



'exp2flux' Package

An R Package to convert expression data to FBA fluxes

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Language: R

Stable: CRAN

Development: gibbslab/exp2flux

License: GPL-2

Binaries: Windows - Linux - Mac

E.C: 1.1.1.1

alcohol[c] + NAD(+)[c] \rightleftharpoons aldehyde[c] + NADH[c]

1.1.1.1

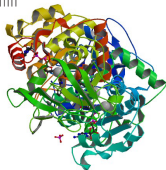
ADH2

ADH1



ADH1: |||||

ADH2: |||||



(ADH2 or ADH1)

sum (ExprADH2 + ExprADH1)

E.C: 3.4.21.5

polypeptides[e] \Rightarrow aminoacids[e]

3.4.21.5

IDE.A

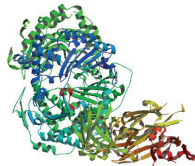
IDE.B

IDE.C

IDE.A: |||||

IDE.B: |||||

IDE.C: |||||



(IDE.A and IDE.B and IDE.C)

min (ExprIDE.A, ExprIDE.B, ExprIDE.C)

GENE EXPRESSION
DATA



exp2flux()
CONVERT GENE
EXPRESSION DATA
TO FBA FLUXES



CONSTRAINED
METABOLIC MODEL



fluxDifferences()
COMPUTE FOLDCHANGE
OF FLUXES BETWEEN
METABOLIC SCENARIOS

METABOLIC MODEL
WITH GPR

