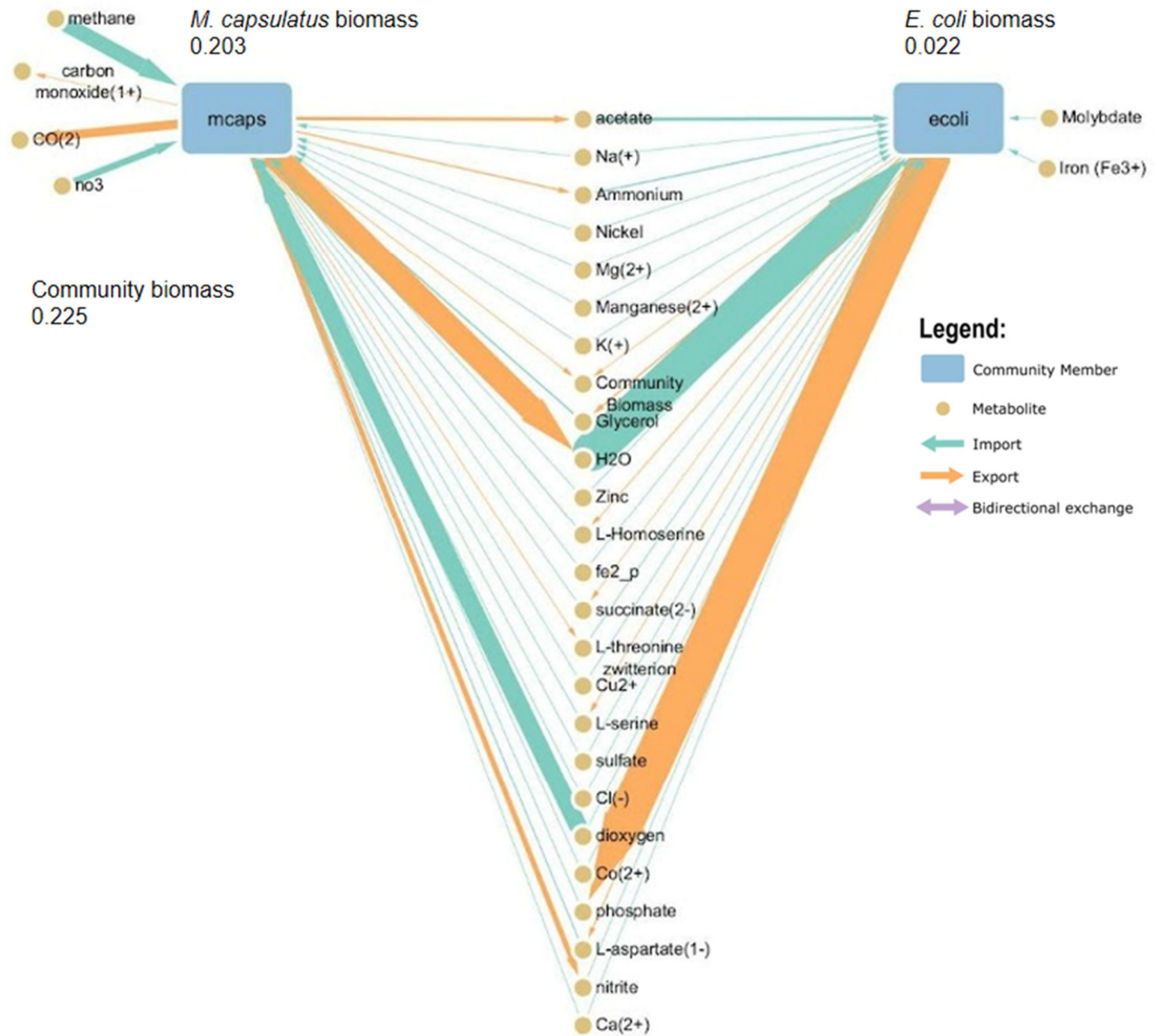


## Supplementary Material

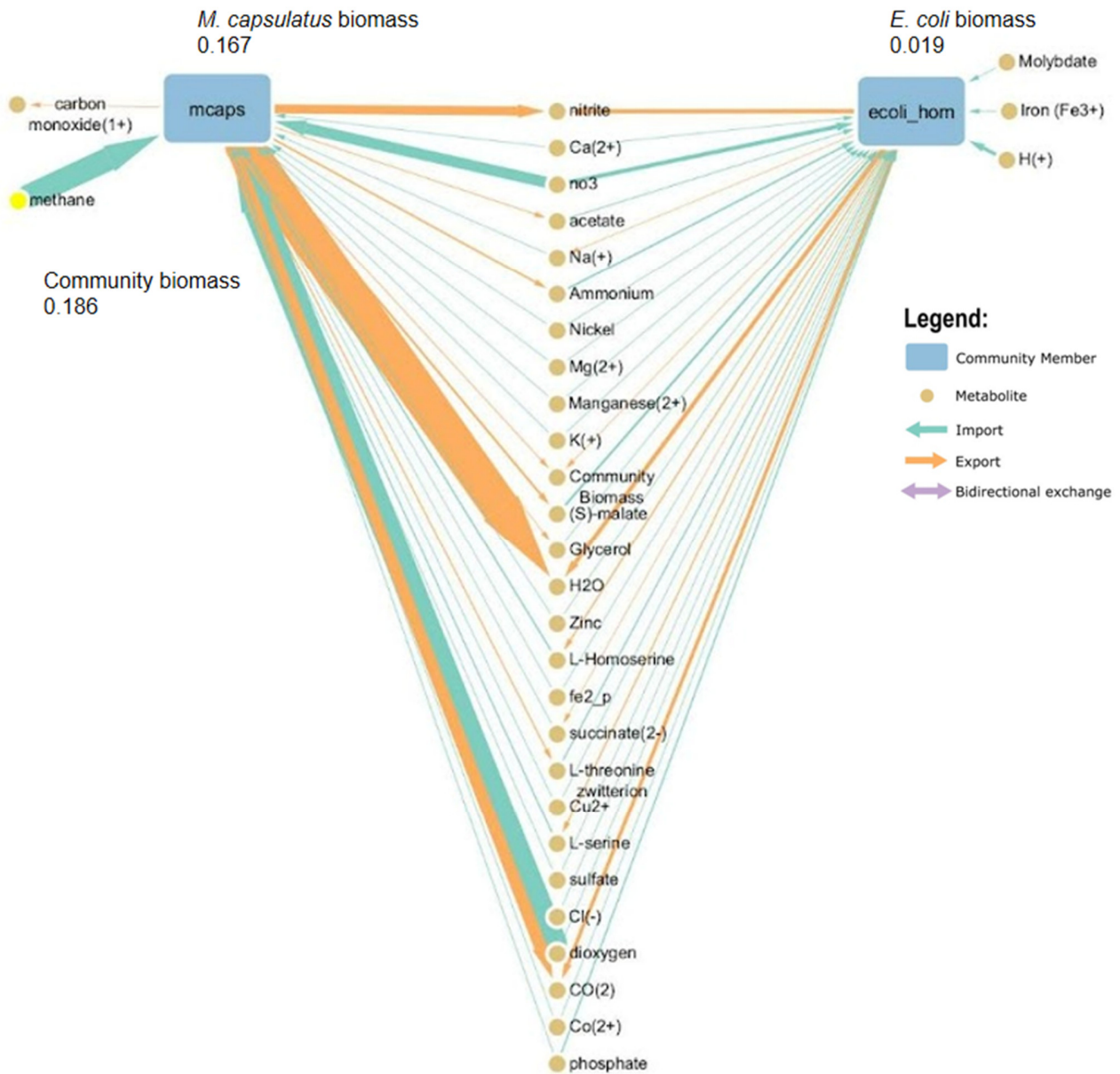
### Supplementary Figures and Tables

#### Supplementary Figures



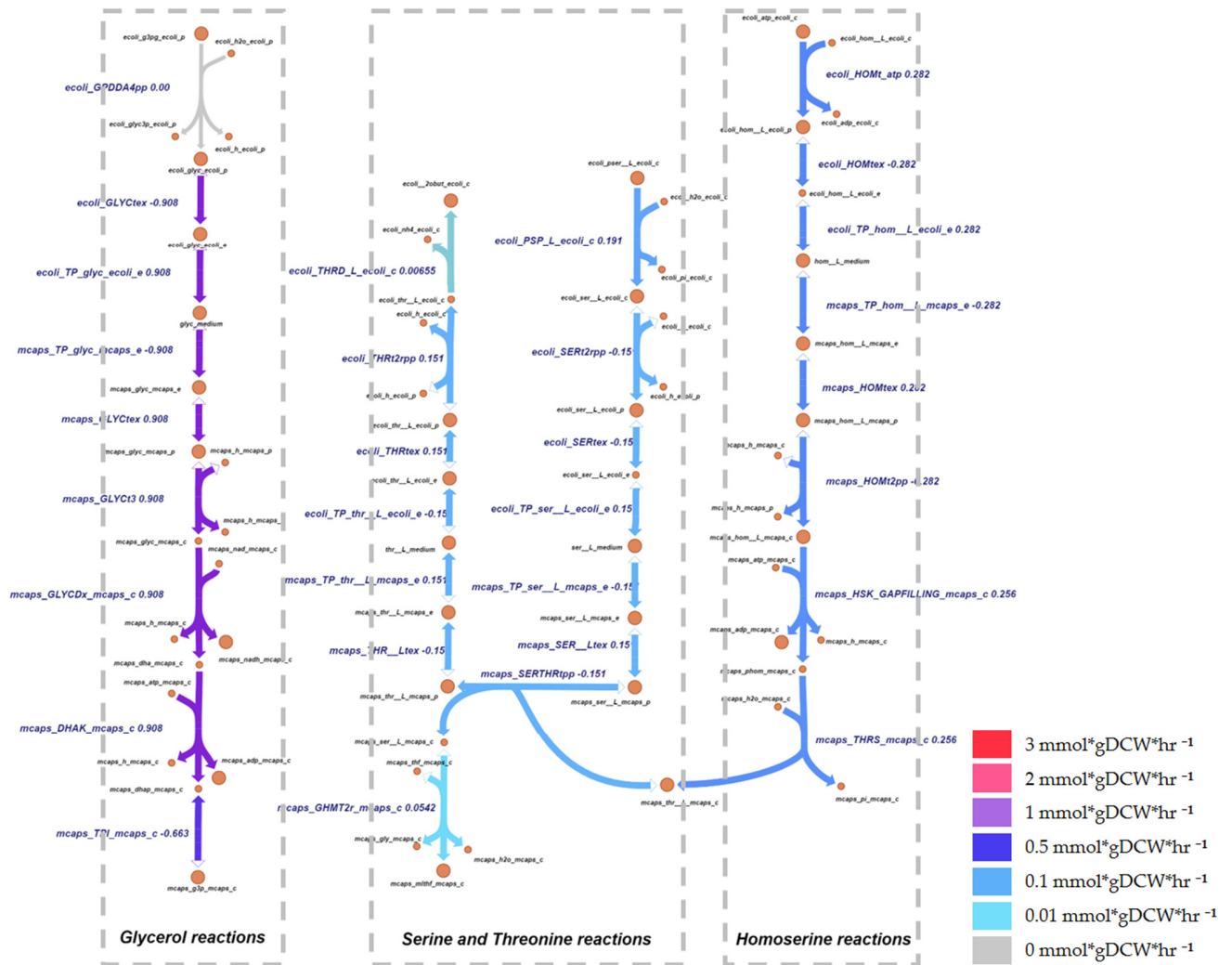
**Supplementary Figure S1.** Visualization of cross-feeding metabolites in the *iMcBath* and *iEC1372\_W3110* community under oxygen-limited conditions using ScyNet. The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.

## Supplementary Material



**Supplementary Figure S2.** Visualization of cross-feeding metabolites in the *i*McBath and modified *i*EC1372\_W3110 community under oxygen-limited conditions using ScyNet. The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.

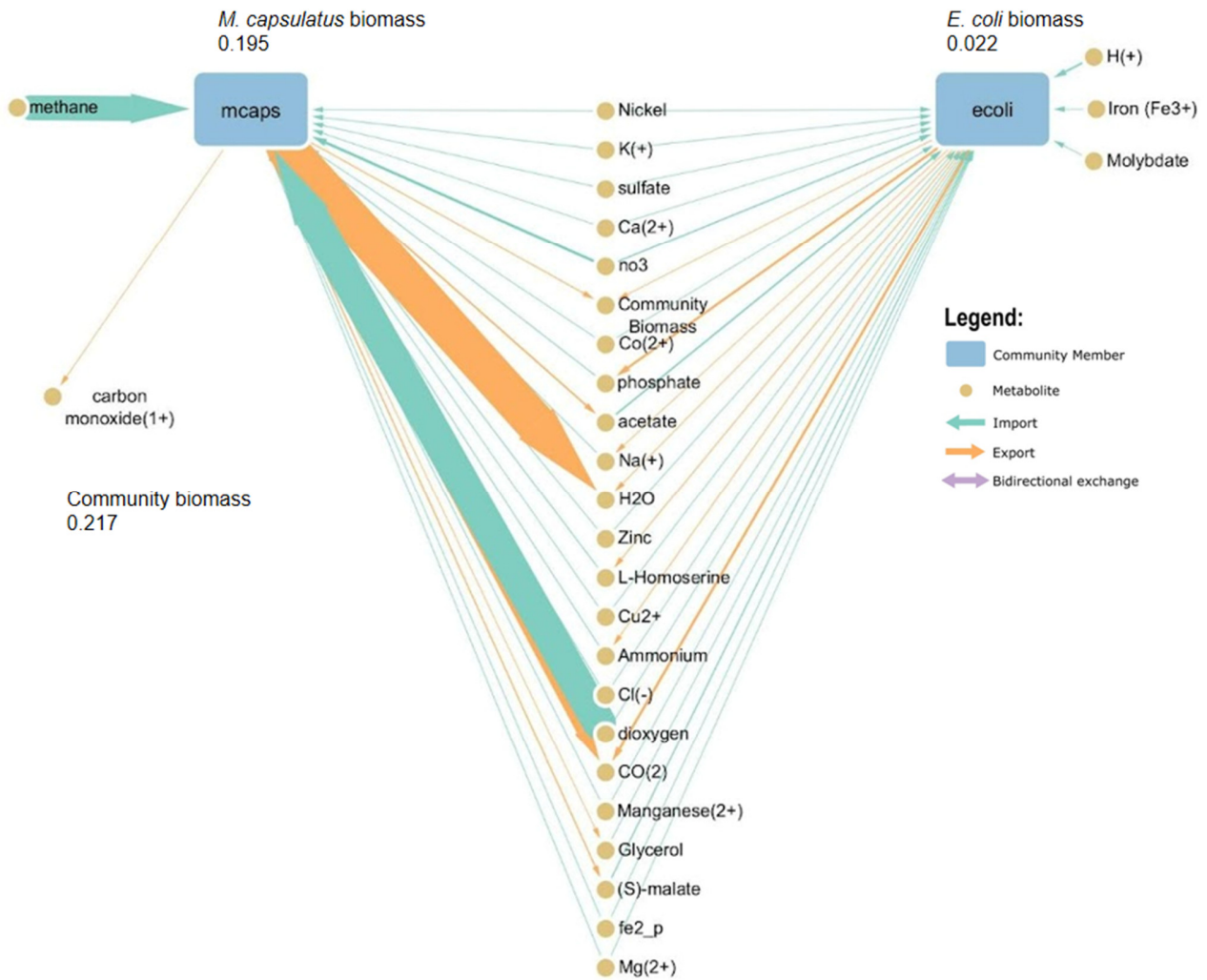
## Supplementary Material



**Supplementary Figure S3.** Visualization with Escher of cross-feeding of glycerol and amino acids in the community model of *iMcBath* and *iEC1372\_W3110* under oxygen-limited conditions. The legend in the figure indicates the flux intensity designations, and dashed lines represent reactions related to the production, exchange, and assimilation of glycerol, serine, threonine, and homoserine.



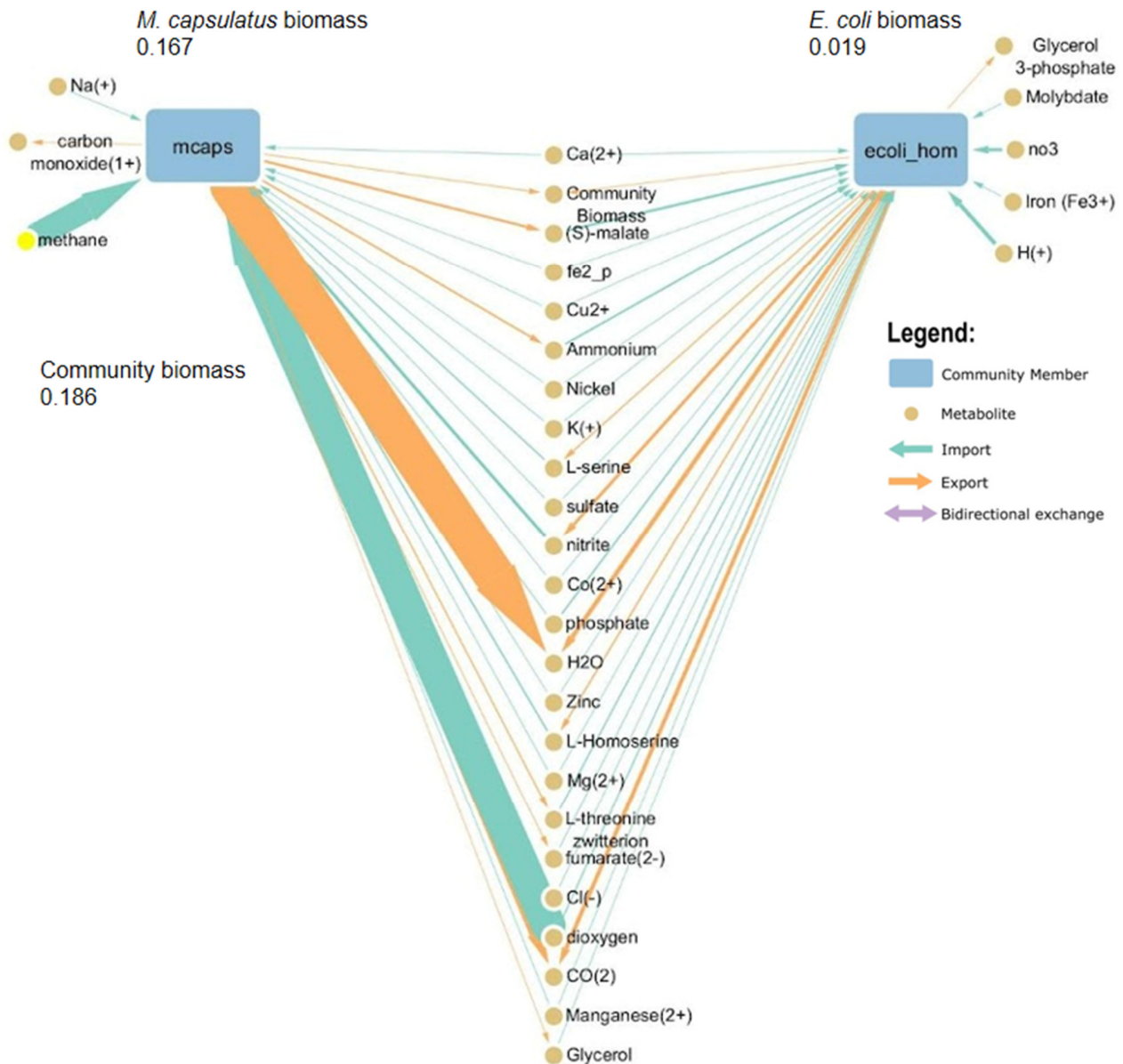
## Supplementary Material



**Supplementary Figure S5.** Visualization of cross-feeding metabolites in the *i*McBath and *i*EC1372\_W3110 community under nitrogen-limited conditions using ScyNet. The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.

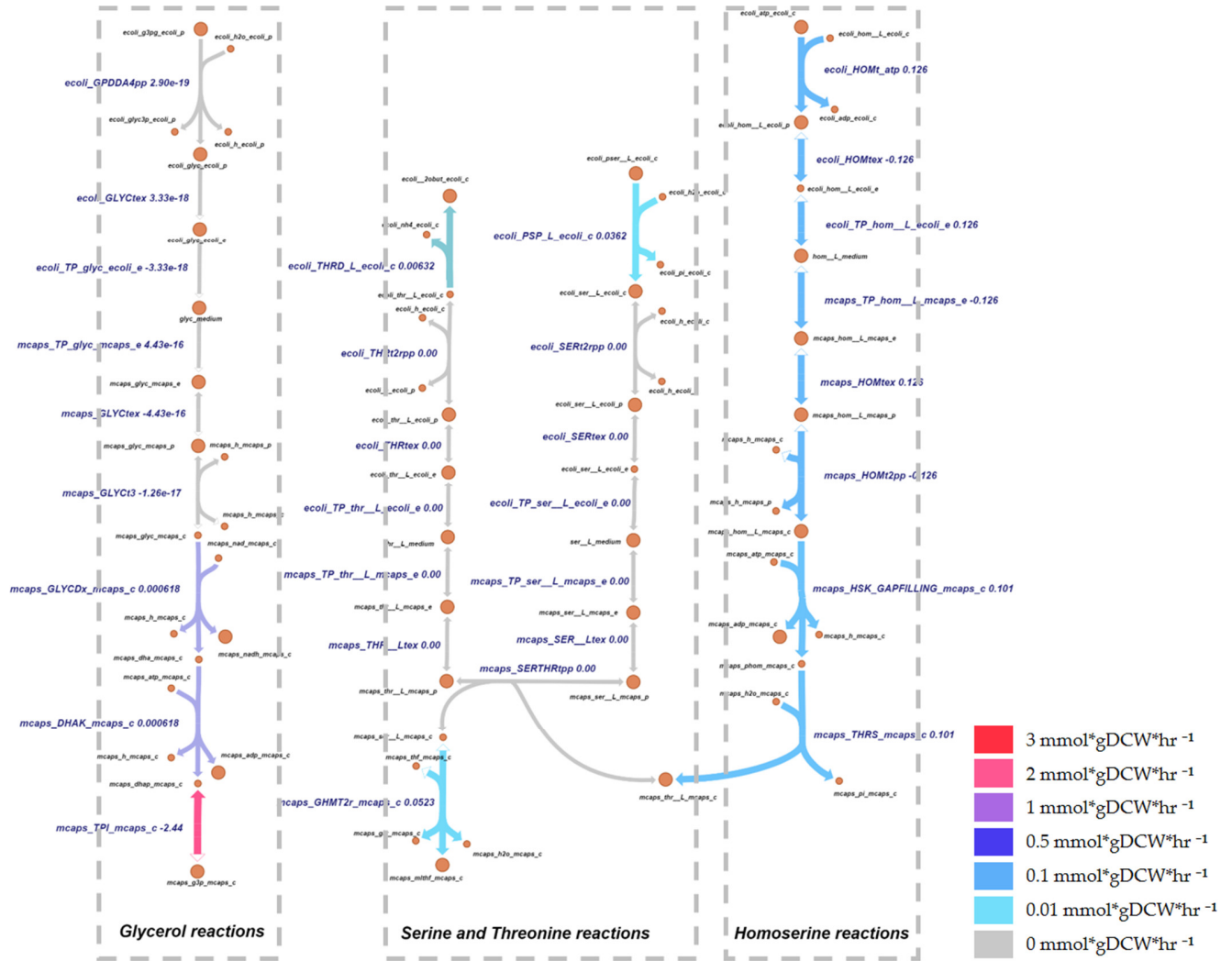


## Supplementary Material



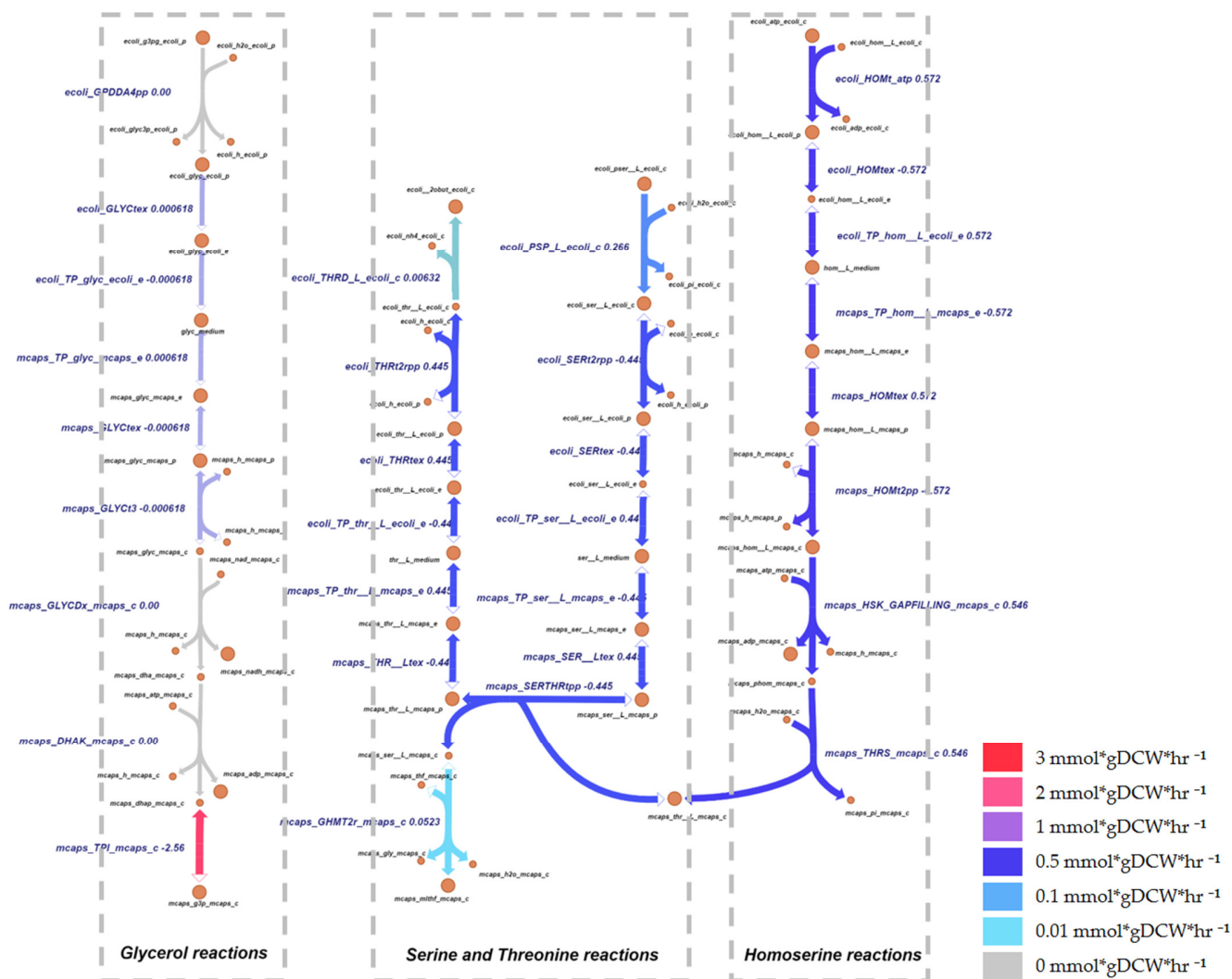
**Supplementary Figure S6.** Visualization of cross-feeding metabolites in the *i*McBath and modified *i*EC1372\_W3110 community under nitrogen-limited conditions using ScyNet. The color shows which metabolites are consumed (turquoise lines) and which are excreted (orange lines) by community members from the environment. The width of the line designates the flux value through this reaction.

## Supplementary Material



**Supplementary Figure S7.** Visualization with Escher of cross-feeding of glycerol and amino acids in the community model of *iMcBath* and *iEC1372\_W3110* under nitrate-limited conditions. The legend in the figure indicates the flux intensity designations, and dashed lines represent reactions related to the production, exchange, and assimilation of glycerol, serine, threonine, and homoserine.

## Supplementary Material



**Supplementary Figure S8.** Visualization with Escher of cross-feeding of glycerol and amino acids in the community model of *iMcBath* and modified *iEC1372\_W3110* under nitrate-limited conditions. The legend in the figure indicates the flux intensity designations, and dashed lines represent reactions related to the production, exchange, and assimilation of glycerol, serine, threonine, and homoserine.



## Supplementary Material

The image shows a web interface for loading models. It is divided into five numbered sections:

- 1**: A text input field labeled "Number of models:" with the value "2".
- 2**: Two rows of model selection. The first row has "Model name 1:" set to "mcaps" and "Select Model 1:" set to "iMcBath\_uphill". The second row has "Model name 2:" set to "ecoli\_hom" and "Select Model 2:" set to "iEC1372\_W3110\_modified". Each row has an "Upload (0)" button.
- 3**: A green button labeled "Load models".
- 4**: A checkbox labeled "Add homoserine transport and exchange rea..." which is checked.
- 5**: A pink button labeled "Create community".

Below the "Load models" button, the following text is displayed:

Model 1 'mcaps' selected from existing models: iMcBath\_uphill  
Model 2 'ecoli\_hom' selected from existing models: iEC1372\_W3110\_modified

**Supplementary Figure S9.** The model loading step includes: **1** Selection of the number of models to be used for community reconstruction; **2** Loading or selecting models used in the study; **3** A button for loading models; **4** Checkbox for adding transport and exchange reactions for homoserine in the *iMcBath\_uphill* model; **5** A button for the community model reconstruction.

The image shows a slider interface for setting the abundance of microorganisms. It includes two sliders:

- mcaps abundance:** A slider with a value of 0.90.
- ecoli\_hom abundance:** A slider with a value of 0.10.

Below the sliders is a purple button labeled "Apply abundance r...".

At the bottom, the text "Abundance ratios applied: {'mcaps': 0.9, 'ecoli\_hom': 0.1}" is displayed.

**Supplementary Figure S10.** A slider for setting the abundance of microorganisms in the community, with the sum required to equal 1.

## Supplementary Material

Supplementary Figure S11 shows a software interface for setting environment parameters. It consists of five numbered components: 1. A 'Select reactions:' dropdown menu with options: EX\_mn2\_medium, EX\_na1\_medium, EX\_ni2\_medium, EX\_no3\_medium (highlighted), EX\_o2\_medium, and EX\_si\_medium. 2. A text input field for 'EX\_no3\_medium' with the value '1.838'. 3. A green button labeled 'Remove reaction'. 4. A green button labeled 'Apply fluxes'. 5. A red button labeled 'Apply medium'.

**Supplementary Figure S11.** The step for set up the environment parameter for the community model consists of: **1** A selector for exchange reactions in the community; **2** A window for setting the boundaries for the chosen reactions; **3** A button to remove a metabolites from the environment; **4** A button for setting a boundary for reactions to continue the modification of metabolites in the environment; **5** A button for adding the configured environment to the community model.

Supplementary Figure S12 shows a software interface for modifying reactions. It consists of six numbered components: 1. A search bar labeled 'Search: Search reactions...'. 2. A 'Select reactions:' dropdown menu with options: mcaps\_GUAtex, mcaps\_H2Otex, mcaps\_H2Otp, mcaps\_HAMtex, mcaps\_HAMtp, mcaps\_Htex, mcaps\_Kabcpp, mcaps\_Kt2pp, mcaps\_Kt3pp, mcaps\_Ktex, and mcaps\_MAL\_Ltex. 3. Two input fields for 'mcaps\_CH4tex' lower and upper bounds, both set to '0'. 4. A green button labeled 'Apply bounds'. 5. A blue button labeled 'Confirm changes'. 6. A green button labeled 'Model summary'.

**Model calculation results**

**Supplementary Figure S12.** The step for modifications of reactions in the community model includes: **1** A window for searching reactions in the community model; **2** A selector to choose a reaction; **3** Changing the upper and lower bounds of the reaction; **4** A button for setting the boundaries of the selected reaction; **5** A button to confirm and apply those modifications, and **6** - a button for displaying the model summary.

## Supplementary Material

Filename:

[Download community](#)

[community\\_model.xml](#)

Filename:

[Download pFBA](#)

[pFBA\\_community.tsv](#)

**Supplementary Figure S13.** The step includes buttons for downloading the built community model in SBML format and pFBA results with all calculated fluxes for the community model.

## Supplementary Tables

**Supplementary Table S1:** Solutions found by OptFlux for the *E. coli* model.

Reaction	Growth rate, h <sup>-1</sup>	Homoserine production, mmol*gDCW <sup>-1</sup> *hr <sup>-1</sup>
R_Pltex = 8.0 R_ICL = 0.5	0.355	5.378
R_Pltex = 8.0 R_FCLT = 32.0	0.361	5.372
R_Pltex = 8.0 R_CU2tpp = 16.0	0.369	5.365
R_Pltex = 8.0	0.369	5.365

**Supplementary Table S2:** Cross-metabolites of the *i*McBath and *i*EC1372\_W3110 community without homoserine production from *i*EC1372\_W3110 and with its production.

Metabolite	Producer	Consumer	o2_lim, mmol* gDCW <sup>-1</sup> * hr <sup>-1</sup>	o2_lim_ homoserine, mmol* gDCW <sup>-1</sup> *hr <sup>-1</sup>	no3_lim, mmol* gDCW <sup>-1</sup> *h r <sup>-1</sup>	no3_lim_ homoserine, mmol* gDCW <sup>-1</sup> *hr <sup>-1</sup>
Acetate	<i>M.capsulatus</i>	<i>E.coli</i>	3.343	0.205	0.612	-

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Aspartate	<i>E.coli</i>	<i>M.capsulatus</i>	0.515	-	-	-
Fumarate	<i>M.capsulatus</i>	<i>E.coli</i>	-	-	-	0.096
Glycerol	<i>M.capsulatus</i>	<i>E.coli</i>	-	5.3E-4	3.3E-18	6.2E-4
Glycerol	<i>E.coli</i>	<i>M.capsulatus</i>	0.908	-	-	-
H <sub>2</sub> O	<i>M.capsulatus</i>	<i>E.coli</i>	30.896	-	-	-
Homoserine	<i>E.coli</i>	<i>M.capsulatus</i>	0.282	0.575	0.126	0.572
Malate	<i>M.capsulatus</i>	<i>E.coli</i>	-	1.144	0.361	1.197
Na <sup>+</sup>	<i>E.coli</i>	<i>M.capsulatus</i>	-	0.007	2.2E-20	-
NH <sub>4</sub>	<i>E.coli</i>	<i>M.capsulatus</i>	-	-	0.071	-
NH <sub>4</sub>	<i>M.capsulatus</i>	<i>E.coli</i>	0.981	0.7755	-	0.777
NO <sub>2</sub>	<i>M.capsulatus</i>	<i>E.coli</i>	0.059	-	-	-
Pi	<i>E.coli</i>	<i>M.capsulatus</i>	0.112	-	0.108	-
Serine	<i>E.coli</i>	<i>M.capsulatus</i>	0.151	0.467	-	0.445
Succinate	<i>E.coli</i>	<i>M.capsulatus</i>	4.06E-4	3.3E-4	-	-
Threonine	<i>M.capsulatus</i>	<i>E.coli</i>	0.151	0.467	-	0.445

**Supplementary Table S3:** Reactions required for considered electron transfer mechanisms in the *i*McBath model.

Electron transfer mechanism/ Reactions	sMMOi	pMMODC ipp	pMMOi pp	CyLCy HORpp	NADH16 pp	NADHNQR2 ipp	NADH5 ppi	CYOR_ q8ppi
<b>Redox-arm</b>	0	-	(0,1000)	-	0	0	-	-
<b>Direct</b>	0	(0,1000)	-	0	-	-	-	-
<b>Uphill</b>	0	-	(0,1000)	-	-	-	0	(-1000,0)

**Supplementary Table S4:** FBA results of the *i*McBath model under different electron transfer mechanisms.

Supplementary Material

<b>Model</b>	<b>Original_model, mmol*gDCW<sup>-1</sup>* hr<sup>-1</sup></b>	<b>Uphill, mmol* gDCW<sup>-1</sup>*hr<sup>-1</sup></b>	<b>Redox-arm, mmol* gDCW<sup>-1</sup>*hr<sup>-1</sup></b>	<b>Direct, mmol* gDCW<sup>-1</sup>*hr<sup>-1</sup></b>
<b>Ratio O2/CH4</b>	1,5 (27,81/18,46)	1,24 (22,84/18,46)	1,5 (27,81/18,46)	1,13 (20,92/18,46)
<b>Biomass</b>	0,178	0,275	0,178	0,313
<b>Uptake</b>				
EX_ca2_e	0,01244	0,01921	0,01244	0,02184
EX_ch4_e	18,46	18,46	18,46	18,46
EX_cl_e	0,03816	0,05895	0,03816	0,067
EX_cobalt2_e	1,03E-05	1,59E-05	1,03E-05	1,80E-05
EX_cu2_e	0,0002689	0,0004154	0,0002689	0,0004721
EX_fe2_e	0,001089	0,001683	0,001089	0,001913
EX_h_e	1,458	2,253	1,458	2,561
EX_k_e	0,03141	0,04853	0,03141	0,05516
EX_mg2_e	0,02197	0,03394	0,02197	0,03858
EX_mn2_e	3,20E-06	4,95E-06	3,20E-06	5,63E-06
EX_na1_e	0,006968	0,01076	0,006968	0,01224
EX_ni2_e	6,05E-06	9,35E-06	6,05E-06	1,06E-05
EX_no3_e	1,459	2,253	1,459	2,561
EX_o2_e	27,81	22,84	27,81	20,92
EX_pi_e	0,09814	0,1516	0,09814	0,1723
EX_so4_e	0,03005	0,04641	0,03005	0,05276
EX_zn2_e	0,000178	0,000275	0,000178	0,0003126
<b>Secretion</b>				
DM_4hba_c	5,10E-06	7,88E-06	5,10E-06	8,95E-06
DM_doxopa_c	0,0001895	0,0002928	0,0001895	0,0003328
DM_h2o2_c	0,05718	0,08834	0,05718	0,1004
DM_rdmmbzi_c	0,0001895	0,0002928	0,0001895	0,0003327
EX_co2_e	12,47	9,204	12,47	7,94



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EX_co_e	5,10E-06	7,88E-06	5,10E-06	8,95E-06
EX_h2o_e	32,96	30,8	32,96	29,97
EX_ac_e	-	-	-	-

**Supplementary Table S5:** Modified reactions with new boundaries in the *iMcBath* model.

Metabolic pathway	Response ID in the model	Set boundaries
<b>TCA</b>	MDH	-1000,1000
	CITL	-1000,1000
	ACONTa	-1000,1000
	ACONTb	-1000,1000
	ACONT	-1000,1000
	SSALx	-1000,0
	SSALy	-1000,0
	SUCCt2_2pp	-1000,1000
	FUM	-1000,1000
	ADSL1i	-1000,1000
	ARGSL	-1000,1000
	ME1	-1000,1000
	FUMt2_2pp	-1000,1000
	MALt2_2pp	-1000,1000
<b>EMP</b>	PFK_ppi	0,1000
	PYK	0,1000
<b>RuMP</b>	HPS	0,1000
	AH6PI	0,1000
	TKT2	0,1000
	RPI	0,1000
	TKT1	0,1000
	TALA	0,1000

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	RPE	0,1000
<b>ED</b>	G6PDH2	0,1000
	PGI	-1000,1000
	PGL	0,1000
	EDD	0,1000
	EDA	0,1000
	GND	0,1000

**Supplementary Table S6:** Impact of changes in EDD pathway flux on EMP reaction fluxes in the *i*McBath model (PFK—phosphofructokinase, PFK3—pyrophosphate-dependent 6-phosphofructokinase, PGM—phosphoglycerate mutase), methane and oxygen consumption, and acetate production.

ED	Biomass, h <sup>-1</sup>	ratio O <sub>2</sub> /CH <sub>4</sub> , mmol* gDCW <sup>-1</sup> *hr <sup>-1</sup>	PFK, mmol* gDCW <sup>-1</sup> *hr <sup>-1</sup>	PFK3, mmol* gDCW <sup>-1</sup> *hr <sup>-1</sup>	PGM, mmol* gDCW <sup>-1</sup> *hr <sup>-1</sup>	Acetate, mmol* gDCW <sup>-1</sup> *hr <sup>-1</sup>
0	0	(-12.515/-8.391)	0	0	0	0
0.503	0.277	(-22.744/-18.46)	2.529	0	1.921	0
1.007	0.275	(-22.824/-18.46)	2.009	0	1.404	0
1.510	0.274	(-22.904/-18.46)	1.488	0	0.887	0
2.014	0.272	(-22.983/-18.46)	0.968	0	0.370	0
2.517	0.270	(-23.089/-18.46)	0.442	0	-0.151	0
3.021	0.268	(-23.224/-18.46)	0	-0.091	-0.678	0
3.524	0.265	(-23.359/-18.46)	0	-0.623	-1.205	0
4.028	0.262	(-23.494/-18.46)	0	-1.155	-1.731	0
4.531	0.260	(-23.630/-18.46)	0	-1.688	-2.258	0
5.035	0.257	(-23.765/-18.46)	0	-2.220	-2.784	0
5.538	0.254	(-23.9/-18.46)	0	-2.753	-3.311	0
6.041	0.246	(-23.95/-18.46)	0	-3.157	-3.697	0.191
6.545	0.188	(-25.082/1.111)	0	-3.377	-3.789	1.111

**Supplementary Table S7:** Additional modifications of the community model.

## Supplementary Material

Reactions of the community model	Boundaries
ecoli_TP_ecoli_eca4colipa_ecoli_e	0,0
ecoli_TP_colipa_ecoli_e	0,0
ecoli_TP_colipap_ecoli_e	0,0
ecoli_TP_btn_ecoli_e	0,0
ecoli_TP_acolipa_ecoli_e	0,0
ecoli_TP_hacolipa_ecoli_e	0,0
ecoli_TP_o16a4colipa_ecoli_e	0,0
ecoli_TP_o6a4colipa_ecoli_e	0,0
ecoli_TP_lipa_ecoli_e	0,0
ecoli_GPDDA1pp	0,0
ecoli_TP_lipa_cold_ecoli_e	0,0
ecoli_hom_TP_ecoli_hom_eca4colipa_ecoli_hom_e	0,0
ecoli_hom_TP_colipa_ecoli_hom_e	0,0
ecoli_hom_TP_colipap_ecoli_hom_e	0,0
ecoli_hom_TP_btn_ecoli_hom_e	0,0
ecoli_hom_TP_acolipa_ecoli_hom_e	0,0
ecoli_hom_TP_hacolipa_ecoli_hom_e	0,0
ecoli_hom_TP_o16a4colipa_ecoli_hom_e	0,0
ecoli_hom_TP_o6a4colipa_ecoli_hom_e	0,0
ecoli_hom_TP_lipa_ecoli_hom_e	0,0
ecoli_hom_GPDDA1pp	0,0
ecoli_hom_TP_lipa_cold_ecoli_hom_e	0,0
ecoli_TP_h_ecoli_e	-1000,0
mcaps_TP_h_mcaps_e	-1000,0
ecoli_hom_TP_h_ecoli_hom_e	-1000,0
ecoli_TP_co2_ecoli_e	0,1000
ecoli_TP_pser__L_ecoli_e	0,0
ecoli_hom_TP_pser__L_ecoli_hom_e	0,0

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ecoli_hom_TP_glyclt_ecoli_hom_e	0,0
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