**Sequences of 12 predicted sRNAs (*Computational homology search for new sRNAs)***

Positions of oligonucleotides used for detection of predicted sRNA sequences by Northern blotting (Figures 1 and 2) are underlined

Str\_1

StrcoelicolorA3\_2\_\_2\_1915678\_1915941\_2e\_30\_SambATCC23877\_GCA\_001267885\_1915854\_1916153

GGGACGGTCACCCCGGTCGTCGCGACGGTACGAGGGACGGTCGCCCCGGTCCCCACGCTCACCACGGTCGTCGCGGCGGAAGGACGGACGGTCACCACCCCGGTCATCGCGACGGAAGCCCCGGTCGCCGCCACGGTCCCGGTCGTCCCGACGCCCGTAGCCGGCACCGCGGTTGTCCTCGCGACGACCGTCGCGGCGGTCATCACGGCCGTCATCCCGACGGTCGTCACGACGGAAGCCGCCGCGCTGCCCACCGCGGTCATCGCGCCGATCGTCACGACGGTCATCACGGCGATC

Str\_2 StrcoelicolorA3\_2\_\_6\_3275271\_3274972\_8e\_80\_Ssca87\_GCA\_000091305\_6167357\_6167656

CCGAGGCGCACCGGGCGGGAGAACTGGGGACCGGGCCGCTCGTCGCCTACGCCGTCACACCGGCGCTGCGCGAGTGGTACCTGTCGGACGACATCGAGGAGCTGGAGTACGCCGCCCTCAACCGGGCCGCCCTGGCCTCGCTGCGCCTGCTGGCGGCCGACCCGGCCGGGGTGCGGCGCCGGGTCGTGGTCGCCGCGGACGTCCCCGACGGCGCCGCCGTGGCCGACCCGGACCGGGGACTCGATCCGGCGGCGCTGGGCGAGGTCCGCCTCGCCGGACCGCTGCCGCTGGCCAAGGCGG

Str\_3 StrcoelicolorA3\_2\_\_14\_1881845\_1881948\_3e\_09\_SgrigriseTsNBRC\_GCA\_000010605\_1691770\_1692069

GGTGCGTGCGATCGCAAGGCGCCGGAGCGCCCTCGTGGCGGAGCCACGCGGGCGCTTCGGCAACGCGGCGAGCGTGCGTGCCAGGCGTCGCCGGGCAGGCGGGAATCATCAGACAGGCCCTAGGTTACCGGGCCGGGCAGACCCCTCCGACAGCCGTCCGCAGGCCCCGGTCACTGCCGGATCGCCCAGCCCCGTTCCTTCAGGGCCGCCGTGAGGACGGCGGCGGCCTTCGGCTCCACCATGAGCTGCACCAGACCCGCCTGCTGCCCGGTCGCGTGCTCGATCCGTACGTCCTCCAC

Str\_4 StrcoelicolorA3\_2\_\_11\_1553780\_1553709\_4e\_07\_SplT\_GCA\_000802245\_939010\_939309\_extended

GCGACCGTTGGGGCGGCGTCTCATGGCGGTCGTCCCCCCTGGACCGAAGCCGGTGAACCGAACGGTCACCACGGTCCCGGCGCCGCGCCCGCACCCCATCGCGCCCGGGACGGGAGCCGCCTGCGCCGCGCGGCGGGGAGGGCCGCCCCGGTCTGATCCCCGAGGACGAGTACCGCACCCGCCGGAGGGTGCGCAACGAATCGCCGTGGGGTGCCCCGGGCACGCAACGATCCGCTCACCGGCGCGCAACAGGTCCGTCTTGTCCGGCCGAGTCCGCCGACCGTACCGTCTATCTGGCCCCCTGAACCCCCCTCGTGACCGGTGAGGAACACGC

Str\_5 Sco\_AL939123\_1\_191892\_192006\_Snod\_GCA\_000819545\_3000867\_3001166\_reconstrTcted\_from\_Save\_BLAST

TGACGCGGGGGCTGAGCGGTGCGGGGCGGTCTTCCGGCGCGGGGTTTCTTCGCCCCCGCCGCCCCTTCCCTTCCCGACCCTGGGGGCGCCACCCCCAGACCCCCGCTTTCGGCCTGAACGGCCTCGTCCTCAAACGCCGGACGGGCTGGGGGCTCAACGGCCTCGTCCTCAAGTGCCGGACGGGCTGGGGGGGCTCAACGGTCTCGTCCTCGAGTGCCGGACGGGCTAAAGTGACCCGCGTGTTCCTCCTCTTGGCCTAGGACCCGCCCCGCACGCGACCGCCGCATCCGGCCGTCGCGC

Str\_6

ScoeA3\_GCA\_000203835\_2249619\_2249798\_-

GGACCGGCCCACCCCGAATCACGGACACCGCGCCGAAAAAGTTCCGCGCGACACCACTTCCCGCATTCTTGCCGCCGTTACCGATTCGTGTCACTCGCCTGTGGACAACTGGCCGCGATATGTCGGCGCTTACGGCCTTTGCGGAGCTTGCACGGCGGGATCGTCGGGGCGGGCCGCCGG

Str\_7

StrcoelicolorA3\_2\_\_4\_4186663\_4186807\_3e\_31\_SambATCC23877\_GCA\_001267885\_4103311\_4103490

GGCCTACGATCGTCACACGAAAGCACTGCCGGGGTGCCGCACAGCAGCGTAACTTAGCGTTCCAAGACACCCGCCGACTGCCGCCACCGCCACTGGCACCGCCGCCACCAACCGCCCGTGTACCGACCGCCGAGGGGTCCCGTTC

Str\_8

ScoeA3\_GCA\_000203835\_3946569\_3946748\_-

CCGTGGATGGCGCAGGCGTACGGAGACCCAGCGGGCCCTGCGGCGCAGGATGCGCGGAATACCCACCCGAAGGTCCGCACCCGCGAGTTGCGGGGTGCCGCCGCGTCGGTGGGTGCTGCTCACGCCGCTCGTGGAGCGGCCGTCGCGTGCTACGTCACTGTAGTCGTGCGTCCAGCCCAT

Str\_9

ScoeA3\_GCA\_000203835\_1671946\_1672125\_+

GCTTCGGGGCGCGAGACTCAGGTGGTGCGGGGGCCCTCTAGAAGGCGCACATTCGGCGGCACATACAACGAGCACCGGGCGTCGTGGTCGCCTCGGTCGCAGGGGTGCGGTCGCTCGTGGTGCTCATGCCGATCAGTAAAGCAGACGTATGCCTCTGGCCGGAGACCGCTGTCCGGATAC

Str\_10

StrcoelicolorA3\_2\_\_1\_5592190\_5592364\_1e\_67\_SambATCC23877\_GCA\_001267885\_5219563\_5219742

CTCATGAGGTGTGACCTGCGTCAAAGAAAACCGGTCCGTATCCATTCGGTGGAAGTGCGTGAGGGCGCGCAGTATCGCAGTCACATCGCCGAATTGAGTGGTTTTGCTCGCGCGCGTTGCCCAAGCGATGCCGACCGATGTTGGTCATCGGGTCCTGGGATGCGGGATAATGGCTGGGAA

Str\_11

StrcoelicolorA3\_2\_\_2\_1609809\_1609633\_2e\_64\_Ssca87\_GCA\_000091305\_8296565\_8296744

TTCCAGGAGCGTCGCGCACCGTCGATGGTGTCGCGGGCAGCCCACCACCACCCGGCTTCCGGGAGCGGTCGGTGGGCCACTCGCGTGCTGCACGTATGTGCCCAGACCAGGGGAGCGGCTGCCCGGCAGGTCCCGAGCGGACCCGGCGGGTTTCCCCGGCTGCGGATTGCGACCTCCCT

Str\_12

ScoeA3\_2\_\_5808519\_5808699\_+\_ML5\_GCA\_000177655\_6788539\_6788718\_+

CGCGTCTGCTCGGCTCTGCCTGGGTCGATGGCGGACGGGATGGGAGCTCCCCGCGCATGCCACTACGGACCCGCAGTCGGAAGCGGCGCTCTTTCCATCCCGGTGCCGGCCGATCCCCCGCCGGAGGCATCATCTTGTGCCTGCGGATGACGTCCCGTCCTTGCCCGCATGCACGCAGCG

**Sequence of Str\_13/src3559/Ms1** ***(final sequence verified by 5´RACE and 3´RACE)***

AACGGCCCGCGAGACCAAGGACATCCGAAAGGATCACCTTAAACACGCATATGGCCCCACGGACCGAGCATGGACACCGGGCACCCACGCGACGTCGACCCGTCGATTACGGGCCAGCCGCACCAGGTCACGGGCGAAGTTCCCGGCCTGATGGGCACATATCGAGGACGCTTGGTAACCGGGTGGTCATGCCAGCGGCGGTACGAGCATTCGTACCGCCGCATTCC

Sequences of biotinylated oligos used for Northern blotting (Figures 1 and 2):

2786 Str1\_F btn-GACGGAAGCCCCGGTCGCCGCCACG

2787 Str1\_R btn-CGTGGCGGCGACCGGGGCTTCCGTC

2788 Str\_2\_F btn-GAGTGGTACCTGTCGGACGACATCG

2789 Str\_2\_R btn-CGATGTCGTCCGACAGGTACCACTC

2790 Str\_3\_F btn-CGTTCCTTCAGGGCCGCCGTGAGGA

2791 Str\_3\_R btn-TCCTCACGGCGGCCCTGAAGGAACG

2792 Str\_4\_F btn-GCACGCAACGATCCGCTCACCGGCG

2793 Str\_4\_R btn-CGCCGGTGAGCGGATCGTTGCGTGC

2794 Str\_5\_F btn-CTGAACGGCCTCGTCCTCAAACGCC

2795 Str\_5\_R btn-GGCGTTTGAGGACGAGGCCGTTCAG

2828 Str6\_F btn-CCGATTCGTGTCACTCGCCTGTGGA

2829 Str6\_R btn-TCCACAGGCGAGTGACACGAATCGG

2830 Str11\_F btn-ACGTATGTGCCCAGACCAGGGGAGC

2831 Str11\_R btn-GCTCCCCTGGTCTGGGCACATACGT

2832 Str8\_F btn-GAATACCCACCCGAAGGTCCGCACC

2833 Str8\_R btn-GGTGCGGACCTTCGGGTGGGTATTC

2834 Str9\_F btn-GTCGCTCGTGGTGCTCATGCCGATC

2835 Str9\_R btn-GATCGGCATGAGCACCACGAGCGAC

2836 Str10\_F btn-CATCGCCGAATTGAGTGGTTTTGCT

2837 Str10\_R btn-AGCAAAACCACTCAATTCGGCGATG

2838 Str7\_F btn-GTAACTTAGCGTTCCAAGACACCCG

2839 Str7\_R btn-CGGGTGTCTTGGAACGCTAAGTTAC

2840 Str12\_F btn-CACTACGGACCCGCAGTCGGAAGCG

2841 Str12\_R btn-CGCTTCCGACTGCGGGTCCGTAGTG

2842 Str\_5S btn-CGCTGTAAGGCTTAGCTTCCGGGTT

2796 Str\_13 (ssrS/scr3559/Ms1) btn-TCCTTGGTCTCGCGGGCCGTTGAGT

3813 Sc\_probe A btn-GGTCCCGAGTAAGCGGAAGTGCTCG

3812 Sc\_probe B btn-GTCCGTGGGGCCATATGCGTGTTA

3811 Sc\_probe C btn- GCTCGTACCGCCGCTGGCATGACCA

Primers used for RT-qPCR validation of Str11/Str13 association with RNA polymerase/HrdB (Figure 3)

3155/Sco\_Str11\_F1 CGTCGCGCACCGTCGATGGT

3156/Sco\_Str11\_R1 TACGTGCAGCACGCGAGTGG

3225/Sco\_Str13\_F GATCACCTTAAACACGCATATGG

3226/Sco\_Str13\_R GAACTTCGCCCGTGACCT

3298/Sco3352\_F CTTGGAGATCGAGGACCTGG

3299/Sco3352\_R CCAGCTCCACCACGTACTC

3300/Sco3710 \_F TTCTGCTACGTCCACCCCAT

3301/Sco3710 \_R CAGGACGAGGAAACCCAGG

3302/Sco2013\_F ctggaggaggaggggtact

3303/Sco2013\_R catcttgggcatcttcacgt

1617/Sco\_16SrRNA\_F TGTCACCCGATTACGGGTAT

1618/Sco\_16SrRNA\_R ACCGAAGTGGTTCATCGTTC

1024/Msmeg\_Ms1\_F GCCGGAAGAGAAGGCTAGAT

1025/Msmeg\_Ms1\_R CGTCCGCTTTTCGAAACTAC

2816/Msmeg\_rpoB\_F CACCGAACCGAGTTTCATTT

2817/Msmeg\_rpoB\_R TCGAAGGAATCCGTCTGAAC

989/Msmeg\_rpoC\_F CGACGAGATCTGGAACACCT

990/Msmeg\_rpoC\_R GGTGAAGTACTCGCCGTAGC

**Supplementary Table S1**. Characteristics of presented expressed *Streptomyces* sRNAs.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| RNA | Predicted function | Gen. locus in S. *coelicolor* A3(2) (GenBank ID AL645882.2) # | Conserved in \* | Approx. length (nts) | Strand | Genomic position | Genomic locus † | Predicted sequence in *S. coelicolor* (oligo for expression verification in lowercase) \*\* |
| Str1 | cis-acting asRNA | - (4 hits at different gen. loci in S. co., also see the 8th column) | Actinobacteria | 90, 120 | + (RNA), - (fragments) | + strand opposite to 'tetratricopeptide repeat protein' that is on the - strand |  | - (impossible to predict 5' and 3' ends for overlapping incomplete BLAST hits in single species) |
| Str3 | cis-acting asRNA | 1882014 : 1882198 | Actinobacteria | 160 | + (RNA), - (fragments) | overlaps both the prephenate dehydrogenase that is on - strand and IGR between 'prephenate dehydrogenase' and '[cytidylate OR (d)CMP] kinase' |  | GUCACUGCCGGAUCGCCCAGCCCcguuccuucagggccgccgugaggacGGCGGCGGCCUUCGGCUCCACCAUGAGCUGCACCAGACCCGCCUGCUGCCCGGUCGCGUGCUCGAUCCGUACGUCCUCCACGUUGACCCCGGCUCGUCCCGCGUCCGCGAAGAUGCGGGCCAGCUGACCGGGCUG |
| Str5 | small noncoding RNA | 5872966 : 5873065 (+ another 8 gapped, but very good BLAST hits at different gen. loci in S. co.) | Streptomyces | 130 | + | IGR between 'methylmalonyl Co-A mutase-associated GTPase MeaB' - 'MFS transporter' (+ a lot other IGRs with different flanking genes) |  | CUUCGCCCCCGCCGCCCCUUCCCUUCCCGACCCUGGGGGCGCCACCCCCAGACCCCCGCUUUCGGCcugaacggccucguccucaaacgccGGACGGGCU |
| Str8 | small noncoding RNA | 3946749 : 3946619 | Streptomyces | 130 | - | IGR between ['colicin V synthesis protein' OR 'serine protease'] - 'alpha/beta hydrolase' |  | CCGUGGAUGGCGCAGGCGUACGGAGACCCAGCGGGCCCUGCGGCGCAGGAUGCGCGgaauacccacccgaagguccgcaccCGCGAGUUGCGGGGUGCCGCCGCGUCGGUGGGUGCUGCUCACGCCGCUC |
| Str10 | small noncoding RNA | 5592268 : 5592388 | Streptomyces | 120 | + | IGR between ['DUF3117 domain-containing protein' OR 'methyltransferase'] - ['enoyl-CoA hydratase' OR 'acyl CoA isomerase'] |  | caucgccgaauugagugguuuugcucGCGCGCGUUGCCCAAGCGAUGCCGACCGAUGUUGGUCAUCGGGUCCUGGGAUGCGGGAUAAUGGCUGGGAAGCAAUGUGUUCGAUGCCGGUGUCG |
| Str11 | small noncoding RNA | 1609864 : 1609645 | Streptomyces | 220 | - | IGR between '30S ribosomal protein S4' - ['AAA family ATPase' OR 'Recombination factor protein RarA' OR 'replication-associated recombination protein A'] (they are synonyms) |  | UUCCAGGAGCGUCGCGCACCGUCGAUGGUGUCGCGGGCAGCCCACCACCACCCGGCUUCCGGGAGCGGUCGGUGGGCCACUCGCGUGCUGCacguaugugcccagaccaggggagcGGCUGCCCGGCAGGUCCCGAGCGGACCCGGCGGGUUUCCCCGGCUGCGGAUUGCGACCUCCCU |
| Str13 | small noncoding RNA | 3934693 : 3934920 | Actinobacteria | 230 | - | IGR between ['IB HAD hydrolase' OR 'inhibition morphological differetiation'] - ['oxidoreductase' OR 'Fic' OR 'hexosaminidase'] |  | AACGGCCCGCGAGACCAAGGACAUCCGAAAGGAUCACCUUAAACACGCAUAUGGCCCCACGGACCGAGCAUGGACACCGGGCACCCACGCGACGUCGACCCGUCGAUUACGGGCCAGCCGCACCAGGUCACGGGCGAAGUUCCCGGCCUGAUGGGCACAUAUCGAGGACGCUUGGUAACCGGGUGGUCAUGCCAGCGGCGGUACGAGCAUUCGUACCGCCGCAUUCCU |

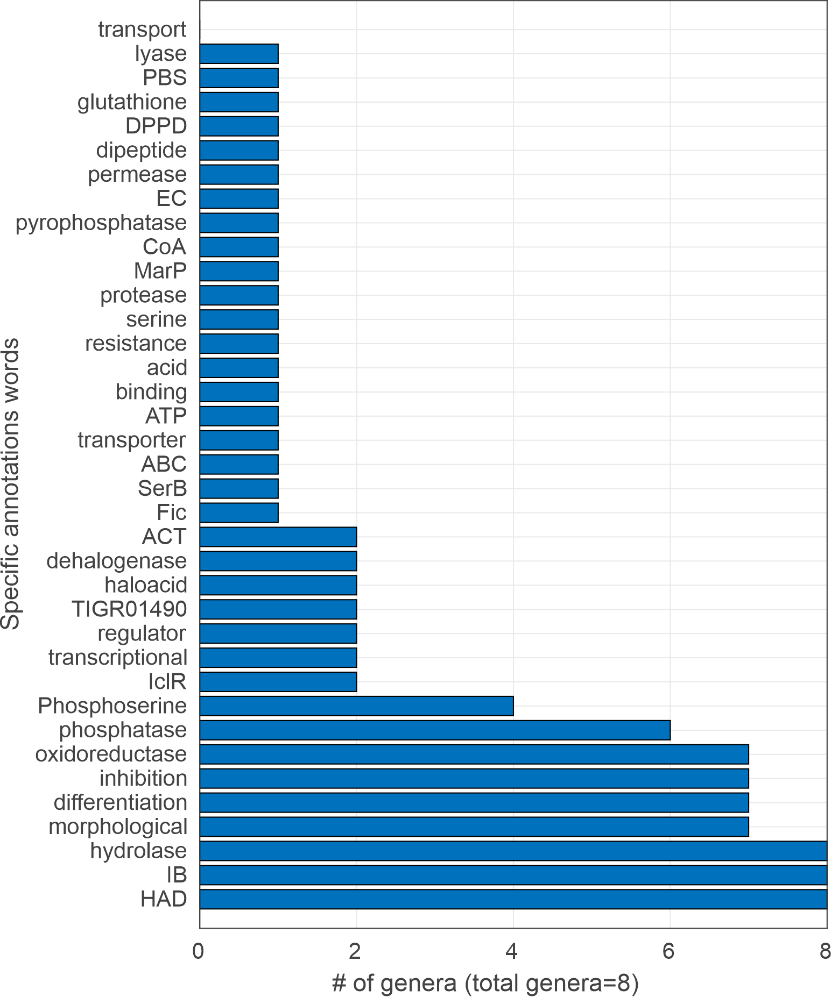
- Not applicable (from reasons shown in parenthesis).

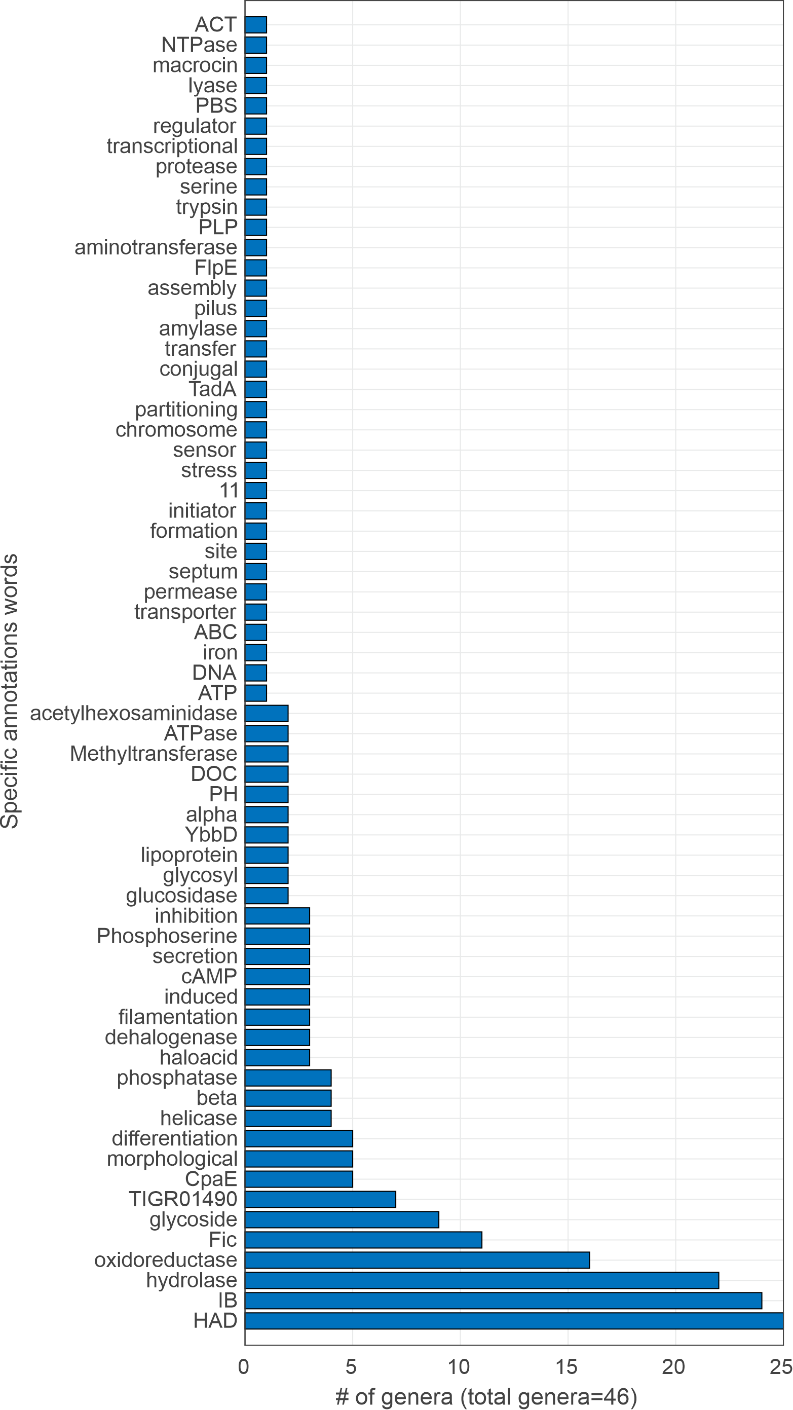
\* Based on sequence similarity by NCBI BLASTn (with parameters Word size = 7, Match/Mismatch Scores = 1, -1, Gap Costs = Existence: 2 Extension: 1), synteny and genomic loci similarity.

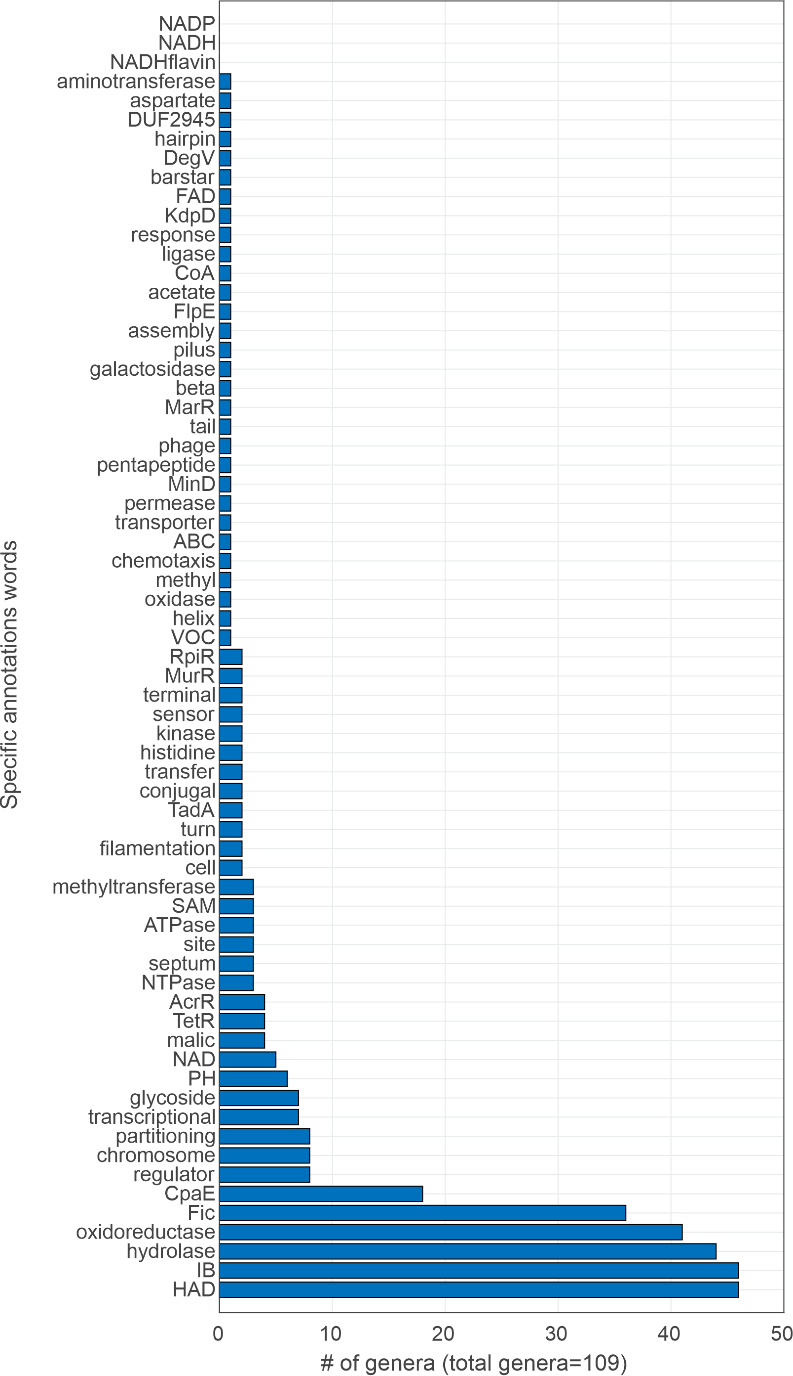
\*\* See Materials and Methods for details on prediction.

† Distribution in first 100 homologs found by BLAST in nt database.

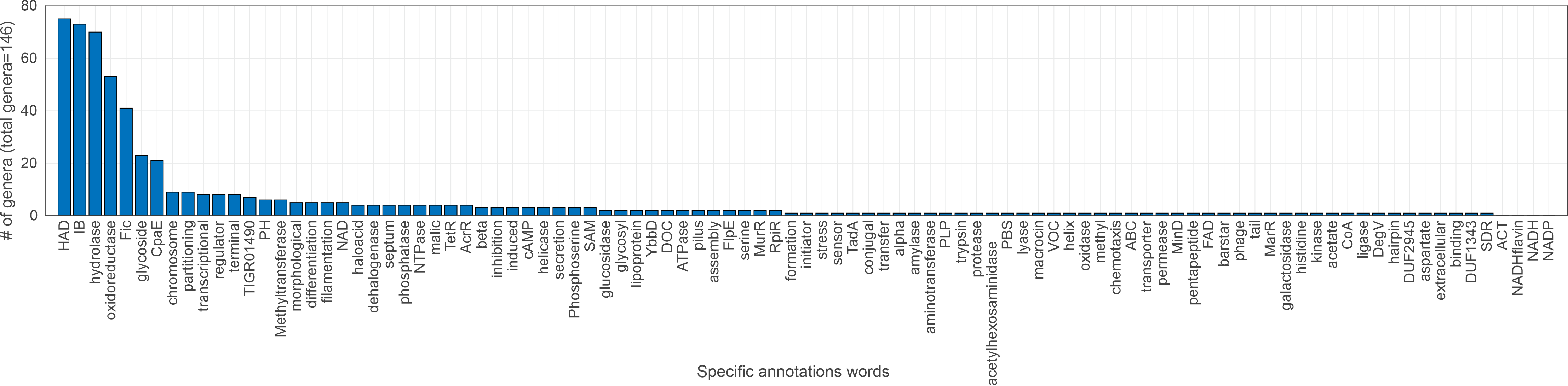
# Computationally predicted based on sequence similarity, except for Str7 5' end identified by 5' RACE.

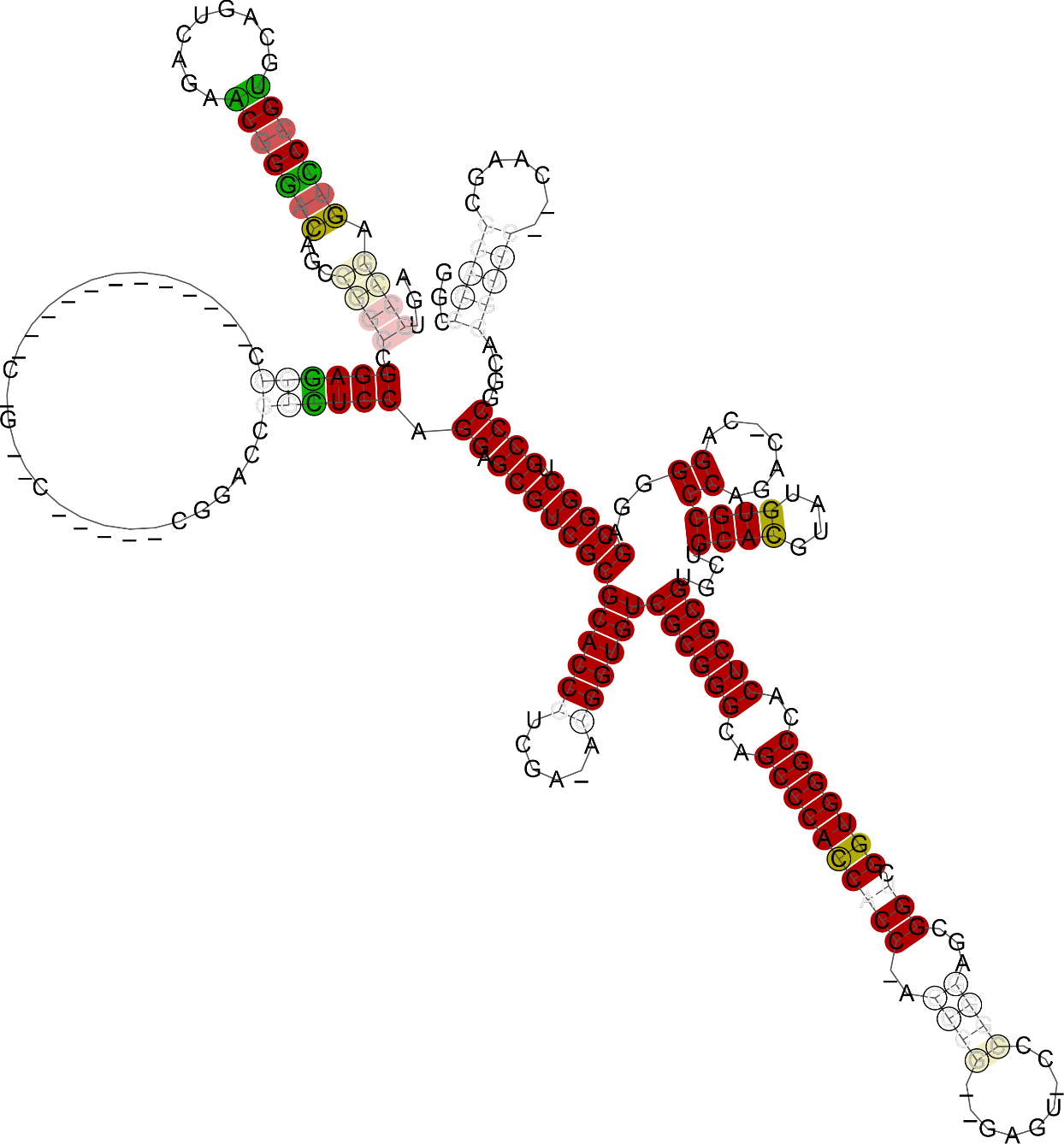
**Supplementary Figure S1**. Specific words and their occurrence in synteny annotations of flanking genes of homologs of *M. smegmatis* Ms1 RNA across eight genera – *Mycobacterium*, *Mycolicibacterium*, *Rhodococcus, Nocardia*, *Gordonia*, *Mycobacteroides*, *Hoyosella* and *Tsukamurella.* The homologs had sequences similar to *M. smegmatis* Ms1 RNA identified by BLAST (with BLAST E-value < 10-20) and conserved Ms1 synteny.

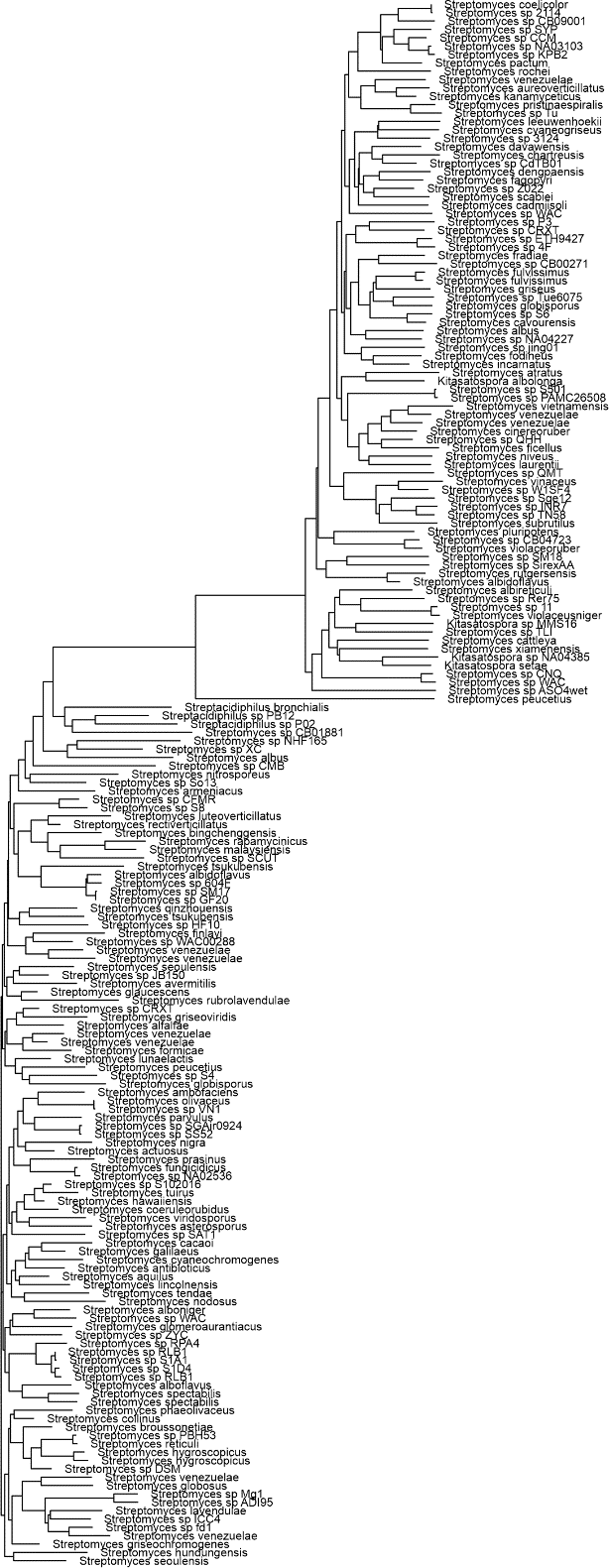
**Supplementary Figure S2**. Specific words and their occurrence in synteny annotations of Ms1 IGRs homologous to the 1st synteny hit in *Streptomyces*. Specific words with higher than average occurrence (3.4 genera), 10 words starting 'HAD' up to 'phosphatase' (see y-axis), were used for the update of the original phrases in Table 1. The updated phrases are shown in Table 2. 'TIGR01490' was not used as it was a part of 'IB HAD hydrolase' annotation. Some of the most occurring specific words semantically bound with other specific words that were not most occurring to form a phrase. Here 'morphological' and 'differentiation' bound with 'inhibition'. Specific word 'beta' occurred in 'beta-N-acetylhexosaminidase' and 'beta-glucosidase-like glycosyl hydrolase' resulting into two new synteny phrases 'beta acetylhexosaminidase ' and 'beta glycosyl glucosidase'. 'glycoside' bound with 'hydrolase' producing 'glycoside hydrolase' phrase and 'phosphatase' bound with 'phosphoserine' producing 'phosphoserine phosphatase' phrase. Phrases 'Fic' and 'CpaE' originated from 'filamentation induced by cAMP protein Fic' and 'helicase/secretion neighborhood CpaE-like protein' annotations, respectively. A CpaE-like protein represented an extended Ms1 RNA synteny and as it is a next Ms1 IGR flanking gene after HAD hydrolase. It occurred here as the HAD hydrolase gene annotation was missing in genomic annotations of some species.

**Supplementary Figure S3**. Specific words and their occurrence in synteny annotations of 708 Ms1 IGRs in 109 genera identified by the first iterative synteny search. Average occurrence of specific words was in 5.4 genera, resulting in 12 most occurring specific words starting 'HAD' up to 'PH' (see y-axis) used for the update the original phrases in Table 2. 7 of the most occurring specific words were the same as before (Supplementary Figure S2). 'transcriptional' and 'regulator' were semantically bound through 'TetR/AcrR family transcriptional regulator' or 'MurR/RpiR family transcriptional regulator' annotations, forming 'transcriptional regulator' phrase (Table 3). 'partitioning' and 'chromosome' originated from 'chromosome partitioning protein' annotation, forming a phrase 'chromosome partitioning'. Phrase 'PH' originated from 'PH domain-containing protein' annotation.

**Supplementary Figure S4.** Specific words and their occurrence in synteny annotations of finally obtained 824 Ms1 IGRs from 146 *Actinobacteria* genera.



**Supplementary Figure S5**. A consensus secondary structure of Str11 (scr1506). The structure was created by RNAalifold [1] from ClustalW2 [2] multiple sequence alignment of sequences from 42 *Streptomyces* species identified by BLAST search of *S. coelicolor* Str11 sequence in nt NCBI nucleotide database.

**Supplementary Figure S6**. A phylogenetic tree of Ms1 IGRs identified in 188 *Streptomyces* species. The tree was generated using ClustalW2. The tree leaves were denoted only with genus and species names. Other details as strain identifiers were left out for readability of the tree.

**Supplementary Table S2**. List of 824 species, in which Ms1 RNAs were predicted in *Actinobacteria*. *Streptomyces* species were not included as they are shown in Supplementary Figure S1 unless found by sequence similarity to the synteny hits. Columns show: genomic sequence ID, species name, genomic loci of BLAST hits with sequence similarity to predicted Ms1 RNAs in evolutionarily related species and genomic locus of IGR with a predicted Ms1 RNA.

|  |  |  |  |
| --- | --- | --- | --- |
| ID | name | BLAST hit genomic locus | IGR genomic locus |
| CP023445.1 | Actinosynnema pretiosum X47 | 275876:275630 | 275382:275972 |
| CP029607.1 | Actinosynnema pretiosum subsp. pretiosum ATCC 31280 | 280450:280204 | 279961:280546 |
| CP024894.1 | Amycolatopsis sp. AA4 | 7906792:7907038 | 7906664:7907296 |
| CP060131.1 | Pseudonocardia sp. CGMCC 4.1532 | 1258061:1257817 | 1257783:1258119 |
| CP016077.1 | Actinoalloteichus sp. GBA129-24 | 299336:299089 | 298803:299520 |
| LN850107.1 | Alloactinosynnema sp. L-07 Alloactinosynnema sp. L-07 I | 6195183:6194939 | 6194735:6195363 |
| HE804045.1 | Saccharothrix espanaensis DSM 44229 | 315710:315466 | 315268:315846 |
| NZ\_CP045480.1 | Amycolatopsis sp. YIM 10 4e-16 | 464448:464708 | 464128:464795 |
| CP016353.1 | Prauserella marina DSM 45268 | 6319114:6319359 | 6318982:6319527 |
| CP064192.1 | Saccharothrix sp. 6-C | 8740658:8740412 | 8740080:8740794 |
| CP054925.1 | Amycolatopsis sp. Hca4 | 6745264:6745018 | 6744621:6745411 |
| NZ\_KB913032.1 | Amycolatopsis alba DSM 44262 scaffold1 2e-07 | 3176975:3176700 | 3176581:3177158 |
| CP022521.1 | Actinoalloteichus hoggarensis DSM 45943 | 289476:289229 | 288923:289661 |
| CP016793.1 | Lentzea guizhouensis DHS C013 | 2553820:2554067 | 2553599:2554309 |
| CP012752.1 | Kibdelosporangium phytohabitans KLBMP1111 | 375401:375153 | 374633:375556 |
| CP053564.1 | Pseudonocardia sp. Gen01 | 1179901:1179654 | 1179616:1179960 |
| CP009110.1 | Amycolatopsis methanolica 239 | 6769674:6769921 | 6769585:6770105 |
| CP012184.1 | Pseudonocardia sp. EC080619-01 | 2445161:2444914 | 2444868:2445307 |
| CP001736.1 | Kribbella flavida DSM 17836 | 567915:567696 | 567680:567951 |
| LT629732.1 | Actinopolymorpha singaporensis DSM 22024 I | 2013151:2012919 | 2012737:2013134 |
| CP049867.1 | Nocardioides sp. HDW12B | 3401637:3401880 | 3401595:3401933 |
| AP012204.1 | Microlunatus phosphovorus NM-1 DNA | 5295527:5295766 | 5295327:5295783 |
| CP025581.1 | Nocardioides houyundeii 78 | 3417894:3418121 | 3417834:3418143 |
| CP033324.1 | Nocardioides sp. 603 | 3157786:3158030 | 3157186:3158414 |
| AP022871.1 | Phytohabitans suffuscus NBRC 105367 DNA | 4056387:4056148 | 4056138:4055653 |
| CP046122.1 | Microlunatus sp. Gsoil 973 | 3298334:3298570 | 3297965:3298590 |
| LT629749.1 | Friedmanniella luteola DSM 21741 I | 271109:270874 | 270839:271345 |
| LT629772.1 | Microlunatus soli DSM 21800 I | 2351268:2351505 | 2350894:2351515 |
| CP041692.1 | Microlunatus sp. KUDC0627 | 816251:816015 | 815744:816568 |
| CP009896.1 | Pimelobacter simplex VKM Ac-2033D | 342461:342222 | 342195:342486 |
| CP038436.1 | Nocardioides seonyuensis MMS17-SY207-3 | 1274084:1274324 | 1274080:1274328 |
| CP060713.1 | Nocardioides mesophilus KACC 16243 | 2170430:2170196 | 2170186:2170456 |
| CP059164.1 | Nocardioides ungokensis LMG 28591 | 441392:441153 | 441142:441394 |
| CP000509.1 | Nocardioides sp. JS614 | 387431:387189 | 386220:387475 |
| CP040748.1 | Nocardioides sp. dk3136 | 3263693:3263929 | 3263651:3263963 |
| CP049866.1 | Nocardioides sp. HDW12A | 683296:683540 | 683283:683551 |
| CP038267.1 | Nocardioides euryhalodurans MMS17-SY117 | 2158069:2158307 | 2158055:2158428 |
| LT629757.1 | Marmoricola scoriae DSM 22127 I | 2587314:2587554 | 2587280:2587600 |
| CP059259.1 | Nocardioidaceae bacterium isolate SSC3 | 464425:464666 | 464458:464799 |
| LT629688.1 | Auraticoccus monumenti MON 2.2 I | 187327:187559 | 187182:187589 |
| CP033729.1 | Actinobacteria bacterium YIM 96077 | 508618:508383 | 508316:508625 |
| LT629791.1 | Jiangella alkaliphila DSM 45079 I | 695996:696236 | 696005:696261 |
| LT629771.1 | Jiangella sp. DSM 45060 I | 6975474:6975234 | 6975101:6975465 |
| CP001738.1 | Thermomonospora curvata DSM 43183 | 5489394:5489629 | 5488756:5490245 |
| CP032402.1 | Thermomonospora amylolytica YIM 77502 | 6609043:6609278 | 6608183:6609310 |
| CP036455.1 | Streptomonospora sp. M2 | 176676:176917 | 176262:177224 |
| CP031320.1 | Streptomyces armeniacus ATCC 15676 | 3246694:3246457 | 3246435:3246786 |
| LT559118.1 | Nonomuraea sp. ATCC 39727 isolate nono1 I | 1037878:1037644 | 0:0 |
| CP017717.1 | Nonomuraea sp. ATCC 55076 | 9673564:9673798 | 9674581:9673814 |
| CP045572.1 | Nonomuraea nitratireducens WYY166 | 410532:410295 | 410265:410633 |
| CP029711.1 | Streptosporangium sp. \_caverna\_ | 46893:46655 | 46625:47848 |
| CP001814.1 | Streptosporangium roseum DSM 43021 | 479835:479600 | 479260:480519 |
| CP001874.1 | Thermobispora bispora DSM 43833 | 254817:254581 | 253843:255271 |
| AP022870.1 | Phytohabitans flavus NBRC 107702 DNA | 7996830:7996586 | 7996569:7996841 |
| CP022753.1 | Nocardiopsis gilva YIM 90087 | 616361:616603 | 615813:616757 |
| CP006272.1 | Actinoplanes friuliensis DSM 7358 | 392931:392691 | 392680:392989 |
| LT629711.1 | Phycicoccus dokdonensis DSM 22329 I | 3602372:3602612 | 3602326:3603201 |
| LR134501.1 | Nocardiopsis dassonvillei NCTC10488 1 | 4300251:4300499 | 4299702:4300776 |
| CP046121.1 | Tetrasphaera sp. HKS02 | 2422696:2422458 | 2422104:2422730 |
| CP060712.1 | Phycicoccus endophyticus JCM 31784 | 2369196:2368958 | 2368588:2369199 |
| CP031194.1 | Streptomyces paludis GSSD-12 | 3171721:3171952 | 3171608:3171992 |
| CP063232.1 | Thermobifida fusca UPMC 901 | 1086203:1086443 | 1085834:1086559 |
| CP000088.1 | Thermobifida fusca YX | 153146:153386 | 0:0 |
| CP049935.1 | Phycicoccus sp. HDW14 | 3949084:3949321 | 3949026:3950231 |
| CP053707.1 | Arthrobacter sp. NEB 688 | 1362445:1362681 | 1362415:1363371 |
| CP041616.1 | Ornithinimicrobium sp. H23M54 | 3847534:3847296 | 3846993:3847529 |
| CP031447.1 | Austwickia chelonae LK16-18 | 494728:494963 | 494715:495362 |
| CP064985.1 | Austwickia sp. isolate Fred\_18-Q3-R57-64\_BATAC.85v2 | 738428:738192 | 737718:738511 |
| CP005929.1 | Actinoplanes sp. N902-109 | 474003:473765 | 473762:473991 |
| LT629758.1 | Actinoplanes derwentensis DSM 43941 I | 7196422:7196662 | 7196202:7196924 |
| AP012319.1 | Actinoplanes missouriensis 431 DNA | 329779:329537 | 329534:329800 |
| AP019371.1 | Actinoplanes sp. OR16 DNA | 2596823:2596579 | 2596574:2596841 |
| CP023865.1 | Actinoplanes teichomyceticus ATCC 31121 | 292747:292507 | 292488:293105 |
| CP023298.1 | Actinoplanes sp. SE50 | 422558:422322 | 422129:423123 |
| AP023355.1 | Actinocatenispora thailandica NBRC 105041 DNA | 213014:212779 | 212540:213116 |
| CP015163.1 | Amycolatopsis albispora WP1 | 5803799:5804044 | 5803687:5804356 |
| LN877229.1 | Kibdelosporangium sp. MJ126-NF4 | 6538888:6538643 | 0:0 |
| CP041306.1 | Amycolatopsis sp. Poz14 | 1220523:1220277 | 0:0 |
| CP034550.1 | Saccharothrix syringae NRRL B-16468 | 317899:317653 | 317453:318024 |
| CP007155.1 | Kutzneria albida DSM 43870 | 328239:327991 | 327985:328452 |
| CP069353.1 | Saccharopolyspora erythraea NRRL 23338 | 485511:485267 | 484264:485622 |
| CP038101.1 | Saccharomonospora sp. 31sw | 4293791:4294039 | 4293708:4294179 |
| NZ\_CP045929.1 | Saccharopolyspora coralli E2A 1e-23 | 310730:311004 | 310549:311094 |
| CP001683.1 | Saccharomonospora viridis DSM 43017 | 3916948:3917196 | 3916855:3917461 |
| NZ\_LT629701.1 | Allokutzneria albata DSM 44149 I 9e-19 | 6577109:6577384 | 6576693:6577483 |
| CP025990.1 | Actinoalloteichus sp. AHMU CJ021 | 2311565:2311808 | 2311501:2312342 |
| CP002593.1 | Pseudonocardia dioxanivorans CB1190 | 448050:448292 | 447912:448397 |
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| NZ\_CP031142.1 | Saccharopolyspora pogona NRRL30141 1e-30 | 6147603:6147328 | 6147235:6147838 |
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| CP014859.1 | Actinoalloteichus hymeniacidonis HPA177T \_DSM 45092T | 294856:294610 | 294406:295031 |
| NZ\_CP022752.1 | Actinopolyspora erythraea YIM 90600 5e-79 | 307994:308270 | 307607:308360 |
| AP018920.1 | Pseudonocardia autotrophica NBRC 12743 DNA | 484940:485186 | 484762:485196 |
| CP013854.1 | Pseudonocardia sp. HH130630-07 | 1916925:1916678 | 1916653:1917068 |
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| CP011862.1 | Pseudonocardia sp. AL041005-10 | 3940600:3940848 | 3940154:3939969 |
| CP001737.1 | Nakamurella multipartita DSM 44233 | 799218:798980 | 798423:799733 |
| CP050902.1 | Nocardioides sp. JQ2195 | 3749594:3749842 | 3749590:3749910 |
| CP038462.1 | Nocardioides daphniae JCM 16608 | 3291364:3291607 | 3291299:3291675 |
| CP040695.2 | Nocardioides sp. S-1144 | 399891:399641 | 399624:399902 |
| CP049257.1 | Nocardioides anomalus HKS04 | 4186364:4186120 | 4186105:4186365 |
| CP015079.1 | Nocardioides dokdonensis FR1436 | 1636696:1636447 | 1636404:1636721 |
| AP019307.1 | Nocardioides baekrokdamisoli KCTC 39748 DNA | 2020661:2020915 | 2020652:2020938 |
| CP060587.1 | Aeromicrobium sp. zg-629 | 176396:176157 | 176138:176362 |
| CP026952.1 | Aeromicrobium sp. 592 | 304101:303862 | 303824:304121 |
| CP027482.1 | Aeromicrobium sp. A1-2 | 2878001:2878240 | 2877991:2878327 |
| CP045737.1 | Aeromicrobium sp. MF47 | 289247:289009 | 288964:289267 |
| LT796768.1 | Aeromicrobium choanae 9H-4 I | 1393541:1393780 | 1393562:1393815 |
| LT629799.1 | Friedmanniella sagamiharensis DSM 21743 I | 4155411:4155179 | 4155098:4155533 |
| LT629710.1 | Nakamurella panacisegetis P4-7KCTC 19426CECT 7604 I | 2553372:2553127 | 2552953:2552840 |
| CP060298.1 | Nakamurella sp. PAMC28650 | 1683530:1683289 | 1683009:1684132 |
| CP034170.1 | Nakamurella sp. s14-144 | 508957:508720 | 508417:509408 |
| CP022434.1 | Nocardiopsis dassonvillei HZNU\_N\_1 | 183738:183986 | 183205:184264 |
| CP017965.1 | Nocardiopsis dassonvillei NOCA502F | 183643:183891 | 183094:184168 |
| CP054933.1 | Nocardiopsis flavescens NA01583 | 194845:195094 | 194338:195319 |
| CP041763.1 | Gordonia sp. HY186 | 2935841:2936130 | 2935775:2936160 |
| CP046320.1 | Gordonia bronchialis FDAARGOS\_676 | 4547805:4548090 | 4547699:4548291 |
| CP023405.1 | Gordonia sp. 1D | 446192:445907 | 445820:446840 |
| CP022580.1 | Gordonia rubripertincta CWB2 | 559827:559543 | 559455:559563 |
| CP059694.1 | Gordonia rubripertincta SD5 | 1543146:1542862 | 1542773:1543809 |
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| CP054691.1 | Gordonia sp. X0973 | 344407:344122 | 344104:344566 |
| CP047235.1 | Gordonia sp. JH63 | 586787:586503 | 586402:587358 |
| CP046257.1 | Gordonia sp. 135 | 527477:527192 | 527104:528142 |
| CP049836.1 | Gordonia terrae RL-JC02 | 5013304:5013588 | 5012733:5013689 |
| CP045810.1 | Gordonia amarae ATCC 27808 | 572569:572284 | 0:0 |
| CP033972.1 | Gordonia insulae MMS17-SY073 | 4371409:4371124 | 4371072:4371648 |
| CP029604.1 | Gordonia terrae NRRL B-16283 | 637698:637414 | 637314:638268 |
| CP002907.1 | Gordonia sp. KTR9 | 491434:491150 | 491051:491921 |
| CP059491.1 | Gordoniaceae bacterium zg-686 | 525708:525422 | 525401:526350 |
| CP045809.1 | Gordonia amarae DSM 43602 | 4663189:4663473 | 0:0 |
| CP003119.1 | Gordonia polyisoprenivorans VH2 | 895644:895360 | 895243:895768 |
| CP027433.1 | Gordonia iterans Co17 | 643106:642823 | 642629:643137 |
| CP025435.1 | Gordonia sp. YC-JH1 | 970806:970511 | 970454:970873 |
| CP011853.1 | Gordonia phthalatica QH-11 | 447791:447500 | 447348:447858 |
| CP001966.1 | Tsukamurella paurometabola DSM 20162 | 4026137:4026409 | 4026041:4026479 |
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| CP019066.1 | Tsukamurella tyrosinosolvens MH1 | 4532801:4533081 | 4532708:4533170 |
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| NZ\_CP074404.1 | Cellulomonas sp. zg-ZUI188 4e-22 | 3060451:3060660 | 3060316:3060662 |
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| NZ\_FOKA01000005.1 | Cellulomonas marina CGMCC 4.6945 2e-20 | 30137:30428 | 30136:30578 |
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| NZ\_CP039291.1 | Cellulomonas shaoxiangyii Z28 1e-18 | 823293:823026 | 822969:823498 |
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| NZ\_JAEINH010000013.1 | Sanguibacter sp. YZGR15 Scaffold13 1e-09 | 12283:12123 | 12109:12327 |
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| NZ\_JACCBT010000001.1 | Actinomadura citrea DSM 43461 Ga0104564\_01 4e-47 | 8930746:8930881 | 8929993:8930906 |
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| NZ\_CP044407.1 | Actinomadura sp. WMMB 499 WMMB499 4e-46 | 4838868:4838736 | 4838686:4839570 |
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| NZ\_SMKB01000257.1 | Actinomadura sp. 7K534 NODE\_257\_length\_9655\_cov\_74.8759 2e-44 | 2126:2265 | 2916:2299 |
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| NZ\_KB903835.1 | Longispora albida DSM 44784 A3G1DRAFT\_scaffold\_5.6 2e-12 | 385842:385720 | 385674:386001 |
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| NZ\_JADBEA010000001.1 | Actinophytocola algeriensis DSM 46746 Ga0415166\_01 0.0004 | 7296075:7296202 | 7295684:7296429 |
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| NZ\_FNON01000002.1 | Amycolatopsis xylanica CPCC 202699 7e-14 | 430578:430306 | 430158:431047 |
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| NZ\_FPJG01000006.1 | Amycolatopsis australiensis DSM 44671 2e-07 | 1558707:1558866 | 1558432:1559088 |
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| NZ\_WMBA01000131.1 | Amycolatopsis pithecellobii RM579 NODE\_131\_length\_3422\_cov\_8.983308 3e-06 | 5:127 | 0:0 |
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| NZ\_QQAU01000014.1 | Lentzea flaviverrucosa DSM 44664 Ga0244493\_114 3e-05 | 148490:148350 | 148054:148686 |
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| NZ\_JABVED010000003.1 | Actinokineospora xionganensis HBU206404 Scaffold3 0.0004 | 243338:243476 | 243121:243730 |
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| NZ\_AUII01000023.1 | Pseudonocardia asaccharolytica DSM 44247 \_ NBRC 16224 DSM 44247 G567DRAFT\_scaffold00022.22\_C 0.001 | 25377:25187 | 25056:25469 |
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| NZ\_FORP01000033.1 | Amycolatopsis sacchari DSM 44468 0.001 | 49391:49237 | 49081:49592 |
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| NZ\_PGGW01000058.1 | Streptomyces carminius TRM SA0054 502 0.003 | 174328:174266 | 174107:174491 |
| NZ\_WIXO01000001.1 | Streptomyces taklimakanensis TRM43335 Contig00001 0.003 | 3208090:3208152 | 3207908:3208413 |
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| NZ\_CP048261.1 | Streptomyces rimosus subsp. rimosus ATCC 10970 0.036 | 7086821:7086865 | 7086658:7086865 |
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| NZ\_WWJL01000018.1 | Streptomyces sp. SID4921 SID4921.c18 0.038 | 599233:599301 | 598932:599381 |

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