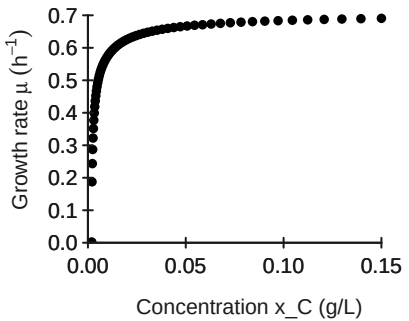
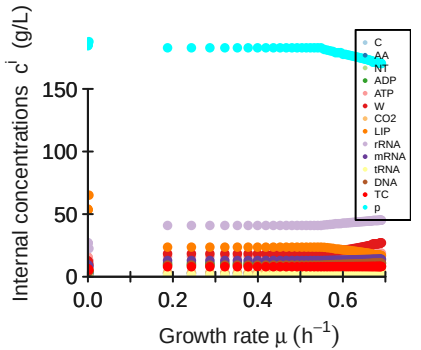
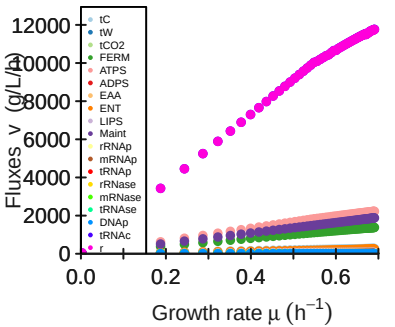
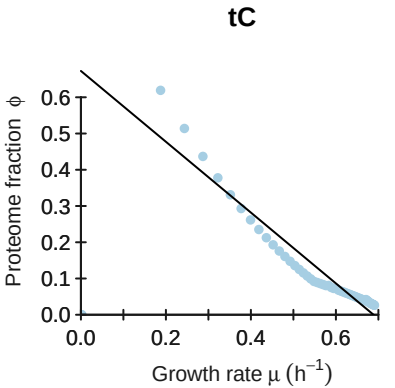
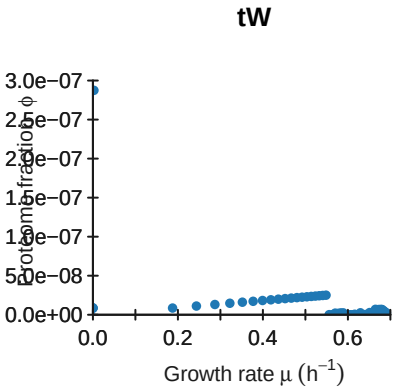
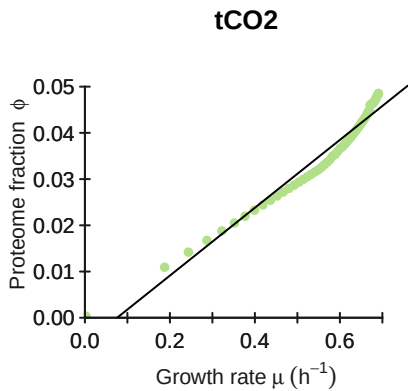

Growth rate μ (h^{-1})
Concentration x_C (g/L)

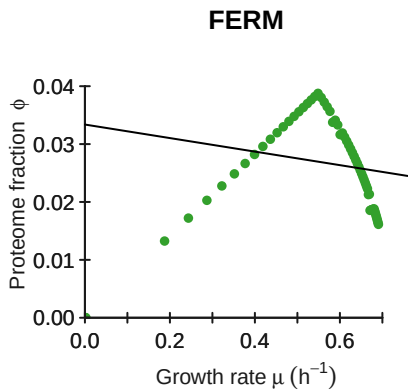

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
W
CO2
LIP
rRNA
mRNA
tRNA
DNA
TC
p

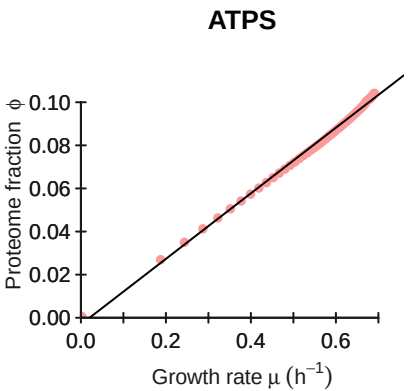

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
tW
tCO2
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc

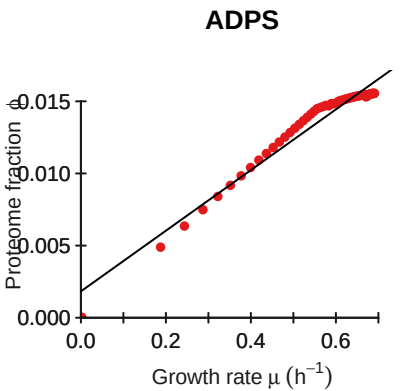

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

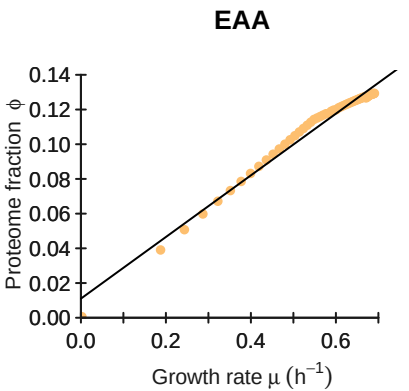

tW
Proteome fraction ϕ
Growth rate μ (h^{-1})

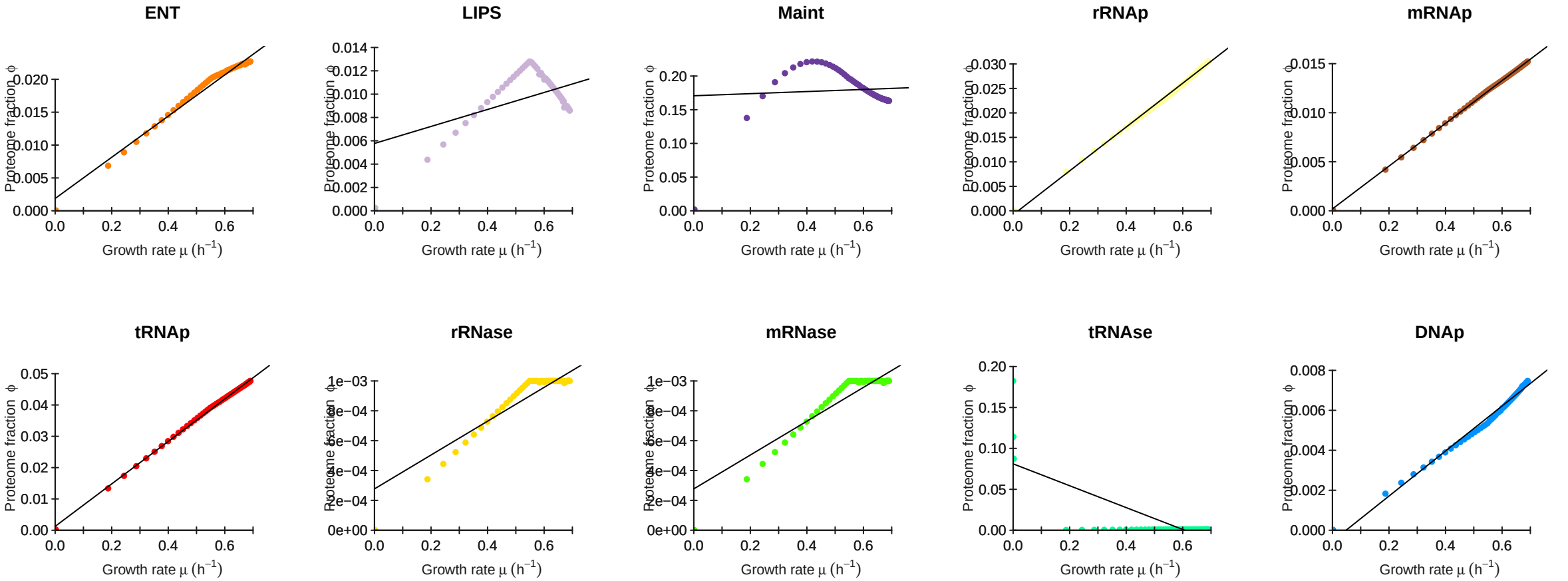

tCO2
Proteome fraction ϕ
Growth rate μ (h^{-1})

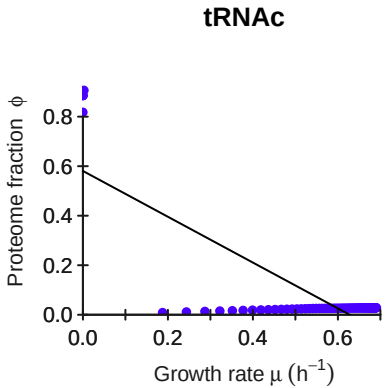

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

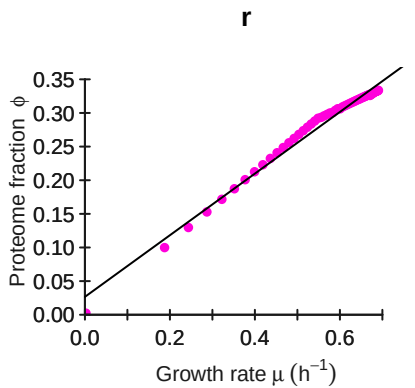

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

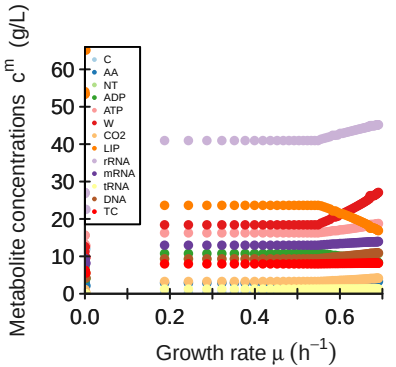

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

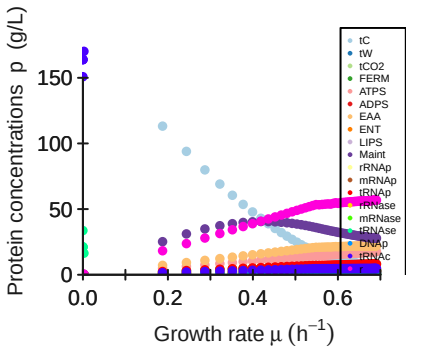

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

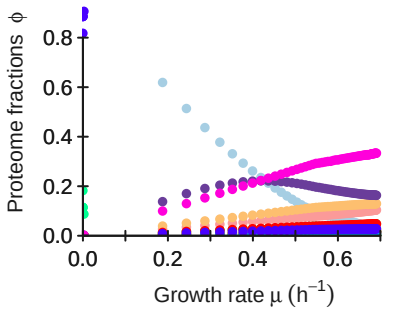

ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

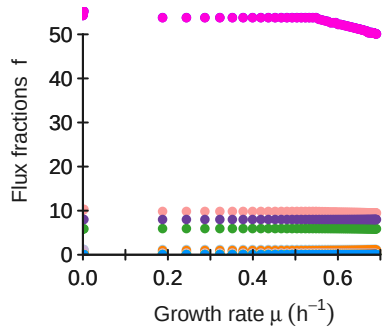

tRNAc
Proteome fraction ϕ
Growth rate μ (h−1)

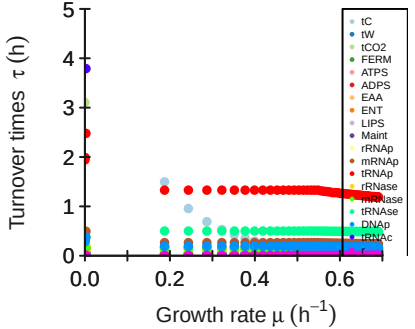

r
Proteome fraction ϕ
Growth rate μ (h−1)

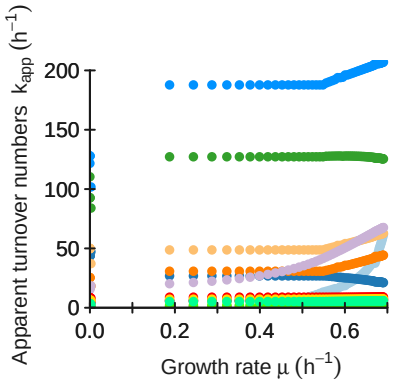

Metabolite concentrations cm (g/L)
C
AA
NT
ADP
ATP
W
CO2
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h−1)

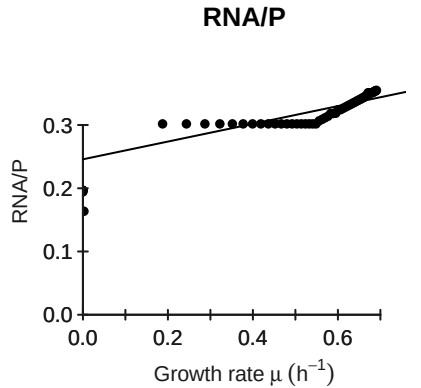

Protein concentrations p (g/L)
tC
tW
tCO2
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h−1)

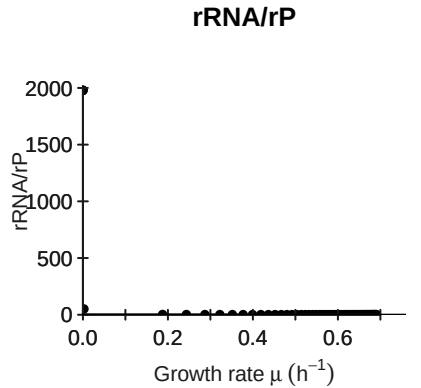

Proteome fractions ϕ
Growth rate μ (h−1)

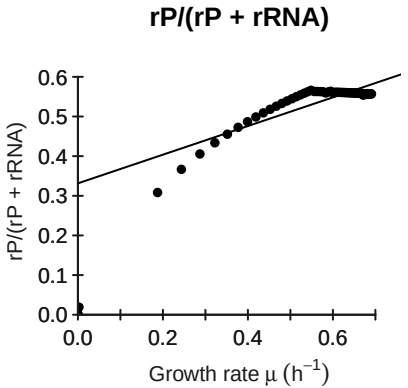

Flux fractions f
Growth rate μ (h−1)

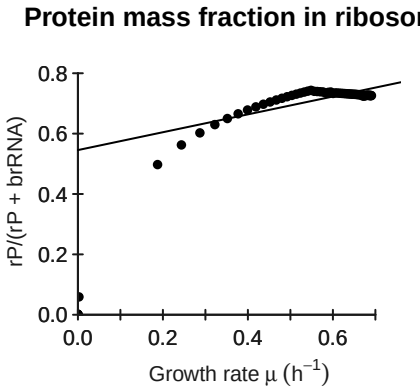

Turnover times τ (h)
tC
tW
tCO2
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h−1)

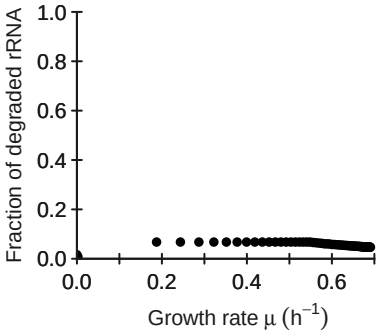

Apparent turnover numbers kapp (h−1)
Growth rate μ (h−1)

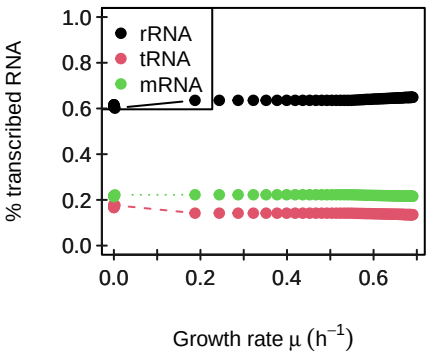

RNA/P
RNA/P
Growth rate μ (h−1)

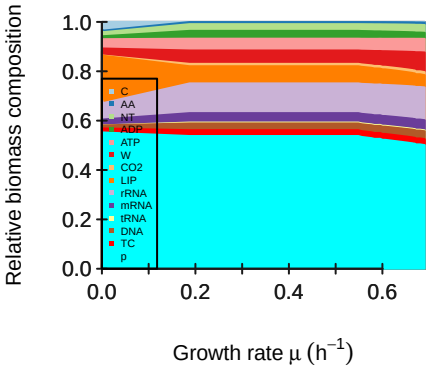

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

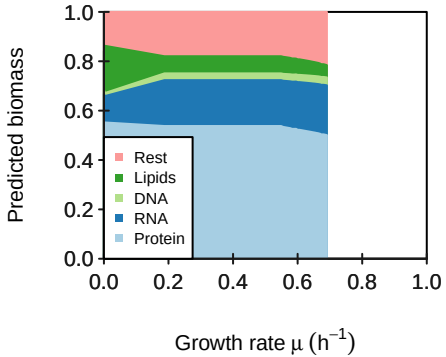

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)

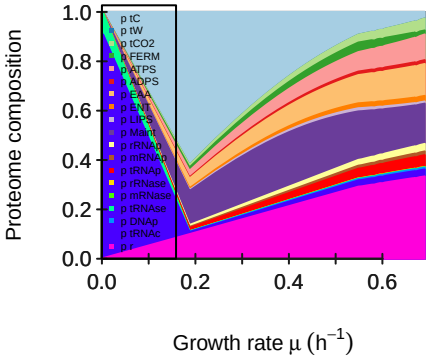

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h−1)

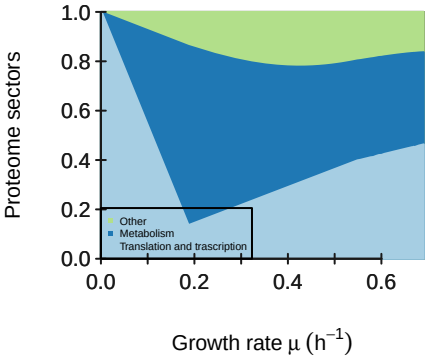

Fraction of degraded rRNA
Growth rate μ (h−1)

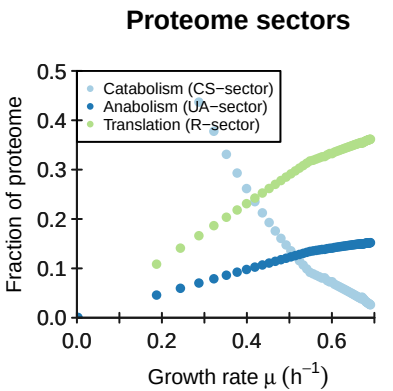

rRNA
tRNA
mRNA
% transcribed RNA
Growth rate μ (h−1)


C
AA
NT
ADP
ATP
W
CO2
LIP
rRNA
mRNA
tRNA
DNA
TC
p
Relative biomass composition
Growth rate μ (h−1)


Rest
Lipids
DNA
RNA
Protein
Predicted biomass
Growth rate μ (h−1)


p tC
p tW
p tCO2
p FERM
p ATPS
p ADPS
p EAA
p BNT
p LIPS
p Maint
p rRNAp
p mRNAp
p tRNAp
p rRNAse
p mRNAse
p tRNAse
p DNAp
p tRNAc
p r
Proteome composition
Growth rate μ (h−1)


Other
Metabolism
Translation and trascription
Proteome sectors
Growth rate μ (h−1)


Proteome sectors
Catabolism (CS−sector)
Anabolism (UA−sector)
Translation (R−sector)
Fraction of proteome
Growth rate μ (h−1)

M

	tC	tW	tCO2	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
C	1	0	0	−0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	1	−0.167	0	0	0	0	0	0	0	0	0	−0.01	0
NT	0	0	0	0	0	−1	0	0.334	0	0	−1	−1	−1	1	1	1	−1	0	0
ADP	0	0	0	−0.8	−0.98	1	0	0.666	0.82	1	0	0	0	0	0	0	0	0.05	0.05
ATP	0	0	0	0.8	0.98	0	0	−0.666	−0.82	−1	0	0	0	0	0	0	0	−0.05	−0.05
W	0	−1	0	0.2	−0.02	0	−1	−0.167	−0.18	0	0	0	0	0	0	0	0	0	0
CO2	0	0	−1	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	0	0.18	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	1	0	0	−1	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	1	0	0	−1	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	−1	0	−0.94	0.94
DNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.95	−0.95
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

K

	tC	tW	tCO2	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_W	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_CO2	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	0.5	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	5	5	0	0	0	0	0	0	0	0	0	6	0
NT	0	0	0	0	0	1	0	10	0	0	4	4	4	0	0	0	6	0	0
ADP	0	0	0	1	2	1	0	1	1	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	5	5	0	0	3	3	3	0	0	0	0	0	0	0	4	4
W	0	1	0	5	3	0	10	2	3	0	0	0	0	0	0	0	0	0	0
CO2	0	0	2	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	1	0
DNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	tW	tCO2	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_CO2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ADP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
W	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CO2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	60	60	60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0	0	0	8	8	8	0	0	0	8	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

kcat

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]	[,18]	[,19]
kcatf	600	100	34	2000	200	14	12	220	73	81	15	10	2	10	10	10	16	15000	800
kcatb	60	10	3	200	20	1	1	22	7	0	0	0	0	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]	[,18]	[,19]
[1,]	100	30	17	500	41.6666666666667	14	6	3.33333333333333	17.3809523809524	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]	[,18]	[,19]
[1,]	0	0	0	0	0	0	0	0	0	0	0	0	0	0.001	0.001	0.001	0	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]	[,18]	[,19]
[1,]	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0