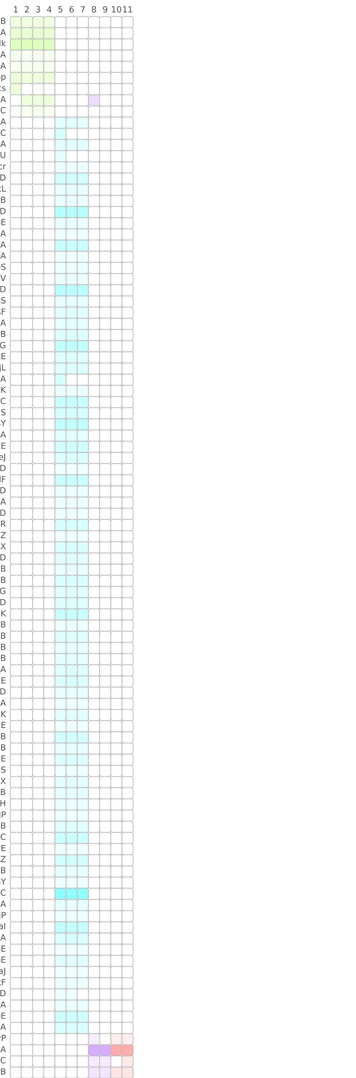
1 2 3 4 5 6 7 8 9 10 11
b1723 - pfkB
b1854 - pykA
b2388 - glk
b3916 - pfkA
b1779 - gapA
b4232 - fbp
b4069 - acs
b1814 - sdaA
b3952 - pflC
b3241 - aaeA
b4175 - hflC
b2813 - mltA
b3263 - yhdU
b2182 - bcr
b1175 - minD
b0652 - gltL
b2351 - gtrB
b0590 - fepD
b0587 - fepE
b1614 - ydgA
b3930 - menA
b0842 - mdfA
b2175 - mepS
b2295 - yfbV
b0722 - sdhD
b0570 - cusS
b0196 - rcsF
b3562 - yiaA
b3009 - yghB
b4032 - malG
b0641 - lptE
b0847 - ybjL
b0489 - qmcA
b1663 - mdtK
b3018 - plsC
b0960 - yccS
b3464 - ftsY
b0970 - yccA
b3523 - yhjE
b1057 - yceJ
b1820 - yobD
b0760 - modF
b1591 - dmsD
b4114 - eptA
b1451 - yncD
b0818 - ybiR
b0380 - yaiZ
b2365 - dsdX
b2611 - ypjD
b1418 - cybB
b2701 - mltB
b3524 - yhjG
b2470 - acrD
b0465 - mscK
b2170 - setB
b4041 - plsB
b1244 - oppB
b1293 - sapB
b3493 - pitA
b1798 - leuE
b0441 - ppiD
b0619 - citA
b4333 - yjiK
b1632 - rsxE
b3494 - uspB
b1859 - znuB
b1816 - yoaE
b1279 - ycjS
b1817 - manX
b3006 - exbB
b2158 - yeiH
b0865 - ybjP
b3668 - uhpB
b2393 - nupC
b3793 - wzyE
b3404 - envZ
b1272 - sohB
b0087 - mraY
b0621 - dcuC
b1216 - chaA
b1948 - fliP
b1785 - yeaI
b0098 - secA
b1520 - yneE
b2195 - dsbE
b1332 - ynaJ
b2558 - mltF
b1132 - hflD
b4189 - bsmA
b1534 - ydeE
b1601 - tqsA
b2903 - gcvP
b2551 - glyA
b4024 - lysC
b4388 - serB
b2898 - ygfZ
1: 3.35 ecg00010:Glycolysis / Gluconeogenesis
2: 1.66 GO:0006006~glucose metabolic process
3: 1.49 GO:0019318~hexose metabolic process
4: 1.2 GO:0005996~monosaccharide metabolic process
5: 1.21 membrane
6: 1.21 cell membrane
7: 1.05 GO:0005886~plasma membrane
8: 3.29 ecm00260:Glycine,serine and threonine metabolism
9: 2.03 GO:0009070~serine family amino acid biosynthetic process
10: 4.33 GO:0006544~glycine metabolic process
11: 2.25 GO:0009069~serine family amino acid metabolic process
group 1: 1.52
group 2: 1.39
group 3: 1.16
group 4: 1.07