

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|---|---|---|---|---|---|
| NGO0090 | 0.0006 | -13.01 | down | transcriptional regulator NrdR\ Context:(NC_002946)-[98397-98849]\ Notes:Best Blastp Hit: pir\|\|A81039 conserved hypothetical protein NMB1816 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227069\|gb\|AAF42151.1\| (AE002531) conserved hypothetical protein [Neisseria meningitidis MC58] COG1327 Uncharacterized BCR | Transcriptional Regulator |
| NGO0602 | 0.0069 | -8.93 | down | MerR family transcriptional regulator\ Context:(NC_002946)+[588393-588800]\ Notes:Best Blastp Hit: pir\|\|E81097 transcription regulator; MerR family NMB1303 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226544\|gb\|AAF41678.1\| (AE002479) transcriptional regulator; MerR family [Neisseria meningitidis MC58] >gi\|7380159\|emb\|CAB84745.1\| (AL162756) putative transcriptional regulator [Neisseria meningitidis] COG0789 Predicted transcriptional regulators | Transcriptional Regulator |
| NGO1182 | 0.0131 | -3.46 | down | putative nitrogen regulatory protein P-II\ Context:(NC_002946)-[1123800-1124138]\ Notes:Best Blastp Hit: pir\|\|B81019 nitrogen regulatory protein P-II NMB1995 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227257\|gb\|AAF42322.1\| (AE002548) nitrogen regulatory protein P-II [Neisseria meningitidis MC58] COG0347 Nitrogen regulatory protein PII | Transcriptional Regulator |
| NGO1185 | 0.0028 | -5.86 | down | ArsR family transcriptional regulator\ Context:(NC_002946)-[1129602-1129913]\ Notes:Best Blastp Hit: pir\|\|D70029 transcription regulator ArsR family homolog yvbA - Bacillus subtilis >gi\|2635892\|emb\|CAB15384.1\| (Z99121) similar to transcriptional regulator (ArsR family) [Bacillus subtilis] COG0640 Predicted transcriptional regulators | Transcriptional Regulator |
| NGO1219 | 0.0399 | -3.25 | down | DeoR family transcriptional regulator\ Context:(NC_002946)-[1169664-1170437]\ Notes:Best Blastp Hit: gb\|AAF41915.1\| (AE002506) transcriptional regulator; DeoR family [Neisseria meningitidis MC58] COG1349 Transcriptional regulators of sugar | Transcriptional Regulator |
| NGO1294 | 0.0008 | -22.04 | down | AsnC family transcriptional regulator\ Context:(NC_002946)-[1249111-1249575]\ Notes:Best Blastp Hit: pir\|\|A81059 leucine-responsive regulatory protein NMB1650 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226901\|gb\|AAF41999.1\| (AE002515) leucine-responsive regulatory protein [Neisseria meningitidis MC58] COG1522 Transcriptional regulators; Lrp family | Transcriptional Regulator |
| NGO1360 | 0.0017 | -13.43 | down | GntR family transcriptional regulator\ Context:(NC_002946)-[1319917-1320696]\ Notes:Best Blastp Hit: emb\|CAB85185.1\| (AL162757) GntR-family transcriptional regulator [Neisseria meningitidis] COG2186 Transcriptional regulators; FadR family | Transcriptional Regulator |
| NGO1511 | 0.0200 | -3.69 | down | putative drug resistance protein\ Context:(NC_002946)-[1477747-1479249]\ Notes:Best Blastp Hit: gb\|AAF08825.1\|AF194079_12 (AF194079) Bcr [Neisseria meningitidis] COG0477 Permeases | Transcriptional Regulator |
| NGO0123 | 0.0520 | -4.42 | down | putative secretion protein\ Context:(NC_002946)+[134372-135646]\ Notes:Best Blastp Hit: gb\|AAF61809.1\| (AF129811) unknown [Moraxella catarrhalis] COG1566 Multidrug resistance efflux pump | Transportation |
| NGO0198 | 0.0026 | -13.55 | down | putative transporter; ammonium\ Context:(NC_002946)-[198352-199818]\ Notes:Best Blastp Hit: possibly phase variable - 8A residue homopolymer repeat in the coding sequence (ON) COG0004 Ammonia permeases | Transportation |
| NGO0377 | 0.0001 | -68.48 | down | putative transport protein\ Context:(NC_002946)-[370891-372306]\ Notes:Best Blastp Hit: pir\|\|G81156 transporter; NadC family NMB0792 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226025\|gb\|AAF41205.1\| (AE002433) transporter; NadC family [Neisseria meningitidis MC58] COG0471 Cation transporters | Transportation |
| NGO0427 | 0.0041 | -11.22 | down | hypothetical protein\ Context:(NC_002946)-[422808-423464]\ Notes:Best Blastp Hit: emb\|CAB84330.1\| (AL162755) putative periplasmic protein [Neisseria meningitidis] COG1101 ATPase components of various transport | Transportation |

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|---|---|---|---|---|---|
| NGO0446 | 0.0259 | -10.04 | down | putative ABC transporter\ Context:(NC_002946)-[441352-442173]\ Notes:Best Blastp Hit: pir\|\|C81147 sulfate ABC transporter; permease protein NMB0880 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226118\|gb\|AAF41291.1\| (AE002440) sulfate ABC transporter; permease protein [Neisseria meningitidis MC58] COG0555 ABC-type cysteine/molybdate transport | Transportation |
| NGO0529 | 0.0076 | -9.10 | down | putative high-affinity choline transport protein\ Context:(NC_002946)+[501653-503635]\ Notes:Best Blastp Hit: pir\|\|E81839 probable transmembrane transport protein NMA1483 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380131\|emb\|CAB84716.1\| (AL162756) putative transmembrane transport protein [Neisseria meningitidis] COG1292 Choline-glycine betaine transporter | Transportation |
| NGO0656 | 0.0075 | -14.87 | down | putative membrane transporter\ Context:(NC_002946)+[646046-647587]\ Notes:Best Blastp Hit: pir\|\|A81850 probable integral membrane transporter NMA1574 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7380215\|emb\|CAB84801.1\| (AL162756) putative integral membrane transporter [Neisseria meningitidis] COG0477 Permeases | Transportation |
| NGO0903 | 0.0247 | -31.07 | down | AgrA\ Context:(NC_002946)-[882770-884176]\ Notes:Best Blastp Hit: emb\|CAB84875.1\| (AL162756) putative integral membrane protein [Neisseria meningitidis] COG0477 Permeases; aminoglycoside resistance efflux transporter protein | Transportation |
| NGO0968 | 0.0299 | -3.33 | down | putative ABC transporter; permease protein; amino acid\ Context:(NC_002946)-[940182-940928]\ Notes:Best Blastp Hit: pir\|\|A81076 amino acid ABC transporter; permease protein NMB1509 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7226752\|gb\|AAF41865.1\| (AE002500) amino acid ABC transporter; permease protein [Neisseria meningitidis MC58] >gi\|7380350\|emb\|CAB84937.1\| (AL162756) putative binding-protein-dependent transport systems inner membrane protein [Neisseria meningitidis] COG0765 Amino acid ABC transporter permease | Transportation |
| NGO0974 | 0.0141 | -8.34 | down | hypothetical protein\ Context:(NC_002946)-[944685-945995]\ Notes:Best Blastp Hit: pir\|\|B81074 transporter; probable NMB1515 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226759\|gb\|AAF41871.1\| (AE002501) transporter; putative [Neisseria meningitidis MC58] | Transportation |
| NGO1290 | 0.0000 | -209.10 | down | putative amino-acid transporter; sodium/alanine symporter\ Context:(NC_002946)-[1245069-1246487]\ Notes:Best Blastp Hit: pir\|\|F81058 amino acid symporter; probable NMB1647 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226898\|gb\|AAF41996.1\| (AE002515) amino acid symporter; putative [Neisseria meningitidis MC58] COG1115 Sodium-alanine symporters | Transportation |
| NGO1355 | 0.0007 | -21.61 | down | putative sodium dependent ion transport protein\ Context:(NC_002946)+[1314593-1315930]\ Notes:Best Blastp Hit: pir\|\|F81050 sodium- and chloride-dependent transporter NMB1707 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7226963\|gb\|AAF42055.1\| (AE002521) sodium- and chloride-dependent transporter [Neisseria meningitidis MC58] COG0733 Sodium-dependent transporters (SNF family) | Transportation |
| NGO1552 | 0.0131 | -7.50 | down | putative sodium/proline symporter; proline permease\ Context:(NC_002946)+[1525688-1527205]\ Notes:Best Blastp Hit: pir\|\|G81202 sodium/proline symporter NMB0402 [imported] - Neisseria meningitidis (group B strain MD58; group A strain Z2491) >gi\|7225624\|gb\|AAF40841.1\| (AE002396) sodium/proline symporter [Neisseria meningitidis MC58] >gi\|7380708\|emb\|CAB85299.1\| (AL162758) sodium/proline symporter [Neisseria meningitidis] COG0591 Na+/proline; Na+/panthothenate symporters | Transportation |

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|---|---|---|---|---|---|
| NGO1807 | 0.0251 | -5.93 | down | putative amino-acid transporter\ Context:(NC_002946)+[1780301-1781692]\ Notes:Best Blastp Hit: pir\|\|B81228 sodium/alanine symporter; probable NMB0177 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7225396\|gb\|AAF40634.1\| (AE002375) sodium/alanine symporter; putative [Neisseria meningitidis MC58] COG1115 Sodium-alanine symporters | Transportation |
| NGO2011 | 0.0013 | -29.62 | down | putative ABC transporter; permease protein; amino acid\ Context:(NC_002946)+[1983007-1983666]\ Notes:Best Blastp Hit: pir\|\|F81391 amino-acid ABC transporter integral membrane protein Cj0467 [imported] - Campylobacter jejuni (strain NCTC 11168) >gi\|6967938\|emb\|CAB75105.1\| (AL139075) amino-acid ABC transporter integral membrane protein [Campylobacter jejuni] COG0765 Amino acid ABC transporter permease | Transportation |
| NGO2012 | 0.0030 | -59.64 | down | putative ABC transporter; permease protein; amino acid\ Context:(NC_002946)+[1983656-1984324]\ Notes:Best Blastp Hit: pir\|\|B64666 glutamine ABC transporter; permease protein - Helicobacter pylori (strain 26695) >gi\|2314329\|gb\|AAD08216.1\| (AE000623) glutamine ABC transporter; permease protein (glnP) [Helicobacter pylori 26695] COG0765 Amino acid ABC transporter permease | Transportation |
| NGO2073 | 0.0048 | -4.59 | down | TnaB\ Context:(NC_002946)-[2051805-2053046]\ Notes:Best Blastp Hit: pir\|\|E81013 tryptophan transporter NMB2031 [imported] - Neisseria meningitidis (group B strain MD58) >gi\|7227293\|gb\|AAF42353.1\| (AE002553) tryptophan transporter [Neisseria meningitidis MC58] COG0814 Amino acid permeases; putative tryptophan transport protein; tryptophan permease | Transportation |
| NGO2077 | 0.0012 | -40.39 | down | GntP\ Context:(NC_002946)-[2055600-2056985]\ Notes:Best Blastp Hit: pir\|\|H81957 probable gluconate permease NMA0413 [imported] - Neisseria meningitidis (group A strain Z2491) >gi\|7379163\|emb\|CAB83712.1\| (AL162753) putative gluconate permease [Neisseria meningitidis] | Transportation |
| NGO2078 | 0.0008 | -31.01 | down | putative ABC transporter; permease protein\ Context:(NC_002946)+[2057326-2058918]\ Notes:Best Blastp Hit: gb\|AAF42349.1\| (AE002552) ABC transporter; permease protein [Neisseria meningitidis MC58] COG1178 Uncharacterized transport system; permease | Transportation |