Supplemental Table S7: Functions enriched amongst gene sets analyzed with PANTHER databases. Sets of gene names corresponding to significant COGs, SNPs, and k-mers were created as described in the Materials and Methods section. FDR means False Discovery Rate.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| PANTHER GO-Slim Biological Process | Staphylococcus aureus - REFLIST (2889) | p0045 (24) | p0045 (expected) | p0045 (over/under) | p0045 (fold Enrichment) | p0045 (raw P-value) | p0045 (FDR) |
| regulation of nucleic acid-templated transcription (GO:1903506) | 45 | 4 | 0.37 | + | 10.7 | 5.87E-04 | 1.17E-01 |
| regulation of RNA biosynthetic process (GO:2001141) | 45 | 4 | 0.37 | + | 10.7 | 5.87E-04 | 8.74E-02 |
| nucleic acid-templated transcription (GO:0097659) | 46 | 4 | 0.38 | + | 10.47 | 6.34E-04 | 7.56E-02 |
| regulation of RNA metabolic process (GO:0051252) | 46 | 4 | 0.38 | + | 10.47 | 6.34E-04 | 6.30E-02 |
| regulation of nucleobase-containing compound metabolic process (GO:0019219) | 47 | 4 | 0.39 | + | 10.24 | 6.84E-04 | 5.83E-02 |
| RNA biosynthetic process (GO:0032774) | 47 | 4 | 0.39 | + | 10.24 | 6.84E-04 | 5.10E-02 |
| regulation of macromolecule biosynthetic process (GO:0010556) | 51 | 4 | 0.42 | + | 9.44 | 9.13E-04 | 6.05E-02 |
| regulation of biosynthetic process (GO:0009889) | 51 | 4 | 0.42 | + | 9.44 | 9.13E-04 | 5.44E-02 |
| regulation of cellular biosynthetic process (GO:0031326) | 51 | 4 | 0.42 | + | 9.44 | 9.13E-04 | 4.95E-02 |
| regulation of cellular macromolecule biosynthetic process (GO:2000112) | 51 | 4 | 0.42 | + | 9.44 | 9.13E-04 | 4.54E-02 |
| regulation of nitrogen compound metabolic process (GO:0051171) | 52 | 4 | 0.43 | + | 9.26 | 9.78E-04 | 4.48E-02 |
| regulation of primary metabolic process (GO:0080090) | 52 | 4 | 0.43 | + | 9.26 | 9.78E-04 | 4.16E-02 |
| regulation of gene expression (GO:0010468) | 52 | 4 | 0.43 | + | 9.26 | 9.78E-04 | 3.89E-02 |
| regulation of cellular metabolic process (GO:0031323) | 53 | 4 | 0.44 | + | 9.08 | 1.05E-03 | 3.90E-02 |
| regulation of macromolecule metabolic process (GO:0060255) | 53 | 4 | 0.44 | + | 9.08 | 1.05E-03 | 3.67E-02 |
| regulation of metabolic process (GO:0019222) | 54 | 4 | 0.45 | + | 8.92 | 1.12E-03 | 3.70E-02 |
| macromolecule biosynthetic process (GO:0009059) | 123 | 6 | 1.02 | + | 5.87 | 4.68E-04 | 2.79E-01 |
| cellular macromolecule biosynthetic process (GO:0034645) | 123 | 6 | 1.02 | + | 5.87 | 4.68E-04 | 1.39E-01 |
| RNA metabolic process (GO:0016070) | 104 | 5 | 0.86 | + | 5.79 | 1.61E-03 | 4.57E-02 |
| nucleic acid metabolic process (GO:0090304) | 148 | 6 | 1.23 | + | 4.88 | 1.20E-03 | 3.78E-02 |
| Nucleobase-  containing compound metabolic process (GO:0006139) | 211 | 7 | 1.75 | + | 3.99 | 1.37E-03 | 4.09E-02 |
| PANTHER Protein Class | Staphylococcus aureus - REFLIST (2889) | p0017 (38) | p0017 (expected) | p0017 (over/under) | p0017 (fold Enrichment) | p0017 (raw P-value) | p0017 (FDR) |
| protein class (PC00000) | 986 | 25 | 12.97 | + | 1.93 | 9.62E-05 | 4.95E-03 |
| Unclassified (UNCLASSIFIED) | 1903 | 13 | 25.03 | - | 0.52 | 9.62E-05 | 9.91E-03 |
| GO biological process complete | Staphylococcus aureus - REFLIST (2889) | p002y (326) | p002y (expected) | p002y (over/under) | p002y (fold Enrichment) | p002y (raw P-value) | p002y (FDR) |
| organic substance metabolic process (GO:0071704) | 878 | 143 | 99.08 | + | 1.44 | 1.62E-06 | 6.35E-04 |
| cellular metabolic process (GO:0044237) | 837 | 136 | 94.45 | + | 1.44 | 4.19E-06 | 1.31E-03 |
| metabolic process (GO:0008152) | 1030 | 167 | 116.23 | + | 1.44 | 6.30E-08 | 3.29E-05 |
| primary metabolic process (GO:0044238) | 748 | 121 | 84.41 | + | 1.43 | 3.14E-05 | 7.01E-03 |
| nitrogen compound metabolic process (GO:0006807) | 717 | 115 | 80.91 | + | 1.42 | 7.77E-05 | 1.52E-02 |
| biological\_process (GO:0008150) | 1496 | 237 | 168.81 | + | 1.4 | 3.16E-13 | 2.48E-10 |
| cellular process (GO:0009987) | 947 | 146 | 106.86 | + | 1.37 | 2.00E-05 | 5.21E-03 |
| Unclassified (UNCLASSIFIED) | 1393 | 89 | 157.19 | - | 0.57 | 3.16E-13 | 4.95E-10 |
| GO molecular function complete | Staphylococcus aureus - REFLIST (2889) | p002y (326) | p002y (expected) | p002y (over/under) | p002y (fold Enrichment) | p002y (raw P-value) | p002y (FDR) |
| ATP binding (GO:0005524) | 275 | 58 | 31.03 | + | 1.87 | 1.37E-05 | 1.23E-03 |
| adenyl ribonucleotide binding (GO:0032559) | 276 | 58 | 31.14 | + | 1.86 | 2.01E-05 | 1.38E-03 |
| adenyl nucleotide binding (GO:0030554) | 277 | 58 | 31.26 | + | 1.86 | 2.07E-05 | 1.34E-03 |
| DNA binding (GO:0003677) | 215 | 45 | 24.26 | + | 1.85 | 2.28E-04 | 1.21E-02 |
| carbohydrate derivative binding (GO:0097367) | 320 | 66 | 36.11 | + | 1.83 | 5.86E-06 | 8.54E-04 |
| drug binding (GO:0008144) | 311 | 64 | 35.09 | + | 1.82 | 1.01E-05 | 1.18E-03 |
| purine ribonucleoside triphosphate binding (GO:0035639) | 302 | 62 | 34.08 | + | 1.82 | 1.80E-05 | 1.50E-03 |
| ribonucleotide binding (GO:0032553) | 312 | 64 | 35.21 | + | 1.82 | 1.06E-05 | 1.12E-03 |
| purine ribonucleotide binding (GO:0032555) | 303 | 62 | 34.19 | + | 1.81 | 1.85E-05 | 1.44E-03 |
| purine nucleotide binding (GO:0017076) | 304 | 62 | 34.3 | + | 1.81 | 1.92E-05 | 1.40E-03 |
| anion binding (GO:0043168) | 378 | 74 | 42.65 | + | 1.73 | 7.40E-06 | 9.58E-04 |
| nucleotide binding (GO:0000166) | 382 | 72 | 43.11 | + | 1.67 | 3.55E-05 | 2.18E-03 |
| nucleoside phosphate binding (GO:1901265) | 382 | 72 | 43.11 | + | 1.67 | 3.55E-05 | 2.07E-03 |
| ion binding (GO:0043167) | 569 | 107 | 64.21 | + | 1.67 | 1.37E-07 | 2.29E-05 |
| small molecule binding (GO:0036094) | 427 | 80 | 48.18 | + | 1.66 | 1.33E-05 | 1.29E-03 |
| nucleic acid binding (GO:0003676) | 353 | 66 | 39.83 | + | 1.66 | 1.20E-04 | 6.65E-03 |
| hydrolase activity (GO:0016787) | 364 | 65 | 41.07 | + | 1.58 | 4.08E-04 | 2.07E-02 |
| heterocyclic compound binding (GO:1901363) | 710 | 126 | 80.12 | + | 1.57 | 1.19E-07 | 2.77E-05 |
| organic cyclic compound binding (GO:0097159) | 710 | 126 | 80.12 | + | 1.57 | 1.19E-07 | 2.31E-05 |
| binding (GO:0005488) | 898 | 156 | 101.33 | + | 1.54 | 2.60E-09 | 7.57E-07 |
| catalytic activity (GO:0003824) | 1105 | 189 | 124.69 | + | 1.52 | 1.10E-11 | 4.27E-09 |
| molecular\_function (GO:0003674) | 1567 | 256 | 176.82 | + | 1.45 | 6.25E-18 | 3.64E-15 |
| Unclassified (UNCLASSIFIED) | 1322 | 70 | 149.18 | - | 0.47 | 6.25E-18 | 7.28E-15 |
| PANTHER GO-Slim Molecular Function | Staphylococcus aureus - REFLIST (2889) | p002y (326) | p002y (expected) | p002y (over/under) | p002y (fold Enrichment) | p002y (raw P-value) | p002y (FDR) |
| catalytic activity (GO:0003824) | 498 | 90 | 56.2 | + | 1.6 | 1.44E-05 | 1.18E-03 |
| molecular\_function (GO:0003674) | 729 | 122 | 82.26 | + | 1.48 | 4.48E-06 | 5.51E-04 |
| Unclassified (UNCLASSIFIED) | 2160 | 204 | 243.74 | - | 0.84 | 4.48E-06 | 1.10E-03 |
| PANTHER Protein Class | Staphylococcus aureus - REFLIST (2889) | p002y (326) | p002y (expected) | p002y (over/under) | p002y (fold Enrichment) | p002y (raw P-value) | p002y (FDR) |
| protein class (PC00000) | 986 | 172 | 111.26 | + | 1.55 | 7.79E-11 | 4.01E-09 |
| metabolite interconversion enzyme (PC00262) | 473 | 78 | 53.37 | + | 1.46 | 1.08E-03 | 3.69E-02 |
| Unclassified (UNCLASSIFIED) | 1903 | 154 | 214.74 | - | 0.72 | 7.79E-11 | 8.02E-09 |
| GO biological process complete | Staphylococcus aureus - REFLIST (2889) | p003p (181) | p003p (expected) | p003p (over/under) | p003p (fold Enrichment) | p003p (raw P-value) | p003p (FDR) |
| Nucleobase-  containing compound metabolic process (GO:0006139) | 331 | 42 | 20.74 | + | 2.03 | 1.74E-05 | 5.45E-03 |
| cellular aromatic compound metabolic process (GO:0006725) | 394 | 46 | 24.68 | + | 1.86 | 4.34E-05 | 1.13E-02 |
| cellular nitrogen compound metabolic process (GO:0034641) | 491 | 56 | 30.76 | + | 1.82 | 8.37E-06 | 4.36E-03 |
| heterocycle metabolic process (GO:0046483) | 408 | 46 | 25.56 | + | 1.8 | 1.30E-04 | 2.26E-02 |
| organic cyclic compound metabolic process (GO:1901360) | 418 | 46 | 26.19 | + | 1.76 | 2.34E-04 | 3.33E-02 |
| nitrogen compound metabolic process (GO:0006807) | 717 | 69 | 44.92 | + | 1.54 | 1.43E-04 | 2.24E-02 |
| cellular metabolic process (GO:0044237) | 837 | 78 | 52.44 | + | 1.49 | 1.05E-04 | 2.05E-02 |
| metabolic process (GO:0008152) | 1030 | 95 | 64.53 | + | 1.47 | 1.03E-05 | 4.05E-03 |
| cellular process (GO:0009987) | 947 | 86 | 59.33 | + | 1.45 | 8.91E-05 | 1.99E-02 |
| organic substance metabolic process (GO:0071704) | 878 | 79 | 55.01 | + | 1.44 | 3.47E-04 | 4.52E-02 |
| biological\_process (GO:0008150) | 1496 | 131 | 93.73 | + | 1.4 | 5.45E-08 | 8.54E-05 |
| Unclassified (UNCLASSIFIED) | 1393 | 50 | 87.27 | - | 0.57 | 5.45E-08 | 4.27E-05 |
| GO molecular function complete | Staphylococcus aureus - REFLIST (2889) | p003p (181) | p003p (expected) | p003p (over/under) | p003p (fold Enrichment) | p003p (raw P-value) | p003p (FDR) |
| nucleotide binding (GO:0000166) | 382 | 43 | 23.93 | + | 1.8 | 2.13E-04 | 3.10E-02 |
| nucleoside phosphate binding (GO:1901265) | 382 | 43 | 23.93 | + | 1.8 | 2.13E-04 | 2.75E-02 |
| heterocyclic compound binding (GO:1901363) | 710 | 74 | 44.48 | + | 1.66 | 3.81E-06 | 8.89E-04 |
| organic cyclic compound binding (GO:0097159) | 710 | 74 | 44.48 | + | 1.66 | 3.81E-06 | 7.41E-04 |
| ion binding (GO:0043167) | 569 | 58 | 35.65 | + | 1.63 | 1.33E-04 | 2.22E-02 |
| binding (GO:0005488) | 898 | 88 | 56.26 | + | 1.56 | 2.31E-06 | 6.75E-04 |
| catalytic activity (GO:0003824) | 1105 | 103 | 69.23 | + | 1.49 | 9.48E-07 | 3.68E-04 |
| molecular\_function (GO:0003674) | 1567 | 137 | 98.17 | + | 1.4 | 7.99E-09 | 9.31E-06 |
| Unclassified (UNCLASSIFIED) | 1322 | 44 | 82.83 | - | 0.53 | 7.99E-09 | 4.66E-06 |
| PANTHER GO-Slim Molecular Function | Staphylococcus aureus - REFLIST (2889) | p003p (181) | p003p (expected) | p003p (over/under) | p003p (fold Enrichment) | p003p (raw P-value) | p003p (FDR) |
| catalytic activity (GO:0003824) | 498 | 52 | 31.2 | + | 1.67 | 2.01E-04 | 1.65E-02 |
| molecular\_function (GO:0003674) | 729 | 72 | 45.67 | + | 1.58 | 3.56E-05 | 4.38E-03 |
| Unclassified (UNCLASSIFIED) | 2160 | 109 | 135.33 | - | 0.81 | 3.56E-05 | 8.76E-03 |
| PANTHER GO-Slim Biological Process | Staphylococcus aureus - REFLIST (2889) | p003p (181) | p003p (expected) | p003p (over/under) | p003p (fold Enrichment) | p003p (raw P-value) | p003p (FDR) |
| nitrogen compound metabolic process (GO:0006807) | 371 | 42 | 23.24 | + | 1.81 | 2.74E-04 | 4.08E-02 |
| cellular metabolic process (GO:0044237) | 425 | 48 | 26.63 | + | 1.8 | 7.05E-05 | 4.20E-02 |
| organic substance metabolic process (GO:0071704) | 415 | 45 | 26 | + | 1.73 | 3.43E-04 | 4.09E-02 |
| metabolic process (GO:0008152) | 443 | 48 | 27.75 | + | 1.73 | 2.16E-04 | 4.30E-02 |
| cellular process (GO:0009987) | 485 | 52 | 30.39 | + | 1.71 | 1.10E-04 | 3.29E-02 |
| PANTHER Protein Class | Staphylococcus aureus - REFLIST (2889) | p003p (181) | p003p (expected) | p003p (over/under) | p003p (fold Enrichment) | p003p (raw P-value) | p003p (FDR) |
| protein class (PC00000) | 986 | 95 | 61.77 | + | 1.54 | 1.16E-06 | 5.99E-05 |
| Unclassified (UNCLASSIFIED) | 1903 | 86 | 119.23 | - | 0.72 | 1.16E-06 | 1.20E-04 |
| GO biological process complete | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| cellular amino acid metabolic process (GO:0006520) | 136 | 19 | 6.87 | + | 2.76 | 1.11E-04 | 1.33E-02 |
| small molecule metabolic process (GO:0044281) | 375 | 45 | 18.95 | + | 2.37 | 4.79E-08 | 9.37E-06 |
| carboxylic acid metabolic process (GO:0019752) | 198 | 23 | 10.01 | + | 2.3 | 4.17E-04 | 3.63E-02 |
| oxoacid metabolic process (GO:0043436) | 202 | 23 | 10.21 | + | 2.25 | 4.69E-04 | 3.67E-02 |
| organic acid metabolic process (GO:0006082) | 222 | 25 | 11.22 | + | 2.23 | 2.56E-04 | 2.50E-02 |
| cellular biosynthetic process (GO:0044249) | 469 | 48 | 23.7 | + | 2.03 | 1.45E-06 | 2.52E-04 |
| organic substance biosynthetic process (GO:1901576) | 476 | 48 | 24.06 | + | 2 | 2.65E-06 | 4.14E-04 |
| biosynthetic process (GO:0009058) | 495 | 49 | 25.02 | + | 1.96 | 3.75E-06 | 5.34E-04 |
| Nucleobase-  containing compound metabolic process (GO:0006139) | 331 | 32 | 16.73 | + | 1.91 | 5.50E-04 | 4.10E-02 |
| organic substance metabolic process (GO:0071704) | 878 | 84 | 44.37 | + | 1.89 | 5.65E-11 | 4.42E-08 |
| cellular metabolic process (GO:0044237) | 837 | 80 | 42.3 | + | 1.89 | 2.49E-10 | 6.50E-08 |
| cellular aromatic compound metabolic process (GO:0006725) | 394 | 37 | 19.91 | + | 1.86 | 2.30E-04 | 2.40E-02 |
| primary metabolic process (GO:0044238) | 748 | 70 | 37.8 | + | 1.85 | 2.87E-08 | 6.41E-06 |
| metabolic process (GO:0008152) | 1030 | 95 | 52.05 | + | 1.83 | 3.57E-12 | 5.59E-09 |
| cellular process (GO:0009987) | 947 | 87 | 47.86 | + | 1.82 | 1.39E-10 | 4.35E-08 |
| heterocycle metabolic process (GO:0046483) | 408 | 37 | 20.62 | + | 1.79 | 4.54E-04 | 3.74E-02 |
| cellular nitrogen compound metabolic process (GO:0034641) | 491 | 43 | 24.81 | + | 1.73 | 3.12E-04 | 2.87E-02 |
| organonitrogen compound metabolic process (GO:1901564) | 514 | 45 | 25.98 | + | 1.73 | 1.79E-04 | 2.00E-02 |
| nitrogen compound metabolic process (GO:0006807) | 717 | 62 | 36.23 | + | 1.71 | 6.12E-06 | 7.98E-04 |
| biological\_process (GO:0008150) | 1496 | 115 | 75.6 | + | 1.52 | 7.10E-11 | 2.78E-08 |
| Unclassified (UNCLASSIFIED) | 1393 | 31 | 70.4 | - | 0.44 | 7.10E-11 | 3.71E-08 |
| GO molecular function complete | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| protein dimerization activity (GO:0046983) | 11 | 5 | 0.56 | + | 8.99 | 6.83E-04 | 3.46E-02 |
| protein binding (GO:0005515) | 28 | 9 | 1.42 | + | 6.36 | 4.22E-05 | 3.08E-03 |
| oxidoreductase activity, acting on CH-OH group of donors (GO:0016614) | 41 | 11 | 2.07 | + | 5.31 | 2.41E-05 | 1.87E-03 |
| magnesium ion binding (GO:0000287) | 53 | 11 | 2.68 | + | 4.11 | 1.80E-04 | 1.10E-02 |
| transition metal ion binding (GO:0046914) | 83 | 16 | 4.19 | + | 3.81 | 1.30E-05 | 1.38E-03 |
| coenzyme binding (GO:0050662) | 111 | 16 | 5.61 | + | 2.85 | 2.92E-04 | 1.62E-02 |
| cofactor binding (GO:0048037) | 154 | 22 | 7.78 | + | 2.83 | 2.19E-05 | 2.13E-03 |
| metal ion binding (GO:0046872) | 271 | 37 | 13.7 | + | 2.7 | 5.05E-08 | 9.82E-06 |
| cation binding (GO:0043169) | 276 | 37 | 13.95 | + | 2.65 | 7.83E-08 | 1.30E-05 |
| oxidoreductase activity (GO:0016491) | 182 | 22 | 9.2 | + | 2.39 | 2.43E-04 | 1.42E-02 |
| transferase activity, transferring phosphorus-  containing groups (GO:0016772) | 161 | 19 | 8.14 | + | 2.34 | 8.91E-04 | 4.33E-02 |
| ion binding (GO:0043167) | 569 | 62 | 28.76 | + | 2.16 | 1.59E-09 | 3.71E-07 |
| small molecule binding (GO:0036094) | 427 | 46 | 21.58 | + | 2.13 | 8.69E-07 | 1.27E-04 |
| nucleotide binding (GO:0000166) | 382 | 39 | 19.3 | + | 2.02 | 2.30E-05 | 2.06E-03 |
| nucleoside phosphate binding (GO:1901265) | 382 | 39 | 19.3 | + | 2.02 | 2.30E-05 | 1.91E-03 |
| transferase activity (GO:0016740) | 366 | 37 | 18.5 | + | 2 | 5.00E-05 | 3.43E-03 |
| drug binding (GO:0008144) | 311 | 31 | 15.72 | + | 1.97 | 3.83E-04 | 2.03E-02 |
| anion binding (GO:0043168) | 378 | 37 | 19.1 | + | 1.94 | 1.03E-04 | 6.69E-03 |
| binding (GO:0005488) | 898 | 85 | 45.38 | + | 1.87 | 7.44E-11 | 2.17E-08 |
| catalytic activity (GO:0003824) | 1105 | 101 | 55.84 | + | 1.81 | 2.43E-13 | 9.43E-11 |
| heterocyclic compound binding (GO:1901363) | 710 | 62 | 35.88 | + | 1.73 | 5.52E-06 | 7.15E-04 |
| organic cyclic compound binding (GO:0097159) | 710 | 62 | 35.88 | + | 1.73 | 5.52E-06 | 6.43E-04 |
| molecular\_function (GO:0003674) | 1567 | 128 | 79.19 | + | 1.62 | 3.24E-17 | 3.78E-14 |
| Unclassified (UNCLASSIFIED) | 1322 | 18 | 66.81 | - | 0.27 | 3.24E-17 | 1.89E-14 |
| GO cellular component complete | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| cytoplasm (GO:0005737) | 332 | 39 | 16.78 | + | 2.32 | 8.66E-07 | 1.01E-04 |
| intracellular (GO:0005622) | 411 | 42 | 20.77 | + | 2.02 | 1.21E-05 | 7.08E-04 |
| PANTHER Pathways | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| Unclassified (UNCLASSIFIED) | 2663 | 117 | 134.58 | - | 0.87 | 8.09E-06 | 5.67E-04 |
| PANTHER GO-Slim Molecular Function | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| catalytic activity (GO:0003824) | 498 | 53 | 25.17 | + | 2.11 | 1.10E-07 | 2.72E-05 |
| molecular\_function (GO:0003674) | 729 | 66 | 36.84 | + | 1.79 | 3.66E-07 | 4.50E-05 |
| Unclassified (UNCLASSIFIED) | 2160 | 80 | 109.16 | - | 0.73 | 3.66E-07 | 3.00E-05 |
| PANTHER GO-Slim Biological Process | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| metabolic process (GO:0008152) | 443 | 44 | 22.39 | + | 1.97 | 1.31E-05 | 7.82E-03 |
| cellular metabolic process (GO:0044237) | 425 | 40 | 21.48 | + | 1.86 | 1.30E-04 | 1.55E-02 |
| organic substance metabolic process (GO:0071704) | 415 | 39 | 20.97 | + | 1.86 | 1.82E-04 | 1.80E-02 |
| cellular process (GO:0009987) | 485 | 45 | 24.51 | + | 1.84 | 4.68E-05 | 1.40E-02 |
| biological\_process (GO:0008150) | 606 | 52 | 30.63 | + | 1.7 | 7.70E-05 | 1.53E-02 |
| Unclassified (UNCLASSIFIED) | 2283 | 94 | 115.37 | - | 0.81 | 7.70E-05 | 1.15E-02 |
| PANTHER GO-Slim Cellular Component | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| cytoplasm (GO:0005737) | 265 | 30 | 13.39 | + | 2.24 | 4.36E-05 | 4.05E-03 |
| cytoplasmic part (GO:0044444) | 184 | 20 | 9.3 | + | 2.15 | 1.82E-03 | 4.22E-02 |
| intracellular part (GO:0044424) | 288 | 31 | 14.55 | + | 2.13 | 8.13E-05 | 3.78E-03 |
| intracellular (GO:0005622) | 292 | 31 | 14.76 | + | 2.1 | 1.46E-04 | 4.54E-03 |
| PANTHER Protein Class | Staphylococcus aureus - REFLIST (2889) | pyo (146) | pyo (expected) | pyo (over/under) | pyo (fold Enrichment) | pyo (raw P-value) | pyo (FDR) |
| metabolite interconversion enzyme (PC00262) | 473 | 50 | 23.9 | + | 2.09 | 4.06E-07 | 1.39E-05 |
| protein class (PC00000) | 986 | 82 | 49.83 | + | 1.65 | 1.68E-07 | 1.73E-05 |
| Unclassified (UNCLASSIFIED) | 1903 | 64 | 96.17 | - | 0.67 | 1.68E-07 | 8.64E-06 |