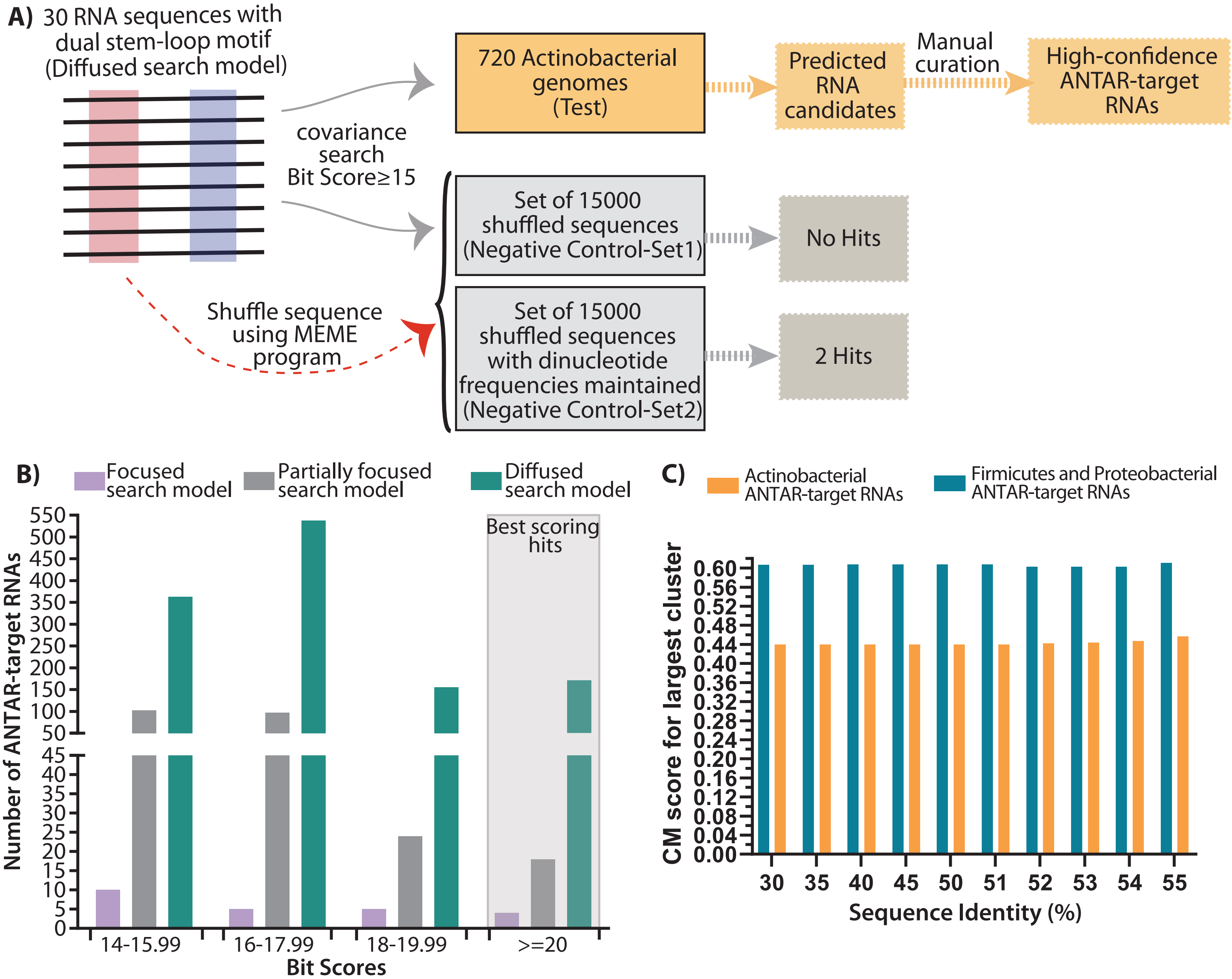
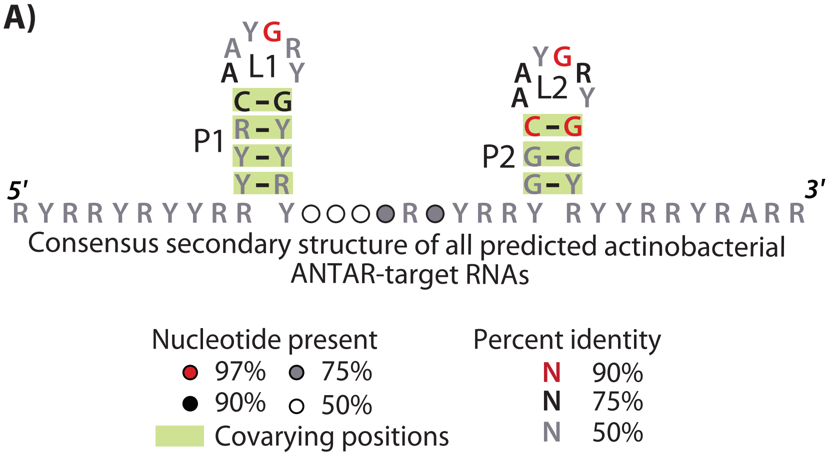


Fig S1. A) Schematic shows the steps followed to identify ANTAR-target RNAs across phylum actinobacteria. Diffused search model consisting of 30 sequences harboring the dual stem-loop (Red and Blue) structure motif was used for covariance searches. As a negative control, the sequences in the diffused search model were taken and shuffled to create 2 sets (gray). First negative control set (Set1) was obtained where the nucleotides in each sequence were shuffled (using kmer=1) and Set2 was obtained by shuffling the sequences such that the dinucleotide frequencies are maintained (using kmer=2). Covariance search was performed using diffused search model against actinobacterial genomes (test set, yellow) and negative control sets with a bit score threshold of 15.00. Our search identified RNA candidates from the test actinobacterial genomes but not from the negative control sets. Predicted RNA candidates from actinobacteria are manually curated to report on high confidence ANTAR-target RNAs. B) Bar plot shows the distribution of bit scores obtained for actinobacterial ANTAR-target RNAs identified using 3 search models (focused/ partially focused/ diffused). Bit scores report on the similarity of each RNA hit to the search model. Diffused search model yields RNAs of higher bit scores. C) RNA sets from firmicutes/ proteobacteria and actinobacteria were clustered using cmbuild. CM score distribution of the largest cluster obtained at varying sequence identity (30%-60%) is shown as bar plots.



Consensus secondary structure of all predicted actinobacterial ANTAR-target RNAs

**B)** ***Parameters for all ANTAR-target RNAs***

| | RNA Pool-1 | RNA Pool-2 |
|---|---|---|
| Number of RNAs | 305 | 306 |
| Mean pairwise identity (mPID) | 33.38 | 33.72 |
| Consensus MFE | -7.88 | -8.06 |
| Structure conservation index (SCI) | 0.49 | 0.50 |
| Mean z-score | -1.07 | -1.04 |
| SVM RNA-class probability (P) | 0.98 | 0.98 |

Fig S2. A) Consensus is drawn for all actinobacterial ANTAR-target RNA sequences using R2R and significantly covarying positions are mapped using R-scape. B) All the actinobacterial RNA hits were randomly divided into 2 pools (RNA Pool-1 and RNA Pool-2) and analyzed using RNAz. Parameters obtained from RNAz for each of the RNA pools are shown.

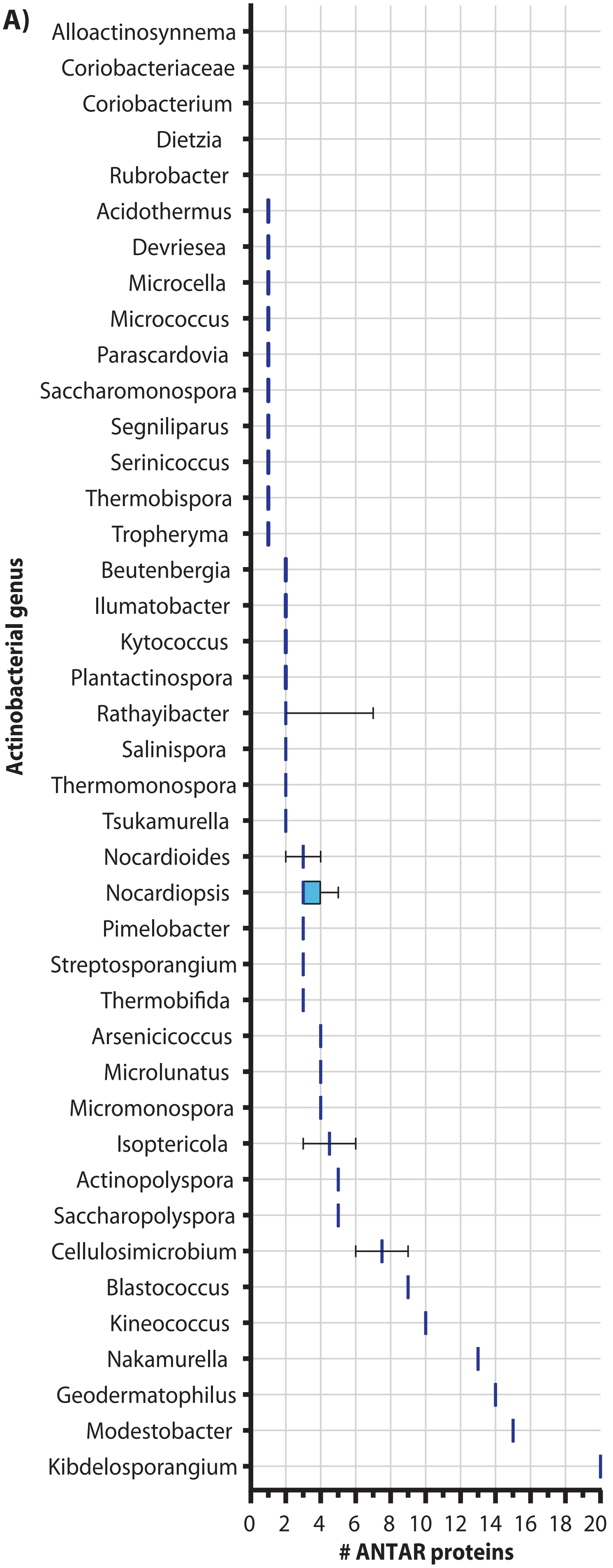


Fig S3. Distribution of ANTAR proteins in actinobacterial genera where ANTAR-target RNAs are not predicted. Box-Whisker plot with median (horizontal line), interquartile range (box) and 1.5 times the interquartile range (whiskers) is shown.

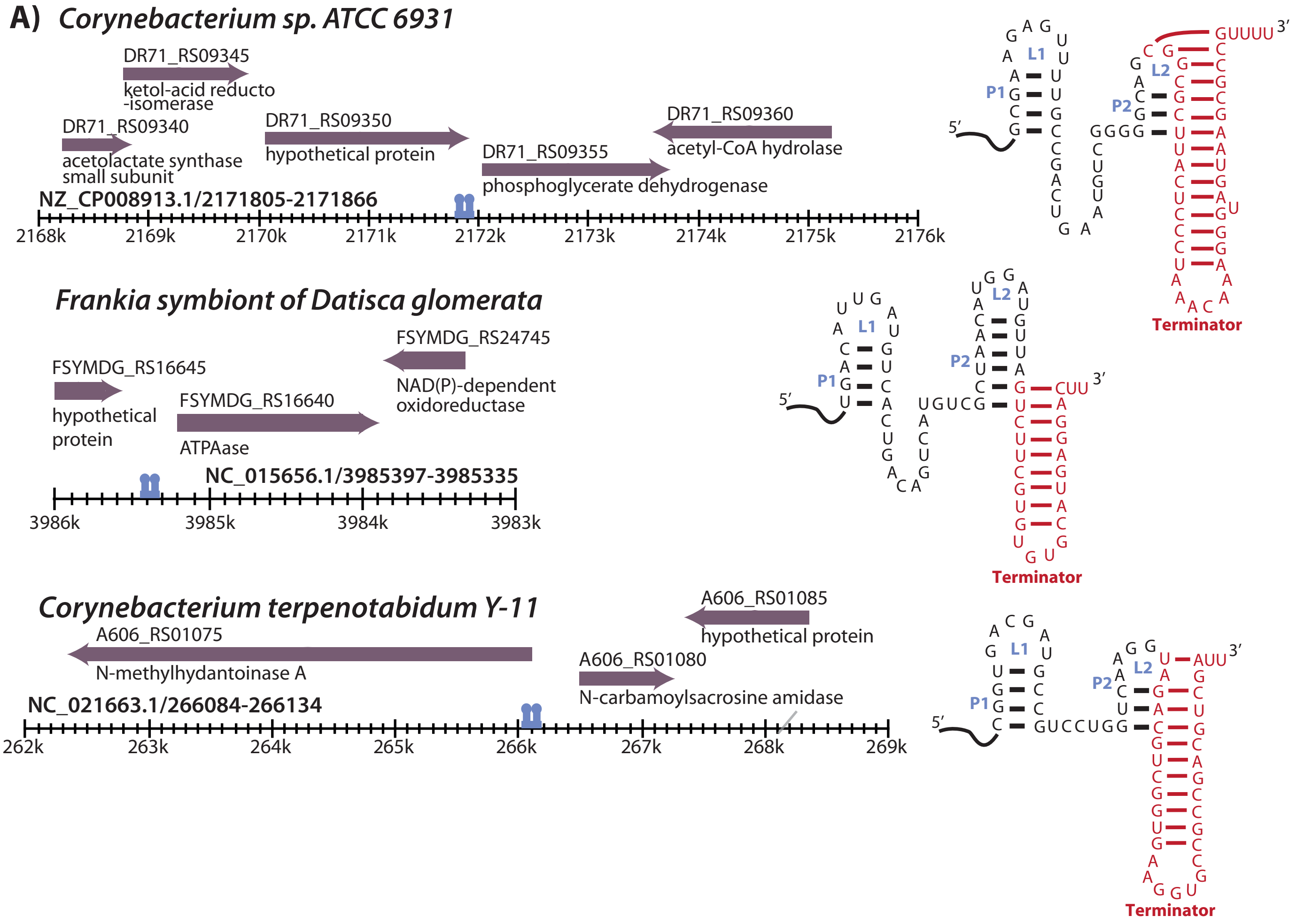
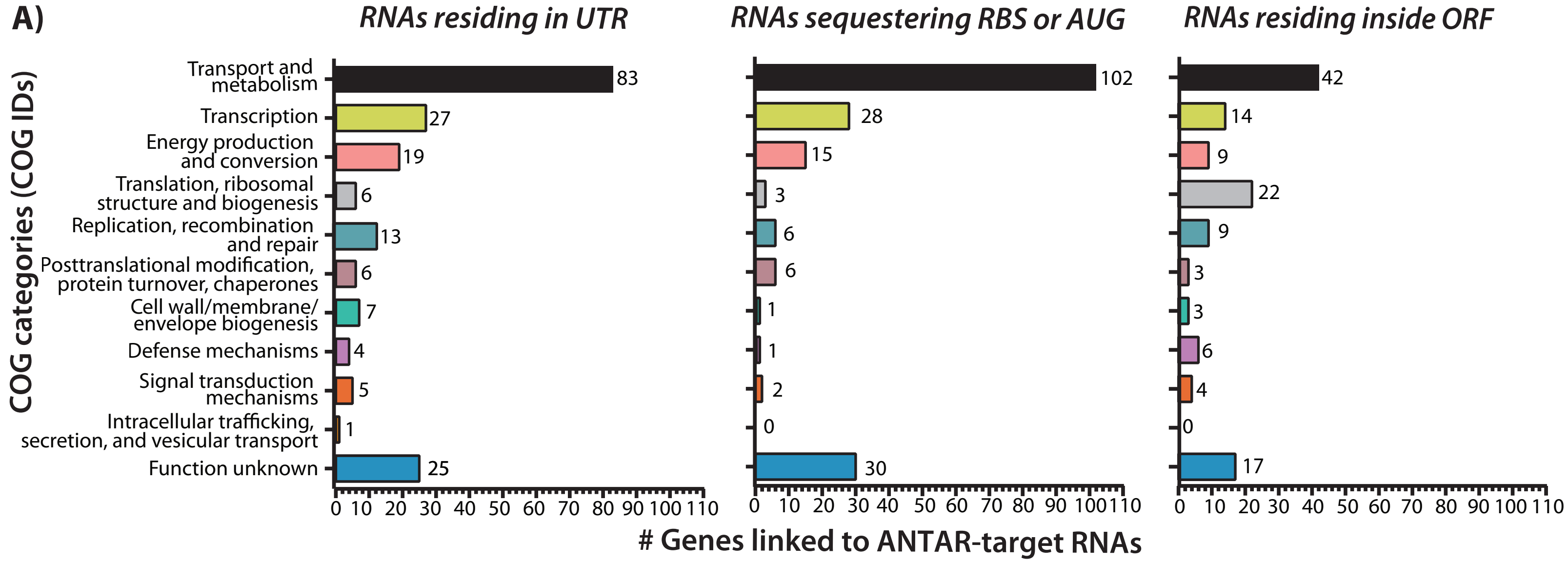


Fig S4: ANTAR-target RNAs categorized as 'intergenic' based on their location, were subjected to rho-independent transcription terminator analyses using TransTerm. Representative RNAs are shown with the predicted transcription terminator (red). The terminator structure is mutually exclusive from the dual stem ANTAR-target RNA structure.



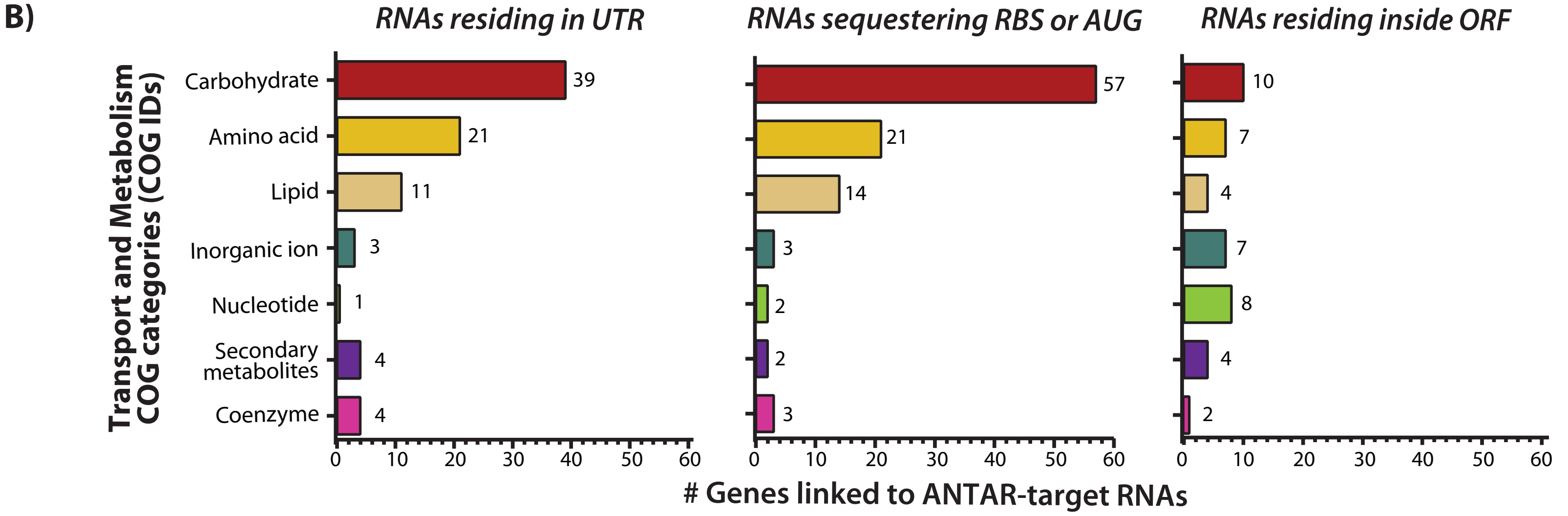


Fig S5. A) Genes linked to ANTAR-target RNAs grouped in UTR, sequester RBS or AUG, inside ORF categories, when analysed individually using EggNOG-mapper, get assigned to 11 COG categories. Bar plot shows distribution of genes linked to ANTAR-target RNAs, in each COG category. B) Bar plot shows distribution of genes linked to ANTAR-target RNAs, within the 'transport and metabolism' COG category. Carbohydrate and amino-acid transport and metabolism are the major processes represented by the targets.

Fig S6. A) Phylogenetic tree obtained from the NCBI taxonomy of actinobacterial species is plotted using iTOL. COG categories of genes linked to ANTAR-target RNAs are plotted using iTOL-binary dataset type with the color notations and abbreviations given in panel B.

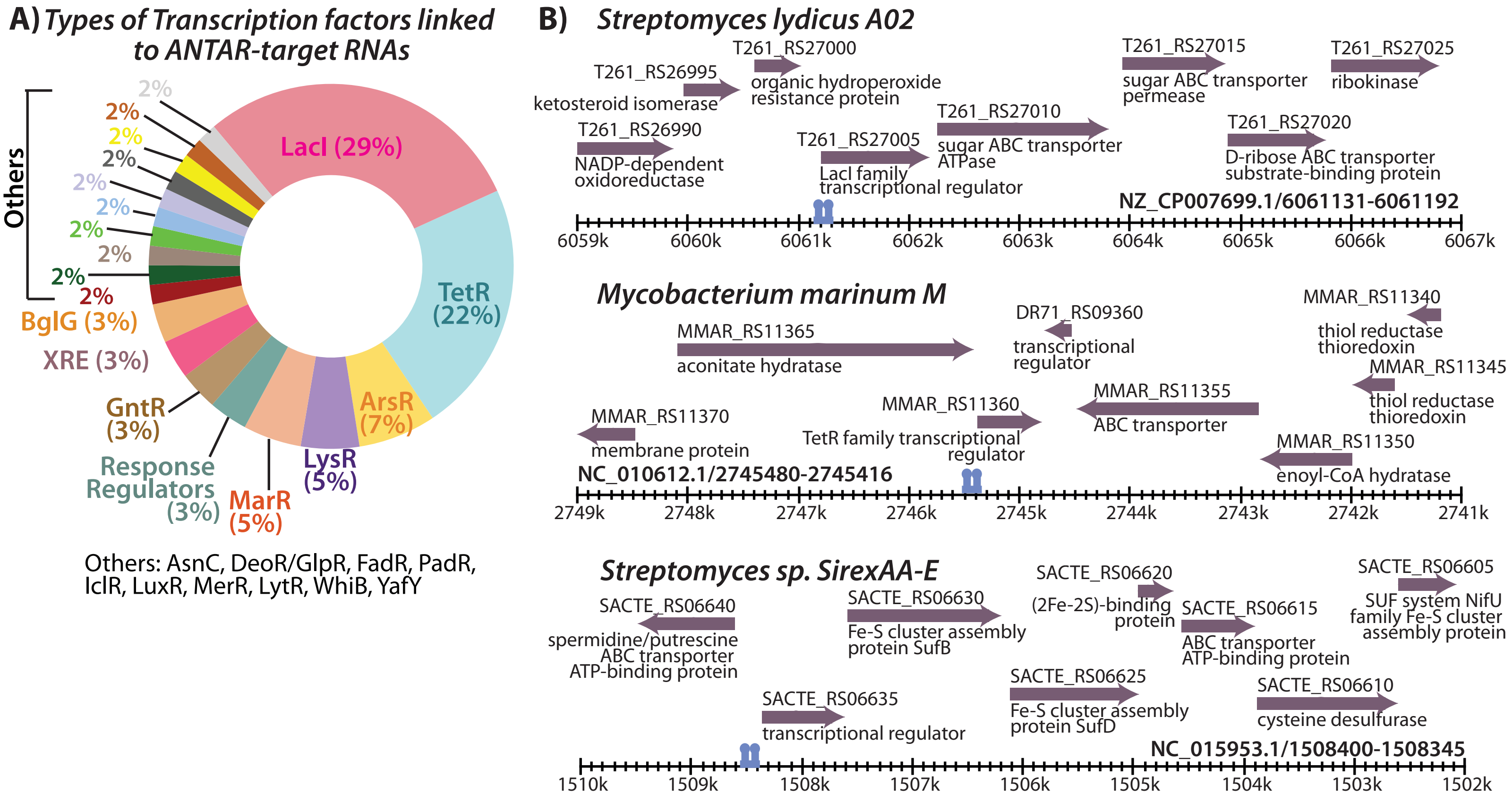


Fig S7. ANTAR-target RNAs linked to genes encoding transcription factors. A) Pie-chart shows the types of transcription factor families linked with ANTAR-target RNAs in actinobacteria. Many of the ANTAR-target RNAs are found upstream to LacI and TetR family transcription factors. (B) Genomic contexts of ANTAR-target RNAs (blue) lying upstream of a transcription factor. ORFs (purple) are shown with their operonic arrangement and labeled with NCBI gene annotations.

*Table S1: Diffused search model for ANTAR-target RNA dual stemloop motif.*
30 representative RNAs from actinobacteria predicted using partially diffused search model are used to make the improvised search model (Diffused search model). Base paired nucleotides in stems are shaded in pink and blue and secondary structure of the RNA is shown in WUSS notation where '<' and '>' indicates base-pairing positions.

| **Accession/Start-End** | **Sequence** |
|---|---|
| NC_019395/1187953-1188002 | .AAAUACAGCuCAGUACUGU-..AUUG--....................UUAUCGGCAUGGACGCCAAUGACGAUG |
| NC_022567/1325289-1325349 | .AAAAAAUCUCUUGCAAUGAU..GCAACGGuc............ggGUUAUCAUAGCAAAGCUGCUUGAGCGGAAG |
| NZ_CP008953/3466226-3466279 | .AAAGUAACAGAUACAACGAC..GUAUC--................-CCUUAUCCAUGACGGUAUGCUCAGCGAAG |
| NC_014218/792299-792362 | .UGCGUGAUAUGCACGAUGAC..GUGCUUUuau.........acgcAUCACUAUGUCAAUGGAGACACUAGAAAAG |
| NZ_CP013200/2964252-2964307 | .AUUUAUAGCAUC-UAAUGGU..GCGAUAU................AUGCACAAUUCAAAGGAGAAUCAUGACAGA |
| NC_013203/420130-420185 | .UUCAUUUCUUACAAAAAGAC..UUGUAG-................AAGUGAUCUGCUAUGAAGCAUAAAAUUUCA |
| NZ_AP017457/676069-676125 | .ACUUACUUCAACAAAAUGGA..UUGUCCG................CGGUUCCGGGCAAAUUCGCCACUAGACUUU |
| NZ_CP007443/1784660-1784721 | .AAAACGGCGACCGCAAAGCU..GCGGUUGcc...........guaACAGAUACGGCAAUGGGGCCGGAAAACCAG |
| NZ_CP009244/915923-915974 | .UAUAACCUAUGGACAAAGAG..GUUGU--................---CAGUAGGCAAUGAAGCCGGUGCACAAC |
| NC_015738/2403432-2403484 | .UCAAUGAUCCCAACAGUGAA..GUUGC--................--CAAAAAGGCAGCGAAGCUUCAAACGGAA |
| NZ_CP014513/1628135-1628207 | .UGACGCCGAUUUACAACGAU..GUAAUAGucgauggagcacccacCCCUACGAAGCAAUGGAGCUCCAUGUCGAC |
| NC_013721/312045-312095 | .AAGAUGAUUGCAGCGAAGAU..GCUGA--................----CGAAAGCAAAGAUGCUGAUAGCAAAA |
| NC_015564/4535773-4535832 | .AAUGAACUAUCUACAACGAU..GUAGAAUu.............ggUGAACUCAUGCAAAGGAGCAUGCGAUGCCA |
| NZ_CP007155/7090364-7090418 | .AAAAUGCAUUCGUGAACGAA..CACGAA-................-AAAUGAUCGCAAUGUAGCGGUUUUUGACA |
| NZ_CP012390/604046-604102 | .AGGUUCUCGACCGCAUUGGU..GUGAUCG................UUGGACAGGGCAACGAUGCCAUGAACGACA |
| NZ_CP014761/2225592-2225649 | .AUCAUGGUCUCUACAACGUU..GUAGUAC...............aACGUUGUAGACAAGGGUGUCACACACCGCG |
| NC_000962/2187261-2187311 | .ACAAAUUCCCAUGCAAAGAA..GCACUU-................-----GUGUACAACGAAGUAUCUUGGUAGU |
| NZ_CP016779/284217-284271 | .GAAAUAACUAAAUCAAUAUC..GGUUCC-................-AAUAAUUGGCAUUGGCGCCGGCAAUGAUU |
| NZ_CP017717/9630535-9630594 | .GAUGCUCUGGCGGCGGUGAC..GCCGACAc.............guCAUUAAAAGGCAAUGGAGCCUGGGAAAAUU |
| NZ_CP016777/10943-11014 | .AACAAAUUCUUAACAAGGCU..GUUGUCCacggcaa.aguaauuuUGUCUUCAGGCAAAGAGGCUGAUUACUACG |
| NZ_CP018002/1543107-1543167 | .AUGAUUUCGGCAACAAUGGU..GUUGUG-.........AAAAACAUGACGGAGCUCGGAGCGGAGCGCCCCAA.. |
| NC_011886/676358-676423 | .AUAUUCGCAACCAGAAUGAC..CUGGGUCacga.......aagccGGAUUACAUGCGAAGGGGCAUCCAGCCAUG |
| NZ_CP012182/279030-279077 | .AUCGAAUUUGCCCCACGGGU..GGGG---................------UAGGCAAGGACGCCGCGGAGCAGA |
| NC_010168/1485495-1485548 | .CAGCAAAGACCGCCAAAGAG..GGCGA--................-UUUUGUGGGCAAGGAAGCCUUGGCAAAGA |
| NC_013521/337151-337201 | .----------UUACAACGUU..GUAAGUGggauu.....cccugaAAGGACACCGCAAUGAAGCGCAU------- |
| NC_013165/1700444-1700501 | .GUACGUGAAAGAGCAACGGU..GCUUUUU...............gAAGGCAAGAGCAAUGGUGGUUCUAUAAAAG |
| NC_013947/4871519-4871574 | .UUGAAUUGAGUCGCAAAGGA..GCGAAG-................AUGUCUGUGGCCAAGUUGCCCAGUGCCGGU |
| NC_016582/1325572-1325634 | .ACAAUAAAACUCACAAAGGU..GUUGUUUuau..........agcAUUGAGCAUGAAUCGGAUCACUCUGUGAAG |
| NZ_CP019606/2506764-2506818 | ACUCUGAUAAUGA-CAGCGGUGUGAUU-..................-UGGACGUAGCAUGGGCGCUAUGUCUGAGG |
| NZ_CP012649/324715-324777 | .AAAAAGCCGUAGCCAAAGCU..GUUUAUGcga..........aagGAAACAAGAACAAUGACGUUUUUGGUUAAC |
| RF | .AaaAaaaauagcACAAaGgc..GUgcUuu................uauuaaAaAGCAAuGaAGCUcauaaaaAaa |
| SS_cons | .::::::::::<<<<______..>>>>---................--------<<<______>>>:::::::::: |

**Table S2**: ANTAR-target RNAs identified with diffused search model using Infernal v1.0.2 are shown for each organism given with the genome accession ID. Bit score is the value assigned by the covariance search to indicate similarity to the search model. A higher score suggests that the predicted RNA is more similar to the search model. RNAs with bit score threshold≥15.00 are reported here. RNA co-ordinates are as predicted by Infernal. Genes in cis to the predicted RNA (gene linked to ANTAR-target RNA) is indicated as NCBI gene annotations and its corresponding distance from the RNAs.

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Brevibacterium flavum strain ATCC 15168 (NZ_CP011309.1) | 16.55 | 641856-641800 | -1 | UDP-glucose 4-epimerase GalE (YH66_RS03105) | 64 |
| | 15.4 | 2690553-2690500 | -1 | phosphate ABC transporter, permease protein PstA (YH66_RS12975) | 5 |
| | 15.31 | 1296793-1296849 | 1 | DEAD/DEAH box helicase (YH66_RS06270) | 7 |
| | 15.24 | 1195547-1195604 | 1 | MFS transporter (YH66_RS05805) | 43 |
| Brevibacterium flavum ZL-1 (NZ_CP004046.1) | 15.4 | 2724657-2724605 | -1 | phosphate ABC transporter, permease protein PstA (C628_RS12840) | 47 |
| | 15.31 | 1333526-1333582 | 1 | ATP-dependent RNA helicase (C628_RS06330) | 7 |
| | 15.24 | 1235481-1235538 | 1 | MFS transporter (C628_RS05870) | 43 |
| Acidimicrobium ferrooxidans DSM 10331 (NC_013124.1) | 15.19 | 1724947-1725012 | 1 | DNA-binding protein (AFER_RS08470) | 42 |
| Acidipropionibacterium acidipropionici ATCC 4875 (NC_019395.1) | 19.36 | 2388629-2388576 | -1 | HTH domain-containing protein (PACID_RS11080) | 19 |
| | 18.01 | 1188010-1187953 | -1 | TetR family transcriptional regulator (PACID_RS05275) | 18 |
| Acidipropionibacterium acidipropionici strain ATCC 55737 (NZ_CP014352.1) | 19.36 | 963025-962972 | -1 | transcriptional regulator (AXH35_RS04620) | 19 |
| | 19.36 | 2384398-2384451 | 1 | transcriptional regulator (ASQ49_RS10630) | 19 |

| Organism<br>(Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs<br>(Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 18.01 | 3485203-3485260 | 1 | TetR family transcriptional regulator (ASQ49_RS15825) | 18 |
| Acidipropionibacterium acidipropionici strain F3E8 (NZ_CP015970.1) | 19.36 | 1261666-1261613 | -1 | HTH domain-containing protein (A8L58_RS06085) | 19 |
|  | 19.36 | 905699-905646 | -1 | Fe-S cluster assembly protein SufB (BWX38_RS04285) | 9 |
|  | 18.01 | 3442803-3442746 | -1 | ABC transporter ATP-binding protein (BWX38_RS15680) | 602 |
| Actinoalloteichus hymeniacidonis strain HPA177(T) (=DSM 45092(T)) (NZ_CP014859.1) | 15.43 | 4943167-4943111 | -1 | YafY family transcriptional regulator (TL08_RS20635) | 254 |
| Actinoalloteichus sp. ADI127-7 (NZ_CP016076.1) | 15.27 | 5692023-5692090 | 1 | LysR family transcriptional regulator (UA74_RS24200) | 17 |
| Actinoalloteichus sp. GBA129-24 (NZ_CP016077.1) | 15.27 | 5778466-5778533 | 1 | LysR family transcriptional regulator (UA75_RS24715) | 17 |
| Actinobacteria bacterium IMCC25003 (NZ_CP015603.1) | 16.63 | 195172-195101 | -1 | orotate phosphoribosyltransferase (IMCC25003_RS00950) | 25 |
| Actinobacteria bacterium IMCC26077 (NZ_CP015606.1) | 15.46 | 213250-213181 | -1 | sugar ABC transporter ATP-binding protein (IMCC26077_RS01135) | 98 |
| Actinobacteria bacterium IMCC26103 (NZ_CP015604.1) | 15.22 | 718815-718864 | 1 | hypothetical protein (IMCC26103_RS03680) | 41 |
| Actinobacteria bacterium IMCC26256 (NZ_CP011489.1) | 18.1 | 1875820-1875760 | -1 | hypothetical protein (IMCC26256_RS08800) | 68 |
|  | 16.24 | 1614744-1614691 | -1 | HNH endonuclease (IMCC26256_RS07585) | 43 |
|  | 15.67 | 878644-878705 | 1 | hypothetical protein (IMCC26256_RS04175) | 86 |
| Actinomyces gaoshouyii strain | 19.82 | 414788-414732 | -1 | MFS transporter (B6G06_RS01630) | 11 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| pika_114 (NZ_CP020468.1) | 16.29 | 646951-647003 | 1 | sugar ABC transporter substrate-binding protein (B6G06_RS02565) | 14 |
| | 15.63 | 2104690-2104738 | 1 | serine/threonine protein kinase (B6G06_RS08790) | 17 |
| Actinomyces meyeri strain W712 (NZ_CP012072.1) | 17.3 | 276999-277055 | 1 | glutamine synthetase (ADJ76_RS01245) | 3 |
| Actinomyces sp. Chiba101 DNA (NZ_AP017896.1) | 16.32 | 593765-593708 | -1 | MFS transporter (CHIBA101_RS02465) | 10 |
| | 15.67 | 773606-773660 | 1 | 2-keto-myo-inositol dehydratase (CHIBA101_RS03265) | 4 |
| | 15.63 | 313776-313728 | -1 | serine/threonine protein kinase (CHIBA101_RS01290) | 17 |
| | 15.25 | 2027467-2027415 | -1 | sugar ABC transporter substrate-binding protein (CHIBA101_RS08425) | 14 |
| Actinomyces sp. Marseille-P2985 strain Marseille-P2985T contig00001 (NZ_LT635457.1) | 15.2 | 581940-581874 | -1 | alpha-mannosidase (BQ7111_RS02600) | 13 |
| Actinomyces sp. oral taxon 414 strain F0588 (NZ_CP012590.1) | 24.28 | 627231-627295 | 1 | LacI family transcriptional regulator (AM609_RS02480) | 91 |
| Actinomyces sp. VUL4_3 (NZ_CP017812.1) | 21.6 | 1397314-1397258 | -1 | recombinase RecA (BK816_RS05805) | 79 |
| | 17.19 | 254992-255054 | 1 | phosphoribosylformylglycinamidine synthase subunit PurL (BK816_RS00900) | 477 |
| | 15.89 | 2085482-2085428 | -1 | hypothetical protein (BK816_RS08520) | 83 |
| Actinoplanes friuliensis DSM 7358 (NC_022657.1) | 18.23 | 9254943-9254997 | 1 | hypothetical protein (AFR_RS42690) | 5 |
| | 15.3 | 7354175-7354127 | -1 | alpha-1,2-mannosidase (AFR_RS33845) | 10 |
| Actinoplanes missouriensis 431 DNA (NC_017093.1) | 15.82 | 7097523-7097475 | -1 | tryptophan 2,3-dioxygenase (AMIS_RS32425) | 6 |
| | 15.42 | 7744888-7744823 | -1 | electron transfer flavoprotein subunit beta | 19 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (AMIS_RS35245) | |
| Actinoplanes sp. N902-109 (NC_021191.1) | 15.77 | 1672608-1672658 | 1 | ribosome silencing factor (L083_RS07555) | 53 |
| Actinosynnema pretiosum strain X47 (NZ_CP023445.1) | 20.39 | 4013130-4013182 | 1 | LacI family transcriptional regulator (CNX65_RS17145) | 17 |
| | 17.87 | 3895160-3895225 | 1 | hypothetical protein (CNX65_RS16655) | 2 |
| Actinotignum schaalii strain CCUG 27420 (NZ_CP008802.1) | 21.11 | 1251722-1251774 | 1 | LacI family transcriptional regulator (FB03_RS05325) | 2 |
| | 15.9 | 1434577-1434519 | -1 | hypothetical protein (FB03_RS06045) | 209 |
| | 15.18 | 1274459-1274527 | 1 | LuxR family transcriptional regulator (FB03_RS05415) | 356 |
| Adlercreutzia equolifaciens DSM 19450 DNA (NC_022567.1) | 32.04 | 1325349-1325289 | -1 | tRNA-Pro (AEQU_RS05195) | 15 |
| | 18.26 | 1426207-1426157 | -1 | 3-methyl-2-oxobutanoate dehydrogenase subunit VorB (AEQU_RS05670) | 5 |
| Aeromicrobium erythreum strain AR18 (NZ_CP011502.1) | 15.47 | 3448673-3448731 | 1 | NAD(P)/FAD-dependent oxidoreductase (Aeryth_RS16260) | 3 |
| Agromyces aureus strain AR33 (NZ_CP013979.1) | 16.26 | 3880103-3880043 | -1 | hypothetical protein (ATC03_RS17315) | 67 |
| Amycolatopsis japonica strain MG417-CF17 (NZ_CP008953.1) | 23.53 | 3466279-3466226 | -1 | TetR/AcrR family transcriptional regulator (AJAP_RS16240) | 12 |
| | 16.49 | 1154197-1154251 | 1 | hypothetical protein (AJAP_RS05720) | 26 |
| Amycolatopsis keratiniphila strain HCCB10007 (NC_021252.1) | 15.72 | 7469565-7469511 | -1 | DUF385 domain-containing protein (AORI_RS74380) | 26 |
| | 15.68 | 4847596-4847645 | 1 | helix-turn-helix domain-containing protein (AORI_RS63105) | 120 |
| Amycolatopsis mediterranei RB (NC_022116.1) | 16.07 | 9478426-9478370 | -1 | gas vesicle protein (B737_RS43515) | 37 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Amycolatopsis mediterranei S699 (NC_017186.1) | 16.23 | 6403001-6403057 | 1 | IS110 family transposase (RAM_RS48360) | 213 |
| | 16.07 | 9468570-9468514 | -1 | gas vesicle protein (RAM_RS43460) | 37 |
| | 16.23 | 6412928-6412984 | 1 | IS110 family transposase (AMES_RS48400) | 213 |
| | 16.07 | 9478482-9478426 | -1 | gas vesicle protein (AMES_RS43515) | 37 |
| Amycolatopsis mediterranei U32 (NC_014318.1) | 16.07 | 9468510-9468454 | -1 | gas vesicle protein GvpA (AMED_8633) | 37 |
| Amycolatopsis orientalis strain B-37 (NZ_CP016174.1) | 15.11 | 3249576-3249634 | 1 | shikimate dehydrogenase (SD37_RS14565) | 36 |
| | 15.02 | 7928691-7928746 | 1 | tripartite tricarboxylate transporter TctB family protein (SD37_RS34325) | 9 |
| Arcanobacterium haemolyticum DSM 20595 (NC_014218.1) | 26.85 | 792299-792362 | 1 | galactose/glucose-binding lipoprotein (ARCH_RS03540) | 8 |
| | 22.68 | 625569-625621 | 1 | hexose-6-phosphate:phosphate antiporter (ARCH_RS02785) | 1 |
| | 19.77 | 40752-40799 | 1 | exo-alpha-sialidase (ARCH_RS09165) | 4 |
| | 17.2 | 88902-88960 | 1 | glycerophosphoryl diester phosphodiesterase (ARCH_RS00310) | 0 |
| | 17.2 | 704515-704578 | 1 | hypothetical protein (ARCH_RS03150) | 36 |
| | 16.57 | 123085-123135 | 1 | ATP-binding protein (ARCH_RS00470) | 2 |
| Arsenicicoccus sp. oral taxon 190 (NZ_CP012070.1) | 15.63 | 2479486-2479551 | 1 | 30S ribosomal protein S1 (ADJ73_RS11475) | 91 |
| Arthrobacter alpinus strain ERGS4:06 (NZ_CP013200.1) | 23.49 | 2964252-2964307 | 1 | alpha/beta hydrolase (AS189_RS13165) | 7 |
| | 19.15 | 2477270-2477335 | 1 | 30S ribosomal protein S1 (AS189_RS10870) | 49 |
| | 17.81 | 1608213-1608269 | 1 | hypothetical protein (AS189_RS07130) | 3 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.34 | 3870920-3870873 | -1 | DNA alkylation repair protein (AS189_RS17180) | 239 |
|  | 15.31 | 1273631-1273692 | 1 | heavy metal translocating P-type ATPase (AS189_RS05655) | 17 |
|  | 15.25 | 4027396-4027453 | 1 | hypothetical protein (AS189_RS17870) | 345 |
|  | 15.21 | 473061-473110 | 1 | DUF3427 domain-containing protein (AOC05_RS02030) | 5 |
|  | 15.1 | 125174-125110 | -1 | ABC transporter substrate-binding protein (AOC05_RS00465) | 72 |
| Arthrobacter arilaitensis RE117 (NC_014550.1) | 20.23 | 976792-976738 | -1 | acyl-CoA carboxylase subunit beta (AARI_RS04880) | 351 |
|  | 15.82 | 3030192-3030140 | -1 | amino acid decarboxylase (AARI_RS14455) | 35 |
| Arthrobacter sp. ATCC 21022 (NZ_CP014196.1) | 18.98 | 506425-506490 | 1 | hypothetical protein (AUT26_RS02425) | 17 |
|  | 17.62 | 523749-523796 | 1 | MFS transporter (AUT26_RS02490) | 5 |
|  | 17.11 | 549492-549436 | -1 | oxidoreductase (AUT26_RS02610) | 80 |
|  | 16.98 | 2015651-2015589 | -1 | sugar ABC transporter substrate-binding protein (AUT26_RS09085) | 3 |
|  | 16.04 | 2275221-2275286 | 1 | 30S ribosomal protein S1 (AUT26_RS10230) | 94 |
|  | 15.76 | 4370883-4370828 | -1 | AUT26_RS20010 (AUT26_RS20010) | 47 |
|  | 15.14 | 3630293-3630349 | 1 | hypothetical protein (AUT26_RS16410) | 11 |
| Arthrobacter sp. ERGS1:01 isolate water (NZ_CP012479.1) | 17.89 | 1014978-1015039 | 1 | hypothetical protein (AL755_RS08425) | 2 |
|  | 15.86 | 386851-386793 | -1 | DUF4245 domain-containing protein (AL755_RS05765) | 209 |
|  | 15.38 | 3422948-3422884 | -1 | universal stress protein (AL755_RS19430) | 25 |

| Organism<br>(Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 15.26 | 98837-98904 | 1 | aldehyde dehydrogenase (AL755_RS04450) | 107 |
| Arthrobacter sp. ERGS1:01 isolate water plasmid unnamed2 (NZ_CP012477.1) | 19.54 | 315774-315838 | 1 | ABC transporter substrate-binding protein (AL755_RS01495) | 17 |
| | 16.68 | 285368-285421 | 1 | ABC transporter ATP-binding protein (AL755_RS01335) | 31 |
| Arthrobacter sp. FB24 plasmid 2 (NC_008538.1) | 18.43 | 84098-84153 | 1 | ferredoxin (ARTH_RS22340) | 17 |
| Arthrobacter sp. FB24 (NC_008541.1) | 24.08 | 399351-399411 | 1 | hypothetical protein (ARTH_RS01920) | 1 |
| | 23 | 3967947-3968005 | 1 | gluconate kinase (ARTH_RS17885) | 17 |
| | 15.34 | 2327690-2327755 | 1 | 30S ribosomal protein S1 (ARTH_RS10440) | 94 |
| Arthrobacter sp. IHBB 11108 (NZ_CP011005.1) | 19.22 | 1447414-1447470 | 1 | amino acid permease (UM93_RS06735) | 280 |
| | 18.47 | 507759-507816 | 1 | death-on-curing protein (UM93_RS02365) | 178 |
| | 16.97 | 2933785-2933728 | -1 | hypothetical protein (UM93_RS13745) | 25 |
| | 15.36 | 3142426-3142370 | -1 | long-chain-fatty-acid--CoA ligase (UM93_RS14870) | 5 |
| Arthrobacter sp. LS16 (NZ_CP012171.1) | 19.15 | 1710406-1710341 | -1 | glyceraldehyde-3-phosphate dehydrogenase (AFL94_RS07635) | 50 |
| Arthrobacter sp. QXT-31 (NZ_CP019304.1) | 19.08 | 3170621-3170678 | 1 | ABC transporter substrate-binding protein (BWQ92_RS14325) | 2 |
| | 18.85 | 4938603-4938520 | -1 | AcrB/AcrD/AcrF family protein (BWQ92_RS22540) | 19 |
| | 17.46 | 4972446-4972392 | -1 | sugar ABC transporter substrate-binding protein (BWQ92_RS22690) | 66 |
| | 17.43 | 1250002-1250061 | 1 | hypothetical protein (BWQ92_RS05620) | 28 |
| | 15.41 | 2070139-2070197 | 1 | gfo/Idh/MocA family oxidoreductase | 44 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (BWQ92_RS09390) | |
| Arthrobacter sp. Rue61a (NC_018531.1) | 18.16 | 2363737-2363795 | 1 | sugar ABC transporter substrate-binding protein (ARUE_RS10720) | 88 |
| | 17.57 | 648665-648604 | -1 | MFS transporter (ARUE_RS03145) | 83 |
| | 15.44 | 4204106-4204050 | -1 | LacI family transcriptional regulator (ARUE_RS19180) | 420 |
| | 15.34 | 2452695-2452760 | 1 | 30S ribosomal protein S1 (ARUE_RS11125) | 94 |
| Arthrobacter sp. U41 (NZ_CP015732.1) | 20.48 | 54483-54428 | -1 | PLP-dependent transferase (ASPU41_RS00255) | 4 |
| | 16.64 | 1628239-1628298 | 1 | hypothetical protein (ASPU41_RS07570) | 2 |
| | 15.96 | 3306175-3306228 | 1 | LacI family DNA-binding transcriptional regulator (ASPU41_RS15065) | 17 |
| | 15.85 | 1748515-1748566 | 1 | acetone carboxylase subunit alpha (ASPU41_RS08160) | 17 |
| | 15.54 | 3982498-3982554 | 1 | hypothetical protein (ASPU41_RS18175) | 48 |
| | 15.27 | 3740542-3740604 | 1 | CsbD family protein (ASPU41_RS17020) | 10 |
| Arthrobacter sp. YC-RL1 (NZ_CP013297.1) | 19.15 | 2161698-2161633 | -1 | glyceraldehyde-3-phosphate dehydrogenase (ATC04_RS10120) | 50 |
| Arthrobacter sp. YN (NZ_CP022436.1) | 21.09 | 2248139-2248195 | 1 | FAD-dependent oxidoreductase (CGK93_RS10185) | 23 |
| | 15.96 | 1910566-1910516 | -1 | sensor histidine kinase (CGK93_RS08610) | 359 |
| | 15.88 | 4224508-4224564 | 1 | hypothetical protein (CGK93_RS19300) | 11 |
| | 15.34 | 2675478-2675543 | 1 | 30S ribosomal protein S1 (CGK93_RS12080) | 94 |
| Arthrobacter sp. ZXY-2 | 17.62 | 3552929-3552882 | -1 | MFS transporter (ARZXY2_RS16210) | 5 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| (NZ_CP017421.1) | 17.11 | 3527274-3527330 | 1 | oxidoreductase (ARZXY2_RS16090) | 80 |
| | 16.04 | 1988906-1988841 | -1 | 30S ribosomal protein S1 (ARZXY2_RS09175) | 94 |
| | 15.76 | 4114296-4114351 | 1 | MFS transporter (ARZXY2_RS18885) | 8 |
| | 15.75 | 304935-304879 | -1 | hypothetical protein (ARZXY2_RS01460) | 11 |
| | 15.05 | 3269070-3269014 | -1 | DNA-binding response regulator (ARZXY2_RS14910) | 64 |
| Arthrobacter sp. ZXY-2 plasmid pZXY21 (NZ_CP017422.1) | 15.66 | 154094-154033 | -1 | FAD-binding oxidoreductase (ARZXY2_RS21385) | 2 |
| Atopobium parvulum DSM 20469 (NC_013203.1) | 19.43 | 420185-420130 | -1 | hypothetical protein (APAR_RS01890) | 17 |
| | 16.32 | 432964-433017 | 1 | hypothetical protein (APAR_RS01945) | 26 |
| Aurantimicrobium minutum DNA, strain: KNC (NZ_AP017457.1) | 19.38 | 676125-676069 | -1 | hypothetical protein (AUMI_RS03320) | 28 |
| | 16.5 | 1187659-1187715 | 1 | NINE protein (AUMI_RS05890) | 64 |
| | 16.44 | 1240808-1240861 | 1 | type I pantothenate kinase (AUMI_RS06085) | 330 |
| | 15.75 | 521488-521549 | 1 | ammonium transporter (AUMI_RS02580) | 2 |
| | 15.3 | 749840-749893 | 1 | propionyl-CoA synthetase (AUMI_RS03660) | 2 |
| Bifidobacterium adolescentis ATCC 15703 DNA (NC_008618.1) | 21.38 | 1609525-1609471 | -1 | sugar ABC transporter permease (BAD_RS06830) | 5 |
| | 16.01 | 534675-534736 | 1 | sugar ABC transporter substrate-binding protein (BAD_RS02255) | 38 |
| | 15.16 | 1278132-1278189 | 1 | mannan endo-1,4-beta-mannosidase (BAD_RS05480) | 4 |
| Bifidobacterium adolescentis strain 22L (NZ_CP007443.1) | 27.95 | 1784660-1784721 | 1 | HAD family hydrolase (BADO_RS07460) | 48 |
| | 21.86 | 2169133-2169079 | -1 | ABC transporter substrate-binding protein | 5 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (BADO_RS08855) | |
| | 16.14 | 542863-542924 | 1 | sugar ABC transporter substrate-binding protein (BADO_RS02270) | 38 |
| | 15.88 | 217067-217115 | 1 | hypothetical protein (BADO_RS00830) | 71 |
| Bifidobacterium adolescentis strain BBMN23 (NZ_CP010437.1) | 25.23 | 2041274-2041213 | -1 | HAD family hydrolase (BBMN23_RS08555) | 14 |
| | 17.56 | 431761-431813 | 1 | MFS transporter (BBMN23_RS01715) | 13 |
| | 17.47 | 550782-550840 | 1 | sugar ABC transporter substrate-binding protein (BBMN23_RS02285) | 38 |
| | 15.88 | 227134-227182 | 1 | hypothetical protein (BBMN23_RS00850) | 71 |
| Bifidobacterium angulatum DSM 20098 = JCM 7096 DNA (NZ_AP012322.1) | 20.47 | 1863117-1863064 | -1 | DUF2142 domain-containing protein (BBAG_RS07490) | 17 |
| | 20 | 787294-787346 | 1 | recombinase RecA (BBAG_RS03180) | 40 |
| | 16.36 | 1197777-1197844 | 1 | YraN family protein (BBAG_RS04860) | 132 |
| | 16.14 | 439087-439148 | 1 | sugar ABC transporter substrate-binding protein (BBAG_RS01745) | 38 |
| | 15.61 | 854184-854242 | 1 | D-tyrosyl-tRNA(Tyr) deacylase (BBAG_RS03410) | 147 |
| | 15.37 | 606590-606650 | 1 | ABC transporter substrate-binding protein (BBAG_RS02440) | 17 |
| | 15.15 | 565546-565592 | 1 | sugar ABC transporter permease (BBAG_RS02280) | 17 |
| Bifidobacterium angulatum strain GT102 (NZ_CP014241.1) | 20 | 1353009-1353061 | 1 | recombinase RecA (Bang102_RS05340) | 40 |
| | 16.14 | 951500-951561 | 1 | sugar ABC transporter substrate-binding protein (Bang102_RS03735) | 38 |
| | 15.59 | 1152771-1152827 | 1 | MFS transporter (Bang102_RS04535) | 93 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 15.15 | 1122454-1122500 | 1 | sugar ABC transporter permease (Bang102_RS04410) | 17 |
| Bifidobacterium animalis strain A6 (NZ_CP010433.1) | 17.58 | 1704615-1704565 | -1 | mannan endo-1,4-beta-mannosidase (BAA6_RS07205) | 12 |
| | 17.28 | 1662665-1662716 | 1 | hypothetical protein (BAA6_RS07010) | 1 |
| | 16.16 | 357064-357123 | 1 | mannose-1-phosphate guanylyltransferase (BAA6_RS01455) | 176 |
| | 16.16 | 357063-357123 | 1 | mannose-1-phosphate guanylyltransferase (BAA6_RS01455) | 176 |
| Bifidobacterium animalis strain BL3 (NZ_CP017098.1) | 17.58 | 1704823-1704773 | -1 | mannan endo-1,4-beta-mannosidase (BGL50_RS07385) | 12 |
| | 17.28 | 1662873-1662924 | 1 | hypothetical protein (BGL50_RS07190) | 1 |
| | 16.16 | 357118-357177 | 1 | mannose-1-phosphate guanylyltransferase (BGL50_RS01545) | 176 |
| Bifidobacterium animalis strain RH (NZ_CP007755.1) | 17.58 | 1693954-1693904 | -1 | mannan endo-1,4-beta-mannosidase (EN10_RS07170) | 12 |
| | 17.28 | 1652004-1652055 | 1 | hypothetical protein (EN10_RS06975) | 1 |
| | 16.16 | 357421-357480 | 1 | mannose-1-phosphate guanylyltransferase (EN10_RS01455) | 176 |
| Bifidobacterium animalis subsp. animalis ATCC 25527 (NC_017834.1) | 17.61 | 1905476-1905417 | -1 | sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC (BANAN_RS07810) | 77 |
| | 16.47 | 363482-363548 | 1 | mannose-1-phosphate guanylyltransferase (BANAN_RS01505) | 176 |
| | 16.18 | 573407-573353 | -1 | hypothetical protein (BANAN_RS08175) | 89 |
| | 16.07 | 1890249-1890201 | -1 | alpha-galactosidase (BANAN_RS07760) | 7 |
| | 15.35 | 1206973-1206922 | -1 | hypothetical protein (BANAN_RS08255) | 228 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Bifidobacterium animalis subsp. animalis strain YL2 (NZ_CP015407.2) | 18.25 | 352928-352862 | -1 | mannose-1-phosphate guanylyltransferase (A4U98_RS01585) | 176 |
| | 17.61 | 750467-750526 | 1 | sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC (A4U98_RS03285) | 77 |
| | 17.28 | 1036659-1036608 | -1 | hypothetical protein (A4U98_RS04475) | 1 |
| | 16.18 | 148239-148293 | 1 | hypothetical protein (A4U98_RS00670) | 89 |
| | 16.07 | 765693-765741 | 1 | alpha-galactosidase (A4U98_RS03340) | 7 |
| | 16.07 | 894076-894146 | 1 | nucleoside hydrolase (A4U98_RS03835) | 6 |
| | 15.35 | 1538414-1538465 | 1 | hypothetical protein (A4U98_RS06450) | 228 |
| Bifidobacterium animalis subsp. lactis AD011 (NC_011835.1) | 17.58 | 830093-830043 | -1 | mannan endo-1,4-beta-mannosidase (BLA_RS03390) | 12 |
| | 17.28 | 788300-788351 | 1 | hypothetical protein (BLA_RS03195) | 1 |
| | 16.16 | 356849-356908 | 1 | mannose-1-phosphate guanylyltransferase (BLA_RS01455) | 176 |
| Bifidobacterium animalis subsp. lactis ATCC 27673 (NC_022523.1) | 18.72 | 1727752-1727699 | -1 | secreted beta-mannosidase (BLAC_RS07285) | 30 |
| | 17.28 | 1678573-1678624 | 1 | hypothetical protein (BLAC_RS07090) | 1 |
| | 16.16 | 357221-357280 | 1 | mannose-1-phosphate guanylyltransferase (BLAC_RS01485) | 176 |
| Bifidobacterium animalis subsp. lactis B420 (NC_017866.1) | 17.58 | 1699160-1699110 | -1 | mannan endo-1,4-beta-mannosidase (W7Y_RS07195) | 12 |
| | 17.28 | 1657210-1657261 | 1 | hypothetical protein (W7Y_RS07000) | 1 |
| | 16.16 | 357061-357120 | 1 | mannose-1-phosphate guanylyltransferase (W7Y_RS01460) | 176 |
| Bifidobacterium animalis subsp. lactis BB-12 (NC_017214.1) | 17.58 | 396461-396411 | -1 | mannan endo-1,4-beta-mannosidase (BIF_RS01600) | 12 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 17.28 | 354579-354630 | 1 | hypothetical protein (BIF_RS01405) | 1 |
| | 16.16 | 992545-992604 | 1 | mannose-1-phosphate guanylyltransferase (BIF_RS03905) | 176 |
| Bifidobacterium animalis subsp. lactis Bi-07 (NC_017867.1) | 17.58 | 1699379-1699329 | -1 | mannan endo-1,4-beta-mannosidase (W91_RS07185) | 12 |
| | 17.28 | 1657429-1657480 | 1 | hypothetical protein (W91_RS06990) | 1 |
| | 16.16 | 357063-357122 | 1 | mannose-1-phosphate guanylyltransferase (W91_RS01455) | 176 |
| Bifidobacterium animalis subsp. lactis Bl-04 (NC_012814.1) | 17.58 | 1699324-1699274 | -1 | mannan endo-1,4-beta-mannosidase (BALAC_RS07185) | 12 |
| | 17.28 | 1657373-1657424 | 1 | hypothetical protein (BALAC_RS06990) | 1 |
| | 16.16 | 357062-357121 | 1 | mannose-1-phosphate guanylyltransferase (BALAC_RS01455) | 176 |
| Bifidobacterium animalis subsp. lactis Bl12 (NC_021593.1) | 17.58 | 1698948-1698898 | -1 | mannan endo-1,4-beta-mannosidase (BL12_RS07185) | 12 |
| | 17.28 | 1656999-1657050 | 1 | hypothetical protein (BL12_RS06990) | 1 |
| | 16.16 | 356921-356980 | 1 | mannose-1-phosphate guanylyltransferase (BL12_RS01455) | 176 |
| Bifidobacterium animalis subsp. lactis BLC1 (NC_017216.2) | 17.58 | 1698969-1698919 | -1 | mannan endo-1,4-beta-mannosidase (BLC1_RS07185) | 12 |
| | 17.28 | 1657019-1657070 | 1 | hypothetical protein (BLC1_RS06990) | 1 |
| | 16.16 | 356927-356986 | 1 | mannose-1-phosphate guanylyltransferase (BLC1_RS01455) | 176 |
| Bifidobacterium animalis subsp. lactis CNCM I-2494 (NC_017215.1) | 17.58 | 1703911-1703861 | -1 | mannan endo-1,4-beta-mannosidase (BALAC2494_RS07200) | 12 |
| | 17.28 | 1661994-1662045 | 1 | hypothetical protein (BALAC2494_RS07005) | 1 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 16.16 | 357074-357133 | 1 | mannose-1-phosphate guanylyltransferase (BALAC2494_RS01455) | 176 |
| Bifidobacterium animalis subsp. lactis DSM 10140 (NC_012815.1) | 17.58 | 1699041-1698991 | -1 | mannan endo-1,4-beta-mannosidase (BALAT_RS07180) | 12 |
|  | 17.28 | 1657091-1657142 | 1 | hypothetical protein (BALAT_RS06985) | 1 |
|  | 16.16 | 357063-357122 | 1 | mannose-1-phosphate guanylyltransferase (BALAT_RS01455) | 176 |
| Bifidobacterium animalis subsp. lactis KLDS2.0603 (NZ_CP007522.1) | 17.58 | 1698786-1698736 | -1 | mannan endo-1,4-beta-mannosidase (U723_RS07185) | 12 |
|  | 17.28 | 1656836-1656887 | 1 | hypothetical protein (U723_RS06990) | 1 |
|  | 16.16 | 356896-356955 | 1 | mannose-1-phosphate guanylyltransferase (U723_RS01450) | 176 |
| Bifidobacterium animalis subsp. lactis strain BF052 (NZ_CP009045.1) | 17.58 | 1698958-1698908 | -1 | mannan endo-1,4-beta-mannosidase (GU89_RS07185) | 12 |
|  | 17.28 | 1657008-1657059 | 1 | hypothetical protein (GU89_RS06990) | 1 |
|  | 16.16 | 356897-356956 | 1 | mannose-1-phosphate guanylyltransferase (GU89_RS01450) | 176 |
| Bifidobacterium animalis subsp. lactis V9 (NC_017217.1) | 17.58 | 1704610-1704560 | -1 | mannan endo-1,4-beta-mannosidase (BALV_RS07195) | 12 |
|  | 17.28 | 1662660-1662711 | 1 | hypothetical protein (BALV_RS07000) | 1 |
|  | 16.16 | 357064-357123 | 1 | mannose-1-phosphate guanylyltransferase (BALV_RS01455) | 176 |
|  | 16.16 | 357063-357123 | 1 | mannose-1-phosphate guanylyltransferase (BAA6_RS01455) | 176 |
| Bifidobacterium asteroides PRL2011 (NC_018720.1) | 18.66 | 1405400-1405348 | -1 | MFS transporter (BAST_RS05485) | 9 |
|  | 16.49 | 389675-389732 | 1 | NAD(P)/FAD-dependent oxidoreductase | 79 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (BAST_RS01530) | |
| | 15.55 | 2013830-2013775 | -1 | type II toxin-antitoxin system antitoxin, RelB/DinJ family (BAST_RS08055) | 62 |
| Bifidobacterium asteroides strain DSM 20089 (NZ_CP017696.1) | 18.66 | 1186153-1186101 | -1 | MFS transporter (BA20089_RS04650) | 87 |
| | 16.49 | 170394-170451 | 1 | NAD(P)/FAD-dependent oxidoreductase (BA20089_RS00705) | 79 |
| | 15.55 | 1794587-1794532 | -1 | type II toxin-antitoxin system antitoxin, RelB/DinJ family (BA20089_RS07265) | 62 |
| Bifidobacterium bifidum ATCC 29521 = JCM 1255 = DSM 20456 DNA (NZ_AP012323.1) | 18.3 | 63952-63901 | -1 | IS256 family transposase (BBBF_RS00250) | 27 |
| | 17.02 | 1140470-1140529 | 1 | PadR family transcriptional regulator (BBBF_RS04740) | 103 |
| | 16.89 | 686128-686184 | 1 | LysM peptidoglycan-binding domain-containing protein (BBBF_RS02700) | 105 |
| | 16.42 | 1744975-1744913 | -1 | thymidylate synthase (BBBF_RS07360) | 102 |
| Bifidobacterium bifidum BGN4 (NC_017999.1) | 18.45 | 647226-647282 | 1 | LysM peptidoglycan-binding domain-containing protein (BBB_RS02605) | 105 |
| | 17.02 | 1082856-1082915 | 1 | PadR family transcriptional regulator (BBB_RS04385) | 103 |
| | 16.42 | 1733401-1733339 | -1 | thymidylate synthase (BBB_RS07205) | 102 |
| Bifidobacterium bifidum PRL2010 (NC_014638.1) | 17.02 | 1134880-1134939 | 1 | family transcriptional regulator PadR (BBPR_0951) | 103 |
| | 16.89 | 681907-681963 | 1 | hypothetical protein (BBPR_0543) | 105 |
| | 16.42 | 1740876-1740814 | -1 | thymidylate synthase (BBPR_1477) | 102 |
| Bifidobacterium bifidum S17 (NC_014616.1) | 18.3 | 480016-480067 | 1 | IS256 family transposase (BBIF_RS02050) | 27 |
| | 17.02 | 1104648-1104707 | 1 | PadR family transcriptional regulator | 103 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (BBIF_RS04590) | |
| | 16.42 | 1713278-1713216 | -1 | thymidylate synthase (BBIF_RS07240) | 102 |
| Bifidobacterium bifidum strain BF3 (NZ_CP010412.1) | 17.02 | 1159989-1160048 | 1 | PadR family transcriptional regulator (RY70_RS04590) | 103 |
| | 16.42 | 1806969-1806907 | -1 | thymidylate synthase (RY70_RS07425) | 102 |
| | 15.09 | 732893-732949 | 1 | LysM peptidoglycan-binding domain-containing protein (RY70_RS02830) | 105 |
| Bifidobacterium breve 12L (NZ_CP006711.1) | 20.6 | 1516065-1516101 | 1 | serpin family protein (B12L_RS06350) | 31 |
| | 17.59 | 775796-775729 | -1 | Txe/YoeB family addiction module toxin (B12L_RS03070) | 59 |
| | 16.26 | 1347579-1347527 | -1 | recombinase RecA (B12L_RS05660) | 55 |
| Bifidobacterium breve 689b (NZ_CP006715.1) | 20.83 | 665275-665329 | 1 | hypothetical protein (B689B_RS02670) | 8 |
| | 20.6 | 1592334-1592390 | 1 | serpin family protein (B689B_RS06770) | 41 |
| | 17.59 | 872602-872535 | -1 | Txe/YoeB family addiction module toxin (B689B_RS03565) | 59 |
| | 17.2 | 602556-602495 | -1 | ATPase AAA (B689B_RS02450) | 1066 |
| | 16.38 | 258222-258273 | 1 | IS3 family transposase (B689B_RS00960) | 183 |
| | 16.26 | 1421977-1421925 | -1 | recombinase RecA (B689B_RS06075) | 55 |
| Bifidobacterium breve ACS-071-V-Sch8b (NC_017218.1) | 20.6 | 652555-652499 | -1 | serpin family protein (HMPREF9228_RS02650) | 5 |
| | 17.59 | 1334083-1334150 | 1 | Txe/YoeB family addiction module toxin (HMPREF9228_RS05665) | 59 |
| | 17.2 | 1591103-1591164 | 1 | ATPase AAA (HMPREF9228_RS06745) | 1066 |
| | 16.38 | 282198-282249 | 1 | IS3 family transposase (HMPREF9228_RS01080) | 183 |
| | 16.26 | 822879-822931 | 1 | recombinase RecA | 55 |

| Organism<br>(Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs<br>(Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (HMPREF9228_RS03350) | |
| Bifidobacterium breve DSM 20213 = JCM 1192 DNA (NZ_AP012324.1) | 20.6 | 1590628-1590684 | 1 | serpin family protein (BBBR_RS06980) | 41 |
| | 17.59 | 788421-788354 | -1 | Txe/YoeB family addiction module toxin (BBBR_RS03210) | 59 |
| | 17.2 | 548890-548829 | -1 | ATPase AAA (BBBR_RS02190) | 1066 |
| | 16.26 | 1382408-1382356 | -1 | recombinase RecA (BBBR_RS05995) | 55 |
| Bifidobacterium breve JCM 7017 (NZ_CP006712.1) | 20.6 | 1542383-1542439 | 1 | serpin family protein (B7017_RS06485) | 41 |
| | 18.02 | 578576-578515 | -1 | ATPase AAA (B7017_RS02265) | 7 |
| | 17.59 | 816831-816764 | -1 | Txe/YoeB family addiction module toxin (B7017_RS03260) | 59 |
| | 16.26 | 1371305-1371253 | -1 | recombinase RecA (B7017_RS05775) | 55 |
| Bifidobacterium breve JCM 7019 (NZ_CP006713.1) | 21.11 | 1022299-1022374 | 1 | sugar ABC transporter permease (B7019_RS04300) | 18 |
| | 20.6 | 1627645-1627701 | 1 | serpin family protein (B7019_RS07170) | 41 |
| | 18.3 | 481305-481356 | 1 | IS256 family transposase (B7019_RS02000) | 27 |
| | 17.67 | 560496-560435 | -1 | ATPase AAA (B7019_RS02290) | 7 |
| | 17.08 | 2153758-2153815 | 1 | hypothetical protein (B7019_RS09445) | 51 |
| | 16.26 | 1449520-1449468 | -1 | recombinase RecA (B7019_RS06425) | 55 |
| Bifidobacterium breve NCFB 2258 (NZ_CP006714.1) | 20.6 | 1543740-1543796 | 1 | serpin family protein (B2258_RS06500) | 41 |
| | 17.59 | 819838-819771 | -1 | Txe/YoeB family addiction module toxin (B2258_RS03295) | 59 |
| | 17.2 | 580193-580132 | -1 | ATPase AAA (B2258_RS02275) | 1066 |
| | 16.38 | 253813-253864 | 1 | IS3 family transposase (B2258_RS00940) | 183 |
| | 16.26 | 1371275-1371223 | -1 | DNA recombination/repair protein RecA | 55 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (B2258_RS05785) | |
| Bifidobacterium breve S27 (NZ_CP006716.1) | 20.6 | 1587761-1587817 | 1 | serpin family protein (BS27_RS06675) | 41 |
| | 17.59 | 860748-860681 | -1 | Txe/YoeB family addiction module toxin (BS27_RS03455) | 59 |
| | 17.2 | 624084-624023 | -1 | ATPase AAA (BS27_RS02455) | 1066 |
| | 16.38 | 285280-285331 | 1 | IS3 family transposase (BS27_RS01055) | 183 |
| | 16.26 | 1420569-1420517 | -1 | recombinase RecA (BS27_RS05990) | 55 |
| Bifidobacterium breve strain BR3 (NZ_CP010413.1) | 20.6 | 521221-521165 | -1 | serpin family protein (RY69_RS02295) | 41 |
| | 17.2 | 1598844-1598905 | 1 | ATPase AAA (RY69_RS07155) | 1066 |
| | 16.13 | 1051877-1051923 | 1 | hypothetical protein (RY69_RS04810) | 208 |
| | 16.01 | 681548-681600 | 1 | recombinase RecA (RY69_RS02960) | 55 |
| Bifidobacterium breve strain LMC520 (NZ_CP019596.1) | 20.6 | 1647336-1647392 | 1 | serpin family protein (BBL520_RS07465) | 41 |
| | 17.2 | 611214-611153 | -1 | ATPase AAA (BBL520_RS02640) | 1066 |
| | 16.13 | 1120327-1120281 | -1 | hypothetical protein (BBL520_RS04915) | 208 |
| | 16.01 | 1476706-1476654 | -1 | recombinase RecA (BBL520_RS06735) | 55 |
| Bifidobacterium breve UCC2003 (NC_020517.1) | 21.11 | 419361-419436 | 1 | sugar ABC transporter permease (BBR_RS11870) | 18 |
| | 20.6 | 1647321-1647377 | 1 | serpin family protein (BBR_RS17245) | 41 |
| | 18.17 | 396084-396033 | -1 | IS256 family transposase (BBR_RS11755) | 27 |
| | 17.59 | 907425-907358 | -1 | Txe/YoeB family addiction module toxin (BBR_RS13945) | 59 |
| | 17.2 | 673882-673821 | -1 | ATPase AAA (BBR_RS12970) | 1066 |
| | 16.38 | 300568-300619 | 1 | IS3 family transposase (BBR_RS11370) | 183 |
| | 16.26 | 1476776-1476724 | -1 | recombinase RecA (BBR_RS16530) | 55 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 16.13 | 1198206-1198160 | -1 | hypothetical protein (BBR_RS15265) | 208 |
| Bifidobacterium catenulatum DSM 16992 = JCM 1194 = LMG 11043 DNA (NZ_AP012325.1) | 21.82 | 603559-603619 | 1 | hypothetical protein (BBCT_RS02540) | 11 |
| | 20.47 | 1858333-1858280 | -1 | DUF2142 domain-containing protein (BBCT_RS07800) | 17 |
| | 18.36 | 1553523-1553467 | -1 | MFS transporter (BBCT_RS06595) | 54 |
| | 17.79 | 279728-279782 | 1 | 50S ribosomal protein L19 (BBCT_RS01090) | 358 |
| | 17.56 | 392162-392214 | 1 | MFS transporter (BBCT_RS01550) | 13 |
| | 16.14 | 500565-500623 | 1 | sugar ABC transporter substrate-binding protein (BBCT_RS02095) | 38 |
| Bifidobacterium coryneforme strain LMG18911 (NZ_CP007287.1) | 23.63 | 1150582-1150528 | -1 | MFS transporter (bcor_RS04490) | 46 |
| | 16.33 | 1691827-1691880 | 1 | VOC family protein (bcor_RS06865) | 17 |
| Bifidobacterium dentium Bd1 (NC_013714.1) | 20.03 | 299280-299223 | -1 | arabinan endo-1,5-alpha-L-arabinosidase (BDP_RS01135) | 39 |
| | 19.4 | 2559866-2559797 | -1 | alpha-glucosidase (BDP_RS10610) | 2 |
| | 17.73 | 1424860-1424909 | 1 | ABC transporter substrate-binding protein (BDP_RS06160) | 8 |
| | 17.32 | 166080-166138 | 1 | sugar ABC transporter substrate-binding protein (BDP_RS00645) | 121 |
| | 16.87 | 672199-672249 | 1 | ABC transporter substrate-binding protein (BDP_RS02780) | 29 |
| | 16.19 | 1524990-1524937 | -1 | alcohol dehydrogenase (BDP_RS06575) | 21 |
| | 15.12 | 212515-212569 | 1 | LacI family DNA-binding transcriptional regulator (BDP_RS00805) | 203 |
| Bifidobacterium dentium JCM 1195 = DSM 20436 DNA (NZ_AP012326.1) | 20.03 | 299282-299225 | -1 | arabinan endo-1,5-alpha-L-arabinosidase (BBDE_RS01135) | 39 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 19.4 | 2559168-2559099 | -1 | threonine ammonia-lyase (BBDE_RS10610) | 2 |
|  | 17.73 | 1424863-1424912 | 1 | ABC transporter substrate-binding protein (BBDE_RS06170) | 8 |
|  | 17.32 | 166081-166139 | 1 | sugar ABC transporter substrate-binding protein (BBDE_RS00645) | 121 |
|  | 16.87 | 672200-672250 | 1 | ABC transporter substrate-binding protein (BBDE_RS02785) | 29 |
|  | 16.19 | 1524993-1524940 | -1 | alcohol dehydrogenase (BBDE_RS06580) | 21 |
|  | 15.12 | 212517-212571 | 1 | LacI family transcriptional regulator (BBDE_RS00805) | 203 |
| Bifidobacterium indicum LMG 11587 = DSM 20214 (NZ_CP006018.1) | 23.23 | 1129914-1129860 | -1 | MFS transporter (BINDI_RS04395) | 46 |
|  | 16.33 | 1664773-1664826 | 1 | VOC family protein (BINDI_RS06740) | 17 |
| Bifidobacterium kashiwanohense JCM 15439 = DSM 21854 DNA (NZ_AP012327.1) | 23.71 | 2246953-2246903 | -1 | sugar ABC transporter substrate-binding protein (BBKW_RS09475) | 154 |
| Bifidobacterium kashiwanohense JCM 15439 = DSM 21854 DNA (NZ_AP012327.1) | 16.87 | 2142313-2142256 | -1 | alpha/beta hydrolase (BBKW_RS09080) | 15 |
|  | 16.87 | 2142324-2142256 | -1 | alpha/beta hydrolase (BBKW_RS09080) | 15 |
|  | 16.14 | 557790-557851 | 1 | sugar ABC transporter substrate-binding protein (BBKW_RS02345) | 38 |
|  | 15.53 | 552772-552725 | -1 | O-acetylhomoserine aminocarboxypropyltransferase/cysteine synthase (BBKW_RS02325) | 12 |
|  | 15.53 | 552810-552725 | -1 | O-acetylhomoserine aminocarboxypropyltransferase/cysteine synthase (BBKW_RS02325) | 12 |
|  | 15.21 | 2152210-2152151 | -1 | sugar ABC transporter substrate-binding protein (BBKW_RS09115) | 20 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Bifidobacterium kashiwanohense PV20-2 (NZ_CP007456.1) | 20.44 | 334680-334711 | 1 | 50S ribosomal protein L19 (AH68_RS01310) | 369 |
| | 20.21 | 2161764-2161708 | -1 | sugar ABC transporter substrate-binding protein (AH68_RS09265) | 147 |
| | 18.59 | 1763578-1763522 | -1 | MFS transporter (AH68_RS07705) | 54 |
| | 17.57 | 560584-560537 | -1 | hypothetical protein (AH68_RS02360) | 12 |
| | 17.55 | 2261564-2261614 | 1 | beta-glucosidase (AH68_RS09650) | 3 |
| | 15.71 | 1901260-1901199 | -1 | hypothetical protein (AH68_RS08170) | 42 |
| | 15.33 | 830090-830149 | 1 | hypothetical protein (AH68_RS03510) | 322 |
| Bifidobacterium longum DJO10A (NC_010816.1) | 18.58 | 1451062-1451004 | -1 | PEGA domain-containing protein (BLD_RS06365) | 10 |
| | 15.38 | 287435-287383 | -1 | aldose 1-epimerase (BLD_RS01220) | 23 |
| Bifidobacterium longum DNA, strain: 105-A (NZ_AP014658.1) | 21.19 | 2161684-2161620 | -1 | glycosyl hydrolase family 43 (BL105A_RS08940) | 31 |
| | 18.58 | 198738-198796 | 1 | serine protease (BL105A_RS00830) | 10 |
| | 16.34 | 631129-631190 | 1 | hypothetical protein (BL105A_RS02540) | 2 |
| | 15.44 | 2064960-2064904 | -1 | glycosyltransferase family 2 protein (BL105A_RS08660) | 73 |
| | 15.38 | 1353107-1353159 | 1 | aldose 1-epimerase (BL105A_RS05765) | 23 |
| Bifidobacterium longum NCC2705 (NC_004307.2) | 15.38 | 261999-261947 | -1 | hypothetical protein (aldose 1-epimerase) (BL1359) | 23 |
| | 18.58 | 208320-208378 | 1 | PEGA domain-containing protein (B624_RS00850) | 10 |
| | 15.44 | 2087311-2087255 | -1 | glycosyltransferase family 2 protein (B624_RS08790) | 73 |
| | 15.38 | 892689-892637 | -1 | aldose 1-epimerase (B624_RS03630) | 23 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Bifidobacterium longum strain BG7 (NZ_CP010453.1) | 18.58 | 221198-221256 | 1 | serine protease (BBG7_RS00940) | 10 |
| | 18.3 | 510354-510303 | -1 | IS256 family transposase (BBG7_RS02240) | 27 |
| | 18.21 | 2252785-2252838 | 1 | cell wall-binding repeat-containing protein (BBG7_RS10960) | 22 |
| | 15.38 | 1508758-1508810 | 1 | aldose 1-epimerase (BBG7_RS06550) | 23 |
| | 15.11 | 667887-667947 | 1 | hypothetical protein (BBG7_RS02825) | 2 |
| Bifidobacterium longum strain BXY01 (NZ_CP008885.1) | 20.6 | 1607611-1607667 | 1 | serpin family protein (GS08_RS06860) | 5 |
| | 16.71 | 1867745-1867806 | 1 | gfo/Idh/MocA family oxidoreductase (GS08_RS07885) | 36 |
| | 16.38 | 239917-239968 | 1 | IS3 family transposase (GS08_RS10520) | 183 |
| | 16.01 | 815425-815493 | 1 | GntR family transcriptional regulator (GS08_RS03335) | 168 |
| Bifidobacterium longum subsp. infantis 157F DNA (NC_015052.1) | 18.58 | 201502-201560 | 1 | serine protease (BLIF_RS00825) | 10 |
| | 16.34 | 629092-629153 | 1 | DUF2975 domain-containing protein (BLIF_RS02475) | 2 |
| | 15.38 | 1482075-1482127 | 1 | aldose 1-epimerase (BLIF_RS06550) | 23 |
| Bifidobacterium longum subsp. infantis ATCC 15697 = JCM 1222 = DSM 20088 DNA (NC_017219.1) | 22.89 | 918066-918010 | -1 | serpin family protein (BLIJ_RS03995) | 41 |
| Bifidobacterium longum subsp. infantis ATCC 15697 = JCM 1222 = DSM 20088 DNA (NC_017219.1) | 20.21 | 47851-47907 | 1 | sugar ABC transporter substrate-binding protein (BLIJ_RS00230) | 147 |
| | 18.17 | 321440-321389 | -1 | IS256 family transposase (BLIJ_RS01405) | 27 |
| | 16.8 | 2786662-2786609 | -1 | glycosyl hydrolase (BLIJ_RS12785) | 78 |
| | 15.91 | 1483251-1483310 | 1 | hypothetical protein (BLIJ_RS06700) | 91 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.84 | 683987-683926 | -1 | gfo/Idh/MocA family oxidoreductase (BLIJ_RS03070) | 36 |
| Bifidobacterium longum subsp. infantis ATCC 15697 (NC_011593.1) | 22.89 | 918275-918219 | -1 | serpin family protein (BLON_RS03995) | 5 |
|  | 20.21 | 48060-48116 | 1 | sugar ABC transporter substrate-binding protein (BLON_RS00235) | 147 |
|  | 18.17 | 321649-321598 | -1 | IS256 family transposase (BLON_RS01410) | 27 |
|  | 16.8 | 2790661-2790608 | -1 | glycosyl hydrolase (BLON_RS12795) | 78 |
|  | 15.91 | 1483460-1483519 | 1 | hypothetical protein (BLON_RS06700) | 91 |
|  | 15.84 | 684195-684134 | -1 | gfo/Idh/MocA family oxidoreductase (BLON_RS03065) | 36 |
| Bifidobacterium longum subsp. infantis genome assembly Bifidobacterium longum subsp. infantis CECT7210 (NZ_LN824140.1) | 18.58 | 2159815-2159873 | 1 | PEGA domain-containing protein (BN1726_RS09745) | 10 |
|  | 16.34 | 153738-153799 | 1 | hypothetical protein (BN1726_RS00600) | 2 |
|  | 16.01 | 278919-278987 | 1 | GntR family transcriptional regulator (BN1726_RS01165) | 168 |
|  | 15.38 | 1010982-1011034 | 1 | aldose 1-epimerase (BN1726_RS04805) | 23 |
| Bifidobacterium longum subsp. infantis strain BT1 (NZ_CP010411.1) | 18.3 | 1097527-1097476 | -1 | IS256 family transposase (RY67_RS04575) | 27 |
|  | 18.3 | 1998526-1998475 | -1 | IS256 family transposase (RY67_RS08410) | 27 |
|  | 17.24 | 343541-343452 | -1 | sugar ABC transporter permease (RY67_RS01365) | 29 |
|  | 16.8 | 686952-686899 | -1 | glycosyl hydrolase (RY67_RS02785) | 78 |
|  | 16.38 | 1001169-1001220 | 1 | IS3 family transposase (RY67_RS04170) | 183 |
|  | 16.19 | 1838541-1838489 | -1 | aldose epimerase (RY67_RS07740) | 23 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 16.01 | 1702086-1702033 | -1 | serpin family protein (RY67_RS07215) | 19 |
| | 15.84 | 1434174-1434113 | -1 | gfo/Idh/MocA family oxidoreductase (RY67_RS06135) | 36 |
| | 15.37 | 473578-473639 | 1 | fucose isomerase (RY67_RS01995) | 7 |
| | 15.11 | 76204-76144 | -1 | hypothetical protein (RY67_RS00360) | 2 |
| Bifidobacterium longum subsp. longum BBMN68 (NC_014656.1) | 21.19 | 1762029-1762093 | 1 | glycosyl hydrolase family 43 (BBMN68_RS07380) | 31 |
| | 18.58 | 1432813-1432755 | -1 | PEGA domain-containing protein (BBMN68_RS06090) | 10 |
| | 16.62 | 304709-304657 | -1 | aldose 1-epimerase (BBMN68_RS01270) | 23 |
| Bifidobacterium longum subsp. longum GT15 (NZ_CP006741.1) | 18.58 | 282168-282226 | 1 | serine protease (BLGT_RS01135) | 10 |
| | 15.38 | 1526578-1526630 | 1 | aldose 1-epimerase (BLGT_RS06480) | 23 |
| | 15.11 | 766087-766147 | 1 | hypothetical protein (BLGT_RS03075) | 2 |
| Bifidobacterium longum subsp. longum JCM 1217 DNA (NC_015067.1) | 21.19 | 2254131-2254067 | -1 | glycosyl hydrolase family 43 (BLLJ_RS09555) | 31 |
| | 18.58 | 216505-216563 | 1 | PEGA domain-containing protein (BLLJ_RS00875) | 10 |
| | 15.38 | 1456774-1456826 | 1 | aldose 1-epimerase (BLLJ_RS06415) | 23 |
| Bifidobacterium longum subsp. longum JDM301 (NC_014169.1) | 20.6 | 1608192-1608228 | 1 | serpin family protein (BLJ_RS06860) | 5 |
| | 16.71 | 1864966-1865027 | 1 | gfo/Idh/MocA family oxidoreductase (BLJ_RS07880) | 36 |
| | 16.38 | 239921-239972 | 1 | IS3 family transposase (BLJ_RS00980) | 183 |
| | 16.01 | 814071-814139 | 1 | GntR family transcriptional regulator (BLJ_RS03330) | 168 |
| Bifidobacterium longum subsp. longum KACC 91563 (NC_017221.1) | 18.58 | 2053635-2053577 | -1 | PEGA domain-containing protein (BLNIAS_RS08605) | 10 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.38 | 858755-858703 | -1 | aldose 1-epimerase (BLNIAS_RS03470) | 23 |
|  | 15.11 | 1643808-1643748 | -1 | hypothetical protein (BLNIAS_RS06980) | 2 |
| Bifidobacterium longum subsp. longum strain AH1206 (NZ_CP016019.1) | 21.19 | 2295601-2295537 | -1 | glycosyl hydrolase family 43 (BL1206_RS09965) | 31 |
|  | 15.38 | 1497218-1497270 | 1 | aldose 1-epimerase (BL1206_RS06775) | 23 |
|  | 15.35 | 134683-134747 | 1 | sugar ABC transporter substrate-binding protein (BL1206_RS00535) | 29 |
| Bifidobacterium longum subsp. longum strain CCUG30698 (NZ_CP011965.1) | 21.19 | 1681266-1681330 | 1 | glycosyl hydrolase family 43 (BBL306_RS07430) | 31 |
|  | 18.58 | 203778-203836 | 1 | serine protease (BBL306_RS00850) | 10 |
|  | 16.34 | 637500-637561 | 1 | hypothetical protein (BBL306_RS02550) | 2 |
|  | 15.38 | 1554627-1554679 | 1 | aldose 1-epimerase (BBL306_RS07005) | 23 |
|  | 18.58 | 193570-193628 | 1 | serine protease (B8809_RS00770) | 10 |
|  | 15.38 | 1367183-1367235 | 1 | aldose 1-epimerase (B8809_RS05795) | 23 |
| Bifidobacterium pseudocatenulatum DSM 20438 = JCM 1200 = LMG 10505 DNA (NZ_AP012330.1) | 20.21 | 2073057-2073001 | -1 | sugar ABC transporter substrate-binding protein (BBPC_RS08455) | 146 |
|  | 18.36 | 1670440-1670384 | -1 | MFS transporter (BBPC_RS06975) | 54 |
|  | 16.79 | 210641-210700 | 1 | alpha-arabinofuranosidase (BBPC_RS00790) | 21 |
|  | 16.61 | 429639-429691 | 1 | MFS transporter (BBPC_RS01680) | 13 |
|  | 16.14 | 582184-582242 | 1 | sugar ABC transporter substrate-binding protein (BBPC_RS02385) | 38 |
|  | 15.46 | 1217386-1217319 | -1 | hypothetical protein (BBPC_RS05115) | 18 |
| Bifidobacterium pseudolongum PV8-2 (NZ_CP007457.1) | 19.39 | 254651-254719 | 1 | alpha-N-arabinofuranosidase (AH67_RS01070) | 10 |
|  | 19.19 | 59994-59941 | -1 | ABC transporter substrate-binding protein | 2 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (AH67_RS00270) | |
| Bifidobacterium pseudolongum strain DSM 20092 (NZ_CP017695.1) | 15.7 | 1636840-1636906 | 1 | LacI family transcriptional regulator (BP20092_RS06750) | 5 |
| Bifidobacterium pseudolongum strain UMB-MBP-01 (NZ_CP022544.1) | 19.19 | 60846-60793 | -1 | sugar ABC transporter ATP-binding protein (BPSOL_RS00270) | 2 |
| | 15.18 | 1884464-1884403 | -1 | ABC transporter substrate-binding protein (BPSOL_RS08000) | 4 |
| Bifidobacterium scardovii JCM 12489 = DSM 13734 DNA (NZ_AP012331.1) | 15.74 | 1087095-1087156 | 1 | hypothetical protein (BBSC_RS04465) | 2 |
| | 15.53 | 2861565-2861616 | 1 | amidohydrolase family protein (BBSC_RS11610) | 6 |
| | 15.32 | 2977285-2977227 | -1 | beta-glucosidase (BBSC_RS12000) | 11 |
| Brachybacterium sp. P6-10-X1 (NZ_CP017297.1) | 20.33 | 3019349-3019293 | -1 | HNH endonuclease (BH708_RS13655) | 24 |
| | 20.33 | 753990-754046 | 1 | HNH endonuclease (BH708_RS03375) | 24 |
| | 20.33 | 3849341-3849285 | -1 | hypothetical protein (BH708_RS17135) | 24 |
| Brevibacterium aurantiacum strain SMQ-1335 (NZ_CP017150.1) | 20.67 | 3576760-3576710 | -1 | DNA-binding response regulator (BLSMQ_RS16455) | 56 |
| | 17.36 | 2225991-2226056 | 1 | SDR family NAD(P)-dependent oxidoreductase (BLSMQ_RS10360) | 34 |
| | 17.32 | 1661339-1661274 | 1 | SAF domain-containing protein (BLSMQ_RS07595) | 84 |
| | 16.49 | 3773876-3773930 | 1 | 50S ribosomal protein L36 (BLSMQ_RS17335) | 2 |
| Brevibacterium linens strain BS258 (NZ_CP014869.1) | 18.51 | 2010339-2010393 | 1 | hypothetical protein (A2T55_RS08990) | 23 |
| | 16.46 | 2170380-2170321 | -1 | 30S ribosomal protein S1 (A2T55_RS09725) | 100 |
| | 15.22 | 378305-378358 | 1 | TetR family transcriptional regulator (A2T55_RS01660) | 167 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Candidatus Nanopelagicus hibericus isolate MMS-21-160 (NZ_CP016771.1) | 23.73 | 508869-508923 | 1 | DNA-binding response regulator (B1s21160_RS02710) | 358 |
| | 15.66 | 1070146-1070090 | -1 | NAD(P)/FAD-dependent oxidoreductase (B1s21160_RS05485) | 67 |
| Candidatus Planktophila dulcis isolate MMS-21-155 (NZ_CP016770.1) | 17.48 | 10956-11027 | 1 | orotate phosphoribosyltransferase (A1s21155_RS00055) | 25 |
| | 17.48 | 10974-11045 | 1 | orotate phosphoribosyltransferase (A1sIA53_RS00060) | 25 |
| Candidatus Planktophila dulcis isolate MMS-IIA-65 (NZ_CP016777.1) | 22.95 | 10943-11014 | 1 | orotate phosphoribosyltransferase (A1sIIA65_RS00055) | 25 |
| Candidatus Planktophila sulfonica isolate MMS-IA-56 (NZ_CP016773.1) | 26.26 | 11044-11115 | 1 | orotate phosphoribosyltransferase (A1sIA56_RS00055) | 25 |
| | 17.87 | 883253-883188 | -1 | 30S ribosome-binding factor RbfA (A1sIA56_RS04440) | 53 |
| | 16.85 | 315907-315957 | 1 | alpha/beta hydrolase (A1sIA56_RS01595) | 154 |
| Candidatus Planktophila versatilis isolate MMS-IA-105 (NZ_CP016775.1) | 20.38 | 10992-11063 | 1 | orotate phosphoribosyltransferase (A1sIA105_RS00055) | 25 |
| | 15.56 | 288544-288594 | 1 | MarR family transcriptional regulator (A1sIA105_RS01510) | 345 |
| Candidatus Rhodoluna planktonica strain MWH-Dar1 (NZ_CP015208.1) | 16.19 | 226162-226228 | 1 | 2-keto-myo-inositol dehydratase (A4Z71_RS01140) | 9 |
| Catenulispora acidiphila DSM 44928 (NC_013131.1) | 19.55 | 8698218-8698252 | 1 | MarR family transcriptional regulator (CACI_RS37065) | 8 |
| | 18.91 | 3728433-3728363 | -1 | peptidase S53 (CACI_RS16775) | 166 |
| Cellulomonas gilvus ATCC 13127 (NC_015671.1) | 22.44 | 2826924-2826867 | -1 | alpha-galactosidase (CELGI_RS12885) | 4 |
| Clavibacter michiganensis strain | 16.87 | 2513441-2513384 | -1 | extracellular solute-binding protein | 5 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| PF008 (NZ_CP012573.1) | | | | (AES38_RS11725) | |
| Clavibacter michiganensis subsp. insidiosus strain R1-1 (NZ_CP011043.1) | 17.58 | 2403997-2403940 | -1 | carbohydrate-binding protein (VO01_RS11345) | 5 |
| Clavibacter michiganensis subsp. michiganensis NCPPB 382 complete genome (NC_009480.1) | 19.13 | 2749746-2749689 | -1 | carbohydrate-binding protein (CMM_RS12990) | 5 |
| | 18.53 | 2521590-2521533 | -1 | sugar ABC transporter substrate-binding protein (CMN_RS11770) | 5 |
| Cnuibacter physcomitrellae strain XA(T) (NZ_CP020715.1) | 15.94 | 3524655-3524708 | 1 | hypothetical protein (B5808_RS16425) | 25 |
| Collinsella aerofaciens strain indica (NZ_CP024160.1) | 22.55 | 94937-94997 | 1 | LysR family transcriptional regulator (CSV91_RS00445) | 135 |
| | 17.26 | 1874478-1874557 | 1 | hypothetical protein (CSV91_RS08165) | 303 |
| | 16.75 | 245313-245260 | -1 | ketopantoate reductase family protein (CSV91_RS01110) | 76 |
| | 16.69 | 1415774-1415725 | -1 | LacI family DNA-binding transcriptional regulator (CSV91_RS06205) | 139 |
| Conexibacter woesei DSM 14684 (NC_013739.1) | 17.68 | 1067939-1067888 | -1 | hypothetical protein (CWOE_RS05070) | 186 |
| Corynebacterium ammoniagenes DSM 20306 strain 9.6 (NZ_CP009244.1) | 19.53 | 2657735-2657682 | -1 | 30S ribosomal protein S6 (CAMM_RS12160) | 113 |
| | 19.1 | 2166420-2166366 | -1 | thymidylate kinase (CAMM_RS09935) | 26 |
| | 16.84 | 2331655-2331593 | -1 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (CAMM_RS10675) | 104 |
| | 15.22 | 2511464-2511408 | -1 | aldehyde dehydrogenase (CAMM_RS11515) | 102 |
| Corynebacterium ammoniagenes | 19.53 | 2744317-2744264 | -1 | 30S ribosomal protein S6 | 113 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| strain KCCM 40472 (NZ_CP019705.1) | | | | (CA40472_RS12530) | |
| | 19.1 | 2253006-2252952 | -1 | thymidylate kinase (CA40472_RS10300) | 26 |
| | 16.84 | 2418238-2418176 | -1 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase (CA40472_RS11040) | 104 |
| | 15.22 | 2598046-2597990 | -1 | aldehyde dehydrogenase (CA40472_RS11885) | 102 |
| Corynebacterium argentoratense DSM 44202 (NC_022198.1) | 18.42 | 34993-34937 | -1 | hypothetical protein (CARG_RS00190) | 349 |
| | 15.49 | 288997-289056 | 1 | adenylate kinase (CARG_RS01425) | 97 |
| | 15.27 | 841374-841433 | 1 | 30S ribosomal protein S1 (CARG_RS04130) | 85 |
| Corynebacterium atypicum strain R2070 (NZ_CP008944.1) | 19.2 | 1161209-1161153 | -1 | PaaI family thioesterase (CATYP_RS05335) | 31 |
| Corynebacterium aurimucosum ATCC 700975 (NC_012590.1) | 18.4 | 844165-844219 | 1 | peptidyl-prolyl cis-trans isomerase (CAURI_RS04070) | 44 |
| Corynebacterium callunae DSM 20147 (NC_020506.1) | 16.89 | 97710-97647 | -1 | hypothetical protein (H924_RS00450) | 276 |
| | 16.27 | 1149035-1149091 | 1 | hypothetical protein (H924_RS05470) | 7 |
| Corynebacterium camporealensis strain DSM 44610 (NZ_CP011311.1) | 15.73 | 906581-906635 | 1 | DUF4245 domain-containing protein (UL81_RS04305) | 149 |
| Corynebacterium casei LMG S-19264 (NZ_CP004350.1) | 19.66 | 282854-282795 | -1 | glycosyltransferase family 2 protein (CCASEI_RS01445) | 421 |
| | 15.69 | 2910386-2910434 | 1 | hypothetical protein (CCASEI_RS13210) | 188 |
| Corynebacterium crudilactis strain JZ16 (NZ_CP015622.1) | 18.11 | 2138588-2138650 | 1 | tRNA-Asn (ccrud_RS09975) | 6 |
| Corynebacterium cystitidis strain NCTC11863 1 (NZ_LT906473.1) | 18.98 | 15053-15109 | 1 | nucleotide exchange factor GrpE (CKV99_RS00075) | 103 |
| Corynebacterium deserti GIMN1.010 | 16.66 | 2493014-2492961 | -1 | glucosamine-6-phosphate deaminase | 4 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| (NZ_CP009220.1) | | | | (CDES_RS11560) | |
| | 15.31 | 1150457-1150513 | 1 | DEAD/DEAH box helicase (CDES_RS05425) | 7 |
| Corynebacterium diphtheriae 241 (NC_016782.1) | 16.24 | 540599-540658 | 1 | membrane protein (CD241_RS02710) | 3 |
| | 15.1 | 1194999-1194943 | -1 | FAD-linked oxidase (CD241_RS05755) | 39 |
| Corynebacterium diphtheriae 31A (NC_016799.1) | 18.12 | 2366685-2366748 | 1 | hypothetical protein (CD31A_RS11190) | 71 |
| | 17.21 | 608792-608851 | 1 | membrane protein (CD31A_RS03035) | 384 |
| Corynebacterium diphtheriae BH8 (NC_016800.1) | 18.12 | 2305800-2305863 | 1 | hypothetical protein (CDBH8_RS11005) | 71 |
| | 16.24 | 562111-562170 | 1 | membrane protein (CDBH8_RS02830) | 3 |
| Corynebacterium diphtheriae C7 (beta) (NC_016801.1) | 17.21 | 564481-564540 | 1 | membrane protein (CDC7B_RS02855) | 384 |
| Corynebacterium diphtheriae CDCE 8392 (NC_016785.1) | 17.21 | 554666-554725 | 1 | membrane protein (CDCE8392_RS02825) | 3 |
| | 15.25 | 1806319-1806266 | -1 | hypothetical protein (CDCE8392_RS11940) | 18 |
| Corynebacterium diphtheriae genome assembly NCTC113971 (NZ_LN831026.1) | 17.21 | 528602-528661 | 1 | membrane protein (AT687_RS02655) | 384 |
| Corynebacterium diphtheriae HC01 (NC_016786.1) | 16.24 | 540570-540629 | 1 | membrane protein (CDHC01_RS02700) | 3 |
| | 15.1 | 1194968-1194912 | -1 | FAD-linked oxidase (CDHC01_RS05760) | 39 |
| Corynebacterium diphtheriae HC02 (NC_016802.1) | 17.37 | 2293876-2293939 | 1 | transposase (CDHC02_RS12255) | 71 |
| | 16.24 | 562291-562350 | 1 | membrane protein (CDHC02_RS02800) | 3 |
| Corynebacterium diphtheriae HC03 (NC_016787.1) | 17.37 | 2287584-2287647 | 1 | transposase (CDHC03_RS12065) | 71 |
| | 17.21 | 542020-542079 | 1 | membrane protein (CDHC03_RS02695) | 384 |
| Corynebacterium diphtheriae HC04 (NC_016788.1) | 17.37 | 2311402-2311465 | 1 | transposase (CDHC04_RS12195) | 71 |
| | 17.21 | 530537-530596 | 1 | membrane protein (CDHC04_RS02615) | 384 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.1 | 1194413-1194357 | -1 | FAD-linked oxidase (CDHC04_RS05780) | 39 |
| Corynebacterium diphtheriae INCA 402 (NC_016783.1) | 16.24 | 544750-544809 | 1 | membrane protein (CDB402_RS02690) | 3 |
| Corynebacterium diphtheriae NCTC 13129 (NC_002935.2) | 17.21 | 582246-582305 | 1 | membrane protein (DIP_RS14365) | 3 |
|  | 15.25 | 1881495-1881442 | -1 | hypothetical protein (DIP_RS23555) | 18 |
| Corynebacterium diphtheriae PW8 (NC_016789.1) | 17.21 | 609691-609750 | 1 | membrane protein (CDPW8_RS03110) | 384 |
| Corynebacterium diphtheriae strain B-D-16-78 (NZ_CP018331.1) | 16.24 | 2272880-2272939 | 1 | membrane protein (BS112_RS11015) | 3 |
| Corynebacterium diphtheriae strain FDAARGOS_197 (NZ_CP020410.1) | 17.21 | 2449468-2449527 | 1 | membrane protein (A6J36_RS11710) | 384 |
|  | 15.25 | 1259703-1259650 | -1 | hypothetical protein (A6J36_RS05950) | 18 |
| Corynebacterium diphtheriae VA01 (NC_016790.1) | 17.37 | 2208578-2208641 | 1 | transposase (CDVA01_RS11645) | 71 |
|  | 17.21 | 519377-519436 | 1 | membrane protein (CDVA01_RS02540) | 384 |
|  | 15.1 | 1161803-1161747 | -1 | FAD-linked oxidase (CDVA01_RS05515) | 39 |
| Corynebacterium efficiens YS-314 DNA (NC_004369.1) | 20.35 | 2288328-2288390 | 1 | hypothetical protein (CE_RS14970) | 245 |
| Corynebacterium efficiens YS-314 DNA (NC_004369.1) | 19.22 | 2797301-2797242 | -1 | nucleotide exchange factor GrpE (CE_RS13010) | 20 |
| Corynebacterium epidermidicanis strain DSM 45586 (NZ_CP011541.1) | 15.51 | 542196-542146 | -1 | O-acetyl-L-homoserine sulfhydrolase (CEPID_RS02575) | 95 |
| Corynebacterium falsenii DSM 44353 strain BL 8171 (NZ_CP007156.1) | 16.91 | 1654540-1654593 | 1 | amino acid-binding ACT domain protein (BI88_RS07010) | 97 |
| Corynebacterium flavescens strain OJ8 (NZ_CP009246.1) | 16.26 | 1947958-1948017 | 1 | ABC transporter ATP-binding protein (CFLV_RS08970) | 294 |
| Corynebacterium glaucum strain DSM 30827 (NZ_CP019688.1) | 15.95 | 718849-718909 | 1 | hypothetical protein (CGLAU_RS03530) | 42 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Corynebacterium glutamicum ATCC 13032 (NC_003450.3) | 17.48 | 2984618-2984562 | -1 | heat shock protein GrpE (NCgl2701) | 21 |
| | 15.4 | 2735190-2735137 | -1 | ABC transporter permease (NCgl2484) | 5 |
| | 15.31 | 1209941-1209997 | 1 | helicase (NCgl1109) | 7 |
| Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5 (NC_006958.1) | 17.48 | 2957923-2957867 | -1 | nucleotide exchange factor GrpE (CGTRNA_RS13835) | 21 |
| | 15.4 | 2706860-2706808 | -1 | phosphate ABC transporter, permease protein PstA (CGTRNA_RS12735) | 47 |
| | 15.31 | 1211409-1211465 | 1 | DEAD/DEAH box helicase (CGTRNA_RS05780) | 7 |
| Corynebacterium glutamicum ATCC 14067 (NZ_CP022614.1) | 16.55 | 638609-638553 | -1 | UDP-glucose 4-epimerase GalE (CEY17_RS03130) | 64 |
| | 15.4 | 2681755-2681703 | -1 | phosphate ABC transporter, permease protein PstA (CEY17_RS13150) | 47 |
| | 15.31 | 1289628-1289684 | 1 | DEAD/DEAH box helicase (CEY17_RS06335) | 7 |
| | 15.24 | 1188383-1188440 | 1 | MFS transporter (CEY17_RS05865) | 43 |
| Corynebacterium glutamicum DNA, strain: AJ1511 (NZ_AP017557.1) | 15.4 | 2685573-2685521 | -1 | phosphate ABC transporter, permease protein PstA (CGBL_RS12700) | 47 |
| | 15.31 | 1316640-1316696 | 1 | ATP-dependent RNA helicase (CGBL_RS06275) | 7 |
| | 15.24 | 1218594-1218651 | 1 | MFS transporter (CGBL_RS05825) | 43 |
| Corynebacterium glutamicum DNA, strain: N24 (NZ_AP017369.1) | 18.59 | 3179973-3179917 | -1 | nucleotide exchange factor GrpE (N24_RS14630) | 21 |
| | 16.52 | 1657111-1657172 | 1 | MerR family transcriptional regulator (N24_RS07815) | 15 |
| | 15.68 | 2337810-2337750 | -1 | NADP-specific glutamate dehydrogenase (N24_RS10865) | 67 |

| Organism<br>(Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs<br>(Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.31 | 1359688-1359744 | 1 | ATP-dependent RNA helicase (N24_RS06480) | 7 |
|  | 15.21 | 2843690-2843740 | 1 | FadR family transcriptional regulator (N24_RS13155) | 82 |
|  | 15.12 | 3237214-3237161 | -1 | PRD domain-containing protein (N24_RS14870) | 10 |
| Corynebacterium glutamicum K051 complete genome, strain ATCC 13032, sub-strain K051 (NC_020519.1) | 17.48 | 2984617-2984561 | -1 | nucleotide exchange factor GrpE (WA5_RS14000) | 21 |
|  | 15.4 | 2735189-2735137 | -1 | phosphate ABC transporter, permease protein PstA (WA5_RS12905) | 47 |
|  | 15.31 | 1209940-1209996 | 1 | helicase (WA5_RS05750) | 7 |
| Corynebacterium glutamicum MB001 (NC_022040.1) | 17.48 | 2754470-2754414 | -1 | nucleotide exchange factor GrpE (CGP_RS12880) | 21 |
|  | 15.4 | 2503403-2503351 | -1 | phosphate ABC transporter, permease protein PstA (CGP_RS11780) | 47 |
|  | 15.31 | 1212837-1212893 | 1 | helicase (CGP_RS05770) | 7 |
| Corynebacterium glutamicum R DNA (NC_009342.1) | 20.62 | 714117-714064 | -1 | PaaI family thioesterase (CGR_RS03420) | 385 |
|  | 17.48 | 2977118-2977062 | -1 | nucleotide exchange factor GrpE (CGR_RS13900) | 21 |
|  | 16.55 | 735566-735510 | -1 | UDP-glucose 4-epimerase GalE (CGR_RS03515) | 64 |
|  | 16.4 | 1256913-1256970 | 1 | MFS transporter (CGR_RS05950) | 43 |
|  | 15.67 | 3018403-3018350 | -1 | PRD domain-containing protein (CGR_RS14090) | 10 |
|  | 15.4 | 2734181-2734129 | -1 | phosphate ABC transporter, permease protein PstA (CGR_RS12865) | 47 |
|  | 15.31 | 1352549-1352605 | 1 | DEAD/DEAH box helicase | 7 |

| Organism<br>(Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (CGR_RS06390) | |
| Corynebacterium glutamicum SCgG1 (NC_021351.1) | 20.62 | 701116-701063 | -1 | PaaI family thioesterase (C624_RS03385) | 385 |
| | 17.48 | 3001152-3001096 | -1 | nucleotide exchange factor GrpE (C624_RS13910) | 21 |
| | 16.55 | 722574-722518 | -1 | UDP-glucose 4-epimerase GalE (C624_RS03480) | 64 |
| | 15.67 | 3044637-3044584 | -1 | PRD domain-containing protein (C624_RS14110) | 10 |
| | 15.4 | 2753889-2753837 | -1 | phosphate ABC transporter, permease protein PstA (C624_RS12865) | 47 |
| | 15.31 | 1401709-1401765 | 1 | DEAD/DEAH box helicase (C624_RS06640) | 7 |
| Corynebacterium glutamicum SCgG2 (NC_021352.1) | 20.62 | 701117-701064 | -1 | PaaI family thioesterase (C629_RS03385) | 385 |
| | 17.48 | 3001151-3001095 | -1 | nucleotide exchange factor GrpE (C629_RS13905) | 21 |
| | 16.55 | 722575-722519 | -1 | UDP-glucose 4-epimerase GalE (C629_RS03480) | 64 |
| | 15.67 | 3044636-3044583 | -1 | PRD domain-containing protein (C629_RS14105) | 10 |
| | 15.4 | 2753888-2753836 | -1 | phosphate ABC transporter, permease protein PstA (C629_RS12860) | 47 |
| | 15.31 | 1401708-1401764 | 1 | DEAD/DEAH box helicase (C629_RS06635) | 7 |
| Corynebacterium glutamicum strain AR1 (NZ_CP007724.1) | 20.62 | 626016-625963 | -1 | PaaI family thioesterase (CGLAR1_RS03095) | 385 |
| | 17.25 | 1164052-1164109 | 1 | MFS transporter (CGLAR1_RS05565) | 44 |
| | 15.4 | 2573691-2573639 | -1 | phosphate ABC transporter, permease | 47 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | protein PstA (CGLAR1_RS12090) | |
| | 15.31 | 1259623-1259679 | 1 | DEAD/DEAH box helicase (CGLAR1_RS06005) | 7 |
| Corynebacterium glutamicum strain ATCC 13869 (NZ_CP016335.1) | 15.4 | 2685568-2685516 | -1 | phosphate ABC transporter, permease protein PstA (BBD29_RS12560) | 47 |
| | 15.31 | 1314970-1315026 | 1 | ATP-dependent RNA helicase (BBD29_RS06195) | 7 |
| | 15.24 | 1216979-1217036 | 1 | MFS transporter (BBD29_RS05735) | 43 |
| Corynebacterium glutamicum strain ATCC 21831 (NZ_CP007722.1) | 20.62 | 656832-656779 | -1 | PaaI family thioesterase (AR0_RS03220) | 385 |
| | 17.25 | 1194869-1194926 | 1 | MFS transporter (AR0_RS05680) | 44 |
| | 15.4 | 2604096-2604044 | -1 | phosphate ABC transporter, permease protein PstA (AR0_RS12200) | 47 |
| | 15.31 | 1290440-1290496 | 1 | DEAD/DEAH box helicase (AR0_RS06120) | 7 |
| Corynebacterium glutamicum strain B253 (NZ_CP010451.1) | 15.4 | 2601352-2601300 | -1 | phosphate ABC transporter, permease protein PstA (SB89_RS12100) | 47 |
| | 15.31 | 1286056-1286112 | 1 | DEAD/DEAH box helicase (SB89_RS06035) | 7 |
| | 15.24 | 1179688-1179745 | 1 | MFS transporter (SB89_RS05560) | 43 |
| Corynebacterium glutamicum strain CP (NZ_CP012194.1) | 15.4 | 2729849-2729797 | -1 | phosphate ABC transporter, permease protein PstA (AC079_RS12905) | 47 |
| | 15.31 | 1355779-1355835 | 1 | DEAD/DEAH box helicase (AC079_RS06490) | 7 |
| | 15.24 | 1257734-1257791 | 1 | MFS transporter (AC079_RS06035) | 43 |
| Corynebacterium glutamicum strain TQ2223 (NZ_CP020658.1) | 17.48 | 3060506-3060562 | 1 | nucleotide exchange factor GrpE (B7P23_RS14495) | 21 |
| | 15.4 | 28885-28938 | 1 | phosphate ABC transporter, permease | 5 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | protein PstA (B7P23_RS00130) | |
| | 15.31 | 1522687-1522631 | -1 | helicase (B7P23_RS07145) | 7 |
| Corynebacterium glutamicum strain USDA-ARS-USMARC-56828 (NZ_CP013991.1) | 17.48 | 2931080-2931024 | -1 | nucleotide exchange factor GrpE (APT58_RS13695) | 21 |
| | 15.67 | 2972568-2972515 | -1 | transcription antiterminator BglG (APT58_RS13885) | 10 |
| | 15.61 | 672726-672673 | -1 | PaaI family thioesterase (APT58_RS03280) | 385 |
| | 15.4 | 2683030-2682978 | -1 | phosphate ABC transporter, permease protein PstA (APT58_RS12645) | 47 |
| | 15.31 | 1310879-1310935 | 1 | DEAD/DEAH box helicase (APT58_RS06245) | 7 |
| | 15.27 | 438395-438335 | -1 | esterase family protein (APT58_RS02155) | 368 |
| Corynebacterium glutamicum strain WM001 (NZ_CP022394.1) | 15.4 | 2237589-2237537 | -1 | phosphate ABC transporter, permease protein PstA (CGB98_RS10580) | 47 |
| | 15.31 | 865646-865702 | 1 | ATP-dependent RNA helicase (CGB98_RS04160) | 7 |
| | 15.24 | 767600-767657 | 1 | MFS transporter (CGB98_RS03710) | 43 |
| Corynebacterium glutamicum strain XV (NZ_CP018175.1) | 15.4 | 2705759-2705707 | -1 | phosphate ABC transporter, permease protein PstA (BSP99_RS12860) | 47 |
| | 15.4 | 2718514-2718462 | -1 | phosphate ABC transporter, permease protein PstA (BSP99_RS12945) | 47 |
| | 15.31 | 1323843-1323899 | 1 | ATP-dependent RNA helicase (BSP99_RS06370) | 7 |
| | 15.24 | 1225797-1225854 | 1 | MFS transporter (BSP99_RS05915) | 43 |
| Corynebacterium glutamicum strain YI (NZ_CP014984.1) | 16.55 | 637028-636972 | -1 | UDP-glucose 4-epimerase GalE (A3654_RS03070) | 64 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.4 | 2676018-2675966 | -1 | phosphate ABC transporter, permease protein PstA (A3654_RS13005) | 47 |
|  | 15.31 | 1289003-1289059 | 1 | DEAD/DEAH box helicase (A3654_RS06260) | 7 |
|  | 15.24 | 1187758-1187815 | 1 | MFS transporter (A3654_RS05790) | 43 |
| Corynebacterium glutamicum ZL-6 (NZ_CP004062.1) | 15.4 | 2716163-2716111 | -1 | phosphate ABC transporter, permease protein PstA (C627_RS12795) | 47 |
|  | 15.31 | 1332273-1332329 | 1 | ATP-dependent RNA helicase (C627_RS06325) | 7 |
|  | 15.24 | 1234226-1234283 | 1 | MFS transporter (C627_RS05865) | 43 |
| Corynebacterium glyciniphilum AJ 3170 (NZ_CP006842.1) | 20.66 | 641835-641767 | -1 | acyl-CoA oxidase (CGLY_RS02960) | 249 |
| Corynebacterium humireducens NBRC 106098 = DSM 45392 (NZ_CP005286.1) | 17.13 | 2213593-2213539 | -1 | tRNA-Asp (B842_RS10925) | 38 |
| Corynebacterium imitans strain DSM 44264 (NZ_CP009211.1) | 15.08 | 817633-817686 | 1 | TrkA family potassium uptake protein (CIMIT_RS03730) | 88 |
| Corynebacterium imitans strain NCTC13015 1 (NZ_LT906467.1) | 15.08 | 899599-899652 | 1 | TrkA family potassium uptake protein (CKV97_RS04135) | 40 |
| Corynebacterium jeikeium strain FDAARGOS_328 (NZ_CP022054.1) | 19.04 | 276098-276155 | 1 | hypothetical protein (CEQ06_RS01215) | 32 |
|  | 15.47 | 2197898-2197951 | 1 | hypothetical protein (CEQ06_RS09770) | 34 |
|  | 15.14 | 1717433-1717377 | -1 | nucleotide exchange factor GrpE (CEQ06_RS07760) | 8 |
| Corynebacterium kroppenstedtii DSM 44385 (NC_012704.1) | 16.99 | 1893895-1893951 | 1 | hypothetical protein (CKROP_RS07925) | 5 |
|  | 16.31 | 1439672-1439725 | 1 | IclR family transcriptional regulator (CKROP_RS05980) | 370 |
| Corynebacterium lactis RW2-5 | 21.46 | 144577-144541 | -1 | glycosyltransferase family 2 protein | 159 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| (NZ_CP006841.1) | | | | (CLAC_RS00545) | |
| | 19.94 | 2631157-2631106 | -1 | hypothetical protein (CLAC_RS11575) | 54 |
| Corynebacterium marinum DSM 44953 plasmid pCmarinum2 (NZ_CP007791.1) | 17.39 | 8792-8740 | -1 | replicase RepA (B840_RS13300) | 357 |
| Corynebacterium mustelae strain DSM 45274 (NZ_CP011542.1) | 16.62 | 1400440-1400500 | 1 | hypothetical protein (CMUST_RS06530) | 54 |
| Corynebacterium phocae strain M408/89/1 (NZ_CP009249.1) | 15.58 | 723165-723214 | 1 | bifunctional folylpolyglutamate synthase/dihydrofolate synthase (CPHO_RS03305) | 93 |
| Corynebacterium pseudotuberculosis 1/06-A (NC_017308.1) | 16.04 | 1945271-1945324 | 1 | cardiolipin synthase (CP106_RS08885) | 26 |
| Corynebacterium pseudotuberculosis 1002 (NC_017300.1) | 16.51 | 1995873-1995926 | 1 | cardiolipin synthase (CP1002_RS09075) | 26 |
| Corynebacterium pseudotuberculosis 258 (NC_017945.2) | 16.04 | 2028099-2028152 | 1 | cardiolipin synthase (CP258_RS09260) | 26 |
| Corynebacterium pseudotuberculosis 267 (NC_017462.1) | 16.04 | 1998436-1998489 | 1 | cardiolipin synthase (CP267_RS09070) | 26 |
| Corynebacterium pseudotuberculosis 3/99-5 (NC_016781.1) | 16.04 | 1998501-1998554 | 1 | cardiolipin synthase (CP3995_RS09100) | 26 |
| Corynebacterium pseudotuberculosis 316 (NC_016932.1) | 16.04 | 1969760-1969813 | 1 | cardiolipin synthase (CP316_RS08945) | 26 |
| Corynebacterium pseudotuberculosis 42/02-A (NC_017306.1) | 16.04 | 1998385-1998438 | 1 | cardiolipin synthase (CP4202_RS09095) | 26 |
| Corynebacterium pseudotuberculosis C231 (NC_017301.1) | 16.04 | 1988938-1988991 | 1 | cardiolipin synthase (CPC231_RS19465) | 26 |
| Corynebacterium pseudotuberculosis CIP 52.97 (NC_017307.2) | 16.04 | 2026638-2026691 | 1 | cardiolipin synthase (CPCIP5297_RS09505) | 26 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Corynebacterium pseudotuberculosis Cp162 (NC_018019.2) | 16.04 | 2024914-2024967 | 1 | cardiolipin synthase (CP162_RS09460) | 26 |
| Corynebacterium pseudotuberculosis FRC41 (NC_014329.1) | 16.04 | 1998568-1998621 | 1 | cardiolipin synthase (CPFRC_RS09100) | 26 |
| Corynebacterium pseudotuberculosis I19 (NC_017303.2) | 16.04 | 1998109-1998162 | 1 | cardiolipin synthase (CPI19_RS09295) | 26 |
| Corynebacterium pseudotuberculosis P54B96 (NC_017031.1) | 16.04 | 1998340-1998393 | 1 | cardiolipin synthase (CPP54B96_RS09090) | 26 |
| Corynebacterium pseudotuberculosis PAT10 (NC_017305.1) | 16.04 | 1995966-1996019 | 1 | cardiolipin synthase (CPPAT10_RS09080) | 26 |
| Corynebacterium pseudotuberculosis strain 1002B (NZ_CP012837.1) | 16.51 | 854171-854118 | -1 | cardiolipin synthase (Cp1002B_RS03865) | 26 |
| Corynebacterium pseudotuberculosis strain 12C (NZ_CP011474.1) | 16.51 | 1998115-1998168 | 1 | cardiolipin synthase (Cp12C_RS09100) | 26 |
| Corynebacterium pseudotuberculosis strain 226 (NZ_CP010889.1) | 16.04 | 1998442-1998495 | 1 | cardiolipin synthase (CP226_RS09090) | 26 |
| Corynebacterium pseudotuberculosis strain 262 (NZ_CP012022.2) | 16.04 | 2021693-2021746 | 1 | cardiolipin synthase (Cp262_RS09400) | 26 |
| Corynebacterium pseudotuberculosis strain 29156 (NZ_CP010795.1) | 16.04 | 854831-854778 | -1 | cardiolipin synthase (Cp29156_RS03900) | 26 |
| Corynebacterium pseudotuberculosis strain 32 (NZ_CP015183.1) | 16.04 | 2060899-2060952 | 1 | cardiolipin synthase (A4R72_RS09470) | 26 |
| Corynebacterium pseudotuberculosis strain 33 (NZ_CP015184.1) | 16.04 | 2060913-2060966 | 1 | cardiolipin synthase (A4R71_RS09485) | 26 |
| Corynebacterium pseudotuberculosis strain 34 (NZ_CP015192.1) | 16.04 | 2060808-2060861 | 1 | cardiolipin synthase (A4R69_RS09465) | 26 |
| Corynebacterium pseudotuberculosis strain 35 (NZ_CP015185.1) | 16.04 | 2060864-2060917 | 1 | cardiolipin synthase (A4R68_RS09485) | 26 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Corynebacterium pseudotuberculosis strain 36 (NZ_CP015186.1) | 16.04 | 2060782-2060835 | 1 | cardiolipin synthase (A4R67_RS09460) | 26 |
| Corynebacterium pseudotuberculosis strain 38 (NZ_CP015187.1) | 16.04 | 2060890-2060943 | 1 | cardiolipin synthase (A4R66_RS09460) | 26 |
| Corynebacterium pseudotuberculosis strain 39 (NZ_CP015188.1) | 16.04 | 2060955-2061008 | 1 | cardiolipin synthase (A4R65_RS09455) | 26 |
| Corynebacterium pseudotuberculosis strain 43 (NZ_CP015189.1) | 16.04 | 2022444-2022497 | 1 | cardiolipin synthase (A4R64_RS09255) | 26 |
| Corynebacterium pseudotuberculosis strain 46 (NZ_CP015190.1) | 16.04 | 2023915-2023968 | 1 | cardiolipin synthase (A4R63_RS09235) | 26 |
| Corynebacterium pseudotuberculosis strain 48 (NZ_CP015191.1) | 16.04 | 2060676-2060729 | 1 | cardiolipin synthase (A4R62_RS09470) | 26 |
| Corynebacterium pseudotuberculosis strain 48252 (NZ_CP008922.1) | 16.04 | 214647-214700 | 1 | cardiolipin synthase (CPTA_RS01030) | 26 |
| Corynebacterium pseudotuberculosis strain ATCC 19410 (NZ_CP021251.1) | 16.04 | 854231-854178 | -1 | cardiolipin synthase (CpATCC19410_RS03970) | 26 |
| Corynebacterium pseudotuberculosis strain Cp13 (NZ_CP014998.1) | 16.51 | 2002902-2002955 | 1 | cardiolipin synthase (CpCp13_RS09135) | 26 |
| Corynebacterium pseudotuberculosis strain CS_10 (NZ_CP008923.1) | 16.04 | 1381691-1381638 | -1 | cardiolipin synthase (CPTB_RS06210) | 26 |
| Corynebacterium pseudotuberculosis strain E19 (NZ_CP012136.1) | 16.04 | 2026360-2026413 | 1 | cardiolipin synthase (CpE19_RS09260) | 26 |
| Corynebacterium pseudotuberculosis strain E55 (NZ_CP014341.1) | 16.04 | 853706-853653 | -1 | cardiolipin synthase (CpE55_RS03870) | 26 |
| Corynebacterium pseudotuberculosis strain E56 (NZ_CP013699.1) | 16.04 | 853708-853655 | -1 | cardiolipin synthase (AN398_RS03860) | 26 |
| Corynebacterium pseudotuberculosis | 16.04 | 1018334-1018281 | -1 | cardiolipin synthase (CPTC_RS04600) | 26 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| strain Ft_2193/67 (NZ_CP008924.1) | | | | | |
| Corynebacterium pseudotuberculosis strain I37 (NZ_CP017384.1) | 16.04 | 2027288-2027341 | 1 | cardiolipin synthase (CPI37_RS09430) | 26 |
| Corynebacterium pseudotuberculosis strain MB11 (NZ_CP013260.1) | 16.04 | 2131290-2131343 | 1 | cardiolipin synthase (ATN02_RS09730) | 26 |
| Corynebacterium pseudotuberculosis strain MB14 (NZ_CP013261.1) | 16.04 | 2027869-2027922 | 1 | cardiolipin synthase (ATN03_RS09285) | 26 |
| Corynebacterium pseudotuberculosis strain MB20 (NZ_CP016829.1) | 16.04 | 971322-971269 | -1 | cardiolipin synthase (CPMB20_RS04670) | 26 |
| Corynebacterium pseudotuberculosis strain MB278 (NZ_CP023395.1) | 16.04 | 2027958-2028011 | 1 | cardiolipin synthase (BFF96_RS09510) | 26 |
| Corynebacterium pseudotuberculosis strain MB30 (NZ_CP013262.2) | 16.04 | 2026744-2026797 | 1 | cardiolipin synthase (ATN04_RS09500) | 26 |
| Corynebacterium pseudotuberculosis strain MB302 (NZ_CP021982.1) | 16.04 | 2025938-2025991 | 1 | cardiolipin synthase (BFG01_RS09500) | 26 |
| Corynebacterium pseudotuberculosis strain MB66 (NZ_CP013263.1) | 16.04 | 971242-971189 | -1 | cardiolipin synthase (ATN05_RS04530) | 26 |
| Corynebacterium pseudotuberculosis strain MEX1 (NZ_CP017711.1) | 16.04 | 854185-854132 | -1 | cardiolipin synthase (CpMEX1_RS03945) | 26 |
| Corynebacterium pseudotuberculosis strain MEX25 (NZ_CP013697.1) | 16.04 | 854204-854151 | -1 | cardiolipin synthase (AN397_RS03870) | 26 |
| Corynebacterium pseudotuberculosis strain MEX29 (NZ_CP016826.1) | 16.04 | 854229-854176 | -1 | cardiolipin synthase (CpMEX29_RS03870) | 26 |
| Corynebacterium pseudotuberculosis strain MEX30 (NZ_CP017291.1) | 16.04 | 2026292-2026345 | 1 | cardiolipin synthase (CpMEX30_RS09515) | 26 |
| Corynebacterium pseudotuberculosis strain MEX31 (NZ_CP017292.1) | 16.04 | 2026049-2026102 | 1 | cardiolipin synthase (CpMEX31_RS09480) | 26 |
| Corynebacterium pseudotuberculosis | 16.04 | 854213-854160 | -1 | cardiolipin synthase (CpMEX9_RS03890) | 26 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| strain MEX9 (NZ_CP014543.1) | | | | | |
| Corynebacterium pseudotuberculosis strain MIC6 (NZ_CP019769.1) | 16.51 | 1997836-1997889 | 1 | cardiolipin synthase (CpMIC6_RS09295) | 26 |
| Corynebacterium pseudotuberculosis strain N1 (NZ_CP013146.1) | 16.04 | 854467-854414 | -1 | cardiolipin synthase (CpN1_RS03870) | 26 |
| Corynebacterium pseudotuberculosis strain PA01 (NZ_CP013327.1) | 16.04 | 1998430-1998483 | 1 | cardiolipin synthase (CpPA01_RS09085) | 26 |
| Corynebacterium pseudotuberculosis strain PA02 (NZ_CP015309.1) | 16.51 | 1989095-1989148 | 1 | cardiolipin synthase (CpPA02_RS09055) | 26 |
| Corynebacterium pseudotuberculosis strain PA04 (NZ_CP019587.1) | 16.04 | 1998550-1998603 | 1 | cardiolipin synthase (CpPa04_RS09295) | 26 |
| Corynebacterium pseudotuberculosis strain phoP (NZ_CP019768.1) | 16.51 | 854156-854103 | -1 | cardiolipin synthase (CpphoP_RS03960) | 26 |
| Corynebacterium pseudotuberculosis strain PO222/4-1 (NZ_CP013698.1) | 16.04 | 854197-854144 | -1 | cardiolipin synthase (AK970_RS03870) | 26 |
| Corynebacterium pseudotuberculosis strain PO269-5 (NZ_CP012695.1) | 16.04 | 854164-854111 | -1 | cardiolipin synthase (AN902_RS03875) | 26 |
| Corynebacterium pseudotuberculosis strain SigmaE (NZ_CP020356.1) | 16.51 | 854123-854070 | -1 | cardiolipin synthase (CpSigmaE_RS03950) | 26 |
| Corynebacterium pseudotuberculosis strain T1 (NZ_CP015100.1) | 16.51 | 1997875-1997928 | 1 | cardiolipin synthase (CpT1_RS09115) | 26 |
| Corynebacterium pseudotuberculosis strain VD57 (NZ_CP009927.1) | 16.51 | 1997850-1997903 | 1 | cardiolipin synthase (cpvd57_RS09075) | 26 |
| Corynebacterium resistens DSM 45100 (NC_015673.1) | 23.06 | 784296-784358 | 1 | bifunctional folylpolyglutamate synthase/dihydrofolate synthase (CRES_RS03270) | 84 |
| Corynebacterium simulans strain PES1 (NZ_CP014634.1) | 19.51 | 2038187-2038240 | 1 | alanine:cation symporter family protein (WM42_RS09435) | 422 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.04 | 1825255-1825308 | 1 | hypoxanthine phosphoribosyltransferase (WM42_RS08480) | 31 |
| Corynebacterium simulans strain Wattiau (NZ_CP014635.1) | 19.51 | 2075643-2075696 | 1 | alanine:cation symporter family protein (AWU68_RS09625) | 422 |
| Corynebacterium singulare strain IBS B52218 (NZ_CP010827.1) | 15.06 | 379234-379174 | -1 | ABC transporter permease (CSING_RS01710) | 51 |
| Corynebacterium sp. ATCC 6931 (NZ_CP008913.1) | 19.04 | 2170035-2170092 | 1 | hypothetical protein (DR71_RS09350) | 32 |
|  | 15.57 | 2171805-2171866 | 1 | phosphoglycerate dehydrogenase (DR71_RS09355) | 158 |
|  | 15.29 | 533505-533558 | 1 | CBS domain-containing protein (DR71_RS02185) | 6 |
| Corynebacterium sp. NML98-0116 genome (NZ_CP017639.1) | 19.17 | 282870-282926 | 1 | nucleotide exchange factor GrpE (BJP05_RS01180) | 39 |
| Corynebacterium stationis strain 622=DSM 20302 (NZ_CP009251.1) | 19.79 | 301620-301569 | -1 | peptidase M23 (CSTAT_RS01510) | 372 |
|  | 19.05 | 658233-658185 | -1 | ribonuclease HI (CSTAT_RS03225) | 5 |
| Corynebacterium striatum strain KC-Na-01 (NZ_CP021252.1) | 19.51 | 737452-737505 | 1 | alanine:cation symporter family protein (CBE89_RS03575) | 422 |
|  | 16.4 | 192948-193016 | 1 | hypothetical protein (CBE89_RS01090) | 25 |
| Corynebacterium terpenotabidum Y-11 (NC_021663.1) | 18.6 | 266084-266134 | 1 | N-carbamoylsarcosine amidase (A606_RS01080) | 361 |
| Corynebacterium testudinoris strain DSM 44614 (NZ_CP011545.1) | 16.85 | 2111774-2111716 | -1 | TetR/AcrR family transcriptional regulator (CTEST_RS10110) | 71 |
| Corynebacterium ulcerans 0102 DNA (NC_018101.1) | 15.6 | 1773540-1773605 | 1 | serine/threonine protein kinase (CULC0102_RS08195) | 315 |
| Corynebacterium ulcerans 809 (NC_017317.1) | 15.6 | 1691258-1691323 | 1 | serine/threonine protein kinase (CULC809_RS07755) | 315 |
| Corynebacterium ulcerans BR-AD22 | 15.6 | 1694931-1694996 | 1 | serine/threonine protein kinase | 315 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| (NC_015683.1) | | | | (CULC22_RS07730) | |
| Corynebacterium ulcerans FRC58 (NZ_CP011913.1) | 15.6 | 1677923-1677988 | 1 | serine/threonine protein kinase (CULFRC58_RS07655) | 315 |
| | 15.17 | 330052-330103 | 1 | hypothetical protein (CULFRC58_RS01565) | 193 |
| Corynebacterium ulcerans strain 05146 (NZ_CP009716.1) | 16.55 | 2091358-2091409 | 1 | Na+/H+ antiporter subunit E (CUL05146_RS09480) | 39 |
| | 15.6 | 1642146-1642211 | 1 | serine/threonine protein kinase (CUL05146_RS07450) | 315 |
| Corynebacterium ulcerans strain 131001 (NZ_CP010818.1) | 15.6 | 1681236-1681301 | 1 | serine/threonine protein kinase (Cul131001_RS07640) | 315 |
| Corynebacterium ulcerans strain 210931 (NZ_CP009583.1) | 16.55 | 2122575-2122626 | 1 | Na+/H+ antiporter subunit E (CUL210931_RS09775) | 39 |
| | 15.6 | 1637127-1637192 | 1 | serine/threonine protein kinase (CUL210931_RS07495) | 315 |
| Corynebacterium ulcerans strain 210932 (NZ_CP009500.1) | 15.6 | 1681546-1681611 | 1 | serine/threonine protein kinase (CUL210932_RS07655) | 315 |
| Corynebacterium ulcerans strain NCTC7910 1 (NZ_LT906443.1) | 15.6 | 661088-661153 | 1 | serine/threonine protein kinase (CKV68_RS02940) | 315 |
| Corynebacterium ulcerans strain PO100/5 (NZ_CP021417.1) | 17.7 | 1615651-1615601 | -1 | terminase (CBE74_RS07650) | 24 |
| | 15.45 | 2207204-2207255 | 1 | Na+/H+ antiporter subunit E (CBE74_RS10395) | 39 |
| | 15.24 | 2530763-2530701 | -1 | aldose epimerase (CBE74_RS11790) | 278 |
| Corynebacterium urealyticum DSM 7109 complete genome (NC_010545.1) | 21.91 | 2341876-2341820 | -1 | NUDIX domain-containing protein (CU_RS10045) | 487 |
| | 19.64 | 547036-547092 | 1 | biotin--[acetyl-CoA-carboxylase] ligase (CU_RS02260) | 435 |

| Organism<br>(Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.54 | 657867-657914 | 1 | PDZ domain-containing protein (CU_RS02720) | 28 |
| Corynebacterium urealyticum DSM 7111 (NC_020230.1) | 19.64 | 536435-536491 | 1 | biotin--[acetyl-CoA-carboxylase] ligase (CU7111_RS02240) | 435 |
|  | 15.54 | 637433-637480 | 1 | PDZ domain-containing protein (CU7111_RS02665) | 28 |
| Corynebacterium urealyticum strain NCTC12011 1 (NZ_LT906481.1) | 21.91 | 1654930-1654874 | -1 | NUDIX domain-containing protein (CKV82_RS07305) | 487 |
|  | 19.64 | 2232424-2232480 | 1 | biotin--[acetyl-CoA-carboxylase] ligase (CKV82_RS09705) | 435 |
|  | 15.54 | 2346331-2346378 | 1 | PDZ domain-containing protein (CKV82_RS10185) | 28 |
| Corynebacterium uterequi strain DSM 45634 (NZ_CP011546.1) | 16.32 | 857566-857513 | -1 | glycogen synthase (CUTER_RS04050) | 88 |
|  | 15.31 | 1596657-1596597 | -1 | heme-copper oxidase subunit III (CUTER_RS07405) | 340 |
| Cryobacterium arcticum strain PAMC 27867 1 (NZ_CP016282.1) | 22.35 | 3698660-3698598 | -1 | LacI family transcriptional regulator (PA27867_RS16790) | 6 |
|  | 16.53 | 2539464-2539403 | -1 | alcohol dehydrogenase (PA27867_RS11370) | 33 |
| Cryobacterium sp. LW097 (NZ_CP021992.1) | 15.46 | 403166-403220 | 1 | sugar ABC transporter substrate-binding protein (B7495_RS01925) | 52 |
| Cryptobacterium curtum DSM 15641 (NC_013170.1) | 18.86 | 1081472-1081416 | -1 | glucan-binding protein (CCUR_RS04640) | 18 |
|  | 18.81 | 205749-205805 | 1 | glucan-binding protein (CCUR_RS00825) | 18 |
| Curtobacterium pusillum strain AA3 (NZ_CP018783.1) | 15.84 | 3814213-3814266 | 1 | peptide ABC transporter substrate-binding protein (BUE88_RS18120) | 14 |
| Curtobacterium sp. MR_MD2014 (NZ_CP009755.1) | 18.57 | 210772-210718 | -1 | gfo/Idh/MocA family oxidoreductase (NI26_RS01060) | 7 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 16.03 | 27231-27283 | 1 | sugar phosphate isomerase/epimerase (NI26_RS00130) | 5 |
| Cutibacterium acnes strain KCOM 1861 (= ChDC B594) (NZ_CP012647.1) | 19.1 | 246678-246614 | -1 | hypothetical protein (RN83_RS01045) | 45 |
| Cutibacterium avidum 44067 (NC_021064.1) | 20.99 | 2362551-2362500 | -1 | LacI family transcriptional regulator (PALO_RS10760) | 45 |
| Cutibacterium avidum strain DPC 6544 (NZ_CP016954.1) | 17.48 | 1895877-1895946 | 1 | hypothetical protein (BFS79_RS08475) | 30 |
| | 15.35 | 2604770-2604819 | 1 | endo-beta-N-acetylglucosaminidase (BFS79_RS11695) | 17 |
| | 15.21 | 1301579-1301520 | -1 | WhiB family transcriptional regulator (BFS79_RS05970) | 292 |
| Cutibacterium granulosum strain NCTC11865 1 (NZ_LT906441.1) | 19.21 | 1211974-1212044 | 1 | putative lysophospholipase (CKV91_RS05110) | 23 |
| Denitrobacterium detoxificans strain NPOH1 (NZ_CP011402.1) | 17.65 | 1421804-1421754 | -1 | 3-methyl-2-oxobutanoate dehydrogenase subunit VorB (AAY81_RS06090) | 5 |
| | 15.74 | 1266680-1266733 | 1 | ribonuclease HII (AAY81_RS05420) | 63 |
| Dermabacter vaginalis strain AD1-86 (NZ_CP012117.1) | 20.61 | 21017-21071 | 1 | restriction endonuclease subunit S (DAD186_RS10515) | 26 |
| | 15.6 | 2034083-2034033 | -1 | cytoplasmic protein (DAD186_RS08980) | 6 |
| Dermacoccus nishinomiyaensis strain M25 (NZ_CP008889.1) | 15.87 | 2422894-2422838 | -1 | TetR/AcrR family transcriptional regulator (HX89_RS10945) | 23 |
| Dermatophilus congolensis strain NCTC13039 1 (NZ_LT906453.1) | 15.04 | 256097-256134 | 1 | citrate synthase (CKV89_RS01045) | 15 |
| Eggerthella lenta DSM 2243 (NC_013204.1) | 15.58 | 1642309-1642246 | -1 | XRE family transcriptional regulator (ELEN_RS06870) | 234 |
| | 15.47 | 3050747-3050800 | 1 | hypothetical protein (ELEN_RS13155) | 70 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 15.09 | 1311510-1311568 | 1 | GGDEF domain-containing protein (ELEN_RS05405) | 68 |
| Eggerthella lenta strain C592 (NZ_CP021140.1) | 15.53 | 2885114-2885061 | -1 | HNH endonuclease (CAB18_RS12525) | 29 |
| | 15.09 | 2331573-2331515 | -1 | GGDEF domain-containing protein (CAB18_RS10165) | 68 |
| Eggerthella sp. YY7918 DNA (NC_015738.1) | 23.92 | 2403484-2403432 | -1 | formate-dependent nitrite reductase (EGYY_RS10130) | 141 |
| | 18.25 | 898918-898968 | 1 | FAD-binding protein (EGYY_RS03605) | 408 |
| | 16.05 | 2989223-2989276 | 1 | serine/threonine-protein phosphatase (EGYY_RS12650) | 11 |
| Eggerthellaceae bacterium Marseille-P3241 contig00001 (NZ_LT821227.1) | 17.89 | 813267-813313 | 1 | hypothetical protein (B5449_RS03580) | 28 |
| | 17.02 | 201358-201305 | -1 | translation initiation factor IF-3 (B5449_RS00945) | 98 |
| | 16.58 | 1387731-1387665 | -1 | hypothetical protein (B5449_RS06055) | 281 |
| Frankia symbiont of Datisca glomerata (NC_015656.1) | 16.08 | 3985397-3985335 | -1 | ATPase (FSYMDG_RS16640) | 17 |
| Frondihabitans sp. PAMC28766 (NZ_CP014513.1) | 22.62 | 1628207-1628135 | -1 | Alpha-L-arabinofuranosidase (AX769_RS07985) | 7 |
| | 19.17 | 4176083-4176027 | -1 | alpha-L-arabinofuranosidase (AX769_RS19925) | 7 |
| | 15.88 | 210467-210404 | -1 | hypothetical protein (AX769_RS00955) | 17 |
| | 15.34 | 1468942-1468876 | -1 | nitronate monooxygenase (AX769_RS07210) | 4 |
| Gardnerella vaginalis ATCC 14018 = JCM 11026 DNA (NZ_AP012332.1) | 20.55 | 713559-713494 | -1 | MFS transporter (GAVG_RS02705) | 39 |
| | 17.78 | 852571-852627 | 1 | elongation factor Ts (GAVG_RS03270) | 58 |
| | 17.14 | 310381-310435 | 1 | ATPase (GAVG_RS01165) | 22 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 16.71 | 84407-84463 | 1 | LacI family transcriptional regulator (GAVG_RS00345) | 107 |
| | 16.53 | 1391978-1391921 | -1 | hypothetical protein (GAVG_RS05255) | 6 |
| | 16.15 | 351111-351171 | 1 | glycosyl transferase (GAVG_RS01325) | 34 |
| Gardnerella vaginalis ATCC 14019 (NC_014644.1) | 20.55 | 852666-852601 | -1 | L-fucose permease (HMPREF0421_20693) | 39 |
| | 17.78 | 991686-991742 | 1 | elongation factor EF1B (HMPREF0421_20808) | 58 |
| | 17.14 | 449487-449541 | 1 | ribulokinase (HMPREF0421_20372) | 22 |
| | 16.71 | 223569-223625 | 1 | hypothetical protein (HMPREF0421_20197) | 107 |
| | 16.53 | 1531081-1531024 | -1 | putative cytoplasmic protein (HMPREF0421_21236) | 6 |
| | 16.15 | 490215-490275 | 1 | group 2 glycosyl transferase (HMPREF0421_20405) | 34 |
| | 15.95 | 1488885-1488834 | -1 | ABC transporter ATP-binding protein (HMPREF0421_21220) | 91 |
| Gardnerella vaginalis HMP9231 (NC_017456.1) | 20.55 | 1045532-1045597 | 1 | MFS transporter (HMPREF9231_RS04225) | 39 |
| | 17.78 | 909641-909585 | -1 | elongation factor Ts (HMPREF9231_RS03690) | 58 |
| | 17.14 | 1437267-1437213 | -1 | ATPase (HMPREF9231_RS05710) | 22 |
| | 16.71 | 86028-86084 | 1 | LacI family DNA-binding transcriptional regulator (HMPREF9231_RS00350) | 107 |
| | 16.42 | 324254-324308 | 1 | cytoplasmic protein (HMPREF9231_RS01430) | 9 |
| | 16.15 | 1396491-1396431 | -1 | glycosyltransferase | 34 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (HMPREF9231_RS05545) | |
| Glutamicibacter halophytocola strain KLBMP 5180 (NZ_CP012750.1) | 17.99 | 3057388-3057338 | -1 | LacI family transcriptional regulator (AOZ07_RS14130) | 13 |
| | 17.72 | 1968178-1968238 | 1 | hypothetical protein (AOZ07_RS18180) | 23 |
| | 17.39 | 1820450-1820512 | 1 | DNA-binding response regulator (AOZ07_RS08370) | 36 |
| | 17 | 2510824-2510880 | 1 | hypothetical protein (AOZ07_RS11560) | 277 |
| | 15.02 | 2883212-2883156 | -1 | spermidine/putrescine ABC transporter substrate-binding protein (AOZ07_RS13370) | 434 |
| Gordonia bronchialis DSM 43247 (NC_013441.1) | 19.06 | 3539668-3539601 | -1 | methyltransferase domain-containing protein (GBRO_RS16465) | 181 |
| | 18.98 | 5147979-5147941 | -1 | ammonium transporter (GBRO_RS23835) | 57 |
| | 16.24 | 1890303-1890247 | -1 | aldehyde oxidase (GBRO_RS08895) | 33 |
| Gordonia phthalatica strain QH-11 (NZ_CP011853.1) | 19.34 | 1991447-1991503 | 1 | DUF4193 domain-containing protein (ACH46_RS09315) | 70 |
| Gordonia sp. KTR9 plasmid pGKT2 (NC_018580.1) | 15.28 | 9243-9187 | -1 | hypothetical protein (KTR9_RS00050) | 7 |
| Gordonia sp. KTR9 (NC_018581.1) | 15.84 | 5108419-5108476 | 1 | DUF2236 domain-containing protein (KTR9_RS23580) | 23 |
| | 15.42 | 5174857-5174799 | -1 | hypothetical protein (KTR9_RS23900) | 11 |
| Gordonibacter sp. Marseille-P2775 contig00001 (NZ_LT827128.1) | 18.89 | 2127191-2127244 | 1 | DNA-binding response regulator (B6F40_RS08985) | 79 |
| Gordonibacter urolithinfaciens strain DSM 27213T (NZ_LT900217.1) | 16.13 | 820786-820735 | -1 | hypothetical protein (BN3560_RS03630) | 489 |
| | 15.77 | 2091859-2091910 | 1 | co-chaperone GroES (BN3560_RS08960) | 35 |
| | 15.58 | 2055612-2055559 | -1 | DNA-binding response regulator (BN3560_RS08800) | 79 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Hoyosella subflava DQS3-9A1 (NC_015564.1) | 31.41 | 4535832-4535773 | -1 | DUF2236 domain-containing protein (AS9A_RS21055) | 5 |
| | 22.4 | 650876-650926 | 1 | alpha/beta hydrolase (AS9A_RS02995) | 188 |
| | 15.5 | 932765-932832 | 1 | lipid-transfer protein (AS9A_RS04405) | 17 |
| Intrasporangium calvum DSM 43043 (NC_014830.1) | 16.22 | 22911-22856 | -1 | hypothetical protein (INTCA_RS00110) | 23 |
| Janibacter indicus strain YFY001 (NZ_CP013290.1) | 16.96 | 2789103-2789043 | -1 | hypothetical protein (ASJ30_RS13585) | 5 |
| Jonesia denitrificans DSM 20603 (NC_013174.1) | 16.56 | 2323554-2323610 | 1 | arabinogalactan endo-1,4-beta-galactosidase (JDEN_RS10685) | 26 |
| | 16.15 | 2592010-2592060 | 1 | anti-sigma factor antagonist (JDEN_RS12130) | 428 |
| | 15.58 | 71727-71779 | 1 | DeoR/GlpR transcriptional regulator (JDEN_RS00320) | 13 |
| | 15.25 | 558606-558552 | -1 | sugar ABC transporter substrate-binding protein (JDEN_RS02550) | 96 |
| | 15.14 | 144170-144235 | 1 | energy-coupling factor ABC transporter ATP-binding protein (JDEN_RS00660) | 76 |
| Jonesia denitrificans strain FDAARGOS_301 (NZ_CP022038.1) | 16.56 | 1554067-1554011 | -1 | arabinogalactan endo-1,4-beta-galactosidase (CEP80_RS07685) | 26 |
| | 16.15 | 1246455-1246405 | -1 | anti-sigma factor antagonist (CEP80_RS05920) | 428 |
| | 15.58 | 1017104-1017052 | -1 | DeoR/GlpR transcriptional regulator (CEP80_RS04895) | 13 |
| | 15.25 | 530242-530296 | 1 | sugar ABC transporter substrate-binding protein (CEP80_RS02640) | 96 |
| | 15.14 | 944662-944597 | -1 | energy-coupling factor ABC transporter ATP-binding protein (CEP80_RS04550) | 76 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Kitasatospora albolonga strain YIM 101047 (NZ_CP020563.1) | 15.64 | 1997191-1997129 | -1 | DUF3052 domain-containing protein (B7C62_RS08665) | 82 |
| Kitasatospora aureofaciens strain DM-1 (NZ_CP020567.1) | 16.58 | 17269-17329 | 1 | hypothetical protein (B6264_RS00060) | 14 |
|  | 16.54 | 651063-651111 | 1 | sugar ABC transporter substrate-binding protein (B6264_RS02840) | 53 |
|  | 15.47 | 6756365-6756418 | 1 | MarR family transcriptional regulator (B6264_RS29625) | 449 |
| Kitasatospora setae KM-6054 DNA (NC_016109.1) | 15.36 | 778009-778069 | 1 | carbohydrate-binding protein (KSE_RS03350) | 186 |
| Kocuria flava strain HO-9041 (NZ_CP013254.1) | 19.86 | 515543-515592 | 1 | hypothetical protein (AS188_RS02400) | 180 |
| Kribbella flavida DSM 17836 (NC_013729.1) | 20.29 | 2485796-2485859 | 1 | ricin B lectin (KFLA_RS11790) | 53 |
| Kutzneria albida DSM 43870 (NZ_CP007155.1) | 25.05 | 7090364-7090418 | 1 | PucR family transcriptional regulator (KALB_RS31050) | 66 |
| Lawsonella clevelandensis strain X1698 (NZ_CP012390.1) | 25.41 | 604102-604046 | -1 | 50S ribosomal protein L13 (AL705_RS02690) | 277 |
|  | 15.58 | 1356990-1357058 | 1 | DNA polymerase III subunit delta' (AL705_RS05785) | 14 |
| Leifsonia xyli strain SE134 (NZ_CP014761.1) | 30.35 | 2225649-2225592 | -1 | hypothetical protein (A0130_RS10910) | 12 |
| Leifsonia xyli subsp. cynodontis DSM 46306 (NC_022438.1) | 19.15 | 1814548-1814589 | 1 | sugar porter family MFS transporter (O159_RS08685) | 2 |
| Lentzea guizhouensis strain DHS C013 (NZ_CP016793.1) | 16.42 | 7916418-7916360 | -1 | hypothetical protein (BBK82_RS38035) | 156 |
|  | 15.85 | 824349-824401 | 1 | hypothetical protein (BBK82_RS48620) | 17 |
| Luteipulveratus mongoliensis strain MN07-A0370 genome (NZ_CP011112.1) | 16.66 | 3020465-3020530 | 1 | 30S ribosomal protein S1 (VV02_RS14365) | 79 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Microbacterium aurum strain KACC 15219 (NZ_CP018762.1) | 16.55 | 817552-817601 | 1 | TetR/AcrR family transcriptional regulator (BOH66_RS04080) | 59 |
| | 15.44 | 3112412-3112459 | 1 | hypothetical protein (BOH66_RS14995) | 0 |
| Microbacterium paludicola strain CC3 (NZ_CP018134.1) | 17.47 | 2473648-2473705 | 1 | carbohydrate-binding protein (BO218_RS11725) | 17 |
| | 15.11 | 2373937-2373993 | 1 | sugar ABC transporter substrate-binding protein (BO218_RS11280) | 4 |
| Microbacterium sp. 1.5R (NZ_CP018151.1) | 18.61 | 1648165-1648105 | -1 | glycerol kinase (BMW26_RS07710) | 9 |
| | 16.89 | 3238250-3238196 | -1 | sugar ABC transporter substrate-binding protein (BMW26_RS15470) | 26 |
| | 15.68 | 3018889-3018838 | -1 | hypothetical protein (BMW26_RS14505) | 33 |
| Microbacterium sp. BH-3-3-3 (NZ_CP017674.1) | 15.95 | 3091177-3091233 | 1 | DUF485 domain-containing protein (BJP65_RS14290) | 7 |
| | 15.89 | 2563384-2563433 | 1 | LacI family DNA-binding transcriptional regulator (BJP65_RS11740) | 31 |
| Microbacterium sp. CGR1 (NZ_CP012299.1) | 18.61 | 661170-661110 | -1 | aquaporin family protein (AKG07_RS03080) | 9 |
| | 16.89 | 2218112-2218058 | -1 | sugar ABC transporter substrate-binding protein (AKG07_RS10695) | 26 |
| Microbacterium sp. PAMC 28756 (NZ_CP014313.1) | 17.56 | 1226223-1226163 | -1 | hypothetical protein (AXH82_RS05985) | 17 |
| Microbacterium sp. TPU 3598 DNA (NZ_AP017975.1) | 18.1 | 1202932-1202999 | 1 | hypothetical protein (MST3598_RS05635) | 45 |
| | 16.19 | 3509660-3509602 | -1 | sugar ABC transporter ATP-binding protein (MST3598_RS16730) | 17 |
| Microbacterium sp. XT11 (NZ_CP013859.1) | 17.63 | 1072688-1072639 | -1 | ABC transporter substrate-binding protein (AB663_RS05085) | 5 |
| | 15.67 | 175856-175802 | -1 | maltose ABC transporter substrate-binding | 39 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  |  |  |  | protein (AB663_RS00910) |  |
| Microbacterium testaceum StLB037 DNA (NC_015125.1) | 18.6 | 3169543-3169487 | -1 | transcriptional regulator (MTES_RS14400) | 138 |
| Microterricola viridarii strain ERGS5:02 (NZ_CP014145.1) | 17.93 | 3382572-3382517 | -1 | sugar phosphate isomerase/epimerase (AWU67_RS15480) | 17 |
|  | 17.44 | 2717332-2717386 | 1 | hypothetical protein (AWU67_RS12465) | 2 |
|  | 17.29 | 15867-15801 | -1 | GntR family transcriptional regulator (AWU67_RS00070) | 214 |
|  | 15.34 | 2872238-2872189 | -1 | FAD-dependent oxidoreductase (AWU67_RS13115) | 8 |
|  | 15.3 | 710315-710365 | 1 | hypothetical protein (AWU67_RS03160) | 266 |
| Mobiluncus curtisii ATCC 43063 (NC_014246.1) | 20.99 | 26853-26799 | -1 | succinate-semialdehyde dehydrogenase (NADP(+)) (HMPREF0573_RS00115) | 5 |
|  | 16.49 | 1518925-1518981 | 1 | 50S ribosomal protein L19 (HMPREF0573_RS06470) | 48 |
|  | 15.62 | 765509-765457 | -1 | hypothetical protein (HMPREF0573_RS03280) | 37 |
|  | 15.54 | 1880212-1880265 | 1 | response regulator (HMPREF0573_RS08165) | 94 |
| Mycobacterium abscessus (NC_010397.1) | 15.93 | 1789584-1789640 | 1 | Bacteriophage protein (MAB_1787) | 81 |
| Mycobacterium abscessus strain FLAC005 (NZ_CP014952.1) | 17.3 | 3098053-3097993 | -1 | malate:quinone oxidoreductase (A3N97_RS15190) | 311 |
| Mycobacterium abscessus strain FLAC013 (NZ_CP014955.1) | 15.93 | 1772773-1772829 | 1 | hypothetical protein (A3O00_RS08870) | 81 |
| Mycobacterium abscessus subsp. bolletii 103 (NZ_CP009407.1) | 15.93 | 1774108-1774164 | 1 | hypothetical protein (LA61_RS08890) | 81 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Mycobacterium abscessus subsp. bolletii 50594 plasmid 2 (NC_021279.1) | 16.96 | 64917-64969 | 1 | hypothetical protein (MASS_RS26665) | 100 |
| Mycobacterium abscessus subsp. bolletii strain MA 1948 (NZ_CP009408.1) | 15.93 | 1789073-1789129 | 1 | hypothetical protein (LA62_RS08980) | 81 |
| Mycobacterium abscessus subsp. bolletii strain MC1518 (NZ_CP009613.1) | 15.93 | 1781082-1781138 | 1 | hypothetical protein (NF82_RS08935) | 81 |
| Mycobacterium africanum GM041182 complete genome (NC_015758.1) | 24.77 | 2187796-2187846 | 1 | monooxygenase (MAF_RS10120) | 73 |
|  | 16.73 | 183316-183369 | 1 | NAD(P) transhydrogenase subunit beta (MAF_RS00845) | 36 |
| Mycobacterium avium subsp. paratuberculosis MAP4 (NC_021200.1) | 15.81 | 2321644-2321703 | 1 | TetR family transcriptional regulator (MAP4_RS10515) | 102 |
| Mycobacterium avium subsp. paratuberculosis str. k10 (NC_002944.2) | 15.81 | 1887618-1887559 | -1 | TetR family transcriptional regulator (MAP_RS08785) | 102 |
| Mycobacterium avium subsp. paratuberculosis strain E1 (NZ_CP010113.1) | 15.81 | 2295420-2295479 | 1 | TetR family transcriptional regulator (RC58_RS10490) | 102 |
| Mycobacterium avium subsp. paratuberculosis strain E93 (NZ_CP010114.1) | 15.81 | 2298051-2298110 | 1 | TetR family transcriptional regulator (RE97_RS10500) | 102 |
| Mycobacterium avium subsp. paratuberculosis strain MAP/TANUVAS/TN/India/2008 (NZ_CP015495.1) | 15.81 | 1887618-1887559 | -1 | TetR family transcriptional regulator (A0V42_RS08815) | 102 |
| Mycobacterium bovis BCG Pasteur | 24.77 | 2189421-2189471 | 1 | monooxygenase (BCG_RS10150) | 73 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| 1173P2 (NC_008769.1) | 16.73 | 214866-214919 | 1 | NAD(P) transhydrogenase subunit beta (BCG_RS01000) | 36 |
| Mycobacterium bovis BCG str. ATCC 35743 (NZ_CP003494.1) | 24.77 | 1889021-1889071 | 1 | monooxygenase (BCGT_RS08920) | 73 |
| | 16.73 | 4234506-4234559 | 1 | NAD(P) transhydrogenase subunit beta (BCGT_RS19940) | 36 |
| Mycobacterium bovis BCG str. Korea 1168P (NC_020245.2) | 24.77 | 2159066-2159116 | 1 | monooxygenase (K60_RS09975) | 73 |
| | 16.73 | 185199-185252 | 1 | NAD(P) transhydrogenase subunit beta (K60_RS00840) | 36 |
| Mycobacterium bovis BCG str. Mexico (NC_016804.1) | 24.77 | 2168786-2168836 | 1 | monooxygenase (BCGMEX_RS10025) | 73 |
| | 16.73 | 185199-185252 | 1 | NAD(P) transhydrogenase subunit beta (BCGMEX_RS00840) | 36 |
| Mycobacterium bovis BCG str. Moreau RDJ complete genome (NZ_AM412059.1) | 24.77 | 2171338-2171388 | 1 | monooxygenase (BCGM_RS10045) | 73 |
| | 16.73 | 185193-185246 | 1 | NAD(P) transhydrogenase subunit beta (BCGM_RS00835) | 36 |
| Mycobacterium bovis BCG str. Tokyo 172 DNA (NC_012207.1) | 24.77 | 2171412-2171462 | 1 | monooxygenase (JTY_RS10050) | 73 |
| | 16.73 | 185199-185252 | 1 | NAD(P) transhydrogenase subunit beta (JTY_RS00845) | 36 |
| Mycobacterium bovis BCG str. Tokyo 172 substrain TRCS (NZ_CP014566.1) | 24.77 | 2171410-2171460 | 1 | monooxygenase (AZH48_RS10030) | 73 |
| | 16.73 | 185199-185252 | 1 | NAD(P) transhydrogenase subunit beta (AZH48_RS00835) | 36 |
| Mycobacterium bovis BCG strain 3281 (NZ_CP008744.1) | 24.77 | 2169564-2169614 | 1 | monooxygenase (GS11_RS10040) | 73 |
| | 16.73 | 185198-185251 | 1 | NAD(P) transhydrogenase subunit beta (GS11_RS00840) | 36 |
| Mycobacterium bovis BCG strain Russia 368 (NZ_CP009243.1) | 24.77 | 2171415-2171465 | 1 | monooxygenase (BCGR_RS10045) | 73 |
| | 16.73 | 185196-185249 | 1 | NAD(P) transhydrogenase subunit beta (BCGR_RS00835) | 36 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Mycobacterium bovis strain 1595 (NZ_CP012095.1) | 24.77 | 2183860-2183910 | 1 | monooxygenase (Mb1595_RS10130) | 73 |
| | 16.73 | 185167-185220 | 1 | NAD(P) transhydrogenase subunit beta (Mb1595_RS00840) | 36 |
| Mycobacterium bovis strain ATCC BAA-935 (NZ_CP009449.1) | 24.77 | 2147621-2147671 | 1 | monooxygenase (LH58_RS10065) | 73 |
| | 16.73 | 184747-184800 | 1 | NAD(P) transhydrogenase subunit beta (LH58_RS00850) | 36 |
| Mycobacterium bovis strain BCG-1 (Russia) (NZ_CP013741.1) | 24.77 | 2171711-2171761 | 1 | monooxygenase (BOVR_RS10050) | 73 |
| | 16.73 | 185196-185249 | 1 | NAD(P) transhydrogenase subunit beta (BOVR_RS00835) | 36 |
| Mycobacterium bovis strain SP38 (NZ_CP015773.1) | 24.31 | 1085783-1085833 | 1 | monooxygenase (SZ58_RS04940) | 73 |
| | 16.73 | 3435305-3435358 | 1 | NAD(P) transhydrogenase subunit beta (SZ58_RS15965) | 36 |
| Mycobacterium canettii CIPT 140010059 complete genome (NC_015848.1) | 16.73 | 191637-191690 | 1 | NAD(P) transhydrogenase subunit beta (MCAN_RS00870) | 36 |
| Mycobacterium chelonae CCUG 47445 (NZ_CP007220.1) | 15.61 | 1991172-1991122 | -1 | leucyl aminopeptidase (BB28_RS09875) | 335 |
| Mycobacterium chubuense NBB4 (NC_018027.1) | 15.84 | 2664513-2664572 | 1 | 30S ribosomal protein S1 (MYCCH_RS12620) | 91 |
| Mycobacterium fortuitum strain CT6 (NZ_CP011269.1) | 20.51 | 6251576-6251522 | -1 | 16S rRNA methyltransferase G (XA26_RS29760) | 7 |
| | 19.98 | 4166635-4166579 | -1 | hypothetical protein (XA26_RS19840) | 43 |
| | 19.55 | 3804230-3804294 | 1 | hypothetical protein (XA26_RS18215) | 17 |
| | 16.6 | 3617008-3616949 | -1 | 30S ribosomal protein S1 (XA26_RS17315) | 91 |
| | 15.11 | 444284-444224 | -1 | MFS transporter (XA26_RS02045) | 72 |
| Mycobacterium gilvum PYR-GCK | 22.54 | 1209116-1209171 | 1 | esterase/ diacyl-glycerol transferase | 60 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| (NC_009338.1) | | | | (MFLV_RS05805) | |
| | 17.57 | 4909773-4909724 | -1 | acyl-CoA dehydrogenase (MFLV_RS23155) | 23 |
| | 16.29 | 4195679-4195623 | -1 | dUTPase (MFLV_RS19775) | 70 |
| | 16.22 | 3798413-3798354 | -1 | 30S ribosomal protein S1 (MFLV_RS17880) | 91 |
| Mycobacterium gilvum Spyr1 (NC_014814.1) | 22.54 | 5213367-5213312 | -1 | hypothetical protein (MSPYR1_RS24685) | 60 |
| | 16.29 | 3405359-3405303 | -1 | dUTPase (MSPYR1_RS16135) | 70 |
| | 16.22 | 3014743-3014684 | -1 | 30S ribosomal protein S1 (MSPYR1_RS14285) | 91 |
| | 15.78 | 3577814-3577873 | 1 | aldehyde dehydrogenase (MSPYR1_RS17045) | 40 |
| Mycobacterium goodii strain X7B (NZ_CP012150.1) | 16.25 | 5969358-5969296 | -1 | SAM-dependent methyltransferase (AFA91_RS27860) | 99 |
| Mycobacterium haemophilum DSM 44634 strain ATCC 29548 (NZ_CP011883.2) | 16.19 | 408604-408663 | 1 | hypothetical protein (B586_RS01890) | 13 |
| | 15.56 | 1112421-1112495 | 1 | hypothetical protein (B586_RS05315) | 161 |
| Mycobacterium immunogenum strain CCUG 47286 (NZ_CP011530.1) | 17.47 | 4394659-4394597 | -1 | AsnC family transcriptional regulator (ABG82_RS21770) | 389 |
| | 15.18 | 3148105-3148046 | -1 | transketolase (ABG82_RS15345) | 2 |
| Mycobacterium liflandii 128FXT (NC_020133.1) | 20.47 | 3552989-3553040 | 1 | hypothetical protein (MULP_RS15355) | 70 |
| | 16.46 | 2276480-2276530 | 1 | hypothetical protein (MULP_RS09850) | 7 |
| | 15.34 | 3623588-3623652 | 1 | TetR family transcriptional regulator (MULP_RS15640) | 85 |
| Mycobacterium marinum E11 main genome (NZ_HG917972.2) | 20.47 | 2705668-2705617 | -1 | hypothetical protein (MMARE11_RS11245) | 70 |
| | 16.54 | 2228845-2228895 | 1 | hypothetical protein | 7 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (MMARE11_RS09125) | |
| | 15.34 | 2608576-2608512 | -1 | TetR family transcriptional regulator (MMARE11_RS10875) | 85 |
| Mycobacterium marinum M (NC_010612.1) | 20.47 | 2842763-2842712 | -1 | hypothetical protein (MMAR_RS11735) | 70 |
| | 16.46 | 2346618-2346668 | 1 | hypothetical protein (MMAR_RS09565) | 7 |
| | 15.34 | 2745480-2745416 | -1 | TetR family transcriptional regulator (MMAR_RS11360) | 85 |
| Mycobacterium neoaurum VKM Ac-1815D (NC_023036.2) | 16.66 | 4181172-4181233 | 1 | hypothetical protein (D174_RS19485) | 63 |
| | 15.99 | 4248495-4248433 | -1 | F0F1 ATP synthase subunit C (D174_RS19810) | 17 |
| Mycobacterium phlei strain CCUG 21000 (NZ_CP014475.1) | 16.65 | 3983075-3983127 | 1 | DNA-3-methyladenine glycosylase (MPHLCCUG_RS19105) | 16 |
| | 16.6 | 2811559-2811500 | -1 | 30S ribosomal protein S1 (MPHLCCUG_RS13480) | 91 |
| Mycobacterium rhodesiae NBB3 (NC_016604.1) | 16.99 | 4624964-4625023 | 1 | 30S ribosomal protein S1 (MYCRHN_RS22435) | 91 |
| | 16.97 | 761121-761068 | -1 | DNA-directed RNA polymerase subunit beta' (MYCRHN_RS03650) | 141 |
| Mycobacterium smegmatis genome assembly NCTC81591 (NZ_LN831039.1) | 16.41 | 3141723-3141672 | -1 | 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (AT701_RS15105) | 36 |
| Mycobacterium smegmatis JS623 plasmid pMYCSM02 (NC_019958.1) | 17.87 | 29809-29757 | -1 | hypothetical protein (MYCSM_RS33235) | 385 |
| Mycobacterium smegmatis JS623 (NC_019966.1) | 17.36 | 2977710-2977769 | 1 | 30S ribosomal protein S1 (MYCSM_RS14600) | 91 |
| | 15.17 | 21645-21589 | -1 | serine/threonine protein kinase (MYCSM_RS00115) | 30 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Mycobacterium smegmatis str. MC2 155 (NC_008596.1) | 16.41 | 3078808-3078757 | -1 | 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (MSMEG_3009) | 36 |
| Mycobacterium smegmatis str. MC2 155 (NC_018289.1) | 16.41 | 3080422-3080371 | -1 | 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (MSMEI_RS14815) | 36 |
| Mycobacterium smegmatis str. MC2 155 (NZ_CP009494.1) | 16.41 | 3078853-3078802 | -1 | 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (LJ00_RS14800) | 36 |
| Mycobacterium smegmatis strain INHR1 (NZ_CP009495.1) | 16.41 | 3078887-3078836 | -1 | 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (LI99_RS14800) | 36 |
| Mycobacterium smegmatis strain INHR2 (NZ_CP009496.1) | 16.41 | 3078875-3078824 | -1 | 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (LI98_RS14795) | 36 |
| Mycobacterium sp. EPa45 (NZ_CP011773.1) | 17.68 | 3780340-3780281 | -1 | 30S ribosomal protein S1 (AB431_RS18105) | 91 |
|  | 16.35 | 4094521-4094465 | -1 | hypothetical protein (AB431_RS19610) | 87 |
|  | 16.22 | 572894-572950 | 1 | hypothetical protein (AB431_RS02575) | 88 |
|  | 15.06 | 5271360-5271312 | -1 | aminoglycoside phosphotransferase (AB431_RS24895) | 3 |
| Mycobacterium sp. JLS (NC_009077.1) | 19.01 | 2700344-2700396 | 1 | ATPase AAA (MJLS_RS12880) | 9 |
|  | 16.1 | 3939077-3939026 | -1 | (2Fe-2S)-binding protein (MJLS_RS18635) | 133 |
|  | 15.84 | 3157092-3157033 | -1 | 30S ribosomal protein S1 (MJLS_RS15115) | 91 |
|  | 15.78 | 1201711-1201770 | 1 | HAD family hydrolase (MJLS_RS05610) | 7 |
|  | 15.33 | 1406291-1406347 | 1 | alpha/beta hydrolase (MJLS_RS06560) | 11 |
| Mycobacterium sp. KMS (NC_008705.1) | 19.01 | 2714603-2714655 | 1 | ATPase AAA (MKMS_RS12840) | 9 |
|  | 15.84 | 3195040-3194981 | -1 | 30S ribosomal protein S1 (MKMS_RS15200) | 91 |
|  | 15.78 | 1198153-1198212 | 1 | hypothetical protein (MKMS_RS05525) | 7 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Mycobacterium sp. MCS (NC_008146.1) | 19.01 | 2696715-2696767 | 1 | ATPase AAA (MMCS_RS12745) | 9 |
| | 15.84 | 3177152-3177093 | -1 | 30S ribosomal protein S1 (MMCS_RS15105) | 91 |
| | 15.78 | 1193844-1193903 | 1 | hypothetical protein (MMCS_RS05500) | 7 |
| Mycobacterium sp. NRRL B-3805 (NZ_CP011022.1) | 16.66 | 4181243-4181304 | 1 | hypothetical protein (MyAD_RS19495) | 63 |
| | 15.99 | 4248566-4248504 | -1 | F0F1 ATP synthase subunit C (MyAD_RS19820) | 17 |
| Mycobacterium sp. QIA-37 (NZ_CP010071.1) | 18.38 | 1151605-1151667 | 1 | cytochrome (Chelonae_RS05625) | 91 |
| Mycobacterium sp. VKM Ac-1817D (NZ_CP009914.1) | 20.51 | 6321182-6321128 | -1 | 16S rRNA methyltransferase G (G155_RS30185) | 7 |
| | 18.79 | 5424084-5424140 | 1 | hypothetical protein (G155_RS25930) | 64 |
| | 16.6 | 3626181-3626122 | -1 | 30S ribosomal protein S1 (G155_RS17390) | 91 |
| | 15.11 | 515037-514977 | -1 | MFS transporter (G155_RS02340) | 72 |
| Mycobacterium tuberculosis 49-02 complete genome (NZ_HG813240.1) | 24.77 | 2173566-2173616 | 1 | alkane 1-monooxygenase (MT49_RS10070) | 73 |
| | 16.73 | 183230-183283 | 1 | NAD(P) transhydrogenase subunit beta (MT49_RS00840) | 36 |
| Mycobacterium tuberculosis 7199-99 complete genome (NC_020089.1) | 24.77 | 2191699-2191749 | 1 | monooxygenase (MT7199_RS10100) | 73 |
| | 16.73 | 185188-185241 | 1 | NAD(P) transhydrogenase subunit beta (MT7199_RS00840) | 36 |
| Mycobacterium tuberculosis BT1 (NZ_CP002883.1) | 24.77 | 2173137-2173187 | 1 | alkane 1-monooxygenase (HKBT1_RS10085) | 73 |
| | 16.73 | 183287-183340 | 1 | NAD(P) transhydrogenase subunit beta (HKBT1_RS00840) | 36 |
| Mycobacterium tuberculosis BT2 | 24.77 | 2166350-2166400 | 1 | alkane 1-monooxygenase | 73 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| (NZ_CP002882.1) | | | | (HKBT2_RS10060) | |
| | 16.73 | 183286-183339 | 1 | NAD(P) transhydrogenase subunit beta (HKBT2_RS00840) | 36 |
| Mycobacterium tuberculosis CCDC5079 (NC_021251.1) | 20.33 | 2174956-2175006 | 1 | alkane 1-monooxygenase (CFBS_RS10115) | 73 |
| | 16.73 | 183231-183284 | 1 | NAD(P) transhydrogenase subunit beta (CFBS_RS00840) | 36 |
| Mycobacterium tuberculosis CCDC5180 (NC_017522.1) | 24.77 | 2168763-2168813 | 1 | alkane 1-monooxygenase (CCDC5180_RS10115) | 73 |
| | 16.73 | 183230-183283 | 1 | NAD(P) transhydrogenase subunit beta (CCDC5180_RS00840) | 36 |
| Mycobacterium tuberculosis CCDC5180 (NZ_CP002885.1) | 24.77 | 2173333-2173383 | 1 | alkane 1-monooxygenase (CFBR_RS10085) | 73 |
| | 16.73 | 183230-183283 | 1 | NAD(P) transhydrogenase subunit beta (CFBR_RS00840) | 36 |
| Mycobacterium tuberculosis CDC1551 (NC_002755.2) | 16.73 | 185137-185190 | 1 | NAD(P) transhydrogenase subunit beta (MT_RS00840) | 36 |
| | 15.69 | 2184593-2184643 | 1 | monooxygenase (MT_RS10100) | 73 |
| Mycobacterium tuberculosis CTRI-2 (NC_017524.1) | 24.77 | 2180824-2180874 | 1 | monooxygenase (MTCTRI2_RS10125) | 73 |
| | 16.73 | 184725-184778 | 1 | NAD(P) transhydrogenase subunit beta (MTCTRI2_RS00845) | 36 |
| Mycobacterium tuberculosis EAI5 (NC_021740.1) | 24.77 | 2181844-2181894 | 1 | monooxygenase (M943_RS10115) | 73 |
| | 16.73 | 184973-185026 | 1 | NAD(P) transhydrogenase subunit beta (M943_RS00845) | 36 |
| Mycobacterium tuberculosis EAI5/NITR206 (NC_021194.1) | 24.77 | 2181480-2181530 | 1 | monooxygenase (J114_RS10135) | 73 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Mycobacterium tuberculosis F11 (NC_009565.1) | 24.77 | 2195516-2195566 | 1 | monooxygenase (TBFG_RS10180) | 73 |
| | 16.73 | 185285-185338 | 1 | NAD(P) transhydrogenase subunit beta (TBFG_RS00840) | 36 |
| Mycobacterium tuberculosis H37Ra (NC_009525.1) | 24.77 | 2197160-2197210 | 1 | monooxygenase (MRA_RS10230) | 73 |
| | 16.73 | 186329-186382 | 1 | NAD(P) transhydrogenase subunit beta (MRA_RS00855) | 36 |
| Mycobacterium tuberculosis H37Rv (NC_000962.3) | 24.77 | 2187261-2187311 | 1 | monooxygenase (Rv1936) | 73 |
| | 16.73 | 184969-185022 | 1 | NAD(P) transhydrogenase subunit beta PntB (Rv0157) | 30 |
| Mycobacterium tuberculosis H37Rv (NC_018143.2) | 24.77 | 2187268-2187318 | 1 | monooxygenase (RVBD_RS10160) | 73 |
| | 16.73 | 184967-185020 | 1 | NAD(P) transhydrogenase subunit beta (RVBD_RS00840) | 36 |
| Mycobacterium tuberculosis H37Rv (NZ_CP009480.1) | 24.77 | 2182565-2182615 | 1 | monooxygenase (LH57_RS10210) | 73 |
| | 16.73 | 184815-184868 | 1 | NAD(P) transhydrogenase subunit beta (LH57_RS00845) | 36 |
| Mycobacterium tuberculosis H37RvSiena (NZ_CP007027.1) | 24.77 | 2186649-2186699 | 1 | monooxygenase (Y980_RS10165) | 73 |
| | 16.73 | 184967-185020 | 1 | NAD(P) transhydrogenase subunit beta (Y980_RS00840) | 36 |
| Mycobacterium tuberculosis HKBS1 (NZ_CP002871.1) | 24.77 | 2172407-2172457 | 1 | alkane 1-monooxygenase (HKBS1_RS10075) | 73 |
| | 16.73 | 183231-183284 | 1 | NAD(P) transhydrogenase subunit beta (HKBS1_RS00840) | 36 |
| Mycobacterium tuberculosis K (NZ_CP007803.1) | 20.21 | 2159806-2159856 | 1 | alkane 1-monooxygenase (MTBK_RS09995) | 73 |
| | 16.73 | 183165-183218 | 1 | NAD(P) transhydrogenase subunit beta (MTBK_RS00840) | 36 |
| Mycobacterium tuberculosis KZN | 24.77 | 2235812-2235762 | -1 | monooxygenase (TBMG_RS10750) | 73 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| 1435 (NC_012943.1) | 16.73 | 184908-184961 | 1 | NAD(P) transhydrogenase subunit beta (TBMG_RS00845) | 36 |
| Mycobacterium tuberculosis KZN 4207 (NC_016768.1) | 24.77 | 2232543-2232493 | -1 | monooxygenase (TBSG_RS10740) | 73 |
| | 16.73 | 184907-184960 | 1 | NAD(P) transhydrogenase subunit beta (TBSG_RS00845) | 36 |
| Mycobacterium tuberculosis KZN 605 (NC_018078.1) | 24.77 | 2235693-2235643 | -1 | monooxygenase (TBXG_RS10755) | 73 |
| | 16.73 | 184906-184959 | 1 | NAD(P) transhydrogenase subunit beta (TBXG_RS00845) | 36 |
| Mycobacterium tuberculosis str. Beijing/NITR203 (NC_021054.1) | 24.99 | 2187067-2187117 | 1 | monooxygenase (J112_RS10210) | 73 |
| | 16.73 | 184956-185009 | 1 | NAD(P) transhydrogenase subunit beta (J112_RS00850) | 36 |
| Mycobacterium tuberculosis str. Erdman = ATCC 35801 DNA (NC_020559.1) | 24.77 | 2178334-2178384 | 1 | monooxygenase (ERDMAN_RS10140) | 73 |
| | 16.73 | 184282-184335 | 1 | NAD(P) transhydrogenase subunit beta (ERDMAN_RS00840) | 36 |
| Mycobacterium tuberculosis str. Haarlem (NC_022350.1) | 24.77 | 2186892-2186942 | 1 | monooxygenase (TBHG_RS10090) | 73 |
| | 16.73 | 185287-185340 | 1 | NAD(P) transhydrogenase subunit beta (TBHG_RS00840) | 36 |
| Mycobacterium tuberculosis str. Kurono DNA (NZ_AP014573.1) | 24.77 | 2192698-2192748 | 1 | monooxygenase (KURONO_RS10185) | 73 |
| | 16.73 | 186176-186229 | 1 | NAD(P) transhydrogenase subunit beta (KURONO_RS00850) | 36 |
| Mycobacterium tuberculosis strain 22103 (NZ_CP010339.1) | 24.77 | 2185332-2185382 | 1 | monooxygenase (RN14_RS10075) | 73 |
| | 16.73 | 185184-185237 | 1 | NAD(P) transhydrogenase subunit beta (RN14_RS00840) | 36 |
| Mycobacterium tuberculosis strain 22115 (NZ_CP010337.1) | 24.77 | 2190192-2190242 | 1 | monooxygenase (RN12_RS10150) | 73 |
| | 16.73 | 185165-185218 | 1 | NAD(P) transhydrogenase subunit beta (RN12_RS00835) | 36 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Mycobacterium tuberculosis strain 26105 (NZ_CP010340.1) | 24.77 | 2199709-2199759 | 1 | alkane 1-monooxygenase (RN15_RS10215) | 73 |
| | 16.73 | 185418-185471 | 1 | NAD(P) transhydrogenase subunit beta (RN15_RS00835) | 36 |
| Mycobacterium tuberculosis strain 37004 (NZ_CP010338.1) | 24.77 | 2182762-2182812 | 1 | monooxygenase (RN13_RS10115) | 73 |
| | 16.73 | 185172-185225 | 1 | NAD(P) transhydrogenase subunit beta (RN13_RS00835) | 36 |
| Mycobacterium tuberculosis strain 96075 (NZ_CP009426.1) | 24.77 | 2167819-2167869 | 1 | alkane 1-monooxygenase (LJ70_RS10085) | 73 |
| | 16.73 | 182314-182367 | 1 | NAD(P) transhydrogenase subunit beta (LJ70_RS00840) | 36 |
| Mycobacterium tuberculosis strain 96121 (NZ_CP009427.1) | 24.77 | 2195453-2195503 | 1 | monooxygenase (HR37_RS10225) | 73 |
| | 16.73 | 185032-185085 | 1 | NAD(P) transhydrogenase subunit beta (HR37_RS00845) | 36 |
| Mycobacterium tuberculosis strain F28 (NZ_CP010330.1) | 24.77 | 2194218-2194268 | 1 | monooxygenase (RN05_RS10215) | 73 |
| | 16.73 | 184967-185020 | 1 | NAD(P) transhydrogenase subunit beta (RN05_RS00835) | 36 |
| Mycobacterium tuberculosis strain KIT87190 (NZ_CP007809.1) | 24.77 | 2166335-2166385 | 1 | alkane 1-monooxygenase (ER17_RS10060) | 73 |
| | 16.73 | 182372-182425 | 1 | NAD(P) transhydrogenase subunit beta (ER17_RS00840) | 36 |
| Mycobacterium tuberculosis strain SCAID 187.0 (NZ_CP012506.1) | 24.77 | 2160992-2161042 | 1 | alkane 1-monooxygenase (AFL40_RS10020) | 73 |
| | 16.73 | 181412-181465 | 1 | NAD(P) transhydrogenase subunit beta (AFL40_RS00825) | 36 |
| Mycobacterium tuberculosis strain ZMC13-264 (NZ_CP009100.1) | 24.77 | 2187257-2187307 | 1 | alkane 1-monooxygenase (IZ84_RS10135) | 73 |

| Organism<br>(Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs<br>(Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 16.73 | 185023-185076 | 1 | NAD(P) transhydrogenase subunit beta (IZ84_RS00845) | 36 |
| Mycobacterium tuberculosis strain ZMC13-88 (NZ_CP009101.1) | 24.77 | 2187289-2187339 | 1 | alkane 1-monooxygenase (JE53_RS10145) | 73 |
|  | 16.73 | 184988-185041 | 1 | NAD(P) transhydrogenase subunit beta (JE53_RS00850) | 36 |
| Mycobacterium tuberculosis W-148 (NZ_CP012090.1) | 24.77 | 1954309-1954359 | 1 | alkane 1-monooxygenase (TBPG_RS08905) | 73 |
|  | 16.73 | 183231-183284 | 1 | NAD(P) transhydrogenase subunit beta (TBPG_RS00835) | 36 |
| Mycobacterium vaccae 95051 (NZ_CP011491.1) | 26.53 | 5794907-5794851 | -1 | esterase/ diacyl-glycerol transferase (MYVA_RS27135) | 58 |
|  | 16 | 3061381-3061433 | 1 | acyl-CoA synthetase (MYVA_RS14355) | 21 |
|  | 15.36 | 505581-505518 | -1 | hypothetical protein (MYVA_RS02330) | 7 |
| Mycobacterium vanbaalenii PYR-1 (NC_008726.1) | 30 | 6033960-6033904 | -1 | esterase/ diacyl-glycerol transferase (MVAN_RS28400) | 61 |
|  | 17.47 | 3573570-3573511 | -1 | 30S ribosomal protein S1 (MVAN_RS16845) | 91 |
|  | 17.16 | 380445-380510 | 1 | putative GAF sensor protein (MVAN_RS01770) | 22 |
|  | 15.13 | 2379314-2379255 | -1 | aldehyde dehydrogenase (MVAN_RS11160) | 40 |
| Neomicrococcus aestuarii strain B18 (NZ_CP018135.1) | 19.92 | 1224527-1224475 | -1 | ABC transporter permease (BHE16_RS05425) | 21 |
|  | 17.46 | 1469870-1469937 | 1 | hypothetical protein (BHE16_RS06505) | 70 |
| Nocardia brasiliensis ATCC 700358 (NC_018681.1) | 16.52 | 466485-466426 | -1 | alpha/beta hydrolase (O3I_RS02080) | 32 |
|  | 16.04 | 3190100-3190039 | -1 | 5-aminolevulinate synthase | 148 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (O3I_RS14450) | |
| Nocardia brasiliensis strain FDAARGOS_352 (NZ_CP022088.1) | 16.52 | 6086749-6086808 | 1 | alpha/beta hydrolase (CEQ30_RS27470) | 32 |
| | 15.19 | 3398943-3399004 | 1 | 5-aminolevulinate synthase (CEQ30_RS15060) | 148 |
| Nocardia cyriacigeorgica GUH-2 complete genome (NC_016887.1) | 19.21 | 425232-425172 | -1 | alpha/beta hydrolase (NOCYR_RS01960) | 32 |
| | 15.23 | 2129230-2129175 | -1 | alpha/beta hydrolase (NOCYR_RS09530) | 1 |
| Nocardia farcinica genome assembly NCTC11134, plasmid : 2 (NZ_LN868939.1) | 15.62 | 363725-363784 | 1 | alpha/beta hydrolase (AMO33_RS18820) | 0 |
| Nocardia farcinica IFM 10152 DNA (NC_006361.1) | 17.88 | 389632-389573 | -1 | alpha/beta hydrolase (NFA_RS01905) | 32 |
| | 15.47 | 4424930-4424995 | 1 | hypothetical protein (NFA_RS30625) | 58 |
| Nocardia nova SH22a (NZ_CP006850.1) | 20.73 | 7697964-7697910 | -1 | alpha/beta hydrolase (NONO_RS34805) | 26 |
| | 15.5 | 7515908-7515859 | -1 | hypothetical protein (NONO_RS39425) | 33 |
| Nocardia seriolae DNA, strain: UTF1 (NZ_AP017900.1) | 22.21 | 6584176-6584229 | 1 | nitrate reductase molybdenum cofactor assembly chaperone (NSERUTF1_RS30720) | 62 |
| | 19.19 | 552477-552424 | -1 | acetoin dehydrogenase dihydrolipoyllysine-residue acetyltransferase subunit (NSERUTF1_RS02545) | 26 |
| Nocardia seriolae DNA, strain: UTF1 (NZ_AP017900.1) | 15.8 | 4227960-4227909 | -1 | cytochrome P450 (NSERUTF1_RS19455) | 34 |
| | 15.75 | 5180104-5180039 | -1 | KR domain-containing protein (NSERUTF1_RS24110) | 79 |
| | 15.72 | 957415-957359 | -1 | IS4 family transposase (NSERUTF1_RS04405) | 398 |
| Nocardia seriolae strain EM150506 (NZ_CP017839.1) | 22.21 | 2300052-2299999 | -1 | nitrate reductase molybdenum cofactor assembly chaperone (NS506_RS10565) | 62 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 19.19 | 204678-204731 | 1 | alpha/beta hydrolase (NS506_RS01055) | 26 |
| | 15.8 | 4746174-4746123 | -1 | cytochrome P450 (NS506_RS21800) | 34 |
| | 15.75 | 6052574-6052509 | -1 | KR domain-containing protein (NS506_RS28010) | 79 |
| Nocardia soli strain Y48 (NZ_CP018082.1) | 15.77 | 376014-376071 | 1 | hypothetical protein (BOX37_RS01685) | 42 |
| Nocardia terpenica strain NC_YFY_NT001 (NZ_CP023778.1) | 17.03 | 7074978-7075034 | 1 | xylose isomerase (CRH09_RS31310) | 7 |
| | 16.58 | 8308608-8308556 | -1 | alpha/beta hydrolase (CRH09_RS37120) | 26 |
| Nonomuraea sp. ATCC 55076 (NZ_CP017717.1) | 20 | 9630594-9630535 | -1 | DUF397 domain-containing protein (BKM31_RS43705) | 1 |
| | 16.45 | 5653656-5653608 | -1 | sugar ABC transporter (BKM31_RS25565) | 30 |
| | 16.07 | 4124855-4124911 | 1 | CBS domain-containing protein (BKM31_RS18760) | 79 |
| Olsenella sp. oral taxon 807 strain F0089 (NZ_CP012069.2) | 17.57 | 2778345-2778401 | 1 | hypothetical protein (ADJ70_RS11980) | 40 |
| Olsenella uli DSM 7084 (NC_014363.1) | 16.27 | 208494-208553 | 1 | LysR family transcriptional regulator (OLSU_RS08990) | 24 |
| | 15.29 | 264364-264414 | 1 | Fic family protein (OLSU_RS01165) | 57 |
| Paenarthrobacter aurescens TC1 (NC_008711.1) | 17.57 | 678612-678551 | -1 | MFS transporter (AAUR_RS03280) | 83 |
| | 17.13 | 2184804-2184862 | 1 | sugar ABC transporter substrate-binding protein (AAUR_RS09910) | 88 |
| | 15.44 | 4054153-4054097 | -1 | LacI family transcriptional regulator (AAUR_RS18450) | 420 |
| | 15.34 | 2273818-2273883 | 1 | 30S ribosomal protein S1 (AAUR_RS10315) | 94 |
| | 16.11 | 2729216-2729267 | 1 | hypothetical protein (BAY61_RS12710) | 36 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.6 | 5375237-5375179 | -1 | TetR/AcrR family transcriptional regulator (BAY61_RS24705) | 17 |
| Propionibacterium acnes ATCC 11828 (NC_017550.1) | 19.1 | 1142938-1142874 | -1 | hypothetical protein (TIIST44_RS05220) | 45 |
| Propionibacterium acnes TypeIA2 P.acn17 (NC_016512.1) | 19.1 | 146843-146779 | -1 | hypothetical protein (TIA2EST22_RS00625) | 45 |
| Propionibacterium acnes TypeIA2 P.acn31 (NC_016511.1) | 19.1 | 146852-146788 | -1 | hypothetical protein (TIA2EST36_RS00620) | 45 |
| Propionibacterium acnes TypeIA2 P.acn33 (NC_016516.1) | 19.1 | 146855-146791 | -1 | hypothetical protein (TIA2EST2_RS00620) | 45 |
| Propionibacterium acnes TypeIA2 P.acn33 (NC_016516.1) | 15.02 | 1290367-1290317 | -1 | 2-deoxyribose-5-phosphate aldolase (TIA2EST2_RS05990) | 24 |
| Propionibacterium freudenreichii strain P.UF1 (NZ_CP018002.1) | 17.83 | 2035851-2035913 | 1 | pyruvate oxidase (BMR99_RS09195) | 44 |
|  | 16.05 | 722929-722867 | -1 | methylmalonyl-CoA mutase small subunit (BMR99_RS03065) | 224 |
|  | 15.39 | 1543147-1543107 | -1 | transcriptional regulator (BMR99_RS06855) | 8 |
|  | 15.07 | 2595505-2595555 | 1 | citrate synthase (BMR99_RS11540) | 45 |
| Propionibacterium freudenreichii subsp. freudenreichii strain DSM 20271 (NZ_CP010341.1) | 17.83 | 510685-510623 | -1 | pyruvate oxidase (RM25_RS02000) | 44 |
|  | 16.05 | 852187-852125 | -1 | methylmalonyl-CoA mutase small subunit (RM25_RS03585) | 224 |
|  | 15.39 | 1613530-1613478 | -1 | transcriptional regulator (RM25_RS07000) | 20 |
|  | 15.07 | 2613515-2613565 | 1 | citrate synthase (RM25_RS11475) | 45 |
| Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1 (NC_014215.1) | 17.83 | 540373-540311 | -1 | pyruvate oxidase (PFREUD_RS02185) | 44 |
|  | 16.05 | 876756-876694 | -1 | methylmalonyl-CoA mutase small subunit (PFREUD_RS03765) | 224 |
|  | 15.39 | 1644669-1644617 | -1 | transcriptional regulator | 20 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | | | | (PFREUD_RS07175) | |
| | 15.07 | 2579483-2579533 | 1 | citrate synthase (PFREUD_RS11405) | 5 |
| Propionibacterium freudenreichii subsp. shermanii isolate PFREUDJS1 (NZ_LN997841.1) | 17.83 | 2329779-2329841 | 1 | pyruvate oxidase (PFREUDJS001_RS10290) | 44 |
| | 16.05 | 755246-755184 | -1 | methylmalonyl-CoA mutase small subunit (PFREUDJS001_RS03180) | 224 |
| | 15.07 | 2620242-2620292 | 1 | citrate synthase (PFREUDJS001_RS11525) | 45 |
| Propionibacterium sp. oral taxon 193 strain F0672 (NZ_CP017040.1) | 15 | 580710-580763 | 1 | homoserine O-acetyltransferase (BCB70_RS02700) | 477 |
| Propionimicrobium sp. Marseille-P3275 strain Marseille-P3275T contig00001 (NZ_LT706985.1) | 23.61 | 1778691-1778741 | 1 | LacI family transcriptional regulator (CZ356_RS08345) | 23 |
| | 19.78 | 764873-764823 | -1 | glycosyltransferase family 2 protein (CZ356_RS03665) | 76 |
| | 18.17 | 581857-581803 | -1 | DNA polymerase III subunit epsilon (CZ356_RS02670) | 255 |
| | 16.68 | 1275582-1275638 | 1 | MFS transporter (CZ356_RS06130) | 4 |
| Pseudarthrobacter chlorophenolicus A6 plasmid pACHL01 (NC_011879.1) | 17.72 | 279963-279898 | -1 | hypothetical protein (ACHL_RS21730) | 16 |
| Pseudarthrobacter chlorophenolicus A6 (NC_011886.1) | 25 | 676358-676423 | 1 | methylmalonate-semialdehyde dehydrogenase (CoA acylating) (ACHL_RS03150) | 2 |
| | 21.97 | 95577-95640 | 1 | tripartite tricarboxylate transporter TctB family protein (ACHL_RS00470) | 23 |
| | 17.17 | 404622-404675 | 1 | alpha-N-arabinofuranosidase (ACHL_RS01895) | 14 |
| | 15.61 | 357905-357964 | 1 | dihydroxyacetone kinase subunit DhaK (ACHL_RS01655) | 73 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.34 | 2039538-2039603 | 1 | 30S ribosomal protein S1 (ACHL_RS09090) | 94 |
| Pseudarthrobacter phenanthrenivorans Sphe3 plasmid pASPHE302 (NC_015147.1) | 18.43 | 75616-75561 | -1 | ferredoxin--NAD(+) reductase (ASPHE3_RS21045) | 183 |
| Pseudarthrobacter phenanthrenivorans Sphe3 (NC_015145.1) | 18.35 | 3706123-3706068 | -1 | sugar ABC transporter substrate-binding protein (ASPHE3_RS17190) | 3 |
|  | 17.88 | 2273699-2273754 | 1 | LacI family DNA-binding transcriptional regulator (ASPHE3_RS10460) | 17 |
|  | 17.13 | 618889-618838 | -1 | 2-hydroxyacid dehydrogenase (ASPHE3_RS03000) | 485 |
|  | 17.04 | 3203787-3203847 | 1 | two-component sensor histidine kinase (ASPHE3_RS21255) | 17 |
|  | 15.27 | 1917982-1918047 | 1 | 30S ribosomal protein S1 (ASPHE3_RS08800) | 94 |
| Pseudarthrobacter sulfonivorans strain Ar51 (NZ_CP013747.1) | 24.63 | 2250041-2249980 | -1 | sugar ABC transporter ATP-binding protein (AU252_RS10090) | 5 |
|  | 18.68 | 1830214-1830155 | -1 | hypothetical protein (AU252_RS08050) | 0 |
|  | 16.76 | 4278609-4278677 | 1 | ribonuclease HII (AU252_RS19425) | 74 |
|  | 16.6 | 3355696-3355746 | 1 | ABC transporter substrate-binding protein (AU252_RS15200) | 35 |
|  | 16.06 | 2996339-2996282 | -1 | copper oxidase (AU252_RS13495) | 45 |
|  | 15.65 | 267906-267857 | -1 | aldehyde dehydrogenase (AU252_RS01160) | 7 |
|  | 15.65 | 262426-262377 | -1 | aldehyde dehydrogenase (AU252_RS01140) | 7 |
|  | 15.62 | 3777164-3777116 | -1 | type I pantothenate kinase (AU252_RS17175) | 33 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.27 | 4860429-4860364 | -1 | 30S ribosomal protein S1 (AU252_RS22125) | 94 |
| Pseudonocardia sp. EC080610-09 plasmid pBCI2-1 (NZ_CP012182.1) | 19.87 | 279077-279030 | -1 | VOC family protein (AD006_RS29515) | 68 |
| Pseudonocardia sp. EC080619-01 plasmid pBCI1-2 (NZ_CP012185.1) | 19.87 | 769514-769561 | 1 | VOC family protein (AD017_RS31735) | 68 |
| Pseudopropionibacterium propionicum F0230a (NC_018142.1) | 16.43 | 301894-301959 | 1 | hypothetical protein (HMPREF9154_RS01395) | 12 |
| Renibacterium salmoninarum ATCC 33209 (NC_010168.1) | 18.03 | 1074795-1074848 | 1 | hypothetical protein (RSAL33209_RS05485) | 10 |
|  | 16.29 | 1070998-1070939 | -1 | hypothetical protein (RSAL33209_RS05450) | 64 |
|  | 16.23 | 1005759-1005815 | 1 | membrane protein (RSAL33209_RS05135) | 92 |
|  | 15.18 | 1611245-1611182 | -1 | methylmalonate-semialdehyde dehydrogenase (CoA acylating) (RSAL33209_RS08115) | 17 |
|  | 15.14 | 2957917-2957855 | -1 | Nif3-like dinuclear metal center hexameric protein (RSAL33209_RS14620) | 231 |
| Rhodococcus aetherivorans strain IcdP1 (NZ_CP011341.1) | 16.81 | 2510931-2510983 | 1 | malate:quinone oxidoreductase (AAT18_RS11550) | 36 |
| Rhodococcus erythropolis CCM2595 (NC_022115.1) | 18.48 | 137578-137631 | 1 | TetR family transcriptional regulator (O5Y_RS00625) | 7 |
|  | 16.01 | 3652209-3652256 | 1 | cytosol aminopeptidase (O5Y_RS16480) | 255 |
| Rhodococcus erythropolis PR4 DNA (NC_012490.1) | 16.01 | 3959281-3959328 | 1 | cytosol aminopeptidase (RER_RS20095) | 255 |
|  | 15.3 | 2862098-2862037 | -1 | D-Ala-D-Ala carboxypeptidase (RER_RS15290) | 34 |
| Rhodococcus erythropolis R138 | 16.01 | 3214398-3214351 | -1 | cytosol aminopeptidase (H351_RS15050) | 255 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| (NZ_CP007255.1) | | | | | |
| Rhodococcus erythropolis strain BG43 (NZ_CP011295.1) | 18.48 | 137863-137916 | 1 | TetR family transcriptional regulator (XU06_RS00630) | 7 |
| | 16.01 | 3690230-3690277 | 1 | cytosol aminopeptidase (XU06_RS16800) | 255 |
| Rhodococcus fascians D188 (NZ_CP015235.1) | 16.47 | 133189-133127 | -1 | gamma-aminobutyraldehyde dehydrogenase (A3L23_RS00625) | 418 |
| Rhodococcus jostii RHA1 (NC_008268.1) | 16.62 | 7784307-7784251 | -1 | NADH dehydrogenase (RHA1_RS35505) | 363 |
| | 16.19 | 2609128-2609176 | 1 | alanine racemase (RHA1_RS12030) | 50 |
| Rhodococcus opacus B4 DNA (NC_012522.1) | 15.99 | 4334716-4334769 | 1 | hypothetical protein (ROP_RS19920) | 49 |
| | 15.69 | 7609996-7610064 | 1 | hypothetical protein (ROP_RS40775) | 144 |
| Rhodococcus sp. B7740 (NZ_CP010797.1) | 18.19 | 4970838-4970892 | 1 | MFS transporter (NY08_RS23335) | 23 |
| | 16.04 | 3887305-3887364 | 1 | DNA-binding protein (NY08_RS18010) | 96 |
| Rhodococcus sp. PBTS2 (NZ_CP015220.1) | 16.47 | 3411253-3411315 | 1 | gamma-aminobutyraldehyde dehydrogenase (A3Q41_RS16235) | 418 |
| Rhodoluna lacicola strain MWH-Ta8 (NZ_CP007490.1) | 15.68 | 1202741-1202801 | 1 | branched-chain amino acid ABC transporter permease (RHOLA_RS05925) | 17 |
| | 15.24 | 330217-330150 | -1 | acetate--CoA ligase (RHOLA_RS01590) | 14 |
| Rothia dentocariosa ATCC 17931 (NC_014643.1) | 17.47 | 1473946-1474000 | 1 | bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase (HMPREF0733_RS06405) | 39 |
| Rothia mucilaginosa DNA, strain: NUM-Rm6536 (NZ_AP014938.1) | 15.97 | 437430-437480 | 1 | RNA-binding S4 domain-containing protein (RM6536_RS01640) | 88 |
| Rothia mucilaginosa DY-18 DNA (NC_013715.1) | 18.33 | 83293-83238 | -1 | ornithine cyclodeaminase (RMDY18_RS00360) | 5 |
| | 15.45 | 1021609-1021661 | 1 | hypothetical protein (RMDY18_RS04100) | 42 |
| Rothia mucilaginosa strain | 15.97 | 761512-761562 | 1 | RNA-binding S4 domain-containing | 88 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| FDAARGOS_369 (NZ_CP023510.1) | | | | protein (CO690_RS03200) | |
| Saccharomonospora viridis DSM 43017 (NC_013159.1) | 17.42 | 3078960-3079028 | 1 | XRE family transcriptional regulator (SVIR_RS13855) | 12 |
| Saccharothrix espanaensis DSM 44229 complete genome (NC_019673.1) | 19.42 | 5436887-5436821 | -1 | hypothetical protein (BN6_RS23530) | 2 |
| | 16.17 | 3146208-3146270 | 1 | hypothetical protein (BN6_RS42935) | 21 |
| Sanguibacter keddieii DSM 10542 (NC_013521.1) | 19.26 | 337201-337151 | -1 | ABC transporter substrate-binding protein (SKED_RS01520) | 10 |
| Scardovia inopinata JCM 12537 DNA (NZ_AP012334.1) | 18.1 | 1529587-1529653 | 1 | putative holin-like toxin (SCIP_RS07835) | 20 |
| | 15.07 | 1500669-1500618 | -1 | hypothetical protein (SCIP_RS06140) | 36 |
| Sinomonas atrocyanea strain KCTC 3377 (NZ_CP014518.1) | 16.5 | 1024306-1024253 | -1 | hypothetical protein (SA2016_RS04845) | 33 |
| | 15.66 | 1617992-1617930 | -1 | nitrite reductase (SA2016_RS07460) | 68 |
| Slackia heliotrinireducens DSM 20476 (NC_013165.1) | 23.09 | 1700501-1700444 | -1 | 3'-phosphoadenosine 5'-phosphosulfate sulfotransferase (SHEL_RS07250) | 413 |
| | 21.59 | 1987700-1987750 | 1 | 3-methyl-2-oxobutanoate dehydrogenase subunit VorB (SHEL_RS08610) | 5 |
| | 20.42 | 1226733-1226789 | 1 | recombinase RecA (SHEL_RS05250) | 82 |
| Stackebrandtia nassauensis DSM 44728 (NC_013947.1) | 20.8 | 4871519-4871574 | 1 | NAD-dependent malic enzyme (SNAS_RS22550) | 29 |
| | 18.92 | 1917023-1917082 | 1 | hypothetical protein (SNAS_RS09010) | 30 |
| Streptomyces albus J1074 (NC_020990.1) | 15.09 | 2012095-2012045 | -1 | ABC transporter permease (XNR_RS08435) | 171 |
| Streptomyces albus strain SM254 (NZ_CP014485.1) | 15.09 | 2289125-2289075 | -1 | ABC transporter permease (Salbus254_RS09635) | 171 |
| Streptomyces avermitilis MA-4680 = NBRC 14893 DNA (NC_003155.5) | 15.7 | 2358373-2358320 | -1 | membrane protein (SAVERM_RS10160) | 398 |
| | 15.36 | 2967279-2967226 | -1 | mannosyltransferase (SAVERM_RS12700) | 159 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Streptomyces bingchenggensis BCW-1 (NC_016582.1) | 22.79 | 1325634-1325572 | -1 | molecular chaperone DnaK (SBI_RS04410) | 32 |
| Streptomyces cyaneogriseus subsp. noncyanogenus strain NMWT 1 (NZ_CP010849.1) | 16.78 | 2043973-2043899 | -1 | transcriptional regulator (TU94_RS08155) | 51 |
| Streptomyces fulvissimus DSM 40593 (NC_021177.1) | 15.64 | 2195512-2195450 | -1 | hypothetical protein (SFUL_RS09650) | 82 |
| Streptomyces glaucescens strain GLA.O (NZ_CP009438.1) | 15.45 | 2684874-2684812 | -1 | hypothetical protein (SGLAU_RS11560) | 55 |
| Streptomyces globisporus C-1027 (NZ_CP013738.1) | 15.24 | 2202150-2202088 | -1 | hypothetical protein (WQO_RS09685) | 82 |
| Streptomyces griseus subsp. griseus NBRC 13350 DNA (NC_010572.1) | 15.24 | 6048357-6048419 | 1 | hypothetical protein (SGR_RS25590) | 82 |
| Streptomyces lividans TK24 (NZ_CP009124.1) | 15.45 | 7213814-7213751 | -1 | LacI family transcriptional regulator (SLIV_RS32445) | 91 |
| Streptomyces lydicus A02 (NZ_CP007699.1) | 21.31 | 6061131-6061192 | 1 | LacI family transcriptional regulator (T261_RS27005) | 9 |
|  | 18.01 | 2624882-2624829 | -1 | hypothetical protein (T261_RS11520) | 302 |
|  | 15.49 | 9065496-9065546 | 1 | type III effector protein (T261_RS39710) | 274 |
| Streptomyces parvulus strain 2297 (NZ_CP015866.1) | 16.28 | 4484722-4484667 | -1 | decaprenylphosphoryl-beta-D-ribose oxidase (Spa2297_RS20440) | 18 |
| Streptomyces pratensis ATCC 33331 (NC_016114.1) | 17.7 | 4725819-4725761 | -1 | hypothetical protein (SFLA_RS20365) | 27 |
| Streptomyces pristinaespiralis strain HCCB 10218 (NZ_CP011340.1) | 18.83 | 8476818-8476874 | 1 | exonuclease SbcC (SPRI_RS36235) | 97 |
|  | 18.83 | 55775-55719 | -1 | exonuclease sbcCD subunit D (SPRI_RS00190) | 97 |
|  | 17.8 | 7513420-7513468 | 1 | sugar ABC transporter (SPRI_RS32325) | 72 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 15.35 | 5557595-5557641 | 1 | agmatinase (SPRI_RS23705) | 11 |
| Streptomyces scabiei 87.22 complete genome (NC_013929.1) | 16.26 | 9274780-9274829 | 1 | L-asparagine permease (SCAB_RS39965) | 7 |
| Streptomyces sp. 4F (NZ_CP013142.1) | 17.52 | 3516700-3516640 | -1 | class II fructose-bisphosphate aldolase (ASR50_RS15530) | 32 |
| Streptomyces sp. CFMR 7 strain CFMR-7 (NZ_CP011522.1) | 15.24 | 6226773-6226835 | 1 | hypothetical protein (ABE83_RS26035) | 82 |
| Streptomyces sp. CNQ-509 (NZ_CP011492.1) | 18.89 | 3795481-3795431 | -1 | 50S ribosomal protein L9 (AA958_RS16065) | 1 |
| Streptomyces sp. PAMC26508 (NC_021055.1) | 19.99 | 2739778-2739819 | 1 | hypothetical protein (F750_RS12050) | 35 |
| Streptomyces sp. S10(2016) (NZ_CP015098.1) | 16.09 | 5995834-5995780 | -1 | MarR family transcriptional regulator (A4E84_RS26725) | 155 |
| Streptomyces sp. SAT1 (NZ_CP015849.1) | 15.79 | 5047550-5047500 | -1 | hypothetical protein (A8713_RS21920) | 38 |
| Streptomyces sp. SirexAA-E (NC_015953.1) | 16.1 | 1565172-1565240 | 1 | TetR family transcriptional regulator (SACTE_RS06915) | 25 |
| | 15.43 | 1508400-1508345 | -1 | transcriptional regulator (SACTE_RS06635) | 32 |
| Streptomyces venezuelae strain ATCC 15439 (NZ_CP013129.1) | 18.23 | 6497952-6497896 | -1 | hypothetical protein (AQF52_RS29165) | 30 |
| | 16.07 | 3448862-3448808 | -1 | hypothetical protein (AQF52_RS15265) | 24 |
| Streptomyces vietnamensis strain GIM4.0001 (NZ_CP010407.1) | 18.68 | 142442-142501 | 1 | hypothetical protein (SVTN_RS00745) | 49 |
| | 16.41 | 2463738-2463683 | -1 | pullulanase-type alpha-1,6-glucosidase (SVTN_RS10835) | 143 |
| | 15.51 | 7881746-7881797 | 1 | succinyl-CoA--3-ketoacid-CoA transferase (SVTN_RS35175) | 24 |
| | 15.38 | 3227892-3227837 | -1 | hypothetical protein (SVTN_RS14300) | 24 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| Tessaracoccus sp. NSG39 (NZ_CP019606.1) | 17.06 | 2506818-2506764 | -1 | DUF3263 domain-containing protein (BW730_RS11675) | 9 |
| | 15.8 | 3143239-3143292 | 1 | MgtC/SapB family protein (BW730_RS14350) | 14 |
| Tessaracoccus sp. T2.5-30 (NZ_CP019229.1) | 16.52 | 146536-146474 | -1 | CsbD family protein (BKM78_RS00755) | 10 |
| | 16 | 1577319-1577267 | -1 | aquaporin family protein (BKM78_RS07235) | 7 |
| Trueperella pyogenes strain 2012CQ-ZSH (NZ_CP012649.1) | 22.62 | 324777-324715 | -1 | dihydroxyacetone kinase (AN946_RS01315) | 17 |
| | 21.51 | 1421966-1422025 | 1 | BMP family ABC transporter substrate-binding protein (AN946_RS06170) | 5 |
| | 19.79 | 305936-305991 | 1 | GntP family permease (AN946_RS01245) | 16 |
| | 19.48 | 1400555-1400498 | -1 | hypothetical protein (AN946_RS06105) | 29 |
| | 17.11 | 1076589-1076642 | 1 | ABC transporter ATP-binding protein (AN946_RS04625) | 46 |
| | 16.74 | 1566665-1566719 | 1 | L-fucose isomerase (AN946_RS06865) | 6 |
| | 16.33 | 2151628-2151567 | -1 | sugar (glycoside-pentoside-Hexuronide) transporter (AN946_RS09515) | 5 |
| | 16.18 | 883231-883287 | 1 | FMN-binding negative transcriptional regulator (AN946_RS03735) | 217 |
| | 15.69 | 1750466-1750525 | 1 | 30S ribosomal protein S1 (AN946_RS07755) | 91 |
| | 15.68 | 277245-277195 | -1 | hypothetical protein (AN946_RS01135) | 326 |
| Trueperella pyogenes strain TP6375 (NZ_CP007519.1) | 21.51 | 848407-848348 | -1 | ABC transporter ATP-binding protein (CQ11_RS04015) | 5 |
| | 19.79 | 1995302-1995247 | -1 | GntP family permease (CQ11_RS09140) | 16 |
| | 19.48 | 869818-869875 | 1 | hypothetical protein (CQ11_RS10670) | 29 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
| | 17.78 | 1401608-1401552 | -1 | FMN-binding negative transcriptional regulator (CQ11_RS06540) | 218 |
| | 17.75 | 1203837-1203784 | -1 | ABC transporter ATP-binding protein (CQ11_RS05610) | 46 |
| | 16.92 | 1802328-1802264 | -1 | hypothetical protein (CQ11_RS08330) | 83 |
| | 16.74 | 659505-659451 | -1 | L-fucose isomerase (CQ11_RS03075) | 6 |
| | 16.33 | 469089-469028 | -1 | hypothetical protein (CQ11_RS02190) | 5 |
| | 15.69 | 65751-65810 | 1 | 30S ribosomal protein S1 (CQ11_RS00345) | 91 |
| | 15.68 | 2022040-2022090 | 1 | MgtC/SapB family protein (CQ11_RS09240) | 325 |
| Trueperella pyogenes TP8 (NZ_CP007003.1) | 21.51 | 794541-794600 | 1 | BMP family ABC transporter substrate-binding protein (X956_RS03620) | 5 |
| | 20.13 | 1952893-1952949 | 1 | sugar ABC transporter substrate-binding protein (X956_RS08895) | 29 |
| | 19.79 | 1911013-1911068 | 1 | GntP family permease (X956_RS08740) | 16 |
| | 19.48 | 773131-773074 | -1 | TetR/AcrR family transcriptional regulator (X956_RS10475) | 29 |
| | 17.11 | 426192-426245 | 1 | ABC transporter ATP-binding protein (X956_RS01940) | 46 |
| | 16.74 | 956842-956896 | 1 | L-fucose isomerase (X956_RS04470) | 6 |
| | 16.33 | 1534199-1534138 | -1 | sugar (glycoside-pentoside-Hexuronide) transporter (X956_RS07145) | 5 |
| | 16.18 | 232466-232522 | 1 | FMN-binding negative transcriptional regulator (X956_RS01025) | 217 |
| | 15.69 | 1174479-1174420 | -1 | 30S ribosomal protein S1 (X956_RS05495) | 91 |

| Organism (Genome ID) | Bit score | ANTAR-target RNA co-ordinates | Strand | Annotation of the gene linked to ANTAR-target RNAs (Locus Tag) | Distance (nt) of RNA from gene linked to ANTAR-target RNA |
|---|---|---|---|---|---|
|  | 15.68 | 82570-82620 | 1 | hypothetical protein (X956_RS00375) | 325 |
|  | 15.68 | 1882450-1882400 | -1 | hypothetical protein (X956_RS08635) | 325 |
| Verrucosispora maris AB-18-032 (NC_015434.1) | 15.07 | 4457207-4457151 | -1 | hypothetical protein (VAB18032_RS19750) | 14 |
| Xylanimonas cellulosilytica DSM 15894 (NC_013530.1) | 19.67 | 474824-474871 | 1 | sugar ABC transporter substrate-binding protein (XCEL_RS02040) | 17 |

*Table S3: Alignment of actinobacterial ANTAR-target RNAs predicted using Infernal.*
Structure based alignment of ANTAR-target RNAs obtained using Infernal are shown sorted according to the bit scores. Alignment is edited using RALEE v0.8 (PMID: 15377506). The stems are shaded in pink and blue. Secondary structure of RNAs is represented by WUSS notation.

| **Accession/Start-End** | **Sequence** |
|---|---|
| NC_022567/1325289-1325349 | AAAAAAUCUCUUGCAAUGAU.GCAACGGuc...............ggGUUAUCAUAGCA..AAGCUGCUUGAGCGGAAG |
| NC_015564/4535773-4535832 | AAUGAACUAUCUACAACGAU.GUAGAAUu...............ggUGAACUCAUGCA..AAGGAGCAUGCGAUGCCA |
| NZ_CP014761/2225592-2225649 | AUCAUGGUCUCUACAACGUU.GUAGUAC..................aACGUUGUAGACA..AGGGUGUCACACACCGCG |
| NC_008726/6033904-6033960 | AGAGAGAUCACCACAAAGGU.GUGGUUG...................ACUACACGGGCA..AAGUGGCCGGUUUUCGGG |
| NZ_CP007443/1784660-1784721 | AAAACGGCGACCGCAAAGCU.GCGGUUGcc..............guaACAGAUACGGCA..AUGGGGCCGGAAAACCAG |
| NC_014218/792299-792362 | UGCGUGAUAUGCACGAUGAC.GUGCUUUuau............acgcAUCACUAUGUCA..AUGGAGACACUAGAAAAG |
| NZ_CP011491/5794851-5794907 | AAAGAGAUCGCCACAAAGGU.GUGGUUG...................ACUACACGGGCA..CAGUGGCCGUUCGUGGGA |
| NZ_CP016773/11044-11115 | AACAAAUUCUUAACAAGGCU.GUUGUCCacggcaa....agucaucuUGUCUUCAGGCA..AGGAAGCCGAUUACUACG |
| NZ_CP012390/604046-604102 | AGGUUCUCGACCGCAUUGGU.GUGAUCG...................UUGGACAGGGCA..ACGAUGCCAUGAACGACA |
| NZ_CP010437/2041213-2041274 | AAAACGGCGACCGCAAAGCU.GCGGUCGcc..............guaACCGAUACGGCA..AUGGGGCCGGAAAACCAG |
| NZ_CP007155/7090364-7090418 | AAAAUGCAUUCGUGAACGAA.CACGAA-...................-AAAUGAUCGCA..AUGUAGCGGUUUUUGACA |
| NC_011886/676358-676423 | AUAUUCGCAACCAGAAUGAC.CUGGGUCacga..........aagccGGAUUACAUGCG..AAGGGGCAUCCAGCCAUG |
| NC_021054/2187067-2187117 | ACAAAUUCCGAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_015758/2187796-2187846 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_008769/2189421-2189471 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP003494/1889021-1889071 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_020245/2159066-2159116 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_016804/2168786-2168836 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_AM412059/2171338-2171388 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_012207/2171412-2171462 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP014566/2171410-2171460 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP008744/2169564-2169614 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP009243/2171415-2171465 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP012095/2183860-2183910 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP009449/2147621-2147671 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP013741/2171711-2171761 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_HG813240/2173566-2173616 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_020089/2191699-2191749 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP002883/2173137-2173187 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP002882/2166350-2166400 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_017522/2168763-2168813 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP002885/2173333-2173383 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_017524/2180824-2180874 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_021740/2181844-2181894 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_021194/2181480-2181530 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_009565/2195516-2195566 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_009525/2197160-2197210 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP009480/2182565-2182615 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_018143/2187268-2187318 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_000962/2187261-2187311 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP007027/2186649-2186699 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP002871/2172407-2172457 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_012943/2235762-2235812 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_016768/2232493-2232543 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_018078/2235643-2235693 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_020559/2178334-2178384 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NC_022350/2186892-2186942 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_AP014573/2192698-2192748 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP010339/2185332-2185382 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP010337/2190192-2190242 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP010340/2199709-2199759 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP010338/2182762-2182812 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP009426/2167819-2167869 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP009427/2195453-2195503 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP010330/2194218-2194268 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP007809/2166335-2166385 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP012506/2160992-2161042 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP009100/2187257-2187307 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP009101/2187289-2187339 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP012090/1954309-1954359 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUCUUGGUAGU |
| NZ_CP013747/2249980-2250041 | CCAGAACCCCCGACAAUGAU.GUCGAUCcu..............cacAUUCUCAUCACG..AAGGAGUGACCAGUGACA |
| NZ_CP015773/1085783-1085833 | ACAAAUUCCCAUGCAAAGAA.GCACU--...................----UGUGUACA..ACGAAGUAUUUUGGUAGU |
| NZ_CP012590/627231-627295 | ACGGGGCGGAUGACAACGAU.GUCAUCGgaau...........agaaCUGUACCUGACA..ACGUUGUCUCCGGUCAAG |
| NC_008541/399351-399411 | AUGAAGCCCACACCAAAGAU.GUUGUGGca...............aaAGAACAUAUACA..AAGGGGUAGAAGUUCAAU |
| NC_015738/2403432-2403484 | UCAAUGAUCCCAACAGUGAA.GUUGC--...................--CAAAAAGGCA..GCGAAGCUUCAAACGGAA |

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NZ_CP016771/508869-508923      AACCUCUCAGCGGCAAAGAC.GCCGUA-...................-CUGACAGGUCA..CUGAUGACAAAACUAAAA
NZ_AP012327/2246903-2246953    ACGCUCAUAAUCGAAACGAU.UCGAA--...................----AGUAAGCG..AAGACGCUGAAAACGAAG
NZ_CP007287/1150528-1150582    GCAAGUAAGGGCUCAAAGUU.GAGCCA-...................-UGAUGAUUGCA..AUGUAGCAAAAUAACAAG
NZ_LT706985/1778691-1778741    ACCUAAAUUGAAACAAAGGA.GUUU---...................---GUCGUGGCA..AAGAAGCCUCCCACUCGA
NZ_CP008953/3466226-3466279    AAAGUAACAGAUACAACGAC.GUAUC--...................-CCUUAUCCAUG..ACGGUAUGCUCAGCGAAG
NZ_CP013200/2964252-2964307    AUUUAUAGCAUC-UAAUGGU.GCGAUAU...................AUGCACAAUUCA..AAGGAGAAUCAUGACAGA
NZ_CP006018/1129860-1129914    GCAAGUAAGGGCUCAAAGUU.GAGCCG-...................-UGAUGAUUGCA..AUGUAGCAAAAUAACAAG
NC_013165/1700444-1700501      GUACGUGAAAGAGCAACGGU.GCUUUUU..................gAAGGCAAGAGCA..AUGGUGGUUCUAUAAAAG
NC_015673/784296-784358        CUUGAUAACGCAGCAAAGAA.GCUGAGCaac.............gagUCCUUCUUGGCA..AAGGCGCCAGAGAAGGUG
NC_008541/3967947-3968005      UUCAUUCCGAAGCCAACGAC.GUCUUCUa.................cGGAGGUAGAACA..AUGAAGUUUCCUGCCAUG
NZ_CP016777/10943-11014        AACAAAUUCUUAACAAGGCU.GUUGUCCacggcaa....aguaauuuUGUCUUCAGGCA..AAGAGGCUGAUUACUACG
NC_017219/918010-918066        UAGCGAUUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NC_011593/918219-918275        UAGCGAUUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NC_016582/1325572-1325634      ACAAUAAAACUCACAAAGGU.GUUGUUUuau.............agcAUUGAGCAUGAA..UCGGAUCACUCUGUGAAG
NC_014218/625569-625621        GUUCAUUCAUUCUCAAUGAA.GAGAA--...................--AGAUACAACA..AAGGAGUUGUAGGCGCAU
NZ_CP014513/1628135-1628207    UGACGCCGAUUUACAACGAU.GUAAUAGucgaugga...gcacccacCCCUACGAAGCA..AUGGAGCUCCAUGUCGAC
NZ_CP012649/324715-324777      AAAAAGCCGUAGCCAAAGCU.GUUUAUGcga.............aagGAAACAAGAACA..AUGACGUUUUUGGUUAAC
NZ_CP024160/94937-94997        GCGAUGGCAGCGGCGAUGAU.GCCGUUGga...............gcCAAACAAUAGCA..AUGCUGCUAAGUACGUAA
NC_009338/1209116-1209171      UGAGAGAUCACCACAAAGGU.GUGGUU-...................GACUACAGGGCA..AUUGGGCCGGACUCGGGG
NC_014814/5213312-5213367      UGAGAGAUCACCACAAAGGU.GUGGUU-...................GACUACAGGGCA..AUUGGGCCGGACUCGGGG
NC_015671/2826867-2826924      CAUGGUUCCUCUACAACGAU.GUAGAAC..................gACGACGAUCGCG..AGGGAGCGAGUCGAUGGG
NC_015564/650876-650926        UACGUCUUAAGCGCAACGAC.GCGCU--...................----UACCGGCA..AUGCUGCCGGAGCCACGA
NZ_CP016282/3698598-3698660    AACGAUUCCAUGGAAACGAU.UCCAUAGgau.............ccaCGCACGUACACA..AGGGAGUGGCUGUGGAAG
NZ_AP017900/6584176-6584229    CUUCCACCAACGGCAACGGC.GCCGC--...................-UGGCAAUGGCA..ACGGAGCCAACGGGAAUG
NZ_CP017839/2299999-2300052    CUUCCACCAACGGCAACGGC.GCCGC--...................-UGGCAAUGGCA..ACGGAGCCAACGGGAAUG
NC_011886/95577-95640          AUUCUAUGAAAUGCAAUGAC.GCGCAGUgaa.............aaggAAUCCAUGACA..ACGGAGUCAGUGACGACG
NC_010545/2341820-2341876      ACGGUUCCCACGGCAAGGGC.GCCGAUA...................AGGGUGCAGGCA..ACGGUGCCGACAAGGGUG
NZ_LT906481/1654874-1654930    ACGGUUCCCACGGCAAGGGC.GCCGAUA...................AGGGUGCAGGCA..ACGGUGCCGACAAGGGUG
NZ_CP007443/2169079-2169133    GUCAUAUCAAUCUAAGCGGU.UAGAUU-...................-GAUAUGAAUCA..AAGGAGAUUUCAAUGAGG
NZ_AP012325/603559-603619      CUAACAGAAUUUGCAACGUU.GCAAAUCcc...............gaAACAGACGGGCG..ACGUUGCCAUAGAAGAAA
NZ_CP017812/1397258-1397314    ACAAAGCUUAUGGCAAAGGU.GCCAUUA...................UGCGUUUGGGUG..AAGAUACUCGUCCCCAAG
NC_013165/1987700-1987750      AUCUGAUGUCUGAGAAAGUC.CUCAUG-...................-----AAGGGCA..ACGAGGCCAUGGCUGAAG
NZ_CP012649/1421966-1422025    AAUGUGAUCACUGCAGAGGA.GCAGUGAa................gcAGACCACUUACG..AAGGAGUAACCUGUGAGG
NZ_CP007519/848348-848407      AAUGUGAUCACUGCAGAGGA.GCAGUGAa................gcAGACCACUUACG..AAGGAGUAACCUGUGAGG
NZ_CP007003/794541-794600      AAUGUGAUCACUGCAGAGGA.GCAGUGAa................gcAGACCACUUACG..AAGGAGUAACCUGUGAGG
NZ_CP006841/144531-144587      CCGGCCUCGUCGACGAAGUU.GUCGAAG...................CCUACGAAGGCA..AAGAGGCCGCCGACAAGG
NC_008618/1609471-1609525      GUAAUAUCAAUCUAAGCGGU.UAGAUU-...................-GAUAUGAAUCA..AAGGAGAUUUCAAUGAGG
NZ_CP007699/6061131-6061192    UACACGUUGGCCGCAACGAC.GCGGACGgc..............acaAGCAGAAUGGCA..ACGGCGCCAUGGCGAACA
NZ_AP014658/2161620-2161684    AUAACAAAUAUUGCGAUGGC.GCAACGAugau...........ccauCACAGUAUUGCA..AAGAAGCAAGGACCCAAG
NC_014656/1762029-1762093      AUAACAAAUAUUGCGAUGGC.GCAACGAugau...........ccauCACAGUAUUGCA..AAGAAGCAAGGACCCAAG
NC_015067/2254067-2254131      AUAACAAAUAUUGCGAUGGC.GCAACGAugau...........ccauCACAGUAUUGCA..AAGAAGCAAGGACCCAAG
NZ_CP016019/2295537-2295601    AUAACAAAUAUUGCGAUGGC.GCAACGAugau...........ccauCACAGUAUUGCA..AAGAAGCAAGGACCCAAG
NZ_CP011965/1681266-1681330    AUAACAAAUAUUGCGAUGGC.GCAACGAugau...........ccauCACAGUAUUGCA..AAGAAGCAAGGACCCAAG
NZ_CP008802/1251722-1251774    ACGUUUCCAUAAACAAAGUA.GUUU---...................-GACACCCUGCA..GCGAGGCAGAUACAUAUG
NZ_CP006713/1022299-1022374    AUUGCAGCAGUAACAAAGAU.GUUGUGUauugcauuccuuuaaggagAGUGAACGAGCA..UGGGCGCUGCAGAAAAAA
NC_020517/419361-419436        AUUGCAGCAGUAACAAAGAU.GUUGUGUauugcauuccuuuaaggagAGUGAACGAGCA..UGGGCGCUGCAGAAAAAA
NZ_CP022436/2248139-2248195    CCACUGAUCAACACAACGUC.GUGUAAA...................ACCCCGGUGGCG..AAGUAGCCGCCGACCAGG
NC_021064/2362500-2362551      UAAUCCAUUUUUACAACGAU.GUAA---...................-CGGAACAUGCA..A-GGNGCACGCCGAGACG
NC_014246/26799-26853          UGGAUGCAUAUCCCAACGAU.GUGAUA-...................-CCGAACUGUCA..AAGGAGACUGUGAUGUCC
NZ_CP006715/665275-665329      GCAGGGAUUCAUACAGUGAU.GUAUGA-...................-ACCAUUUGGCA..AUGAUGCUGAGAGAAAGG
NC_013947/4871519-4871574      UUGAAUUGAGUCGCAAAGGA.GCGAAG-...................AUGUCUGUGGCC..AAGUUGCCCAGUGCCGGU
NZ_CP006850/7697910-7697964    GAUCAGUAACACACAAAGGA.GUGUUC-...................-UGAUGCAGGCA..UCGUUGCCCAGCAUGGUG
NZ_CP017150/3576710-3576760    AAAAAGACGGUGACAAUGAC.GUUGA--...................----CGGUGACA..AGGGUGUCAGCACAGUGG
NZ_CP006842/641767-641835      AUCAACAGCCCGGCAAUGAU.GCCGACAgcguag.......gacaccAGCAAGGAGUCG..ACGAAGACCUCACUGAAU
NC_009342/714064-714117        CCGUCGAUAUCGACAAAGUU.GUCGC--...................-GCUUGUUUGCA..CCGGAGCACAUGGCGAGU
NC_021351/701063-701116        CCGUCGAUAUCGACAAAGUU.GUCGC--...................-GCUUGUUUGCA..CCGGAGCACAUGGCGAGU
NC_021352/701064-701117        CCGUCGAUAUCGACAAAGUU.GUCGC--...................-GCUUGUUUGCA..CCGGAGCACAUGGCGAGU
NZ_CP007724/625963-626016      CCGUCGAUAUCGACAAAGUU.GUCGC--...................-GCUUGUUUGCA..CCGGAGCACAUGGCGAGU
NZ_CP007722/656779-656832      CCGUCGAUAUCGACAAAGUU.GUCGC--...................-GCUUGUUUGCA..CCGGAGCACAUGGCGAGU
NZ_CP012117/21017-21071        AAGUAGUCCUAAGCAAUGGC.GCUCUC-...................-UGCCUAAGUCA..GCGAUGACAGCGACGGGA
NZ_CP006711/1516055-1516111    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP006715/1592334-1592390    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NC_017218/652499-652555        CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_AP012324/1590628-1590684    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP006712/1542383-1542439    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP006713/1627645-1627701    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP006714/1543740-1543796    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP006716/1587761-1587817    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP010413/521165-521221      CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP019596/1647336-1647392    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NC_020517/1647321-1647377      CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
NZ_CP008885/1607611-1607667    CAGGGGCUUCGUGCAAUGAU.GCACGAG...................CCGAUCCAAGCA..AAGGGGCUGACCAUGAGC
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NC_014644/852601-852666        AGAAUUAUUCUCACACAGGA.GUGACGAugac..........uacaaAAGAAAACGACA..AUGCCGUCGUUAAGAAUA
NC_017456/1045532-1045597      AGAAUUAUUCUCACACAGGA.GUGACGAugac..........uacaaAAGAAAACGACA..AUGCCGUCGUUAAGAAUA
NZ_CP011269/6251522-6251576    GAGUUCUUAGUUACAAAGGU.GUAGUU-...................-CGAUUGCGGCG..ACGGUGCCGUAGGGAGUG
NZ_CP009914/6321128-6321182    GAGUUCUUAGUUACAAAGGU.GUAGUU-...................-CGAUUGCGGCG..ACGGUGCCGUAGGGAGUG
NZ_CP015732/54428-54483        UACUUGCGGAAUUCAACGGU.GAAUAU-...................UCAUAAGGAGCA..AGGGUGCUUUCUCAAGAC
NZ_AP012322/1863064-1863117    AUUUUCUGUGGCAAACAGCA.UUGUU--...................-UUAACGAUGCA..AUGGCGCAUUGGGCCAGA
NZ_AP012325/1858280-1858333    AUUUUCUGUGGCAAACAGCA.UUGUU--...................-UUAACGAUGCA..AUGGCGCAUUGGGCCAGA
NC_020133/3552989-3553040      GUUAUACCGACGGCAGAGUG.GUCGU--...................---GCCUUUGCA..AAGGCGCAGCCAACUAAG
NZ_HG917972/2705617-2705668    GUUAUACCGACGGCAGAGUG.GUCGU--...................---GCCUUUGCA..AAGGCGCAGCCAACUAAG
NC_010612/2842712-2842763      GUUAUACCGACGGCAGAGUG.GUCGU--...................---GCCUUUGCA..AAGGCGCAGCCAACUAAG
NZ_CP007456/334670-334721      UGCGAAAUCAGCACAAUGAA.GUGCA--...................---UAUCAUGCA..UAGGAGCAGUAUUUUCCG
NC_013165/1226733-1226789      AUAAGAAGUUCGGCAAAGGU.GCCAUCA...................UGAAGCUUGGCG..AAGAUGCCGAAAAGCUGG
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