**Table S4.** Net flux values for the central metabolic pathways*a* of *Pseudomonas putida* KT2440 grown on glucose.

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional block** | **Reaction code** | **BiGG ID** | **Flux value** (mmol gCDW-1 h-1) **± SE***b* |
| **Peripheral**  **pathways** | 1 | GLCDpp | 5.51 ± 0.04 |
| 2 | GAD2ktpp | 0.72 ± 0.06 |
| 4 | GNK | 4.79 ± 0.07 |
| 5 | 2DHGLCK | 0.72 ± 0.06 |
| 6 | PGLCNDH | 0.72 ± 0.06 |
| **Pentose phosphate**  **pathway** | 7 | G6PDH2 / PGL | 1.17 ± 0.07 |
| 10 | GND | 0.59 ± 0.03 |
| 11 | RPE | 0.15 ± 0.59 |
| 12 | RPI | 0.44 ± 0.59 |
| 13 | TKT1 | 0.15 ± 0.01 |
| 14 | TKT2 | 0.01 ± 0.01 |
| **Entner-Doudoroff**  **pathway** | 8 | EDD | 6.11 ± 0.04 |
| 9 | EDA | 6.11 ± 0.04 |
| **Embden-Meyerhof-Parnas pathway** | 3 | GLK | 0.63 ± 0.04 |
| 15 | TALA | 0.15 ± 0.01 |
| 16 | PGI | 0.57 ± 0.04 |
| 17 | FBP | 0.46 ± 0.03 |
| 18 | FBA | 0.46 ± 0.03 |
| 19 | TPI | 0.46 ± 0.03 |
| 20 | GAPD/PGK | 5.11 ± 0.04 |
| 21 | PGM/ENO | 4.36 ± 0.07 |
| **Tricarboxylic acid cycle / Glyoxylate shunt** | 22 | PYK | 3.89 ± 0.08 |
| 23 | PDH | 6.67 ± 0.18 |
| 24 | CS | 5.44 ± 0.21 |
| 25 | ACONTa/b | 5.44 ± 0.21 |
| 26 | ICDHyr | 5.44 ± 0.21 |
| 27 | AKGDH/SUCOAS | 4.71 ± 0.22 |
| 28 | SUCDi | 4.71 ± 0.22 |
| 29 | FUM | 4.71 ± 0.22 |
| 30 | MDH | 2.01 ± 0.11 |
| 31 | ICL/MALS | 0.00 ± 0.00 |
| **Anaplerosis / Gluconeogenesis** | 32 | OOADC | 4.44 ± 0.15 |
| 33 | PPC | 0.15 ± 0.13 |
| 34 | ME2 | 2.69 ± 0.18 |

*a* The functional classification and the codes of the biochemical reactions is the same as depicted in **Fig. 1** in the main textand **Table S3** in the Supplemental Data. The distribution of normalized values for each metabolic flux with respect to the specific rate of glucose consumption is shown in **Fig. 4** in the main text.

*b* SE, standard error.