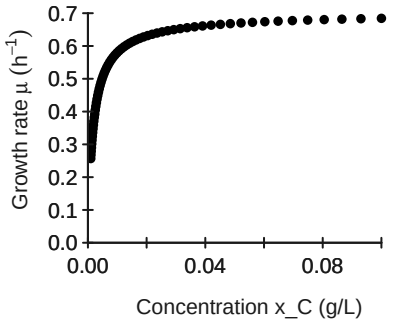
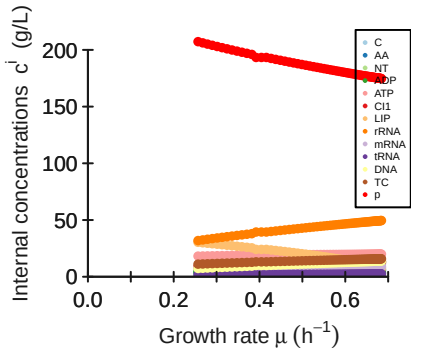
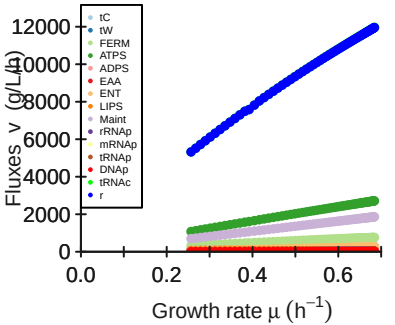
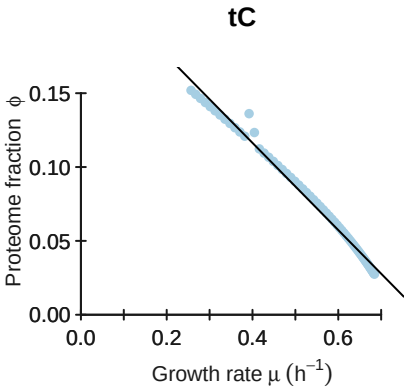
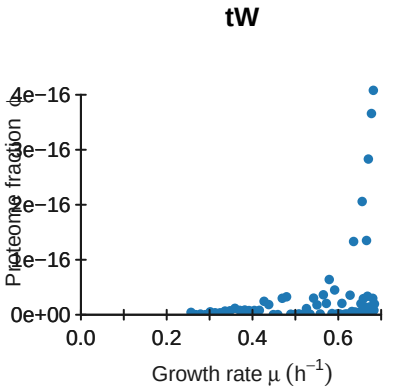
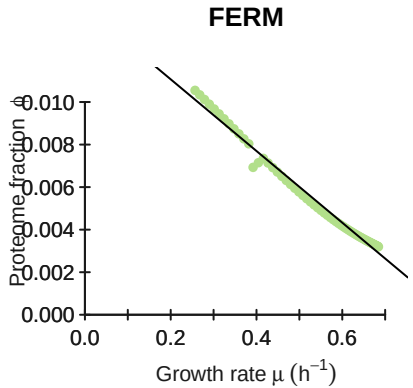

Growth rate μ (h^{-1})
Concentration x_C (g/L)

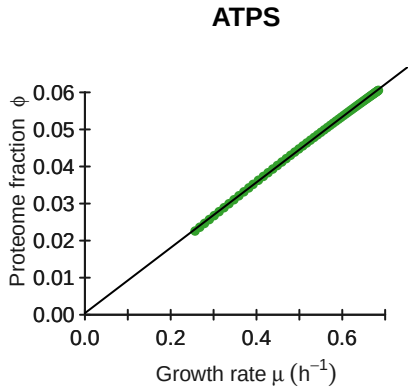

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
Cl1
LIP
rRNA
mRNA
tRNA
DNA
TC
p

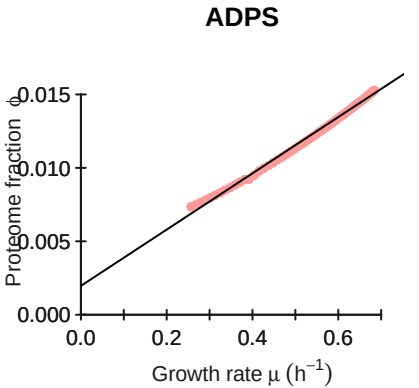

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
tW
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

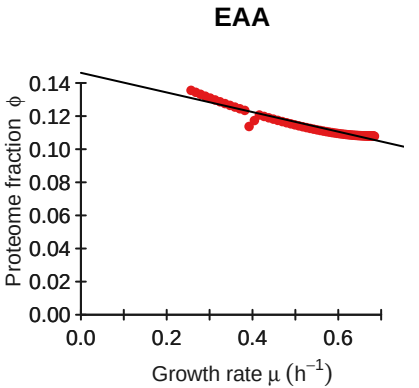

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

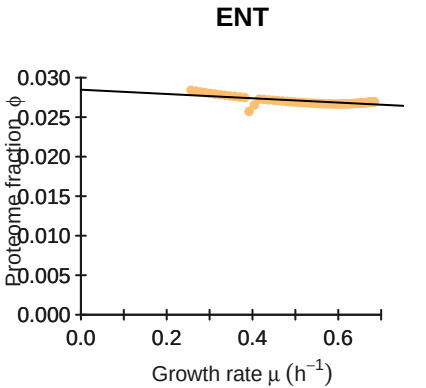

tW
Proteome fraction ϕ
Growth rate μ (h^{-1})

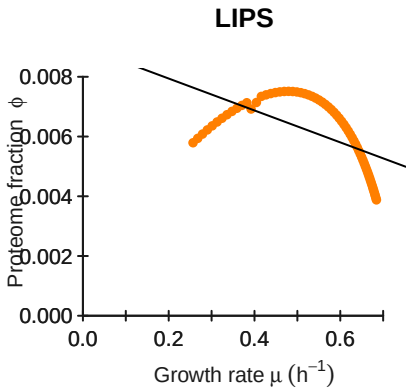

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

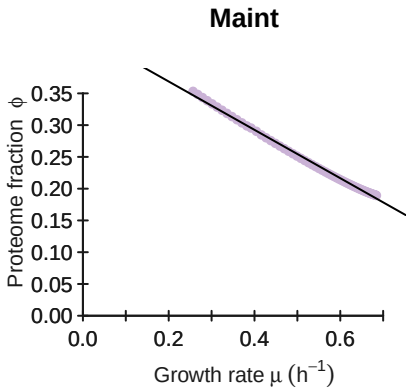

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

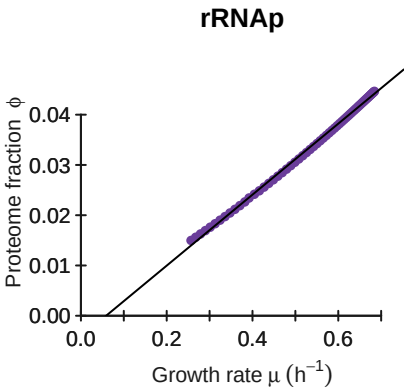

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

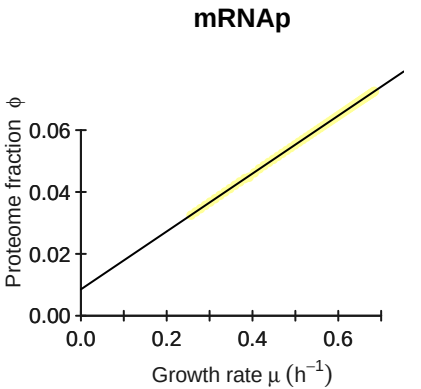

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

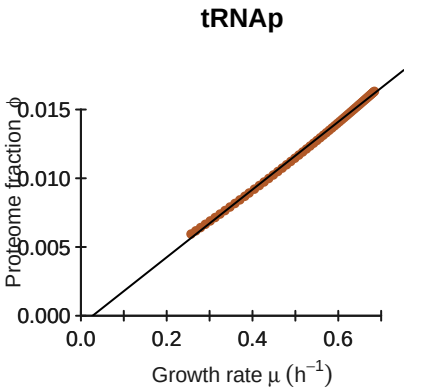

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

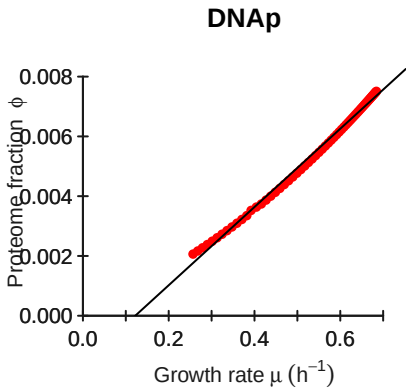

LIPS
Proteome fraction ϕ
Growth rate μ (h⁻¹)

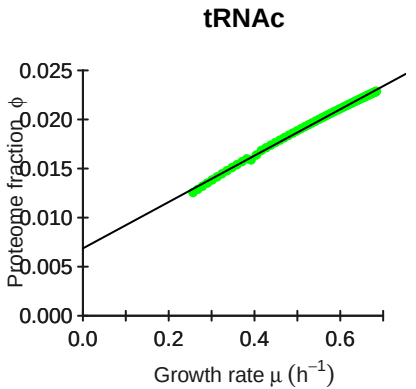

Maint
Proteome fraction ϕ
Growth rate μ (h⁻¹)

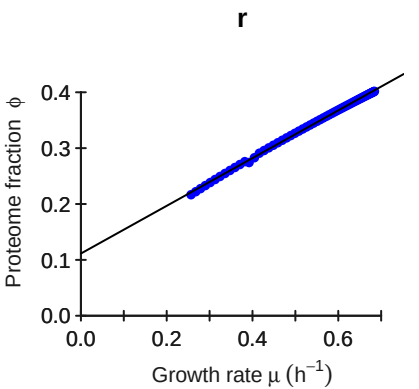

rRNAp
Proteome fraction ϕ
Growth rate μ (h⁻¹)

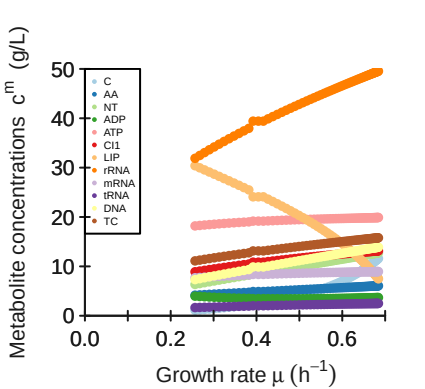

mRNAp
Proteome fraction ϕ
Growth rate μ (h⁻¹)

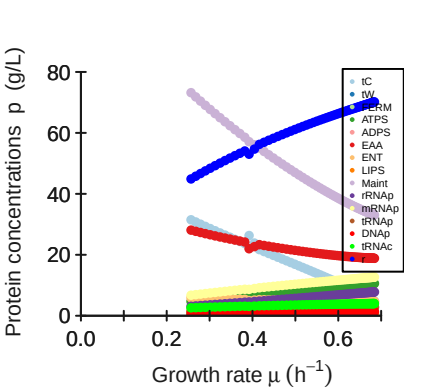

tRNAp
Proteome fraction ϕ
Growth rate μ (h⁻¹)

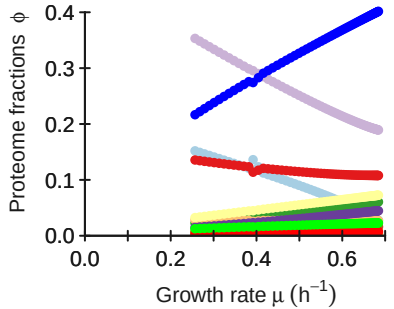

DNAp
Proteome fraction ϕ
Growth rate μ (h⁻¹)

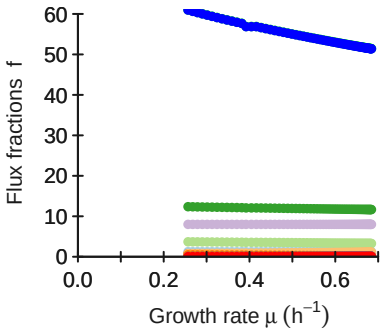

tRNAc
Proteome fraction ϕ
Growth rate μ (h⁻¹)

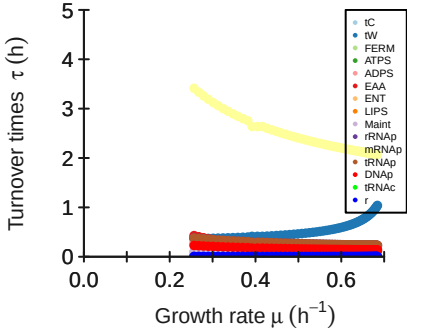

r
Proteome fraction ϕ
Growth rate μ (h⁻¹)

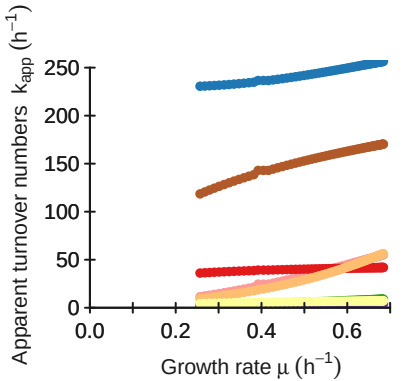

Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
Ci1
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h⁻¹)

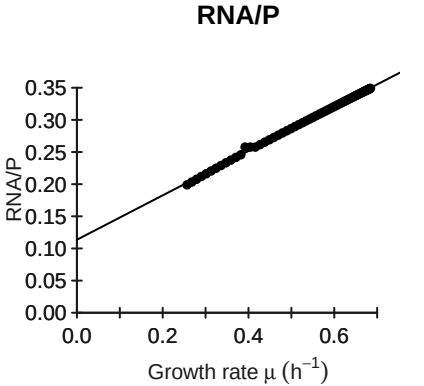

Protein concentrations p (g/L)
tC
tW
eTRM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r
Growth rate μ (h⁻¹)

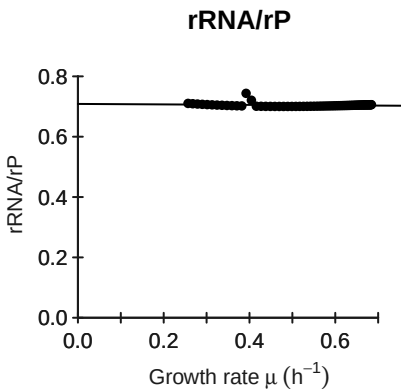


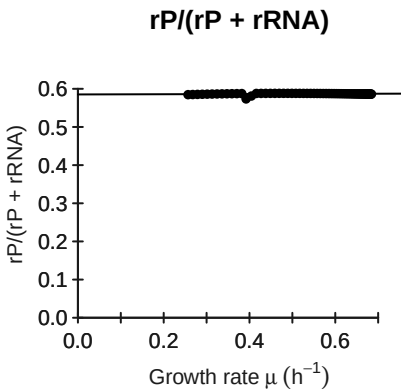


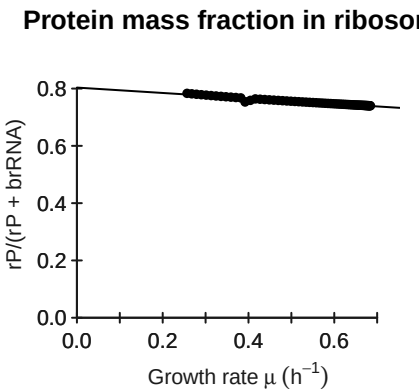


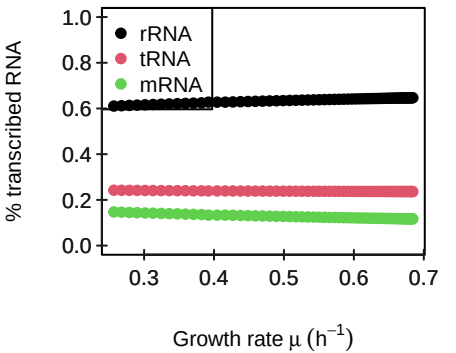


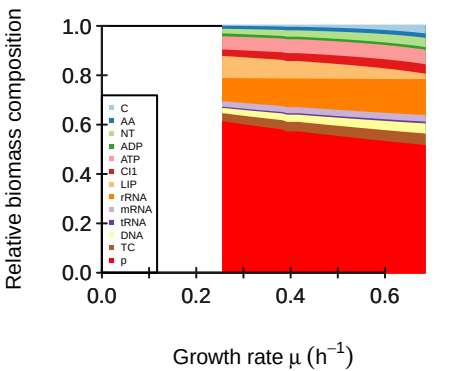








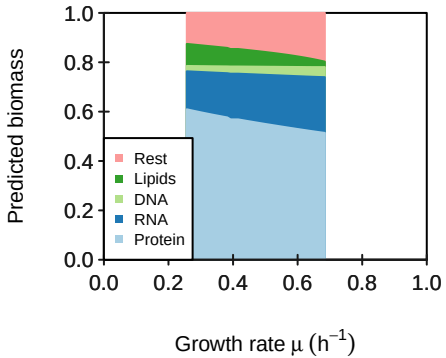


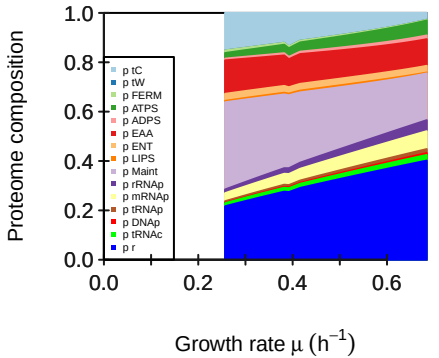


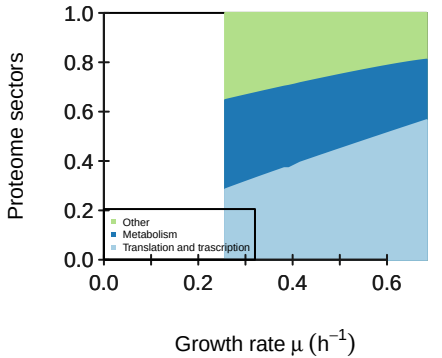
rRNA/rP

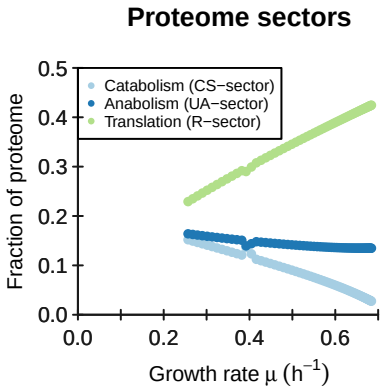
rP/(rP + rRNA)

Protein mass fraction in ribosome


Predicted biomass
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Rest
Lipids
DNA
RNA
Protein
Growth rate μ (h−1)


Proteome composition
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
p tC
p tW
p FERM
p ATPS
p ADPS
p EAA
p ENT
p LIPS
p Maint
p rRNAp
p mRNAp
p tRNAp
p DNAp
p tRNAc
p r
Growth rate μ (h−1)


Proteome sectors
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)


Proteome sectors
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.2
0.4
0.6
Catabolism (CS−sector)
Anabolism (UA−sector)
Translation (R−sector)
Fraction of proteome
Growth rate μ (h−1)

M

	tC	tW	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
C	1	0	−0.2	0	0	−0.5	−0.167	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	1	−0.167	0	0	0	0	0	0	−0.01	0
NT	0	0	0	0	−1	0	0.334	0	0	−1	−1	−1	−1	0	0
ADP	0	0	−0.8	−0.98	1	0	0.666	0.82	1	0	0	0	0	0.05	0.05
ATP	0	0	0.8	0.98	0	0	−0.666	−0.82	−1	0	0	0	0	−0.05	−0.05
CI1	0	−1	0.2	−0.02	0	−0.5	0	−0.18	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	0.18	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	1	0	−0.94	0.94
DNA	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	0.95	−0.95
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

K

	tC	tW	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0.05	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
x_CO2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	12	0	4	3.6	0	4	4	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	12	4	0	0	0	0	0	0	4	0
NT	0	0	0	0	4	0	12	0	0	4	4	4	4	0	0
ADP	0	0	1	0.9	2	0	2	2	0	0	0	0	0	0	0
ATP	0	0	7	6.3	0	0	3	3	3	0	0	0	0	3	3
Cl1	0	2	4	3.6	0	2	0	2	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	35	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
DNA	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	3
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	tW	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0	0.005	0	0	0	0	0	0
x_W	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
C	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
NT	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
ATP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cl1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	60	60	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	50
mRNA	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
DNA	0	0	0	0	0	0	0	0	0	8	8	8	8	0	0
TC	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

kcat

	tC	tW	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
kcatf	1126	10	4710	471	12	14	152	58	68	9	1	9	15	10310	626
kcatb	113	1	471	47	1	1	15	6	0	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
[1,]	2391.50442477876	15	70	19.4858156028369	6	21	5.06666666666667	112.777777777778	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
[1,]	0.002	0.02	0.041	0.046	0.005	0.165	0.023	0.031	0.287	0.0426	0.0213	0.0071	0.002	0.023	0.284

average saturation input

3

minimal phi constraint

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

minimal f constraint

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