Supplementary Data

1. Chinese Hamster Ovary (CHO)
The model and reported flux distribution are cited from Llaneras and Pico (2007).

Llaneras, F. Pico, J. An interval approach for dealing with flux distributions and elementary modes activity patterns. *J. Theor. Biol.* 2007, *246*, 290-308.

Table S1 Prediction results for the flux distribution of CHO cells by Quadratic programming (QP) , the maximum entropy principle (MEP), and Linear Programming in Enzyme Control Flux (ECFLP)

No	Reactions	Exp	QP	MEP	ECFLP
R1	G ==> G6P	4.05	4.05	4.05	4.05
R2	G6P ==> DAP + G3P	3.76	4.05	3.92	3.93
R3	G6P ==> R5P + CO_2	0.28	0.00	0.13	0.12
R4	DAP ==> G3P	3.76	4.05	3.92	3.93
R5	G3P ==> PYR	7.53	8.10	7.84	7.87
R6	PYR ==> L	7.39	7.39	7.39	7.39
R7	PYR + GLU ==> A + AKG	0.26	0.26	0.26	0.26
R8	PYR ==> CO_2 + ACA	0.34	1.63	1.06	1.12
R9	ACA + OXA ==> CIT	0.34	1.63	1.06	1.12
R10	CIT ==> CO_2 + AKG	0.34	1.63	1.06	1.12
R11	AKG ==> CO_2 + MAL	1.10	2.81	2.06	2.14
R12	MAL ==> OXA	0.63	1.63	1.19	1.24
R13	MAL ==> CO_2 + PYR	0.47	1.18	0.87	0.9
R14	GLU + OXA ==> ASP + AKG	0.28	0.00	0.13	0.12
R15	GLU ==> NH4 + AKG	0.20	0.92	0.61	0.64
R16	Q ==> GLU + NH4	0.75	1.18	1.00	1.02
R17	R5P + ASP + Q ==> PU	0.14	0.00	0.08	0.07
R18	R5P + ASP + 2 Q ==> PY	0.14	0.00	0.05	0.05
R19	GX ==> G	4.05	4.05	4.05	4.05
R20	L ==> LX	7.39	7.39	7.39	7.39
R21	NH4 ==> NH4X	0.96	2.10	1.61	1.66
R22	PU ==> PUX	0.14	0.00	0.08	0.07
R23	QX ==> Q	1.18	1.18	1.18	1.18
R24	A ==> AX	0.26	0.26	0.26	0.26
R25	CO_2 ==> CO_2x	2.61	7.25	5.19	5.4
R26	PY ==> PYX	0.14	0.00	0.05	0.05

<==> reversible reaction; => irreversible reaction. Exp: Experimental fluxes.

Metabolites:
G, Glucose; L, Lactate; NH4, Ammonia; PU, Purine; Q, Glutamine; A, Alamime; CO_2, Carbon Dioxide; PY, Pyrimidine; G6P, Glucose-6-phosphate; DAP, Dihydroxy-acetone Phosphate; R5P, Ribose-5-Phosphate; Cit, Citrate; Mal, Malate; Glu, Glutamate; G3P, Glyceraldehyde-3-phosphate; PYR, pyruvate; ACA, acetyl-coenzyme A; OXA, Oxaloacetate; AKG, α-ketoglutarase; ASP, Aspartate; GX, extracellular glucose; LX, extracelluar lactate; NH4X, extracellular ammonia; PUX, product purine; QX, extracellular glutamine; AX, extracellular alanine; CO_2X, extracellular carbon dioxide; PYX, product pyrimidine.

2. *Escherichia coli*

The experimental flux distribution is cited from Burgard and Maranas (2003)

Burgard, A.P., Maranas, C.D. Optimization-based framework for inferring and testing hypothesized metabolic objective functions. *Biotechnol. Bioeng.* 2003, *82*, 670-677.

The external flux for acetate is set to be 0 and glucose uptake is set to be 115 under aerobic conditions. The prediction results are shown in Table S2. Under anaerobic conditions, the external fluxes for acetate, ethanol, lactate and succinate are set to be 34.1, 65.3, 69.8 and 3.9, respectively. The uptake of glucose is set to be 115. The prediction results are shown in Table S3.

Table S2 Prediction results for the flux distribution of *E. coli* under aerobic conditions by Quadratic programming (QP), Linear programming (LP) , the maximum entropy principle (MEP) and Linear Programming in Enzyme Control Flux (ECFLP)

Genes	Reactions	Exp	QP	LP	MEP	ECFLP
TKTA	2 P5P <==> GAP + S7P	18.90	-0.21	-2.51	28.14	29.76
TKTB	P5P + E4P <==> GAP + F6P	9.60	-6.23	-8.59	24.13	26.26
PCK	CO_2 + PEP <==> OAA	21.40	43.67	44.13	29.14	25.36
MDH	MAL <==> OAA	45.00	0.21	0.00	48.34	66.66
PYK	PEP <==> PYR	26.60	-0.25	0.78	9.79	18.18
CO_2EXT	CO_2 <==> CO_2EXT	254.90	75.94	69.24	280.13	333.34
PGI	G6P <==> F6P	61.00	105.22	111.96	23.61	19.67
FUM	FUM <==> MAL	45.00	0.21	0.00	48.34	66.66
TAL	GAP + S7P <==> F6P + E4P	18.90	-0.21	-2.51	28.14	29.76
GLCEXT	GLCXT ==> GLC	115.00	115.02	115.00	115.00	115.00
PDH	PYR ==> ACCOA + CO_2	126.10	72.85	73.42	96.82	108.84
ENO	P3G ==> PEP	181.20	165.79	167.35	158.84	162.81
SDH	SUC ==> FUM	45.00	0.21	0.00	48.34	66.66
GND	D6PGL ==> CO_2 + P5P	53.10	6.80	0.00	89.39	93.59
CS	ACCOA + OAA ==> ICIT	52.00	16.76	16.72	59.38	76.26
GAP	GAP ==> P3G	193.00	186.15	187.93	172.43	174.63
ACEXT	AC ==> ACEXT	0.00	0.00	0.00	0.00	0.00
ZWF	G6P ==> D6PGL	53.10	6.80	0.00	89.39	93.59
ICDH	ICIT ==> CO_2 + AKG	52.00	16.76	16.72	59.38	76.26
ACK	ACCOA ==> AC	0.00	0.00	0.00	0.00	0.00
GROWTH	3.058 PYR + 0.219 G6P + 4.093 ACCOA + 0.165 GAP + 0.537 PEP + 0.982 P5P + 0.106 F6P + 1.979 OAA + 0.439 E4P + 1.207 AKG + 1.485 P3G ==> 1.677 CO_2 + BIOMASS	7.00	13.71	13.85	9.15	7.96
AKD	AKG ==> CO_2 + SUC	45.00	0.21	0.00	48.34	66.66
PFK	F6P ==> 2 GAP	89.10	97.32	99.40	74.90	74.84
PTS	PEP + GLC ==> PYR + G6P	115.00	115.02	115.00	115.00	115.00

<==> reversible reaction; => irreversible reaction. Exp: Experimental fluxes;

Metabolites:

G6P, glucose-6-phosphate; ACCOA , acetyl-coenzyme A; CO_2, carbon dioxide; S7P, sedoheptulose-7-phosphate; PEP, phosphoenolpyruvate; P5P, pentose-5-phosphate; SUC, succinate; OAA, oxaloacetate; ICIT, isocitrate; P3G, 3-phosphoglycerate; LAC, lactate; PYR, pyruvate; ETH, ethanol; GAP, glyceraldehydes-3-phosphate; D6PGL, d-6-phosphate gluconate; MAL, malate; F6P, fructose-6-phosphate; AC, acetate; GLC, glucose; FUM, fumarate; E4P, erythrose-4-phosphate; AKG, α-ketoglutarase; ACEXT, external acetate; BIOMASS, biomass; GLCXT, external glucose; CO_2EXT, external carbon dioxide.

Table S3 Prediction results for the flux distribution of *Escherichia coli* under anaerobic conditions by Quadratic programming (QP), Linear programming (LP), the maximum entropy principle (MEP), and Linear Programming in Enzyme Control Flux (ECFLP)

Genes	Reactions	Exp	QP	LP	MEP	ECFLP
MDH	MAL <==> OAA	0.80	0.00	0.00	3.44	4.91
PCK	CO_2 + PEP <==> OAA	6.10	6.88	14.07	8.33	10.31
PGI	G6P <==> F6P	30.00	2.40	114.30	35.27	70.43
TAL	S7P + GAP <==> F6P + E4P	28.20	37.29	-0.58	26.22	14.35
TKTA	2 P5P <==> S7P + GAP	28.20	37.29	-0.58	26.22	14.35
TKTB	P5P + E4P <==> GAP + F6P	26.90	36.88	-1.98	25.61	13.46
PYK	PEP <==> PYR	69.10	65.92	84.78	73.16	79.81
CO2EXT	CO2 <==> CO_2EXT	199.60	224.27	123.15	203.91	176.11
FUM	FUM <==> MAL	0.80	0.00	0.00	3.44	4.91
ENO	P3G ==> PEP	194.60	188.31	215.56	197.24	206.20
SDH	SUC ==> FUM	0.80	0.00	0.00	3.44	4.91
GND	D6PGL ==> CO_2 + P5P	84.90	112.39	0.00	79.43	44.13
SUCCEXT	SUC ==> SUCEXT	3.90	3.90	3.90	3.90	3.90
ACEXT	AC ==> ACEXT	34.10	34.10	34.10	34.10	34.10
ICDH	ICIT ==> CO_2 + AKG	4.80	5.03	7.75	9.02	11.24
ZWF	G6P ==> D6PGL	84.90	112.39	0.00	79.43	44.13
LDH	PYR ==> LAC	69.80	69.80	69.80	69.80	69.80
ACK	ACCOA ==> AC	34.10	34.10	34.10	34.10	34.10
PTS	PEP + GLC ==> G6P + PYR	115.00	115.00	115.00	115.00	115.00
GLCEXT	GLCXT ==> GLC	115.00	115.00	115.00	115.00	115.00
PDH	PYR ==> ACCOA + CO_2	111.40	108.26	120.22	114.11	118.86
CS	ACCOA + OAA ==> ICIT	4.80	5.03	7.75	9.02	11.24
GAP	GAP ==> P3G	205.00	189.70	220.31	199.30	209.18
ETHEXT	ETH ==> ETHEXT	65.30	65.30	65.30	65.30	65.30
LACEXT	LAC ==> LACEXT	69.80	69.80	69.80	69.80	69.80
GROWTH	0.219 G6P + 4.093 ACCOA + 0.537 PEP + 0.982 P5P + 1.979 OAA + 1.485 P3G + 3.058 PYR + 0.165 GAP + 0.106 F6P + 0.439 E4P + 1.207 AKG ==> 1.677 CO_2 + BIOMASS	2.00	0.94	3.19	1.39	2.01
AKD	AKG ==> CO_2 + SUC	4.70	3.90	3.90	7.34	8.81
ADH	ACCOA ==> ETH	65.30	65.30	65.30	65.30	65.30
PFK	F6P ==> 2 GAP	84.90	76.48	111.41	86.96	98.03

<==> reversible reaction; => irreversible reaction. Exp: Experimental fluxes;

Metabolites:
G6P, glucose-6-phosphate; ACCOA , acetyl-coenzyme A; CO_2, carbon dioxide; S7P, sedoheptulose-7-phosphate; PEP, phosphoenolpyruvate; P5P, pentose-5-phosphate; SUC, succinate; OAA, oxaloacetate; ICIT, isocitrate; P3G, 3-phosphoglycerate; LAC, lactate; PYR, pyruvate; ETH, ethanol; GAP, glyceraldehydes-3-phosphate; D6PGL, d-6-phosphate gluconate; MAL, malate; F6P, fructose-6-phosphate; AC, acetate; GLC, glucose; FUM, fumarate; E4P, erythrose-4-phosphate; AKG, α-ketoglutarase; ACEXT, external acetate; BIOMASS, biomass; SUCEXT, external succinate; ETHEXT , external ethanol; GLCXT, external glucose; LACEXT, external lactate; CO_2EXT, external carbon dioxide.

3. *Saccharomyces cerevisiae*

The experimental flux distribution is cited from Frick and Wittmann (2005).

Frick, O., Wittmann, C. Characterization of the metabolic shift between oxidative and fermentative growth in *Saccharomyces cerevisiae* by comparative ^{13}C flux analysis, *Microb Cell Fact*, 2005, *4*, 30.

The external fluxes of glucose, acetate, ethanol and glycerol are set to be the same value as the experimental data.

Metabolites (Table S4-S6):

R5P, ribose-5-phosphate; G6P, glucose-6-phosphate; CO_2, carbon dioxide; S7P, sedoheptulose-7-phosphate; PEP, phosphoenolpyruvate; ACE, acetate; ACCOACYT, cytosolic acetyl-coenzyme A; SUC, succinate; DHAP, dihydroxyacetong phosphate; SUCCOA, succinyl-coenzyme A; OAA, cytosolic oxaloacetate; P3G, 3-phosphoglycerate; PYR, cytosolic pyruvate; P6G, 6-phospho-gluconate; GA3P, glyceraldehydes-3-phosphate; MAL, malate; G15L, 6-phospho-glucono-1,5-lactone; RU5P, ribulose-5-phosphate; ACA, acetate; ICI, isocitrate; OAAMIT, mitochondrial oxaloacetate ; F6P, fructose-6-phosphate; ACCOAMIT, mitochondrial acetyl-coenzyme A; PYRMIT, mitochondrial pyruvate; X5P, xylulose-5-phosphate; GP, glycerone-3-phosphate; E4P, erythrose-4-phosphate; FUM, fumarate; AKG, α-ketoglutarase; ACEX, external acetate; CO_2EX, external carbon dioxide; BIOMASS, biomass; ETH, ethanol; GLYC, glycerol; GLC, glucose; ETHEXT, external ethanol; GLCEXT, external glucose; GLYCEXT, external glycerol.

<==> reversible reaction;
=> irreversible reaction.

Exp: Experimental fluxes;

Table S4. Prediction results for the flux distribution of *Saccharomyces cerevisiae* (μ=0.15 h^{-1}) by Quadratic programming (QP), Linear programming (LP), the maximum entropy principle (MEP), and Linear Programming in Enzyme Control Flux (ECFLP)

Genes	Reactions	Exp	QP	LP	MEP	ECFLP
ENO	P3G <==> PEP	128.70	107.54	110.48	124.78	132.21
SDH	SUC <==> FUM	63.40	4.84	0.00	44.56	61.83
TPI	DHAP <==> GA3P	58.30	53.19	59.60	60.41	63.45
MDH	MAL <==> OAAMIT	56.20	-12.06	-16.59	17.75	30.75
RKI	RU5P <==> R5P	20.00	12.83	3.98	12.66	12.70
TAL	S7P + GA3P <==> F6P + E4P	18.70	9.13	0.00	9.77	10.17
TKL	R5P + X5P <==> S7P + GA3P	18.70	9.13	0.00	9.77	10.17
TKI	X5P + E4P <==> GA3P + F6P	16.30	5.43	-3.98	6.88	7.63
RPE	RU5P <==> X5P	30.00	14.55	-3.98	16.65	17.80
TDH	GA3P <==> P3G	134.10	114.94	118.45	130.56	137.28
LSC	SUCCOA <==> SUC	63.40	4.84	0.00	44.56	61.83
FUM	FUM <==> MAL	63.40	4.84	0.00	44.56	61.83
FBA	F6P <==> DHAP + GA3P	60.20	56.33	62.83	63.27	66.19
ACS	ACE ==> ACCOACYT	73.60	44.93	41.15	48.03	49.67
GPD	DHAP ==> GP	2.20	3.14	3.23	2.86	2.74
ACEX	ACE ==> ACEX	0.00	0.00	0.00	0.00	0.00
GND	P6G ==> CO_2 + RU5P	54.70	27.38	0.00	29.31	30.50
HXK	GLC ==> G6P	100.00	100.00	100.00	100.00	100.00
CO2EX	CO_2 ==> CO_2EX	270.00	76.76	37.47	190.24	239.94
ZWF	G6P ==> G15L	54.70	27.38	0.00	29.31	30.50
BIOMASS	3 R5P + 25 G6P + 6 PEP + 24 ACCOACYT + 10 OAA + 6 P3G + 3 ACCOAMIT + 18 PYRMIT + GP + 3 E4P + 11 AKG ==> 100 BIOMASS	0.60	1.23	1.33	0.96	0.84
PYC	CO_2 + PYR ==> OAA	23.80	42.81	44.47	47.02	48.82
PGI	G6P ==> F6P	25.20	41.77	66.81	46.62	48.40
KGD	AKG ==> CO_2 + SUCCOA	63.40	4.84	0.00	44.56	61.83
IDP	ICI ==> CO_2 + AKG	73.10	18.41	14.60	55.15	71.12
CAT	ACCOACYT ==> ACCOAMIT	53.40	15.32	9.29	24.92	29.41
ALD	ACA ==> ACE	73.60	44.93	41.15	48.03	49.67
MAE	MAL ==> CO_2 + PYRMIT	7.20	16.90	16.59	26.80	31.09
PYK	PEP ==> PYR	124.30	100.14	102.52	119.00	127.15
SOL	G15L ==> P6G	54.70	27.38	0.00	29.31	30.50
GPP	GP ==> GLYC	1.90	1.91	1.90	1.90	1.90
PDC	PYR ==> CO_2 + ACA	73.30	45.23	41.45	48.33	49.97
PDB	PYRMIT ==> CO_2 + ACCOAMIT	21.80	6.79	9.29	33.12	44.25
OAAT	OAA ==> OAAMIT	16.80	30.47	31.20	37.39	40.38
ADH	ACA ==> ETH	0.30	0.30	0.30	0.30	0.30
CIT	OAAMIT + ACCOAMIT ==> ICI	73.10	18.41	14.60	55.15	71.12
YEL006W	PYR ==> PYRMIT	27.00	12.10	16.59	23.65	28.35
GLCup	GLCEXT ==> GLC	100.00	100.00	100.00	100.00	100.00
ETHEXT	ETH ==> ETHEXT	0.30	0.30	0.30	0.30	0.30
GLYCEXT	GLYC ==> GLYCEXT	1.90	1.91	1.90	1.90	1.90

Table S5. Prediction results for the flux distribution of *Saccharomyces cerevisiae* (μ=0.30 h^{-1}) by Quadratic programming (QP), Linear programming (LP), the maximum entropy principle (MEP), and Linear Programming in Enzyme Control Flux (ECFLP)

Genes	Reaction	Exp	QP	LP	MEP	ECFLP
ENO	P3G <==> PEP	156.90	128.60	136.87	150.53	147.52
SDH	SUC <==> FUM	47.20	2.93	0.00	43.87	35.75
TPI	DHAP <==> GA3P	73.10	55.92	69.18	69.37	68.64
MDH	MAL <==> OAAMIT	22.70	-7.19	-10.91	22.76	16.75
RKI	RU5P <==> R5P	16.00	19.38	2.62	11.90	11.03
TAL	S7P + GA3P <==> F6P + E4P	10.20	17.17	0.00	10.37	9.31
TKL	R5P + X5P <==> S7P + GA3P	10.20	17.17	0.00	10.37	9.31
TKI	X5P + E4P <==> GA3P + F6P	8.50	14.95	-2.62	8.84	7.60
RPE	RU5P <==> X5P	14.00	32.12	-2.62	19.21	16.92
TDH	GA3P <==> P3G	159.80	133.03	142.11	153.58	150.94
LSC	SUCCOA <==> SUC	47.20	2.93	0.00	43.87	35.75
FUM	FUM <==> MAL	47.20	2.93	0.00	43.87	35.75
FBA	F6P <==> DHAP + GA3P	78.70	62.15	75.55	75.37	74.71
ACS	ACE ==> ACCOACYT	19.50	26.93	27.07	31.27	31.59
GPD	DHAP ==> GP	6.00	6.24	6.37	6.01	6.07
ACEX	ACE ==> ACEX	14.70	14.70	14.70	14.70	14.70
GND	P6G ==> CO_2 + RU5P	29.60	51.50	0.00	31.11	27.94
HXK	GLC ==> G6P	100.00	99.99	100.00	100.00	100.00
CO2EX	CO_2 ==> CO_2EX	250.00	145.37	88.85	241.38	215.58
ZWF	G6P ==> G15L	29.60	51.50	0.00	31.11	27.94
BIOMASS	3 R5P + 25 G6P + 6 PEP + 24 ACCOACYT + 10 OAA + 6 P3G + 3 ACCOAMIT + 18 PYRMIT + GP + 3 E4P + 11 AKG ==> 100 BIOMASS	0.40	0.74	0.87	0.51	0.57
PYC	CO_2 + PYR ==> OAA	27.40	25.62	29.25	31.80	30.98
PGI	G6P ==> F6P	60.00	30.03	78.17	56.16	57.79
KGD	AKG ==> CO_2 + SUCCOA	47.10	2.93	0.00	43.87	35.75
IDP	ICI ==> CO_2 + AKG	54.40	11.05	9.60	49.47	42.03
CAT	ACCOACYT ==> ACCOAMIT	6.40	9.22	6.11	19.06	17.89
ALD	ACA ==> ACE	34.20	41.63	41.77	45.97	46.29
MAE	MAL ==> CO_2 + PYRMIT	14.50	10.12	10.91	21.11	19.00
PYK	PEP ==> PYR	153.20	124.17	131.63	147.47	144.10
SOL	G15L ==> P6G	29.60	51.50	0.00	31.11	27.94
GPP	GP ==> GLYC	5.50	5.50	5.50	5.50	5.50
PDC	PYR ==> CO_2 + ACA	82.90	91.33	91.47	95.67	95.99
PDB	PYRMIT ==> CO_2 + ACCOAMIT	49.50	4.05	6.11	31.94	25.85
OAAT	OAA ==> OAAMIT	21.70	18.24	20.52	26.71	25.28
ADH	ACA ==> ETH	49.70	49.70	49.70	49.70	49.70
CIT	OAAMIT + ACCOAMIT ==> ICI	54.40	11.05	9.60	49.47	42.03
YEL006W	PYR ==> PYRMIT	42.80	7.21	10.91	20.00	17.12
GLCup	GLCEXT ==> GLC	100.00	99.99	100.00	100.00	100.00
ETHEXT	ETH ==> ETHEXT	49.70	49.70	49.70	49.70	49.70
GLYCEXT	GLYC ==> GLYCEXT	5.50	5.50	5.50	5.50	5.50

Table S6. Prediction results for the flux distribution of *Saccharomyces cerevisiae* (μ=0.40 h^{-1}) by Quadratic programming (QP), Linear programming (LP), the maximum entropy principle (MEP) , and Linear Programming in Enzyme Control Flux (ECFLP)

Genes	Reactions	Exp	QP	LP	MEP	ECFLP
ENO	P3G <==> PEP	167.40	145.19	157.62	159.11	162.97
SDH	SUC <==> FUM	16.80	1.49	0.00	17.78	20.49
TPI	DHAP <==> GA3P	80.50	59.10	77.73	71.97	76.33
MDH	MAL <==> OAAMIT	-4.10	-3.66	-6.80	7.43	9.18
RKI	RU5P <==> R5P	6.00	24.62	1.63	12.50	7.77
TAL	S7P + GA3P <==> F6P + E4P	5.30	23.49	0.00	11.46	6.69
TKL	R5P + X5P <==> S7P + GA3P	5.30	23.49	0.00	11.46	6.69
TKI	X5P + E4P <==> GA3P + F6P	3.80	22.36	-1.63	10.41	5.61
RPE	RU5P <==> X5P	10.00	45.85	-1.63	21.87	12.30
TDH	GA3P <==> P3G	171.00	147.45	160.88	161.20	165.14
LSC	SUCCOA <==> SUC	16.80	1.49	0.00	17.78	20.49
FUM	FUM <==> MAL	16.80	1.49	0.00	17.78	20.49
FBA	F6P <==> DHAP + GA3P	87.10	65.98	84.78	78.82	83.20
ACS	ACE ==> ACCOACYT	11.10	13.71	16.85	17.78	19.28
GPD	DHAP ==> GP	6.80	6.88	7.04	6.85	6.86
ACEX	ACE ==> ACEX	5.00	5.00	5.00	5.00	5.00
GND	P6G ==> CO_2 + RU5P	15.10	70.47	0.00	34.37	20.07
HXK	GLC ==> G6P	100.00	100.00	100.00	100.00	100.00
CO2EX	CO_2 ==> CO_2EX	191.60	197.98	127.72	209.93	204.14
ZWF	G6P ==> G15L	15.10	70.47	0.00	34.37	20.07
BIOMASS	3 R5P + 25 G6P + 6 PEP + 24 ACCOACYT + 10 OAA + 6 P3G + 3 ACCOAMIT + 18 PYRMIT + GP + 3 E4P + 11 AKG ==> 100 BIOMASS	0.30	0.38	0.54	0.35	0.36
PYC	CO_2 + PYR ==> OAA	31.40	13.05	18.21	17.64	18.90
PGI	G6P ==> F6P	77.90	20.13	86.41	56.95	70.90
KGD	AKG ==> CO_2 + SUCCOA	16.80	1.49	0.00	17.78	20.49
IDP	ICI ==> CO_2 + AKG	22.90	5.63	5.98	21.60	24.46
CAT	ACCOACYT ==> ACCOAMIT	0.60	4.69	3.81	9.44	10.61
ALD	ACA ==> ACE	16.10	18.71	21.85	22.78	24.28
MAE	MAL ==> CO_2 + PYRMIT	20.90	5.16	6.80	10.35	11.31
PYK	PEP ==> PYR	164.60	142.94	154.36	157.03	160.80
SOL	G15L ==> P6G	15.10	70.47	0.00	34.37	20.07
GPP	GP ==> GLYC	6.50	6.50	6.50	6.50	6.50
PDC	PYR ==> CO_2 + ACA	123.50	126.21	129.35	130.28	131.78
PDB	PYRMIT ==> CO_2 + ACCOAMIT	23.70	2.06	3.81	13.20	14.93
OAAT	OAA ==> OAAMIT	27.10	9.29	12.78	14.17	15.28
ADH	ACA ==> ETH	107.50	107.50	107.50	107.50	107.50
CIT	OAAMIT + ACCOAMIT ==> ICI	22.90	5.63	5.98	21.60	24.46
YEL006W	PYR ==> PYRMIT	9.70	3.67	6.80	9.10	10.12
GLCup	GLCEXT ==> GLC	100.00	100.00	100.00	100.00	100.00
ETHEXT	ETH ==> ETHEXT	107.50	107.50	107.50	107.50	107.50
GLYCEXT	GLYC ==> GLYCEXT	6.50	6.50	6.50	6.50	6.50