Convert a reconstruction into a flux balance analysis model

Author: Ronan Fleming, Ines Thiele, University of Luxembourg

Reviewers:

INTRODUCTION

Even with quality control during the reconstruction process, it is not appropriate to assume that any reconstruction can be converted directly into a model and used to make predictions. A model must satisfy certain assumptions before it can be used to make reliable predictions. Depending on the type of model model, these assumptions will be different. Each assumption should be chemically or biologically motivated and expressed in an unambiguous manner and preferably both intuitively and mathematically. Flux balance analysis is a mathematical method widely used for studying genome-scale biochemical network. Here one aims to predict steady-state reaction fluxes, where there is a balance between production and consumption of each molecular species that is not exchanged across the specified boundary of a system. In this situation, one might obtain erroneous predictions if the system boundary is incorrectly specified. If a reconstruction contains one or more supposedly mass balanced reactions, but which are actually not mass balanced, such reactions in a model can lead to inadvertent leakage of a metabolite from the model, in violation of mass balance. Similarly, when generating a model for flux balance analysis, it is important to ensure that the network is flux consistent, that is, each reaction can carry a non-zero steady state flux.

Given a reconstruction with $\hat{m}$ reactants involved in $\hat{n}$ reactions, this tutorial demonstrates a method to identify and extract the largest subset of the reconstruction whose internal reactions are both stoichoimetrically and flux consistent and whose external reactions are flux consistent. This model is then mathematically consistent with the basic requirements for generation of predictions using flux balance analysis. The identification of the component of the reconstruction that does not satisfy the aforementioned modelling conditions is also useful for targeting reconstruction effort towards resolving stoichiometric inconsistency or resolving flux inconsistency. The example used in this tutorial illustrates the process of extracting a model consistent with flux balance analsis, from a ReconX reconstruction.

PROCEDURE

Select reconstruction to convert into a model and enter parameters

Load the ReconX reconstruction, and save the original reconstruction in the workspace, unless it is already loaded into the workspace.

```
clear model
if ~exist('modelOrig','var')
    %select your own model, or use Recon2.0model instead
    if 0
        filename='Recon3.0model';
        directory='~/work/sbgCloud/programReconstruction/projects/recon2models/data/reconXComparisonModels';
        model = loadIdentifiedModel(filename,directory);
    else
        filename='Recon2.0model.mat';
        if exist('Recon2.0model.mat','file')==2
            model = readCbModel(filename);
        end
    end
    model.csense(1:size(model.S,1),1)='E';
    modelOrig = model;
else
    model=modelOrig;
end
```

Set the level of printing, zero for silent, higher for more output.

```
printLevel=2;
```

Choose the directory to place the results

```
basePath='~/work/sbgCloud/';
resultsPath=[basePath '/programReconstruction/projects/recon2models/results/reconXs/' model.modelID];
resultsFileName=[resultsPath filesep model.modelID];
```

Create and enter the folder for the results if it does not already exist

```
if ~exist(resultsPath,'dir')
    mkdir(resultsPath)
end
cd(resultsPath)
```

Optionally create a diary to save the output in case it is very long, this makes it easier to search, especially when debugging the process during the early stages.

```
if 0
    diary([resultsFileName '_diary.txt'])
end
```

Overview some of the key properties of the reconstruction

Noting the initial size of the reconstruction is useful for comparisons later with subsets derived according to mathematical specifications.

```
[nMet,nRxn]=size(model.S);
fprintf('%6s\t%6s\n','#mets','#rxns')
```

```
  #mets  #rxns
```

```
fprintf('%6u\t%6u\t%s\n',nMet,nRxn,' totals.')
```

```
    5063   7335  totals.
```

Make sure the stoichiometric matrix is stored in a sparse format as this accelerates computations with large networks

```
model.S=sparse(model.S);
```

Check in case the reconstruction is a model that is already ready for flux balance analysis

There is no need to run this live script any further if the reconstruction already satisfies the conditions necessary for flux balance analysis. That is if all internal reactants and reactions are stoichiometrically consistent, and all reactions are flux consistent, then the reconstruction satisfies the criteria to designate it a model ready for flux balance analysis.

SIntMetBool	m x 1 Boolean of metabolites heuristically though to be involved in mass balanced reactions.
SIntRxnBool	n x 1 Boolean of reactions heuristically though to be mass balanced.
SConsistentMetBool	m x 1 Boolean vector indicating consistent mets
SConsistentRxnBool	n x 1 Boolean vector indicating consistent rxns
fluxConsistentMetBool	m x 1 Boolean vector indicating flux consistent mets
fluxConsistentRxnBool	n x 1 Boolean vector indicating flux consistent rxns

```
if all(isfield(model,{'SIntMetBool','SIntRxnBool','SConsistentMetBool',...
        'SConsistentRxnBool','fluxConsistentMetBool','fluxConsistentRxnBool'}))
    if all(model.SIntMetBool & model.SConsistentMetBool)...
            && nnz(model.SIntRxnBool & model.SConsistentRxnBool)==nnz(model.SIntRxnBool)...
            && all(model.fluxConsistentMetBool)...
            && all(model.fluxConsistentRxnBool)
        fullyStoichAndFluxConsistent=1;
        fprintf('%s\n','Reconstruction is a model that is already ready for flux balance analysis')
    end
    return
else
    fullyStoichAndFluxConsistent=0;
    fprintf('%s\n','Reconstruction must be tested to check if it is ready for flux balance analysis')
end
```

```
Reconstruction must be tested to check if it is ready for flux balance analysis
```

Manually remove certain reactions from the reconstruction

Before attempting to algorithmically remove stoichiometrically or flux inconsistent supposed internal reactions from a reconstruction to generate a model, there is an option to review the content of the reconstruction and manually identify reactions for removal. That is, there are two options:

A. Skip manual review of reconstruction content. Move to the next step.

B. Review the content of the reconstruction and omit any reactions that are assumed to be stoichiometrically or flux inconsistent. With respect to stoichiometric inconsistency, such reactions may be obviously mass imbalanced and not satisfy the heuristic conditions for indentification as an exernal reaction. Alternatively, such reactions may be identified by a previous pass through of this tutorial as being of unknown stoichometric consistent (model.unknownSConsistencyRxnBool(j)==1), after the largest stoichiometrically consistent subset of the network has been is identified. This is an iterative process where multiple rounds of identification of the largest stoichiometrically consistent set and manual curation of the remainder that is of unknown stoichiometric consistency is necessary.

```
if strcmp(filename,'Recon3.0model')
    modelOrig=model;
    if 0
        if 1
            %Rename some of the biomass reactions to make them more obviously exchange
            %reactions
            model.rxns{strcmp(model.rxns,'biomass_reaction')}= 'EX_biomass_reaction';
            model.rxns{strcmp(model.rxns,'biomass_maintenance')}= 'EX_biomass_maintenance';
            model.rxns{strcmp(model.rxns,'biomass_maintenance_noTrTr')}= 'EX_biomass_maintenance_noTrTr';

            %ATP hydrolysis is not imbalanced like all the other demand reactions so
            %give it a different accronym ATPM = ATP Maintenance
            bool=strcmp('DM_atp_c_',model.rxns);
            model.rxns{bool}='ATPM';
        end
        [model,removeMetBool,removeRxnBool] = manuallyAdaptRecon3(model,printLevel);
    else
        [model,removeMetBool,removeRxnBool] = manuallyAdaptRecon3Ines(model,printLevel);
    end
    [nMet0,nRxn0]=size(modelOrig.S);
    [nMet,nRxn]=size(model.S);
    if nMet0==nMet && nRxn0==nRxn && printLevel>0
        fprintf('%s\n','--- Manually removing rows and columns of the stoichiometric matrix----')
        fprintf('%6s\t%6s\n','#mets','#rxns')
        fprintf('%6u\t%6u\t%s\n',nMet0,nRxn0,' totals.')
        fprintf('%6u\t%6u\t%s\n',nMet0-nMet,nRxn0-nRxn,' manually removed.')
        fprintf('%6u\t%6u\t%s\n',nMet,nRxn,' remaining.')
    end
end
```

Remove any trivial rows and columns of the stoichiometric matrix

Remove any zero rows or columns of the stoichiometric matrix

```
modelOrig=model;
model=removeTrivialStoichiometry(model);
[nMet0,nRxn0]=size(modelOrig.S);
[nMet,nRxn]=size(model.S);
if nMet0==nMet && nRxn0==nRxn && printLevel>0
    fprintf('%s\n','---Checking for Remove any trivial rows and columns of the stoichiometric matrix----')
    fprintf('%6s\t%6s\n','#mets','#rxns')
    fprintf('%6u\t%6u\t%s\n',nMet0,nRxn0,' totals.')
    fprintf('%6u\t%6u\t%s\n',nMet0-nMet,nRxn0-nRxn,' duplicates removed.')
```

```
    fprintf('%6u\t%6u\t%s\n',nMet,nRxn,' remaining.')
end
```

```
---Checking for Remove any trivial rows and columns of the stoichiometric matrix----
 #mets  #rxns
  5063   7335  totals.
     0      0  duplicates removed.
  5063   7335  remaining.
```

Check for duplicate columns by detecting the columns of the S matrix that are identical upto scalar multiplication.

```
modelOrig=model;
dupDetectMethod='FR';
dupDetectMethod='S';
removeFlag=0;
[modelOut,removedRxnInd, keptRxnInd] = checkDuplicateRxn(model,dupDetectMethod,removeFlag,printLevel-2);
```

Remove any duplicate reactions, and uniquely involved reactants, from the stoichiometric matrix.

```
if length(removedRxnInd)>0
    irrevFlag=0;
    metFlag=1;
    %set all reactions reversible that are duplicates
    model.lb(removedRxnInd)=-model.ub(removedRxnInd);
    %remove duplicates
    model = removeRxns(model,model.rxns(removedRxnInd),irrevFlag,metFlag);
end
```

Display the statistics on the duplicate reactions,

```
[nMet0,nRxn0]=size(modelOrig.S);
[nMet,nRxn]=size(model.S);
if nMet0==nMet && nRxn0==nRxn && printLevel>0
    fprintf('%s\n','---Remove any duplicate reactions----')
    [nMet0,nRxn0]=size(modelOrig.S);
    [nMet,nRxn]=size(model.S);
    fprintf('%6s\t%6s\n','#mets','#rxns')
    fprintf('%6u\t%6u\t%s\n',nMet0,nRxn0,' totals.')
    fprintf('%6u\t%6u\t%s\n',nMet0-nMet,nRxn0-nRxn,' duplicates removed.')
    fprintf('%6u\t%6u\t%s\n',nMet,nRxn,' remaining.')
end
```

```
---Remove any duplicate reactions----
 #mets  #rxns
  5063   7335  totals.
     0      0  duplicates removed.
  5063   7335  remaining.
```

Remove any duplicate reactions upto protons

Remove reactions reactions that differ only in the number of protons involved as substrates or products. Also remove exclusively involved reactants.

Save a temporary model for testing, before making any changes.

```
modelH=model;
```

Find the proton indicies in different compartments. A proton, with index i, is asumed to be represented by an abbreviation within model.mets{i} like h[*], where * denotes the compartment symbol.

```
nMetChars=zeros(length(modelH.mets),1);
for m=1:length(modelH.mets)
    nMetChars(m,1)=length(modelH.mets{m});
end
protonMetBool=strncmp(modelH.mets,'h',1) & nMetChars==length('h[*]');
if printLevel>2
    disp(modelH.mets(protonMetBool))
end
```

Zero out the proton stoichiometric coefficients from the temporary model for testing

```
modelH.S(protonMetBool,:)=0;
```

Check for duplicate columns, upto protons, by detecting the columns of the S matrix that are identical upto scalar multiplication.

```
dupDetectMethod='FR';
removeFlag=0;
[modelOut,removedRxnInd, keptRxnInd] = checkDuplicateRxn(modelH,dupDetectMethod,removeFlag,printLevel-1);
```

```
Checking for reaction duplicates by stoichiometry (up to orientation) ...
     Keep:  BTNt2 btn[e]  <=> btn[c]
Duplicate:  BTNt4i btn[e]  -> btn[c]
Warning: EX_h(e) has more than one replicate
     Keep:  EX_h(e)  <=>
Duplicate:  Htr  <=>
     Keep:  GLCt1r glc_D[e]  <=> glc_D[c]
Duplicate:  GLCt2_2 glc_D[e]  <=> glc_D[c]
     Keep:  NACUP nac[e]  -> nac[c]
Duplicate:  NACDe nac[c]  -> nac[e]
     Keep:  ORNt4m orn[m] + citr_L[c]  <=> orn[c] + citr_L[m]
Duplicate:  r0947 orn[m] + citr_L[c]  -> orn[c] + citr_L[m]
```

Remove any duplicate reactions from the stoichiometric matrix, but do not remove the protons.

```
if length(removedRxnInd)>0
    irrevFlag=0;
    metFlag=0;%dont remove the protons
    model = removeRxns(model,model.rxns(removedRxnInd),irrevFlag,metFlag);
end
```

Display statistics of the removed reactions

```
if printLevel>0
    [nMet0,nRxn0]=size(modelOrig.S);
    [nMet,nRxn]=size(model.S);
    fprintf('%6s\t%6s\n','#mets','#rxns')
    fprintf('%6u\t%6u\t%s\n',nMet0,nRxn0,' totals.')
    fprintf('%6u\t%6u\t%s\n',nMet0-nMet,nRxn0-nRxn,' duplicate reactions upto protons removed.')
    fprintf('%6u\t%6u\t%s\n',nMet,nRxn,' remaining.')
end
```

```
  #mets  #rxns
   5063   7335  totals.
      0      5  duplicate reactions upto protons removed.
   5063   7330  remaining.
```

```
%model size
[nMet,nRxn]=size(model.S);
```

Heuristically identify exchange reactions and metabolites exclusively involved in exchange reactions

An external reaction is one that is heuristically identified by a single stoichiometric coefficient in the corresponding column of S, or an (abbreviated) reaction name matching a pattern (e.g. prefix EX_) or an external subsystem assignment. Any remaining reaction is assumed to be an internal reaction. If a reaction is not external then it is denoted an internal reaction. External reactants are exclusively involved in exchange reactions, and internal reactants otherwise. The findSExRxnInd function finds the external reactions in the model which export or import mass from or to the model, e.g. Exchange reactions, Demand reactions, Sink reactions.

```
if ~isfield(model,'SIntMetBool')  ||  ~isfield(model,'SIntRxnBool')
     model = findSExRxnInd(model,[],printLevel-1);
end
```

EXPECTED RESULTS

In the returned model, model.SIntRxnBool, is a boolean of reactions heuristically though to be mass balanced, while model.SIntMetBool is a boolean of metabolites heuristically though to be involved in mass balanced reactions.

CAUTION

The aforementioned assignments of external and internal reactions and reactants is the result of a heuristic and might result in one or more errors, either due to misspecification or because the names of external reactions and external subsystems often vary between laboratories.

Find the reactions that are flux inconsistent

Ultimately we seek to identify the set of stoichiometrically consistent reactions that are also flux consistent, with no bounds on reaction rates. However, finiding the stoichiometrically consistent subset can be demanding for large models so first we identify the subset of reactions that are flux consistent and focus on them.

```
modelOrig=model;
model.lb(~model.SIntRxnBool)=-1000;
model.ub(~model.SIntRxnBool)= 1000;
if 1
    if ~isfield(model,'fluxConsistentMetBool') || ~isfield(model,'fluxConsistentRxnBool')
        param.epsilon=1e-4;
        param.modeFlag=0;
        param.method='null_fastcc';
        %param.method='fastcc';
        [fluxConsistentMetBool,fluxConsistentRxnBool,fluxInConsistentMetBool,fluxInConsistentRxnBool,model] = findFluxConsistentSubset(model
    end
    % Remove reactions that are flux inconsistent
    if any(fluxInConsistentRxnBool)
        irrevFlag=0;
        metFlag=1;
        model = removeRxns(model,model.rxns(fluxInConsistentRxnBool),irrevFlag,metFlag);
        [nMet0,nRxn0]=size(modelOrig.S);
        [nMet,nRxn]=size(model.S);

        if printLevel>0
            fprintf('%s\n','-------')
            fprintf('%6s\t%6s\n','#mets','#rxns')
            fprintf('%6u\t%6u\t%s\n',nMet0,nRxn0,' totals.')
            fprintf('%6u\t%6u\t%s\n',nMet0-nMet,nRxn0-nRxn,' flux inconsistent reactions removed.')
```

```
            fprintf('%6u\t%6u\t%s\n',nMet,nRxn,' remaining.')
            fprintf('%s\n','-------')
            if printLevel>1
                for n=1:nRxn0
                    if fluxInConsistentRxnBool(n)
                        fprintf('%15s\t%-100s\n',modelOrig.rxns{n},modelOrig.rxnNames{n})
                    end
                end
            end
        end
        %revise model size
        [nMet,nRxn]=size(model.S);

        %Recompute
        %Heuristically identify exchange reactions and metabolites exclusively involved in exchange reactions
        %finds the reactions in the model which export/import from the model
        %boundary i.e. mass unbalanced reactions
        %e.g. Exchange reactions
        %     Demand reactions
        %     Sink reactions

        model = findSExRxnInd(model,[],0);
        if printLevel>0
            fprintf('%s\n','------end------')
        end
    end
end
```

```
-------
 #mets  #rxns
  5063   7330  totals.
  2123   2140  flux inconsistent reactions removed.
  2940   5190  remaining.
-------
1a_24_25VITD2Hm 1-alpha-Vitamin D-24,25-hydroxylase (D2)
1a_24_25VITD3Hm 1-alpha-Vitamin D-24,25-hydroxylase (D3)
   1a_25VITD2Hm 1-alpha,24R,25-Vitamin D-hydroxylase (D2)
   1a_25VITD3Hm 1-alpha,24R,25-Vitamin D-hydroxylase (D3)
  24_25DHVITD2t 24,25-Dihydroxyvitamin D2 transport from cytoplasm
 24_25DHVITD2tm 24,25-Dihydroxyvitamin D2 transport from mitochondria
   24_25VITD2Hm 24R-Vitamin D-25-hydroxylase (D2)
      25HVITD2t 25-hydroxyvitamin D2 transport from cytoplasm
  25HVITD2tin_m 25-hydroxyvitamin D2 transport in mitochondria
      25VITD2Hm 1-alpha-Vitamin D-25-hydroxylase (D2)
      25VITD3Hm 1-alpha-Vitamin D-25-hydroxylase (D3)
      34DHPHAMT 3,4-Dihydroxyphenylacetate:amet O-methyltransferase
      3HPCOAHYD 3-hydroxyisobutyryl-Coenzyme A hydrolase
          3HPPD 3-hydroxypropionate dehydrogenase
      3HXKYNDCL 3-Hydroxykynurenamine decarboxy-lyase
     3HXKYNOXDA 3-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)
      3M4HDXPAC 3-Methoxy-4-hydroxyphenylacetaldehyde:NAD+ oxidoreductase
      3MOXTYROX 3-Methoxytyramine:oxygen oxidoreductase (deaminating)
         3NTD7l 3'-nucleotidase (AMP), lysosome
      42A12BOOX 4-(2-Aminoethyl)-1,2-benzenediol:oxygen oxidoreductase(deaminating)(flavin-containing)
       4MPTNLtr 4-methylpentanal transport (ER)
  5HOXINDACTOXm 5-Hydroxyindoleacetaldehyde:NAD+ oxidoreductase (mito)
     5HOXINOXDA 5-Hydroxytryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)
       5HTRPDOX 5-Hydroxy-L-tryptophan:oxygen 2,3-dioxygenase (indole-decyclizing)
      5HXKYNDCL 5-Hydroxykynurenamine decarboxy-lyase
     5HXKYNOXDA 5-Hydroxykynurenamine:oxygen oxidoreductase(deaminating)(flavin-containing)
       A_MANASE alpha-mannosidase
        A4GALTc Lactosylceramide 4-alpha-galactosyltransferase
        A4GNT1g alpha 1,4-N-acetylglucosaminyltransferase, Golgi apparatus
       ABUTt2rL 4-aminobutyrate reversible transport in via proton symport (lysosome)
        ACACT8p acetyl-CoA acyltransferase (hexadecanoyl-CoA), peroxisomal
        ACACT9p acetyl-CoA acyltransferase (tetracosanoyl-CoA), peroxisomal
          ACGSm N-acteylglutamate synthase, mitochondrial
         ACOATA Acetyl-CoA ACP transacylase
          ACODA acetylornithine deacetylase
          ACSOMT S-Adenosyl-L-methionine:N-acetylserotonin O-methyltransferase
       ACSRTNMT S-Adenosyl-L-homocysteine:N-acetylserotonin O-methyltransferase
           ACtg acetate transport, Golgi apparatus
          ADEtl adenine facilated transport from lysosome
       ADHAPtx intracellular transport (peroxisome)
          ADNtl adenosine facilated transport from lysosome
         ADPGLC ADPglucose diphosphatase
         ADPMAN ADPmannose diphosphatase
       ADPRDPm ADPribose diphosphatase (mitochondrial)
        ADSELK adenylyl-selenate kinase
          AGLPC alkyl acylglycerol phosphocholine transferase
         AGLPED alkyl acyl glycerophosphoethanolamine desaturase
         AGLPET alkyl acylglycerol phosphoethanolamine transferase
          AGLPH alkyl glycerol phosphate hydrolase
```

AGLPR alkyl glycerol phospnate reductase
AGLPT alkyl glycerol phosphate acyltransferase
AGPex alkyl glycerol phosphate transport
AGPRim N-acetyl-g-glutamyl-phosphate reductase, irreversible, mitochondrial
AGPSx alkylglycerone phosphate synthase
AHANDROSTANGLCte glucuronidated compound transport
AHANDROSTANGLCtr glucuronidated compound transport
AHCYStn S-adenosyl-L-homocysteine nuclear transport
ALAt2rL L-alanine reversible transport via proton symport (lysosome)
ALDD20x aldehyde dehydrogenase (indole-3-acetaldehyde, NAD)
ALDD20xm aldehyde dehydrogenase (indole-3-acetaldehyde, NAD), mitochondrial
ALKP alkaline phosphatase
ALOX12 Arachidonate 12-lipoxygenase
ALOX12R Arachidonate 12-lipoxygenase R
ALOX15 Arachidonate 15-lipoxygenase
AMACR2r alpha-methylacyl-CoA racemase (reductase)
AMACRr alpha-methylacyl-CoA racemase
AMETtn S-adenosyl-L-methionine nuclear transport
AMPtr AMP transporter, endoplasmic reticulum
AP4AH1 Ap4A hydrolase, asymmetrically
APRTO2 N-acetylputrescine: oxygen oxireductase (deaminating)
AQCOBALt Aquacob(III)alamin uptake
ARTFR11 R group artificial flux
ARTFR12 R group artificial flux (C16:1)
ARTFR13 R group artificial flux
ARTFR202 R group artificial flux (C18:3, n-3)
ARTFR203 R group artificial flux
ARTFR204 R group artificial flux
ARTFR205 R group artificial flux
ARTFR206 R group artificial flux
ARTFR207 R group artificial flux
ARTFR208 R group artificial flux
ARTFR209 R group artificial flux
ARTFR210 R group artificial flux
ARTFR211 R group artificial flux
ARTFR212 R group artificial flux
ARTFR213 R group artificial flux
ARTFR31 R group artificial flux
ARTFR32 R group artificial flux
ARTFR33 R group artificial flux
ARTFR34 R group artificial flux
ARTFR41 R group artificial flux
ARTFR42 R group artificial flux
ARTFR43 R group artificial flux
ARTFR44 R group artificial flux
ARTFR45 R group artificial flux
ARTFR46 R group artificial flux
ARTFR51 R group artificial flux
ARTFR52 R group artificial flux
ARTFR53 R group artificial flux
ARTFR54 R group artificial flux
ARTFR55 R group artificial flux
ARTFR56 R group artificial flux
ARTFR57 R group artificial flux
ARTFR61 R group artificial flux
ARTPLM1 R group to palmitate conversion
ARTPLM1m R group to palmitate conversion
ARTPLM2 R group to palmitate conversion
ARTPLM2m R group to palmitate conversion
ARTPLM3 R group to palmitate conversion
ARTPLM3m R group to palmitate conversion
BAMPPALDOXm beta-Aminopropion aldehyde:NAD+ oxidoreductase (m)
BBHOX 4-Trimethylammoniobutanoate,2-oxoglutarate:oxygen oxidoreductase (3-hydroxylating)
BDG2HCGHD beta-D-Glucosyl-2-coumarinate glucohydrolase
BTNt2m Biotin reversible transport via proton symport, mitochondria
BZt benzoate transport (diffusion)
BZtr Benzene transporter, endoplasmic reticulum
C2M26DCOAHLm cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (m)
C2M26DCOAHLx cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (x)
CBL2OR NADH:cob(III)alamine oxidoreductase
CBL2tm Cob(II)alamine transport, mitochondrial
CBLATm cob(I)alamin adenosyltransferase, mitochondrial
CBPPer Carbamoyl phosphate phosphotransferase, endoplasmic reticulum
CBPter carbamoyl phosphate transport, endoplasmic reticulum
CBR1 Carbonyl reductase [NADPH] 1
CCA_D3t Calcitroic acid transport from cytosol
CCA_D3tm Calcitroic acid transport from mitochondria
CHSTEROLtg cholesterol efflux (ATP depedent), golgi
CHTNASE chitinase
CITMCOAHm L-Citramalyl-CoA hydro-lyase, mitochondrial
CITMCOALm L-Citramalyl-CoA pyruvate-lyase

CLPNDCPT1 carnitine O-palmitoyltransferase
CLPNDCPT2 carnitine transferase
CLPNDCRNt transport into the mitochondria (carnitine)
CO2tg CO2 Golgi transport
CO2tn CO2 nuclear transport via diffusion
COKECBESr Carboxylesterase (cocaine) (er)
CPCTDTX choline-phosphate cytidylyltransferase
CRTNsyn Creatinine synthase
CRTSLtr cortisol intracellular transport
CRTSTRNtr corticosterone intracellular transport
CSPG_At chondroitin sulfate A transport, golgi to extracellular
CSPG_Bt chondroitin sulfate B transport, golgi to extracellular
CSPG_Ct chondroitin sulfate C transport, golgi to extracellular
CSPG_Dt chondroitin sulfate D transport, golgi to extracellular
CSPG_Et chondroitin sulfate E transport, golgi to extracellular
CYOOm2 cytochrome c oxidase, mitochondrial Complex IV
CYSLYSL L-Cystine Lysteine-lyase (deaminating)
CYSTAm cysteine transaminase (mitochondrial)
CYTDtl Cytidine facilated transport from lysosome
DALAt2rL D-alanine transport via proton symport (lysosome)
DARGOp D-arginine oxidase, perixosomal
DASCBH L-Dehydroascorbate lactonohydrolase
DCIm dodecenoyl-Coenzyme A delta isomerase
DCK1m Deoxycytidine kinase, mitochondrial (ATP)
DEDOLP1_L dehydrodolichol diphosphate phosphatase (liver)
DEDOLP1_U dehydrodolichol diphosphate phosphatase (uterus)
DEDOLP2_L dehydrodolichol phosphate phosphatase (liver)
DEDOLP2_U dehydrodolichol phosphate phosphatase (uterus)
DEDOLR_L dehydrodolichol reductase (liver)
DEDOLR_U dehydrodolichol reductase (uterus)
DHAPA dihydroxyacetone phosphate acyltransferase
DHAPAx dihydroxyacetone phosphate acyltransferase
DHEAStr dheas intracellular transport
D_LACtm D-lactate transport, mitochondrial
DM_m_em_3gacpail_prot_hs_r_ DM m(em)3gacpail prot hs(r)
DMHPTCRNCPT1 carnitine fatty-acyl transferase
DNAMTn DNA (cytosine-5-)-methyltransferase, nucleus
DNAMTSEn DNA (cytosine-5-)-methyltransferase, nucleus
DOGULND1 2,3-dioxo-L-gulonate decarboxylase (L-lyxonate-forming)
DOGULND2 2,3-dioxo-L-gulonate decarboxylase (L-xylonate-forming)
DOGULNO1 2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase
DOGULNO2 2,3-dioxo-L-gulonate:hydrogen peroxide oxireductase
DOPAMT Dopamine:amet O-methyltransferase
DORNOp D-ornithine oxidase, perixosomal
DPROOp D-proline oxidase, perixosomal
ECGISOr Ecgonine isomerase (ER)
ECOAH1x 3-hydroxyacyl-CoA dehydratase (3-hydroxybutanoyl-CoA) (perioxisome)
EGMESTr ecgonine methyl esterase (ER)
EHGLAT L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase
ENGASE endo-beta-N-acetylglucosaminidase
ENGASE2 endo-beta-N-acetylglucosaminidase
ENMAN1g Endomannosidase (glc1man-producing), Golgi apparatus
ENMAN2g Endomannosidase (glc2man-producing), Golgi apparatus
ENMAN3g Endomannosidase (glc3man-producing), Golgi apparatus
ENMAN4g Endomannosidase (m6masnC-producing), Golgi apparatus
ENMAN5g Endomannosidase (m6masnB2-producing), Golgi apparatus
ENMAN6g Endomannosidase (m5masnB1-producing), Golgi apparatus
EPCTX ethanolamine-phosphate cytidylyltransferase
ESTRIOLGLCte glucuronidated compound transport
ESTRIOLGLCtr glucuronidated compound transport
ESTRIOLtr estriol intracellular transport
EX_2425dhvitd2(e) 24R,25-Dihyoxyvitamin D2 exchange
EX_25hvitd2(e) 25-Hydroxyvitamin D2 exchange
EX_ahandrostanglc(e) Etiocholan-3alpha-ol-17-one 3-glucuronide exchange
EX_aqcobal(e) Aquacob(III)alamin exchange
EX_bz(e) Benzoate exchange
EX_ca2(e) Calcium exchange
EX_cca_d3(e) Calcitroic acid (D3) exchange
EX_estriolglc(e) 16-Glucuronide-estriol exchange
EX_hom_L(e) L-Homoserine exchange
EX_k(e) K+ exchange
EX_lipoate(e) Lipoate exchange
EX_na1(e) exchange reaction for Sodium
EX_nifedipine(e) nifedipine exchange
EX_peplys(e) Peptidyl-L-lysine exchange
EX_phyQ(e) Phylloquinone exchange
EX_pro_D(e) D-Proline exchange
EX_sel(e) Selenate exchange
EX_ser_D(e) D-Serine exchange
EX_vitd2(e) Vitamin D2 exchange

EX_androsterone(e) 17-hydroxy-testosterone exchange
EX_xolest_hs(e) cholesterol ester exchange
FA120ACPH fatty-acyl-ACP hydrolase
FA140ACPH fatty-acyl-ACP hydrolase
FA141ACPH fatty-acyl-ACP hydrolase
FA160ACPH fatty-acyl-ACP hydrolase
FA161ACPH fatty-acyl-ACP hydrolase
FA180ACPH fatty-acyl-ACP hydrolase
FA181ACPH fatty-acyl-ACP hydrolase
FA1821ACPH fatty-acyl-ACP hydrolase
FA1822ACPH fatty-acyl-ACP hydrolase
FA182ACPH fatty-acyl-ACP hydrolase
FORtrn Formate transport, nuclear
FRTT farnesyltranstransferase
FT farnesyltranstransferase (trans,trans,cis-geranylgeranyl diphosphate-generating)
G1M6MASNB1terg g1m6masnB1 endoplasmic reticulum to Golgi transport
G1M7MASNBterg g1m7masnC endoplasmic reticulum to Golgi transport
G1M7MASNCterg g1m7masnC endoplasmic reticulum to Golgi transport
G1M8MASNterg g1m8masn transport from endoplasmic reticulum to Golgi apparatus
G1PTT glucose-1-phosphate thymidylyltransferase
G2M8MASNterg g2m8masn transport from endoplasmic reticulum to Golgi apparatus
G3M8MASNterg g3m8masn transport from endoplasmic reticulum to Golgi apparatus
GALNACT1g UDPGal-chondroitin acetylgalactosaminyltransferase I, Golgi
GALNACT2g uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
GALNACT3g uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
GALNACT4g uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
GALNACT5g uridine diphosphoacetylgalactosamine-chondroitin acetylgalactosaminyltransferase II, Golgi
GALOR D-Galactose:NADP+ 1-oxidoreductase
GALT2g UDP-D-galactose:galactosylxylose galactosyltransferase, Golgi apparatus
GALTg UDP-D-galactose:D-xylose galactosyltransferase, Golgi apparatus
GAO1 Ganglioside O-acetylation
GAO2 Ganglioside O-acetylation
GCALDDm Glycolaldehyde dehydrogenase, mitochondrial
GGT_L geranylgeranyltransferase (liver)
GGT_U geranylgeranyltransferase (uterus)
GHMT3 glycine hydroxymethyltransferase
GHMT3m glycine hydroxymethyltransferase, mitochondrial
GK1m guanylate kinase (GMP:ATP), mitochondrial
GLACO D-Glucuronolactone:NAD+ oxidoreductase
GLACOm D-Glucuronolactone:NAD+ oxidoreductase, mitochondrial
GLCAE1g chondroitin-glucuronate 5-epimerase
GLCAE2g heparosan-N-sulfate-glucuronate 5-epimerase
GLCAT2g chondroitin glucuronyltransferase II, Golgi apparatus
GLCAT3g chondroitin glucuronyltransferase II, Golgi apparatus
GLCAT4g chondroitin glucuronyltransferase II, Golgi apparatus
GLCAT5g chondroitin glucuronyltransferase II, Golgi apparatus
GLCAT6g heparan glucuronyltransferase II
GLCAT7g heparan glucuronyltransferase II
GLCAT8g heparan glucuronyltransferase II
GLCAT9g heparan glucuronyltransferase II
GLCATg UDP-D-glucuronate:galactosylgalactosylxylose glucuronosyltransferase, Golgi apparatus
GLCNACDASg GlcNAc N-deacetylase / N-sulfotransferase
GLCNACT1g alpha-N-acetylglucosaminyltransferase I, Golgi apparatus
GLCNACT2g alpha-N-acetylglucosaminyltransferase II
GLCNACT3g alpha-N-acetylglucosaminyltransferase II
GLCNACT4g alpha-N-acetylglucosaminyltransferase II
GLCNACT5g alpha-N-acetylglucosaminyltransferase II
GLYCLTDym Glycolate dehydrogenase (NADP), mitochondrial
GLYOXm hydroxyacylglutathione hydrolase, mitochondrial
GLYt2rL glycine reversible transport via proton symport (lysosome)
GPAMm_hs glycerol-3-phosphate acyltransferase
GSNKm guanosine kinase (mitochondrial)
GSNtl guanosine facilated transport from lysosome
GSNtm guanosine facilated transport in mitochondria
GTPCI GTP cyclohydrolase I
GTPCIn GTP cyclohydrolase I, nuclear
GTPtn GTP diffusion in nucleus
H2CO3Dm carboxylic acid dissociation
H8MTer_L H8 mannosyltransferase, endoplasmic reticulum
H8MTer_U H8 mannosyltransferase, endoplasmic reticulum
HACD1x 3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) (peroxisome)
HEXCCPT1 carnitine O-palmitoyltransferase
HEXCCPT2 carnitine transferase
HEXCCRNt transport into the mitochondria (carnitine)
HISTASE Histaminase
HMGCOARr Hydroxymethylglutaryl CoA reductase (ir)
HPYRDCm hydroxypyruvate decarboxylase, mitochondria
HSD3B13 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type I
HSPGt heparan sulfate transport, golgi to extracellular
HXANtl hypoxanthine facilated transport from lysosome
IMACTD Imidazole acetaldeyde dehydrogenase

IMACTD_m Imidazole acetaldeyde dehydrogenase (mito)
INSKm inosine kinase, mitochondrial
INStl inosine facilated transport from lysosome
INStm inosine facilated transport in mitochondria
IPDPtr Isopentenyl diphosphate transport (ER)
Kt3g potassium transport via proton antiport
LACZly b-galactosidase,lysosomal
LCADi_Dm lactaldehyde dehydrogenase, mitochondrial
LCADim lactaldehyde dehydrogenase, mitochondrial
LCTStl lactose transport from cytosol to lysosome (via autophagocytosis)
LCYSTATm L-Cysteate:2-oxoglutarate aminotransferase, mitochondrial
LDH_Lm L-lactate dehydrogenase
LEUKTRB4tr leukotriene intracellular transport
LGNCCPT1 carnitine O-palmitoyltransferase
LGNCCPT2 transport into the mitochondria (carnitine)
LGNCCRNt transport into the mitochondria (carnitine)
LIPOti Lipoate transport via sodium symport
L_LACtcm L-lactate transport via diffusion (cytosol to mitochondria)
LNS14DM cytochrome P450 lanosterol 14-alpha-demethylase (NADP)
LS3 Lumisterol 3 formation
LTDCL L-Tryptophan decarboxy-lyase
LYSMTF1n histone-lysine N-methyltransferase, nuclear
LYSMTF2n histone-lysine N-methyltransferase, nuclear
LYSMTF3n histone-lysine N-methyltransferase, nuclear
M4ATAer M4A transamidase, endoplasmic reticulum
M4BET2er M4B phosphoethanolaminyl transferase, endoplasmic reticulum
MALTly alpha-glucosidase, lysosomal
MAN1_6B1er mannosidase I, endoplasmic reticulum (g1m6masnB1-producing)
MAN1_7Ber mannosidase I, endoplasmic reticulum (g1m7masnB-producing)
MAN2_6B1er mannosidase II, endoplasmic reticulum (g1m6masnB1-producing)
MAN2_7Cer mannosidase II, endoplasmic reticulum (g1m7masnC-producing)
MAOLNOR monoamine oxidase (L-Normetanephrine)
MCDp Malonyl-CoA Decarboxylase peroxisomal
MCOATA Malonyl-CoA-ACP transacylase
MCOATAm Malonyl-CoA-ACP transacylase, mitochondrial
MELATN23DOX Melatonin:oxygen 2,3-dioxygenase (indole-decyclizing)
MEOHtr Methanol transporter, endoplasmic reticulum
MESCOALm Mesaconyl-CoA pyruvate-lyase
MGACONm methylglutaconase, mitochondrial
MI13456PK inositol-1,3,4,5,6-pentakisphosphate 2-kinase
MI13456Ptn inositol 1,3,4,5,6-pentakisphosphate nuclear transport (diffusion)
MI1345PKn inositol-1,3,4,5-triphosphate 6-kinase, nucleus
MI1346PKn inositol-1,3,4,6-tetrakisphosphate 5-kinase, nucleus
MI1346Ptn 1D-myo-Inositol 1,3,4,6-tetrakisphosphate nuclear transport (diffusion)
MI134PK inositol-1,3,4-trisphosphate 6-kinase
MI1456PKn inositol-1,4,5,6- tetrakisphosphate 3-kinase, nucleus
MI145P6Kn inositol-1,4,5-triphosphate 6-kinase, nucleus
MI145PKn inositol-1,4,5-trisphosphate 3-kinase, nucleus
MI3456PK inositol-3,4,5,6-tetrakisphosphate 1-kinase
MICITDr 2-methylisocitrate dehydratase
MINOHPtn inositol hexakisphosphate nuclear transport (diffusion)
MLTG1 Maltodextrin glucosidase (maltotriose)
MLTG1ly Maltodextrin glucosidase (maltotriose), lysosome
MMCD Methylmalonyl-CoA decarboxylase
MMCDp Methylmalonyl-CoA decarboxylase, peroxisomal
NABTNO N4-Acetylaminobutanal:NAD+ oxidoreductase
NABTNOm N4-Acetylaminobutanal:NAD+ oxidoreductase (m)
NADK NAD kinase
NADPN NADP nucleosidase
NAt3_1g sodium proton antiporter (H:NA is 1:1)
NDPK10m nucleoside-diphosphate kinase (ATP:dIDP), mitochondrial
NDPK2m nucleoside-diphosphate kinase (ATP:UDP), mitochondrial
NDPK9m nucleoside-diphosphate kinase (ATP:IDP), mitochondrial
NIFEDIPINEte xenobiotic transport
NMNATm nicotinamide-nucleotide adenylyltransferase, mitochondrial
NMPTRCOX N-Methylputrescine:oxygen oxidoreductase (deaminating)
NNATm nicotinate-nucleotide adenylyltransferase, mitochondrial
NRVNCCPT1 carnitine O-palmitoyltransferase
NRVNCCPT2 carnitine transferase
NRVNCCRNt transport into the mitochondria (carnitine)
NTD12 5'-nucleotidase (dIMP)
NTD2l 5'-nucleotidase (UMP), lysosome
NTD2m 5'-nucleotidase (UMP), mitochondrial
NTD3l 5'-nucleotidase (dCMP), lysosomal
NTD4l 5'-nucleotidase (CMP), lysosome
NTD5l 5'-nucleotidase (dTMP), lysosomal
NTD6l 5'-nucleotidase (dAMP), lysosome
NTD7l 5'-nucleotidase (AMP), lysosome
NTD8l 5'-nucleotidase (dGMP), lysosomal
NTD9l 5'-nucleotidase (GMP), lysosome

NTMELYStner protein trimethyl lysine transport (nucleus to ER)
NTPP10 Nucleoside triphosphate pyrophosphorylase (ditp)
NTPP11 Nucleoside triphosphate pyrophosphorylase (xtp)
NTPP9 Nucleoside triphosphate pyrophosphorylase (itp)
P4503A4 cytochrome P450 3A4
P4503A43r cytochrome p450 P450 3A43
P4504B1r cytochrome P450 4B1
P4504F121r cytochrome p450 4F12/4F2
P4504F122r cytochrome p450 4F12/4F2
P4504F81r cytochrome p450 4F8
P450LTB4r cytochrome p450 leukotriene B4
PCLYSOX Procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase
PDE1g 3',5'-cyclic-nucleotide phosphodiesterase,Golgi
PDE4g 3',5'-cyclic-nucleotide phosphodiesterase, Golgi
PE_HStg phosphatidylethanolamine scramblase
PECGONCOATr Pseudoecgonine CoA transferase (ER)
PEPLYStn peptide (lysine) nuclear transport via diffusion
PGDIr Prostaglandin-H2 D-isomerase [Precursor]
PGESr Prostaglandin E synthase
PGLYCP Phosphoglycolate phosphatase
PHETA1 phenylalanine transaminase
PHETA1m phenylalanine transaminase (m)
PI45PLCn phosphatidylinositol 4,5-bisphosphate phospholipase C, nucleus
PI4P3Ker phosphatidylinositol 4-phosphate 3-kinase, endoplasmic reticulum
PI5P3Ker phosphatidylinositol-5-phosphate 3-kinase, endoplasmic reticulum
PIt2m phosphate transporter, mitochondrial
PLA2 phospholipase A2
PLYSPSer protein lysine peptidase (endoplasmic reticulum)
PMI12346PH 5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase
PMI12346PHn 5-diphosphoinositol-1,2,3,4,6-pentakisphosphate diphosphohydrolase, nuclear
PMI1346PH diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase
PMI1346PHn diphosphoinositol-1,3,4,6-tetrakisphosphate diphosphohydrolase, nucleus
PNTKm pantothenate kinase (mitochondrial)
PPA2 inorganic triphosphatase
PPA2m inorganic triphosphatase, mitochondrial
PPMI12346Ptn 5-diphosphatidylinositol pentakisphosphate nuclear transport (diffusion)
PPMI1346Ptn diphosphatidylinositol tetrakisphosphate nuclear transport (diffusion)
PPOR Phenylpyruvate:oxygen oxidoreductase (hydroxylating,decarboxylating)
PPPItn Inorganic triphosphate transport through nuclear pore
PROAKGOX1r L-Proline,2-oxoglutarate:oxygen oxidoreductase (4-hydroxylating) (ER)
PRODt2r D-proline reversible transport via proton symport
PRODt2rL D-proline reversible transport via proton symport (lysosome)
PROt2rL L-proline reversible transport via proton symport (lysosome)
PROtm L-proline transport, mitochondrial
PRPNCOAHYDx Propenoyl-CoA hydrolase (x)
PS_HSter phosphatidylserine scramblase
PS_HStg phosphatidylserine scramblase
PTE2x peroxisomal acyl-CoA thioesterase
PTE5x peroxisomal acyl-CoA thioesterase
PTHPS 6-pyruvoyltetrahydropterin synthase
PTHPSn 6-pyruvoyltetrahydropterin synthase, nuclear
PTRCAT1 Putrescine acetyltransferase
PYAM5Ptm Pyridoxamine 5'-phosphate transport via diffusion, mitochondrial
PYDX5Ptm Pyridoxal 5'-phosphate transport via diffusion, mitochondrial
PYLALDOX Perillyl aldehyde:NAD+ oxidoreductase
PYLALDOXm Perillyl aldehyde:NAD+ oxidoreductase (m)
QUILSYN Quinolinate Synthase (Eukaryotic)
RAtn Retinoate transport, nuclear
RBK_D D-ribulokinase
RETNCOA Retinoyl CoA formation
RTOT_2 R total flux 2 position
RTOT_3 R total flux 3 position
RTOT1 R total flux
RTOT2 R total flux
RTOT3 R total flux
RTOT4 R total flux
RTOT5 R total flux
RTOT6 R total flux
RTOTAL2CRNCPT1 carnitine fatty-acyl transferase
RTOTAL2CRNCPT2 R group transport into the mitochondria
RTOTAL2CRNt R group transport into the mitochondria
RTOTAL3CRNCPT1 carnitine fatty-acyl transferase
RTOTAL3CRNCPT2 R group transport into the mitochondria
RTOTAL3CRNt R group transport into the mitochondria
RTOTALCRNCPT1 carnitine fatty-acyl transferase
RTOTALCRNCPT2 R group transport into the mitochondria
RTOTALCRNt R group transport into the mitochondria
Rtotaltp fatty acid intracellular transport
S2T1g chondroitin 2-sulfotransferase, Golgi
S2T2g chondroitin 2-sulfotransferase, Golgi
S2T3g uronyl 2-sulfotransferase, Golgi

S2T4g uronyl 2-sulfotransferase, Golgi
S3T1g heparin-glucosamine 3-O-sulfotransferase
S3T2g heparin-glucosamine 3-O-sulfotransferase
S3T3g heparin-glucosamine 3-O-sulfotransferase
S4T1g chondroitin 4-sulfotransferase, Golgi apparatus
S4T2g chondroitin 4-sulfotransferase, Golgi apparatus
S4T3g chondroitin 4-sulfotransferase, Golgi apparatus
S4T4g chondroitin 4-sulfotransferase, Golgi apparatus
S4T5g chondroitin 4-sulfotransferase, Golgi apparatus
S4T6g chondroitin 4-sulfotransferase, Golgi apparatus
S6T19g chondroitin 6-sulfotransferase, Golgi apparatus
S6T20g chondroitin 6-sulfotransferase, Golgi apparatus
S6T21g chondroitin 6-sulfotransferase, Golgi apparatus
S6T22g chondroitin 6-sulfotransferase, Golgi apparatus
S6T23g chondroitin 6-sulfotransferase, Golgi apparatus
S6T24g chondroitin 6-sulfotransferase, Golgi apparatus
S6T25g heparan sulfate 6-sulfotransferase, Golgi apparatus
SALMCOM S-Adenosyl-L-methionine:catechol O-methyltransferase
SARCOXp sarcosine oxidase, peroxisomal
SARCStp Sarcosine transport (peroxisomal)
SEAHCYSHYD Se-Adenosylselenohomocysteine hydrolase
SEAHCYStn Se-adenosyl-seleno-L-homocysteine nuclear transport
SEASMETtn Se-adenosyl-seleno-L-methionine nuclear transport
SELADT selenate adenylyltransferase
SELCYSLY selenocysteine lyase
SELCYSLY2 selenocysteine lyase
SELCYSTGL selanocystathionine g-lyase
SELCYSTS selanocystathionine beta-synthase
SELMETAT selenomethionine adenosyltransferase
SELNPS Selenophosphate synthase
SELt4_3 selenate transport via sodium symport
SGPL11r Sphingosine-1-phosphate lyase 1
SIAASE sialidase
SLDxm L-sulfolactate dehydrogenase (NAD+), mitochondrial
SOAT11 sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
SOAT11r sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
SOAT12 sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
SOAT12r sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1
SPR sepiapterin reductase
SPRn sepiapterin reductase, nuclear
SRTN23OX 5-Hydroxytryptamine:oxygen 2,3-dioxygenase (indole-decyclizing)
SRTNACT Acetyl-CoA:aralkylamine N-acetyltransferase
SRTNMTX S-Adenosyl-L-methionine:amine N-methyltransferase (srtn)
STS1r Steryl-sulfatase
STS2r Steryl-sulfatase
T2M26DCOAHLm trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (m)
T2M26DCOAHLx trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA hydro-lyase (x)
T4HCINNOX 4-Coumarate:oxygen oxidoreductase
TDPDRE dTDP-4-dehydrorhamnose 3,5-epimerase
TDPDRR dTDP-4-dehydrorhamnose reductase
TDPGDH dTDPglucose 4,6-dehydratase
TETPENT3CPT1 carnitine O-palmitoyltransferase
TETPENT3CPT2 carnitine transferase
TETPENT3CRNt transport into the mitochondria (carnitine)
TETPENT6CPT1 carnitine O-palmitoyltransferase
TETPENT6CPT2 carnitine transferase
TETPENT6CRNt transport into the mitochondria (carnitine)
TETTET6CPT1 carnitine O-palmitoyltransferase
TETTET6CPT2 carnitine transferase
TETTET6CRNt transport into the mitochondria (carnitine)
THMt2m Thiamine transport in via proton symport, mitochondrial
THRS threonine synthase
THYMDtl thymidine facilated transport from lysosome
TMABADH 4-trimethylaminobutyraldehyde dehydrogenase
TMLYSOX trimethyllysine dioxygenase
TMLYSter trimethyl-L-lysine transport (ER to cytosol)
TRDRm thioredoxin reductase (NADPH)
TREH alpha,alpha-trehalase
TRYPTAOX Tryptamine:oxygen oxidoreductase(deaminating)(flavin-containing)
TS3 Tachysterol 3 formation
UDPGALt2g UDPgalactose transport (Golgi)
UDPGLCAtg UDPGlcA Golgi transport via UMP antiport
UDPGLCtg UDP-Glc Golgi transport via CMP antiport
UDPGLDCg UDP-D-glucuronate decarboxylase, Golgi apparatus
UDPXYLter UDP-Xyl endoplasmic reticular transport via CMP antiport
UDPXYLtg UDP-Xyl Golgi transport via CMP antiport
UGALNACter UDP-GalNAc endoplasmic reticulum transport via CMP antiport
UGT1A7r UDP-glucuronosyltransferase 1-10 precursor, microsomal
UGT1A8r UDP-glucuronosyltransferase 1-10 precursor, microsomal
UMPKm UMP kinase (mitochondrial, ATP)

```
        UridtU uridine facilated transport from lysosome
         Uritm uridine facilated transport in mitochondria
         UTPtn UTP diffusion in nucleus
       VITD2Hm Vitamin D-25-hydroxylase (D2)
        VITD2t Vitamin D2 release
       VITD2tm Vitamin D2 transport from mitochondria
       VITD3Hm Vitamin D-25-hydroxylase (D3)
       VITD3tm Vitamin D3 transport from mitochondria
WHTSTSTERONEte omega hydroxy testosterone transport
     XOL7AH2tr lipid, flip-flop intracellular transport
  XOLDIOLONEtm lipid, flip-flop intracellular transport
      XOLESTte cholesterol ester transporter
    XOLTRIOLtr lipid, flip-flop intracellular transport
        XSERtg Xyl-L-Ser (protein) transport from endoplasmic reticulum to Golgi apparatus
        XYLTer UDP-xylose:protein xylosyltransferase, endoplasmic reticulum
 EX_HC01440(e) Exchange of 3-Keto-beta-D-galactose
 EX_HC01441(e) Exchange of Lactose-6P
 EX_HC01446(e) Exchange of 3-Ketolactose
 EX_HC01577(e) Exchange of gamma-Glutamyl-beta-cyanoalanine
 EX_HC01700(e) Exchange of gamma-Glutamyl-3-aminopropiononitrile
 EX_HC02160(e) Exchange of GM2-pool
 EX_HC02161(e) Exchange of GM1-pool
         r0001 Virtual reaction/potential definition
         r0023 NADH:ferricytochrome-b5 oxidoreductase Aminosugars metabolism EC:1.6.2.2
         r0024 N-(omega)-Hydroxyarginine,NADPH:oxygen oxidoreductase (nitric-oxide-forming) Arginine and proline metabolism EC:1.14.13.39
         r0120 GTP 7,8-8,9-dihydrolase Folate biosynthesis EC:3.5.4.16
         r0121 r0121
         r0205 sn-Glycerol-3-phosphate:(acceptor) 2-oxidoreductase Glycerophospholipid metabolism EC:1.1.5.3
         r0220 Propinol adenylate:CoA ligase (AMP-forming) Propanoate metabolism EC:6.2.1.17 EC:6.2.1.1
         r0221 Propinol adenylate:CoA ligase (AMP-forming) Propanoate metabolism EC:6.2.1.17
         r0318 Propanoate:CoA ligase (AMP-forming) Propanoate metabolism EC:6.2.1.1 EC:6.2.1.17
         r0319 Propanoate:CoA ligase (AMP-forming) Propanoate metabolism EC:6.2.1.1 EC:6.2.1.17
         r0366 [Acyl-carrier-protein] 4-pantetheine-phosphohydrolase Pantothenate and CoA biosynthesis EC:3.1.4.14
         r0368 CoA:apo-[acyl-carrier-protein] pantetheinephosphotransferase Pantothenate and CoA biosynthesis EC:2.7.8.7
         r0380 Lactose 6-phosphate galactohydrolase Galactose metabolism EC:3.2.1.23
         r0402 Tetrahydrobiopterin:NADP+ oxidoreductase Folate biosynthesis EC:1.1.1.153
         r0430 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0431 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0432 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0433 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0438 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0439 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0440 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0444 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0445 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0446 Palmitoyl-CoA:L-carnitine O-palmitoyltransferase Fatty acid metabolism EC:2.3.1.21
         r0465 L-Histidine:4-aminobutanoate ligase (AMP-forming) Urea cycle and metabolism of amino groups EC:6.3.2.11
         r0466 alpha-Aminobutyryl histidine hydrolase Urea cycle and metabolism of amino groups EC:3.4.13.3
         r0510 steroyl-CoA,hydrogen-donor:oxygen oxidoreductase Polyunsaturated fatty acid biosynthesis EC:1.14.19.1
         r0511 steroyl-CoA,hydrogen-donor:oxygen oxidoreductase Polyunsaturated fatty acid biosynthesis EC:1.14.19.1
         r0537 Sphinganine-1-phosphate pamlmitaldehyde-lyase Sphingolipid metabolism EC:4.1.2.27
         r0546 Phenylacetaldehyde:NAD+ oxidoreductase Phenylalanine metabolism / Styrene degradation EC:1.2.1.5 EC:1.2.1.39
         r0548 Aldehyde:NADP+ oxidoreductase Phenylalanine metabolism EC:1.2.1.5
         r0598 L-Fucose ketol-isomerase Fructose and mannose metabolism EC:5.3.1.25
         r0625 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholestan-26-al:NAD+ 26-oxidoreductase Bile acid biosynthesis EC:1.2.1.40
         r0626 5beta-Cholestane-3alpha,7alpha,12alpha,26-tetraol:NAD+ 26-oxidoreductase Bile acid biosynthesis EC:1.1.1.161
         r0648 (5-Glutamyl)-peptide:amino-acid 5-glutamyltransferase Cyanoamino acid metabolism EC:2.3.2.2
         r0649 (5-Glutamyl)-peptide:amino-acid 5-glutamyltransferase Cyanoamino acid metabolism EC:2.3.2.2
         r0673 6-Lactoyl-5,6,7,8-tetrahydropterin:NADP+ 2-oxidoreductase Folate biosynthesis EC:1.1.1.220
         r0678 Acyl-[acyl-carrier-protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating) Fatty acid biosynthesis EC:2.3.1.85
         r0681 (3R)-3-Hydroxybutanoyl-[acyl-carrier-protein] hydro-lyase Fatty acid biosynthesis EC:2.3.1.85
         r0682 Butyryl-[acyl-carrier protein]:malonyl-CoA C-acyltransferase(decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydrolysin
         r0691 (3R)-3-Hydroxybutanoyl-[acyl-carrier protein]:NADP+ oxidoreductase Fatty acid biosynthesis EC:2.3.1.85
         r0692 (3R)-3-Hydroxydecanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase Fatty acid biosynthesis EC:2.3.1.85
         r0693 (3R)-3-Hydroxybutanoyl-[acyl-carrier-protein] hydro-lyase Fatty acid biosynthesis EC:2.3.1.85
         r0694 (3R)-3-Hydroxyoctanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase Fatty acid biosynthesis EC:2.3.1.85
         r0695 (3R)-3-Hydroxybutanoyl-[acyl-carrier-protein] hydro-lyase; (3R)-3-Hydroxyoctanoyl-[acyl-carrier-protein] hydro-lyase Fatty acid bi
         r0696 (3R)-3-Hydroxypalmitoyl-[acyl-carrier-protein]:NADP+ oxidoreductase Fatty acid biosynthesis EC:2.3.1.85
         r0697 (3R)-3-Hydroxypalmitoyl-[acyl-carrier-protein] hydro-lyase Fatty acid biosynthesis EC:2.3.1.85
         r0701 (3R)-3-Hydroxytetradecanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase Fatty acid biosynthesis EC:2.3.1.85
         r0702 (3R)-3-Hydroxypalmitoyl-[acyl-carrier-protein] hydro-lyase Fatty acid biosynthesis EC:2.3.1.85
         r0708 2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl) dihydropteridine triphosphate 7,8-8,9-dihydrolase Folate biosynthesis EC:3.5.
         r0709 r0709
         r0712 Dodecanoyl-[acyl-carrier protein]: malonyl-CoA C-acyltransferase(decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydrol
         r0713 dodecanoyl-[acyl-carrier-protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating) Fatty acid biosynthesis EC:2.
         r0737 3-Ketolactose galactohydrolase Galactose metabolism EC:3.2.1.23
         r0760 butyryl-[acyl-carrier protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating) Fatty acid biosynthesis EC:2.3.1
         r0761 (3R)-3-Hydroxyhexanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase Fatty acid biosynthesis EC:2.3.1.85
         r0762 (3R)-3-Hydroxybutanoyl-[acyl-carrier-protein] hydro-lyase Fatty acid biosynthesis EC:2.3.1.85
         r0763 Hexanoyl-[acyl-carrier protein]:oxoacyl- and enoyl-reducing and thioester-hydrolysing) Fatty acid biosynthesis EC:2.3.1.85
         r0764 hexanoyl-[acyl-carrier protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating) Fatty acid biosynthesis EC:2.3.
```

r0765 Octanoyl-[acyl-carrier protein]:malonyl-CoA C-acyltransferase(decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydrolysi
r0766 Octanoyl-[acyl-carrier protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating) Fatty acid biosynthesis EC:2.3.
r0767 Decanoyl-[acyl-carrier protein]:malonyl-CoA C-acyltransferase(decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydrolysi
r0768 Decanoyl-[acyl-carrier protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating) Fatty acid biosynthesis EC:2.3.
r0769 (3R)-3-Hydroxydodecanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase Fatty acid biosynthesis EC:2.3.1.85
r0770 (3R)-3-Hydroxybutanoyl-[acyl-carrier-protein] hydro-lyase Fatty acid biosynthesis EC:2.3.1.85
r0771 Tetradecanoyl-[acyl-carrier protein]:malonyl-CoA C-acyltransferase(decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydr
r0772 Tetradecanoyl-[acyl-carrier protein]:malonyl-[acyl-carrier-protein] C-acyltransferase (decarboxylating) Fatty acid biosynthesis EC
r0773 Hexadecanoyl-[acyl-carrier protein:malonyl-CoA C-acyltransferase(decarboxylating, oxoacyl- and enoyl-reducing and thioester-hydrol
r0775 Formamidopyrimidine nucleoside triphosphate 7,8-8,9-dihydrolase Folate biosynthesis EC:3.5.4.16
r0776 r0776
r0777 GTP 7,8-8,9-dihydrolase Folate biosynthesis EC:3.5.4.16
r0778 r0778
r0786 sphinganine-1-phosphate palmitaldehyde-lyase Sphingolipid metabolism EC:4.1.2.27
r0800 Virtual reaction/potential definition
r0802 Vesicular transport
r0803 Vesicular transport
r0804 Vesicular transport
r0805 Vesicular transport
r0806 Vesicular transport
r0807 Vesicular transport
r0808 Vesicular transport
r0825 Vesicular transport
r0826 Transport reaction
r0859 Postulated transport reaction
r0886 Postulated transport reaction
r0925 Vesicular transport
r0927 Free diffusion
r0988 Postulated transport reaction
r0992 Na(+)/bile acid cotransporter Active transport
r1000 Facilitated diffusion
r1001 Facilitated diffusion
r1002 Facilitated diffusion
r1003 Facilitated diffusion
r1004 Facilitated diffusion
r1005 Facilitated diffusion
r1006 Facilitated diffusion
r1021 Postulated transport reaction
r1027 Active transport
r1033 Vesicular transport
r1034 Vesicular transport
r1048 Vesicular transport
r1049 Vesicular transport
r1054 Vesicular transport
r1055 Vesicular transport
r1056 Vesicular transport
r1057 Vesicular transport
r1059 Major Facilitator(MFS) TCDB:2.A.18.6.7
r1061 Vesicular transport
r1062 Vesicular transport
r1063 Vesicular transport
r1064 Postulated transport reaction
r1067 Vesicular transport
r1068 Vesicular transport
r1071 Transport reaction
r1073 Transport reaction
r1074 Vesicular transport
r1076 Postulated transport reaction
r1077 Vesicular transport
r1080 Vesicular transport
r1081 Vesicular transport
r1082 Vesicular transport
r1092 albumin Protein assembly
r1093 serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 Protein assembly
r1094 serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 Protein assembly
r1095 apolipoprotein B Protein assembly
r1096 NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 Protein assembly
r1097 ACP Protein assembly
r1098 Apo-CIB Protein assembly
r1099 Apo-CII Protein assembly
r1100 Apo-CIII Protein assembly
r1101 Fibrinogen alpha chain Protein assembly
r1102 Haptoglobin Protein assembly
r1103 Plasminogen Protein assembly
r1104 Prothrombin Protein assembly
r1105 T9 Protein assembly
r1112 Apo-E Protein assembly
r1113 Apo-AI Protein assembly
r1127 Transport reaction
r1128 Transport reaction

r1129 Transport reaction
r1130 Transport reaction
r1131 Transport reaction
r1132 Transport reaction
r1133 Transport reaction
r1134 methylsterol monooxygenase Biosynthesis of steroids EC:1.14.13.72
r1135 hydroxysteroid (17-beta) dehydrogenase 7 Biosynthesis of steroids EC:1.1.1.270
r1136 sterol-4alpha-carboxylate 3-dehydrogenase (decarboxylating) Biosynthesis of steroids EC:1.1.1.170
r1137 NAD(P) dependent steroid dehydrogenase-like EC:1.1.1.170
r1140 Vesicular transport
r1146 Biosynthesis of steroids Enzyme catalyzed
r1159 Vesicular transport
r1165 EC:2.3.1.26
r1166 EC:2.3.1.26
r1169 EC:2.3.1.26
r1170 EC:2.3.1.26
r1171 EC:2.3.1.26
r1173 EC:3.1.1.13
r1174 EC:3.1.1.13
r1175 EC:3.1.1.13
r1176 EC:3.1.1.13
r1178 EC:3.1.1.13
r1180 EC:3.1.1.13
r1181 EC:3.1.1.13
r1182 EC:3.1.1.13
r1183 EC:3.1.1.13
r1184 EC:3.1.1.13
r1185 EC:2.3.1.15
r1186 EC:2.3.1.15
r1187 EC:2.3.1.15
r1188 EC:2.3.1.15
r1189 EC:2.3.1.15
r1190 EC:2.3.1.15
r1251 EC:6.2.1.3
r1253 EC:6.2.1.3
r1290 Postulated transport reaction
r1293 ADF Protein assembly
r1294 MTRX Protein assembly
r1313 3-oxoacyl-ACP synthase, mitochondrial Polyunsaturated fatty acid biosynthesis EC:2.3.1.85
r1314 fatty acid synthase Polyunsaturated fatty acid biosynthesis EC:2.3.1.85
r1315 fatty acid synthase Polyunsaturated fatty acid biosynthesis EC:2.3.1.85
r1316 fatty acid synthase Polyunsaturated fatty acid biosynthesis EC:2.3.1.85
r1317 oleoyl-ACP hydrolase EC:2.3.1.85
r1319 Virtual reaction/potential definition
r1320 Virtual reaction/potential definition
r1321 Virtual reaction/potential definition
r1322 Virtual reaction/potential definition
r1323 Virtual reaction/potential definition
r1324 Virtual reaction/potential definition
r1325 Virtual reaction/potential definition
r1326 Virtual reaction/potential definition
r1327 Virtual reaction/potential definition
r1328 Virtual reaction/potential definition
r1329 Virtual reaction/potential definition
r1330 Virtual reaction/potential definition
r1331 Virtual reaction/potential definition
r1332 Virtual reaction/potential definition
r1333 Protein degradation
r1334 Protein degradation
r1335 Protein degradation
r1336 Protein degradation
r1337 Protein degradation
r1338 Protein degradation
r1339 Protein degradation
r1340 Protein degradation
r1341 Protein degradation
r1342 Protein degradation
r1343 Protein degradation
r1344 Protein degradation
r1345 Protein degradation
r1346 Protein degradation
r1347 Protein degradation
r1348 Protein degradation
r1349 Protein degradation
r1350 Protein degradation
r1351 Protein degradation
r1352 Protein degradation
r1353 Protein degradation
r1354 Protein degradation
r1355 Protein degradation
r1356 Protein degradation

r1357 Protein degradation
r1358 Protein degradation
r1359 Protein degradation
r1382 folylpolyglutamyl synthetase EC:6.3.2.17
r1383 gamma-glutamyl hydrolase EC:3.4.19.9
r1386 Virtual reaction/potential definition
r1391 amylo-1,6-glucosidase, 4-alpha-glucanotransferase EC:2.4.1.25
r1392 amylo-1,6-glucosidase, 4-alpha-glucanotransferase EC:3.2.1.33
r1393 EC:2.4.1.1
r1394 EC:2.3.1.21
r1395 carnitine acetyltransferase EC:2.3.1.7
r1398 EC:2.3.1.21
r1399 carnitine acetyltransferase EC:2.3.1.7
r1402 glycogenin Protein assembly
r1403 Protein degradation
r1411 D-Galactosyl-N-acetyl-D-galactosaminyl-(N-acetylneuraminyl)-D- galactosyl-D-glucosylceramide galactohydrolase EC:3.2.1.23
r1430 [Acyl-carrier-protein] 4-pantetheine-phosphohydrolase Pantothenate and CoA biosynthesis EC:3.1.4.14
r1431 2-Deoxyuridine 5-diphosphate:oxidized-thioredoxin 2-oxidoreductase Pyrimidine metabolism EC:1.17.4.1
r1432 2-Deoxyuridine 5-diphosphate:oxidized-thioredoxin 2-oxidoreductase Pyrimidine metabolism EC:1.17.4.1
r1436 Transport reaction
r1437 Transport reaction
r1440 Transport reaction
r1441 Active transport
r1455 Transport reaction
r1457 hexadecanal:NADP+ delta2-oxidoreductase EC:1.3.1.27
r1468 Postulated transport reaction
r1472 long-chain-acyl-CoA dehydrogenase EC:1.3.99.13
r1474 EC:4.2.1.17
r1477 EC:1.1.1.35
r1479 EC:2.3.1.16
r1481 EC:2.3.1.16
r1501 Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter TCDB:2.A.28.1.1
r1502 Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter TCDB:2.A.28.1.1
r1503 Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter TCDB:2.A.28.1.1
r1526 ATP-binding Cassette (ABC) TCDB:3.A.1.211.1
r1531 ATP-binding Cassette (ABC) TCDB:3.A.1.208.15
r1532 ATP-binding Cassette (ABC) TCDB:3.A.1.208.15
r1533 ATP-binding Cassette (ABC) TCDB:3.A.1.208.15
r2073 Zinc (Zn2+)-Iron (Fe2+) Permease (ZIP), TCDB:2.A.55.2.3
r2143 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2146 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2147 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2148 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2149 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2151 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2152 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2153 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2154 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2155 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2156 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2157 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2158 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2159 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2160 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2161 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2162 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2163 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2164 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2165 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2166 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2167 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2168 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2169 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2170 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2171 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2172 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2173 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2174 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2175 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2176 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2177 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2178 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2179 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2180 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2181 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2182 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2183 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2184 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2185 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2186 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14

r2187 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2188 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2189 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2190 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2191 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2192 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2203 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2204 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2205 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2206 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2207 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2208 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2209 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2210 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2211 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2212 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2213 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2214 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2215 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2216 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2217 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2218 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2219 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2220 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2221 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2222 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2223 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2224 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2225 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2226 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2227 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2228 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2229 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2230 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2231 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2232 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2233 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2234 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2235 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2236 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2237 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2238 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2239 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2240 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2241 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2242 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2243 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2244 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2245 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2246 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2247 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2248 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2249 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2250 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2251 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2252 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2253 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2254 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2255 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2256 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2257 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2258 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2259 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2260 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2261 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2262 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2263 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2264 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2265 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2266 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2267 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2268 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2269 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2270 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2271 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2272 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2273 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2274 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2275 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2276 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2277 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5

r2278 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2279 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2280 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2281 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2282 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2283 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2284 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2285 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2286 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2287 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2288 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2289 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2290 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2291 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2292 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2293 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2294 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2295 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2296 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2297 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2298 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2299 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2300 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2301 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2302 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2303 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2304 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2305 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2306 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2307 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.5
r2436 Mitochondrial Carrier (MC) TCDB:2.A.29.8.3
r2438 Mitochondrial Carrier (MC) TCDB:2.A.29.8.3
r2482 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2483 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2484 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2485 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2486 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2487 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2488 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2489 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2490 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2491 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2492 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2493 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2494 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2495 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2496 Resistance-Nodulation-Cell Division (RND) TCDB:2.A.60.1.14
r2498 ATP-binding Cassette (ABC) TCDB:3.A.1.203.3
r2502 ATP-binding Cassette (ABC) TCDB:3.A.1.203.3
EX_so3(e) Sulfite exchange
RE0066C RE0066
RE0066M RE0066
RE0066R RE0066
RE0124C RE0124
RE0344M RE0344
RE0344X RE0344
RE0452N RE0452
RE0456M RE0456
RE0456N RE0456
RE0512C RE0512
RE0512X RE0512
RE0549C RE0549
RE0569C RE0569
RE0570C RE0570
RE0571C RE0571
RE0572N RE0572
RE0573N RE0573
RE0574C RE0574
RE0575C RE0575
RE0576C RE0576
RE0577M RE0577
RE0577X RE0577
RE0578C RE0578
RE0578M RE0578
RE0578X RE0578
RE0579C RE0579
RE0579M RE0579
RE0579X RE0579
RE0580L RE0580
RE0580R RE0580

RE0581C RE0581
RE0581R RE0581
RE0582N RE0582
RE0583N RE0583
RE0688C RE0688
RE0688X RE0688
RE0689C RE0689
RE0689X RE0689
RE0690C RE0690
RE0690X RE0690
RE0702C RE0702
RE0702L RE0702
RE0702M RE0702
RE0702N RE0702
RE0827C RE0827
RE0827X RE0827
RE0828C RE0828
RE0828X RE0828
RE0864C RE0864
RE0875C RE0875
RE0908G RE0908
RE0908R RE0908
RE0915C RE0915
RE0916C RE0916
RE0916G RE0916
RE0916R RE0916
RE0918C RE0918
RE0918G RE0918
RE0918R RE0918
RE0919C RE0919
RE0919R RE0919
RE0920C RE0920
RE0920R RE0920
RE0921C RE0921
RE0921R RE0921
RE0922C RE0922
RE0922R RE0922
RE0923C RE0923
RE0923R RE0923
RE0924C RE0924
RE0924R RE0924
RE0925C RE0925
RE0925R RE0925
RE0926C RE0926
RE0927C RE0927
RE0927R RE0927
RE0928C RE0928
RE0928R RE0928
RE0935C RE0935
RE0936C RE0936
RE0937C RE0937
RE0938C RE0938
RE0944C RE0944
RE0958C RE0958
RE1050C RE1050
RE1050E RE1050
RE1050L RE1050
RE1050N RE1050
RE1062C RE1062
RE1062M RE1062
RE1063C RE1063
RE1064C RE1064
RE1077C RE1077
RE1096C RE1096
RE1096M RE1096
RE1096R RE1096
RE1099C RE1099
RE1099G RE1099
RE1099L RE1099
RE1099R RE1099
RE1100G RE1100
RE1100L RE1100
RE1100R RE1100
RE1134C RE1134
RE1134M RE1134
RE1134R RE1134
RE1135G RE1135
RE1135L RE1135
RE1135R RE1135
RE1233M RE1233
RE1234C RE1234

RE1235C RE1235
RE1236C RE1236
RE1238X RE1238
RE1240C RE1240
RE1266C RE1266
RE1308C RE1308
RE1308M RE1308
RE1309C RE1309
RE1309M RE1309
RE1310C RE1310
RE1310M RE1310
RE1311C RE1311
RE1311M RE1311
RE1317C RE1317
RE1441G RE1441
RE1473C RE1473
RE1508C RE1508
RE1514M RE1514
RE1514X RE1514
RE1516X RE1516
RE1517X RE1517
RE1518X RE1518
RE1519X RE1519
RE1520X RE1520
RE1521X RE1521
RE1522X RE1522
RE1523X RE1523
RE1525C RE1525
RE1525X RE1525
RE1526C RE1526
RE1526X RE1526
RE1527C RE1527
RE1527X RE1527
RE1531X RE1531
RE1532X RE1532
RE1533X RE1533
RE1534X RE1534
RE1537C RE1537
RE1537X RE1537
RE1538C RE1538
RE1538X RE1538
RE1539C RE1539
RE1539X RE1539
RE1573X RE1573
RE1582C RE1582
RE1582L RE1582
RE1582R RE1582
RE1587C RE1587
RE1587L RE1587
RE1587R RE1587
RE1627C RE1627
RE1628C RE1628
RE1629C RE1629
RE1630C RE1630
RE1630R RE1630
RE1631C RE1631
RE1632C RE1632
RE1632R RE1632
RE1635C RE1635
RE1635M RE1635
RE1635R RE1635
RE1635X RE1635
RE1651C RE1651
RE1653C RE1653
RE1699C RE1699
RE1700C RE1700
RE1701C RE1701
RE1702C RE1702
RE1711C RE1711
RE1711M RE1711
RE1796C RE1796
RE1803C RE1803
RE1806C RE1806
RE1806R RE1806
RE1808R RE1808
RE1809C RE1809
RE1809R RE1809
RE1811C RE1811
RE1811R RE1811
RE1812C RE1812

RE1812R RE1812
RE1815C RE1815
RE1815M RE1815
RE1815R RE1815
RE1815X RE1815
RE1816C RE1816
RE1816M RE1816
RE1816R RE1816
RE1816X RE1816
RE1817C RE1817
RE1817M RE1817
RE1817R RE1817
RE1817X RE1817
RE1818C RE1818
RE1818M RE1818
RE1818R RE1818
RE1818X RE1818
RE1819C RE1819
RE1819M RE1819
RE1819X RE1819
RE1826M RE1826
RE1827C RE1827
RE1827M RE1827
RE1828C RE1828
RE1828M RE1828
RE1829C RE1829
RE1829M RE1829
RE1830C RE1830
RE1830M RE1830
RE1834M RE1834
RE1834X RE1834
RE1835M RE1835
RE1835X RE1835
RE1836C RE1836
RE1836M RE1836
RE1846C RE1846
RE1846X RE1846
RE1860C RE1860
RE1899C RE1899
RE1904C RE1904
RE1904R RE1904
RE1905C RE1905
RE1905R RE1905
RE1906C RE1906
RE1906R RE1906
RE1907C RE1907
RE1915C RE1915
RE1916C RE1916
RE1916X RE1916
RE1917C RE1917
RE1918C RE1918
RE1919C RE1919
RE1920C RE1920
RE1921C RE1921
RE1922C RE1922
RE1923C RE1923
RE1925C RE1925
RE1927C RE1927
RE1933C RE1933
RE1938C RE1938
RE1938R RE1938
RE1941C RE1941
RE1941R RE1941
RE1942C RE1942
RE1942R RE1942
RE1943C RE1943
RE1943R RE1943
RE1944C RE1944
RE1952C RE1952
RE1952R RE1952
RE1952X RE1952
RE1954C RE1954
RE1956C RE1956
RE1956R RE1956
RE1956X RE1956
RE1957G RE1957
RE1978C RE1978
RE2026C RE2026
RE2027C RE2027
RE2028C RE2028
RE2029C RE2029

RE2030M RE2030
RE2031M RE2031
RE2032M RE2032
RE2034C RE2034
RE2040C RE2040
RE2041C RE2041
RE2048N RE2048
RE2048R RE2048
RE2049C RE2049
RE2050C RE2050
RE2050R RE2050
RE2051C RE2051
RE2051G RE2051
RE2051R RE2051
RE2067C RE2067
RE2068C RE2068
RE2070C RE2070
RE2078M RE2078
RE2080C RE2080
RE2081C RE2081
RE2111M RE2111
RE2112C RE2112
RE2112R RE2112
RE2117M RE2117
RE2122C RE2122
RE2124C RE2124
RE2127C RE2127
RE2128C RE2128
RE2129C RE2129
RE2130C RE2130
RE2131C RE2131
RE2132C RE2132
RE2133C RE2133
RE2138C RE2138
RE2139C RE2139
RE2140C RE2140
RE2141C RE2141
RE2146C RE2146
RE2146R RE2146
RE2147R RE2147
RE2149C RE2149
RE2149R RE2149
RE2150C RE2150
RE2150R RE2150
RE2151C RE2151
RE2151R RE2151
RE2152C RE2152
RE2154C RE2154
RE2155C RE2155
RE2155R RE2155
RE2156M RE2156
RE2202C RE2202
RE2203C RE2203
RE2220C RE2220
RE2221C RE2221
RE2221M RE2221
RE2223M RE2223
RE2235C RE2235
RE2235R RE2235
RE2248C RE2248
RE2249C RE2249
RE2250C RE2250
RE2251C RE2251
RE2252C RE2252
RE2265C RE2265
RE2269C RE2269
RE2270C RE2270
RE2272C RE2272
RE2272L RE2272
RE2273C RE2273
RE2292C RE2292
RE2296C RE2296
RE2296X RE2296
RE2306C RE2306
RE2318C RE2318
RE2318M RE2318
RE2318R RE2318
RE2318X RE2318
RE2319C RE2319
RE2319M RE2319

RE2319R RE2319
RE2319X RE2319
RE2327C RE2327
RE2333C RE2333
RE2334C RE2334
RE2335C RE2335
RE2346C RE2346
RE2349M RE2349
RE2360C RE2360
RE2360N RE2360
RE2373C RE2373
RE2375C RE2375
RE2377C RE2377
RE2382C RE2382
RE2382R RE2382
RE2383C RE2383
RE2383R RE2383
RE2384C RE2384
RE2386C RE2386
RE2387C RE2387
RE2387R RE2387
RE2398C RE2398
RE2398R RE2398
RE2404R RE2404
RE2405R RE2405
RE2407C RE2407
RE2410C RE2410
RE2410N RE2410
RE2427M RE2427
RE2428M RE2428
RE2429M RE2429
RE2439C RE2439
RE2440C RE2440
RE2442C RE2442
RE2443C RE2443
RE2443M RE2443
RE2444C RE2444
RE2445C RE2445
RE2452C RE2452
RE2453M RE2453
RE2454M RE2454
RE2459C RE2459
RE2474C RE2474
RE2474R RE2474
RE2476C RE2476
RE2477C RE2477
RE2493C RE2493
RE2513C RE2513
RE2513L RE2513
RE2513N RE2513
RE2514C RE2514
RE2514L RE2514
RE2514N RE2514
RE2520C RE2520
RE2521C RE2521
RE2522C RE2522
RE2522X RE2522
RE2523C RE2523
RE2523X RE2523
RE2524C RE2524
RE2524X RE2524
RE2525C RE2525
RE2525X RE2525
RE2526C RE2526
RE2533C RE2533
RE2541L RE2541
RE2562C RE2562
RE2563C RE2563
RE2591C RE2591
RE2594C RE2594
RE2596C RE2596
RE2601C RE2601
RE2605C RE2605
RE2622C RE2622
RE2622R RE2622
RE2624M RE2624
RE2624X RE2624
RE2632C RE2632
RE2632M RE2632
RE2633C RE2633
RE2633R RE2633

RE2635C RE2635
RE2635R RE2635
RE2636C RE2636
RE2636R RE2636
RE2637C RE2637
RE2637X RE2637
RE2638C RE2638
RE2638X RE2638
RE2640C RE2640
RE2642C RE2642
RE2644C RE2644
RE2649X RE2649
RE2658C RE2658
RE2677N RE2677
RE2677R RE2677
RE2680C RE2680
RE2680G RE2680
RE2704C RE2704
RE2705C RE2705
RE2717L RE2717
RE2718C RE2718
RE2718G RE2718
RE2722C RE2722
RE2722G RE2722
RE2746C RE2746
RE2766C RE2766
RE2768C RE2768
RE2768M RE2768
RE2768R RE2768
RE2782C RE2782
RE2813C RE2813
RE2848C RE2848
RE2849C RE2849
RE2850C RE2850
RE2851C RE2851
RE2852C RE2852
RE2853C RE2853
RE2854C RE2854
RE2856C RE2856
RE2857C RE2857
RE2858C RE2858
RE2859C RE2859
RE2860C RE2860
RE2861C RE2861
RE2862C RE2862
RE2863C RE2863
RE2864C RE2864
RE2865C RE2865
RE2866C RE2866
RE2867C RE2867
RE2868C RE2868
RE2869C RE2869
RE2870C RE2870
RE2871C RE2871
RE2872C RE2872
RE2873C RE2873
RE2874C RE2874
RE2875C RE2875
RE2876C RE2876
RE2877C RE2877
RE2878C RE2878
RE2880C RE2880
RE2888C RE2888
RE2888N RE2888
RE2897C RE2897
RE2898C RE2898
RE2899C RE2899
RE2908C RE2908
RE2908M RE2908
RE2908X RE2908
RE2909C RE2909
RE2909M RE2909
RE2909X RE2909
RE2910C RE2910
RE2910M RE2910
RE2910X RE2910
RE2911C RE2911
RE2912M RE2912
RE2912X RE2912
RE2913M RE2913

RE2913X RE2913
RE2914M RE2914
RE2914X RE2914
RE2915M RE2915
RE2915X RE2915
RE2916M RE2916
RE2916X RE2916
RE2917M RE2917
RE2917X RE2917
RE2919M RE2919
RE2919X RE2919
RE2920M RE2920
RE2920X RE2920
RE2921M RE2921
RE2921X RE2921
RE2948C RE2948
RE2958C RE2958
RE2972G RE2972
RE2972R RE2972
RE2973G RE2973
RE2974G RE2974
RE2975C RE2975
RE2975M RE2975
RE2977C RE2977
RE2985M RE2985
RE2989X RE2989
RE2990X RE2990
RE2991X RE2991
RE2992M RE2992
RE2992X RE2992
RE2993X RE2993
RE2994X RE2994
RE2995M RE2995
RE2995X RE2995
RE2997X RE2997
RE3010C RE3010
RE3010M RE3010
RE3010R RE3010
RE3010X RE3010
RE3011M RE3011
RE3012C RE3012
RE3012M RE3012
RE3013C RE3013
RE3013R RE3013
RE3014C RE3014
RE3015C RE3015
RE3018C RE3018
RE3018R RE3018
RE3019C RE3019
RE3019R RE3019
RE3020C RE3020
RE3020R RE3020
RE3021C RE3021
RE3022C RE3022
RE3033C RE3033
RE3033N RE3033
RE3033R RE3033
RE3036C RE3036
RE3036N RE3036
RE3038C RE3038
RE3038N RE3038
RE3038R RE3038
RE3038X RE3038
RE3039C RE3039
RE3040C RE3040
RE3040R RE3040
RE3040X RE3040
RE3041C RE3041
RE3041N RE3041
RE3044C RE3044
RE3044N RE3044
RE3045C RE3045
RE3051C RE3051
RE3052C RE3052
RE3053C RE3053
RE3066X RE3066
RE3072X RE3072
RE3073X RE3073
RE3075C RE3075
RE3075X RE3075
RE3076X RE3076

RE3079C RE3079
RE3081X RE3081
RE3082X RE3082
RE3083X RE3083
RE3084X RE3084
RE3086X RE3086
RE3087X RE3087
RE3088X RE3088
RE3089X RE3089
RE3090X RE3090
RE3092X RE3092
RE3093X RE3093
RE3095C RE3095
RE3095L RE3095
RE3095X RE3095
RE3097X RE3097
RE3103C RE3103
RE3103R RE3103
RE3104C RE3104
RE3104R RE3104
RE3106C RE3106
RE3106R RE3106
RE3108C RE3108
RE3110C RE3110
RE3110R RE3110
RE3111C RE3111
RE3111M RE3111
RE3111R RE3111
RE3112C RE3112
RE3112R RE3112
RE3113C RE3113
RE3113R RE3113
RE3114R RE3114
RE3119C RE3119
RE3119R RE3119
RE3120C RE3120
RE3120R RE3120
RE3121C RE3121
RE3121R RE3121
RE3122C RE3122
RE3122R RE3122
RE3123C RE3123
RE3123R RE3123
RE3124C RE3124
RE3124R RE3124
RE3125C RE3125
RE3125R RE3125
RE3126C RE3126
RE3126R RE3126
RE3129N RE3129
RE3132C RE3132
RE3132R RE3132
RE3134C RE3134
RE3134R RE3134
RE3136C RE3136
RE3139X RE3139
RE3140X RE3140
RE3141X RE3141
RE3144C RE3144
RE3144M RE3144
RE3145X RE3145
RE3146C RE3146
RE3146R RE3146
RE3147C RE3147
RE3147R RE3147
RE3148C RE3148
RE3148R RE3148
RE3150C RE3150
RE3150R RE3150
RE3151C RE3151
RE3151R RE3151
RE3152C RE3152
RE3152R RE3152
RE3153C RE3153
RE3153R RE3153
RE3154C RE3154
RE3154R RE3154
RE3155C RE3155
RE3155R RE3155
RE3156X RE3156

RE3157X RE3157
RE3158X RE3158
RE3159X RE3159
RE3160C RE3160
RE3160R RE3160
RE3161C RE3161
RE3161R RE3161
RE3162C RE3162
RE3162R RE3162
RE3163C RE3163
RE3163R RE3163
RE3164C RE3164
RE3164R RE3164
RE3165C RE3165
RE3165R RE3165
RE3166C RE3166
RE3166R RE3166
RE3167C RE3167
RE3167R RE3167
RE3168C RE3168
RE3168R RE3168
RE3169C RE3169
RE3169R RE3169
RE3170C RE3170
RE3170R RE3170
RE3171C RE3171
RE3171R RE3171
RE3172C RE3172
RE3172R RE3172
RE3173C RE3173
RE3173R RE3173
RE3174C RE3174
RE3174R RE3174
RE3175C RE3175
RE3175R RE3175
RE3176C RE3176
RE3176R RE3176
RE3177M RE3177
RE3178M RE3178
RE3179M RE3179
RE3180C RE3180
RE3181C RE3181
RE3184M RE3184
RE3185M RE3185
RE3186M RE3186
RE3189M RE3189
RE3190M RE3190
RE3191M RE3191
RE3192M RE3192
RE3193M RE3193
RE3194M RE3194
RE3195M RE3195
RE3201C RE3201
RE3218L RE3218
RE3218R RE3218
RE3220C RE3220
RE3220L RE3220
RE3220R RE3220
RE3224C RE3224
RE3224R RE3224
RE3225C RE3225
RE3225R RE3225
RE3226C RE3226
RE3226R RE3226
RE3227C RE3227
RE3227R RE3227
RE3228C RE3228
RE3228R RE3228
RE3229C RE3229
RE3229R RE3229
RE3230C RE3230
RE3230R RE3230
RE3231C RE3231
RE3231R RE3231
RE3232C RE3232
RE3232R RE3232
RE3233C RE3233
RE3233G RE3233
RE3233L RE3233
RE3234C RE3234
RE3234R RE3234

RE3235C RE3235
RE3235R RE3235
RE3236C RE3236
RE3236R RE3236
RE3237C RE3237
RE3238C RE3238
RE3239C RE3239
RE3247M RE3247
RE3247X RE3247
RE3248M RE3248
RE3248X RE3248
RE3250C RE3250
RE3250M RE3250
RE3250X RE3250
RE3251M RE3251
RE3258C RE3258
RE3258R RE3258
RE3259C RE3259
RE3259R RE3259
RE3260C RE3260
RE3260R RE3260
RE3261C RE3261
RE3261R RE3261
RE3263C RE3263
RE3264C RE3264
RE3264R RE3264
RE3265C RE3265
RE3265R RE3265
RE3267E RE3267
RE3267G RE3267
RE3267M RE3267
RE3267N RE3267
RE3267R RE3267
RE3268C RE3268
RE3273G RE3273
RE3273R RE3273
RE3286C RE3286
RE3286R RE3286
RE3287C RE3287
RE3287R RE3287
RE3288C RE3288
RE3288R RE3288
RE3289C RE3289
RE3289R RE3289
RE3295C RE3295
RE3301G RE3301
RE3301R RE3301
RE3307C RE3307
RE3307M RE3307
RE3307X RE3307
RE3308C RE3308
RE3308M RE3308
RE3308R RE3308
RE3308X RE3308
RE3310C RE3310
RE3310R RE3310
RE3334M RE3334
RE3334X RE3334
RE3335C RE3335
RE3335M RE3335
RE3335R RE3335
RE3335X RE3335
RE3336M RE3336
RE3336X RE3336
RE3337M RE3337
RE3337X RE3337
RE3338C RE3338
RE3338M RE3338
RE3338X RE3338
RE3339C RE3339
RE3339M RE3339
RE3339X RE3339
RE3340C RE3340
RE3340M RE3340
RE3340X RE3340
RE3341M RE3341
RE3341X RE3341
RE3342M RE3342
RE3342X RE3342
RE3343C RE3343

RE3343M RE3343
RE3343X RE3343
RE3344M RE3344
RE3344X RE3344
RE3345C RE3345
RE3345M RE3345
RE3345R RE3345
RE3345X RE3345
RE3346R RE3346
RE3352C RE3352
RE3367C RE3367
RE3367X RE3367
RE3370C RE3370
RE3370R RE3370
RE3372C RE3372
RE3378C RE3378
RE3381L RE3381
RE3383M RE3383
RE3384M RE3384
RE3385M RE3385
RE3386M RE3386
RE3387M RE3387
RE3388M RE3388
RE3389M RE3389
RE3390M RE3390
RE3391M RE3391
RE3392M RE3392
RE3393M RE3393
RE3394M RE3394
RE3395M RE3395
RE3396M RE3396
RE3397M RE3397
RE3398M RE3398
RE3399M RE3399
RE3400M RE3400
RE3401M RE3401
RE3402M RE3402
RE3403M RE3403
RE3404M RE3404
RE3407C RE3407
RE3408C RE3408
RE3409C RE3409
RE3410C RE3410
RE3411C RE3411
RE3412C RE3412
RE3413C RE3413
RE3414C RE3414
RE3415C RE3415
RE3417C RE3417
RE3420C RE3420
RE3421M RE3421
RE3422C RE3422
RE3423C RE3423
RE3430C RE3430
RE3430M RE3430
RE3430X RE3430
RE3431C RE3431
RE3432C RE3432
RE3432M RE3432
RE3432X RE3432
RE3434C RE3434
RE3434R RE3434
RE3435C RE3435
RE3435R RE3435
RE3436C RE3436
RE3436R RE3436
RE3437C RE3437
RE3440C RE3440
RE3440R RE3440
RE3443M RE3443
RE3443X RE3443
RE3444C RE3444
RE3444M RE3444
RE3444X RE3444
RE3445M RE3445
RE3445X RE3445
RE3446C RE3446
RE3446M RE3446
RE3446R RE3446
RE3446X RE3446
RE3447M RE3447

RE3447X RE3447
RE3448C RE3448
RE3448M RE3448
RE3448X RE3448
RE3449C RE3449
RE3450C RE3450
RE3451C RE3451
RE3452C RE3452
RE3453C RE3453
RE3454C RE3454
RE3455C RE3455
RE3456C RE3456
RE3457C RE3457
RE3458C RE3458
RE3459C RE3459
RE3460C RE3460
RE3464C RE3464
RE3464R RE3464
RE3469C RE3469
RE3470C RE3470
RE3470M RE3470
RE3470X RE3470
RE3474C RE3474
RE3474R RE3474
RE3475C RE3475
RE3475N RE3475
RE3476C RE3476
RE3476M RE3476
RE3476X RE3476
RE3477C RE3477
RE3485C RE3485
RE3485N RE3485
RE3486C RE3486
RE3488C RE3488
RE3488N RE3488
RE3488R RE3488
RE3488X RE3488
RE3490C RE3490
RE3491C RE3491
RE3492C RE3492
RE3493C RE3493
RE3494C RE3494
RE3495C RE3495
RE3496C RE3496
RE3496N RE3496
RE3498N RE3498
RE3498R RE3498
RE3499C RE3499
RE3500C RE3500
RE3500R RE3500
RE3500X RE3500
RE3501C RE3501
RE3501R RE3501
RE3501X RE3501
RE3502C RE3502
RE3502X RE3502
RE3503C RE3503
RE3503N RE3503
RE3506C RE3506
RE3506R RE3506
RE3511C RE3511
RE3511M RE3511
RE3511R RE3511
RE3513C RE3513
RE3513N RE3513
RE3513R RE3513
RE3514C RE3514
RE3514R RE3514
RE3515C RE3515
RE3518C RE3518
RE3518R RE3518
RE3519C RE3519
RE3519R RE3519
RE3519X RE3519
RE3520C RE3520
RE3520M RE3520
RE3520N RE3520
RE3521C RE3521
RE3521M RE3521
RE3521R RE3521

RE3521X RE3521
RE3522C RE3522
RE3522R RE3522
RE3525C RE3525
RE3525M RE3525
RE3525N RE3525
RE3525R RE3525
RE3525X RE3525
RE3526C RE3526
RE3526M RE3526
RE3526X RE3526
RE3532C RE3532
RE3532M RE3532
RE3532R RE3532
RE3533C RE3533
RE3533M RE3533
RE3533R RE3533
RE3534C RE3534
RE3534M RE3534
RE3534R RE3534
RE3535R RE3535
RE3536C RE3536
RE3537C RE3537
RE3550X RE3550
RE3551X RE3551
RE3552X RE3552
RE3554C RE3554
RE3554M RE3554
RE3554R RE3554
RE3557C RE3557
RE3557M RE3557
RE3557R RE3557
RE3559M RE3559
RE3559X RE3559
RE3560C RE3560
RE3560M RE3560
RE3560X RE3560
RE3561M RE3561
RE3561X RE3561
RE3562C RE3562
RE3562M RE3562
RE3562R RE3562
RE3562X RE3562
RE3563M RE3563
RE3563X RE3563
RE3564C RE3564
RE3564M RE3564
RE3564X RE3564
RE3570C RE3570
RE3571C RE3571
RE3571R RE3571
RE3572X RE3572
RE3573X RE3573
RE3574X RE3574
RE3575X RE3575
RE3576X RE3576
RE3577X RE3577
RE3578X RE3578
RE3580X RE3580
RE3581X RE3581
RE3582X RE3582
RE3583X RE3583
RE3586X RE3586
RE3587C RE3587
RE3587N RE3587
RE3596C RE3596
RE3596M RE3596
RE3596X RE3596
RE3597C RE3597
RE3597M RE3597
RE3597X RE3597
RE3624X RE3624
RE3627C RE3627
RE3627X RE3627
RE3631C RE3631
RE3633C RE3633
RE3636C RE3636
RE3637C RE3637
RN0001C RN0001
RN0001R RN0001
RN0002N RN0002

```
        RN0002R RN0002
        RN0013C RN0013
        RN0014R RN0014
        RN0020C RN0020
        RN0020R RN0020
        RN0021C RN0021
        RN0021R RN0021
        RN0021X RN0021
        RN0022C RN0022
        RN0022R RN0022
        RN0022X RN0022
        RN0023C RN0023
        RN0023R RN0023
        RN0023X RN0023
        RN0027C RN0027
        RN0027R RN0027
        RN0028C RN0028
        RN0028R RN0028
        RN0028X RN0028
        RN0029C RN0029
        RN0029R RN0029
        RN0030C RN0030
        RN0030R RN0030
        RN0031C RN0031
        RN0031R RN0031
        RN0031X RN0031
        RN0032C RN0032
        RN0032R RN0032
  EX_HC00955(e) L-3-Cyanoalanine exchange
  EX_HC00001(e) Albumin exchange
  EX_HC00002(e) Antichymotrypsin exchange
  EX_HC00003(e) Antitrypsin exchange
  EX_HC00004(e) ApoA1 exchange
  EX_HC01787(e) Lepidimoide exchange
  EX_HC01852(e) Fibrinogen exchange
  EX_HC01939(e) Haptoglobin exchange
  EX_HC01942(e) Plasminogen exchange
  EX_HC01943(e) Prothrombin exchange
  EX_HC01944(e) ApoTransferin exchange
  EX_HC02192(e) taurolithocholate exchange
  EX_HC02193(e) glycolithocholate exchange
  EX_HC02195(e) tauroursodeoxycholate exchange
  EX_HC02196(e) glycoursodeoxycholate exchange
  EX_HC02220(e) sulfochenodeoxycholate exchange
  EX_HC02154(e) GM4-pool exchange
  EX_HC02175(e) caprate exchange
  EX_HC02199(e) glutathionyl-leuc4 exchange
  EX_HC02200(e) S-glutathionyl-2-4-dinitrobenzene exchange
  EX_HC02201(e) S-glutathionyl-ethacrynic-acid exchange
  EX_HC02172(e) Zinc exchange
  EX_HC02191(e) lithocholate exchange
  EX_HC02194(e) ursodeoxycholate exchange
  EX_HC02197(e) sulfoglycolithocholate(2-) exchange
  EX_HC02198(e) 2-[(4R)-4-[(1S,2S,5R,7R,10R,11S,14R,15R)-2,15-dimethyl-5-(sulfonatooxy)tetracyclo[8.7.0.0^{2,7}.0^{11,15}]heptadecan-14-yl]pentana
  EX_HC02187(e) reverse-triiodthyronine exchange
  EX_HC02180(e) thromboxane-b2 exchange
  EX_HC02179(e) 20-hydroxy-arachidonate exchange
  EX_HC02208(e) prostaglandin-d1 exchange
  EX_HC02210(e) prostaglandin-d3 exchange
  EX_HC02213(e) prostaglandin-e3 exchange
  EX_HC02214(e) prostaglandin-f1alpha exchange
  EX_HC02216(e) prostaglandin-f2beta exchange
  EX_HC02217(e) prostaglandin-g2 exchange
   EX_CE1950(e) cyanosulfurous acid anion exchange
      EX_cynt(e) Cyanate exchange
    EX_cdpea(e) CDP-ethanolamine(1-) exchange
 EX_12dgr120(e) 1,2-Diacyl-sn-glycerol (didodecanoyl, n-C12:0) exchange
 FAOXC11BRC9BRx fatty acid beta oxidation(C11br-->C9br)x
FAOXC13BRC11BRx fatty acid beta oxidation(C13br-->C11br)x
FAOXC15BRC13BRx fatty acid beta oxidation(C15br-->C13br)x
  FAOXC9BRC7BRm fatty acid beta oxidation(C9br-->C7br)m
       CARhPTtc Transport of L-Carnosine by hPT3 or hPT4 peptide transporter.
         CBLTDe release of B12 by simple diffusion
      BIDGLCURr bilirubin di-glucuronide production
   EX_adpcbl(e) exchange reaction for Adenosylcobalamin
       EX_oh1(e) exchange reaction for hydroxide ion
           FADtm Transport of fad into mitochondria
           NADtm transport of NAD into mitochondria
------end------
```

Find mass leaks or siphons within the heuristically internal part, without using the bounds given by the model

```
if 1
    modelBoundsFlag=0;
    leakParams.epsilon=1e-4;
    leakParams.method='dc';
    leakParams.theta=0.5;
    [leakMetBool,leakRxnBool,siphonMetBool,siphonRxnBool,leakY,siphonY,statp,statn] =...
        findMassLeaksAndSiphons(model,model.SIntMetBool,model.SIntRxnBool,...
        modelBoundsFlag,leakParams,printLevel);
end
```

```
   2940   4559  subset tested for leakage (dc method, with infinite flux bounds)...
      0      0  semipositive leaking metabolites (and exclusive reactions).
      0      0  seminegative siphon metabolites (and exclusive reactions).
```

Find the maximal set of reactions that are stoichiometrically consistent

```
if ~isfield(model,'SConsistentMetBool') || ~isfield(model,'SConsistentRxnBool')
    if strcmp(model.modelID,'HMRdatabase2_00')
        massBalanceCheck=0;
    else
        massBalanceCheck=1;
    end
    if 1
        [SConsistentMetBool,SConsistentRxnBool,SInConsistentMetBool,SInConsistentRxnBool,unknownSConsistencyMetBool,unknownSConsistencyRxnBo
            =findStoichConsistentSubset(model,massBalanceCheck,printLevel);
    else
        %print out problematic reactions to file
        resultsFileName=[resultsPath filesep model.modelID];
        [SConsistentMetBool,SConsistentRxnBool,SInConsistentMetBool,SInConsistentRxnBool,unknownSConsistencyMetBool,unknownSConsistencyRxnBo
            =findStoichConsistentSubset(model,massBalanceCheck,printLevel,resultsFileName);
    end
end
```

```
-------
 #mets  #rxns
  2940   5190  totals.
-------
     0    631  heuristically exchange.
  2940   4559  heuristically non-exchange.
  2203   4534  seemingly elementally balanced.
  2203   4534  seemingly elementally balanced and stoichiometrically consistent.
   737    656  seemingly elementally imbalanced.
-------
  2203   4534  heuristically non-exchange and seemingly elementally balanced.
  2203   4534  seemingly elementally balanced and stoichiometrically consistent.
   737     25  heuristically non-exchange and seemingly elementally imbalanced.
-------
Iteration #1 minimum cardinality of conservation relaxation vector.
  2940   4559  unknown consistency.
  2940   4559  being tested.
  2940   4559  ... of which are stoichiometrically consistent by min cardinality of stoich consistency relaxation.
  2940   4559 Confirmed stoichiometrically consistent by leak/siphon testing.
     0      0  ... of which are of unknown consistency.
--- Summary of stoichiometric consistency ----
  2940   5190  totals.
     0    631  heuristically exchange.
  2940   4559  heuristically non-exchange:
  2940   4559  ... of which are stoichiometrically consistent.
     0      0  ... of which are stoichiometrically inconsistent.
     0      0  ... of which are of unknown consistency.
---
     0      0  heuristically non-exchange and stoichiometrically inconsistent or unknown consistency.
     0      0  ... of which are elementally imbalanced (inclusively involved metabolite).
     0      0  ... of which are elementally imbalanced (exclusively involved metabolite).
  2940   4559  Confirmed stoichiometrically consistent by leak/siphon testing.
--- END ----
```

```
rxnBool=model.SInConsistentRxnBool & model.SIntRxnBool;
if any(rxnBool)
    if printLevel>0
        fprintf('%s\n','Stoichiometrically inconsistent heuristically non-exchange reactions:')
    end
    for n=1:nRxn
        if rxnBool(n)
            fprintf('%20s\t%50s\t%s\n',model.rxns{n},model.rxnNames{n},model.subSystems{n})
        end
    end
    if printLevel>0
        fprintf('%s\n','---------------')
    end
end

rxnBool=model.unknownSConsistencyRxnBool & model.SIntRxnBool;
if any(rxnBool)
    if printLevel>0
        fprintf('%s\n','Unknown consistency heuristically non-exchange reactions:')
    end
    for n=1:nRxn
```

```
        if rxnBool(n)
            fprintf('%20s\t%50s\t%s\n',model.rxns{n},model.rxnNames{n},model.subSystems{n})
        end
    end
    if printLevel>0
        fprintf('%s\n','---------------')
    end
end
```

Sanity check of stoichiometric and flux consistency of model with open external reactions

```
    if  all(model.SIntMetBool & model.SConsistentMetBool)...
            && nnz(model.SIntRxnBool & model.SConsistentRxnBool)==nnz(model.SIntRxnBool)...
            && all(model.fluxConsistentMetBool)...
            && all(model.fluxConsistentRxnBool)

        [nMet,nRxn]=size(model.S);
        if printLevel>1
            fprintf('%6s\t%6s\n','#mets','#rxns')
            fprintf('%6u\t%6u\t%s\n',nMet,nRxn,' totals.')
            fprintf('%6u\t%6u\t%s\n',nnz(~model.SIntMetBool),nnz(~model.SIntRxnBool),' heuristically exchange.')
        end

        checksPassed=0;
        %Check that all heuristically non-exchange reactions are also stoichiometrically consistent

        %exchange reactions
        model.EXRxnBool=strncmp('EX_', model.rxns, 3)==1;
        %demand reactions going out of model
        model.DMRxnBool=strncmp('DM_', model.rxns, 3)==1;
        %sink reactions going into or out of model
        model.SinkRxnBool=strncmp('sink_', model.rxns, 5)==1;
        %all heuristic non-exchanges, i.e., supposedly all external reactions
        bool=~(model.EXRxnBool | model.DMRxnBool | model.SinkRxnBool);
        if nnz(bool & model.SIntRxnBool & model.SConsistentRxnBool)==nnz(model.SConsistentRxnBool)
            checksPassed=checksPassed+1;
            if printLevel>1
                fprintf('%6u\t%6u\t%s\n',nnz(model.SIntMetBool),nnz(model.SIntRxnBool),' All internally stoichiometrically consistent. (Chec
            end
        end

        %Check for mass leaks or siphons in the stoichiometrically consistent part
        %There should be no leaks or siphons in the stiochiometrically consistent part
        modelBoundsFlag=0;
        leakParams.epsilon=1e-4;
        leakParams.eta = getCobraSolverParams('LP', 'feasTol')*100;
        leakParams.method='dc';
        [leakMetBool,leakRxnBool,siphonMetBool,siphonRxnBool,leakY,siphonY,statp,statn]...
            =findMassLeaksAndSiphons(model,model.SConsistentMetBool,model.SConsistentRxnBool,modelBoundsFlag,leakParams,printLevel);

        if nnz(leakMetBool)==0 && nnz(leakRxnBool)==0 && nnz(siphonMetBool)==0 && nnz(siphonRxnBool)==0
            checksPassed=checksPassed+1;
            if printLevel>1
                fprintf('%6u\t%6u\t%s\n',nnz(leakMetBool | siphonMetBool),nnz(leakRxnBool | siphonRxnBool),' No internal leaks or siphons. (
            end
        end

        %Check that the maximal conservation vector is nonzero for each the
        %internal stoichiometric matrix
        maxCardinalityConsParams.epsilon=1e-4;%1/epsilon is the largest mass considered, needed for numerical stability
        maxCardinalityConsParams.method = 'quasiConcave';%seems to work the best, but sometimes infeasible
        maxCardinalityConsParams.theta = 0.5;
        maxCardinalityConsParams.eta=getCobraSolverParams('LP', 'feasTol')*100;
        [maxConservationMetBool,maxConservationRxnBool,solution]=maxCardinalityConservationVector(model.S(model.SConsistentMetBool,model.SCo

        if nnz(maxConservationMetBool)==size(model.S,1) && nnz(maxConservationRxnBool)==nnz(model.SIntRxnBool)
            checksPassed=checksPassed+1;
            if printLevel>1
                fprintf('%6u\t%6u\t%s\n',nnz(maxConservationMetBool),nnz(maxConservationRxnBool),' All internally stoichiometrically consist
            end
        end

        %Check that each of the reactions in the model (with open external reactions) is flux consistent
        modelOpen=model;
        modelOpen.lb(~model.SIntRxnBool)=-1000;
        modelOpen.ub(~model.SIntRxnBool)= 1000;
        param.epsilon=1e-4;
        param.modeFlag=0;
        param.method='null_fastcc';
        [fluxConsistentMetBool,fluxConsistentRxnBool,fluxInConsistentMetBool,fluxInConsistentRxnBool,modelOpen] = findFluxConsistentSubset(m

        if nnz(fluxConsistentMetBool)==size(model.S,1) && nnz(fluxConsistentRxnBool)==size(model.S,2)
            checksPassed=checksPassed+1;
            if printLevel>1
                fprintf('%6u\t%6u\t%s\n',nnz(fluxConsistentMetBool),nnz(fluxConsistentRxnBool),' All flux consistent. (Check 4: maximim car
            end
        end

        if checksPassed==4
```

```
            %save the model with open exchanges as the default generic
            %model
            model=modelOpen;
            if printLevel>0
                fprintf('%s\n','Open external reactions is stoichiometrically and flux consistent. A flux balance model generated from a re
            end
        end
        save([resultsFileName '_consistent.mat'],'model')
    end
```

REFERENCES

Gevorgyan, A., Poolman, M. G., Fell D., Detection of stoichiometric inconsistencies in biomolecular models. Bioinformatics, 24(19):2245–51, 2008.

Fleming, R.M.T., et al., Cardinality optimisation in constraint-based modelling: Application to Recon 3D (submitted), 2017.

Brunk, E. et al. Recon 3D: A resource enabling a three-dimensional view of gene variation in human metabolism. (submitted) 2017.