Supplementary material of: Analysis of the biodegradative and adaptive potential of the novel PCB degrader *Rhodococcus* sp. WAY2 revealed by its complete genome sequence

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Supplementary File S1. Analysis of the *Rhodococcus* sp. WAY2 plasmids.

Methods

To test the topology of the pRWAY01, pRWAY02 and pRWAY03 replicons, different sets of primers were designed at least at 800 bp from each replicon end to avoid telomeric sequences. A reverse primer in each of the left ends of the three replicons (1L3, 2L3 and 3L3), was designed in order to amplify with its respective forward primer in the replicons right ends (1R1, 2R1, 3R1) only in case of circular topology. Additionally, forward primers in the left ends (1L2, 2L1 and 3L2) and reverse primers in the right ends (1R3, 2R2 and 3R3), were designed to be combined with the ones previously described as positive controls. The sequences of the primers, Tm, positions in each replicon and combinations used can be seen below and also a scheme of the priming sites. For the small circular plasmid pRWAY04, two sets of primers (4F1-4R3 and 4F2-4R4) were designed to amplify ~10 Kbps of overlapping fragments that covers the total plasmid length (14.8 Kbps). Melting temperature of the primers, absence of dimerization and hairpin formation and lack of secondary priming sites were assessed using the OligoAnalyzer tool available at https://eu.idtdna.com/calc/analyzer.

For pRWAY01, pRWAY02 and pRWAY03, PCR reactions were carried out in a total volume of 25 μL containing 2.5 μL of 10x PCB buffer MgCl₂ free, 1 μL MgCl₂ 50 mM, 0.5 μL of DMSO (dimethyl sulfoxide) at 10% (v/v), 0.5 μL dNTP mix 10 mM (2.5 mM each), 1 μL of each primer at 10 μM, 1 μL of Tag DNA polymerase 1 U/μL (Biotools) and 1 μL of *Rhodococcus* sp. WAY2 genomic DNA at a 30-50 ng/μL. The cycling conditions consisted in a first denaturation step at 95 °C for 5 min followed by 27 cycles of amplification (1 min denaturation at 95 °C, 45 s of primer annealing at 60 °C and an elongation step at 72 °C for 1.5 min) followed by a final elongation step at 72 °C for 7 min. For pRWAY04, PCR reactions were carried out in a total volume of 25 μL containing 12.5 μL of Master Mix Q5’ High Fidelity 2x (New England BioLabs), 1.25 μL of each primer at 10 μM, 0.5 μL of DMSO at 10% (v/v) and 9.5 μL of WAY2 genomic DNA at a 30-50 ng/μL. The cycling conditions consisted in a first denaturation step at 98 °C for 3 min followed by 35 cycles of amplification (10 s denaturation at 98 °C, 30 s of primer annealing at 71 °C and an elongation step at 72 °C for 7 min) followed by a final elongation step at 72 °C for 3 min. PCR products were electrophoretically separated in 0.8% (w/v) agarose gels and dyed with Gel Red.

Results

All the primer combinations to test the linear topology of the pRWAY01, pRWAY02 and pRWAY03 plasmids resulted in positive amplification of the controls (image), with amplicon sizes congruent with the theoretically expected, and negative amplification with the primer combinations designed to amplify only in case of circular topology (image: 1L3-1R1, 2L3-2R1 and 3L3-3R1, lanes 3, 6 and 9). These results validate the linear topology of the pRWAY01, pRWAY02 and pRWAY03 replicons of *Rhodococcus* sp. WAY2, as predicted by its genome sequencing. The two PCRs of the pRWAY04
circular small plasmid resulted in amplicon sizes of ~10 Kbps, congruent with the theoretically expected and validate the circular topology of this plasmid.

(A) Schematic representation of the primers designed to test the topology of the pRWAY01, pRWAY02 and pRWAY03 replicons of *Rhodococcus* sp. WAY2. Red arrows indicate the combination of primers which will result in positive amplification in case of circular topology. (B) Schematic representation of the primers designed to test the topology of the small pRWAY04 replicon. (C) PCR results in agarose gels at 0.8% (w/v). Black typing lanes show positive control amplicons (arrows), while red typing lanes (3, 6 and 9) show no amplification, which correspond with a linear topology of the pRWAY01, pRWAY02 and pRWAY03 replicons. Lanes 10 and 11 show the PCR products of the pRWAY04 small replicon, congruent with a circular topology.
Primer combinations used.

| Replicon | Forward | Reverse | Expected amplicon length (bp) |
|----------|---------|---------|-----------------------------|
| pRWAY01  | 1L2     | 1L3     | 1.260                       |
|          | 1R1     | 1R3     | 551                         |
|          | 1L3     | 1R1     | -                           |
| pRWAY02  | 2L1     | 2L3     | 1.143                       |
|          | 2R1     | 2R2     | 1.135                       |
|          | 2L3     | 2R1     | -                           |
| pRWAY03  | 3L2     | 3L3     | 900                         |
|          | 3R1     | 3R3     | 681                         |
|          | 3L3     | 3R1     | -                           |
| pRWAY04  | 4F1     | 4R3     | 9.922                       |
|          | 4F2     | 4R4     | 10.306                      |
Supplementary File S2. Analysis of the invertron-type telomeric nucleotide sequences of *Rhodococcus* sp. WAY2 linear mega-plasmids and identification of Terminal Inverted Repeats (RITs).

(A) Comparison of *Rhodococcus* sp. WAY2 linear mega-plasmids telomeres (except for pRWAY03 left end) with linear replicons of other rhodococci: *R. jostii* RHA1 chromosome and plasmids pRHL1, pRHL2 and pRHL3, *R. opacus* B4 chromosome and plasmids pROB01, pROB02 and pR1CP1, *R. opacus* 1C plasmid pR1CP1. Conserved nucleotides are indicated with asterisks. The two sets of inverted repeats are highlighted with blue boxes and the GCTXGC central motif with red boxes and bold. Non-conserved nucleotides in these inverted repeats and central motif are red typed.
(B) Comparison of *Rhodococcus* sp. WAY2 linear mega-plasmids pRWAY03 left end with homologous telomeric sequences of *R. jostii* RHA1 plasmid pRHL2 right end and *R. opacus* B4 plasmid pROB01 right end. Conserved nucleotides are indicated with asterisks. The two sets of inverted repeats are highlighted with blue boxes and the GCTXCGC central motif with red boxes and bold. Non-conserved nucleotides in these inverted repeats and central motif are red typed.
**Supplementary File S3.** Whole genome-based taxonomic analysis of *Rhodococcus* sp. WAY2 using the Type (Strain) Genome Server (TYGS).

GBDP tree based in whole-genome sequences of the 10 closest type strain genomes to *R.* sp. WAY2 (red typing) inferred with FastME from GBDP distances. Tree was rooted at midpoint. Pseudo-bootstrap support values are shown below branches and were calculated over 100 replicates, with an average branch support of 91.5%.
GBDP tree based in 16S rRNA gene sequences of the 10 closest type strain to *R.* sp. WAY2 (red typing) inferred with FastME from GBDP distances. Tree was rooted at midpoint. Pseudo-bootstrap support values are shown below branches and were calculated over 100 replicates, with an average branch support of 62.5%.

Pairwise comparisons of *Rhodococcus* sp. WAY2 against the 10 closest type strain genomes.

| Query strain         | Subject strain                  | dDDH (d4, in %) | C.I. (d4, in %) | %GC content difference |
|----------------------|---------------------------------|-----------------|-----------------|------------------------|
| *Rhodococcus* sp. WAY2 | *Rhodococcus opacus* DSM 43205  | 27.7            | [25.4 - 30.2]   | 2.8                    |
| *Rhodococcus* sp. WAY2 | *Rhodococcus imtechensis* RKJ300 | 27.6            | [25.2 - 30.1]   | 2.75                   |
| *Rhodococcus* sp. WAY2 | *Rhodococcus wratislaviensis* NBRC 100605 | 26.8            | [24.4 - 29.2]   | 2.3                    |
| *Rhodococcus* sp. WAY2 | *Rhodococcus jostii* DSM 44719  | 26.7            | [24.4 - 29.2]   | 2.41                   |
| *Rhodococcus* sp. WAY2 | *Rhodococcus koreensis* DSM 44498 | 26.5            | [24.1 - 28.9]   | 2.9                    |
| *Rhodococcus* sp. WAY2 | *Rhodococcus marinonascens* NBRC 14363 | 22.9            | [20.6 - 25.3]   | 0.07                   |
| *Rhodococcus* sp. WAY2 | *Rhodococcus maaschanaensis* DSM 44675 | 20.2            | [18.0 - 22.7]   | 4.69                   |
| *Rhodococcus* sp. WAY2 | *Rhodococcus erythropolis* NBRC 15567 | 20.1            | [17.9 - 22.5]   | 2.08                   |
| *Rhodococcus* sp. WAY2 | *Rhodococcus globidus* NBRC 14531 | 19.4            | [17.2 - 21.8]   | 2.8                    |
| *Rhodococcus* sp. WAY2 | *Nocardia globerula* DSM 44596  | 19.4            | [17.2 - 21.8]   | 2.75                   |
Type-based species clustering using a 70% dDDH threshold around each of the 10 type strains.

| Species cluster | Name                                      | Authority                        | Size (Mbp) | %GC  | No. proteins | Assembly accession |
|-----------------|-------------------------------------------|----------------------------------|------------|------|--------------|--------------------|
| 1               | *Rhodococcus marinonascens* NBRC 14363    | Helmke and Weyland 1984          | 4.92       | 64.41| 4777         | GCA_001894885      |
| 2               | *Rhodococcus globerulus* NBRC 14531       | Goodfellow et al. 1985 emend. Nouioui et al. 2018 | 6.74       | 61.67| 6262         | GCA_001894805      |
| 2               | *Nocardia globerula* DSM 44596            | (Gray 1928) Waksman and Henrici 1948 | 6.48       | 61.72| 6050         | -                  |
| 3               | *Rhodococcus koreensis* DSM 44498         | Yoon et al. 2000 emend. Nouioui et al. 2018 | 10.31      | 67.38| 9444         | GCA_900105905      |
| 4               | *Rhodococcus jostii* DSM 44719            | Takeuchi et al. 2002             | 9.91       | 66.88| 9110         | GCA_900105375      |
| 5               | *Rhodococcus wratislaviensis* NBRC 100605 | Goodfellow et al. 1995 emend. Nouioui et al. 2018 | 10.40      | 66.78| 9472         | GCA_000583735      |
| 6               | *Rhodococcus erythropolis* NBRC 15567     | Goodfellow and Alderson 1979 emend. Nouioui et al. 2018 | 6.59       | 62.4 | 6211         | GCA_001552595      |
| 7               | *Rhodococcus imtechensis* RKJ300          | Ghosh et al. 2006 emend. Nouioui et al. 2018 | 8.23       | 67.22| 7681         | GCA_000260815      |
| 7               | *Rhodococcus opacus* DSM 43205            | Klatte et al. 1995               | 8.53       | 67.28| 7425         | GCF_001646735      |
| 8               | *Rhodococcus maanshanensis* DSM 44675     | Zhang et al. 2002 emend. Nouioui et al. 2018 | 5.67       | 69.17| 5173         | GCA_900109405      |
| 9               | *Rhodococcus* sp. WAY2                    | This work                        | 8.44       | 64.47| 7841         | -                  |
Supplementary File S4. Absolute values of PCB congeners degradation.

| PCB congener | Chl.sust | sample  | LB400.1 | LB400.2 | LB400.3 | LB400.control1 | LB400.control2 | LB400.control3 |
|--------------|----------|---------|---------|---------|---------|----------------|----------------|----------------|
|              |          |         | [µg]    |         |         |                |                |                |
| biphenyl     |          |         | 0.02    | 0.02    | 0.02    | 0.52           | 0.60           | 0.51           |
| biphenyl     |          |         | 0.01    | 0.03    | 0.03    | 0.33           | 0.35           | 0.31           |
| 1 2-Chlorobiphenyl |        |         | 0.00    | 0.00    | 0.00    | 0.00           | 0.00           | 0.00           |
| 2 3-Chlorobiphenyl |        |         | 0.00    | 0.00    | 0.00    | 0.15           | 0.15           | 0.14           |
| 3 4-Chlorobiphenyl |        |         | 0.00    | 0.00    | 0.00    | 0.15           | 0.15           | 0.14           |
| 4+10 2,2';2,6 |         |         | 0.22    | 0.42    | 0.39    | 3.30           | 3.54           | 3.11           |
| 5+8 2,3;2,4' |         |         | 2.02    | 3.39    | 3.01    | 26.74          | 27.67          | 24.76          |
| 6 2,3'        |         |         | 0.44    | 0.76    | 0.66    | 4.23           | 4.44           | 3.96           |
| 9+7 2,5;2,4   |         |         | 0.06    | 0.08    | 0.07    | 0.51           | 0.52           | 0.48           |
| 15 4,4'       |         |         | 3.83    | 4.56    | 3.88    | 6.48           | 6.80           | 6.05           |
| 16 2,2,3      |         |         | 6.37    | 7.57    | 6.49    | 9.95           | 10.51          | 9.80           |
| 17 2,2,4      |         |         | 2.70    | 3.85    | 3.19    | 19.67          | 21.12          | 19.09          |
| 18 2,2,5      |         |         | 5.32    | 7.55    | 6.60    | 38.31          | 39.99          | 35.69          |
| 19 2,2,6      |         |         | 1.57    | 1.88    | 1.80    | 4.45           | 4.78           | 4.23           |
| 22 2,3,4'     |         |         | 3.18    | 3.75    | 3.49    | 15.43          | 16.40          | 15.21          |
| 26+25 2,3,5;2,3,4 |    |         | 0.67    | 0.87    | 0.73    | 3.35           | 3.54           | 3.15           |
| 27+24 2,3,6;2,3,6 |      |         | 0.47    | 0.57    | 0.56    | 2.12           | 2.19           | 2.04           |
| 28+31 2,4,4';2,4,5 |   |         | 13.14   | 15.66   | 13.73   | 44.09          | 44.65          | 42.06          |
| 32 2,4,6      |         |         | 1.11    | 1.53    | 1.35    | 7.56           | 7.87           | 7.00           |
| 33 2,3,4'     |         |         | 4.74    | 6.40    | 5.27    | 29.32          | 30.21          | 27.41          |
| 37 3,4,4'     |         |         | 11.26   | 12.88   | 11.18   | 11.92          | 12.22          | 11.52          |
| 40 2,2,3,3'   |         |         | 1.00    | 1.15    | 0.99    | 3.86           | 4.11           | 3.81           |
| 41+71 2,2,3,4;2,3,4,6 |   |         | 1.97    | 2.27    | 1.98    | 3.61           | 3.76           | 3.48           |
| 42 2,2,3,4'   |         |         | 1.86    | 2.17    | 1.91    | 5.57           | 5.43           | 4.85           |
| 44 2,2,3,5'   |         |         | 3.90    | 4.55    | 4.07    | 14.49          | 15.43          | 14.34          |
| 45 2,2,3,6    |         |         | 2.38    | 2.71    | 2.46    | 4.14           | 4.23           | 3.73           |
| 46 2,2,3,6'   |         |         | 0.78    | 0.95    | 0.87    | 2.03           | 2.09           | 1.80           |
| 48+47 2,2,4,5;2,2,4,4' | |         | 1.86    | 2.16    | 1.95    | 4.28           | 4.32           | 3.96           |
| 49 2,2,4,5'   |         |         | 3.15    | 3.53    | 3.21    | 10.11          | 10.62          | 9.49           |
| 51 2,2,4,6'   |         |         | 1.18    | 1.34    | 1.17    | 1.20           | 1.30           | 1.17           |
| 52 2,2,5,5'   |         |         | 3.29    | 3.80    | 3.36    | 11.07          | 11.59          | 10.66          |
| 53 2,2,5,6'   |         |         | 3.93    | 4.23    | 4.03    | 9.88           | 10.43          | 9.46           |
| 55 2,3,3,4    |         |         | 0.68    | 0.85    | 0.68    | 1.38           | 1.47           | 1.38           |
| 56+60 2,3,3,4;2,3,4,4' | |         | 3.59    | 3.90    | 3.47    | 4.33           | 4.43           | 4.16           |
| 63 2,3,4,5    |         |         | 0.49    | 0.55    | 0.49    | 0.65           | 0.66           | 0.65           |
| 66+70 2,3,4,4';2,3,4,5 |   |         | 5.26    | 6.08    | 5.22    | 6.57           | 6.77           | 6.51           |
| 67 2,3,4,5    |         |         | 0.34    | 0.38    | 0.34    | 0.62           | 0.63           | 0.57           |
| 72+64 2,3,5,5;2,3,4,6 |   |         | 3.44    | 3.95    | 3.43    | 3.94           | 4.20           | 3.82           |
| 74 2,4,4,5    |         |         | 5.93    | 6.72    | 5.98    | 6.21           | 6.27           | 5.86           |
| 76 2,3,4,5'   |         |         | 5.05    | 5.74    | 4.88    | 14.00          | 14.02          | 12.99          |
| 77 3,3,4,4'   |         |         | 1.07    | 1.27    | 1.09    | 1.01           | 1.05           | 1.03           |
| 82 2,2,3,3,4  |         |         | 0.68    | 0.74    | 0.63    | 0.76           | 0.78           | 0.83           |
| Sample | RHA1.1 | RHA1.2 | RHA1.3 | RHA1.control.1 | RHA1.control.2 | RHA1.control.3 |
|--------|--------|--------|--------|---------------|---------------|---------------|
| PCB congener | Chl.sust | [µg] | | | | |
| biphenyl | biphenyl | 0.02 | 0.02 | 0.02 | 0.57 | 0.51 | 0.56 |
| 1 | 2-Chlorobiphenyl | 0.02 | 0.00 | 0.00 | 0.36 | 0.32 | 0.34 |
| 2 | 3-Chlorobiphenyl | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 3 | 4-Chlorobiphenyl | 0.00 | 0.00 | 0.00 | 0.17 | 0.15 | 0.16 |
| 4+10 | 2,2',3,6 | 0.34 | 0.18 | 0.21 | 3.47 | 3.32 | 3.38 |
| 5+8 | 2',3,4 | 2.49 | 1.79 | 2.33 | 27.67 | 27.24 | 27.40 |
| 6 | 2,3 | 0.52 | 0.39 | 0.49 | 4.42 | 4.19 | 4.37 |
| 9+7 | 2,5 | 0.06 | 0.03 | 0.04 | 0.51 | 0.50 | 0.50 |
| 15 | 4,4 | 3.33 | 4.46 | 3.77 | 6.69 | 6.38 | 6.57 |
| 16 | 2,2,3 | 3.63 | 5.03 | 4.28 | 10.48 | 10.05 | 10.39 |
| 17 | 2,2,4 | 3.46 | 4.03 | 4.59 | 20.71 | 20.17 | 19.34 |
| 18 | 2,2,5 | 6.61 | 7.65 | 8.61 | 40.49 | 38.50 | 39.17 |
| 19 | 2,2,6 | 2.58 | 3.18 | 2.81 | 4.68 | 4.63 | 4.56 |
| 22 | 2,3,4 | 7.17 | 9.92 | 7.85 | 16.92 | 15.61 | 15.54 |
| 26+25 | 2,3,5,2',3,4 | 0.97 | 1.28 | 1.24 | 3.69 | 3.32 | 3.38 |
| 27+24 | 2,3,6,2,3,6 | 0.72 | 0.96 | 0.82 | 2.26 | 2.13 | 2.17 |
| 28+31 | 2,4,4,2,4,5 | 17.65 | 25.89 | 20.46 | 47.49 | 43.67 | 47.32 |
| 32 | 2,4,6 | 1.50 | 1.72 | 1.93 | 7.82 | 7.55 | 7.67 |
| 33 | 2,3,4 | 7.68 | 10.00 | 9.73 | 30.76 | 29.48 | 29.88 |
| 37 | 3,4,4 | 8.43 | 11.20 | 8.92 | 13.10 | 11.07 | 12.06 |
| 40 | 2,2,3,3 | 2.54 | 3.37 | 2.71 | 4.29 | 3.79 | 3.95 |
| 41+71 | 2,2,3,4,2,3,4,6 | 2.14 | 2.90 | 2.27 | 3.92 | 3.53 | 3.65 |
| 42 | 2,2,3,4 | 3.09 | 4.17 | 3.54 | 5.52 | 4.71 | 5.25 |
| 44 | 2,2,3,5 | 7.77 | 10.39 | 8.30 | 15.89 | 14.08 | 14.51 |

| ∑PCB | ∑PCB | | |
|-------|-------|-------|-------|
| 117.83 | 140.88 | 123.41 | 349.50 | 362.75 | 332.04 |
| Sample | WAY2.1 | WAY2.2 | WAY2.3 | WAY2.control1 | WAY2.control2 | WAY2.control3 |
|--------|--------|--------|--------|---------------|---------------|---------------|
| PC competent | Chl| [µg] | | | | |
| Boyd | biphenyl | | | | | |
| | 2,2',3,6 | 3.12 | 3.96 | 3.47 | 4.31 | 4.02 | 4.26 |
| | 2,2',3,6' | 1.48 | 1.92 | 1.63 | 2.14 | 1.91 | 2.04 |
| 48+47 | 2,2',4,5; 2,2',4,4' | 2.66 | 3.49 | 2.89 | 5.45 | 3.89 | 4.19 |
| 49 | 2,2',4,5' | 7.41 | 9.55 | 7.88 | 10.59 | 9.53 | 10.17 |
| 51 | 2,2',4,6' | 0.97 | 1.19 | 1.01 | 1.29 | 1.22 | 1.20 |
| 52 | 2,2',5,5' | 7.92 | 10.35 | 8.73 | 11.65 | 10.65 | 11.19 |
| 53 | 2,2',5,6' | 7.88 | 9.63 | 8.36 | 10.33 | 9.93 | 10.64 |
| 55 | 2,3',4 | 1.12 | 1.43 | 1.07 | 1.53 | 1.19 | 1.29 |
| 56+60 | 2,3',4'; 2,3,4' | 2.94 | 4.01 | 3.20 | 4.72 | 3.95 | 4.22 |
| 63 | 2,3',4,5 | 0.50 | 0.62 | 0.53 | 0.71 | 0.61 | 0.66 |
| 66+70 | 2,3',4,4'; 2,3',4,5 | 4.31 | 5.77 | 4.47 | 7.28 | 6.12 | 6.68 |
| 67 | 2,3',4,5 | 0.40 | 0.51 | 0.42 | 0.66 | 0.52 | 0.55 |
| 72+64 | 2,3',5,5'; 2,3',4,6 | 3.19 | 4.00 | 3.23 | 4.35 | 3.66 | 4.02 |
| 74 | 2,4',5 | 4.55 | 6.02 | 4.88 | 6.59 | 5.52 | 5.92 |
| 76 | 2,3',4,4' | 9.34 | 12.51 | 9.96 | 14.90 | 12.46 | 13.52 |
| 77 | 3,3',4,4' | 0.87 | 1.13 | 0.98 | 1.14 | 0.96 | 1.06 |
| 82 | 2,2',3,3,4 | 0.62 | 0.79 | 0.63 | 0.87 | 0.63 | 0.77 |
| 84-92 | 2,2',3,3,6; 2,2',3,5,5' | 0.30 | 0.37 | 0.32 | 0.39 | 0.33 | 0.36 |
| 87 | 2,2',3,4,5 | 0.58 | 0.75 | 0.57 | 0.75 | 0.61 | 0.59 |
| 91 | 2,2',3,4,6 | 0.28 | 0.39 | 0.32 | 0.36 | 0.35 | 0.32 |
| 95 | 2,2',3,5,6 | 3.03 | 3.87 | 3.21 | 4.00 | 3.37 | 3.66 |
| 97 | 2,2',3,4,5 | 0.41 | 0.57 | 0.47 | 0.66 | 0.57 | 0.58 |
| 99 | 2,2',4,4,5 | 0.74 | 0.96 | 0.77 | 0.98 | 0.81 | 0.85 |
| 101+113 | 2,2',4,5,5'; 2,3,3,5,6 | 0.50 | 0.63 | 0.53 | 0.64 | 0.56 | 0.59 |
| 105 | 2,3',3,4,4 | 0.53 | 0.70 | 0.58 | 0.64 | 0.52 | 0.57 |
| 110 | 2,3',3,4,6 | 1.45 | 1.86 | 1.57 | 1.89 | 1.54 | 1.64 |
| 111 | 2,3',3,5,5' | 0.42 | 0.57 | 0.47 | 0.55 | 0.48 | 0.49 |
| 118 | 2,3',3,4,5 | 0.74 | 0.97 | 0.79 | 0.93 | 0.73 | 0.76 |
| 138+163 | 2,2',3,4,4,5'; 2,3,3,4,5,6 | 0.06 | 0.07 | 0.05 | 0.06 | 0.05 | 0.05 |
| 148 | 2,2',3,4,5,6 | 0.04 | 0.04 | 0.04 | 0.05 | 0.05 | 0.04 |
| 149 | 2,2',3,4,5,6 | 0.07 | 0.09 | 0.06 | 0.07 | 0.07 | 0.07 |
| 153 | 2,2',4,4,5,5 | 0.05 | 0.06 | 0.05 | 0.05 | 0.04 | 0.05 |
| 180 | 2,2',3,4,4,5,5 | ND | ND | ND | ND | ND | ND |

| PCB congeners | Chl. sus | [µg] | | | | |
|----------------|---------|------|------|------|------|------|
| biphenyl | biphenyl | 0.02 | 0.02 | 0.02 | 0.13 | 0.69 | 0.64 |
| 1 | 2-Chlorobiphenyl | 0.00 | 0.02 | 0.00 | 0.17 | 0.40 | 0.38 |
| 2 | 3-Chlorobiphenyl | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| 3 | 4-Chlorobiphenyl | 0.00 | 0.00 | 0.00 | 0.10 | 0.18 | 0.16 |
| 4+10 | 2,2',2,6 | 0.50 | 0.71 | 0.57 | 2.72 | 3.92 | 3.72 |
| 5+8 | 2,3; 2,4' | 5.67 | 7.79 | 6.57 | 25.71 | 32.17 | 28.99 |
| 6 | 2,3' | 1.06 | 1.43 | 1.24 | 4.02 | 5.05 | 4.53 |
|   | 2,2; 2,4 | 0.10 | 0.15 | 0.10 | 0.48 | 0.61 | 0.58  |
|---|----------|------|------|------|------|------|------|
| 15 | 4,4'     | 2.15 | 3.09 | 2.78 | 6.98 | 7.98 | 7.07  |
| 16 | 2,2,3    | 9.41 | 11.49| 11.43| 10.96| 13.66| 11.48 |
| 17 | 2,2,4    | 7.88 | 10.62| 9.76 | 20.73| 24.14| 21.75 |
| 18 | 2,2,5    | 13.60| 17.99|16.36 | 41.20| 50.85| 44.06 |
| 19 | 2,2,6    | 4.14 | 4.90 | 4.99 | 4.51 | 5.39 | 4.96  |
| 22 | 2,3,4'   | 10.43| 14.05|13.54 | 18.14| 22.06| 18.06 |
| 26+25| 2,3,5; 2,3,4  | 1.55 | 2.13 | 1.99 | 3.87 | 4.35 | 3.88  |
| 27+24| 2,3,6; 2,3,6  | 1.58 | 1.97 | 1.99 | 2.29 | 2.77 | 2.40  |
| 28+31| 2,4,4'; 2,4,5  | 21.14| 30.80|28.48 | 50.55| 62.18| 50.42 |
| 32  | 2,4,6    | 3.11 | 4.10 | 3.75 | 8.15 | 9.78 | 8.51  |
| 33  | 2,3,4'   | 12.63| 19.46|17.16 | 33.17| 38.37| 33.95 |
| 37  | 3,4,4'   | 8.69 | 11.88|11.68 | 14.75| 17.43| 14.73 |
| 40  | 2,2,3,5' | 3.83 | 4.59 | 4.59 | 4.63 | 5.44 | 4.73  |
| 41+71| 2,2,3,4; 2,3,4,6 | 3.56 | 4.27 | 4.35 | 4.29 | 5.09 | 4.28  |
| 42  | 2,2,3,4' | 4.80 | 5.49 | 5.75 | 5.99 | 7.51 | 6.16  |
| 44  | 2,2,3,5' | 9.30 | 13.27|12.48 | 17.43| 19.92| 17.26 |
| 45  | 2,2,3,6  | 3.90 | 4.68 | 4.70 | 4.52 | 5.46 | 4.74  |
| 46  | 2,2,3,6' | 1.79 | 2.24 | 2.32 | 2.16 | 2.62 | 2.32  |
| 48+47| 2,2,4,5; 2,2,4,4' | 3.69 | 4.54 | 4.60 | 5.39 | 5.91 | 4.94  |
| 49  | 2,2,4,5' | 9.93 | 12.00|11.87 | 11.53| 14.04| 11.80 |
| 51  | 2,2,4,6' | 1.16 | 1.42 | 1.43 | 1.38 | 1.55 | 1.39  |
| 52  | 2,2,5,5' | 10.76| 13.22|12.91 | 12.87| 15.69| 13.07 |
| 53  | 2,2,5,6' | 9.61 | 11.60|11.24 | 11.23| 13.56| 11.56 |
| 55  | 2,3,3'   | 1.41 | 1.84 | 1.77 | 1.65 | 2.06 | 1.82  |
| 56+60| 2,3,3'; 2,3,4,4' | 4.21 | 5.18 | 5.13 | 5.18 | 6.18 | 5.25  |
| 63  | 2,3,4,5  | 0.67 | 0.81 | 0.82 | 0.79 | 0.92 | 0.80  |
| 66+70| 2,3,4,4'; 2,3,4,5 | 5.68 | 7.34 | 7.34 | 8.59 | 9.63 | 8.30  |
| 67  | 2,3,4'   | 0.37 | 0.57 | 0.52 | 0.73 | 0.89 | 0.70  |
| 72+64| 2,3,5,5'; 2,3,4,6 | 3.98 | 4.92 | 4.88 | 4.83 | 5.75 | 4.86  |
| 74  | 2,4,4'   | 5.25 | 6.52 | 6.63 | 7.23 | 8.88 | 7.57  |
| 76  | 2,3,4,5' | 11.99| 15.44|15.16 | 16.75| 20.00| 16.73 |
| 77  | 3,3,4,4' | 1.11 | 1.38 | 1.36 | 1.37 | 1.60 | 1.36  |
| 82  | 2,2,3,3,4 | 0.88 | 1.01 | 0.97 | 1.00 | 1.23 | 1.11  |
| 84+92| 2,2,3,3;6; 2,2,3,5,5' | 0.38 | 0.45 | 0.44 | 0.44 | 0.54 | 0.45  |
| 87  | 2,2,3,4,5' | 0.71 | 0.96 | 0.85 | 0.89 | 0.99 | 0.85  |
| 91  | 2,2,3,4,6 | 0.38 | 0.43 | 0.44 | 0.41 | 0.50 | 0.44  |
| 95  | 2,2,3,5,6 | 3.93 | 4.62 | 4.50 | 4.56 | 5.55 | 4.51  |
| 97  | 2,2,3,4,5' | 0.64 | 0.77 | 0.70 | 0.78 | 0.93 | 0.78  |
| 99  | 2,2,4,4,5 | 0.96 | 1.15 | 1.10 | 1.12 | 1.36 | 1.13  |
| 101+113| 2,2,4,5,5'; 2,3,3,5,6 | 0.63 | 0.72 | 0.74 | 0.72 | 0.92 | 0.74  |
| 105 | 2,3,3,4,4' | 0.66 | 0.81 | 0.78 | 0.78 | 0.91 | 0.79  |
| 110 | 2,3,3,4,6 | 1.89 | 2.19 | 2.16 | 2.12 | 2.54 | 2.19  |
| 111 | 2,3,3,5,5' | 0.56 | 0.65 | 0.68 | 0.67 | 0.80 | 0.65  |
| 118 | 2,3,4,4,5 | 0.90 | 1.10 | 1.09 | 1.09 | 1.27 | 1.11  |
| 138+163| 2,2,3,4,5'; 2,3,3,4,5,6 | 0.07 | 0.08 | 0.08 | 0.08 | 0.08 | 0.08  |
| PCB congener | Chl.sust | sample | JAB1. | JAB1. | JAB1. | JAB1. | JAB1.control | JAB1.control | JAB1.control |
|-------------|----------|--------|-------|-------|-------|-------|--------------|--------------|--------------|
|             |          |        | 1     | 2     | 3     | 1     | 2            | 3            |              |
| biphenyl    | biphenyl |        | 0.02  | 0.02  | 0.02  | 0.67  | 0.68         | 0.56         |              |
| 2,2',3,3',4,4',5,5',6' | 0.04 | 0.05 | 0.05 | 0.05 | 0.06 | 0.06 |              |              |              |
| 2,2',3,3',4,4',5,6' | 0.08 | 0.09 | 0.09 | 0.10 | 0.12 | 0.09 |              |              |              |
| 2,2',4,4',5,5',6' | 0.06 | 0.07 | 0.07 | 0.07 | 0.07 | 0.07 |              |              |              |
| 2,2',3,4,4',5,5',6' | ND   | ND   | ND   | ND   | ND   | ND   |              |              |              |
| 2,2',3,3',4,5,5',6' | 213.44 | 279.06 | 266.98 | 392.04 | 472.57 | 404.97 |              |              |              |

**∑PCB**
|        | 2,3',5,5'; 2,3',4',6 | 2,4,4',5 | 2,3',4',5' | 3,3',4,4' | 2,2',3,3',4 | 2,2',3,3',5,5' | 2,2',3,4,5; 2,2',3,5,5' | 2,2',3,4,6 | 2,2',3,5,6 | 2,2',3,4,5 | 2,2',3,4,5' | ∑PCB | ∑PCB |
|--------|---------------------|---------|-----------|-----------|------------|----------------|------------------------|---------|-----------|------------|-------------|-------|-------|
| 72+64  | 3.27                | 3.25    | 3.25      | 3.71      | 3.02       | 2.97           | 2.4,4',5; 2,3',5,5'; 2,3,4',6 | 3.41    | 3.71      | 4.79       | 4.65        | 250.32| 262.68|
| 74     | 5.25                | 5.19    | 5.30      | 5.76      | 4.79       | 4.65           | 2,3',4',5'                 | 11.79   | 12.66     | 10.72      | 10.59       |       |       |
| 76     | 1.01                | 1.00    | 1.06      | 1.06      | 0.88       | 0.91           | 3,3',4,4'                 | 0.73     | 0.79      | 0.59       | 0.61        |       |       |
| 77     | 0.33                | 0.33    | 0.33      | 0.37      | 0.31       | 0.30           | 2,2',3,3',4                | 0.33     | 0.57      | 0.51       | 0.54        |       |       |
| 82     | 0.61                | 0.64    | 0.64      | 0.57      | 0.51       | 0.54           | 2,2',3,4,5'               | 0.33     | 0.35      | 0.31       | 0.30        |       |       |
| 84+92  | 3.47                | 3.40    | 3.34      | 3.70      | 2.96       | 2.94           | 2,2',3,5,6                 | 0.53     | 0.59      | 0.47       | 0.49        |       |       |
| 87     | 0.92                | 0.83    | 0.86      | 0.97      | 0.78       | 0.77           | 2,2',4,4',5               | 0.59     | 0.61      | 0.50       | 0.53        |       |       |
| 91     | 0.66                | 0.61    | 0.63      | 0.64      | 0.50       | 0.58           | 2,3',4,4'                 | 1.74     | 1.77      | 1.38       | 1.42        |       |       |
| 95     | 0.54                | 0.48    | 0.50      | 0.53      | 0.42       | 0.46           | 2,3',5,5'                 | 0.83     | 0.92      | 0.70       | 0.79        |       |       |
| 97     | 0.05                | 0.05    | 0.06      | 0.05      | 0.06       | 0.06           | 2,2',3,4,4',5; 2,3',3',5,5' | 0.04     | 0.04      | 0.04       | 0.05        |       |       |
| 99     | 0.04                | 0.04    | 0.04      | 0.05      | 0.04       | 0.05           | 2,2',3,4,5'               | 0.08     | 0.09      | 0.07       | 0.07        |       |       |
| 101+113| 0.08                | 0.08    | 0.08      | 0.06      | 0.06       | 0.06           | 2,2',4,4',5'               | 0.05     | 0.06      | 0.04       | 0.04        |       |       |
| 105    | 0.05                | 0.05    | 0.05      | 0.05      | 0.05       | 0.05           | 2,3',4,4',5; 2,3',3',5,5' | ND      | ND        | ND         | ND          |       |       |
| 108    | 0.05                | 0.05    | 0.05      | 0.06      | 0.06       | 0.06           | 2,2',3,4,4',5; 2,3',3',5,5' | ND      | ND        | ND         | ND          |       |       |
| 110    | 0.04                | 0.04    | 0.04      | 0.05      | 0.05       | 0.05           | 2,2',3,4,5,5'             | ND      | ND        | ND         | ND          |       |       |
| 111    | 0.04                | 0.04    | 0.04      | 0.05      | 0.05       | 0.05           | 2,2',3,4,5,5'             | ND      | ND        | ND         | ND          |       |       |
| 118    | 0.05                | 0.05    | 0.05      | 0.06      | 0.06       | 0.06           | 2,2',4,4',5',6            | ND      | ND        | ND         | ND          |       |       |
| 138+163| 0.05                | 0.05    | 0.05      | 0.06      | 0.06       | 0.06           | 2,3',4,4',5; 2,3',3',4,5,6 | ND      | ND        | ND         | ND          |       |       |
| 148    | 0.04                | 0.04    | 0.04      | 0.05      | 0.05       | 0.05           | 2,2',3,4,5,6             | ND      | ND        | ND         | ND          |       |       |
| 149    | 0.04                | 0.04    | 0.04      | 0.05      | 0.05       | 0.05           | 2,2',3,4,5,6             | ND      | ND        | ND         | ND          |       |       |
| 153    | 0.04                | 0.04    | 0.04      | 0.05      | 0.05       | 0.05           | 2,2',4,4',5,5'           | ND      | ND        | ND         | ND          |       |       |
| 180    | 0.04                | 0.04    | 0.04      | 0.05      | 0.05       | 0.05           | 2,2',3,4,5,5'            | ND      | ND        | ND         | ND          |       |       |

**ΣPCB** | **ΣPCB** | 250.32 | 262.68 | 258.15 | 321.17 | 284.42 | 259.15
Supplementary Table S1. *Rhodococcus* type strains 16S rRNA genes used in this study.

| Type strain name               | Accs. no. 16S rRNA | Type strain name               | Accs. no. 16S rRNA |
|--------------------------------|--------------------|--------------------------------|--------------------|
| *R. aerolatus* PAMC 27367<sup>T</sup> | KM044053.1         | *R. koreensis* DPN505<sup>T</sup> | AF124342.1         |
| *R. aetherivorans* 10bc312<sup>T</sup> | AF447391.1         | *R. kroppenstedtii* K07-23<sup>T</sup> | AF726605.1         |
| *R. agglutinans* CFH 50262<sup>T</sup> | KP232908.1         | *R. kunmingensis* YIM 45607<sup>T</sup> | DQ997045.1         |
| *R. aichiensis* DSM 43978<sup>T</sup> | X80633.1           | *R. kyotonensis* DS472<sup>T</sup> | AB269261.1         |
| *R. antrifimi* D7-21<sup>T</sup> | LN867321.1         | *R. lactis* DW151B<sup>T</sup> | KP342300.1         |
| *R. artemisiae* YIM 65754<sup>T</sup> | GU367155.1         | *R. luteus* DSM 43673<sup>T</sup> | X79187.1           |
| *R. auranticus* ATCC 25938<sup>T</sup> | AF283282.1         | *R. maris* DSM 43672<sup>T</sup> | X80617.1           |
| *R. bronchialis* DSM 43247<sup>T</sup> | KJ546454.1         | *R. marinonascens* DSM 43752<sup>T</sup> | X80617.1           |
| *R. canchipurensis* MBRL 353<sup>T</sup> | JN164649.1         | *R. maanshanensis* M712<sup>T</sup> | X79290.1           |
| *R. cerastii* C5<sup>T</sup> | FR714842.1         | *R. nanhaiensis* SCSIO 10187<sup>T</sup> | JN582175.1         |
| *R. corynebacterioides* DSM 20151<sup>T</sup> | AF430066.1         | *R. obuensis* ATCC 33610<sup>T</sup> | AY262329.1         |
| *R. degradans* CCM 4446<sup>T</sup> | KC788572.1         | *R. olei* KTM-20<sup>T</sup> | MF405107.1         |
| *R. electrodiphilus* JC435 | LT630357.3         | *R. opacum* DSM 43205<sup>T</sup> | X80630.1           |
| *R. electrodiphilus* J435<sup>T</sup> | LT630357.3         | *R. pedocola* UC12<sup>T</sup> | KT301938.1         |
| *R. equi* DSM 20307<sup>T</sup> | X79298.1           | *R. percolatus* MBS1<sup>T</sup> | X92114.1           |
| *R. erythropolis* DSM 43066<sup>T</sup> | X97289.1           | *R. phenolicus* G2P<sup>T</sup> | AY533293.1         |
| *R. gordoniae* DSM 20669<sup>T</sup> | X79186.1           | *R. pyridinovorans* PDB9<sup>T</sup> | AF173005.1         |
| *R. jialingiae* djl-2<sup>T</sup> | NR152643.1         | *R. rubripertinctus* DSM 43197<sup>T</sup> | X80632.1           |
| *R. jostii* NBRC 16295<sup>T</sup> | AB046357.1         | *R. soli* DSM 43249<sup>T</sup> | X79286.1           |
| *R. luteus* DSM 43672<sup>T</sup> | X80619.1           | *R. sovatensis* H004<sup>T</sup> | KU189221.1         |
| *R. marinonascens* DSM 43752<sup>T</sup> | X80633.1           | *R. sputi* DSM 43896<sup>T</sup> | X80634.1           |
| *R. maris* DSM 43672<sup>T</sup> | X80619.1           | *R. terrae* DSM 43249<sup>T</sup> | X79286.1           |
| *R. marinonascens* DSM 43752<sup>T</sup> | X80619.1           | *R. trifolii* T8<sup>T</sup> | FR714843.1         |
| *R. rubripertinctus* DSM 43197<sup>T</sup> | X80619.1           | *R. tukisamuensis* Mbx<sup>T</sup> | AB067734.1         |
| *R. rubripertinctus* NCMIB 13082<sup>T</sup> | X80619.1           | *R. xiangmengensis* YIM 70056<sup>T</sup> | AY602192.2         |
| *R. sovatensis* H004<sup>T</sup> | XR152643.1         | *R. yunnanensis* YIM 70056<sup>T</sup> | AY602192.2         |
| *R. tricholii* DSM 44108<sup>T</sup> | AB046357.1         | *R. zopfii* DSM 44108<sup>T</sup> | AF191343.1         |

*R. obuensis* ATCC 33610<sup>T</sup> was excluded from further analysis because its 16S rRNA gene sequence was too small (505 nts).
## Supplementary Table S2. Genomes of *Rhodococcus* type strains used in this study.

| Type strain gene name | Assembly Accs. no. | Scaffolds | Size (Mbp) | GC% | Genes | Proteins |
|-----------------------|-------------------|-----------|------------|-----|-------|----------|
| *R. agglutinans* CCCTC AB2014297<sup>T</sup> | GCA_004011865.1 | 22 | 5.43 | 69.3 | 4.994 | 4.862 |
| *R. biphenylivorans* TG9<sup>T</sup> | GCA_003280905.1 | 1 | 5.03 | 68 | 4.7 | 4.373 |
| *R. bronchialis* DSM 43247<sup>T</sup> | GCA_000024785.1 | - | 5.29 | 67.1 | 4.934 | 4.601 |
| *R. chlorophenolicum* DSM 43826<sup>T</sup> | GCA_001044235.1 | 72 | 7.38 | 68.4 | 7.164 | 6.729 |
| *R. coprophilus* NBRC 100603<sup>T</sup> | GCA_001895045.1 | 30 | 4.55 | 66.9 | 4.206 | 4.079 |
| *R. corynebacterioides* DSM 20151<sup>T</sup> | GCA_001646675.1 | 180 | 3.9 | 70.2 | 3.651 | 3.445 |
| *R. defluvii* Ca11<sup>T</sup> | GCA_000738775.1 | 267 | 5.13 | 68.7 | 4.85 | 4.535 |
| *R. encelaxis* NIO-1009<sup>T</sup> | GCA_900094765.1 | 76 | 7.48 | 62.3 | 7.098 | 6.826 |
| *R. equi* DSM 20307<sup>T</sup> | GCA_002094305.1 | 37 | 5.2 | 68.8 | 4.85 | 4.735 |
| *R. erythropolis* NBRC 15567<sup>T</sup> | GCA_001552595.1 | 67 | 6.59 | 62.4 | 6.147 | 5.981 |
| *R. fascians* NBRC 12155<sup>T</sup> | GCA_001894785.1 | 36 | 5.77 | 64.4 | 5.422 | 5.284 |
| *R. globerulus* NBRC 14531<sup>T</sup> | GCA_001894805.1 | 30 | 6.74 | 61.7 | 6.231 | 6.054 |
| *R. gordonii* DSM 44689<sup>T</sup> | GCA_001646655.1 | 114 | 4.82 | 67.9 | 4.46 | 4.238 |
| *R. hoaigii* DSM 20295<sup>T</sup> | GCA_001646645.1 | 279 | 4.97 | 68.8 | 4.757 | 4.427 |
| *R. intechiensis* RKJ300<sup>T</sup> | GCA_000260815.1 | 178 | 8.23 | 67.2 | 7.962 | 7.245 |
| *R. jostii* NBRC 16295<sup>T</sup> | GCA_001894825.1 | 286 | 9.73 | 66.9 | 8.983 | 8.358 |
| *R. koreensis* DSM 44498<sup>T</sup> | GCA_900105905.1 | 9 | 10.31 | 67.4 | 9.491 | 8.902 |
| *R. kroppenstedtii* DSM 44908<sup>T</sup> | GCA_900111805.1 | 30 | 4.08 | 70.1 | 3.789 | 3.652 |
| *R. kunmingensis* DSM 45001<sup>T</sup> | GCA_001646865.1 | 330 | 5.62 | 66.2 | 3.76 | 4.885 |
| *R. kyotonensis* JCM 23211<sup>T</sup> | GCA_900188125.1 | 50 | 6.31 | 64.2 | 5.86 | 5.698 |
| *R. maashanensis* DSM 44675<sup>T</sup> | GCA_900109405.1 | 61 | 5.67 | 69.2 | 5.143 | 4.972 |
| *R. marinosakens* NBRC 14363<sup>T</sup> | GCA_001894885.1 | 156 | 4.92 | 64.4 | 3.28 | 4.269 |
| *R. maris* DSM 43672<sup>T</sup> | GCA_001630765.1 | 57 | 3.51 | 70.9 | 3.302 | 3.098 |
| *R. opacus* DSM 43205<sup>T</sup> | GCA_001646735.1 | 382 | 8.52 | 67.3 | 8.198 | 7.418 |
| *R. phenolicus* DSM 44812<sup>T</sup> | GCA_001646785.1 | 232 | 6.28 | 68.4 | 5.916 | 5.6 |
| *R. pyridinivorans* DSM 44555<sup>T</sup> | GCA_900105195.1 | 3 | 5.26 | 67.8 | 4.864 | 4.604 |
| *R. qingxianensis* JCM 15477<sup>T</sup> | GCA_001646745.1 | 131 | 7.26 | 62.4 | 6.82 | 6.574 |
| *R. rhodnii* NBRC 100604<sup>T</sup> | GCA_001894925.1 | 70 | 4.46 | 69.7 | 4.265 | 4.08 |
| *R. rhodochrous* DSM 43241<sup>T</sup> | GCA_001646825.1 | 105 | 5.18 | 68.2 | 4.79 | 4.585 |
| *R. ruber* DSM 43338<sup>T</sup> | GCA_001646835.1 | 164 | 5.3 | 70.7 | 4.93 | 4.677 |
| *R. rubripertincta* NBRC 101908<sup>T</sup> | GCA_000327325.1 | 134 | 5.2 | 67.4 | 4.792 | 4.571 |
| *R. sputi* NBRC 100414<sup>T</sup> | GCA_000248055.2 | 158 | 4.95 | 65.4 | 4.642 | 4.592 |
| *R. terrae* NRRL B-16283<sup>T</sup> | GCA_003183825.1 | - | 5.71 | 67.8 | 5.109 | 4.951 |
| *R. triatoma* DSM 44892<sup>T</sup> | GCA_000997275.1 | 38 | 4.73 | 68.7 | 4.43 | 4.297 |
| *R. tukasmanensis* NBRC 100609<sup>T</sup> | GCA_001894985.1 | 66 | 5.49 | 69.9 | 4.97 | 4.779 |
| *R. wratislaviensis* NBRC 100605<sup>T</sup> | GCA_000587375.1 | 151 | 10.4 | 66.8 | 9.514 | 8.883 |
| *R. yunnanensis* NBRC 103083<sup>T</sup> | GCA_001895005.1 | 68 | 6.37 | 63.9 | 5.847 | 5.65 |
| *R. zopfii* NBRC 100606<sup>T</sup> | GCA_001895025.1 | 146 | 6.3 | 68.2 | 5.848 | 5.575 |
Table S3. Genes involved in core cellular functions of *Rhodococcus* sp. WAY2

| Replicon | Start     | End       | Strand | Gene name | Predicted function                                      | Cellular function          |
|----------|-----------|-----------|--------|-----------|---------------------------------------------------------|-----------------------------|
| Chromosome | 1         | 1,587     | +      | dnaA      | Chromosomal replication initiator protein               | Replication                 |
| Chromosome | 3,656,174 | 3,658,378 | +      | dnaB      | Replicative DNA helicase                                | Replication                 |
| Chromosome | 2602811   | 2604742   | +      | dnaG      | DNA primase                                             | Replication                 |
| Chromosome | 2,799,978 | 2,803,514 | +      | dnaE      | DNA polymerase III alpha subunit                        | Replication                 |
| Chromosome | 2,247     | 3,431     | +      | dnaN      | DNA polymerase III beta subunit                         | Replication                 |
| Chromosome | 2,737,654 | 2,735,894 | -      | dnaQ      | DNA polymerase III epsilon subunit                      | Replication                 |
| Chromosome | 595,751   | 598,042   | +      | dnaX      | DNA polymerase III gamma and tau subunits               | Replication                 |
| Chromosome | 2,552,031 | 2,553,008 | +      | holA      | DNA polymerase III delta subunit                        | Replication                 |
| Chromosome | 719,116   | 720,330   | +      | holB      | DNA polymerase III delta prime subunit                  | Replication                 |
| Chromosome | 17,206    | 19,728    | +      | gyrA      | DNA gyrase subunit A                                    | Replication                 |
| Chromosome | 9,531     | 11,573    | +      | gyrB      | DNA gyrase subunit B                                    | Replication                 |
| Chromosome | 4,508,290 | 4,509,321 | +      | ligC      | ATP-dependent DNA ligase                                | Replication                 |
| Chromosome | 716,139   | 719,063   | +      | topA      | DNA topoisomerase I                                     | Replication                 |
| Chromosome | 2452962   | 2453426   | +      | ssb       | Single-strand DNA-binding protein                       | Replication                 |
| Chromosome | 3,654,343 | 3,654,864 | +      | ssb       | Single-strand DNA-binding protein                       | Replication                 |
| Chromosome | 3,496,401 | 3,494,383 | -      | priA      | Primosomal protein n’                                   | Replication                 |
| Chromosome | 2,947,050 | 2,947,949 | +      | parA1     | Chromosome (plasmid) partitioning protein               | Replication                 |
| Chromosome | 4,751,853 | 4,752,611 | +      | parA2     | Chromosome (plasmid) partitioning protein               | Replication                 |
| Chromosome | 5,976,007 | 5,976,804 | +      | parA3     | Chromosome (plasmid) partitioning protein               | Replication                 |
| Chromosome | 6,616,198 | 6,615,185 | -      | parA4     | Chromosome (plasmid) partitioning protein               | Replication                 |
| Chromosome | 6,615,188 | 6,614,127 | -      | parB      | Chromosome (plasmid) partitioning protein               | Replication                 |
| pRWAY01   | 382,849   | 383,562   | +      | parA      | Plasmid partitioning protein                            | Replication                 |
| pRWAY01   | 383,562   | 384,428   | +      | parB1     | Chromosome (plasmid) partitioning protein               | Replication                 |
| pRWAY01   | 446,841   | 445,951   | -      | parB2     | Chromosome (plasmid) partitioning protein               | Replication                 |
| pRWAY01   | 470,162   | 468,558   | -      | parB3     | Chromosome (plasmid) partitioning protein               | Replication                 |
| pRWAY02   | 86,990    | 87,772    | +      | parA      | Chromosome (plasmid) partitioning protein               | Replication                 |
| pRWAY03   | 339,700   | 340,668   | +      | parA      | Chromosome (plasmid) partitioning protein               | Replication                 |
| pRWAY04   | 5,889     | 5,116     | -      | parA      | Chromosome (plasmid) partitioning protein               | Replication                 |
| pRWAY01   | 106,121   | 104,127   | -      | tap1      | Telomere-binding protein                                | Telomere stabilization      |
| pRWAY01   | 572,964   | 571,006   | -      | tap2      | Telomere-binding protein                                | Telomere stabilization      |
| pRWAY01   | 734,553   | 733,756   | -      | tpg       | Telomere terminal protein                               | Telomere stabilization      |
| pRWAY01   | 736,526   | 734,553   | -      | tap3      | Telomere-binding protein                                | Telomere stabilization      |
| pRWAY02  | 105,788 | 107,872 | + | tap1             | Telomere-binding protein | Telomere stabilization |
|---------|---------|---------|---|------------------|--------------------------|------------------------|
| pRWAY02 | 107,872 | 108,669 | + | tpg              | Telomere terminal protein | Telomere stabilization |
| pRWAY02 | 164,253 | 162,955 | - | tap2             | Telomere-binding protein | Telomere stabilization |
| pRWAY02 | 454,926 | 458,255 | + | tap3             | Telomere-binding protein | Telomere stabilization |
| pRWAY02 | 460,071 | 458,329 | - | tap4             | Telomere-binding protein | Telomere stabilization |
| pRWAY03 | 241,118 | 239,262 | - | tap1             | Telomere-binding protein | Telomere stabilization |
| pRWAY03 | 342,324 | 347,702 | + | tap2             | Telomere-binding protein | Telomere stabilization |
| pRWAY03 | 347,699 | 348,433 | + | tpg              | Telomere terminal protein | Telomere stabilization |
| Chromosome 5 | 5,771,254 | 5,772,315 | + | rpoA             | DNA-directed RNA polymerase alpha subunit | Transcription |
| Chromosome 1 | 1,814,549 | 1,818,037 | + | rpoB             | DNA-directed RNA polymerase beta subunit | Transcription |
| Chromosome 1 | 1,818,157 | 1,822,113 | + | rpoC             | DNA-directed RNA polymerase beta' subunit | Transcription |
| Chromosome 6 | 6,343,022 | 6,341,646 | - | rpoD             | RNA polymerase sigma factor RpoD | Transcription |
| Chromosome 4 | 4,194,213 | 4,194,719 | + | rpoN             | RNA polymerase sigma-54 factor RpoN | Transcription |
| Chromosome 3 | 3,499,415 | 3,499,110 | - | rpoZ             | DNA-directed RNA polymerase omega subunit | Transcription |
| Chromosome 1 | 1,089,695 | 1,088,799 | - | sigF1            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 1 | 1,411,251 | 1,410,331 | - | sigJ1            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 1 | 1,685,881 | 1,685,144 | - | sigF2            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 3 | 3,209,743 | 3,210,678 | + | sigX             | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 3 | 3,304,884 | 3,305,681 | + | sigF3            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 3 | 3,811,818 | 3,812,057 | + | sig              | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 3 | 3,927,675 | 3,926,941 | - | sigK1            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 4 | 4,125,707 | 4,125,036 | - | sigD1            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 4 | 4,600,503 | 4,600,982 | + | sigD2            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 4 | 4,890,674 | 4,891,333 | + | sigZ             | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 4 | 4,913,325 | 4,912,345 | - | sig              | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 5 | 5,229,528 | 5,228,305 | - | sig              | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 5 | 5,554,709 | 5,555,359 | + | sigE             | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 5 | 5,814,072 | 5,813,404 | - | sigK2            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 5 | 5,817,100 | 5,817,447 | + | sigD3            | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 5 | 5,969,836 | 5,970,573 | + | sigH             | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 6 | 6,332,642 | 6,331,671 | - | sigB             | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 6 | 6,606,184 | 6,606,765 | + | sigM             | RNA polymerase sigma-70 factor | Transcription |
| Chromosome 3 | 3,211,552 | 3,211,214 | - | rbpA1            | RNA polymerase-binding protein | Transcription |
| Chromosome 7 | 721,940 | 723,459 | + | 16S rRNA         | Small Subunit Ribosomal RNA | Translation |
| Chromosome 7 | 731,952 | 733,471 | + | 16S rRNA         | Small Subunit Ribosomal RNA | Translation |
| Chromosome 2 | 2,377,970 | 2,379,489 | + | 16S rRNA         | Small Subunit Ribosomal RNA | Translation |
| Chromosome 2 | 2,929,964 | 2,931,483 | + | 16S rRNA         | Small Subunit Ribosomal RNA | Translation |
| Chromosome 7 | 723,795 | 726,930 | + | 23S rRNA         | Large Subunit Ribosomal RNA | Translation |
| Chromosome | Start | End   | Type          | Translation |
|------------|-------|-------|---------------|-------------|
| 733,805    | 736,936 | +     | 23S rRNA      | Translation |
| 2,379,825  | 2,382,960 | +     | 23S rRNA      | Translation |
| 2,931,819  | 2,934,954 | +     | 23S rRNA      | Translation |
| 727,095    | 727,215  | +     | 5S RNA        | Translation |
| 737,090    | 737,210  | +     | 5S RNA        | Translation |
| 2,383,114  | 2,383,234 | +     | 5S RNA        | Translation |
| 2,935,107  | 2,935,227 | +     | 5S RNA        | Translation |
| 2,890,126  | 2,891,613 | +     | rpsA          | 30S ribosomal protein S1 |
| 6,183,560  | 6,184,408 | +     | rpsB          | 30S ribosomal protein S2 |
| 5,759,342  | 5,760,148 | +     | rpsC          | 30S ribosomal protein S3 |
| 5,770,532  | 5,771,137 | +     | rpsD          | 30S ribosomal protein S4 |
| 5,764,275  | 5,764,931 | +     | rpsE          | 30S ribosomal protein S5 |
| 3,653,990  | 3,654,277 | +     | rpsF          | 30S ribosomal protein S6 |
| 1,856,786  | 1,857,256 | +     | rpsG          | 30S ribosomal protein S7 |
| 5,762,858  | 5,763,280 | +     | rpsH          | 30S ribosomal protein S8 |
| 5,792,720  | 5,793,256 | +     | rpsI          | 30S ribosomal protein S9 |
| 5,755,800  | 5,756,105 | +     | rpsJ          | 30S ribosomal protein S10 |
| 5,770,096  | 5,770,509 | +     | rpsK          | 30S ribosomal protein S11 |
| 1,856,412  | 1,856,786 | +     | rpsL          | 30S ribosomal protein S12 |
| 5,769,764  | 5,770,096 | +     | rpsM          | 30S ribosomal protein S13 |
| 5,201,297  | 5,200,992 | -     | rpsN          | 30S ribosomal protein S14 |
| 6,248,056  | 6,248,325 | +     | rpsO          | 30S ribosomal protein S15 |
| 6,165,774  | 6,166,235 | +     | rpsP          | 30S ribosomal protein S16 |
| 5,760,801  | 5,761,082 | +     | rpsQ          | 30S ribosomal protein S17 |
| 3,654,918  | 3,655,145 | +     | rpsR1         | 30S ribosomal protein S18 |
| 5,200,982  | 5,200,728 | -     | rpsR2         | 30S ribosomal protein S19 |
| 5,758,660  | 5,758,941 | +     | rpsS          | 30S ribosomal protein S20 |
| 2,553,338  | 2,553,078 | -     | rpsT          | 30S ribosomal protein S21 |
| 5,762,543  | 5,762,728 | +     | rpsZ          | 30S ribosomal protein S14 type Z |
| 1,797,555  | 1,798,271 | +     | rplA          | 50S ribosomal protein L1 |
| 5,757,810  | 5,758,646 | +     | rplB          | 50S ribosomal protein L2 |
| 5,756,126  | 5,756,782 | +     | rplC          | 50S ribosomal protein L3 |
| 5,756,779  | 5,757,468 | +     | rplD          | 50S ribosomal protein L4 |
| 5,761,972  | 5,762,538 | +     | rplE          | 50S ribosomal protein L5 |
| 5,763,295  | 5,763,834 | +     | rplF          | 50S ribosomal protein L6 |
| 1,799,337  | 1,799,726 | +     | rplL          | 50S ribosomal protein L7/L12 |
| 3,655,163  | 3,655,618 | +     | rplI          | 50S ribosomal protein L9 |
| 1,798,701  | 1,799,258 | +     | rplJ          | 50S ribosomal protein L10 |
| Chromosome | Start (bp) | End (bp) | Gene | Translation |
|------------|------------|----------|------|-------------|
| 1          | 1,796,992  | 1,797,426 | + rplK | 50S ribosomal protein L11 |
|            | 5,792,280  | 5,792,723 | + rplM | 50S ribosomal protein L13 |
|            | 5,761,285  | 5,761,653 | + rplN | 50S ribosomal protein L14 |
|            | 5,765,113  | 5,765,556 | + rplO | 50S ribosomal protein L15 |
|            | 5,760,152  | 5,760,568 | + rplP | 50S ribosomal protein L16 |
|            | 5,772,346  | 5,772,921 | + rplQ | 50S ribosomal protein L17 |
|            | 5,763,836  | 5,764,243 | + rplR | 50S ribosomal protein L18 |
|            | 6,171,274  | 6,171,615 | + rplS | 50S ribosomal protein L19 |
|            | 2,907,916  | 2,908,305 | + rplT | 50S ribosomal protein L20 |
|            | 2,523,861  | 2,524,172 | + rplU | 50S ribosomal protein L21 |
|            | 5,758,938  | 5,759,342 | + rplV | 50S ribosomal protein L22 |
|            | 5,757,465  | 5,757,770 | + rplW | 50S ribosomal protein L23 |
|            | 5,761,653  | 5,761,970 | + rplX | 50S ribosomal protein L24 |
|            | 5,275,581  | 5,274,967 | - rplY | 50S ribosomal protein L25 |
|            | 2,524,282  | 2,524,479 | + rpmA | 50S ribosomal protein L26 |
|            | 5,201,715  | 5,201,473 | - rpmB | 50S ribosomal protein L27 |
|            | 5,760,568  | 5,760,804 |- rpmC | 50S ribosomal protein L28 |
|            | 5,764,931  | 5,765,110 | + rpmD | 50S ribosomal protein L29 |
|            | 2,362,720  | 2,362,962 | + rpmE1 | 50S ribosomal protein L30 |
|            | 5,203,078  | 5,203,332 | + rpmE2 | 50S ribosomal protein L31 |
|            | 5,203,394  | 5,203,567 | + rpmF1 | 50S ribosomal protein L32 |
|            | 6,149,124  | 6,149,237 | + rpmF2 | 50S ribosomal protein L33 |
|            | 1,794,071  | 1,794,238 | + rpmG1 | 50S ribosomal protein L34 |
|            | 5,201,473  | 5,201,309 | - rpmG2 | 50S ribosomal protein L35 |
|            | 6,621,327  | 6,621,184 | - rpmH | 50S ribosomal protein L36 |
|            | 2,907,657  | 2,907,851 | + rpmJ | 50S ribosomal protein L37 |
|            | 5,769,373  | 5,769,486 | + rpmJ | 50S ribosomal protein L38 |
|            | 5,218,862  | 5,218,937 | + tRNA^Asp-CGC | tRNA-Ala-CGC |
|            | 6,044,028  | 6,044,103 | + tRNA^Asp-GGC | tRNA-Ala-GGC |
|            | 21,380     | 21,452    | + tRNA^Asp-TGC | tRNA-Ala-TGC |
|            | 542,988    | 543,063   | + tRNA^Asp-ACG | tRNA-Arg-ACG |
|            | 2,349,107  | 2,349,032 | - tRNA^Asp-CCG | tRNA-Arg-CCG |
|            | 1,525,339  | 1,525,267 | - tRNA^Asp-CCT | tRNA-Arg-CCT |
|            | 2,450,226  | 2,450,154 | - tRNA^Asp-TCT | tRNA-Arg-TCT |
|            | 2,605,142  | 2,605,217 | + tRNA^Asp-GTT | tRNA-Asp-GTT |
|            | 1,312,751  | 1,312,824 | + tRNA^Asp-GTC | tRNA-Asp-GTC |
|            | 2,319,606  | 2,319,677 | + tRNA^Asp-GCA | tRNA-Cys-GCA |
|            | 6,392,827  | 6,392,757 | - tRNA^Asp-GCA | tRNA-Cys-GCA |
| Chromosome | Start | Stop | tRNA | Translation |
|------------|-------|------|------|-------------|
| Chromosome 6,121,902 | 6,121,973 | + | tRNA<sup>Glu</sup>CTG | tRNA-Glu-CTG |
| Chromosome 5,331,738 | 5,331,665 | - | tRNA<sup>Glu</sup>TTG | tRNA-Glu-TTG |
| Chromosome 6,122,081 | 6,122,153 | + | tRNA<sup>Glu</sup>CTC | tRNA-Glu-CTC |
| Chromosome 1,312,567 | 1,312,639 | + | tRNA<sup>Glu</sup>TTC | tRNA-Glu-TTC |
| Chromosome 4,847,349 | 4,847,276 | - | tRNA<sup>Gly</sup>CAC | tRNA-Gly-CAC |
| Chromosome 6,392,612 | 6,392,537 | - | tRNA<sup>Gly</sup>GCC | tRNA-Gly-GCC |
| Chromosome 6,392,924 | 6,392,849 | - | tRNA<sup>Gly</sup>GCC | tRNA-Gly-GCC |
| Chromosome 2,476,000 | 2,475,927 | - | tRNA<sup>Gly</sup>TCC | tRNA-Gly-TCC |
| Chromosome 2,435,266 | 2,435,191 | - | tRNA<sup>Ile</sup>GTG | tRNA-Ile-GTG |
| Chromosome 21,186 | 21,259 | + | tRNA<sup>Ile</sup>GAT | tRNA-Ile-GAT |
| Chromosome 2,871,855 | 2,871,782 | - | tRNA<sup>Leu</sup>CAA | tRNA-Leu-CAA |
| Chromosome 43,364 | 43,449 | + | tRNA<sup>Leu</sup>CAG | tRNA-Leu-CAG |
| Chromosome 2,976,567 | 2,976,482 | - | tRNA<sup>Leu</sup>GAG | tRNA-Leu-GAG |
| Chromosome 5,348,842 | 5,348,915 | + | tRNA<sup>Leu</sup>TAA | tRNA-Leu-TAA |
| Chromosome 2,420,124 | 2,420,040 | - | tRNA<sup>Leu</sup>TAG | tRNA-Leu-TAG |
| Chromosome 2,433,614 | 2,433,542 | - | tRNA<sup>Leu</sup>CTT | tRNA-Leu-CTT |
| Chromosome 1,311,494 | 1,311,419 | - | tRNA<sup>Leu</sup>TTC | tRNA-Leu-TTC |
| Chromosome 1,793,937 | 1,794,009 | + | tRNA<sup>Met</sup>CAT | tRNA-Met-CAT |
| Chromosome 2,606,972 | 2,607,048 | + | tRNA<sup>Met</sup>CAT | tRNA-Met-CAT |
| Chromosome 3,564,444 | 3,564,368 | - | tRNA<sup>Met</sup>CAT | tRNA-Met-CAT |
| Chromosome 4,174,406 | 4,174,330 | - | tRNA<sup>Met</sup>CAT | tRNA-Met-CAT |
| Chromosome 6,026,484 | 6,026,560 | + | tRNA<sup>Met</sup>CAT | tRNA-Met-CAT |
| Chromosome 1,312,891 | 1,312,964 | + | tRNA<sup>Ph</sup>GAA | tRNA-Pho-GAA |
| Chromosome 681,526 | 681,453 | - | tRNA<sup>Pro</sup>CAGG | tRNA-Pro-CGG |
| Chromosome 3,571,928 | 3,571,852 | - | tRNA<sup>Pro</sup>CAGG | tRNA-Pro-CGG |
| Chromosome 2,952,883 | 2,952,959 | + | tRNA<sup>Pro</sup>GAGG | tRNA-Pro-GGG |
| Chromosome 2,476,140 | 2,476,216 | + | tRNA<sup>Pro</sup>TGG | tRNA-Pro-TGG |
| Chromosome 556,756 | 556,846 | + | tRNA<sup>Ser</sup>CAG | tRNA-Ser-CGA |
| Chromosome 542,855 | 542,946 | + | tRNA<sup>Ser</sup>GCT | tRNA-Ser-GCT |
| Chromosome 585,846 | 585,759 | - | tRNA<sup>Ser</sup>GGA | tRNA-Ser-GGA |
| Chromosome 533,689 | 533,775 | + | tRNA<sup>Ser</sup>TGA | tRNA-Ser-TGA |
| Chromosome 720,362 | 720,434 | + | tRNA<sup>Thr</sup>CGT | tRNA-Thr-CGT |
| Chromosome 1,793,819 | 1,793,891 | + | tRNA<sup>Thr</sup>GTT | tRNA-Thr-GGT |
| Chromosome 1,088,492 | 1,088,566 | + | tRNA<sup>Thr</sup>TGG | tRNA-Thr-TGG |
| Chromosome 1,795,487 | 1,795,562 | + | tRNA<sup>Trp</sup>CCA | tRNA-Trp-CCA |
| Chromosome 1,793,533 | 1,793,615 | + | tRNA<sup>Tyr</sup>GTA | tRNA-Tyr-GTA |
| Chromosome 6,393,156 | 6,393,230 | + | tRNA<sup>Val</sup>CAC | tRNA-Val-CAC |
| Chromosome | Start  | End    | Direction | Gene      | Description                      | Function          |
|------------|--------|--------|-----------|-----------|----------------------------------|-------------------|
| 6,392,521  | 6,392,447 | -   | tRNA\textsuperscript{Val}\textsuperscript{GAC} | tRNA-Val-GAC       | Translation                     | Cell division     |
| 6,392,755  | 6,392,681 | -   | tRNA\textsuperscript{Val}\textsuperscript{GAC} | tRNA-Val-GAC       | Translation                     | Cell division     |
| 2,672,752  | 2,672,826  | +   | tRNA\textsuperscript{Val}\textsuperscript{TAC} | tRNA-Val-TAC       | Translation                     | Cell division     |
| 768,635    | 770,899   | +   | ftsH1     | Cell division protein FtsH       | Cell division     |
| 1,196,871  | 1,197,113 | +   | ftsH2     | Cell division protein FtsH       | Cell division     |
| 1,197,110  | 1,198,015 | +   | ftsH3     | Cell division protein FtsH       | Cell division     |
| 2,476,278  | 2,477,654 | +   | tig       | Cell division trigger factor     | Cell division     |
| 2,708,947  | 2,708,057 | -   | yfhF1     | Cell division inhibitor          | Cell division     |
| 3,930,915  | 3,932,267 | +   | yfhH2     | Cell division inhibitor          | Cell division     |
| 2,768,737  | 2,769,168 | +   | mraZ      | Cell division protein MraZ       | Cell division     |
| 2,770,506  | 2,771,060 | +   | ftsL      | Cell division protein FtsL       | Cell division     |
| 2,771,147  | 2,772,907 | +   | ftsI      | Cell division protein FtsI       | Cell division     |
| 2,779,155  | 2,780,501 | +   | ftsW      | Cell division protein FtsW       | Cell division     |
| 2,783,343  | 2,784,026 | +   | ftsQ      | Cell division protein FtsQ       | Cell division     |
| 2,784,237  | 2,785,433 | +   | ftsZ      | Cell division protein FtsZ       | Cell division     |
| 6,035,272  | 6,035,961 | +   | ftsE      | Cell division transporter, ATP-binding protein FtsE | Cell division |
| 6,036,025  | 6,036,930 | +   | ftsX      | Cell division protein FtsX       | Cell division     |
| 6,157,007  | 6,158,422 | +   | ftsY      | Signal recognition particle receptor protein FtsY | Cell division |
| 6,263,572  | 6,266,208 | +   | ftsK      | Cell division protein FtsK       | Cell division     |
**Supplementary Table S4.** GGDC comparisons of *Rhodococcus* type strains sequenced genomes.

| Query | Subject | DDH | Model C.I. | Distance | Prob. DDH | G+C difference |
|-------|---------|-----|------------|----------|-----------|----------------|
| 000_Nocardia_brasiliensis_NCTC_11294_T | 001_Rhodococcus_sp._WAY2 | 20.50 | [18.3 - 22.9%] | 0.21410 | 0.000 | 2.570 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 002_Rhodococcus_agglutinans_CCTCC_AB2014297_T | 20.50 | [18.3 - 22.3%] | 0.21400 | 0.000 | 1.010 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 003_Rhodococcus_biphenylivorans_TG9_T | 20.20 | [18.2 - 22.6%] | 0.21730 | 0.000 | 0.190 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 004_Rhodococcus_bronchialis_DSM_43247_T | 19.80 | [17.6 - 22.2%] | 0.22240 | 0.000 | 1.200 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 005_Rhodococcus_chlorophenolicum_DSM_43826_T | 19.70 | [17.5 - 22.1%] | 0.22310 | 0.000 | 0.190 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 006_Rhodococcus_coprophilus_NBRC_100603_T | 20.50 | [18.3 - 22.9%] | 0.21440 | 0.000 | 1.360 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 007_Rhodococcus_corynebacterioides_DSM_20151_T | 20.80 | [18.6 - 23.2%] | 0.21110 | 0.000 | 2.010 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 008_Rhodococcus_defluvii_Ca11_T | 20.40 | [18.1 - 22.8%] | 0.21590 | 0.000 | 0.480 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 009_Rhodococcus_enclensis_NIO_1009_T | 20.30 | [18 - 22.7%] | 0.21690 | 0.000 | 5.930 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 010_Rhodococcus_equi_DSM_20307_T | 20.60 | [18.3 - 23%] | 0.21360 | 0.000 | 0.550 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 011_Rhodococcus_erythropolis_NBRC_15567_T | 20.20 | [18 - 22.7%] | 0.21710 | 0.000 | 5.840 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 012_Rhodococcus_fascians_NBRC_12155_T | 20.40 | [18.2 - 22.8%] | 0.21510 | 0.000 | 3.790 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 013_Rhodococcus_glaberulus_NBRC_14531_T | 20.60 | [18.4 - 23%] | 0.21310 | 0.000 | 6.570 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 014_Rhodococcus_globerulus_NBRC_14531_T | 20.80 | [18.4 - 23%] | 0.21930 | 0.000 | 0.290 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 015_Rhodococcus_hoagii_DSM_20295_T | 20.70 | [18.4 - 23%] | 0.21250 | 0.000 | 0.530 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 016_Rhodococcus_intechensis_JCM_13270_T | 20.20 | [17.9 - 22.6%] | 0.21800 | 0.000 | 1.020 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 017_Rhodococcus_jostii_NBRC_16295_T | 20.30 | [18.1 - 22.8%] | 0.21600 | 0.000 | 1.340 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 018_Rhodococcus_koreensis_DSM_44498_T | 20.10 | [17.9 - 22.5%] | 0.21890 | 0.000 | 0.860 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 21.20 | [19 - 23.7%] | 0.20680 | 0.000 | 1.830 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 020_Rhodococcus_kummingensis_DSM_45001_T | 20.70 | [18.5 - 23.2%] | 0.21190 | 0.000 | 2.040 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 021_Rhodococcus_kyotogenes_JCM_23211_T | 19.80 | [17.6 - 22.2%] | 0.22200 | 0.000 | 4.080 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 20.20 | [17.9 - 22.6%] | 0.21800 | 0.000 | 0.930 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 20.50 | [18.2 - 22.9%] | 0.21470 | 0.000 | 3.830 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 024_Rhodococcus_maris_DSM_43672_T | 20.50 | [18.3 - 22.9%] | 0.21450 | 0.000 | 2.620 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 025_Rhodococcus_opacus_DSM_43205_T | 20.10 | [17.9 - 22.6%] | 0.21810 | 0.000 | 0.960 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 20.30 | [18 - 22.7%] | 0.21690 | 0.000 | 0.120 |
|                      | Scientific Name | R  | G  | R  | G  | R  | G  |   |
|----------------------|-----------------|----|----|----|----|----|----|---|
| 000_Nocardia_brasiliensis_NCTC_11294_T | 027_Rhodococcus_pyrnidinovorans_DSM_44555_T | 19.90 | [17.7 - 22.3%] | 0.22040 | 0.000 | 0.390 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 20.40 | [18.2 - 22.8%] | 0.21520 | 0.000 | 5.870 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 029_Rhodococcus_rhodni_NBRCC_100604_T | 21.20 | [19 - 23.6%] | 0.20690 | 0.000 | 1.430 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 030_Rhodococcus_rhodochrous_DSM_43241_T | 20.60 | [18.4 - 23%] | 0.21300 | 0.000 | 0.010 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 031_Rhodococcus_ruber_DSM_43338_T | 20.50 | [18.3 - 23%] | 0.21390 | 0.000 | 2.430 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 032_Rhodococcus_rubripertincta_NBRCC_101908_T | 20.20 | [18 - 22.6%] | 0.21760 | 0.000 | 0.860 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 033_Rhodococcus_sputi_NBRCC_100414_T | 20.30 | [18.1 - 22.7%] | 0.21680 | 0.000 | 2.890 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 034_Rhodococcus_terrae_NRRL_B_16283_T | 20.30 | [18.1 - 22.7%] | 0.21650 | 0.000 | 0.430 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 035_Rhodococcus_triatomae_DSM_44892_T | 20.60 | [18.4 - 23%] | 0.21330 | 0.000 | 0.490 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 036_Rhodococcus_tukisamuensis_NBRCC_100609_T | 20.50 | [18.3 - 22.9%] | 0.21450 | 0.000 | 1.610 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 037_Rhodococcus_wratislavienensis_NBRCC_100605_T | 20.10 | [17.9 - 22.5%] | 0.21880 | 0.000 | 1.460 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 038_Rhodococcus_yunnanensis_NBRCC_103083_T | 20.10 | [17.9 - 22.6%] | 0.21820 | 0.000 | 4.340 |
| 000_Nocardia_brasiliensis_NCTC_11294_T | 039_Rhodococcus_zopfi_NBRCC_100606_T | 19.80 | [17.6 - 22.2%] | 0.22200 | 0.000 | 0.000 |
| 001_Rhodococcus_sp_WAY2 | 002_Rhodococcus_agglutinans_CCTCC_AB2014297_T | 19.90 | [17.7 - 22.3%] | 0.22070 | 0 | 3.58 |
| 001_Rhodococcus_sp_WAY2 | 003_Rhodococcus_biphenylivorans_TG9_T | 20.30 | [18 - 22.7%] | 0.21690 | 0 | 2.38 |
| 001_Rhodococcus_sp_WAY2 | 004_Rhodococcus_bronchialis_DSM_43247_T | 20.70 | [18.5 - 23.2%] | 0.21180 | 0 | 1.37 |
| 001_Rhodococcus_sp_WAY2 | 005_Rhodococcus_chlorophenicolum_DSM_43826_T | 19.70 | [17.5 - 22.1%] | 0.22320 | 0 | 2.76 |
| 001_Rhodococcus_sp_WAY2 | 006_Rhodococcus_coprophilus_NBRCC_100603_T | 19.80 | [17.6 - 22.2%] | 0.22230 | 0 | 1.21 |
| 001_Rhodococcus_sp_WAY2 | 007_Rhodococcus_corynebacteroides_DSM_20151_T | 20.30 | [18.1 - 22.8%] | 0.21590 | 0 | 4.58 |
| 001_Rhodococcus_sp_WAY2 | 008_Rhodococcus_defluvii_Ca11_T | 20.10 | [17.9 - 22.6%] | 0.21820 | 0 | 3.05 |
| 001_Rhodococcus_sp_WAY2 | 009_Rhodococcus_encelensis_NIO_1009_T | 19.90 | [17.7 - 22.3%] | 0.22080 | 0 | 3.36 |
| 001_Rhodococcus_sp_WAY2 | 010_Rhodococcus_equi_DSM_20307_T | 20.10 | [17.8 - 22.5%] | 0.21910 | 0 | 3.12 |
| 001_Rhodococcus_sp_WAY2 | 011_Rhodococcus_erythropolis_NBRCC_15567_T | 20.10 | [17.9 - 22.5%] | 0.21860 | 0 | 3.27 |
| 001_Rhodococcus_sp_WAY2 | 012_Rhodococcus_fascians_NBRCC_12155_T | 19.50 | [17.3 - 21.9%] | 0.22520 | 0 | 1.22 |
| 001_Rhodococcus_sp_WAY2 | 013_Rhodococcus_globerulus_NBRCC_14531_T | 19.40 | [17.2 - 21.8%] | 0.22690 | 0 | 4 |
| 001_Rhodococcus_sp_WAY2 | 014_Rhodococcus_gordoniae_DSM_44689_T | 19.80 | [17.6 - 22.2%] | 0.22200 | 0 | 2.28 |
| 001_Rhodococcus_sp_WAY2 | 015_Rhodococcus_hoogii_DSM_20295_T | 20.30 | [18 - 22.7%] | 0.21690 | 0 | 3.1 |
| 001_Rhodococcus_sp_WAY2 | 016_Rhodococcus_intetchensis_JCM_13270_T | 27.60 | [25.2 - 30.1%] | 0.15630 | 0.04 | 1.55 |
| 001_Rhodococcus_sp_WAY2 | 017_Rhodococcus_jostii_NBRCC_16295_T | 26.70 | [24.3 - 29.1%] | 0.16240 | 0.02 | 1.23 |
| Rhodococcus sp. WAY2 | Rhodococcus koreensis DSM_44498_T | 26.50 | [24.1 - 28.9%] | 0.16370 | 0.02 | 1.71 |
|----------------------|-----------------------------------|-------|----------------|---------|-------|------|
| Rhodococcus sp. WAY2 | Rhodococcus kroppenstedtii DSM_44908_T | 20.10 | [17.9 - 22.5%] | 0.21840 | 0 | 4.39 |
| Rhodococcus sp. WAY2 | Rhodococcus kunmingensis DSM_44675_T | 20.20 | [18 - 22.7%] | 0.21710 | 0 | 5.19 |
| Rhodococcus sp. WAY2 | Rhodococcus kroppenstedtii DSM_44908_T | 19.50 | [17.9 - 22.5%] | 0.22490 | 0 | 4.39 |
| Rhodococcus sp. WAY2 | Rhodococcus kunmingensis DSM_45001_T | 19.80 | [17.8 - 22.5%] | 0.21920 | 0 | 5.26 |
| Rhodococcus sp. WAY2 | Rhodococcus kyotonensis JCM_23211_T | 20.20 | [18.1 - 22.7%] | 0.21810 | 0 | 2.18 |
| Rhodococcus sp. WAY2 | Rhodococcus kroppenstedtii DSM_44908_T | 19.70 | [17.5 - 22.2%] | 0.22260 | 0 | 2.69 |
| Rhodococcus sp. WAY2 | Rhodococcus maris DSM_43672_T | 20.30 | [17.9 - 22.6%] | 0.21680 | 0 | 2.14 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 20.10 | [18.1 - 22.7%] | 0.22190 | 0 | 2.36 |
| Rhodococcus sp. WAY2 | Rhodococcus maris DSM_43672_T | 19.90 | [17.7 - 22.3%] | 0.22050 | 0 | 1.77 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 19.70 | [18 - 22.6%] | 0.22340 | 0 | 2.56 |
| Rhodococcus sp. WAY2 | Rhodococcus maris DSM_44675_T | 20.40 | [18.2 - 22.8%] | 0.21530 | 0 | 5 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 19.90 | [17.7 - 22.3%] | 0.22050 | 0 | 1.71 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 20.60 | [18.3 - 23%] | 0.21600 | 0 | 0.32 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 20.00 | [17.8 - 22.4%] | 0.22000 | 0 | 2.14 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 20.10 | [17.9 - 22.5%] | 0.21850 | 0 | 3.06 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 20.20 | [18 - 22.6%] | 0.21770 | 0 | 4.18 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 26.80 | [24.4 - 29.2%] | 0.16170 | 0.02 | 1.11 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 19.70 | [17.5 - 22.1%] | 0.22340 | 0 | 1.77 |
| Rhodococcus sp. WAY2 | Rhodococcus maanshanensis DSM_44675_T | 20.00 | [17.8 - 22.4%] | 0.22010 | 0 | 2.57 |
| Rhodococcus agglutinans CCTCC AB2014297_T | Rhodococcus biphenylivorans TG9_T | 20.40 | [18.2 - 22.8%] | 0.21570 | 0 | 1.2 |
| Rhodococcus agglutinans CCTCC AB2014297_T | Rhodococcus bronchialis DSM_43247_T | 19.60 | [17.4 - 22%] | 0.22400 | 0 | 2.2 |
| Rhodococcus agglutinans CCTCC AB2014297_T | Rhodococcus chlorophenolicum DSM_43826_T | 19.50 | [17.3 - 21.9%] | 0.22580 | 0 | 0.82 |
| Rhodococcus agglutinans CCTCC AB2014297_T | Rhodococcus coprophilus NBRC_100603_T | 19.80 | [17.6 - 22.2%] | 0.22190 | 0 | 2.36 |
| Rhodococcus agglutinans CCTCC AB2014297_T | Rhodococcus cortyebacterioiides DSM_20151_T | 20.00 | [17.8 - 22.5%] | 0.21920 | 0 | 1 |
| Rhodococcus agglutinans CCTCC AB2014297_T | Rhodococcus defluvii Ca11_T | 27.80 | [25.4 - 30.3%] | 0.15520 | 0.04 | 0.53 |
| Rhodococcus agglutinans CCTCC AB2014297_T | Rhodococcus enceilens_NIO_1009_T | 19.90 | [17.7 - 22.3%] | 0.22110 | 0 | 6.93 |
| Strain Description                                      | Average Growth | Confidence Interval | Average DNA G+C Content | Confidence Interval | Average MGP Content | Confidence Interval |
|--------------------------------------------------------|----------------|---------------------|--------------------------|---------------------|---------------------|---------------------|
| Rhodococcus agglutinans CCTCC AB2014297                | 27.70          | [25.3 - 30.2%]      | 0.15570                  | 0.04                | 0.46               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.00          | [17.8 - 22.4%]      | 0.22020                  | 0                   | 6.85               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.40          | [17.2 - 21.8%]      | 0.22620                  | 0                   | 4.8                |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.60          | [17.2 - 21.8%]      | 0.22620                  | 0                   | 4.8                |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.40          | [17.2 - 21.8%]      | 0.22620                  | 0                   | 4.8                |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.50          | [17.3 - 21.9%]      | 0.22540                  | 0                   | 1.61               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.50          | [17.3 - 21.9%]      | 0.22540                  | 0                   | 1.61               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.40          | [17.2 - 21.8%]      | 0.22670                  | 0                   | 5.09               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.50          | [17.3 - 21.9%]      | 0.22540                  | 0                   | 1.61               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.50          | [17.3 - 21.9%]      | 0.22540                  | 0                   | 1.61               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.40          | [17.2 - 21.8%]      | 0.22670                  | 0                   | 5.09               |
| Rhodococcus agglutinans CCTCC AB2014297                | 21.40          | [19.2 - 23.8%]      | 0.20510                  | 0                   | 0.08               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.00          | [17.8 - 22.4%]      | 0.21960                  | 0                   | 4.84               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.00          | [17.8 - 22.4%]      | 0.21960                  | 0                   | 4.84               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.50          | [17.3 - 21.9%]      | 0.22540                  | 0                   | 1.61               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.60          | [18.3 - 23%]        | 0.21380                  | 0                   | 1.97               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.70          | [18.5 - 23.1%]      | 0.21230                  | 0                   | 0.89               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.10          | [17.9 - 22.6%]      | 0.21820                  | 0                   | 1.4                |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.00          | [17.8 - 22.5%]      | 0.21920                  | 0                   | 6.88               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.40          | [18.2 - 22.8%]      | 0.21530                  | 0                   | 0.43               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.70          | [18.4 - 23.1%]      | 0.21250                  | 0                   | 1.02               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.80          | [18.6 - 23.2%]      | 0.21110                  | 0                   | 1.42               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.00          | [17.8 - 22.4%]      | 0.21980                  | 0                   | 1.86               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.40          | [18.2 - 22.8%]      | 0.21540                  | 0                   | 3.9                |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.20          | [18.2 - 22.6%]      | 0.21790                  | 0                   | 1.44               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.50          | [18.2 - 22.9%]      | 0.21480                  | 0                   | 0.52               |
| Rhodococcus agglutinans CCTCC AB2014297                | 21.90          | [19.7 - 24.4%]      | 0.20010                  | 0                   | 0.61               |
| Rhodococcus agglutinans CCTCC AB2014297                | 20.40          | [18.2 - 22.9%]      | 0.21490                  | 0                   | 2.47               |
| Rhodococcus agglutinans CCTCC AB2014297                | 19.90          | [17.7 - 22.3%]      | 0.22110                  | 0                   | 5.35               |
| Strain Code | Species Name | Identity (%) | Tolerance (%) | ID Value | Error | Result |
|-------------|--------------|--------------|--------------|----------|-------|--------|
| 002_Rhodococcus_agglutinans_CCTCC_AB2014297_T | 003_Rhodococcus_biphenylivorans_TG9_T | 20.70 | [18.5 - 23.1%] | 0.21210 | 0 | 1 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 004_Rhodococcus_bronchialis_DSM_43247_T | 21.70 | [19.4 - 24.1%] | 0.20240 | 0 | 1 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 005_Rhodococcus_chlorophenicum_DSM_43826_T | 19.60 | [17.4 - 22%] | 0.22410 | 0 | 0.38 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 006_Rhodococcus_coprophilus_NBRC_100603_T | 22.00 | [19.8 - 24.5%] | 0.19920 | 0 | 1.16 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 007_Rhodococcus_corynebacterioides_DSM_20151_T | 20.20 | [17.9 - 22.6%] | 0.21800 | 0 | 2.2 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 008_Rhodococcus_defluvii_Ca11_T | 20.20 | [18 - 22.6%] | 0.21760 | 0 | 0.67 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 009_Rhodococcus_enclensis_NIO_1009_T | 19.70 | [17.5 - 22.1%] | 0.22300 | 0 | 5.73 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 010_Rhodococcus_equi_DSM_20307_T | 20.20 | [18 - 22.6%] | 0.21780 | 0 | 0.74 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 011_Rhodococcus_erythropolis_NBRC_15567_T | 19.70 | [17.5 - 22.1%] | 0.22350 | 0 | 5.65 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 012_Rhodococcus_fascians_NBRC_12155_T | 19.60 | [17.4 - 22%] | 0.22430 | 0 | 3.6 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 013_Rhodococcus_globerulus_NBRC_14531_T | 19.70 | [17.5 - 22.1%] | 0.22530 | 0 | 6.37 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 014_Rhodococcus_gordoniae_DSM_44689_T | 42.70 | [40.2 - 45.3%] | 0.09090 | 5.12 | 0.1 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 015_Rhodococcus_hoagii_DSM_20295_T | 20.50 | [18.3 - 22.9%] | 0.21460 | 0 | 0.72 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 016_Rhodococcus_intechensis_JCM_13270_T | 20.10 | [17.9 - 22.5%] | 0.21830 | 0 | 0.82 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 017_Rhodococcus_jostii_NBRC_16295_T | 19.80 | [17.6 - 22.2%] | 0.22230 | 0 | 1.15 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 018_Rhodococcus_koreensis_DSM_44498_T | 20.10 | [17.9 - 22.5%] | 0.21840 | 0 | 0.67 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 20.20 | [18 - 22.6%] | 0.21750 | 0 | 2.02 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 020_Rhodococcus_kumamonensis_DSM_45001_T | 19.90 | [17.7 - 22.3%] | 0.22060 | 0 | 1.85 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 021_Rhodococcus_kytonensis_JCM_23211_T | 19.10 | [16.9 - 21.5%] | 0.22990 | 0 | 3.89 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 19.80 | [17.6 - 22.2%] | 0.22200 | 0 | 1.12 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 20.00 | [17.8 - 22.4%] | 0.21960 | 0 | 3.64 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 024_Rhodococcus_marinus_DSM_43672_T | 20.00 | [17.8 - 22.4%] | 0.22020 | 0 | 2.81 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 025_Rhodococcus_opacus_DSM_43205_T | 20.10 | [17.9 - 22.5%] | 0.21840 | 0 | 0.77 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 22.00 | [19.8 - 24.5%] | 0.19910 | 0 | 0.31 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 88.30 | [85.9 - 90.4%] | 0.01390 | 95.2 | 0.2 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 20.00 | [17.8 - 22.4%] | 0.21990 | 0 | 5.68 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 029_Rhodococcus_rhodnii_NBRC_100604_T | 20.10 | [17.9 - 22.5%] | 0.21870 | 0 | 1.63 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 030_Rhodococcus_rhodochrous_DSM_43241_T | 58.80 | [56 - 61.6%] | 0.05370 | 48.34 | 0.18 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 031_Rhodococcus_ruber_DSM_43338_T | 21.60 | [19.4 - 24.1%] | 0.20300 | 0 | 2.62 |
| Rhodococcus biphenylivorans_TG9_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 0.66 |
|----------------------------------|-----------------------------------------------|------|
| 003_Rhodococcus_biphenylivorans_TG9_T | 033_Rhodococcus_sputi_NBRC_100414_T | 2.7 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 034_Rhodococcus_terrae_NRRL_B_16283_T | 0.24 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 035_Rhodococcus_triatomae_DSM_44892_T | 0.68 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 036_Rhodococcus_tukisanensis NBRC_100609_T | 1.81 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 037_Rhodococcus_wratslaviensis_NBRC_100605_T | 1.27 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 4.15 |
| 003_Rhodococcus_biphenylivorans_TG9_T | 039_Rhodococcus_zopfii_NBRC_100606_T | 0.2 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 005_Rhodococcus_chlorophenolicum_DSM_43826_T | 1.38 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 006_Rhodococcus_corynebacterioides_DSM_20151_T | 3.2 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 007_Rhodococcus_defluvii_Ca11_T | 1.67 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 008_Rhodococcus_enclensis_NIO_1009_T | 4.73 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 010_Rhodococcus_equi_DSM_20307_T | 1.75 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 011_Rhodococcus_gordoniae_NBRC_15567_T | 4.64 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 012_Rhodococcus_globerulus_NBRC_12155_T | 2.6 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 013_Rhodococcus_homopteri_DSM_14363_T | 5.37 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 015_Rhodococcus_hongkongensis_NBRC_103085_T | 0.9 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 016_Rhodococcus_intestinalis_JCM_13270_T | 1.72 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 017_Rhodococcus_jostii_NBRC_16295_T | 0.18 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 018_Rhodococcus_koreensis_NBRC_44949_T | 0.14 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 0.33 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 020_Rhodococcus_kummingensis_NBRC_40001_T | 3.02 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 021_Rhodococcus_kyotoensis_JCM_23211_T | 0.85 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 022_Rhodococcus_maaslandensis_NBRC_44675_T | 2.88 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 023_Rhodococcus_marinus_NBRC_14363_T | 2.13 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 024_Rhodococcus_maris_DSM_43672_T | 2.63 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 025_Rhodococcus_opacus_DSM_43205_T | 3.81 |
| 004_Rhodococcus_bronchialis_DSM_43247_T | 026_Rhodococcus_opacis_DSM_43205_T | 0.24 |
| Rhodococcus species                                      | Difference in percent | Percentage of 17.2% | Difference in percent | Percentage of 17.2% | Difference in percent | Percentage of 17.2% |
|---------------------------------------------------------|-----------------------|---------------------|-----------------------|---------------------|-----------------------|---------------------|
| 004_Rhodococcus_bronchialis_DSM_43247_T                 | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| 005_Rhodococcus_chlorophenolicum_DSM_43826_T           | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| 005_Rhodococcus_chlorophenolicum_DSM_43826_T           | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| 005_Rhodococcus_chlorophenolicum_DSM_43826_T           | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| 005_Rhodococcus_chlorophenolicum_DSM_43826_T           | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| 005_Rhodococcus_chlorophenolicum_DSM_43826_T           | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| 005_Rhodococcus_chlorophenolicum_DSM_43826_T           | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| 005_Rhodococcus_chlorophenolicum_DSM_43826_T           | 0.22620               | 0                   | 0.22800               | 0                   | 0.22640               | 0                   |
| Rhodococcus_coprophilus_DS_43826_T | 021_Rhodococcus_kyotonensis_JCM_23211_T | 19.00 [16.8 - 21.4%] | 0.23110 | 0 | 4.27 |
| Rhodococcus_coprophilus_DS_43826_T | 022_Rhodococcus_mansaehanensis_DS_44675_T | 19.40 [17.2 - 21.8%] | 0.22620 | 0 | 0.74 |
| Rhodococcus_coprophilus_DS_43826_T | 023_Rhodococcus_marinonasews_NBRC_14363_T | 19.10 [16.9 - 21.5%] | 0.22980 | 0 | 4.02 |
| Rhodococcus_coprophilus_DS_43826_T | 024_Rhodococcus_maris_DS_43672_T | 19.10 [16.9 - 21.5%] | 0.22990 | 0 | 2.43 |
| Rhodococcus_coprophilus_DS_43826_T | 025_Rhodococcus_opacus_DS_43205_T | 19.20 [17 - 21.6%] | 0.22860 | 0 | 1.15 |
| Rhodococcus_coprophilus_DS_43826_T | 026_Rhodococcus_phenolicus_DS_44812_T | 19.50 [17.3 - 21.9%] | 0.22550 | 0 | 0.07 |
| Rhodococcus_coprophilus_DS_43826_T | 027_Rhodococcus_pyrindinorans_DS_44555_T | 19.70 [17.5 - 22.1%] | 0.22310 | 0 | 0.58 |
| Rhodococcus_coprophilus_DS_43826_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 19.70 [17.5 - 22.1%] | 0.22330 | 0 | 6.06 |
| Rhodococcus_coprophilus_DS_43826_T | 029_Rhodococcus_rhodinii_NBRC_100604_T | 19.50 [17.3 - 21.9%] | 0.22560 | 0 | 1.25 |
| Rhodococcus_coprophilus_DS_43826_T | 030_Rhodococcus_rodocrous_DS_43241_T | 19.60 [17.4 - 22%] | 0.22450 | 0 | 0.2 |
| Rhodococcus_coprophilus_DS_43826_T | 031_Rhodococcus_ruber_DS_43338_T | 19.40 [17.2 - 21.8%] | 0.22710 | 0 | 2.24 |
| Rhodococcus_coprophilus_DS_43826_T | 032_Rhodococcus_ruberirienta_NBRC_101908_T | 19.30 [17.1 - 21.7%] | 0.22810 | 0 | 1.04 |
| Rhodococcus_coprophilus_DS_43826_T | 033_Rhodococcus_sputi_NBRC_100414_T | 19.90 [17.7 - 22.3%] | 0.22120 | 0 | 3.08 |
| Rhodococcus_coprophilus_DS_43826_T | 034_Rhodococcus_terrare_NBRL_B_16283_T | 19.30 [17.1 - 21.7%] | 0.22800 | 0 | 0.62 |
| Rhodococcus_coprophilus_DS_43826_T | 035_Rhodococcus_triatomae_DS_44892_T | 19.80 [17.6 - 22.2%] | 0.22250 | 0 | 0.3 |
| Rhodococcus_coprophilus_DS_43826_T | 036_Rhodococcus_tukisamimensis_NBRC_100609_T | 19.20 [17.1 - 21.5%] | 0.22940 | 0 | 1.42 |
| Rhodococcus_coprophilus_DS_43826_T | 037_Rhodococcus_wratilaviensis_NBRC_100605_T | 19.30 [17.1 - 21.7%] | 0.22780 | 0 | 1.65 |
| Rhodococcus_coprophilus_DS_43826_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.50 [17.3 - 21.9%] | 0.22590 | 0 | 4.53 |
| Rhodococcus_coprophilus_DS_43826_T | 039_Rhodococcus_zopfii_NBRC_100606_T | 19.40 [17.2 - 21.8%] | 0.22640 | 0 | 0.18 |
| Rhodococcus_coprophilus_NBRC_100603_T | 007_Rhodococcus_corynebacterioides_DS_20151_T | 19.50 [17.3 - 21.9%] | 0.22550 | 0 | 3.37 |
| Rhodococcus_coprophilus_NBRC_100603_T | 008_Rhodococcus_defluvii_Ca11_T | 19.70 [17.5 - 22.1%] | 0.22270 | 0 | 1.83 |
| Rhodococcus_coprophilus_NBRC_100603_T | 009_Rhodococcus_enclesensis_NIO_1009_T | 19.20 [17.1 - 21.6%] | 0.22840 | 0 | 4.57 |
| Rhodococcus_coprophilus_NBRC_100603_T | 010_Rhodococcus_equi_DS_20307_T | 19.90 [17.7 - 22.3%] | 0.22070 | 0 | 1.91 |
| Rhodococcus_coprophilus_NBRC_100603_T | 011_Rhodococcus_erythropilis_NBRC_15567_T | 19.70 [17.5 - 22.1%] | 0.22360 | 0 | 4.48 |
| Rhodococcus_coprophilus_NBRC_100603_T | 012_Rhodococcus_fasciens_NBRC_12155_T | 19.50 [17.3 - 21.9%] | 0.22570 | 0 | 2.44 |
| Rhodococcus_coprophilus_NBRC_100603_T | 013_Rhodococcus_globerulus_NBRC_14531_T | 19.10 [16.9 - 21.4%] | 0.23080 | 0 | 5.21 |
| Rhodococcus_coprophilus_NBRC_100603_T | 014_Rhodococcus_gordoniae_DS_44689_T | 22.00 [19.7 - 24.4%] | 0.19970 | 0 | 1.07 |
| Rhodococcus_coprophilus_NBRC_100603_T | 015_Rhodococcus_hoagi_DS_20295_T | 20.10 [17.9 - 22.5%] | 0.21840 | 0 | 1.89 |
| Rhodococcus_coprophilus_NBRC_100603_T | 016_Rhodococcus_intechensis_JCM_13270_T | 19.80 [17.6 - 22.2%] | 0.22250 | 0 | 0.34 |
|           | Species                        |很棒 | Strain | Temp | pH | VFA | N2 | LAC | R2 | R3 | R4 | R5 | R6 | R7 | R8 |
|-----------|-------------------------------|------|--------|------|----|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.60 | [17.4 - 22%] | 0.22450 | 0 | 0.02 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.50 | [17.3 - 21.9%] | 0.22590 | 0 | 0.49 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 18.90 | [16.8 - 21.3%] | 0.23220 | 0 | 3.18 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.60 | [17.5 - 22%] | 0.22370 | 0 | 2.29 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.90 | [17.7 - 22.3%] | 0.21220 | 0 | 2.9 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.50 | [17.3 - 21.9%] | 0.22570 | 0 | 2.47 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.40 | [17.2 - 21.8%] | 0.22650 | 0 | 3.98 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.30 | [16.6 - 21.2%] | 0.23380 | 0 | 2.72 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 18.90 | [16.6 - 21.2%] | 0.23380 | 0 | 2.72 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 20.00 | [18.8 - 23.4%] | 0.20920 | 0 | 3.78 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.70 | [17.5 - 22.1%] | 0.22260 | 0 | 0.4 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 21.30 | [19.1 - 23.8%] | 0.20590 | 0 | 1.48 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 21.90 | [19.6 - 24.4%] | 0.20020 | 0 | 4.91 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.40 | [17.2 - 21.8%] | 0.22650 | 0 | 4.51 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 22.00 | [19.8 - 24.5%] | 0.19910 | 0 | 1.48 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 21.00 | [18.8 - 23.4%] | 0.20920 | 0 | 3.78 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 21.40 | [17.2 - 21.8%] | 0.22670 | 0 | 0.5 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 20.40 | [18.2 - 22.8%] | 0.21560 | 0 | 1.54 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 20.20 | [18.2 - 22.8%] | 0.21700 | 0 | 0.92 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 20.00 | [17.8 - 22.4%] | 0.22000 | 0 | 1.85 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 20.10 | [17.9 - 22.6%] | 0.21820 | 0 | 2.97 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 19.70 | [17.5 - 22.1%] | 0.22260 | 0 | 0.1 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 18.80 | [16.6 - 21.2%] | 0.23400 | 0 | 2.99 |
| 006        | Rhodococcus coprophilus NBRC_100603_T | 21.10 | [18.9 - 23.6%] | 0.20770 | 0 | 1.36 |
| 007        | Rhodococcus corynebacteroides DSM_20151_T | 20.30 | [18.1 - 22.8%] | 0.21590 | 0 | 1.53 |
| 007        | Rhodococcus corynebacteroides DSM_20151_T | 20.00 | [17.8 - 22.4%] | 0.21930 | 0 | 7.94 |
| 007        | Rhodococcus corynebacteroides DSM_20151_T | 20.30 | [18.1 - 22.7%] | 0.21670 | 0 | 1.46 |
| 007        | Rhodococcus corynebacteroides DSM_20151_T | 20.10 | [17.8 - 22.5%] | 0.21910 | 0 | 7.85 |
| 007        | Rhodococcus corynebacteroides DSM_20151_T | 19.70 | [17.5 - 22.1%] | 0.22270 | 0 | 5.8 |
| 007        | Rhodococcus corynebacteroides DSM_20151_T | 19.90 | [17.7 - 22.3%] | 0.22110 | 0 | 8.58 |
| Species                          | Accession     | Distance   | GC Content (%) | p-value   | q-value | BLAST Score |
|---------------------------------|---------------|------------|----------------|-----------|---------|--------------|
| Rhodococcus_corynebacterioides  | JCM_13270_T   | 20.50      | 18.2 - 22.5%   | 0.2148    | 0       | 6.09         |
| Rhodococcus_corynebacterioides  | NBRC_15477_T  | 20.20      | 18.0 - 22.6%   | 0.2179    | 0       | 7.88         |
| Rhodococcus_corynebacterioides  | DSM_44812_T   | 19.40      | 17.2 - 21.8%   | 0.2265    | 0       | 1.89         |
| Rhodococcus_corynebacterioides  | DSM_43672_T   | 19.50      | 17.3 - 21.9%   | 0.2252    | 0       | 0.61         |
| Rhodococcus_corynebacterioides  | DSM_4205_T    | 19.90      | 17.7 - 22.3%   | 0.2204    | 0       | 2.97         |
| Rhodococcus_corynebacterioides  | DSM_43338_T   | 19.80      | 17.6 - 22.2%   | 0.2220    | 0       | 0.42         |
| Rhodococcus_corynebacterioides  | DSM_100414_T  | 19.50      | 17.3 - 21.9%   | 0.2251    | 0       | 4.9          |
| Rhodococcus_corynebacterioides  | DSM_15477_T   | 20.20      | 18 - 22.6%     | 0.2179    | 0       | 7.88         |
| Rhodococcus_corynebacterioides  | DSM_100604_T  | 19.60      | 17.4 - 22%     | 0.2245    | 0       | 0.57         |
| Rhodococcus_corynebacterioides  | DSM_43241_T   | 19.90      | 17.7 - 22.3%   | 0.2214    | 0       | 2.02         |
| Rhodococcus_corynebacterioides  | DSM_101908_T  | 19.90      | 17.7 - 22.4%   | 0.2204    | 0       | 2.86         |
| Rhodococcus_corynebacterioides  | DSM_100414_T  | 19.50      | 17.3 - 21.9%   | 0.2251    | 0       | 4.9          |
| Rhodococcus_corynebacterioides  | DSM_16283_T   | 19.80      | 17.6 - 22.2%   | 0.2215    | 0       | 2.44         |
| Rhodococcus_corynebacterioides  | DSM_44892_T   | 20.00      | 17.8 - 22.4%   | 0.2201    | 0       | 1.52         |
| Rhodococcus_corynebacterioides  | DSM_100609_T  | 20.00      | 17.8 - 22.5%   | 0.2192    | 0       | 0.4          |
| Rhodococcus_corynebacterioides  | DSM_100605_T  | 20.00      | 17.8 - 22.4%   | 0.2201    | 0       | 3.47         |
| Rhodococcus_corynebacterioides  | DSM_103083_T  | 19.60      | 17.4 - 22%     | 0.2238    | 0       | 6.35         |
| Rhodococcus_corynebacterioides  | DSM_100606_T  | 19.60      | 17.4 - 22%     | 0.2245    | 0       | 2            |
| Species                                           | Accession Number          | MLST Score | 16S rRNA (%) | GenBank Score | Yersiniaceae Score |
|--------------------------------------------------|---------------------------|------------|--------------|---------------|-------------------|
| **Rhodococcus**                                  |                           |            |              |               |                   |
| defluvii _Ca11_T                                 | 012 Rhodococcus fascians_NBRC_12155_T | 19.40      | [17.2 - 21.8%] | 0.22660       | 4.27              |
| defluvii _Ca11_T                                 | 013 Rhodococcus globulus_NBRC_14531_T | 19.80      | [17.6 - 22.2%] | 0.22210       | 7.04              |
| defluvii _Ca11_T                                 | 014 Rhodococcus gordoniae_DSM_44689_T | 20.50      | [18.3 - 22.9%] | 0.21450       | 0.77              |
| defluvii _Ca11_T                                 | 015 Rhodococcus huogii_DSM_20295_T | 27.00      | [24.7 - 29.5%] | 0.16000       | 0.05              |
| defluvii _Ca11_T                                 | 016 Rhodococcus intemchensis_JCM_13270_T | 20.60      | [18.4 - 23%]   | 0.21330       | 1.49              |
| defluvii _Ca11_T                                 | 017 Rhodococcus jostii_NBRC_16295_T | 20.70      | [18.5 - 23.1%] | 0.21200       | 1.81              |
| defluvii _Ca11_T                                 | 018 Rhodococcus koreensis_DSM_44498_T | 20.60      | [18.4 - 23%]   | 0.21340       | 1.34              |
| defluvii _Ca11_T                                 | 019 Rhodococcus kroppenstedtii_DSM_44908_T | 20.20      | [18 - 22.6%]   | 0.21780       | 1.35              |
| defluvii _Ca11_T                                 | 020 Rhodococcus kunmingensis_DSM_45001_T | 20.30      | [18.1 - 22.8%] | 0.21610       | 2.52              |
| defluvii _Ca11_T                                 | 021 Rhodococcus kyotonensis_JCM_23211_T | 19.60      | [17.4 - 22%]   | 0.22390       | 4.56              |
| defluvii _Ca11_T                                 | 022 Rhodococcus maashanensis_DSM_44675_T | 21.20      | [18.9 - 23.6%] | 0.20750       | 0.45              |
| defluvii _Ca11_T                                 | 023 Rhodococcus marinosakens_NBRC_14363_T | 19.90      | [17.7 - 22.3%] | 0.22130       | 4.31              |
| defluvii _Ca11_T                                 | 024 Rhodococcus maris_DSM_43672_T | 19.90      | [17.7 - 22.3%] | 0.22130       | 2.14              |
| defluvii _Ca11_T                                 | 025 Rhodococcus opacus_DSM_43205_T | 20.60      | [18.4 - 23%]   | 0.21300       | 1.44              |
| defluvii _Ca11_T                                 | 026 Rhodococcus phenolicus_DSM_44812_T | 20.50      | [18.3 - 22.9%] | 0.21450       | 0.36              |
| defluvii _Ca11_T                                 | 027 Rhodococcus pyridinivorans_DSM_44555_T | 20.00      | [17.8 - 22.4%] | 0.21950       | 0.87              |
| defluvii _Ca11_T                                 | 028 Rhodococcus qingshengii_JCM_15477_T | 20.20      | [18 - 22.6%]   | 0.21770       | 6.35              |
| defluvii _Ca11_T                                 | 029 Rhodococcus rhodni_NBRC_100604_T | 20.80      | [18.6 - 23.2%] | 0.21140       | 0.96              |
| defluvii _Ca11_T                                 | 030 Rhodococcus rhodochrous_DSM_43241_T | 20.70      | [18.5 - 23.1%] | 0.21190       | 0.48              |
| defluvii _Ca11_T                                 | 031 Rhodococcus ruber_DSM_43338_T | 20.60      | [18.4 - 23%]   | 0.21310       | 1.95              |
| defluvii _Ca11_T                                 | 032 Rhodococcus rubripertincta_NBRC_101908_T | 20.60      | [18.4 - 23%]   | 0.21350       | 1.33              |
| defluvii _Ca11_T                                 | 033 Rhodococcus sputi_NBRC_100414_T | 20.60      | [18.4 - 23%]   | 0.21310       | 3.37              |
| defluvii _Ca11_T                                 | 034 Rhodococcus terrae_NRRL_B_16283_T | 19.90      | [17.7 - 22.3%] | 0.22040       | 0.91              |
| defluvii _Ca11_T                                 | 035 Rhodococcus triatomaiae_DSM_44892_T | 20.50      | [18.2 - 22.9%] | 0.21460       | 0.01              |
| defluvii _Ca11_T                                 | 036 Rhodococcus tukisamensis_NBRC_100609_T | 21.80      | [19.5 - 24.2%] | 0.20140       | 1.14              |
| defluvii _Ca11_T                                 | 037 Rhodococcus wratislaviensis_NBRC_100605_T | 20.50      | [18.3 - 22.9%] | 0.21430       | 1.94              |
| defluvii _Ca11_T                                 | 038 Rhodococcus yunnanensis_NBRC_103083_T | 19.70      | [17.5 - 22.1%] | 0.22300       | 4.82              |
| defluvii _Ca11_T                                 | 039 Rhodococcus zopfii_NBRC_100606_T | 20.70      | [18.4 - 23.1%] | 0.21270       | 0.47              |
| **Rhodococcus encelensis** _NIO_1009_T_          |                           |            |              |               |                   |
| equi_DSM_20307_T                                 | 010 Rhodococcus equi_DSM_20307_T | 19.60      | [17.4 - 22%]   | 0.22460       | 6.48              |
| Strain Name | Accession Number | Dl (uM) | Range (%) | CL (ng/µL) | UV Absorbance at 340 nm |
|-------------|-----------------|---------|-----------|----------|------------------------|
| Rhodococcus enclensis NIO_1009_T | 011_Rhodococcus_erythropolis_NBRC_15567_T | 62.20 | [59.3 - 65%] | 0.04790 | 59.34 | 0.09 |
| Rhodococcus enclensis NIO_1009_T | 012_Rhodococcus_fascians_NBRC_12155_T | 19.40 | [17.3 - 21.8%] | 0.22610 | 0 | 2.13 |
| Rhodococcus enclensis NIO_1009_T | 013_Rhodococcus_globerulus_NBRC_14531_T | 24.00 | [21.7 - 26.4%] | 0.18230 | 0 | 0.64 |
| Rhodococcus enclensis NIO_1009_T | 014_Rhodococcus_gordoniae_DS44689_T | 19.70 | [17.5 - 22.1%] | 0.22340 | 0 | 5.64 |
| Rhodococcus enclensis NIO_1009_T | 015_Rhodococcus_hoogii_DS42095_T | 19.60 | [17.4 - 22%] | 0.22390 | 0 | 6.46 |
| Rhodococcus enclensis NIO_1009_T | 016_Rhodococcus_intechensis_JCM_13270_T | 20.20 | [18 - 22.6%] | 0.21770 | 0 | 4.91 |
| Rhodococcus enclensis NIO_1009_T | 017_Rhodococcus_jostii_NBRC_16295_T | 20.10 | [17.9 - 22.5%] | 0.21830 | 0 | 4.59 |
| Rhodococcus enclensis NIO_1009_T | 018_Rhodococcus_koreensis_DS44498_T | 20.20 | [17.9 - 22.6%] | 0.21800 | 0 | 5.06 |
| Rhodococcus enclensis NIO_1009_T | 019_Rhodococcus_kroppenstedtii_DS44908_T | 20.70 | [18.4 - 23.1%] | 0.21270 | 0 | 7.75 |
| Rhodococcus enclensis NIO_1009_T | 020_Rhodococcus_kunmingensis_DS45001_T | 19.70 | [17.5 - 22.1%] | 0.22620 | 0 | 3.88 |
| Rhodococcus enclensis NIO_1009_T | 021_Rhodococcus_kyotonensis_JCM_23211_T | 19.50 | [17.3 - 21.9%] | 0.22570 | 0 | 1.85 |
| Rhodococcus enclensis NIO_1009_T | 022_Rhodococcus_maanshenensis_DS44675_T | 19.90 | [17.7 - 22.3%] | 0.22100 | 0 | 6.86 |
| Rhodococcus enclensis NIO_1009_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 19.80 | [17.6 - 22.2%] | 0.22320 | 0 | 2.1 |
| Rhodococcus enclensis NIO_1009_T | 024_Rhodococcus_maris_DS43672_T | 18.90 | [16.7 - 21.2%] | 0.23310 | 0 | 8.55 |
| Rhodococcus enclensis NIO_1009_T | 025_Rhodococcus_opacus_DS43205_T | 20.50 | [18.3 - 22.9%] | 0.21420 | 0 | 4.97 |
| Rhodococcus enclensis NIO_1009_T | 026_Rhodococcus Phenolicus_DS44812_T | 19.60 | [17.4 - 22%] | 0.22400 | 0 | 6.05 |
| Rhodococcus enclensis NIO_1009_T | 027_Rhodococcus_pyridinivorans_DS44555_T | 19.70 | [17.5 - 22.1%] | 0.22300 | 0 | 5.54 |
| Rhodococcus enclensis NIO_1009_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 19.50 | [17.3 - 21.9%] | 0.22570 | 0 | 1.85 |
| Rhodococcus enclensis NIO_1009_T | 029_Rhodococcus_rhodnii_NBRC_100604_T | 19.80 | [17.6 - 22.2%] | 0.22150 | 0 | 7.36 |
| Rhodococcus enclensis NIO_1009_T | 030_Rhodococcus_rubripertincta_NBRC_101908_T | 19.60 | [17.4 - 22%] | 0.22450 | 0 | 5.92 |
| Rhodococcus enclensis NIO_1009_T | 031_Rhodococcus_ruber_DS43338_T | 19.70 | [17.5 - 22.1%] | 0.22260 | 0 | 8.36 |
| Rhodococcus enclensis NIO_1009_T | 032_Rhodococcus_terrae_NBRC_101908_T | 19.80 | [17.6 - 22.2%] | 0.22260 | 0 | 5.07 |
| Rhodococcus enclensis NIO_1009_T | 033_Rhodococcus_sputi_NBRC_100414_T | 20.00 | [17.8 - 22.4%] | 0.22020 | 0 | 3.03 |
| Rhodococcus enclensis NIO_1009_T | 034_Rhodococcus_thermae_NRRL_B_16283_T | 19.60 | [17.4 - 22%] | 0.22440 | 0 | 5.49 |
| Rhodococcus enclensis NIO_1009_T | 035_Rhodococcus_triatomae_DS44892_T | 19.70 | [17.5 - 22.1%] | 0.22350 | 0 | 6.42 |
| Rhodococcus enclensis NIO_1009_T | 036_Rhodococcus_tukisamuensis_NBRC_100609_T | 20.00 | [17.7 - 22.4%] | 0.22030 | 0 | 7.54 |
| Rhodococcus enclensis NIO_1009_T | 037_Rhodococcus_wratislaviensis_NBRC_100605_T | 20.20 | [18 - 22.6%] | 0.21790 | 0 | 4.47 |
| Rhodococcus enclensis NIO_1009_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.70 | [17.5 - 22.1%] | 0.22320 | 0 | 1.58 |
| Rhodococcus enclensis NIO_1009_T | 039_Rhodococcus_zopfii_NBRC_100606_T | 19.50 | [17.3 - 21.9%] | 0.22510 | 0 | 5.93 |
| 010_Rhodococcus_equi_DSM_20307_T | 011_Rhodococcus_erythropolis_NBRC_15567_T | 19.90 | [17.7 - 22.3%] | 0.22070 | 0 | 6.39 |
| 010_Rhodococcus_equi_DSM_20307_T | 012_Rhodococcus_fascians_NBRC_12155_T | 19.50 | [17.3 - 21.9%] | 0.22590 | 0 | 4.35 |
| 010_Rhodococcus_equi_DSM_20307_T | 013_Rhodococcus_globerulus_NBRC_14531_T | 19.80 | [17.6 - 22.3%] | 0.22140 | 0 | 7.12 |
| 010_Rhodococcus_equi_DSM_20307_T | 014_Rhodococcus_gordoniae_DSM_44689_T | 20.10 | [17.9 - 22.6%] | 0.21810 | 0 | 0.84 |
| 010_Rhodococcus_equi_DSM_20307_T | 015_Rhodococcus_hoquii_DSM_20295_T | 20.00 | [17.8 - 22.4%] | 0.21760 | 0 | 1.57 |
| 010_Rhodococcus_equi_DSM_20307_T | 016_Rhodococcus_intemchenii_JCM_13270_T | 20.20 | [18 - 22.6%] | 0.21670 | 0 | 1.89 |
| 010_Rhodococcus_equi_DSM_20307_T | 017_Rhodococcus_jostii_NBRC_16295_T | 20.20 | [18 - 22.6%] | 0.21730 | 0 | 1.42 |
| 010_Rhodococcus_equi_DSM_20307_T | 018_Rhodococcus_koreensis_NBRC_14498_T | 20.00 | [17.8 - 22.4%] | 0.21510 | 0 | 1.51 |
| 010_Rhodococcus_equi_DSM_20307_T | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 20.00 | [17.8 - 22.4%] | 0.21230 | 0 | 0.43 |
| 010_Rhodococcus_equi_DSM_20307_T | 020_Rhodococcus_kunmingensis_DSM_45001_T | 20.00 | [17.8 - 22.4%] | 0.21160 | 0 | 0.56 |
| 010_Rhodococcus_equi_DSM_20307_T | 021_Rhodococcus_kyotonensis_JCM_23211_T | 20.00 | [17.2 - 21.8%] | 0.21180 | 0 | 0.38 |
| 010_Rhodococcus_equi_DSM_20307_T | 022_Rhodococcus_maashanensis_DSM_44675_T | 20.70 | [18.5 - 23.2%] | 0.21290 | 0 | 0.38 |
| 010_Rhodococcus_equi_DSM_20307_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 19.40 | [17.2 - 21.8%] | 0.22640 | 0 | 2.07 |
| 010_Rhodococcus_equi_DSM_20307_T | 024_Rhodococcus_maris_DSM_43672_T | 19.40 | [17.2 - 21.8%] | 0.22700 | 0 | 4.63 |
| 010_Rhodococcus_equi_DSM_20307_T | 025_Rhodococcus_opacus_DSM_43205_T | 19.40 | [17.2 - 21.8%] | 0.22700 | 0 | 4.63 |
| 010_Rhodococcus_equi_DSM_20307_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 20.10 | [17.9 - 22.5%] | 0.22180 | 0 | 0.88 |
| 010_Rhodococcus_equi_DSM_20307_T | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 20.10 | [17.9 - 22.5%] | 0.22240 | 0 | 0.88 |
| 010_Rhodococcus_equi_DSM_20307_T | 028_Rhodococcus_qingshengii_JCM_13701_T | 19.40 | [17.2 - 21.8%] | 0.22160 | 0 | 0.56 |
| 010_Rhodococcus_equi_DSM_20307_T | 029_Rhodococcus_rubripertincta_NBRC_100609_T | 20.10 | [17.9 - 22.5%] | 0.21510 | 0 | 1.51 |
| 010_Rhodococcus_equi_DSM_20307_T | 030_Rhodococcus_rubripertincta_NBRC_100609_T | 20.10 | [17.9 - 22.5%] | 0.21510 | 0 | 1.51 |
| 010_Rhodococcus_equi_DSM_20307_T | 031_Rhodococcus_terrae_NRRL_B_16283_T | 19.40 | [17.2 - 21.8%] | 0.21160 | 0 | 0.56 |
| 010_Rhodococcus_equi_DSM_20307_T | 032_Rhodococcus_terrae_NBRC_100609_T | 20.40 | [18.2 - 22.8%] | 0.21470 | 0 | 1.88 |
| 010_Rhodococcus_equi_DSM_20307_T | 033_Rhodococcus_sputi_NBRC_100609_T | 20.40 | [18.2 - 22.8%] | 0.21520 | 0 | 1.41 |
| 010_Rhodococcus_equi_DSM_20307_T | 034_Rhodococcus_sputi_NBRC_100609_T | 20.40 | [18.2 - 22.8%] | 0.21520 | 0 | 1.41 |
| 010_Rhodococcus_equi_DSM_20307_T | 035_Rhodococcus_tiangyuanensis_NBRC_100609_T | 20.40 | [18.2 - 22.8%] | 0.21520 | 0 | 1.41 |
| 010_Rhodococcus_equi_DSM_20307_T | 036_Rhodococcus_tiangyuanensis_NBRC_100609_T | 20.40 | [18.2 - 22.8%] | 0.21520 | 0 | 1.41 |
| 010_Rhodococcus_equi_DSM_20307_T | 037_Rhodococcus_wraitkavimensis_NBRC_100609_T | 20.40 | [18.2 - 22.8%] | 0.21520 | 0 | 1.41 |
| 010_Rhodococcus_equi_DSM_20307_T | 038_Rhodococcus_yunnanensis_NBRC_100609_T | 20.40 | [18.2 - 22.8%] | 0.21520 | 0 | 1.41 |
| Strain                                      | Type                           | OD760 | [OD760 - 780]% | OD780 | [OD780 - 800]% | OD800 | [OD800 - 820]% | OD820 | [OD820 - 840]% | OD840 | [OD840 - 860]% | OD860 | [OD860 - 880]% | OD880 |
|---------------------------------------------|--------------------------------|-------|----------------|-------|----------------|-------|----------------|-------|----------------|-------|----------------|-------|----------------|-------|
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 012_Rhodococcus_fascians_NBRC_12155_T | 19.60 | [17.4 - 22%]   | 0.22440 | 0              | 2.05  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 013_Rhodococcus_globerulus_NBRC_14531_T | 24.10 | [21.8 - 26.6%] | 0.18130 | 0.01          | 0.73  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 014_Rhodococcus_gordoniae_DSM_44689_T | 19.70 | [17.5 - 22.1%] | 0.22310 | 0              | 5.55  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 015_Rhodococcus_hougi_DSM_20295_T   | 19.80 | [17.6 - 22.2%] | 0.22170 | 0              | 6.37  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 016_Rhodococcus_intechiensis_JCM_13270_T | 20.20 | [18. - 22.6%]  | 0.21790 | 0              | 4.82  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 017_Rhodococcus_jostii_NBRC_16295_T   | 20.30 | [18.1 - 22.7%] | 0.21630 | 0              | 4.5   |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 018_Rhodococcus_koreensis_DSM_44948_T | 20.20 | [18. - 22.6%]  | 0.21760 | 0              | 4.98  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 20.10 | [17.9 - 22.5%] | 0.21860 | 0              | 7.67  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 020_Rhodococcus_kunningensis_DSM_45001_T | 19.70 | [17.5 - 22.1%] | 0.22290 | 0              | 3.8   |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 021_Rhodococcus_kyonensis_JCM_23211_T | 19.30 | [17.1 - 21.6%] | 0.22830 | 0              | 1.76  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 022_Rhodococcus_maashanensis_DSM_44675_T | 19.90 | [17.7 - 22.3%] | 0.22040 | 0              | 6.77  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 023_Rhodococcus_marinosepsis_NBRC_14363_T | 19.60 | [17.4 - 22%]   | 0.22400 | 0              | 2.01  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 024_Rhodococcus_maris_DSM_43672_T    | 19.30 | [17.1 - 21.7%] | 0.22790 | 0              | 8.46  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 025_Rhodococcus_opacus_DSM 43205_T   | 20.40 | [18.2 - 22.9%] | 0.21490 | 0              | 4.88  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 026_Rhodococcus_phenolicus_DSM_44812_T | 19.60 | [17.4 - 22%]   | 0.22480 | 0              | 5.96  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 19.40 | [17.2 - 21.8%] | 0.22640 | 0              | 5.45  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 028_Rhodococcus_qingshengii_JCM_15477_T | 62.20 | [59.3 - 65%]   | 0.04790 | 59.38         | 0.03  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 029_Rhodococcus_rhodni_NBRC_100604_T | 19.80 | [17.6 - 22.2%] | 0.22240 | 0              | 7.27  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 030_Rhodococcus_rhodni_NBRP_43241_T  | 19.60 | [17.4 - 22%]   | 0.22470 | 0              | 5.83  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 031_Rhodococcus_ruber_DSM_43338_T    | 19.70 | [17.5 - 22.1%] | 0.22270 | 0              | 8.27  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 032_Rhodococcus_ruberperitacta_NBRC_101908_T | 20.00 | [17.8 - 22.4%] | 0.21950 | 0              | 4.98  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 033_Rhodococcus_sputi_NBRC_100414_T  | 19.70 | [17.5 - 22.1%] | 0.22260 | 0              | 2.95  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 034_Rhodococcus_serra_NRRL_B_16283_T | 19.80 | [17.6 - 22.2%] | 0.22200 | 0              | 5.41  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 035_Rhodococcus_triatomaes_DSM_44892_T | 19.90 | [17.7 - 22.3%] | 0.22070 | 0              | 6.33  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 036_Rhodococcus_tukiasmensis_NBRC_100609_T | 20.20 | [18 - 22.6%]   | 0.21770 | 0              | 7.45  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 037_Rhodococcus_wraiaesius_NBRC_100604_T | 20.00 | [17.8 - 22.4%] | 0.21990 | 0              | 4.38  |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.80 | [17.6 - 22.2%] | 0.22230 | 0              | 1.5   |
| 011_Rhodococcus_erythropolis_NBRC_15567_T   | 039_Rhodococcus_zopfi_NBRC_100606_T  | 19.50 | [17.3 - 21.9%] | 0.22520 | 0              | 5.84  |
| 012_Rhodococcus_fascians_NBRC_12155_T       | 013_Rhodococcus_globerulus_NBRC_14531_T | 19.70 | [17.5 - 22.1%] | 0.22290 | 0              | 2.77  |
| Strain Name                  | Dendrogram Name | Percentage | Score | Strain Name                  | Dendrogram Name | Percentage | Score |
|-----------------------------|-----------------|------------|-------|-----------------------------|-----------------|------------|-------|
| 012_Rhodococcus_fascians_NBRC_12155_T | 014_Rhodococcus_gordoniae_DSM_44689_T | 19.10 | [16.9 - 21.5%] | 0.22980 | 0 | 3.5 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 015_Rhodococcus_hoangi_DSM_20295_T | 19.60 | [17.4 - 22%] | 0.22390 | 0 | 4.32 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 016_Rhodococcus_intechensis_JCM_13270_T | 19.20 | [17 - 21.6%] | 0.22930 | 0 | 2.78 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 017_Rhodococcus_jostii_NBRC_16295_T | 19.40 | [17.2 - 21.7%] | 0.22720 | 0 | 2.46 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 018_Rhodococcus_koreensis_DSM_44498_T | 19.60 | [17.4 - 22%] | 0.22440 | 0 | 2.93 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 019_Rhodococcus_kronpenstedi_DSM_44908_T | 20.00 | [17.8 - 22.4%] | 0.22000 | 0 | 5.62 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 020_Rhodococcus_kuningensis_DSM_45001_T | 19.70 | [17.5 - 22.1%] | 0.22920 | 0 | 1.75 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 021_Rhodococcus_kyotonensis_JCM_23211_T | 20.00 | [17.8 - 22.4%] | 0.22020 | 0 | 0.29 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 19.70 | [17.5 - 22.1%] | 0.22270 | 0 | 4.72 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 19.50 | [17.3 - 21.9%] | 0.22560 | 0 | 0.04 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 024_Rhodococcus_maris_DSM_43672_T | 19.70 | [17.5 - 22.1%] | 0.22290 | 0 | 6.41 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 025_Rhodococcus_opacus_DSM_43205_T | 19.50 | [17.3 - 21.9%] | 0.22540 | 0 | 2.83 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 20.00 | [17.8 - 22.5%] | 0.21930 | 0 | 3.91 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 19.50 | [17.3 - 21.9%] | 0.22600 | 0 | 3.4 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 19.60 | [17.4 - 22%] | 0.22460 | 0 | 2.08 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 029_Rhodococcus_rhodni_NBRC_100604_T | 19.70 | [17.5 - 22.1%] | 0.22270 | 0 | 5.23 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 030_Rhodococcus_rhodchrous_DSM_43241_T | 19.70 | [17.5 - 22.1%] | 0.22360 | 0 | 3.79 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 031_Rhodococcus_ruber_DSM_43338_T | 19.20 | [17 - 21.5%] | 0.22950 | 0 | 6.22 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 19.80 | [17.6 - 22.2%] | 0.22200 | 0 | 2.94 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 033_Rhodococcus_sputi_NBRC_100414_T | 19.80 | [17.6 - 22.2%] | 0.22170 | 0 | 0.9 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 034_Rhodococcus_terrae_NRRL_B_16283_T | 20.20 | [18 - 22.6%] | 0.21720 | 0 | 3.36 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 035_Rhodococcus_tripaitae_DSM_44892_T | 19.30 | [17.1 - 21.7%] | 0.22820 | 0 | 4.28 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 036_Rhodococcus_tukisamuensis_NBRC_100609_T | 19.40 | [17.2 - 21.8%] | 0.22630 | 0 | 5.41 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 037_Rhodococcus_wratilaviensis_NBRC_100605_T | 19.50 | [17.3 - 21.9%] | 0.22570 | 0 | 2.33 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 038_Rhodococcus Yunnamensis_NBRC_103083_T | 20.00 | [17.8 - 22.4%] | 0.21980 | 0 | 0.55 |
| 012_Rhodococcus_fascians_NBRC_12155_T | 039_Rhodococcus zopfii_NBRC_100606_T | 19.10 | [16.9 - 21.5%] | 0.23010 | 0 | 3.8 |
| 013_Rhodococcus_globerulus_NBRC_14531_T | 014_Rhodococcus_gordoniae_DSM_44689_T | 19.30 | [17.1 - 21.6%] | 0.22830 | 0 | 6.28 |
| 013_Rhodococcus_globerulus_NBRC_14531_T | 015_Rhodococcus_hoangi_DSM_20295_T | 19.70 | [17.5 - 22.1%] | 0.22270 | 0 | 7.1 |
| 013_Rhodococcus_globerulus_NBRC_14531_T | 016_Rhodococcus_intechensis_JCM_13270_T | 19.80 | [17.6 - 22.2%] | 0.22170 | 0 | 5.55 |
| Strain | Name | Accession | Survival (%) | Bioavailability (%) | Other Parameters |
|--------|------|-----------|--------------|---------------------|-----------------|
| 014_Rhodococcus_gordoniae_DSM_44689_T | 021_Rhodococcus_kyotenensis_JCM_23211_T | 19.10 | [17 - 21.5%] | 0.22980 | 0 | 3.79 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 19.90 | [17.7 - 22.3%] | 0.22130 | 0 | 1.22 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 19.40 | [17.2 - 21.8%] | 0.22660 | 0 | 3.54 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 024_Rhodococcus_maris_DS_43672_T | 19.50 | [17.3 - 21.9%] | 0.22580 | 0 | 2.91 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 025_Rhodococcus_opacus_DS_43205_T | 19.70 | [17.5 - 22.1%] | 0.22350 | 0 | 0.67 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 026_Rhodococcus_phenolicus_DS_44812_T | 22.00 | [19.7 - 24.5%] | 0.19930 | 0 | 0.41 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 027_Rhodococcus_pyridinivorans_DS_44555_T | 43.10 | [40.6 - 45.7%] | 0.08970 | 5.58 | 0.1 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 19.50 | [17.3 - 21.9%] | 0.22560 | 0 | 5.58 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 029_Rhodococcus_rhodnii_NBRC_100604_T | 20.00 | [17.8 - 22.4%] | 0.21950 | 0 | 1.73 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 030_Rhodococcus_rhodcirovus_DS_43241_T | 41.70 | [39.2 - 44.3%] | 0.09380 | 4.12 | 0.28 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 031_Rhodococcus_ruber_DS_43338_T | 21.40 | [19.1 - 23.8%] | 0.20560 | 0 | 2.72 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 032_Rhodococcus_ruberpertincta_NBRC_101908_T | 20.00 | [17.8 - 22.4%] | 0.22000 | 0 | 0.56 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 033_Rhodococcus_spiniti_NBRC_100414_T | 20.10 | [17.9 - 22.6%] | 0.21820 | 0 | 2.6 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 034_Rhodococcus_terreix_NBRL_B_16283_T | 20.00 | [17.8 - 22.4%] | 0.22000 | 0 | 0.14 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 035_Rhodococcus_triataomae_DS_44892_T | 20.50 | [18.3 - 22.9%] | 0.21420 | 0 | 0.78 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 036_Rhodococcus_tukiaumensis_NBRC_100609_T | 20.40 | [18.1 - 22.8%] | 0.21580 | 0 | 1.9 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 037_Rhodococcus_wratlaviensis_NBRC_100605_T | 19.90 | [17.7 - 22.3%] | 0.22110 | 0 | 1.17 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.40 | [17.3 - 21.8%] | 0.22610 | 0 | 4.05 |
| 014_Rhodococcus_gordoniae_DSM_44689_T | 039_Rhodococcus_zopfii_NBRC_100606_T | 21.90 | [19.6 - 24.3%] | 0.20980 | 0 | 0.3 |

| Strain | Name | Accession | Survival (%) | Bioavailability (%) | Other Parameters |
|--------|------|-----------|--------------|---------------------|-----------------|
| 015_Rhodococcus_hoagii_DSM_20295_T | 016_Rhodococcus_intechensis_JCM_13270_T | 20.50 | [18.3 - 22.9%] | 0.21410 | 0 | 1.55 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 017_Rhodococcus_jostii_NBRC_16295_T | 20.30 | [18.1 - 22.8%] | 0.21600 | 0 | 1.87 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 018_Rhodococcus_koreensis_DS_44498_T | 20.50 | [18.3 - 22.9%] | 0.21460 | 0 | 1.39 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 019_Rhodococcus_kroppenstedtii_DS_44908_T | 20.30 | [18.1 - 22.7%] | 0.21660 | 0 | 1.3 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 020_Rhodococcus_kummingensis_DS_45001_T | 20.40 | [18.1 - 22.8%] | 0.21590 | 0 | 2.57 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 021_Rhodococcus_kyotenensis_JCM_23211_T | 19.50 | [17.3 - 21.8%] | 0.22600 | 0 | 4.61 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 022_Rhodococcus_maanshanensis_DS_44675_T | 20.90 | [18.7 - 23.4%] | 0.20960 | 0 | 0.4 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 20.20 | [18.2 - 22.6%] | 0.21750 | 0 | 4.36 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 024_Rhodococcus_maris_DS_43672_T | 19.50 | [17.3 - 21.8%] | 0.22600 | 0 | 2.09 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 025_Rhodococcus_opacus_DS_43205_T | 20.70 | [18.5 - 23.1%] | 0.21220 | 0 | 1.49 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 21.10 [18.9 - 23.5%] | 0.20800 | 0 | 0.41 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 20.40 [18.2 - 22.8%] | 0.21520 | 0 | 0.92 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 19.70 [17.5 - 22.1%] | 0.22300 | 0 | 6.4 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 029_Rhodococcus_rhodnii_NBRC_100604_T | 20.50 [18.3 - 22.9%] | 0.21420 | 0 | 0.91 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 030_Rhodococcus_rhodochrous_DSM_43241_T | 21.00 [18.8 - 23.4%] | 0.20900 | 0 | 0.54 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 031_Rhodococcus_ruber_DSM_43338_T | 20.70 [18.4 - 23.1%] | 0.21260 | 0 | 1.9 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 20.60 [18.4 - 23%] | 0.21330 | 0 | 1.38 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 033_Rhodococcus_sputi_NBRC_100414_T | 20.40 [18.2 - 22.8%] | 0.21550 | 0 | 0.96 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 034_Rhodococcus_terrae_NRRL_B_16283_T | 20.60 [18.4 - 23%] | 0.21320 | 0 | 3.44 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 035_Rhodococcus_triatomae_DSM_44892_T | 20.20 [17.9 - 22.6%] | 0.21800 | 0 | 0.99 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 036_Rhodococcus_tukisamuensis_NBRC_100605_T | 20.50 [18.3 - 22.9%] | 0.21400 | 0 | 1.38 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 037_Rhodococcus_yunnanensis_NBRC_103083_T | 19.40 [17.2 - 21.8%] | 0.22620 | 0 | 4.87 |
| 015_Rhodococcus_hoagii_DSM_20295_T | 038_Rhodococcus_zopfii_NBRC_100606_T | 20.70 [18.4 - 23.1%] | 0.21260 | 0 | 0.52 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 017_Rhodococcus_jostii_NBRC_16295_T | 41.60 [39.1 - 44.2%] | 0.09410 | 4.03 | 0.32 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 018_Rhodococcus_koreensis_DSM_44498_T | 44.30 [41.8 - 46.9%] | 0.08610 | 7.23 | 0.15 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 19.70 [17.5 - 22.1%] | 0.22290 | 0 | 2.84 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 020_Rhodococcus_kummingensis_DSM_45001_T | 19.90 [17.7 - 22.3%] | 0.22140 | 0 | 1.03 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 021_Rhodococcus_leydenensis_JCM_23211_T | 19.40 [17.2 - 21.8%] | 0.22620 | 0 | 1.95 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 20.60 [18.4 - 23%] | 0.21350 | 0 | 3.64 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 27.10 [24.7 - 29.5%] | 0.15970 | 0.03 | 2.81 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 024_Rhodococcus_marinus_DSM_43672_T | 19.30 [17.1 - 21.7%] | 0.22740 | 0 | 0.66 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 025_Rhodococcus_opacus_DSM_43205_T | 81.20 [78.3 - 83.8%] | 0.02190 | 91.47 | 0.06 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 20.00 [17.8 - 22.5%] | 0.21930 | 0 | 1.14 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 20.00 [17.8 - 22.4%] | 0.21960 | 0 | 0.63 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 20.20 [18 - 22.6%] | 0.21750 | 0 | 4.85 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 029_Rhodococcus_rhodnii_NBRC_100604_T | 19.70 [17.5 - 22.1%] | 0.22280 | 0 | 2.45 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 030_Rhodococcus_rhodochrous_DSM_43241_T | 19.90 [17.7 - 22.3%] | 0.22090 | 0 | 1.01 |
| 016_Rhodococcus_imtechensis_JCM_13270_T | 031_Rhodococcus_ruber_DSM_43338_T | 20.40 [18.2 - 22.9%] | 0.21500 | 0 | 3.44 |
| Rhodococcus_intechensis_ICM_13270_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 19.50  | [17.3 - 21.9%] | 0.22540 | 0 | 0.16 |
|-----------------------------------|---------------------------------------------|--------|----------------|--------|---|------|
| 016_Rhodococcus_intechensis_ICM_13270_T | 033_Rhodococcus_sputi_NBRC_100414_T | 20.30  | [18 - 22.7%]  | 0.21700 | 0 | 1.88 |
| 016_Rhodococcus_intechensis_ICM_13270_T | 034_Rhodococcus_terrae_NRRL_B_16283_T | 19.90  | [17.7 - 22.3%] | 0.22060 | 0 | 0.58 |
| 016_Rhodococcus_intechensis_ICM_13270_T | 035_Rhodococcus_triatomae_DSM_44892_T | 20.80  | [18.5 - 23.2%] | 0.21150 | 0 | 1.51 |
| 016_Rhodococcus_intechensis_ICM_13270_T | 036_Rhodococcus_tukisanensis_NBRC_100609_T | 20.90  | [18.7 - 23.3%] | 0.20990 | 0 | 2.63 |
| 016_Rhodococcus_intechensis_ICM_13270_T | 037_Rhodococcus_wratislaviensis_NBRC_100605_T | 57.40  | [54.6 - 60.1%] | 0.05630 | 43.39 | 0.44 |
| 016_Rhodococcus_intechensis_ICM_13270_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.20  | [17 - 21.6%]  | 0.22930 | 0 | 3.33 |
| 016_Rhodococcus_intechensis_ICM_13270_T | 039_Rhodococcus_zopfii_NBRC_100606_T | 20.10  | [17.9 - 22.5%] | 0.21840 | 0 | 1.02 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 018_Rhodococcus_koreensis_DSM_44498_T | 38.80  | [36.4 - 41.4%] | 0.10340 | 2.02 | 0.47 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 19.70  | [17.5 - 22.1%] | 0.22340 | 0 | 3.16 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 020_Rhodococcus_kunningensis_DSM_45001_T | 20.00  | [17.8 - 22.4%] | 0.22020 | 0 | 0.71 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 021_Rhodococcus_kytonensis_ICM_23211_T | 19.10  | [16.9 - 21.5%] | 0.23040 | 0 | 2.74 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 20.60  | [18.4 - 23.1%] | 0.21280 | 0 | 2.27 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 023_Rhodococcus_marinascens_NBRC_14363_T | 26.90  | [24.6 - 29.4%] | 0.16070 | 0.03 | 2.49 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 024_Rhodococcus_maris_DSM_43672_T | 19.20  | [17.1 - 21.6%] | 0.22850 | 0 | 3.96 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 025_Rhodococcus_opacus_DSM_43205_T | 42.50  | [40 - 45.1%]  | 0.09140 | 4.94 | 0.38 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 20.10  | [17.9 - 22.6%] | 0.21820 | 0 | 1.46 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 19.70  | [17.5 - 22.1%] | 0.22320 | 0 | 0.95 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 028_Rhodococcus_qingshengii_ICM_15477_T | 20.20  | [18 - 22.6%]  | 0.21720 | 0 | 4.53 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 029_Rhodococcus_rhodii_NBRC_100604_T | 19.50  | [17.3 - 21.9%] | 0.22490 | 0 | 2.77 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 030_Rhodococcus_rhodochrous_DSM_43241_T | 19.80  | [17.6 - 22.2%] | 0.22230 | 0 | 1.33 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 031_Rhodococcus_ruber_DSM_43338_T | 20.30  | [18.1 - 22.7%] | 0.21620 | 0 | 3.77 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 19.50  | [17.3 - 21.9%] | 0.22580 | 0 | 0.48 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 033_Rhodococcus_sputi_NBRC_100414_T | 19.60  | [17.4 - 22%]   | 0.22410 | 0 | 1.56 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 034_Rhodococcus_terrae_NRRL_B_16283_T | 19.50  | [17.3 - 21.9%] | 0.22500 | 0 | 0.9 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 035_Rhodococcus_triatomae_DSM_44892_T | 20.50  | [18.2 - 22.9%] | 0.21470 | 0 | 1.83 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 036_Rhodococcus_tukisanensis_NBRC_100609_T | 20.80  | [18.6 - 23.3%] | 0.21080 | 0 | 2.95 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 037_Rhodococcus_wratislaviensis_NBRC_100605_T | 41.90  | [39.4 - 44.5%] | 0.09320 | 4.3 | 0.12 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.40  | [17.2 - 21.8%] | 0.22660 | 0 | 3.01 |
| 017_Rhodococcus_jostii_NBRC_16295_T | 039_Rhodococcus_zopfii_NBRC_100606_T | 20.10 | [17.9 - 22.5%] | 0.21880 | 0.00 | 1.34 |
|-----------------------------------|----------------------------------------|-------|----------------|--------|-------|-------|
| 018_Rhodococcus_koreensis_DSM_44498_T | 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 19.80 | [17.6 - 22.2%] | 0.22180 | 0.00 | 2.69 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 020_Rhodococcus_kunningensis_DSM_45001_T | 20.10 | [17.9 - 22.6%] | 0.21810 | 0.00 | 1.18 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 021_Rhodococcus_kyotonensis_JCM_23211_T | 19.20 | [17 - 21.6%] | 0.22910 | 0.00 | 3.22 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 20.60 | [18.4 - 23%] | 0.21340 | 0.00 | 1.79 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 26.60 | [24.2 - 29.1%] | 0.16300 | 0.02 | 2.97 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 024_Rhodococcus_maris_DSM_43672_T | 19.40 | [17.2 - 21.8%] | 0.22620 | 0.00 | 3.48 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 025_Rhodococcus_opacus_DSM_43205_T | 44.00 | [41.4 - 46.5%] | 0.08710 | 6.7 | 0.1 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 20.10 | [17.9 - 22.5%] | 0.21830 | 0.00 | 0.98 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 027_Rhodococcus_pyridinivorans_DSM_44555_T | 19.80 | [17.6 - 22.2%] | 0.22180 | 0.00 | 0.47 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 028_Rhodococcus_qingshengii_JCM_15477_T | 20.40 | [18.2 - 22.8%] | 0.21550 | 0.00 | 5.01 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 029_Rhodococcus_rhodni_NBRC_100604_T | 19.80 | [17.6 - 22.2%] | 0.22170 | 0.00 | 2.3 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 030_Rhodococcus_rochochorous_DSM_43241_T | 20.00 | [17.8 - 22.4%] | 0.21950 | 0.00 | 0.85 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 031_Rhodococcus_ruber_DSM_43338_T | 20.60 | [18.4 - 23%] | 0.21310 | 0.00 | 3.29 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 19.70 | [17.5 - 22.1%] | 0.22340 | 0.00 | 0.01 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 033_Rhodococcus_sputi_NBRC_100414_T | 20.60 | [18.4 - 23.1%] | 0.21290 | 0.00 | 2.03 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 034_Rhodococcus_terrae_NRRL_B_16283_T | 19.70 | [17.5 - 22.1%] | 0.22310 | 0.00 | 0.43 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 035_Rhodococcus_triatomae_DSM_44892_T | 20.30 | [18.1 - 22.8%] | 0.21600 | 0.00 | 1.35 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 036_Rhodococcus_tukisamuensis_NBRC_100609_T | 20.80 | [18.6 - 23.2%] | 0.21100 | 0.00 | 2.48 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 037_Rhodococcus_wratilaviensis_NBRC_100605_T | 43.30 | [40.7 - 45.8%] | 0.08920 | 5.77 | 0.6 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.50 | [17.3 - 21.9%] | 0.22590 | 0.00 | 3.48 |
| 018_Rhodococcus_koreensis_DSM_44498_T | 039_Rhodococcus_zopfii_NBRC_100606_T | 20.10 | [17.9 - 22.5%] | 0.21870 | 0.00 | 0.87 |
| 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 020_Rhodococcus_kunningensis_DSM_45001_T | 19.80 | [17.6 - 22.2%] | 0.22250 | 0.00 | 3.87 |
| 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 021_Rhodococcus_kyotonensis_JCM_23211_T | 19.90 | [17.7 - 22.3%] | 0.22080 | 0.00 | 5.91 |
| 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 022_Rhodococcus_maanshanensis_DSM_44675_T | 20.00 | [17.8 - 22.5%] | 0.21930 | 0.00 | 0.9 |
| 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 023_Rhodococcus_marinonascens_NBRC_14363_T | 20.10 | [17.9 - 22.5%] | 0.21900 | 0.00 | 5.66 |
| 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 024_Rhodococcus_maris_DSM_43672_T | 18.80 | [16.6 - 21.2%] | 0.23390 | 0.00 | 0.79 |
| 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 025_Rhodococcus_opacus_DSM_43205_T | 19.70 | [17.5 - 22.1%] | 0.22290 | 0.00 | 2.79 |
| 019_Rhodococcus_kroppenstedtii_DSM_44908_T | 026_Rhodococcus_phenolicus_DSM_44812_T | 19.40 | [17.2 - 21.8%] | 0.22620 | 0.00 | 1.71 |
| Rhodococcus spp. | Reference | T | 
|------------------|-----------|---|
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 20.20 | [18 - 22.6%] | 0.21760 | 0.00 | 2.22 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 20.30 | [18.1 - 22.7%] | 0.21620 | 0.00 | 7.7 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.70 | [17.5 - 22.1%] | 0.22350 | 0.00 | 0.39 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 20.00 | [17.8 - 22.4%] | 0.21980 | 0.00 | 1.83 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.80 | [17.6 - 22.2%] | 0.22150 | 0.00 | 0.6 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.80 | [17.6 - 22.2%] | 0.22220 | 0.00 | 2.68 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.70 | [17.5 - 22.1%] | 0.22280 | 0.00 | 4.72 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 20.20 | [17.9 - 22.6%] | 0.21800 | 0.00 | 2.26 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.80 | [17.8 - 22.4%] | 0.21920 | 0.00 | 1.34 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 20.00 | [17.8 - 22.4%] | 0.21940 | 0.00 | 0.21 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.60 | [17.4 - 22%] | 0.22450 | 0.00 | 3.29 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.90 | [17.7 - 22.3%] | 0.22120 | 0.00 | 6.17 |
| Rhodococcus kroppenstedtii DSM_44908_T | 019 | 19.40 | [17.2 - 21.8%] | 0.22640 | 0.00 | 1.82 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.40 | [17.2 - 21.8%] | 0.22680 | 0.00 | 2.04 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.90 | [17.7 - 22.4%] | 0.22030 | 0.00 | 2.97 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.00 | [16.9 - 21.4%] | 0.23080 | 0.00 | 1.79 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.30 | [17.2 - 21.7%] | 0.22730 | 0.00 | 4.66 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.70 | [17.5 - 22.1%] | 0.22280 | 0.00 | 1.08 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.40 | [17.2 - 21.8%] | 0.22660 | 0.00 | 2.16 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.50 | [17.3 - 21.9%] | 0.22550 | 0.00 | 1.65 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.70 | [17.5 - 22.1%] | 0.22260 | 0.00 | 3.83 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 20.30 | [18.1 - 22.8%] | 0.21600 | 0.00 | 3.48 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.80 | [17.6 - 22.2%] | 0.22240 | 0.00 | 2.04 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 20.00 | [17.8 - 22.4%] | 0.21990 | 0.00 | 4.47 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 19.90 | [17.7 - 22.4%] | 0.22040 | 0.00 | 1.19 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 20.10 | [17.9 - 22.5%] | 0.21870 | 0.00 | 0.85 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 20.10 | [17.9 - 22.5%] | 0.21880 | 0.00 | 1.61 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 20.30 | [18.1 - 22.7%] | 0.21660 | 0.00 | 2.53 |
| Rhodococcus kunmingensis DSM_45001_T | 020 | 20.00 | [17.8 - 22.4%] | 0.21950 | 0.00 | 3.66 |
| Culture Name                                      | Similarity to Reference | Similarity to Literature | Genotype | 16S rRNA | 16S rRNA Other |
|-------------------------------------------------|-------------------------|--------------------------|----------|---------|---------------|
| Rhodococcus kunmingensis DSM 45001 T            | 0.97                    | 97.1%                    | 0.58     | 0.00    | 0.12          |
| Rhodococcus kunmingensis DSM 45001 T            | 0.98                    | 98.0%                    | 2.3      | 0.00    | 0.05          |
| Rhodococcus kunmingensis DSM 45001 T            | 0.98                    | 98.1%                    | 2.05     | 0.00    | 0.00          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.97                    | 97.1%                    | 0.58     | 0.00    | 0.12          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.0%                    | 2.3      | 0.00    | 0.05          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.1%                    | 2.05     | 0.00    | 0.00          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.97                    | 97.1%                    | 0.58     | 0.00    | 0.12          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.0%                    | 2.3      | 0.00    | 0.05          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.1%                    | 2.05     | 0.00    | 0.00          |

*Notes: Similarity values are calculated using blastn and blastp, with the corresponding Genotype, 16S rRNA, and 16S rRNA Other values are reported.*

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**Table:**

| Culture Name                                      | Similarity to Reference | Similarity to Literature | Genotype | 16S rRNA | 16S rRNA Other |
|-------------------------------------------------|-------------------------|--------------------------|----------|---------|---------------|
| Rhodococcus kunmingensis DSM 45001 T            | 0.97                    | 97.1%                    | 0.58     | 0.00    | 0.12          |
| Rhodococcus kunmingensis DSM 45001 T            | 0.98                    | 98.0%                    | 2.3      | 0.00    | 0.05          |
| Rhodococcus kunmingensis DSM 45001 T            | 0.98                    | 98.1%                    | 2.05     | 0.00    | 0.00          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.97                    | 97.1%                    | 0.58     | 0.00    | 0.12          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.0%                    | 2.3      | 0.00    | 0.05          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.1%                    | 2.05     | 0.00    | 0.00          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.97                    | 97.1%                    | 0.58     | 0.00    | 0.12          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.0%                    | 2.3      | 0.00    | 0.05          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.1%                    | 2.05     | 0.00    | 0.00          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.97                    | 97.1%                    | 0.58     | 0.00    | 0.12          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.0%                    | 2.3      | 0.00    | 0.05          |
| Rhodococcus kunmingensis JCM 23211 T            | 0.98                    | 98.1%                    | 2.05     | 0.00    | 0.00          |

*Notes: Similarity values are calculated using blastn and blastp, with the corresponding Genotype, 16S rRNA, and 16S rRNA Other values are reported.***
| Species 1                                      | Species 2                                      | Percentage | Tolerance | Growth | Temperature | Type       |
|------------------------------------------------|------------------------------------------------|------------|-----------|---------|-------------|------------|
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus ruber DSM 43338 T                  | 20.30      | [18.1 - 22.7%] | 0.21640 | 0.00 | 1.5 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus rubripertincta NBRC 101908 T       | 19.90      | [17.7 - 22.3%] | 0.22140 | 0.00 | 1.78 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus sputi NBRC 100414 T                | 20.00      | [17.8 - 22.4%] | 0.21970 | 0.00 | 3.82 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus terrae NRRL B_16283 T              | 19.90      | [17.7 - 22.3%] | 0.22100 | 0.00 | 1.36 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus triatomae DSM 44892 T              | 20.40      | [18.2 - 22.8%] | 0.21510 | 0.00 | 0.44 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus tuksamensis NBRC 100609 T          | 24.20      | [21.9 - 26.6%] | 0.18060 | 0.01 | 0.68 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus wratislaviensis NBRC 100605 T      | 20.50      | [18.3 - 22.9%] | 0.21440 | 0.00 | 2.39 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus yunnanensis NBRC 103083 T         | 20.50      | [18.2 - 22.8%] | 0.21440 | 0.00 | 5.27 |
| Rhodococcus maanshanensis DSM 44675 T          | Rhodococcus zopfii NBRC 100606 T               | 24.20      | [21.9 - 26.6%] | 0.18060 | 0.01 | 0.68 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus maris DSM 43672 T                  | 19.30      | [17.1 - 21.7%] | 0.22820 | 0.00 | 6.45 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus opacus DSM 43205 T                 | 27.20      | [24.8 - 29.7%] | 0.15900 | 0.03 | 2.87 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus phenolicus DSM 44812 T             | 19.60      | [17.4 - 22%]  | 0.22410 | 0.00 | 3.95 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus pyridinivorans DSM 44555 T         | 20.00      | [17.8 - 22.4%] | 0.22000 | 0.00 | 3.44 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus qingshengii JCM 15477 T           | 20.00      | [17.8 - 22.4%] | 0.22010 | 0.00 | 2.04 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus rhodnii NBRC 100604 T             | 19.80      | [17.6 - 22.2%] | 0.22150 | 0.00 | 5.26 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus rhodochrous DSM 43241 T            | 19.90      | [17.7 - 22.3%] | 0.22130 | 0.00 | 3.82 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus ruber DSM 43338 T                  | 19.80      | [17.6 - 22.2%] | 0.22250 | 0.00 | 6.26 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus rubripertincta NBRC 101908 T       | 19.60      | [17.5 - 22%]  | 0.22370 | 0.00 | 2.97 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus sputi NBRC 100414 T                | 20.60      | [18.4 - 23%]  | 0.21340 | 0.00 | 0.94 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus terrae NRRL B_16283 T              | 19.90      | [17.7 - 22.3%] | 0.22100 | 0.00 | 3.4  |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus triatomae DSM 44892 T              | 20.20      | [17.9 - 22.6%] | 0.21800 | 0.00 | 4.32 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus tuksamensis NBRC 100609 T          | 20.10      | [17.9 - 22.5%] | 0.21890 | 0.00 | 5.44 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus wratislaviensis NBRC 100605 T      | 27.20      | [24.9 - 29.7%] | 0.15860 | 0.03 | 2.37 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus yunnanensis NBRC 103083 T         | 19.60      | [17.4 - 22%]  | 0.22420 | 0.00 | 0.51 |
| Rhodococcus marinonascens NBRC 14363 T         | Rhodococcus zopfii NBRC 100606 T               | 19.50      | [17.4 - 21.9%] | 0.22490 | 0.00 | 3.83 |
| Rhodococcus maris DSM 43672 T                   | Rhodococcus opacus DSM 43205 T                  | 19.80      | [17.6 - 22.2%] | 0.22160 | 0.00 | 3.58 |
| Rhodococcus maris DSM 43672 T                   | Rhodococcus phenolicus DSM 44812 T             | 19.40      | [17.2 - 21.8%] | 0.22630 | 0.00 | 2.5  |
| Rhodococcus maris DSM 43672 T                   | Rhodococcus pyridinivorans DSM 44555 T         | 19.80      | [17.6 - 22.2%] | 0.22190 | 0.00 | 3.01 |
| Rhodococcus maris DSM 43672 T                   | Rhodococcus qingshengii JCM 15477 T           | 19.60      | [17.4 - 22%]  | 0.22420 | 0.00 | 8.49 |
| Species                                             | Strain Code                        | Growth (%) | Dissimilarity (%) | Dissimilarity Index |
|-----------------------------------------------------|------------------------------------|------------|-------------------|---------------------|
| Rhodococcus maris DSM 43672_T                       | 024                                 |            |                   |                     |
| Rhodococcus maris DSM 43672_T                       | 024                                 | 19.20      | 17 - 21.6%        | 0.22930             | 0.00               | 1.18               |
| Rhodococcus maris DSM 43672_T                       | 029                                 | 19.60      | 17.4 - 21.9%      | 0.22480             | 0.00               | 2.63               |
| Rhodococcus maris DSM 43672_T                       | 030                                 | 19.70      | 17.5 - 22.1%      | 0.22350             | 0.00               | 0.19               |
| Rhodococcus maris DSM 43672_T                       | 031                                 | 19.90      | 17.7 - 22.3%      | 0.22580             | 0.00               | 3.05               |
| Rhodococcus maris DSM 43672_T                       | 032                                 | 20.10      | 17.9 - 22.5%      | 0.22490             | 0.00               | 0.19               |
| Rhodococcus maris DSM 43672_T                       | 033                                 | 20.30      | 18.1 - 22.7%      | 0.21630             | 0.00               | 5.51               |
| Rhodococcus maris DSM 43672_T                       | 034                                 | 20.40      | 18.1 - 22.8%      | 0.21560             | 0.00               | 3.05               |
| Rhodococcus maris DSM 43672_T                       | 035                                 | 20.50      | 18.2 - 22.8%      | 0.21580             | 0.00               | 3.05               |
| Rhodococcus maris DSM 43672_T                       | 036                                 | 21.90      | 19.7 - 24.4%      | 0.19980             | 0.00               | 0.51               |
| Rhodococcus maris DSM 43672_T                       | 037                                 | 22.00      | 19.7 - 24.5%      | 0.19930             | 0.00               | 0.13               |
| Strain                          | Metabolite                                | Percentage | Peak Area | RSD  | Retention Time |
|--------------------------------|-------------------------------------------|------------|-----------|------|----------------|
| 026_Rhodococcus_phenolicus_DSM_44812_T | 031_Rhodococcus_ruber_DSM_43338_T         | 22.60      | [20.4 - 25.1%] | 0.19360 | 0.00          | 2.31 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 20.10      | [17.9 - 22.5%] | 0.21850 | 0.00          | 0.98 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 033_Rhodococcus_sputi_NBRC_100414_T       | 20.10      | [17.9 - 22.5%] | 0.21850 | 0.00          | 3.01 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 034_Rhodococcus_terrea_NBRL_B_16283_T     | 19.90      | [17.7 - 22.4%] | 0.22040 | 0.00          | 0.55 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 035_Rhodococcus_triatorae_DSM_44892_T     | 20.10      | [17.9 - 22.5%] | 0.21890 | 0.00          | 0.37 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 036_Rhodococcus_tukisauensis_NBRC_100609_T | 20.60      | [18.3 - 23%]   | 0.21360 | 0.00          | 1.49 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 037_Rhodococcus_wratislaviensis_NBRC_100605_T | 20.10     | [17.9 - 22.5%] | 0.21880 | 0.00          | 1.58 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.70      | [17.5 - 22.1%] | 0.22340 | 0.00          | 4.46 |
| 026_Rhodococcus_phenolicus_DSM_44812_T | 039_Rhodococcus_zopfii_NBRC_100606_T      | 36.40      | [34 - 39%]    | 0.11230 | 1.03          | 0.12 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 028_Rhodococcus_qingshengii_JCM_15477_T  | 19.90      | [17.7 - 22.3%] | 0.22070 | 0.00          | 5.48 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 029_Rhodococcus_rhodini_NBRC_100604_T    | 20.00      | [17.8 - 22.4%] | 0.21950 | 0.00          | 1.83 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 030_Rhodococcus_rhodochrous_DSM_43241_T  | 58.60      | [55.8 - 61.4%] | 0.05410 | 47.65         | 0.38 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 031_Rhodococcus_ruber_DSM_43338_T        | 21.50      | [19.3 - 24%]   | 0.20380 | 0.00          | 2.82 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 20.30     | [18 - 22.7%]   | 0.21700 | 0.00          | 0.46 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 033_Rhodococcus_sputi_NBRC_100414_T      | 21.50      | [19.2 - 23.9%] | 0.20420 | 0.00          | 2.5  |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 034_Rhodococcus_terrea_NRRL_B_16283_T    | 20.00      | [17.8 - 22.5%] | 0.21930 | 0.00          | 0.04 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 035_Rhodococcus_triatorae_DSM_44892_T    | 20.20      | [18 - 22.7%]   | 0.21710 | 0.00          | 0.88 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 036_Rhodococcus_tukisauensis_NBRC_100609_T | 20.00    | [17.8 - 22.4%] | 0.21970 | 0.00          | 2    |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 037_Rhodococcus_wratislaviensis_NBRC_100605_T | 19.90    | [17.7 - 22.3%] | 0.22140 | 0.00          | 1.07 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 038_Rhodococcus_yunnanensis_NBRC_103083_T | 19.20      | [17 - 21.6%]   | 0.22940 | 0.00          | 3.95 |
| 027_Rhodococcus_pyridinivorans_DSM_44555_T | 039_Rhodococcus_zopfii_NBRC_100606_T     | 22.10      | [19.8 - 24.5%] | 0.19870 | 0.00          | 0.4  |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 029_Rhodococcus_rhodini_NBRC_100604_T    | 19.90      | [17.7 - 22.3%] | 0.22110 | 0.00          | 7.3  |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 030_Rhodococcus_rhodochrous_DSM_43241_T  | 19.60      | [17.4 - 22%]   | 0.22440 | 0.00          | 5.86 |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 031_Rhodococcus_ruber_DSM_43338_T        | 19.80      | [17.6 - 22.2%] | 0.22220 | 0.00          | 8.3  |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 032_Rhodococcus_rubripertincta_NBRC_101908_T | 20.00     | [17.8 - 22.5%] | 0.21920 | 0.00          | 5.01 |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 033_Rhodococcus_sputi_NBRC_100414_T      | 20.30      | [18.1 - 22.7%] | 0.21660 | 0.00          | 2.98 |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 034_Rhodococcus_terrea_NBRL_B_16283_T    | 20.10      | [17.9 - 22.5%] | 0.21820 | 0.00          | 5.44 |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 035_Rhodococcus_triatorae_DSM_44892_T    | 19.90      | [17.7 - 22.3%] | 0.22100 | 0.00          | 6.36 |
| 028_Rhodococcus_qingshengii_JCM_15477_T | 036_Rhodococcus_tukisauensis_NBRC_100609_T | 20.10    | [17.9 - 22.6%] | 0.21820 | 0.00          | 7.48 |
| Rhodococcus qingshengii_JCM_15477_T | Rhodococcus wratislaviensis_NBRC_100605_T | 20.20 | [18 - 22.6%] | 0.21760 | 0.00 | 4.41 |
| Rhodococcus qingshengii_JCM_15477_T | Rhodococcus yunnanensis_NBRC_103083_T | 19.90 | [17.7 - 22.3%] | 0.22140 | 0.00 | 1.53 |
| Rhodococcus qingshengii_JCM_15477_T | Rhodococcus zopfii_NBRC_100606_T | 19.40 | [17.3 - 21.8%] | 0.22610 | 0.00 | 5.87 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus rhodnii_NBRC_100604_T | 20.00 | [17.8 - 22.4%] | 0.21980 | 0.00 | 1.44 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus ruber_DSM_43338_T | 19.80 | [17.6 - 22.2%] | 0.22150 | 0.00 | 0.99 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus rubripertincta_NBRC_101908_T | 19.80 | [17.6 - 22.2%] | 0.22200 | 0.00 | 2.29 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus sputi_NBRC_100414_T | 20.30 | [18.1 - 22.7%] | 0.21660 | 0.00 | 4.33 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus terrae_NRRL_B_16283_T | 19.70 | [17.5 - 22.1%] | 0.22260 | 0.00 | 1.87 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus triatomae_DSM_44892_T | 20.50 | [18.2 - 22.9%] | 0.21480 | 0.00 | 0.94 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus tukisamuensis_NBRC_100609_T | 20.00 | [17.7 - 22.4%] | 0.22030 | 0.00 | 0.18 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus wratislaviensis_NBRC_100605_T | 19.90 | [17.7 - 22.3%] | 0.22100 | 0.00 | 2.9 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus yunnanensis_NBRC_103083_T | 19.40 | [17.2 - 21.8%] | 0.22650 | 0.00 | 5.78 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus zopfii_NBRC_100606_T | 19.70 | [17.5 - 22.1%] | 0.22310 | 0.00 | 1.43 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus ruber_DSM_43338_T | 21.70 | [19.4 - 24.1%] | 0.20260 | 0.00 | 2.44 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus rubripertincta_NBRC_101908_T | 20.00 | [17.8 - 22.5%] | 0.21920 | 0.00 | 0.85 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus sputi_NBRC_100414_T | 20.20 | [18 - 22.6%] | 0.21770 | 0.00 | 2.89 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus terrae_NRRL_B_16283_T | 20.10 | [17.9 - 22.5%] | 0.21840 | 0.00 | 0.43 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus triatomae_DSM_44892_T | 20.30 | [18.1 - 22.7%] | 0.21640 | 0.00 | 0.5 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus tukisamuensis_NBRC_100609_T | 20.50 | [18.2 - 22.9%] | 0.21470 | 0.00 | 1.62 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus wratislaviensis_NBRC_100605_T | 19.80 | [17.6 - 22.2%] | 0.22170 | 0.00 | 1.45 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus yunnanensis_NBRC_103083_T | 19.30 | [17.2 - 21.7%] | 0.22730 | 0.00 | 4.33 |
| Rhodococcus rhodnii_NBRC_100604_T | Rhodococcus zopfii_NBRC_100606_T | 21.90 | [19.6 - 24.3%] | 0.20060 | 0.00 | 0.01 |
| Rhodococcus ruber_DSM_43338_T | Rhodococcus ruber_DSM_43338_T | 20.10 | [17.9 - 22.5%] | 0.21830 | 0.00 | 3.28 |
| Rhodococcus ruber_DSM_43338_T | Rhodococcus sputi_NBRC_100414_T | 20.60 | [18.4 - 23%] | 0.21330 | 0.00 | 5.32 |
| Rhodococcus ruber_DSM_43338_T | Rhodococcus terrae_NRRL_B_16283_T | 19.70 | [17.5 - 22.1%] | 0.22270 | 0.00 | 2.86 |
| Rhodococcus ruber_DSM_43338_T | Rhodococcus triatomae_DSM_44892_T | 20.10 | [17.9 - 22.5%] | 0.21860 | 0.00 | 1.94 |
| Rhodococcus ruber_DSM_43338_T | Rhodococcus tukisamuensis_NBRC_100609_T | 20.60 | [18.4 - 23.1%] | 0.21280 | 0.00 | 0.82 |
| Rhodococcus ruber_DSM_43338_T | Rhodococcus wratislaviensis_NBRC_100605_T | 20.50 | [18.3 - 22.9%] | 0.21450 | 0.00 | 3.89 |
| Rhodococcus ruber_DSM_43338_T | Rhodococcus yunnanensis_NBRC_103083_T | 19.20 | [17 - 21.5%] | 0.22950 | 0.00 | 6.77 |
| Species                                           | Accession      | 19.40 | 19.70 | 19.80 | 20.00 | 20.20 | 20.00 | 19.70 | 20.80 |
|--------------------------------------------------|----------------|-------|-------|-------|-------|-------|-------|-------|-------|
| Rhodococcus rubripertincta_NBRC_101908_T         | 032            |       |       |       |       |       |       |       |       |
| Rhodococcus sputi_NBRC_100414_T                  | 033            | 0.227 | 0.223 | 0.217 | 0.224 | 0.227 | 0.219 | 0.220 | 0.184 |
| Rhodococcus terraie_NRRL_B_16283_T              | 034            | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  |
| Rhodococcus vquinens_NBRC_100609_T              | 035            | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  |
| Rhodococcus sputi_NBRC_100414_T                  | 036            | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  |
| Rhodococcus terraie_NRRL_B_16283_T              | 037            | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  |
| Rhodococcus vquinens_NBRC_100609_T              | 038            | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  |
| Rhodococcus sputi_NBRC_100414_T                  | 039            | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  |
### Table S5. Genes involved in the central metabolism of *Rhodococcus* sp. WAY2

| Replicon  | Start    | End      | Strand | Gene name | Predicted function | Function, pathway                      |
|-----------|----------|----------|--------|-----------|--------------------|----------------------------------------|
| Chromosome| 654,458  | 655,462  | +      | glkA      | Glucokinase        | Glycolysis                             |
| Chromosome| 2,747,596| 2,748,597| +      | glk       | Glucokinase        | Glycolysis                             |
| Chromosome| 4,167,043| 4,167,567| +      | gntk      | Glucokinase thermoresistant | Glycolysis                             |
| Chromosome| 6,343,896| 6,343,144| -      | ppgK      | Polyphosphate glucokinase | Glycolysis                             |
| Chromosome| 227,909  | 229,564  | +      | pgi1      | Glucose-6-phosphate isomerase | Glycolysis, gluconeogenesis, pentose phosphate pathway |
| Chromosome| 5,115,499| 5,114,198| -      | pgi2      | Glucose-6-phosphate isomerase | Glycolysis, gluconeogenesis, pentose phosphate pathway |
| Chromosome| 6,102,346| 6,103,377| +      | pfkA      | 6-phosphofructokinase | Glycolysis                             |
| Chromosome| 6,297,174| 6,296,194| -      | fruK      | 1-phosphofructokinase | Glycolysis                             |
| Chromosome| 5,083,954| 5,084,988| +      | fba       | Fructose-bisphosphate aldolase | Glycolysis, gluconeogenesis             |
| Chromosome| 3,474,588| 3,473,803| -      | tpiA      | Triose-phosphate isomerase | Glycolysis                             |
| Chromosome| 3,476,836| 3,475,817| -      | gap       | Glyceraldehyde 3-phosphate dehydrogenase | Glycolysis, gluconeogenesis             |
| Chromosome| 3,475,745| 3,474,588| -      | pgk       | Phosphoglycerate kinase | Glycolysis, gluconeogenesis             |
| Chromosome| 1,728,074| 1,728,829| +      | gpmA1     | Phosphoglycerate mutase | Glycolysis, gluconeogenesis             |
| Chromosome| 5,975,937| 5,975,323| -      | gpmA2     | Phosphoglycerate mutase | Glycolysis, gluconeogenesis             |
| Chromosome| 5,345,257| 5,346,543| +      | eno       | Phosphopyruvate hydratase / enolase | Glycolysis, gluconeogenesis             |
| Chromosome| 2,865,568| 2,866,986| +      | pyk       | Pyruvate kinase | Glycolysis, purine metabolism           |
| Chromosome| 4,159,399| 4,161,252| +      | edd       | Phosphogluconate dehydratase | Glycolysis (ED)                        |
| Chromosome| 4,161,265| 4,161,891| +      | eda       | 4-hydroxy-2-oxoglutarate aldolase | Glycolysis (ED)                        |
| Chromosome| 5,389,671| 5,388,631| -      | glpX      | Fructose-1,6-bisphosphatase class II | Gluconeogenesis                        |
| prWAY01   | 292,410  | 293,354  | +      | glpX      | Fructose-1,6-bisphosphatase | Gluconeogenesis                        |
| Chromosome| 4,553,850| 4,555,679| +      | pckG      | Phosphoenolpyruvate carboxykinase | Gluconeogenesis                        |
| prWAY02   | 385,109  | 383,205  | -      | pckG      | Phosphoenolpyruvate carboxykinase | Gluconeogenesis                        |
| Chromosome| 241,101  | 238,750  | -      | pdh       | Pyruvate dehydrogenase E1 component | Acetyl-CoA synthesis                   |
| Chromosome| 2,029,413| 2,030,396| +      | pdhA1     | Pyruvate dehydrogenase E1 component, alpha subunit | Acetyl-CoA synthesis                   |
| Chromosome| 2,295,245| 2,294,148| -      | pdhA2     | Pyruvate dehydrogenase E1 component, alpha subunit | Acetyl-CoA synthesis                   |
| Chromosome| 3,673,818| 3,672,730| -      | pdhA3     | Pyruvate dehydrogenase E1 component, alpha subunit | Acetyl-CoA synthesis                   |
| Chromosome| 2,030,393| 2,031,412| +      | pdhB1     | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit | Acetyl-CoA synthesis                   |
| Chromosome| 2,294,151| 2,293,168| -      | pdhB2     | Pyruvate dehydrogenase E1 component beta subunit | Acetyl-CoA synthesis                   |
| Chromosome| 3,672,733| 3,671,741| -      | pdhB3     | Pyruvate dehydrogenase E1 component beta subunit | Acetyl-CoA synthesis                   |
| Chromosome | Start | End   | Gene/Function                                      | Reaction/Pathway                      |
|------------|-------|-------|---------------------------------------------------|---------------------------------------|
| 2,031,440  | 2,032,741 | +     | pdhC1 Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex | Acetyl-CoA synthesis                  |
| 2,293,124  | 2,291,898 | -     | pdhC2 Dihydrolipoamide acyltransferase component of pyruvate dehydrogenase complex | Acetyl-CoA synthesis                  |
| 3,671,719  | 3,670,391 | -     | pdhC3 Dihydrolipoamide acyltransferase component of pyruvate dehydrogenase complex | Acetyl-CoA synthesis                  |
| 3,744,757  | 3,743,195 | -     | pdhC4 Dihydrolipoamide acyltransferase component of pyruvate dehydrogenase complex | Acetyl-CoA synthesis                  |
| 2,670,866  | 2,668,014 |     | aceE1 Pyruvate dehydrogenase E1 component a        | Acetyl-CoA synthesis                  |
| 3,153,897  | 3,151,561 | +     | aceE2 Pyruvate dehydrogenase E1 component a        | Acetyl-CoA synthesis                  |
| 1,458,004  | 1,456,874 |     | citA Citrate synthase (si)                         | TCA cycle                            |
| 1,461,733  | 1,462,974 | +     | citA Citrate synthase (si)                         | TCA cycle                            |
| 3,439,278  | 3,442,082 | +     | acnA Aconitate hydratase                           | TCA cycle                            |
| 1,484,368  | 1,486,602 | +     | icd1 Isocitrate dehydrogenase (NADP+)              | TCA cycle                            |
| 5,857,767  | 5,858,990 | +     | icd2 Isocitrate dehydrogenase (NADP+)              | TCA cycle                            |
| 5,591,157  | 5,587,378 | -     | sucA 2-Oxoglutarate dehydrogenase, E1 and E2 components | TCA cycle                            |
| 5,124,137  | 5,125,306 | +     | succC Succinyl-CoA ligase (ADP-forming) beta chain | TCA cycle                            |
| 5,125,323  | 5,126,225 | +     | succD Succinyl-CoA ligase (ADP-forming) alpha chain | TCA cycle                            |
| 2,824,678  | 2,826,609 | +     | sdhA1 Succinate dehydrogenase flavoprotein subunit | TCA cycle                            |
| 5,870,475  | 5,868,724 | -     | sdhA2 Succinate dehydrogenase flavoprotein subunit | TCA cycle                            |
| 2,826,611  | 2,827,360 | +     | sdhB1 Succinate dehydrogenase iron-sulfur protein | TCA cycle                            |
| 5,868,724  | 5,867,945 | -     | sdhB2 Succinate dehydrogenase iron-sulfur protein | TCA cycle                            |
| 5,495,768  | 5,494,071 | -     | fumB Fumarate hydratase class I                    | TCA cycle                            |
| 6,208,259  | 6,209,806 | +     | mgo Malate dehydrogenase (quinone oxidoreductase) | TCA cycle                            |
| 1,941,117  | 1,942,310 | +     | mdh1 Malate dehydrogenase                          | TCA cycle                            |
| 2,149,115  | 2,150,170 | +     | mdh2 Malate dehydrogenase                          | TCA cycle                            |
| 4,840,775  | 4,841,710 | +     | mdh3 Malate dehydrogenase                          | TCA cycle                            |
| 5,577,218  | 5,578,411 | +     | mdh4 Malate dehydrogenase                          | TCA cycle                            |
| 27,337     | 28,536   | +     | mdh1 Malate dehydrogenase                          | TCA cycle                            |
| 632,113    | 630,920  | -     | mdh2 Malate dehydrogenase                          | TCA cycle                            |
| 3,467,019  | 3,468,557 | +     | zwf1 Glucose-6-phosphate 1-dehydrogenase           | Pentose phosphate pathway, glycolysis (ED) |
| 4,157,906  | 4,159,402 | +     | zwf2 Glucose-6-phosphate 1-dehydrogenase           | Pentose phosphate pathway, glycolysis (ED) |
| 5,223,741  | 5,222,395 | -     | zwf3 Glucose-6-phosphate 1-dehydrogenase           | Pentose phosphate pathway, glycolysis (ED) |
| Chromosome   | Start (bp) | End (bp) | Type                | Gene          | Description                                                                 |
|-------------|------------|----------|---------------------|---------------|-----------------------------------------------------------------------------|
| Chromosome  | 6,488,580  | 6,490,118 | +                   | zwf4          | Glucose-6-phosphate 1-dehydrogenase                                          |
| Chromosome  | 3,469,462  | 3,470,205 | +                   | pgl           | 6-phosphogluconolactonase                                                   |
| pRWAY01     | 276,334    | 275,534  | -                   | pgl           | 6-phosphogluconolactonase                                                   |
| Chromosome  | 3,495      | 4,406    | +                   | gnd1          | 6-Phosphogluconate dehydrogenase, decarboxylating                           |
| Chromosome  | 226,045    | 226,911  | +                   | gnd2          | 6-Phosphogluconate dehydrogenase, decarboxylating                           |
| Chromosome  | 3,355,733  | 3,357,181 | +                   | gnd3          | 6-Phosphogluconate dehydrogenase, decarboxylating                           |
| Chromosome  | 6,488,387  | 6,487,479 | -                   | gnd4          | 6-Phosphogluconate dehydrogenase, decarboxylating                           |
| pRWAY01     | 291,430    | 292,347  | +                   | gnd           | Ribulose-phosphate 3-epimerase                                              |
| Chromosome  | 3,486,888  | 3,486,205 | -                   | rpe           | Ribose 5-phosphate isomerase B                                              |
| Chromosome  | 3,465,885  | 3,467,009 | +                   | rpiB          | Transaldolase                                                               |
| pRWAY01     | 296,705    | 297,859  | +                   | tal           | Transaldolase                                                               |
| Chromosome  | 294,587    | 296,695  | +                   | tkt1          | Transketolase                                                               |
| Chromosome  | 3,463,767  | 3,465,875 | +                   | tkt2          | Transketolase                                                               |
| Chromosome  | 1,276,787  | 1,278,370 | +                   | purF          | Amidophosphoribosyltransferase                                              |
| Chromosome  | 1,231,769  | 1,233,022 | +                   | purD          | Phosphoribosylamine-glycine ligase                                           |
| Chromosome  | 5,130,043  | 5,130,483 | +                   | purN          | Phosphoribosylglycinamide formyltransferase                                  |
| Chromosome  | 1,278,489  | 1,279,568 | +                   | purM          | Phosphoribosylformylglycinamide cyclo-ligase                                 |
| Chromosome  | 1,271,293  | 1,273,578 | +                   | purL          | Phosphoribosylformylglycinamide synthase, synthetase subunit                |
| Chromosome  | 1,262,421  | 1,262,660 | +                   | purS          | Phosphoribosylformylglycinamide synthase, PurS subunit                      |
| Chromosome  | 1,262,657  | 1,263,334 | +                   | purQ          | Phosphoribosylformylglycinamide synthase, glutamine amidotransferase subunit |
| Chromosome  | 5,926,967  | 5,928,157 | +                   | purK          | Phosphoribosylaminomimidazole carboxylase ATPase subunit                    |
| Chromosome  | 5,928,150  | 5,928,668 | +                   | purE          | Phosphoribosylamidazole carboxylase catalytic subunit                        |
| Chromosome  | 1,246,819  | 1,247,703 | +                   | purC          | Phosphoribosylaminomimidazole-succinocarboxamide synthase                    |
| Chromosome  | 1,238,668  | 1,240,089 | +                   | purB          | Adenylosuccinate lyase                                                      |
| Chromosome  | 5,130,476  | 5,132,032 | +                   | purH          | Phosphoribosylaminomimidazolecarboxamide formyltransferase                   |
| Chromosome  | 5,097,130  | 5,098,419 | +                   | purA          | Adenylosuccinate synthetase                                                  |
| Chromosome  | 1,238,668  | 1,240,089 | +                   | purB          | Adenylosuccinate lyase                                                      |
| Chromosome  | 5,767,055  | 5,767,600 | +                   | adk1          | Adenylate kinase                                                            |
| Chromosome | Start | End | Direction | Gene | Function | Metabolism Pathway |
|------------|-------|-----|-----------|------|----------|-------------------|
| 3,300,576  | 3,301,157 | + | adk2 | Adenylate kinase | Purine metabolism |
| 2,519,189  | 2,519,608 | + | ndk | Nucleoside diphosphate kinase | Purine and pyrimidine metabolism |
| 3,499,983  | 3,499,465 | - | gmk | Guanylate kinase | Purine metabolism |
| 5,823,892  | 5,825,463 | + | guaA | GMP synthase | Purine metabolism |
| 3,359,549  | 3,360,985 | + | guaB1 | Inosine-5'-monophosphate dehydrogenase | Purine metabolism |
| 4,127,515  | 4,127,069 | - | guaB2 | Inosine-5'-monophosphate dehydrogenase | Purine metabolism |
| 5,819,152  | 5,820,675 | + | guaB3 | Inosine-5'-monophosphate dehydrogenase | Purine metabolism |
| 5,820,702  | 5,821,841 | + | guaB4 | Inosine-5'-monophosphate dehydrogenase | Purine metabolism |
| 843,891    | 841,156 | - | xdhA1 | Xanthine dehydrogenase, molybdenum binding subunit | Purine metabolism |
| 1,475,762  | 1,478,485 | + | xdhA2 | Xanthine dehydrogenase, molybdenum binding subunit | Purine metabolism |
| 844,697    | 843,888 | - | xdhB1 | Xanthine dehydrogenase, FAD binding subunit | Purine metabolism |
| 845,696    | 844,767 | - | xdhB2 | Xanthine dehydrogenase, FAD binding subunit | Purine metabolism |
| 846,028    | 845,699 | - | pucM | 5'-Hydroxyisourate hydrolase | Purine metabolism |
| 846,540    | 846,028 | - | uraD | 2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline (OHCU) decarboxylase | Purine metabolism |
| 867,465    | 866,470 | - | alc | Allantoicase | Purine metabolism |
| 3,505,899  | 3,504,739 | - | carA | Carbamoyl-phosphate synthase large chain | Pyrimidine metabolism |
| 3,504,739  | 3,501,371 | - | carB | Carbamoyl-phosphate synthase small chain | Pyrimidine metabolism |
| 3,507,772  | 3,506,456 | - | pyrC | Dihydroorotase | Pyrimidine metabolism |
| 3,508,743  | 3,507,799 | - | pyrR | Aspartate carbamoyltransferase | Pyrimidine metabolism |
| 2,979,743  | 2,978,673 | - | pyrD | Dihydroorotate dehydrogenase | Pyrimidine metabolism |
| 5,063,466  | 5,063,999 | + | pyrE | Orotate phosphoribosyltransferase | Pyrimidine metabolism |
| 3,501,374  | 3,500,535 | - | pyrF | Orotidine 5'-phosphate decarboxylase | Pyrimidine metabolism |
| 6,185,523  | 6,186,251 | + | pyrH | Uridine monophosphate kinase | Pyrimidine metabolism |
| 2,943,519  | 2,945,288 | - | pyrG | CTP synthase | Pyrimidine metabolism |
| 6,061,354  | 6,063,537 | + | nrdE | Ribonucleotide reductase, class Ib, alpha subunit | Pyrimidine metabolism |
| 6,063,615  | 6,064,580 | + | nrdF | Ribonucleotide reductase, class Ib, beta subunit | Pyrimidine metabolism |
| 6,060,544  | 6,060,831 | + | nrdH | Glutaredoxin-like protein NrdH, required for reduction of Ribonucleotide reductase class Ib | Pyrimidine metabolism |
| 6,060,920  | 6,061,392 | + | nrdI | Ribonucleotide reduction protein | Pyrimidine metabolism |
| 4,849,022  | 4,849,591 | + | dcd | Deoxycytidine triphosphate deaminase | Pyrimidine metabolism |
| 6,347,206  | 6,347,652 | + | dut | Deoxyuridine 5'-triposphate nucleotide hydrolase | Pyrimidine metabolism |
| 1,539,932  | 1,539,132 | - | thyA | Thymidylate synthase | Pyrimidine metabolism |
| 5,949,443  | 5,950,141 | + | tmk1 | Thymidylate kinase | Pyrimidine metabolism |
| 5,373,059  | 5,375,026 | + | tmk2 | Thymidylate kinase | Pyrimidine metabolism |
| Chromosome  | Start (bp) | End (bp) | Description | Location |
|-------------|------------|----------|-------------|----------|
| 152,600     | 154,102    | +        | fadD1       | Long-chain-fatty-acid--CoA ligase |
| 502,624     | 500,777    | -        | fadD2       | Long-chain-fatty-acid--CoA ligase |
| 917,717     | 916,167    | -        | fadD3       | Long-chain-fatty-acid--CoA ligase |
| 1,040,510   | 1,042,186  | +        | fadD4       | Long-chain-fatty-acid--CoA ligase |
| 1,044,931   | 1,043,360  | -        | fadD5       | Long-chain-fatty-acid--CoA ligase |
| 1,171,757   | 1,170,342  | -        | fadD6       | Long-chain-fatty-acid--CoA ligase |
| 1,878,765   | 1,880,564  | +        | fadD7       | Long-chain-fatty-acid--CoA ligase |
| 2,744,757   | 2,742,946  | -        | fadD8       | Long-chain-fatty-acid--CoA ligase |
| 3,907,778   | 3,906,096  | -        | fadD9       | Long-chain-fatty-acid--CoA ligase |
| 4,051,539   | 4,050,073  | -        | fadD10      | Long-chain-fatty-acid--CoA ligase |
| 4,224,541   | 4,226,064  | +        | fadD11      | Long-chain-fatty-acid--CoA ligase |
| 4,288,207   | 4,289,730  | +        | fadD12      | Long-chain-fatty-acid--CoA ligase |
| 5,543,473   | 5,545,248  | +        | fadD13      | Long-chain-fatty-acid--CoA ligase |
| 5,605,565   | 5,606,755  | +        | fadD14      | Long-chain-fatty-acid--CoA ligase |
| 5,618,475   | 5,616,709  | -        | fadD15      | Long-chain-fatty-acid--CoA ligase |
| 5,681,092   | 5,682,729  | +        | fadD16      | Long-chain-fatty-acid--CoA ligase |
| 5,742,135   | 5,743,724  | +        | fadD17      | Long-chain-fatty-acid--CoA ligase |
| pRWAY01     | 606,992    | 605,433  | -        | fadD       | Long-chain-fatty-acid--CoA ligase |
| 1,751,879   | 1,749,999  | -        | acx         | Acyl-CoA oxidase                       |
| 202,429     | 203,574    | +        | fadE1       | Butyryl-CoA dehydrogenase              |
| 217,813     | 216,650    | -        | fadE2       | Branched-chain acyl-CoA dehydrogenase |
| 500,744     | 499,575    | -        | fadE3       | Butyryl-CoA dehydrogenase              |
| 821,632     | 823,794    | +        | fadE4       | Butyryl-CoA dehydrogenase              |
| 823,877     | 824,917    | +        | fadE5       | Acyl-CoA dehydrogenase                 |
| 824,902     | 826,053    | +        | fadE6       | Acyl-CoA dehydrogenase                 |
| 913,176     | 912,118    | -        | fadE7       | Butyryl-CoA dehydrogenase              |
| 914,141     | 913,173    | -        | fadE8       | Butyryl-CoA dehydrogenase              |
| 915,298     | 914,138    | -        | fadE9       | Butyryl-CoA dehydrogenase              |
| 1,046,049   | 1,044,928  | -        | fadE10      | Butyryl-CoA dehydrogenase              |
| 1,135,137   | 1,133,836  | -        | fadE11      | Butyryl-CoA dehydrogenase              |
| 1,331,093   | 1,332,352  | +        | fadE12      | Acyl-CoA dehydrogenase, short-chain specific |
| 1,852,221   | 1,853,411  | +        | fadE13      | Butyryl-CoA dehydrogenase              |
| 2,034,972   | 2,036,204  | +        | fadE14      | Butyryl-CoA dehydrogenase              |
| 2,054,090   | 2,055,238  | +        | fadE15      | Butyryl-CoA dehydrogenase              |
| 2,342,932   | 2,344,032  | +        | fadE16      | Butyryl-CoA dehydrogenase              |
| 2,839,029   | 2,840,972  | +        | fadE17      | Butyryl-CoA dehydrogenase              |
| 3,867,347   | 3,868,498  | +        | fadE18      | Butyryl-CoA dehydrogenase              |
| 4,055,055   | 4,053,814  | -        | fadE19      | Butyryl-CoA dehydrogenase              |

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| Chromosome | Start | End | Operator | Gene | Annotation | Location |
|------------|-------|-----|----------|------|------------|----------|
| Chromosome 4,087,431 | 4,088,747 | + | fadE20 | Butyryl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,184,512 | 4,185,747 | + | fadE21 | Butyryl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,235,387 | 4,234,230 | - | fadE22 | Butyryl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,354,022 | 4,351,809 | - | fadE23 | Acyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,390,385 | 4,389,225 | - | fadE24 | Butyryl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,525,431 | 4,526,666 | + | fadE25 | Butyryl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 6,031,073 | 6,029,661 | - | fadE26 | Butyryl-CoA dehydrogenase | Beta-oxidation |
| pRWAY02 | 154,775 | 155,296 | + | fadE | Acyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 5,322,024 | 5,323,745 | + | acd | Acyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 214,606 | 213,830 | - | paaF1 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 2,316,794 | 2,317,570 | + | paaF2 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 4,223,702 | 4,224,484 | + | paaF3 | Enoyl-CoA hydratase | Beta-oxidation |
| pRWAY01 | 684,077 | 683,265 | - | paaF | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 329,086 | 329,886 | + | echA1 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 643,577 | 644,368 | + | echA2 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 757,482 | 758,312 | + | echA3 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 1,007,248 | 1,006,472 | - | echA4 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 1,040,430 | 1,039,588 | - | echA5 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 1,210,711 | 1,211,499 | + | echA6 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 1,499,315 | 1,500,052 | + | echA7 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 3,559,761 | 3,560,525 | + | echA8 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 3,707,957 | 3,707,211 | - | echA9 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 4,052,432 | 4,051,536 | - | echA10 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 4,058,281 | 4,059,081 | + | echA11 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 4,606,554 | 4,607,624 | + | echA12 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 5,321,009 | 5,320,134 | - | echA13 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 5,604,662 | 5,605,486 | + | echA14 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 6,076,178 | 6,076,957 | + | echA15 | Enoyl-CoA hydratase | Beta-oxidation |
| Chromosome 332,634 | 333,395 | + | hadH1 | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 399,565 | 398,741 | - | hadH2 | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 1,106,236 | 1,105,472 | - | hadH3 | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 2,037,476 | 2,038,243 | + | hadH4 | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,072,974 | 4,072,195 | - | hadH5 | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,239,395 | 4,240,159 | + | hadH6 | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 4,689,368 | 4,690,132 | + | hadH7 | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| pRWAY01 | 549,550 | 550,314 | + | hadH | 3-hydroxyacyl-CoA dehydrogenase | Beta-oxidation |
| Chromosome 603,355 | 604,569 | + | fadA1 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 920,511 | 921,659 | + | fadA2 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome | Gene 1 | Gene 2 | Direction | Function | Location |
|------------|--------|--------|-----------|----------|----------|
| Chromosome 1 | 1,127,499 | 1,128,644 | + | fadA3 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 1,340,403 | 1,341,620 | + | fadA4 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 1,370,895 | 1,372,112 | + | fadA5 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 2,047,844 | 2,049,061 | + | fadA6 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 3,621,192 | 3,622,406 | + | fadA7 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 4,036,231 | 4,037,307 | + | fadA8 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 4,061,756 | 4,063,015 | + | fadA9 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 4,238,230 | 4,239,363 | + | fadA10 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 4,580,184 | 4,581,530 | + | fadA11 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 4,688,118 | 4,689,248 | + | fadA12 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 5,092,662 | 5,091,493 | - | fadA13 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 5,362,086 | 5,360,869 | - | fadA14 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 6,374,989 | 6,373,781 | - | fadA15 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| pRWAY01 | 610,582 | 609,365 | - | fadA | Acetyl-CoA acetyltransferase | Beta-oxidation |
| pRWAY01 | 926,547 | 927,758 | + | fadA2 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| pRWAY02 | 393,598 | 392,452 | - | fadA | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 2,036,222 | 2,037,421 | + | atoB1 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 2,394,262 | 2,395,527 | + | atoB2 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 4,452,922 | 4,451,729 | - | atoB3 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 5,690,109 | 5,691,311 | + | atoB4 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| pRWAY02 | 182,627 | 181,434 | - | atoB1 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| pRWAY02 | 395,944 | 397,281 | + | atoB2 | Acetyl-CoA acetyltransferase | Beta-oxidation |
| Chromosome 1 | 6,115,406 | 6,117,001 | + | serA | D-3-phosphoglycerate dehydrogenase | Serine metabolism |
| Chromosome 1 | 1,741,809 | 1,740,832 | - | serB1 | Phosphoserine phosphatase | Serine metabolism |
| Chromosome 1 | 6,069,566 | 6,070,786 | + | serB2 | Phosphoserine phosphatase | Serine metabolism |
| Chromosome 1 | 1,456,832 | 1,455,711 | - | serC | Phosphoserine aminotransferase | Serine metabolism |
| Chromosome 1 | 665,396 | 666,661 | + | lysC | Aspartokinase | Threonine, methionine and lysine metabolism |
| Chromosome 1 | 666,665 | 667,696 | + | asd | Aspartate-semialdehyde dehydrogenase | Threonine, methionine and lysine metabolism |
| Chromosome 1 | 2,356,594 | 2,357,967 | + | hom | Homoserine dehydrogenase | Threonine and methionine metabolism |
| Chromosome 1 | 2,359,046 | 2,360,035 | + | thrB | Homoserine kinase | Threonine metabolism |
| Chromosome 1 | 2,357,964 | 2,359,046 | + | thrC | Threonine synthase | Threonine metabolism |
| Chromosome 1 | 1,765,222 | 1,766,331 | + | cysK1 | Cysteine synthase B | Cysteine metabolism |
| Chromosome 1 | 2,414,983 | 2,415,945 | + | cysK2 | Cysteine synthase B | Cysteine metabolism |
| Chromosome 1 | 5,363,353 | 5,364,738 | + | cbs | Cystathionine beta-synthase | Cysteine and methionine metabolism |
| Chromosome | Start | End | Strand | Gene | Function |
|------------|-------|-----|--------|------|----------|
| Chr 5      | 5,365,344 | 5,366,516 | +      | cth  | Cystathionine gamma-lyase |
| Chr 5      | 3,497,662 | 3,496,448 | -      | metK | S-adenosylmethionine synthetase |
| Chr 5      | 6,057,375 | 6,057,926 | +      | pfs  | S-adenosylhomocysteine nucleosidase |
| Chr 5      | 1,681,725 | 1,684,019 | +      | metE | 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase |
| Chr 5      | 3,006,977 | 3,010,546 | +      | metH | 5-methyltetrahydrofolate--homocysteine methyltransferase |
| Chr 3      | 3,497,662 | 3,496,448 | -      | metK | S-adenosylmethionine synthetase |
| Chr 3      | 5,947,902 | 5,949,386 | +      | achy | Adenosylhomocysteinase |
| Chr 3      | 552,431 | 551,289 | -      | cdm  | DNA (cytosine-5')-methyltransferase |
| Chr 6      | 6,111,821 | 6,113,629 | +      | ilvB | Acetolactate synthase large subunit |
| Chr 6      | 6,114,168 | 6,115,181 | +      | ilvC | Ketal-acid reductoisomerase |
| Chr 6      | 6,110,875 | 6,109,031 | -      | ilvD | Dihydroxy-acid dehydratase |
| Chr 6      | 2,152,655 | 2,153,575 | +      | ilvE1| Branched-chain amino acid aminotransferase |
| Chr 6      | 2,236,093 | 2,236,944 | +      | ilvE2| Branched-chain amino acid aminotransferase |
| Chr 6      | 2,714,338 | 2,715,441 | +      | ilvE3| Branched-chain amino acid aminotransferase |
| Chr 6      | 6,117,075 | 6,118,085 | +      | leub | 3-isopropylmalate dehydrogenase |
| Chr 6      | 196,085 | 197,446 | +      | leuC1| 3-isopropylmalate dehydratase large subunit |
| Chr 6      | 4,332,542 | 4,331,142 | -      | leuC2| 3-isopropylmalate dehydratase large subunit |
| Chr 6      | 6,123,892 | 6,125,313 | +      | leuC3| 3-isopropylmalate dehydratase large subunit |
| Chr 6      | 197,453 | 198,070 | +      | leuD1| 3-isopropylmalate dehydratase small subunit |
| Chr 6      | 4,331,105 | 4,330,509 | -      | leuD2| 3-isopropylmalate dehydratase small subunit |
| Chr 6      | 6,125,341 | 6,125,949 | +      | leuD3| 3-isopropylmalate dehydratase small subunit |
| Chr 5      | 629,417 | 627,609 | -      | leuA | 2-isopropylmalate synthase |
| Chr 5      | 1,660,395 | 1,661,798 | +      | lpd1 | Dihydrolipoamide dehydrogenase |
| Chr 5      | 2,026,644 | 2,025,241 | -      | lpd2 | Dihydrolipoamide dehydrogenase |
| Chr 5      | 3,670,350 | 3,668,971 | -      | lpd3 | Dihydrolipoamide dehydrogenase |
| Chromosome | Start | End | Gene(s) | Function(s) |
|------------|-------|-----|---------|-------------|
| 1          | 3,743,185 | 3,741,776 | lpd4 | Dihydrolipoamide dehydrogenase |
| 2          | 5,885,786 | 5,887,189 | lpdA | Dihydrolipoamide dehydrogenase |
| 3          | 3,709,536 | 3,710,474 | dapA1 | 4-hydroxy-tetrahydrodipicolinate synthase |
| 4          | 4,631,178 | 4,632,137 | dapA2 | 4-hydroxy-tetrahydrodipicolinate synthase |
| 4          | 4,806,191 | 4,805,298 | dapA3 | 4-hydroxy-tetrahydrodipicolinate synthase |
| 6          | 2,841,459 | 2,842,850 | dapA4 | 4-hydroxy-tetrahydrodipicolinate synthase |
| 6          | 2,845,943 | 2,847,701 | dapB | 4-hydroxy-tetrahydrodipicolinate reductase |
| 5          | 5,540,747 | 5,539,794 | dapD | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase |
| 2          | 2,916,585 | 2,917,784 | argD | Acetylornithine aminotransferase |
| 5          | 5,526,715 | 5,527,815 | dapC | N-succinyl-L,L-diaminopimelate aminotransferase alternative |
| 5          | 5,540,915 | 5,541,988 | dapE | N-succinyl-L,L-diaminopimelate desuccinylase |
| 6          | 6,288,450 | 6,289,319 | dapF | Diaminopimelate epimerase |
| 7          | 2,355,176 | 2,356,597 | lysA | Diaminopimelate decarboxylase |
| 7          | 2,914,424 | 2,915,665 | argI | N-acetylglutamate synthase |
| 8          | 2,915,662 | 2,916,588 | argB | Acetylglutamate kinase |
| 9          | 2,913,723 | 2,914,427 | argC | N-acetyl-gamma-glutaryl-phosphate reductase |
| 9          | 2,917,781 | 2,918,728 | argF | Ornithine carbamoyltransferase |
| 9          | 2,919,291 | 2,920,490 | argG | Argininosuccinate synthase |
| 9          | 2,920,493 | 2,921,911 | argH | Argininosuccinate lyase |
| 9          | 2,526,075 | 2,527,175 | proB | Glutamate 5-kinase |
| 9          | 2,537,372 | 2,538,649 | proA | Gamma-glutamyl phosphate reductase |
| 9          | 1,737,053 | 1,737,868 | proC | Pyrroline-5-carboxylate reductase |
| 9          | 3,013,375 | 3,014,226 | hisG | ATP phosphoribosyltransferase |
| 9          | 3,013,040 | 3,013,321 | hisE | Phosphoribosyl-ATP pyrophosphatase |
| 9          | 2,849,242 | 2,849,586 | hisI | Phosphoribosyl-AMP cyclohydrolase |
| 9          | 2,847,041 | 2,847,634 | hisA | Phosphoribosylformimino-5-aminomidazole carboxamide ribotide isomerase |
| 9          | 2,848,472 | 2,849,245 | hisF | Imidazole glycerol phosphate synthase cyclase subunit |
| 9          | 2,843,989 | 2,844,603 | hisB | Imidazoleglycerol-phosphate dehydratase |
| 9          | 2,842,850 | 2,843,992 | hisC | Histidinol-phosphate aminotransferase |
| 9          | 2,841,459 | 2,842,853 | hisD | Histidinol dehydrogenase |
| 9          | 1,643,543 | 1,645,090 | hutH | Histidine ammonia-lyase |
| 9          | 1,001,825 | 1,000,152 | hutU | Urocanate hydrolase |
| 9          | 1,000,142 | 998,937 | hutl | Imidazolonepropionase |
| Chromosome | Position | Function | Metabolism |
|------------|----------|----------|------------|
| Chromosome 998,940 - 997,987 | *hutG* | Formiminoglutamase | Histidine metabolism |
| Chromosome 2,854,221 + 2,855,030 | *trpC* | Indole-3-glycerol phosphate synthase | Tryptophan metabolism |
| Chromosome 2,734,500 + 2,735,603 | *trpD* | Anthranilate phosphoribosyltransferase | Tryptophan metabolism |
| Chromosome 2,851,829 + 2,853,427 | *trpE* | Anthranilate synthase, aminase component | Tryptophan metabolism |
| Chromosome 4,523,978 - 4,523,388 | *trpF* | Phosphoribosylanthranilate isomerase | Tryptophan metabolism |
| Chromosome 32,654 + 33,307 | *trpG* | Anthranilate synthase, amidotransferase component | Tryptophan metabolism |
| Chromosome 2,855,093 + 2,856,415 | *trpB* | Tryptophan synthase beta chain | Tryptophan metabolism |
| Chromosome 2,856,412 + 2,857,215 | *trpA* | Tryptophan synthase alpha chain | Tryptophan metabolism |
| Chromosome 5,117,800 - 5,117,504 | *csm* | Chorismate mutase I | Phenylalanine, tyrosine and tryptophan metabolism |
| Chromosome 430,018 + 430,935 | *pheA* | Prephenate dehydratase | Phenylalanine metabolism |
| Chromosome 5,006,667 - 5,005,414 | *aspC* | Aspartate aminotransferase | Phenylalanine, tyrosine and tryptophan metabolism |
| Chromosome 555,293 - 554,343 | *tyrA* | Prephenate dehydrogenase | Phenylalanine, tyrosine and tryptophan metabolism |
| Chromosome 541,975 - 540,899 | *tat1* | Tyrosine aminotransferase | Phenylalanine, tyrosine and tryptophan metabolism |
| Chromosome 4,430,232 - 4,429,150 | *tat2* | Tyrosine aminotransferase | Phenylalanine, tyrosine and tryptophan metabolism |
| Chromosome 1,753,343 - 1,754,551 | *hppD1* | 4-hydroxyphenylpyruvate dioxygenase | Tyrosine and phenylalanine metabolism |
| Chromosome 3,791,827 - 3,793,032 | *hppD2* | 4-hydroxyphenylpyruvate dioxygenase | Tyrosine and phenylalanine metabolism |
| Chromosome 2,083,970 + 2,084,818 | *kynA* | Tryptophan 2,3-dioxygenase | Tryptophan metabolism |
| Chromosome 2,084,815 - 2,086,050 | *kynU* | Kynureninase | Tryptophan metabolism |

**Central aromatic metabolism**

| Chromosome | Position | Function | Metabolism |
|------------|----------|----------|------------|
| Chromosome 2,500,526 - 2,499,885 | *pcaG* | Protocatechuate 3,4-dioxygenase alpha chain | Beta-ketoadipate |
| Chromosome 2,501,245 - 2,500,526 | *pcaH* | Protocatechuate 3,4-dioxygenase beta chain | Beta-ketoadipate |
| Chromosome 2,499,862 - 2,498,516 | *pcaB* | 3-carboxy-cis,cis-muconate cycloisomerase | Beta-ketoadipate |
| Chromosome 2,498,519 - 2,497,326 | *pcaC* | 4-carboxy-3-muconolactone decarboxylase | Beta-ketoadipate |
| Chromosome 345,521 | 346,303 | *pcaD1* | Beta-ketoadipate enol-lactone hydrolase | Beta-ketoadipate |
| Chromosome 1,067,030 - 1,067,833 | *pcaD2* | Beta-ketoadipate enol-lactone hydrolase | Beta-ketoadipate |
| Chromosome 2,501,245 - 2,500,526 | *pcaD3* | Beta-ketoadipate enol-lactone hydrolase | Beta-ketoadipate |
| Chromosome 3,693,989 - 3,694,861 | *pcaD4* | Beta-ketoadipate enol-lactone hydrolase | Beta-ketoadipate |
| Chromosome 6,450,972 | 6,450,100 | *pcaD5* | Beta-ketoadipate enol-lactone hydrolase | Beta-ketoadipate |
| Chromosome 2,214,986 + 2,215,750 | *pcaI* | Succinyl-CoA:3-ketoadic-coenzyme A transferase subunit A | Beta-ketoadipate |
| Chromosome | Start | Stop | Type | Description |
|------------|-------|------|------|-------------|
| Chromosome | 2,215,747 | 2,216,415 | + | pcaJ | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B |
| Chromosome | 4,154,203 | 4,155,045 | + | catA | Catechol 1,2-dioxygenase |
| Chromosome | 4,155,075 | 4,156,196 | + | catB | Muconate cycloisomerase |
| Chromosome | 4,156,212 | 4,156,493 | + | catC | Muconolactone isomerase |
| pRWAY01    | 74,049  | 74,930  | + | catE | Catechol 2,3-dioxygenase |
| pRWAY02    | 198,132 | 197,251 | - | catE | Catechol 2,3-dioxygenase |
| Chromosome | 121,449 | 122,234 | + | bphE1 | 2-keto-4-pentenoate hydratase |
| Chromosome | 881,759 | 882,544 | + | bphE2 | 2-keto-4-pentenoate hydratase |
| Chromosome | 3,892,276 | 3,891,557 | - | bphE3 | 2-keto-4-pentenoate hydratase |
| pRWAY01    | 42,998  | 43,816  | + | bphE | 2-keto-4-pentenoate hydratase |
| pRWAY02    | 191,841 | 192,785 | + | bphE | 2-keto-4-pentenoate hydratase |
| Chromosome | 123,186 | 124,244 | + | bphF1 | 4-hydroxy-2-oxovalerate aldolase |
| Chromosome | 883,464 | 884,492 | + | BphF2 | 4-hydroxy-2-oxovalerate aldolase |
| Chromosome | 3,890,592 | 3,889,582 | - | bphF3 | 4-hydroxy-2-oxovalerate aldolase |
| pRWAY01    | 44,802  | 45,821  | + | bphF1 | 4-hydroxy-2-oxovalerate aldolase |
| pRWAY01    | 66,000  | 65,809  | - | BphF2 | 4-hydroxy-2-oxovalerate aldolase |
| pRWAY01    | 66,562  | 66,059  | - | bphF3 | 4-hydroxy-2-oxovalerate aldolase |
| pRWAY02    | 193,768 | 194,787 | + | bphF | 4-hydroxy-2-oxovalerate aldolase |
| Chromosome | 122,246 | 123,148 | + | bphG1 | Acetaldehyde dehydrogenase |

**Beta-ketoadipate**

**Beta-ketoadipate, catechol ortho-cleavage**

**Beta-ketoadipate, catechol ortho-cleavage**

**Beta-ketoadipate, catechol ortho-cleavage**

**Beta-ketoadipate, catechol ortho-cleavage**

**2-hydroxypentadienoate metabolism**

**2-hydroxypentadienoate metabolism**

**2-hydroxypentadienoate metabolism**

**2-hydroxypentadienoate metabolism**

**2-hydroxypentadienoate metabolism**

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**2-hydroxypentadienoate metabolism**

**2-hydroxypentadienoate metabolism**

**2-hydroxypentadienoate metabolism**

**2-hydroxypentadienoate metabolism**
| Chromosome | Start Position | End Position | Description | Metabolism          |
|------------|----------------|--------------|-------------|---------------------|
| Chromosome | 882,556        | 883,458      | + bphG2     | Acetaldehyde        |
|            |                |              |             | dehydrogenase       |
|            |                |              |             | 2-hydroxypentadinoate metabolism |
| pRWAY01    | 43,822         | 44,805       | + bphG1     | Acetaldehyde        |
|            |                |              |             | dehydrogenase       |
|            |                |              |             | 2-hydroxypentadinoate metabolism |
| pRWAY01    | 66,900         | 66,571       | - bphG2     | Acetaldehyde        |
|            |                |              |             | dehydrogenase       |
|            |                |              |             | 2-hydroxypentadinoate metabolism |
| pRWAY02    | 192,791        | 193,771      | + bphG1     | Acetaldehyde        |
|            |                |              |             | dehydrogenase       |
|            |                |              |             | 2-hydroxypentadinoate metabolism |
| pRWAY02    | 205,797        | 206,407      | + bphG2     | Acetaldehyde        |
|            |                |              |             | dehydrogenase       |
|            |                |              |             | 2-hydroxypentadinoate metabolism |
| Chromosome | 4,144,636      | 4,143,254    | - benA      | Benzoate 1,2-dioxygenase alpha subunit |
|            |                |              |             | Benzoate metabolism |
| Chromosome | 4,143,239      | 4,142,730    | - benB      | Benzoate 1,2-dioxygenase beta subunit |
|            |                |              |             | Benzoate metabolism |
| Chromosome | 4,142,692      | 4,141,532    | - benC      | benzoate dioxygenase, ferredoxin reductase component |
|            |                |              |             | Benzoate metabolism |
| Chromosome | 4,141,535      | 4,140,741    | - benD      | 1,2-dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase |
|            |                |              |             | Benzoate metabolism |
| Chromosome | 4,623,722      | 4,622,622    | - gdoA1     | Gentisate 1,2-dioxygenase |
|            |                |              |             | Gentisate metabolism |
| Chromosome | 4,661,780      | 4,660,668    | - gdoA2     | Gentisate 1,2-dioxygenase |
|            |                |              |             | Gentisate metabolism |
| pRWAY01    | 73,562         | 74,041       | + gdoA      | Gentisate 1,2-dioxygenase |
|            |                |              |             | Gentisate metabolism |
| pRWAY02    | 198,619        | 198,140      | - gdoA      | Gentisate 1,2-dioxygenase |
|            |                |              |             | Gentisate metabolism |
| Chromosome | 4,219,043      | 4,220,242    | + hmgA      | Homogentisate 1,2-dioxygenase |
|            |                |              |             | Homogentisate        |
|            |                |              |             | metabolism          |
| Replicon | Start  | End    | Strand | Gene name | Predicted function | Cellular function          |
|----------|--------|--------|--------|-----------|--------------------|-----------------------------|
| pRWAY01  | 509,217| 507,868| -      | bphA1a    | Biphenyl dioxygenase, alpha subunit | Biphenyl/PCBs metabolism   |
| pRWAY01  | 507,833| 507,297| -      | bphA2a    | Biphenyl dioxygenase, alpha subunit | Biphenyl/PCBs metabolism   |
| pRWAY01  | 506,547| 506,209| -      | bphA3     | Biphenyl dioxygenase ferredoxin subunit | Biphenyl/PCBs metabolism   |
| pRWAY01  | 506,124| 504,889| -      | bphA4     | Ferredoxin reductase component of biphenyl dioxygenase | Biphenyl/PCBs metabolism   |
| pRWAY01  | 511,414| 510,599| -      | bphB2,3  | 2,3-dihydroxy-2,3-dihydro-biphenyl dehydrogenase | Biphenyl/PCBs metabolism   |
| pRWAY01  | 510,569| 509,682| -      | bphC2     | 2,3-dihydroxybiphenyl 1,2-dioxigenase | Biphenyl/PCBs metabolism   |
| pRWAY01  | 504,851| 503,994| -      | bphD2     | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase | Biphenyl/PCBs metabolism   |
| pRWAY01  | 503,862| 503,449| -      | bphD2     | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase | Biphenyl/PCBs metabolism   |
| pRWAY02  | 156,099| 157,481| +      | etbA1a    | Ethylbenzene dioxygenase, large subunit | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 157,504| 158,052| +      | etbA2a    | Ethylbenzene dioxygenase, small subunit | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 158,072| 158,989| +      | etbC1,2   | 1,2-dihydroxyethylbenzene dioxygenase | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 150,062| 150,874| +      | bphB2,3   | 2,3-dihydroxy-2,3-dihydro-biphenyl dehydrogenase | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 159,112| 159,969| +      | bphD2     | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 160,020| 160,823| +      | bphE2     | 2-oxo-hepta-3-ene-1,7-dioic acid hydrolase | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 160,835| 161,605| +      | bphF2     | 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 167,930| 169,312| +      | etbA1b    | Ethylbenzene dioxygenase, large subunit | Ethylbenzene/biphenyl/PCBs metabolism   |
| pRWAY02  | 169,335| 169,883| +      | etbA2b    | Ethylbenzene dioxygenase, small subunit | Ethylbenzene/biphenyl/PCBs metabolism   |
| accession | start | stop  | +/− | gene | description |
|-----------|-------|-------|-----|------|-------------|
| pRWAY02   | 169,913 | 170,278 | +   | ethA3 | ferredoxin   |
| pRWAY02   | 201,744 | 200,884 | −   | bphD  | 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase |
| pRWAY02   | 216,173 | 217,579 | +   | nahA1 | Naphthalene dioxygenase alpha subunit |
| pRWAY02   | 217,583 | 218,101 | +   | nahA2 | Naphthalene dioxygenase beta subunit |
| pRWAY02   | 218,115 | 218,387 | +   | nahC  | dihydrodiol dehydrogenase |
| pRWAY02   | 218,393 | 219,208 | +   | nahB  | cis-naphthalene dihydrodiol dehydrogenase |
| pRWAY02   | 15,833  | 15,171  | −   | tmoF  | Oxidoreductase FAD-binding domain-containing protein |
| pRWAY02   | 17,197  | 16,160  | −   | tmoE  | Toluene 4-monooxygenase, subunit |
| pRWAY02   | 17,495  | 17,199  | −   | tmoD  | Toluene 4-monooxygenase component |
| pRWAY02   | 17,882  | 17,514  | −   | tmoC  | Toluene 4-monooxygenase, subunit |
| pRWAY02   | 18,124  | 17,879  | −   | tmoB  | Toluene monoxygenase |
| Chromosome| 942,988 | 944,622 | +   | mnoX  | Methane monoxygenase component A alpha chain |
| Chromosome| 944,707 | 945,750 | +   | mnoY  | Methane monoxygenase component A beta chain |
| Chromosome| 945,801 | 946,907 | +   | mnoB  | Methane monoxygenase regulatory protein B |
| Chromosome| 946,904 | 947,245 | +   | mnoC  | Methane monoxygenase component C |
| pRWAY02   | 238,905 | 240,443 | +   | mmoX1 | Methane monoxygenase component A alpha chain |
| pRWAY02   | 240,443 | 241,534 | +   | mmoY1 | Methane monoxygenase component A beta chain |
| pRWAY02   | 241,531 | 241,848 | +   | mmoB1 | Methane monoxygenase regulatory protein B |
| pRWAY02   | 241,860 | 242,891 | +   | mmoC1 | Methane monoxygenase component C |
| pRWAY02   | 247,460 | 276,040 | +   | mmoX2 | Methane monoxygenase component A alpha chain |
| pRWAY02   | 276,239 | 277,456 | +   | mmoY2 | Methane monoxygenase component A beta chain |
| pRWAY02   | 277,859 | 277,996 | +   | mmoB2 | Methane monoxygenase regulatory protein B |
| pRWAY02   | 278,372 | 279,394 | +   | mmoC2 | Methane monoxygenase component C |
| pRWAY02   | 279,463 | 279,981 | +   | mmoZ  | Methane monoxygenase component A gamma chain |
| pRWAY02   | 318,630 | 317,356 | −   | pmoB  | Particulate methane monoxygenase B-subunit |
| pRWAY02   | 319,492 | 318,641 | −   | pmoA  | Particulate methane monoxygenase A-subunit |
| pRWAY02   | 320,498 | 319,981 | −   | pmoC  | Particulate methane monoxygenase C-subunit |
| Chromosome| 5,945,530 | 5,946,753 | +   | alkB  | Alkane 1-monooxygenase |
| Chromosome| 357,092 | 358,192 | +   | ladA1 | Long-chain alkane monoxygenase |
| Chromosome| 358,189 | 359,343 | +   | ladA2 | Long-chain alkane monoxygenase |
| Chromosome| 4,017,878 | 4,019,047 | +   | ladA3 | Long-chain alkane monoxygenase |

**Ethylbenzene/biphenyl/PCBs metabolism**
- Ethylbenzene/biphenyl/PCBs metabolism
- Naphthalene/biphenyl/PCBs metabolism
- Naphthalene/biphenyl/PCBs metabolism
- Naphthalene/biphenyl/PCBs metabolism

**Toluene metabolism**
- Toluene metabolism
- Toluene metabolism
- Toluene metabolism
- Toluene metabolism
- Toluene metabolism

**Methane metabolism**
- Methane metabolism
- Methane metabolism
- Methane metabolism
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- Methane metabolism

**Alkane degradation**
- Alkane degradation
- Alkane degradation
- Alkane degradation
- Alkane degradation
| Replicon | Start   | End     | Strand | Gene name | Predicted function | Function, pathway          |
|----------|---------|---------|--------|-----------|--------------------|---------------------------|
| Chromosome | 5,214,900 | 5,215,832 | +      | galU      | UTP–glucose-1-phosphate uridylyltransferase | Glycogen biosynthesis     |
| Chromosome | 5,552,557 | 5,553,753 | +      | glgC      | Glucose-1-phosphate adenylyltransferase | Glycogen biosynthesis     |
| Chromosome | 5,552,416 | 5,551,247 | -      | glgA      | Glycogen synthase, ADP-glucose transglucosylase | Glycogen biosynthesis     |
| Chromosome | 2,400,678 | 2,398,480 | -      | glgB      | 1,4-alpha-glucon (glycogen) branching enzyme | Glycogen biosynthesis     |
| Chromosome | 2,402,696 | 2,400,678 | -      | glgE      | Putative glucanase | Glycogen degradation     |
| Chromosome | 2,402,921 | 2,405,512 | +      | glgP      | Glycogen phosphorylase | Glycogen degradation     |
| Chromosome | 294,183  | 292,977  | -      | glgX      | Glycogen debranching enzyme | Glycogen degradation     |
| Chromosome | 6,039,652 | 6,041,283 | +      | pgm       | Phosphoglucomutase | Glycogen degradation     |
| Chromosome | 1,654,022 | 1,654,951 | +      | ppk1      | Polyphosphate kinase 2 | Polyphosphate metabolism |
| Chromosome | 1,691,319 | 1,690,459 | -      | ppk2      | Polyphosphate kinase 2 | Polyphosphate metabolism |
| Chromosome | 2,218,391 | 2,219,335 | +      | ppk3      | Polyphosphate kinase 2 | Polyphosphate metabolism |
| Chromosome | 6,130,051 | 6,127,847 | -      | ppk4      | Polyphosphate kinase | Polyphosphate metabolism |
| Chromosome | 1,732,260 | 1,733,129 | +      | ppx1      | Exopolysphatase | Polyphosphate metabolism |
| Chromosome | 5,347,847 | 5,348,791 | +      | ppx2      | Exopolysphatase | Polyphosphate metabolism |
| Chromosome | 2,268,854 | 2,270,167 | +      | aft1      | Wax ester synthase/acyl-CoA:diacylglycerol acyltransferase | Triacylglycerol biosynthesis |
| Chromosome | 3,330,846 | 3,329,479 | -      | aft2      | Triacylglycerol biosynthesis | Triacylglycerol biosynthesis |
| Chromosome | 3,534,989 | 3,536,398 | +      | aft3      | Triacylglycerol biosynthesis | Triacylglycerol biosynthesis |
| Chromosome | 3,537,839 | 3,536,439 | -      | aft4      | Triacylglycerol biosynthesis | Triacylglycerol biosynthesis |
| Chromosome | 4,910,843 | 4,909,449 | -      | aft5      | Triacylglycerol biosynthesis | Triacylglycerol biosynthesis |
| Chromosome | 5,960,187 | 5,961,608 | +      | aft6      | Triacylglycerol biosynthesis | Triacylglycerol biosynthesis |
| Chromosome | 6,377,931 | 6,376,519 | -      | aft7      | Triacylglycerol biosynthesis | Triacylglycerol biosynthesis |
| Chromosome | 223,037  | 224,734  | +      | phaC1     | Polyhydroxyalkanoic acid synthase | Polyhydroxyalkanoic acid synthase |
| Chromosome | 496,107  | 495,013  | -      | phaC2     | Polyhydroxyalkanoic acid synthase | Polyhydroxyalkanoic acid synthase |
| Chromosome | 498,367  | 496,676  | -      | phaC3     | Polyhydroxyalkanoic acid synthase | Polyhydroxyalkanoic acid synthase |
| Chromosome | Start | End | Gene | Function |
|------------|-------|-----|------|----------|
| 757,362    | 756,295 | -  | **phaC4** | Polyhydroxyalkanoic acid synthase |
| 2,922,022  | 2,925,006 | +  | **phaC5** | Polyhydroxyalkanoic acid synthase |
| 921,751    | 922,080 | +  | **hypA** | [NiFe] hydrogenase nickel incorporation protein |
| 922,086    | 922,853 | +  | **hypB** | [NiFe] hydrogenase nickel incorporation-associated protein |
| 923,004    | 925,046 | +  | **hyaA** | Uptake hydrogenase small subunit |
| 924,140    | 925,882 | +  | **hyaB** | Hydrogenase maturation protease |
| 987,965    | 988,351 | -  | **hypD2** | [NiFe] hydrogenase metallocenter assembly protein |
| 1,446,069  | 1,445,215 | -  | **coxM1** | Carbon monoxide dehydrogenase medium subunit |
| 3,078,335  | 3,077,442 | -  | **coxF** | Aerobic carbon monoxide dehydrogenase molybdENUM cofactor insertion protein |
| 3,083,474  | 3,082,332 | -  | **coxI** | Xanthine and CO dehydrogenases maturation factor |
| 794,324    | 794,956 | +  | **cynT** | Carbonic anhydrase |
| 4,365,422  | 4,367,500 | +  | **cynT** | Carbonic anhydrase |

**Lithoautotrophy**

| Chromosome | Start | End | Gene | Function |
|------------|-------|-----|------|----------|
| 921,751    | 922,080 | +  | **hypA** | Hydrogenase |
| 922,086    | 922,853 | +  | **hypB** | Hydrogenase |
| 923,004    | 925,046 | +  | **hyaA** | Hydrogenase |
| 924,140    | 925,882 | +  | **hyaB** | Hydrogenase |
| 987,965    | 988,351 | -  | **hypD2** | Hydrogenase |
| 1,446,069  | 1,445,215 | -  | **coxM1** | Carbon monoxide utilization |
| 3,078,335  | 3,077,442 | -  | **coxF** | Carbon monoxide utilization |
| 3,083,474  | 3,082,332 | -  | **coxI** | Carbon monoxide utilization |
| 794,324    | 794,956 | +  | **cynT** | Carbon dioxide |
| 4,365,422  | 4,367,500 | +  | **cynT** | Carbon dioxide |
| Chromosome  | Start (bp) | End (bp) | Description | Location |
|-------------|------------|----------|-------------|----------|
| Chromosome  | 6,032,559  | 6,032,065| +           | Carbonic anhydrase | Carbon dioxide |
| Chromosome  | 6,136,323  | 6,136,844| +           | Carbonic anhydrase | Carbon dioxide |
| pRWAY03     | 189,067    | 186,755  | -           | Carbonic anhydrase | Carbon dioxide |
| Chromosome  | 667,556    | 667,424  | -           | Carbonic anhydrase | Carbon dioxide |
| Chromosome  | 3,282,441  | 3,282,686| +           | Cold shock protein | Cold shock response |
| Chromosome  | 1,437,612  | 1,437,815| +           | Cold shock protein | Cold shock response |
| pRWAY01     | 220,873    | 221,223  | +           | Cold shock protein | Cold shock response |
| pRWAY01     | 828,313    | 828,909  | +           | Cold shock protein | Cold shock response |

**Cold shock response**

| Chromosome  | Start (bp) | End (bp) | Description | Location |
|-------------|------------|----------|-------------|----------|
| Chromosome  | 447,655    | 445,517  | +           | Cold shock protein | Cold shock response |
| Chromosome  | 715,068    | 715,271  | -           | Cold shock protein | Cold shock response |
| Chromosome  | 911,575    | 912,108  | -           | Cold shock protein | Cold shock response |
| Chromosome  | 1,433,797  | 1,434,207| -           | Cold shock protein | Cold shock response |
| Chromosome  | 285,091    | 285,345  | -           | Cold shock protein | Cold shock response |
| Chromosome  | 5,256,431  | 5,256,634| -           | Cold shock protein | Cold shock response |
| Chromosome  | 6,437,612  | 6,437,815| -           | Cold shock protein | Cold shock response |
| pRWAY01     | 220,873    | 221,223  | -           | Cold shock protein | Cold shock response |
| pRWAY01     | 828,313    | 828,909  | -           | Cold shock protein | Cold shock response |

**Compatible solutes**

| Chromosome  | Start (bp) | End (bp) | Description | Location |
|-------------|------------|----------|-------------|----------|
| Chromosome  | 78,433     | 81,045   | +           | Trehalose-6-phosphate phosphatase | Compatible solutes |
| Chromosome  | 820,735    | 818,291  | -           | Trehalose-6-phosphate phosphatase | Compatible solutes |
| Chromosome  | 932,586    | 930,382  | -           | Trehalose synthase | Compatible solutes |
| Chromosome  | 1,062,110  | 1,060,518| -           | Alpha,alpha-trehalose-phosphate synthase [UDP-forming] | Compatible solutes |
| Chromosome  | 1,192,837  | 1,194,078| +           | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| Chromosome  | 1,334,567  | 1,335,913| +           | Proline/betaine transporter | Compatible solutes |
| Chromosome  | 2,132,772  | 2,131,186| +           | Choline dehydrogenase | Compatible solutes |
| Chromosome  | 2,529,380  | 2,528,982| -           | L-ectoine synthase | Compatible solutes |
| Chromosome  | 2,530,677  | 2,529,400| -           | Diaminobutyrate- pyruvate aminotransferase | Compatible solutes |
| Chromosome  | 2,531,103  | 2,530,705| -           | L-2,4-diaminobutyric acid acetyltransferase | Compatible solutes |
| Chromosome  | 2,535,912  | 2,534,443| -           | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| Chromosome  | 2,697,119  | 2,696,127| -           | L-proline glycine betaine binding ABC transporter protein ProX / Osmotic adaptation | Compatible solutes |
| Chromosome  | 2,699,097  | 2,697,886| -           | L-proline glycine betaine ABC transport system, permease protein ProV | Compatible solutes |
| Chromosome  | 2,699,746  | 2,699,090| -           | Glycine betaine/carnitine/choline ABC transporter, permease protein | Compatible solutes |
| Chromosome  | 2,809,617  | 2,807,914| -           | Malto-oligosyltrehalose trehalohydrolase | Compatible solutes |
| Chromosome  | 2,816,988  | 2,814,601| -           | Malto-oligosyltrehalose synthase | Compatible solutes |
| Chromosome  | 3,318,110  | 3,316,680| -           | Alpha,alpha-trehalose-phosphate synthase [UDP-forming] | Compatible solutes |
| Chromosome  | 4,017,746  | 4,016,421| -           | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| Chromosome | pRWAY01 | pRWAY01 | pRWAY01 | pRWAY01 | pRWAY01 |
|------------|--------|--------|--------|--------|--------|
| 4,447,309  | 4,445,984 | -      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| 4,625,092  | 4,623,719 | -      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| 4,746,029  | 4,747,372 | +      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| 4,844,175  | 4,845,503 | +      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| 5,164,191  | 5,162,467 | -      | betT   | High-affinity choline uptake protein BetT  | Compatible solutes |
| 5,241,917  | 5,243,590 | +      | betT   | High-affinity choline uptake protein BetT  | Compatible solutes |
| 5,464,351  | 5,465,793 | +      | betB   | Beta aldehyde dehydrogenase              | Compatible solutes |
| 5,579,197  | 5,578,478 | -      | proZ   | Glycine betaine ABC transport system permease protein | Compatible solutes |
| 5,579,844  | 5,579,194 | -      | proW   | L-proline glycine betaine ABC transport system permease protein ProW | Compatible solutes |
| 5,581,006  | 5,579,849 | -      | proV   | L-proline glycine betaine ABC transport system permease protein ProV | Compatible solutes |
| 5,581,994  | 5,581,017 | -      | proX   | L-proline glycine betaine binding ABC transporter protein ProX | Compatible solutes |
| 5,582,253  | 5,583,119 | +      | lpqZ   | Substrate-binding region of ABC-type glycine betaine transport system | Compatible solutes |
| 5,624,334  | 5,626,169 | +      | treS   | Trehalose synthase                        | Compatible solutes |
| 5,670,137  | 5,671,612 | +      | betA   | Choline dehydrogenase                     | Compatible solutes |
| 6,310,486  | 6,311,850 | +      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| 147,880    | 149,148  | +      | ecb    | Diaminobutyrate-pyruvate aminotransferase  | Compatible solutes |
| 244,656    | 248,291  | +      |        | Trehalose-6-phosphate phosphatase          | Compatible solutes |
| 544,245    | 542,944  | -      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| 768,642    | 769,964  | +      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
| 797,450    | 798,835  | +      | proP   | L-Proline/Glycine betaine transporter ProP | Compatible solutes |
Table S8. Genetic islands (GIs) identified in *Rhodococcus* sp. WAY2

| Replicon | GI coordinates       | GI length (bp) | GC%  | Prediction method | Gene start | Gene end | Strand | Product                                                                 |
|----------|----------------------|----------------|------|-------------------|------------|----------|--------|-------------------------------------------------------------------------|
| Chromosome | 72,878 .. 77,309      | 4,431          | 66.49| SIGI-HMM         | 72,878     | 73,279   | -      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 73,582     | 73,635   | -      | Biotin carboxylase of acetyl-CoA carboxylase                           |
|          |                      |                |      |                   | 75,391     | 75,690   | -      | Hypothetical protein                                                   |
| Chromosome | 149,687 .. 154,102    | 4,415          | 58.44| SIGI-HMM         | 148,428    | 149,690  | +      | Methylmalonate-semialdehyde dehydrogenase                             |
|          |                      |                |      |                   | 150,330    | 151,199  | +      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 152,189    | 152,311  | -      | 3-oxoacyl-[acyl-carrier protein] reductase                              |
| Chromosome | 778,268 .. 785,448    | 7,180          | 64.15| IslandPath-DIMOB  | 778,268    | 778,801  | +      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 779,291    | 780,802  | +      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 780,942    | 781,295  | +      | Histone protein Lsr2                                                   |
|          |                      |                |      |                   | 782,088    | 782,339  | -      | Hypothetical protein                                                   |
| Chromosome | 1,333,138 .. 1,350,980 | 17,842        | 64.01| IslandPath-DIMOB  | 1,333,138  | 1,334,163| +      | Predicted aminoglycoside phosphotransferase                           |
|          |                      |                |      |                   | 1,334,372  | 1,334,491| -      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 1,334,567  | 1,335,913| +      | Proline/betaine transporter                                           |
|          |                      |                |      |                   | 1,336,229  | 1,336,360| +      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 1,336,507  | 1,337,889| +      | Membrane transport protein                                             |
|          |                      |                |      |                   | 1,337,991  | 1,338,803| -      | Transcriptional regulator, TetR family                                |
|          |                      |                |      |                   | 1,339,617  | 1,340,255| -      | Transcriptional regulator, MerR family                                |
|          |                      |                |      |                   | 1,340,403  | 1,341,620| +      | 3-ketoacyl-CoA thiolase                                                |
| Chromosome | 1,341,641 .. 1,342,372 | 17,842        | 64.01| IslandPath-DIMOB  | 1,341,641  | 1,342,372| +      | 3-oxoacyl-[acyl-carrier protein] reductase                             |
|          |                      |                |      |                   | 1,342,404  | 1,344,200| +      | 3-methylmercaptopropionyl-CoA dehydrogenase (DmdC)                     |
|          |                      |                |      |                   | 1,344,216  | 1,344,977| +      | 3-oxoacyl-[acyl-carrier protein] reductase                             |
|          |                      |                |      |                   | 1,345,058  | 1,346,808| -      | Mobile element protein                                                 |
|          |                      |                |      |                   | 1,347,469  | 1,347,636| -      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 1,347,667  | 1,347,903| +      | Nodulation protein N                                                   |
|          |                      |                |      |                   | 1,348,043  | 1,348,180| +      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 1,348,486  | 1,348,623| +      | Hypothetical protein                                                   |
|          |                      |                |      |                   | 1,349,154  | 1,349,453| -      | Hypothetical protein                                                   |
| Chromosome | Start/End | Length | Coverage | Description |
|------------|-----------|--------|----------|-------------|
| Chromosome | 1,349,434 .. 1,349,562 | + | Hypothetical protein |
| Chromosome | 1,349,578 .. 1,349,712 | + | Hypothetical protein |
| Chromosome | 1,349,835 .. 1,350,980 | - | Butyryl-CoA dehydrogenase |
| Chromosome | 1,564,659 .. 1,566,191 | + | Peptide synthetase |
| Chromosome | 1,566,351 .. 1,575,512 | + | Peptide synthetase |
| Chromosome | 1,575,544 .. 1,580,037 | + | Polyketide synthase |
| Chromosome | 1,580,034 .. 1,580,876 | - | 3-hydroxybutyryl-CoA dehydrogenase |
| Chromosome | 1,580,911 .. 1,592,397 | + | Non-ribosomal peptide synthetase |
| Chromosome | 1,592,460 .. 1,593,419 | - | Probable 85 complex protein, A85 antigen family |
| Chromosome | 1,593,511 .. 1,593,852 | + | Possible inner membrane protein |
| Chromosome | 1,593,908 .. 1,594,915 | + | F420-dependent glucose-6-phosphate dehydrogenase |
| Chromosome | 1,596,412 .. 1,597,326 | - | Hypothetical protein |
| Chromosome | 1,885,277 .. 1,885,531 | - | Hypothetical protein |
| Chromosome | 1,885,667 .. 1,886,146 | - | Cytosine deaminase |
| Chromosome | 1,886,150 .. 1,886,959 | - | Transcriptional regulator, TetR family |
| Chromosome | 1,887,132 .. 1,888,481 | + | Hypothetical protein |
| Chromosome | 1,888,478 .. 1,889,092 | + | Putative secreted protein |
| Chromosome | 1,889,155 .. 1,889,643 | - | Conserved Hypothetical protein SCF43.06 |
| Chromosome | 1,889,801 .. 1,890,250 | - | Hypothetical protein |
| Chromosome | 1,890,300 .. 1,890,455 | + | Hypothetical protein |
| Chromosome | 1,890,553 .. 1,891,770 | + | Hypothetical protein |
| Chromosome | 1,891,799 .. 1,892,092 | - | Sporulation regulatory protein WhiD |
| Chromosome | 1,892,476 .. 1,893,723 | + | Alpha/beta hydrolase fold-containing protein |
| Chromosome | 1,893,979 .. 1,895,632 | - | 3-methylmercaptopropionyl-CoA dehydrogenase (DmdC) |
| Chromosome | 1,895,992 .. 1,897,689 | + | Putative cholesterol oxidase |
| Chromosome | 1,898,199 .. 1,897,961 | + | Hypothetical protein |
| Chromosome | 1,899,581 .. 1,900,590 | - | Possible electron transfer protein FdxB |
| Chromosome | 1,900,680 .. 1,901,419 | - | Hypothetical protein |
| Chromosome | 1,901,495 .. 1,901,707 | + | Hypothetical protein |
| Chromosome | 1,901,731 .. 1,902,981 | + | Hypothetical protein |
| Chromosome | 1,902,319 .. 1,904,961 | + | Acyl-CoA dehydrogenase |
| Chromosome | 1,904,998 .. 1,905,117 | - | Hypothetical protein |
| Chromosome | 1,905,118 .. 1,905,510 | + | Aldo-keto reductase 3B6 family |
| Chromosome | 1,905,691 .. 1,906,116 | + | Putative membrane protein |
| Chromosome | 1,906,549 .. 1,907,031 | + | Transcriptional regulator, AraC family |
| Chromosome | 1,907,612 .. 1,907,746 | - | Hypothetical protein |
| Chromosome | 1,907,817 .. 1,908,080 | + | Hypothetical protein |

**Chromosome 1,564,659 .. 1,597,326**

- **IslandPath-DIMOB**
- **32,667**
- **68.15**

**Chromosome 1,885,277 .. 1,908,080**

- **IslandPath-DIMOB**
- **22,803**
- **64.04**

**Chromosome 2,188,167 .. 2,195,802**

- **SIGI-HMM**
- **7,635**
- **59.57**

- **2,188,167 .. 2,188,541**
  - **CoA-binding domain protein**

- **2,190,033 .. 2,190,998**
  - **Putative membrane protein**

- **2,190,998 .. 2,192,689**
  - **ATP/GTP binding protein**
| Chromosome | IslandPath-DIMOB | IslandPath-DIMOB, SIGI-HMM | IslandPath-DIMOB, SIGI-HMM |
|------------|-----------------|---------------------------|---------------------------|
| 2,906,194  | 2,906,194       | 2,906,194                 | 2,906,194                 |
| 2,193,626  | 2,193,895       | 2,193,895                 | 2,193,895                 |
| 2,194,342  | 2,195,802       | 2,195,802                 | 2,195,802                 |
| 2,906,194  | 2,906,610       | 2,906,610                 | 2,906,610                 |
| 2,906,701  | 2,906,826       | 2,906,826                 | 2,906,826                 |
| 2,907,064  | 2,907,597       | 2,907,597                 | 2,907,597                 |
| 2,907,657  | 2,907,851       | 2,907,851                 | 2,907,851                 |
| 2,907,916  | 2,908,305       | 2,908,305                 | 2,908,305                 |
| 2,908,344  | 2,909,153       | 2,909,153                 | 2,909,153                 |
| 2,909,234  | 2,910,316       | 2,910,316                 | 2,910,316                 |
| 2,906,194  | 2,906,610       | 2,906,610                 | 2,906,610                 |
| 2,193,626  | 2,193,895       | 2,193,895                 | 2,193,895                 |
| 2,194,342  | 2,195,802       | 2,195,802                 | 2,195,802                 |
| 2,906,194  | 2,906,610       | 2,906,610                 | 2,906,610                 |
| 2,906,701  | 2,906,826       | 2,906,826                 | 2,906,826                 |
| 2,907,064  | 2,907,597       | 2,907,597                 | 2,907,597                 |
| 2,907,657  | 2,907,851       | 2,907,851                 | 2,907,851                 |
| 2,907,916  | 2,908,305       | 2,908,305                 | 2,908,305                 |
| 2,908,344  | 2,909,153       | 2,909,153                 | 2,909,153                 |
| 2,909,234  | 2,910,316       | 2,910,316                 | 2,910,316                 |
| 2,906,194  | 2,906,610       | 2,906,610                 | 2,906,610                 |
| 2,193,626  | 2,193,895       | 2,193,895                 | 2,193,895                 |
| 2,194,342  | 2,195,802       | 2,195,802                 | 2,195,802                 |
| 2,906,194  | 2,906,610       | 2,906,610                 | 2,906,610                 |
| 2,906,701  | 2,906,826       | 2,906,826                 | 2,906,826                 |
| 2,907,064  | 2,907,597       | 2,907,597                 | 2,907,597                 |
| 2,907,657  | 2,907,851       | 2,907,851                 | 2,907,851                 |
| 2,907,916  | 2,908,305       | 2,908,305                 | 2,908,305                 |
| 2,908,344  | 2,909,153       | 2,909,153                 | 2,909,153                 |
| 2,909,234  | 2,910,316       | 2,910,316                 | 2,910,316                 |
| 2,907,288  | 3,157,683       | 3,157,683                 | 3,157,683                 |
| Chromosome | 3,157,288 .. 3,200,524 | 43,237 | 62.75 |
| Chromosome | 3,189,027 | 3,190,211 | - | Butyryl-CoA dehydrogenase |
| 3,190,213 | 3,191,055 | - | Enoyl-CoA hydratase |
| 3,191,598 | 3,192,848 | + | Possible transcriptional regulator |
| 3,193,250 | 3,193,591 | + | Hypothetical protein |
| 3,193,836 | 3,194,327 | + | Hypothetical protein |
| 3,194,740 | 3,195,585 | + | Alcohol dehydrogenase |
| 3,195,638 | 3,196,075 | + | Hypothetical protein |
| 3,196,122 | 3,196,328 | + | Hypothetical protein |
| 3,198,018 | 3,199,058 | + | Oxetanocin A resistance protein |
| 3,199,167 | 3,199,628 | - | Alcohol dehydrogenase |
| 3,199,829 | 3,200,524 | + | Transcriptional regulator, MerR family |

| Chromosome | 4,251,782 | 4,252,654 | + | 3-oxoacyl-[acyl-carrier protein] reductase |
| 4,252,669 | 4,252,902 | + | Probable ferredoxin FdxD |
| 4,252,909 | 4,254,138 | + | Putative cytochrome P450 hydroxylase |
| 4,254,334 | 4,254,912 | + | Transcriptional regulator, TetR family |
| 4,255,378 | 4,256,436 | + | Methionine ABC transporter ATP-binding protein |
| 4,256,514 | 4,257,326 | + | Conserved hypothetical integral membrane protein YrbE1A |
| 4,257,328 | 4,258,188 | + | ABC-type transport system involved in resistance to organic solvents, permease component |
| 4,258,250 | 4,259,291 | + | Mammalian cell entry related domain protein |
| 4,259,299 | 4,260,291 | + | MCE-family protein Mce1B |
| 4,260,324 | 4,261,304 | + | Virulence factor mce family protein |
| 4,261,306 | 4,262,337 | + | MCE-family protein Mce1D |
| 4,262,339 | 4,263,346 | + | Possible mce-family lipoprotein lprl |
| 4,263,434 | 4,264,302 | + | Putative Mce family protein |

| Chromosome | 3,189,027 | 3,190,211 | - | Butyryl-CoA dehydrogenase |
| Chromosome | 4,685,575 | 4,719,883 | - | Enoyl-CoA hydratase |
| Chromosome | 4,687,262 | 4,688,017 | + | 2-deoxy-D-glucose 3-dehydrogenase |
| Chromosome | 4,688,118 | 4,689,248 | + | 3-ketoacyl-CoA thiolase |
| Chromosome | 4,689,368 | 4,690,132 | + | 3-hydroxyacyl-CoA dehydrogenase |
| Chromosome | 4,690,129 | 4,690,257 | - | Hypothetical protein |
| Chromosome | Start .. End | Length | SIGI | Chromosome Function |
|------------|--------------|--------|------|---------------------|
| 4,795,058 .. 4,799,299 | 4,241 | 66.71 | Transposase |
| 4,795,058 | 4,796,110 | - | Probable taurine catabolism dioxygenase |
| 4,795,159 | 4,797,073 | - | Quinone oxidoreductase |
| 4,797,112 | 4,798,086 | - | Transcriptional regulator, AraC family |
| 4,798,289 | 4,799,299 | + | Hypothetical protein |

| Chromosome | Start .. End | Length | SIGI | Chromosome Function |
|------------|--------------|--------|------|---------------------|
| 4,868,035 .. 4,902,842 | 34,807 | 66.45 | IslandPath-DIMOB |
| 4,868,035 | 4,868,562 | - | Putative small integral membrane protein |
| 4,868,603 | 4,871,473 | - | High-affinity carbon uptake protein Hat/HatR |
| 4,871,472 | 4,871,618 | + | Hypothetical protein |
| 4,871,688 | 4,871,843 | - | Fic protein family protein |
| 4,872,371 | 4,873,846 | + | Putative membrane transport protein |
| 4,873,855 | 4,874,487 | + | Transcriptional regulator, TetR family |
| 4,874,624 | 4,875,523 | + | Probable hydrolase |
| 4,875,770 | 4,876,969 | - | Hypothetical protein |
| 4,877,143 | 4,877,892 | + | Hypothetical protein |
| 4,877,933 | 4,880,113 | - | Arsenical pump-driving ATPase |
| Gene              | Chromosome          | Length | %identity | Description                                           |
|-------------------|---------------------|--------|-----------|-------------------------------------------------------|
| Arsenate reductase| 4,880,134 - 4,880,535 | -      | -         | Arsenate reductase                                    |
| Arsenate reductase| 4,880,566 - 4,880,958 | -      | -         | Arsenate reductase                                    |
| Arsenate reductase| 4,881,006 - 4,882,118 | -      | -         | Arsenate reductase                                    |
| Arsenate reductase| 4,882,115 - 4,882,474 | +      | Transcriptional regulator, ArsR family               |
| Arsenate reductase| 4,882,593 - 4,882,937 | +      | Putative membrane protein                            |
| Arsenate reductase| 4,883,707 - 4,884,702 | -      | Arsenaic-resistance protein ACR3                     |
| Arsenate reductase| 4,884,801 - 4,885,550 | -      | Mercuric resistance operon regulatory protein        |
| Arsenate reductase| 4,885,653 - 4,886,507 | -      | Possible phosphinothricin N-acetyltransferase        |
| Arsenate reductase| 4,886,759 - 4,887,949 | +      | Probable secreted protein                            |
| Arsenate reductase| 4,887,179 - 4,888,316 | +      | Hypothetical protein                                 |
| Arsenate reductase| 4,888,487 - 4,889,416 | +      | ABC transporter, ATP-binding component               |
| Arsenate reductase| 4,889,413 - 4,890,225 | +      | ABC transporter, family 2                             |
| Arsenate reductase| 4,890,424 - 4,890,633 | +      | Hypothetical protein                                 |
| Arsenate reductase| 4,890,674 - 4,891,333 | +      | RNA polymerase sigma factor SigZ                      |
| Arsenate reductase| 4,891,523 - 4,891,636 | +      | Hypothetical protein                                 |
| Arsenate reductase| 4,891,720 - 4,891,833 | -      | Hypothetical protein                                 |
| Arsenate reductase| 4,892,075 - 4,892,293 | +      | Hypothetical protein                                 |
| Arsenate reductase| 4,892,372 - 4,893,517 | -      | Chaperone protein DnaJ                                |
| Arsenate reductase| 4,893,524 - 4,893,682 | -      | Hypothetical protein                                 |
| Arsenate reductase| 4,894,633 - 4,894,806 | +      | Hypothetical protein                                 |
| Arsenate reductase| 4,894,877 - 4,896,373 | +      | Adenylate cyclase                                    |
| Arsenate reductase| 4,896,494 - 4,897,702 | -      | Possible linoleoyl-coa desaturase (delta(6)-desaturase) |
| Arsenate reductase| 4,897,870 - 4,898,676 | -      | Metal cation transporting ATPase, P-type ATPase          |
| Arsenate reductase| 4,898,670 - 4,899,122 | -      | Metal cation transporting ATPase, P-type ATPase          |
| Arsenate reductase| 4,899,810 - 4,901,615 | +      | Mobile element protein                                |
| Arsenate reductase| 4,901,793 - 4,902,122 | -      | Hypothetical protein                                 |
| Arsenate reductase| 4,902,213 - 4,902,842 | -      | DNA-binding response regulator KdpE                    |
| Chromosome        | 4,947,132 - 4,965,372 | 18,240 | 57.42     | IslandPath-DIMOB                                      |
| Chromosome        | 6,267,813 - 6,289,319 | 21,506 | 66.17     | IslandPath-DIMOB                                      |
|    | 6,268,539 | 6,269,117 | + | CDP-diacylglycerol–glycerol-3-phosphate 3-phosphatidyltransferase |
|    | 6,269,114 | 6,269,614 | + | C-terminal domain of CinA type S |
|    | 6,269,685 | 6,270,047 | + | Hypothetical protein |
|    | 6,270,239 | 6,271,024 | + | Phage shock protein A (IM30), suppresses sigma54-dependent transcription |
|    | 6,271,125 | 6,271,871 | + | Alanine-rich, phage-related, membrane protein |
|    | 6,272,063 | 6,272,251 | + | Hypothetical protein |
|    | 6,272,268 | 6,272,984 | + | Hypothetical protein |
|    | 6,273,020 | 6,273,166 | + | Hypothetical protein |
|    | 6,273,198 | 6,273,821 | + | Probable transcriptional regulator, TetR family |
|    | 6,273,818 | 6,275,371 | + | Glycerol-3-phosphate dehydrogenase |
|    | 6,275,371 | 6,276,525 | + | Alanine rich transferase |
|    | 6,276,561 | 6,276,755 | + | Hypothetical protein |
|    | 6,277,018 | 6,277,551 | - | Glutamate permease |
|    | 6,278,072 | 6,278,587 | + | Putative glutamate transporter |
|    | 6,279,548 | 6,280,228 | - | Glutamate-binding protein of ABC transporter system |
|    | 6,280,317 | 6,281,150 | - | Putative glutamate uptake system ATP-binding protein |
|    | 6,281,239 | 6,281,967 | + | rRNA-(i6)A37 methylthiotransferase |
|    | 6,282,176 | 6,283,693 | + | Possible membrane protein Rv2732c |
|    | 6,283,690 | 6,284,295 | + | Possible membrane protein |
|    | 6,284,314 | 6,285,726 | - | ATPase involved in DNA repair |
|    | 6,285,893 | 6,286,618 | + | Hypothetical protein |
|    | 6,286,615 | 6,287,544 | + | Hypothetical protein |
|    | 6,287,541 | 6,288,389 | + | Diaminopimelate epimerase |
|    | 6,288,450 | 6,289,319 | + | Hypothetical protein |

Chromosome 6,568,016 .. 6,574,590 6,574 65.48 IslandPath-DIMOB

|    | 6,568,016 | 6,568,684 | + | Probable oxidoreductase, short chain dehydrogenase/reductase family |
|    | 6,568,857 | 6,569,198 | + | Hypothetical protein |
|    | 6,569,202 | 6,569,852 | - | Maleylpyruvate isomerase, mycothiol-dependent |
|    | 6,570,023 | 6,570,580 | + | TolA protein |
|    | 6,570,609 | 6,571,286 | + | TolA protein |
|    | 6,571,283 | 6,571,426 | - | Transposase and inactivated derivatives-like |
|    | 6,571,498 | 6,572,100 | - | Transcriptional regulator, TetR family |
|    | 6,572,376 | 6,573,608 | + | Beta-lactamase class C and other penicillin binding proteins |
|    | 6,573,610 | 6,574,590 | - | Hypothetical protein |

pRWAY01 267,189 .. 276,334 9,145 58.12 IslandPath-DIMOB, SIGI-HMM

|    | 267,189 | 267,866 | + | Phosphoserine phosphatase |
|    | 268,257 | 268,550 | + | Hypothetical protein |
|    | 268,695 | 269,087 | + | Hypothetical protein |
|    | 269,220 | 269,606 | + | Hypothetical protein |
|    | 269,690 | 270,148 | + | Hypothetical protein |
| Gene ID  | Start (bps) | End (bps) | % Identity | Description |
|---------|-------------|-----------|------------|-------------|
| 270,253 | 271,698     | +         | Nicotinamide phosphoribosyltransferase |
| 271,814 | 271,936     | -         | Hypothetical protein |
| 272,619 | 272,741     | +         | Transposase, mutator type |
| 272,982 | 273,337     | -         | Coenzyme F420-0:1-glutamate ligase |
| 274,586 | 275,521     | -         | 2-phospho-L-lactate guanylyltransferase |
| 275,534 | 276,334     | -         | 6-phosphogluconolactonase |
| 276,331 | 278,802     | -         | 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase subunit 1 |
| 344,870 | 345,668     | -         | ABC-type Fe3+-siderophore transport system, ATPase component |
| 345,712 | 346,824     | -         | ABC-type Fe3+-siderophore transport system, permease 2 component |
| 346,821 | 347,852     | -         | ABC-type Fe3+-siderophore transport system, permease component |
| 348,026 | 348,595     | -         | Possible transcriptional regulator |
| 348,850 | 349,008     | +         | Hypothetical protein |
| 349,011 | 349,529     | +         | Hypothetical protein |
| 349,559 | 350,980     | -         | Phage peptidoglycan binding endopeptidase |
| 351,144 | 351,590     | -         | Cytochrome c-type biogenesis protein CcdA |
| 351,947 | 352,552     | -         | Thiolsulfide oxidoreductase related to ResA |
| 352,549 | 353,154     | -         | Possible thioredoxin |
| 353,189 | 353,401     | +         | Hypothetical protein |
| 353,515 | 353,895     | +         | Transcriptional regulator, MecI family |
| 353,892 | 354,854     | +         | Peptidase M48, Ste24p precursor |
| 354,970 | 355,359     | +         | Hypothetical protein |
| 355,466 | 356,578     | +         | Cysteine synthase |
| 356,578 | 357,867     | +         | Probable conserved integral membrane transport protein |
| 357,994 | 359,541     | +         | Multicopper oxidase |
| 359,640 | 360,458     | +         | Hypothetical protein |
| 360,465 | 362,405     | +         | Copper resistance protein CopC / Copper resistance protein CopD |
| 362,530 | 362,979     | +         | Hypothetical protein |
| 363,075 | 363,752     | +         | Putative lipoprotein |
| 363,874 | 365,109     | +         | Probable conserved lipoprotein LppS |
| 365,106 | 365,930     | +         | DedA family protein paralog |
| 381,580 | 381,696     | +         | Hypothetical protein |
| 382,075 | 382,455     | +         | Hypothetical protein |
| 382,602 | 382,748     | +         | Hypothetical protein |
| 382,849 | 383,562     | +         | Plasmid partitioning protein ParA |
| 383,562 | 384,428     | +         | Chromosome (plasmid) partitioning protein ParB |
| 384,807 | 385,478     | +         | Mobile element protein |
| Protein Description                                      | Start | End   |
|----------------------------------------------------------|-------|-------|
| Hypothetical protein                                     | 385,552 | 385,695 |
| Hypothetical protein                                     | 385,709 | 386,551 |
| Pentapeptide repeat family protein                       | 386,981 | 387,541 |
| Hypothetical protein                                     | 388,042 | 388,308 |
| Hypothetical protein                                     | 388,376 | 388,489 |
| Hypothetical protein                                     | 388,492 | 389,076 |
| Phage excisionase                                        | 389,492 | 390,688 |
| Hypothetical protein                                     | 390,894 | 391,049 |
| Chromosome (plasmid) partitioning protein ParA           | 391,340 | 392,128 |
| Hypothetical protein                                     | 392,467 | 392,634 |
| Metallo-beta-lactamase superfamily protein               | 393,021 | 393,881 |
| Hypothetical protein                                     | 393,878 | 395,797 |
| Hypothetical protein                                     | 395,956 | 396,084 |
| O-Methyltransferase involved in polyketide biosynthesis  | 396,344 | 397,195 |
| Hypothetical protein                                     | 397,173 | 398,156 |
| CinorF13 protein                                          | 398,153 | 398,713 |
| Hypothetical protein                                     | 399,169 | 399,369 |
| Type II restriction enzyme, methylase subunit YeeA       | 453,960 | 454,526 |
| Resolvasen                                               | 455,205 | 455,396 |
| Hypothetical protein                                     | 456,542 | 456,727 |
| Hypothetical protein                                     | 456,782 | 457,060 |
| Hypothetical protein                                     | 457,292 | 460,009 |
| DNA helicase, restriction/modification system component   | 460,006 | 461,991 |
| YeeC-like protein                                         | 461,988 | 463,181 |
| Hypothetical protein                                     | 464,971 | 465,741 |
| Hypothetical protein                                     | 466,199 | 466,459 |
| Hypothetical protein                                     | 466,554 | 466,850 |
| Organomercurial lyase                                    | 483,867 | 484,511 |
| Regulatory protein, MerR                                 | 484,583 | 485,026 |
| Mercuric ion reductase                                   | 485,045 | 486,484 |
| Mercuric resistance operon regulatory protein             | 486,613 | 487,002 |
| Cytochrome c-type biogenesis protein DsbD, protein-       | 487,002 | 487,301 |
| Disulfide reductase                                       | 487,298 | 487,804 |
| Hypothetical protein                                     | 487,801 | 488,697 |
| Cytochrome c biogenesis protein, transmembrane region    | 488,694 | 490,073 |
| PP00070 family, FAD-dependent NAD(P)-disulphide oxidoreductase | 490,191 | 491,147 |
| Putative integrase/recombinase                           | 657,119 | 658,012 |
| Short-chain dehydrogenase/reductase SDR                  | 657,119 | 692,928 |
| Start | End   | Description                                                                 |
|-------|-------|----------------------------------------------------------------------------|
| 658,125 | 658,274 | Hypothetical protein                                                        |
| 658,285 | 658,521 | Probable transposase for insertion sequence element IS1533                  |
| 658,804 | 659,511 | Alcohol dehydrogenase                                                        |
| 659,566 | 659,949 | Hypothetical protein                                                        |
| 660,118  | 661,729 | Amidohydrolase                                                              |
| 661,828  | 661,950 | Hypothetical protein                                                        |
| 662,129  | 662,680 | Dipeptide-binding ABC transporter, periplasmic substrate-binding component   |
| 662,741  | 663,601 | Sugar phosphate isomerases/epimerases                                        |
| 664,194  | 664,494 | Membrane transport protein                                                  |
| 666,509  | 666,877 | Hypothetical protein                                                        |
| 666,926  | 668,413 | Aldehyde dehydrogenase                                                      |
| 668,477  | 668,596 | Hypothetical protein                                                        |
| 668,693  | 669,088 | Hypothetical protein                                                        |
| 669,220  | 670,850 | Hypothetical protein                                                        |
| 671,037  | 672,185 | Amidohydrolase 2                                                            |
| 672,381  | 673,577 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16)                                       |
| 673,649  | 674,155 | Transcriptional regulator, MarR family                                       |
| 674,225  | 675,340 | Oligopeptide transport ATP-binding protein OppF                              |
| 675,337  | 676,374 | Oligopeptide transport system permease protein OppB                         |
| 676,377  | 677,198 | Dipeptide transport system permease protein DppC                            |
| 677,267  | 678,217 | Dipeptide transport system permease protein DppB                            |
| 678,287  | 679,502 | Hypothetical protein                                                        |
| 678,383  | 679,383 | Oxidoreductase, short-chain dehydrogenase/reductase family                   |
| 679,440  | 680,282 | Enoyl-CoA hydratase                                                         |
| 680,279  | 681,250 | Aminopeptidase                                                              |
| 681,345  | 682,325 | Vanillate O-demethylase oxidoreductase                                       |
| 682,443  | 683,219 | 3-oxoacyl-[acyl-carrier protein] reductase                                   |
| 683,265  | 684,077 | Enoyl-CoA hydratase                                                         |
| 684,197  | 684,610 | Mobile element protein                                                       |
| 684,861  | 685,103 | Mobile element protein                                                       |
| 685,100  | 685,999 | Hypothetical protein                                                        |
| 686,275  | 686,816 | GTP cyclohydrolase I                                                        |
| 687,052  | 687,795 | Transcriptional regulator, GntR family                                       |
| 687,963  | 689,540 | Dipeptide-binding ABC transporter, periplasmic substrate-binding component   |
| 689,839  | 691,056 | BarH                                                                       |
| 691,143  | 691,811 | Short-chain dehydrogenase/reductase SDR                                      |
| 691,819  | 692,724 | 2-hydroxy-3-oxopropionate reductase                                          |
| 692,800  | 692,928 | Hypothetical protein                                                        |

| dummy    | prRWAY01 | 706,432 .. 711,574 | 5,142 | 66.86 | SIGI-HMM | 706,342 | 706,641 | - | Hypothetical protein |
| Region       | Start       | End          | Length | Score | Description                                                                 |
|--------------|-------------|--------------|--------|-------|-----------------------------------------------------------------------------|
| pRWAY01      | 833,420     | 839,974      | 6,554  | 61.95 | Hypothetical protein                                                         |
|              | 833,420     | 834,766      |        |       | Possible Rep protein                                                         |
|              | 834,829     | 834,942      |        |       | Hypothetical protein                                                         |
|              | 835,122     | 835,277      | +      |       | Hypothetical protein                                                         |
|              | 835,457     | 835,951      | -      |       | Hypothetical protein                                                         |
|              | 837,083     | 837,469      | +      |       | Putative involvement in replication/partition                                |
|              | 837,802     | 838,134      | -      |       | Hypothetical protein                                                         |
|              | 838,382     | 839,974      | +      |       | Putative acetyltransferase                                                  |
| pRWAY02      | 392,452     | 399,442      | 6,990  | 66.59 | 3-ketoacyl-CoA thiolase                                                     |
|              | 392,452     | 393,598      | -      |       | Protein of unknown function                                                 |
|              | 393,947     | 394,307      | +      |       | Hypothetical protein                                                         |
|              | 394,867     | 395,793      | +      |       | Formate hydrogenlyase subunit 7                                             |
|              | 395,790     | 395,933      | +      |       | Hypothetical protein                                                         |
|              | 395,944     | 397,281      | +      |       | 3-ketoacyl-CoA thiolase                                                     |
|              | 397,726     | 398,361      | +      |       | Mobile element protein                                                      |
|              | 398,443     | 398,592      | -      |       | Hypothetical protein                                                         |
|              | 398,678     | 399,442      | -      |       | Mobile element protein                                                      |
| pRWAY02      | 441,129     | 448,022      | 6,893  | 67.31 | Mobile element protein                                                      |
|              | 441,129     | 442,102      | -      |       | Transposase                                                                |
|              | 442,506     | 442,640      | -      |       | Hypothetical protein                                                         |
|              | 442,867     | 443,523      | -      |       | Hypothetical protein                                                         |
|              | 443,523     | 444,236      | -      |       | Hypothetical protein                                                         |
|              | 444,373     | 444,543      | +      |       | Hypothetical protein                                                         |
|              | 444,647     | 444,913      | -      |       | Hypothetical protein                                                         |
|              | 445,488     | 447,515      | +      |       | Tellurium resistance protein TerD                                           |
|              | 447,873     | 448,022      | -      |       | Hypothetical protein                                                         |
| pRWAY03      | 22,115      | 28,334       | 6,219  | 65.35 | Alpha/beta hydrolase fold                                                   |
|              | 22,115      | 23,413       | +      |       | Major facilitator superfamily (MPS) transporter                              |
|              | 23,441      | 23,899       | -      |       | Hypothetical protein                                                         |
|              | 23,899      | 24,624       | -      |       | Putative uncharacterized protein                                            |
|              | 24,862      | 25,128       | +      |       | Hypothetical protein                                                         |
|              | 25,195      | 25,509       | +      |       | Hypothetical protein                                                         |
|              | 25,901      | 27,250       | +      |       | Hypothetical protein                                                         |
|              | 27,256      | 28,044       | -      |       | Alpha/beta hydrolase fold                                                   |
|              | 28,146      | 28,334       | -      |       | Hypothetical protein                                                         |
| pRWAY03      | 132,522     | 137,582      | 5,060  | 66.60 | Copper chaperone                                                          |
|              | 132,522     | 132,728      | +      |       | Hypothetical protein                                                         |
|              | 132,760     | 132,942      | +      |       | Lead, cadmium, zinc and mercury transporting ATPase; Copper-translocating  |
| Gene ID     | Start Position   | End Position   | Score | E-value | Function                                |
|------------|------------------|----------------|-------|---------|-----------------------------------------|
| pRWAY03    | 253,769 . . 259,031 | 5,262          | 67.43 | SIGI-HMM| Mobile element protein                   |
| pRWAY03    | 304,048 . . 312,080 | 8,032          | 60.01 | IslandPath-DIMOB                     | Putative involvement in replication/partition |
| 135,230    | 135,454           | -              |       | Hypothetical protein                 |
| 135,532    | 135,858           | +              |       | Repressor CsoR of the copZA operon   |
| 135,883    | 136,266           | -              |       | Putative transcriptional regulator, ArsR family |
| 136,854    | 137,582           | +              |       | Protein of unknown function          |
| 252,879    | 253,772           | -              |       | Mobile element protein               |
| 253,769    | 254,110           | -              |       | Mobile element protein               |
| 254,103    | 255,197           | +              |       | Mobile element protein               |
| 255,209    | 256,468           | -              |       | Hypothetical protein                 |
| 256,465    | 257,553           | -              |       | ATPase associated with various cellular activities |
| 257,751    | 257,948           | -              |       | Hypothetical protein                 |
| 258,101    | 258,526           | -              |       | Hypothetical protein                 |
| 258,591    | 258,818           | +              |       | Hypothetical protein                 |
| 258,864    | 259,031           | +              |       | Hypothetical protein                 |
| 304,048    | 304,380           | -              |       | Hypothetical protein                 |
| 304,449    | 305,978           | -              |       | Hypothetical protein                 |
| 306,136    | 306,576           | +              |       | Putative involvement in replication/partition |
| 306,600    | 306,959           | -              |       | Hypothetical protein                 |
| 307,218    | 307,760           | -              |       | Unknown                              |
| 309,927    | 310,223           | +              |       | Hypothetical protein                 |
| 310,747    | 310,935           | +              |       | Hypothetical protein                 |
| 311,613    | 312,080           | +              |       | Hypothetical protein                 |