

Supplemental Table 3. Min\_max\_span\_internal

| Reactions     | minWT | maxWT | spanW | minKO | maxKO | spanKC | spanKO | Name                                   | Equation | Subsystem                |
|---------------|-------|-------|-------|-------|-------|--------|--------|--|----------|--------------------------|
| 2HBO          | -2    | 0     | 2     | -3    | 0     | 3      | 1.5    | 2-Hydroxybut [c] : 2hb + na            |          | Propanoate Metabolism    |
| 2HBt2         | -2    | 0     | 2     | -3    | 0     | 3      | 1.5    | 2-hydroxybut 2hb[e] + h[e]             |          | Transport, Extracellular |
| 2MCITt        | 0     | 2     | 2     | 0     | 3     | 3      | 1.5    | 2-methylcitra 2mcit[c] <==>            |          | Transport, Extracellular |
| 34HPLFM       | 0     | 1     | 1     | 0     | 2     | 2      | 2      | 3-(4-hydroxy) [m] : 34hpp + Ubiquinone |          | Biosynthesis             |
| 3DSPHR        | 0     | 1     | 1     | 0     | 37.54 | 37.54  | 37.536 | 3-Dehydrospl [c] : 3dsphgn             |          | Sphingolipid Metabolism  |
| 4HOXPACDOX(N/ | 0     | 1     | 1     | 0     | 2     | 2      | 2      | 4-Hydroxyph [c] : 4hoxpac              |          | Tyrosine metabolism      |
| AACTOOR       | 0     | 2     | 2     | 0     | 24.58 | 24.58  | 12.291 | Aminoaceton [c] : aact + h2            |          | Gly, Ser, Thr Metabolism |
| AACTtm        | 0     | 2     | 2     | 0     | 24.58 | 24.58  | 12.291 | Aminoaceton aact[m] --> a              |          | Transport, Mitochondrial |
| ACAct2m       | -217  | 260.7 | 478.1 | -219  | 149.7 | 368.6  | 0.771  | Acetoacetate acac[c] + h[c]            |          | Transport, Mitochondrial |
| ACActx        | -254  | 0     | 254.4 | -130  | 0     | 129.9  | 0.5105 | acetoacetate acac[c] <==>              |          | Transport, Peroxisomal   |
| ACGAMtly      | 0     | 56.44 | 56.44 | 0     | 5     | 5      | 0.0886 | N-acetyl-gluc acgam[l] --> e           |          | Transport, Lysosomal     |
| ADK3m         | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41  | 3.5666 | adentylate ki [m] : amp + g            |          | Nucleotides              |
| ADNK1m        | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41  | 3.5666 | adenosine kir [m] : adn + at           |          | Nucleotides              |
| ADNtm         | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41  | 3.5666 | adenosine far adn[c] <==> a            |          | Transport, Mitochondrial |
| ADSL2         | 0     | 2     | 2     | 0     | 10.51 | 10.51  | 5.2563 | adenylosuccii [c] : 25aics -->         |          | IMP Biosynthesis         |
| AHC           | 0     | 2     | 2     | 0     | 3     | 3      | 1.5    | adenosylhom [c] : ahcys + h            |          | Methionine Metabolism    |
| AICART        | 0     | 2     | 2     | 0     | 10.51 | 10.51  | 5.2563 | phosphoribo [c] : 10fthf + i           |          | IMP Biosynthesis         |
| AIRCr         | 0     | 2     | 2     | 0     | 10.51 | 10.51  | 5.2563 | phosphoribo [c] : air + co2            |          | IMP Biosynthesis         |
| AKGMALtm      | -708  | 5E+05 | 5E+05 | -710  | 170   | 879.9  | 0.0018 | alpha-ketogl akg[m] + mal              |          | Transport, Mitochondrial |
| ALCD1         | -2    | 0     | 2     | -3    | 0     | 3      | 1.5    | alcohol dehy [c] : meoh + r            |          | Miscellaneous            |
| AOBUTDsm      | 0     | 2     | 2     | 0     | 24.58 | 24.58  | 12.291 | L-2-amino-3-[m] : 2aobut               |          | Gly, Ser, Thr Metabolism |
| BETALDHxm     | 0     | 1     | 1     | 0     | 2     | 2      | 2      | betaine-alde [m] : betald +            |          | Gly, Ser, Thr Metabolism |
| BHMT          | 0     | 1     | 1     | 0     | 2     | 2      | 2      | betaine-hom [c] : glyb + hc            |          | Gly, Ser, Thr Metabolism |
| BPNT          | 0     | 1     | 1     | 0     | 2     | 2      | 2      | 3',5'-bisphos [c] : h2o + pa           |          | Nucleotides              |
| BUP2          | 0     | 1.3   | 1.3   | 0     | 27.65 | 27.65  | 21.268 | beta-ureidop [c] : 3uib + (2           |          | Pyrimidine Catabolism    |
| CAMPt         | 0     | 3.3   | 3.3   | 0     | 9.45  | 9.45   | 2.8636 | cAMP transp atp[c] + cam               |          | Transport, Extracellular |
| CGMPt         | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45   | 63     | cGMP transp 35cgmp[c] + :              |          | Transport, Extracellular |
| CHLtm         | 0     | 1     | 1     | 0     | 2     | 2      | 2      | choline trans chol[c] <==>             |          | Transport, Mitochondrial |
| CHOLD2m       | 0     | 1     | 1     | 0     | 2     | 2      | 2      | choline dehy [m] : chol + f            |          | Gly, Ser, Thr Metabolism |
| CHOLtu        | 0     | 1     | 1     | -0.33 | 1     | 1.333  | 1.3333 | Choline unipc chol[e] <==>             |          | Transport, Extracellular |
| CLFORtex      | 0     | 1     | 1     | 0     | 1.5   | 1.5    | 1.5    | chloride tran: cl[e] + (2) fo          |          | Transport, Extracellular |
| COAAtm        | -108  | 234.8 | 342.7 | -108  | 0     | 108.2  | 0.3158 | CoA transpor coa[c] <==>               |          | Transport, Mitochondrial |
| COAtp         | -254  | 0     | 254.4 | -130  | 0     | 129.9  | 0.5105 | coenzyme A t coa[c] <==>               |          | Transport, Peroxisomal   |
| CRNCARtp      | 0     | 254.4 | 254.4 | 0     | 129.9 | 129.9  | 0.5105 | carnitine-ace acrn[x] + crn            |          | Transport, Peroxisomal   |
| CSNATp        | 0     | 254.4 | 254.4 | 0     | 129.9 | 129.9  | 0.5105 | carnitine O-a [x] : accoa + c          |          | Fatty Acid Metabolism    |
| CYTDt         | -1.15 | 0.15  | 1.3   | -13.2 | 0.15  | 13.35  | 10.269 | cytidine facil cytd[e] <==>            |          | Transport, Extracellular |
| D-3AIBt       | 0     | 1.3   | 1.3   | 0     | 27.65 | 27.65  | 21.268 | D-3-amino-isi 3aib-D[c] -->            |          | Transport, Extracellular |
| DATPtn        | 0     | 3.3   | 3.3   | 0     | 9.45  | 9.45   | 2.8636 | dATP diffusio datp[c] <==>             |          | Transport, Nuclear       |
| DCTPtn        | 0     | 1.3   | 1.3   | 0     | 13.35 | 13.35  | 10.269 | dCTP diffusio dctp[c] <==>             |          | Transport, Nuclear       |
| DCYTt         | -1.3  | 0     | 1.3   | -13.4 | 0     | 13.35  | 10.269 | deoxycytidin dcyt[e] <==>              |          | Transport, Extracellular |
| DGK1          | -4.6  | 0     | 4.6   | -16.5 | 0     | 16.46  | 3.5779 | deoxyguanyl [c] : atp + dgr            |          | Nucleotides              |
| DGK2m         | 0     | 4.6   | 4.6   | 0     | 16.33 | 16.33  | 3.5507 | deoxyguanyl [m] : datp + d             |          | Nucleotides              |
| DGNSKm        | 0     | 4.6   | 4.6   | 0     | 16.33 | 16.33  | 3.5507 | deoxyguanos [m] : atp + dg             |          | Nucleotides              |
| DGSNt         | -0.15 | 0     | 0.15  | -9.45 | 0     | 9.45   | 63     | deoyguanosir dgsn[e] <==>              |          | Transport, Extracellular |
| DGSNtm        | 0     | 4.6   | 4.6   | 0     | 16.33 | 16.33  | 3.5507 | deoyguanosir dgsn[c] <==>              |          | Transport, Mitochondrial |
| DGTPtn        | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45   | 63     | dGTP diffusio dgtp[c] <==>             |          | Transport, Nuclear       |
| DHCRD1        | 0     | 1     | 1     | 0     | 37.31 | 37.31  | 37.309 | dihydroceran [c] : dhcrm_h             |          | Sphingolipid Metabolism  |
| DHFR          | 0     | 1.3   | 1.3   | 0     | 27.65 | 27.65  | 21.268 | dihydrofolate [c] : dhf + h +          |          | Folate Metabolism        |
| DHPM1         | 0     | 1.3   | 1.3   | 0     | 47.17 | 47.17  | 36.287 | dihydropyrim [c] : 56dura +            |          | Pyrimidine Catabolism    |
| DHPM2         | 0     | 1.3   | 1.3   | 0     | 27.65 | 27.65  | 21.268 | dihydropyrim [c] : 56dthm              |          | Pyrimidine Catabolism    |
| DMGDHm        | 0     | 1     | 1     | 0     | 2     | 2      | 2      | dimethylglyci [m] : dmgly +            |          | Gly, Ser, Thr Metabolism |
| DMGtm         | 0     | 1     | 1     | 0     | 2     | 2      | 2      | dimethylglyci dmgly[c] <==             |          | Transport, Mitochondrial |
| DNDPt12m      | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41  | 3.5666 | dADP transpc adp[m] + dad              |          | Transport, Mitochondrial |
| DNDPt13m      | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41  | 3.5666 | dADP transpc atp[m] + dad              |          | Transport, Mitochondrial |

|            |       |       |       |       |       |       |        |   |                             |
|------------|-------|-------|-------|-------|-------|-------|--------|---|-----------------------------|
| DNDPt18m   | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41 | 3.5666 | dUDP transpc adp[m] + dud                 | Transport, Mitochondrial    |
| DNDPt19m   | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41 | 3.5666 | dUDP transpc atp[m] + dud                 | Transport, Mitochondrial    |
| DNDPt1m    | 0     | 3.95  | 3.95  | 0     | 10.27 | 10.27 | 2.5995 | dATP transpo adp[m] + dat                 | Transport, Mitochondrial    |
| DNDPt20m   | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41 | 3.5666 | dTDP transpc atp[m] + dtd                 | Transport, Mitochondrial    |
| DNDPt21m   | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41 | 3.5666 | dTDP transpc adp[m] + dtd                 | Transport, Mitochondrial    |
| DNDPt2m    | 0     | 3.95  | 3.95  | 0     | 10.27 | 10.27 | 2.5995 | dATP transpo atp[m] + dat                 | Transport, Mitochondrial    |
| DNDPt30m   | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41 | 3.5666 | dCDP transpc adp[m] + dcd                 | Transport, Mitochondrial    |
| DNDPt31m   | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41 | 3.5666 | dCDP transpc atp[m] + dcd                 | Transport, Mitochondrial    |
| DNDPt32m   | 0     | 4.6   | 4.6   | 0     | 16.41 | 16.41 | 3.5666 | dGDP transpc atp[m] + dgd                 | Transport, Mitochondrial    |
| DNDPt3m    | 0     | 7.9   | 7.9   | 0     | 20.48 | 20.48 | 2.5925 | dATP transpo datp[c] + dcd                | Transport, Mitochondrial    |
| DNDPt44m   | 0     | 1.3   | 1.3   | 0     | 14.91 | 14.91 | 11.472 | dTTP transpo atp[m] + dttp                | Transport, Mitochondrial    |
| DNDPt45m   | 0     | 1.3   | 1.3   | 0     | 14.91 | 14.91 | 11.472 | dTTP transpo adp[m] + dttp                | Transport, Mitochondrial    |
| DNDPt46m   | 0     | 1.3   | 1.3   | 0     | 14.91 | 14.91 | 11.472 | dTTP transpo dttp[c] + dud                | Transport, Mitochondrial    |
| DNDPt47m   | 0     | 1.3   | 1.3   | 0     | 14.91 | 14.91 | 11.472 | dTTP transpo dtdp[m] + dti                | Transport, Mitochondrial    |
| DNDPt48m   | 0     | 1.3   | 1.3   | 0     | 14.91 | 14.91 | 11.472 | dTTP transpo dgdp[m] + dti                | Transport, Mitochondrial    |
| DNDPt49m   | 0     | 1.3   | 1.3   | 0     | 14.91 | 14.91 | 11.472 | dTTP transpo dadp[m] + dti                | Transport, Mitochondrial    |
| DNDPt4m    | 0     | 7.9   | 7.9   | 0     | 20.48 | 20.48 | 2.5925 | dATP transpo datp[c] + dud                | Transport, Mitochondrial    |
| DNDPt50m   | 0     | 1.3   | 1.3   | 0     | 14.91 | 14.91 | 11.472 | dTTP transpo dcdp[m] + dti                | Transport, Mitochondrial    |
| DNDPt51m   | 0     | 1.3   | 1.3   | 0     | 13.35 | 13.35 | 10.269 | dCTP transpo dcdp[m] + dc                 | Transport, Mitochondrial    |
| DNDPt52m   | 0     | 1.3   | 1.3   | 0     | 13.35 | 13.35 | 10.269 | dCTP transpo dctp[c] + dud                | Transport, Mitochondrial    |
| DNDPt53m   | 0     | 1.3   | 1.3   | 0     | 13.35 | 13.35 | 10.269 | dCTP transpo dctp[c] + dgd                | Transport, Mitochondrial    |
| DNDPt54m   | 0     | 1.3   | 1.3   | 0     | 13.35 | 13.35 | 10.269 | dCTP transpo dadp[m] + dc                 | Transport, Mitochondrial    |
| DNDPt55m   | 0     | 1.3   | 1.3   | 0     | 13.35 | 13.35 | 10.269 | dCTP transpo adp[m] + dct                 | Transport, Mitochondrial    |
| DNDPt56m   | 0     | 1.3   | 1.3   | 0     | 13.35 | 13.35 | 10.269 | dCTP transpo atp[m] + dct                 | Transport, Mitochondrial    |
| DNDPt57m   | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | dGTP transpc atp[m] + dgt                 | Transport, Mitochondrial    |
| DNDPt58m   | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | dGTP transpc adp[m] + dgt                 | Transport, Mitochondrial    |
| DNDPt59m   | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | dGTP transpc dadp[m] + dg                 | Transport, Mitochondrial    |
| DNDPt5m    | 0     | 7.9   | 7.9   | 0     | 20.48 | 20.48 | 2.5925 | dATP transpo datp[c] + dtd                | Transport, Mitochondrial    |
| DNDPt60m   | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | dGTP transpc dgtp[c] + dud                | Transport, Mitochondrial    |
| DNDPt61m   | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | dGTP transpc dgtp[c] + dtd                | Transport, Mitochondrial    |
| DNDPt62m   | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | dGTP transpc dgdp[m] + dg                 | Transport, Mitochondrial    |
| DNDPt63m   | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | dGTP transpc dcdp[m] + dg                 | Transport, Mitochondrial    |
| DNDPt6m    | 0     | 7.9   | 7.9   | 0     | 20.48 | 20.48 | 2.5925 | dATP transpo datp[c] + dgd                | Transport, Mitochondrial    |
| DNDPt7m    | 0     | 7.9   | 7.9   | 0     | 20.48 | 20.48 | 2.5925 | dATP transpo dadp[m] + da                 | Transport, Mitochondrial    |
| DOPAtu     | ##### | 388.4 | 5E+05 | 0     | 389.6 | 389.6 | 0.0008 | Dopamine un dopa[e] <==>                  | Transport, Extracellular    |
| DSAT       | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | dihydrosphin[c] : Rtotalco                | Sphingolipid Metabolism     |
| DTMPK      | 0     | 1.3   | 1.3   | 0     | 15.67 | 15.67 | 12.051 | dTMP kinase [c] : atp + dtn               | Nucleotides                 |
| DTTPtn     | 0     | 1.3   | 1.3   | 0     | 15.67 | 15.67 | 12.051 | dTTP diffusio dttp[c] <==>                | Transport, Nuclear          |
| DURAD      | -1.3  | 0     | 1.3   | -47.2 | 0     | 47.17 | 36.287 | dihydrouacil [c] : 56dura                 | + Pyrimidine Catabolism     |
| DURAD2     | -1.3  | 0     | 1.3   | -27.6 | 0     | 27.65 | 21.268 | dihydrothymi [c] : 56dthm                 | - Pyrimidine Catabolism     |
| DURIPP     | -1.3  | 0     | 1.3   | -27.8 | 0     | 27.78 | 21.371 | deoxyuridine [c] : duri + pi              | - Nucleotides               |
| DURit      | -1.3  | 0     | 1.3   | -19.7 | 0     | 19.74 | 15.188 | deoxyuridine duri[e] <==>                 | Transport, Extracellular    |
| FACOAL160i | 0     | 22.48 | 22.48 | 0     | 38.31 | 38.31 | 1.7043 | C160 fatty ac [c] : atp + coa             | Fatty acid activation       |
| FALDH      | -1    | 1     | 2     | -1    | 2     | 3     | 1.5    | formaldehyd[c] : fald + gtf               | Tyrosine metabolism         |
| FALDtm     | 0     | 1     | 1     | 0     | 2     | 2     | 2      | formaldehyd[c] : fald[m] <==>             | Transport, Mitochondrial    |
| FORT2m     | -2    | 0     | 2     | -3    | 0     | 3     | 1.5    | formate mito for[m] <==>                  | f Transport, Mitochondrial  |
| FTHFL      | 0     | 2     | 2     | 0     | 3     | 3     | 1.5    | formate-tetr[c] : atp + for               | Folate Metabolism           |
| FTHFLm     | 0     | 2     | 2     | 0     | 3     | 3     | 1.5    | formate-tetr[m] : atp + fo                | Folate Metabolism           |
| GARFT      | 0     | 2     | 2     | 0     | 10.51 | 10.51 | 5.2563 | phosphoribo[c] : 10fthf + i               | IMP Biosynthesis            |
| GLUPRT     | 0     | 2     | 2     | 0     | 10.51 | 10.51 | 5.2563 | glutamine ph [c] : gln-L + h              | IMP Biosynthesis            |
| GLUt2m     | -562  | 5E+05 | 5E+05 | -565  | 160.6 | 725.3 | 0.0014 | L-glutamate r glu-L[c] + h[c]             | Transport, Mitochondrial    |
| GLYATm     | 0     | 2     | 2     | 0     | 24.58 | 24.58 | 12.291 | glycine C-ace [m] : accoa + Gly, Ser, Thr | Metabolism                  |
| GLYBtm     | 0     | 1     | 1     | 0     | 2     | 2     | 2      | Glycine betai glyb[m] <==>                | Transport, Mitochondrial    |
| GLYOp      | 0     | 2     | 2     | 0     | 26.22 | 26.22 | 13.112 | glycine oxida: [x] : gly + h2o            | Gly, Ser, Thr Metabolism    |
| GLYtm      | -3    | 1     | 4     | -3    | 24.58 | 27.58 | 6.8953 | glycine passiv gly[c] <==>                | gl Transport, Mitochondrial |
| GLYtp      | 0     | 2     | 2     | 0     | 26.22 | 26.22 | 13.112 | glycine passiv gly[c] <==>                | gl Transport, Peroxisomal   |

|          |       |       |       |       |       |       |        |   |
|----------|-------|-------|-------|-------|-------|-------|--------|---|
| GMPR     | 0     | 0.15  | 0.15  | 0     | 86.92 | 86.92 | 579.45 | GMP reducta [c] : gmp + (2 Nucleotides                          |
| GSNt     | 0     | 0.15  | 0.15  | -9.3  | 0.15  | 9.45  | 63     | guanosine fa gsn[e] <==> g Transport, Extracellular             |
| GUAD     | 0     | 0.15  | 0.15  | 0     | 11.81 | 11.81 | 78.75  | guanine dean [c] : gua + h + Purine Catabolism                  |
| H2Otlly  | 0     | 110.9 | 110.9 | 0     | 9     | 9     | 0.0812 | H2O transpor h2o[c] <==> f Transport, Lysosomal                 |
| HDCATER  | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | palmitate ER hdca[r] --> hc Transport, ER                       |
| HMGCOAtm | -235  | 107.9 | 342.7 | 0     | 108.2 | 108.2 | 0.3158 | Hydroxymeth hmgcoa[c] <= Transport, Mitochondrial               |
| HMGCOAtx | 0     | 254.4 | 254.4 | 0     | 129.9 | 129.9 | 0.5105 | Hydroxymeth hmgcoa[c] <= Transport, Peroxisomal                 |
| HMGLm    | 0     | 296.8 | 296.8 | 0     | 108.2 | 108.2 | 0.3646 | hydroxymeth [m] : hmgcoa Cholesterol Metabolism                 |
| HMGLx    | 0     | 254.4 | 254.4 | 0     | 129.9 | 129.9 | 0.5105 | hydroxymeth [x] : hmgcoa · Cholesterol Metabolism               |
| HPACTr   | 0     | 1     | 1     | 0     | 2     | 2     | 2      | hydroxyphen 4hphac[c] <== Transport, Extracellular              |
| HXANTx   | 0     | 3.3   | 3.3   | 0     | 11.81 | 11.81 | 3.5795 | hypoxanthine hxan[c] --> hx Transport, Peroxisomal              |
| ILEtec   | 0     | 1     | 1     | ##### | 0.568 | 5E+05 | 500001 | L-isoleucine t ile-L[e] <==> i Transport, Extracellular         |
| IMPC     | -2    | 0     | 2     | -10.5 | 0     | 10.51 | 5.2563 | IMP cyclohyd [c] : h2o + im IMP Biosynthesis                    |
| MCITS    | 0     | 2     | 2     | 0     | 3     | 3     | 1.5    | 2-methylcitra [c] : h2o + oa. Propanoate Metabolism             |
| MEOHt2   | -2    | 0     | 2     | -3    | 0     | 3     | 1.5    | Methanol difi meoh[e] <==> Transport, Extracellular             |
| METAT    | 0     | 2     | 2     | 0     | 3     | 3     | 1.5    | methionine a [c] : atp + h2c Methionine Metabolism              |
| MTHFC    | -1.3  | 2     | 3.3   | -5    | 20.36 | 25.36 | 7.6843 | methenyltetr [c] : h2o + me Folate Metabolism                   |
| MTHFD    | -1.3  | 0     | 1.3   | -7    | 18.53 | 25.53 | 19.635 | methylenetet [c] : mlthf + n Folate Metabolism                  |
| NDPK4    | 0     | 1.3   | 1.3   | 0     | 15.67 | 15.67 | 12.051 | nucleoside-di [c] : atp + dtd Nucleotides                       |
| NRPPHRtu | ##### | 388.4 | 5E+05 | 0     | 389.6 | 389.6 | 0.0008 | Norepinephri nrpphr[e] <== Transport, Extracellular             |
| NTD8     | 0     | 4.6   | 4.6   | 0     | 16.46 | 16.46 | 3.5779 | 5'-nucleotida [c] : dgmp + f Nucleotides                        |
| OBDHc    | 0     | 2     | 2     | 0     | 3     | 3     | 1.5    | 2-Oxobutano [c] : 2obut + c Gly, Ser, Thr Metabolism            |
| OCOAT1m  | -221  | 289.9 | 511.3 | -223  | 150.4 | 373.4 | 0.7301 | 3-oxoacid Co. [m] : acac + s Val, Leu, ileu Metabolism          |
| Pit2m_2  | ##### | 540   | 5E+05 | -236  | 542   | 777.9 | 0.0016 | Pit2m_2 (2) h[c] + pi[c] Oxidative Phosphorylation              |
| Pit9     | -3    | 24.83 | 27.83 | -3    | 54.19 | 57.19 | 2.0554 | phosphate tr: (2) na1[e] + p Transport, Extracellular           |
| PRAGSr   | 0     | 2     | 2     | 0     | 10.51 | 10.51 | 5.2563 | phosphoribo: [c] : atp + gly IMP Biosynthesis                   |
| PRAIS    | 0     | 2     | 2     | 0     | 10.51 | 10.51 | 5.2563 | phosphoribo: [c] : atp + fpr: IMP Biosynthesis                  |
| PRASCS   | 0     | 2     | 2     | 0     | 10.51 | 10.51 | 5.2563 | phosphoribo: [c] : 5aizc + a: IMP Biosynthesis                  |
| PRFGS    | 0     | 2     | 2     | 0     | 10.51 | 10.51 | 5.2563 | phosphoribo: [c] : atp + fga IMP Biosynthesis                   |
| PSDm_hs  | 0     | 1     | 1     | 0     | 5.5   | 5.5   | 5.5    | Phosphatidyl: [m] : h + ps_f Glycerophospholipid Met.           |
| PSFLIPm  | 0     | 1     | 1     | 0     | 5.5   | 5.5   | 5.5    | phosphatidyl: atp[c] + h2o[ <i>c</i> ] Transport, Mitochondrial |
| PYNP2r   | 0     | 1.3   | 1.3   | 0     | 47.29 | 47.29 | 36.378 | pyrimidine-n1 [c] : pi + uri <= Pyrimidine Catabolism           |
| RNDR2    | 0     | 0.15  | 0.15  | 0     | 9.45  | 9.45  | 63     | ribonucleosid [c] : gdp + trd Nucleotides                       |
| SADT     | 0     | 1     | 1     | 0     | 2     | 2     | 2      | sulfate adeny [c] : atp + h + Nucleotides                       |
| SERPT    | 0     | 1     | 1     | 0     | 37.54 | 37.54 | 37.536 | serine C-palr [c] : h + pmtc Sphingolipid Metabolism            |
| SFGTH    | -1    | 1     | 2     | -1    | 2     | 3     | 1.5    | S-Formylglut: [c] : Sfglutth - Tyrosine metabolism              |
| SGPL12r  | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | Sphingosine-: [r] : h2o + spl Sphingolipid Metabolism           |
| SLCBK1   | 0     | 1     | 1     | 0     | 9.255 | 9.255 | 9.2546 | sphingolipid l [c] : atp + sph Sphingolipid Metabolism          |
| SMPD4    | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | sphingomyeli [c] : h2o + spr Sphingolipid Metabolism            |
| SMS      | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | Sphingomyeli [c] : crm_hs + Sphingolipid Metabolism             |
| SPC_HSt  | 0     | 1     | 1     | 0     | 1.333 | 1.333 | 1.3333 | sphingosylph spc_hs[c] <== Transport, Extracellular             |
| SPH1Pte  | 0     | 1     | 1     | 0     | 9.255 | 9.255 | 9.2546 | sph1p transp sph1p[c] <==> Transport, Extracellular             |
| SPHK21c  | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | sphingosine k [c] : atp + sph Sphingolipid Metabolism           |
| SPHMDAc  | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | sphingomyeli [c] : h2o + spl Sphingolipid Metabolism            |
| SPHS1Pte | 0     | 1     | 1     | 0     | 9.09  | 9.09  | 9.0903 | sphingosine-1 sphs1p[c] <== Transport, Extracellular            |
| SPHS1Ptr | 0     | 1     | 1     | 0     | 37.31 | 37.31 | 37.309 | sphingosine-1 sphs1p[c] <== Transport, ER                       |
| TMDPP    | 0     | 1.3   | 1.3   | 0     | 27.65 | 27.65 | 21.268 | thymidine ph [c] : pi + thyr Pyrimidine Catabolism              |
| TMDS     | 0     | 1.3   | 1.3   | 0     | 27.65 | 27.65 | 21.268 | thymidylate s [c] : dump + r Nucleotides                        |
| TYMSft   | 0     | 1     | 1     | 0     | 2     | 2     | 2      | Tyramine O-s tymsf[c] --> t Transport, Extracellular            |
| TYMSULT  | 0     | 1     | 1     | 0     | 2     | 2     | 2      | Tyramine Suli [c] : paps + ty Tyrosine metabolism               |
| TYRCBOX  | 0     | 1     | 1     | 0     | 2     | 2     | 2      | L-Tyrosine ca [c] : h + tyr-L Tyrosine metabolism               |
| TYROXDAC | 0     | 1     | 1     | 0     | 2     | 2     | 2      | Tyramine:oxy [c] : h2o + o2 Tyrosine metabolism                 |
| UPPN     | 0     | 1.3   | 1.3   | 0     | 47.17 | 47.17 | 36.287 | b-ureidoprop [c] : cala + (2) Pyrimidine Catabolism             |
| URATet   | 0     | 3.3   | 3.3   | 0     | 11.81 | 11.81 | 3.5795 | urate export urate[c] --> u Transport, Extracellular            |
| URATetx  | 0     | 3.3   | 3.3   | 0     | 11.81 | 11.81 | 3.5795 | urate export urate[x] --> u Transport, Peroxisomal              |
| URit     | -0.15 | 1.15  | 1.3   | -18.9 | 1.15  | 20.03 | 15.404 | uridine facilit uri[e] <==> ur Transport, Extracellular         |

|        |   |      |      |       |       |       |        |                              |                          |
|--------|---|------|------|-------|-------|-------|--------|------------------------------|--------------------------|
| VALtec | 0 | 1    | 1    | ##### | 0.73  | 5E+05 | 500001 | L-valine trans val-L[e] <==> | Transport, Extracellular |
| XANTx  | 0 | 0.15 | 0.15 | 0     | 11.81 | 11.81 | 78.75  | xanthine diff xan[c] --> xan | Transport, Peroxisomal   |
| XAO2x  | 0 | 3.3  | 3.3  | 0     | 11.81 | 11.81 | 3.5795 | xanthine oxid [x] : h2o + hx | Purine Catabolism        |
| XAOx   | 0 | 3.3  | 3.3  | 0     | 11.81 | 11.81 | 3.5795 | xanthine oxi [x] : h2o + o2  | Purine Catabolism        |

MULTISPECIFIC DRUG TRANSPORTER Slc22a8 (Oat3) REGULATES MULTIPLE METABOLIC PATHWAYS.

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DRUG METABOLISM AND DISPOSITION.