**Table S1 The amino acid homology of BT/DBT biodesulfurization enzymes.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | | RIPI90APR | | | A11-2PR | | | X7BPR | | | IGTS8PP | | |
| DszA | DszB | DszC | TdsA | TdsB | TdsC | DszA | DszB | DszC | DszA | DszB | DszC |
| C-6PR | BdsC | 12.4Id | 13.3Id | 9.6Id | 12.5Id | 11.4Id | 12.2Id | 13.0Id | 11.1Id | 10.3Id | 11.7Id | 10.1Id | 9.8Id |
| BdsA | 10.6Id | 22.9Id | 10.4Id | 9.3Id | 16.6Id | 11.1Id | 10.3Id | 16.6Id | 11.1Id | 10.3Id | 23.2Id | 9.1Id |
| BdsB | 13.7Id | 14.3Id | 12.2Id | 13.9Id | 14.8Id | 9.6Id | 13.7Id | 13.5Id | 11.3Id | 14.4Id | 13.0Id | 12.4Id |
| RIPI90APR | DszA |  |  |  | 59.8Id |  |  | 75.0Id |  |  | 87.1Id |  |  |
| DszB |  |  |  |  | 50.0Id |  |  | 62.4Id |  |  | 86.9Id |  |
| DszC |  |  |  |  |  | 50.6Id |  |  | 72.4Id |  |  | 90.4Id |
| A11-2PR | TdsA |  |  |  |  |  |  | 61.9Id |  |  | 61.9Id |  |  |
| TdsB |  |  |  |  |  |  |  | 52.2Id |  |  | 51.1Id |  |
| TdsC |  |  |  |  |  |  |  |  | 50.2Id |  |  | 49.5Id |
| X7BPR | DszA |  |  |  |  |  |  |  |  |  | 77.3Id |  |  |
| DszB |  |  |  |  |  |  |  |  |  |  | 63.2Id |  |
| DszC |  |  |  |  |  |  |  |  |  |  |  | 71.2Id |

Note: PR, Protein Resource; Id, Identities percentage; C-6, *Gordonia terrae* C-6; RIPI90A, *Gordonia alkanivorans* RIPI90A; A11-2, *Paenibacillus* sp. strain A11-2; X7B, *Mycobacterium goodii* X7B; IGTS8, *Rhodococcus* sp. IGTS8. DszA and TdsA, dibenzothiophene-5,5-dioxide monooxygenase; DszB and TdsB, 2-hydroxybiphenyl-2-sulfinate sulfinolyase; DszC and TdsC, dibenzothiophene monooxygenase; BdsA, desulfinase; BdsB, FMNH2-dependent monooxygenase; BdsC, alkanesulfonate monooxygenase.

**Table S2 Sulfur resource specificity of *Gordonia terrae* C-6.**

|  |  |  |
| --- | --- | --- |
| **Sulfur resource** | ***OD*600** | **Gibbs′ assay** |
| control | 0.00 | − |
| sodium sulfate | 0.92 | − |
| yeast extract | 1.26 | − |
| casein hydrolysate | 1.17 | − |
| dimethyl sulfoxide | 1.50 | − |
| benzothiophene | 1.44 | + |
| 2-methyl-benzothiophene | 0.96 | + |
| 3-methyl-benzothiophene | 0.82 | + |
| 5-methyl-benzothiophene | 1.33 | + |
| 2-carboxyl-benzothiophene | 0.23 | − |
| dibenzothiophene | 0.15 | − |
| 1-methyl- dibenzothiophene | 0.15 | − |
| 2-methyl- dibenzothiophene | 0.13 | − |
| 3-methyl- dibenzothiophene | 0.16 | − |
| 4-methyl- dibenzothiophene | 0.19 | − |

Note: +, indicates positive result in the Gibbs′ assay; −, indicates negative result in the Gibbs′ assay;

**Table S3 Primers used for RT-qPCR.**

|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Forward primer (5′→3′)** | **Reverse primer(5′→3′)** |
| GTC6\_00280 | CCTCGAAGGGCTGGAACTGC | CGGTCCCGTCCGCAGATCTAC |
| GTC6\_00275 | GTCTTCGATGCTGCCCTGTT | GTGCTCGAAGGGCTCCTACAT |
| GTC6\_00260 | CGTCGTGCGTCACCAGCAAG | CCTGGCCGTCCACGCTCTC |
| GTC6\_00255 | TCGTTCATCAGAAAGCCCAATC | AGGCGGGATGGGAACTGAT |
| GTC6\_04560 | CAGACGGCGTGCTCATCG | GGGAAGAGCGGCGACCTG |
| GTC6\_10396 | TGGCGGGCCTGGATGTCTC | CAGGGCAGTTATCCGCACCAG |
| GTC6\_10391 | AGATGAGGCGGCTCAAGATG | CACGACTATCCCGTCATCCAG |
| GTC6\_10386 | GCCGGGAGGATGAGGTGA | TACGGCGTTCGGCAACAC |
| GTC6\_11646 | GTCGGCATCAATGTCACCAAT | CGTGAACTGAGCGAAACCGT |
| GTC6\_11651 | GGCAGCATCGGCGACCTC | GAGTGCGGGCAGCAGCAGAT |
| GTC6\_11656 | GTTCCCGATCCCCGTTGTG | GCGTGATGCCGAGGATCAG |
| GTC6\_11661 | GCGGACAGAAGCAGCGAGTG | CGGTGTGACGCACGGTGATC |
| GTC6\_13080 | GGCGACGGCGAGAGGATG | CGCAGCAGCACCGCTTCAAC |
| GTC6\_13085 | CCGAACGCCATCACCCTCAAC | TTGTGCGGGTTGGGACTGTCC |
| GTC6\_13090 | ACGGCGATCTCGGCATCTC | GACGGTTTCGGCGATCACC |
| GTC6\_13095 | GCTCGTGGTTCTCGCCCTGT | GGTCGCCGCCTCGATGTAGG |
| GTC6\_13100 | AATCGCTGACCGCTCATGGT | GCCTTGCCGCTGAACGACT |
| GTC6\_15154 | CGATTCCCGCCTGGATGAGC | CGCCTTCTTCGCCGACCTG |
| GTC6\_15124 | CATCGCCGTCCTCGTGCTC | CACCGATGCCGAACCACAAG |
| GTC6\_15119 | CAGCGGCAGTGGCAAGTCG | GGCGAGGGAGACCCGTTGTG |
| GTC6\_15114 | CGCCTCCCTACAGGACCTCAC | GAACGCCGACAACGCATCT |
| GTC6\_15109 | GCGCGAGACCTCGGAGGAG | GCCTTCGGCGAACCAGTGC |
| GTC6\_01585 | GCCAGTTCCTCGGGATGCTG | GGTTTCACGCCACCGATCAC |
| GTC6\_01590 | GTTGATGTGCGGCGGGATC | CCTGGGCCGACGACCTGAC |
| GTC6\_01595 | GGCGGAATCGGTCGTGCTC | CACCGCAACTCGCACAGACG |
| GTC6\_01600 | GGATGGATGTCGCCGTGTTCC | CCGTTGCCAAAGGCGTATG |
| GTC6\_01605 | GCAGGTCCAGCCGCTCCTC | ATCGGTGCCGTCGGGATTT |
| GTC6\_01610 | GCCGAAGGTGCCGTCCGACAG | ACCATCAGGCGCGGCGAGTTC |
| GTC6\_01615 | TCGACAAGCAGATCCGCAGTG | CCGTTGTTCATCGCCTGGTTC |
| GTC6\_01620 | CGGAAGGCGACGATGGTG | GGCGGGCAAGGGTGAGTAC |
| GTC6\_06509 | TCGTGAGGCGGGCATCTTC | CCGCTGGCGTAGGACTGGT |
| GTC6\_06474 | TCGACACCGACGCCCACTC | CCGAGGTGGTGGCGATCCT |
| GTC6\_06469 | GAAGCCGCCCAGGATGAGGT | AGCCCAAGCCGCTCAACAC |
| GTC6\_06464 | AGGTAGGTGTCGGCGTGCTT | CCACCGAGAGCCTCAAGTTCC |
| GTC6\_15606 | GGTGAGCACGATGATCCGACT | GGAGTTCCTGGTGCTGGTGG |
| GTC6\_15611 | GGTGTTCACGACCTCGGGAT | CCGATCTCAAGGGCAAGCG |
| GTC6\_15616 | TTGACCACGCCACCGATTC | TGACCGCCGTTGGCCTACTT |

S-Fig 1.tif

**Figure S1 Histogram of clusters of orthologous groups (COG) classification.**

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

S-Fig 2.tif

**Figure S2 MS spectra of the phenolic compound produced by cell extracts of *E. coli* Rosetta (DE3) conceived with pET28a-*bds*ABC during BT biodesulfurization.**

Metabolites of BT in the cell extracts reaction system was extracted directly with ethyl acetate without adjusting its pH to 2.0, and analyzed by GC-MS according to the previously described method [25]. *o*-hydroxystyrene was identified by MS spectra corresponding to the peak with retention time of 3.67 in the GC profile. The molecular weight of *o*-hydroxystyrene decreased by 1 (the hydroxyl of *o*-hydroxystyrene exists in the form of negative ions) due to the extracting procedure.