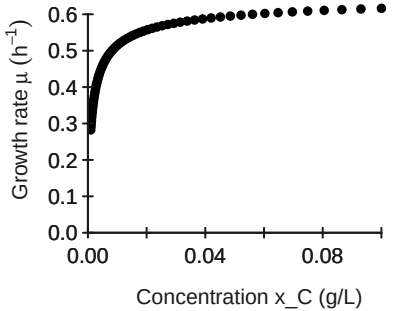
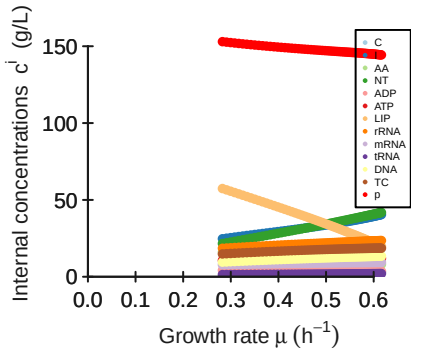
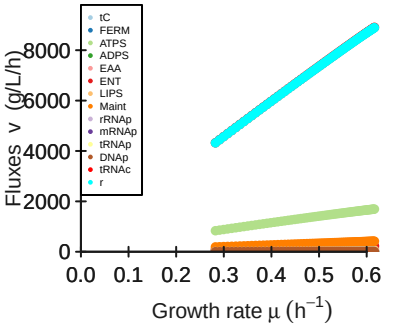
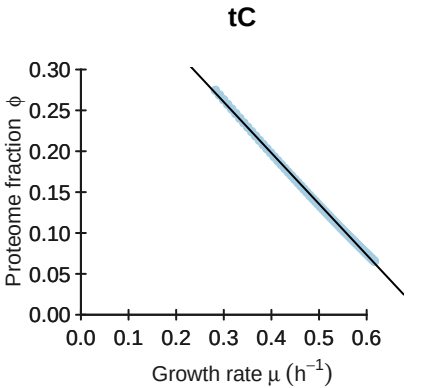
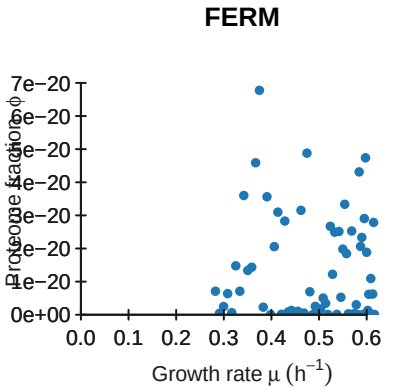
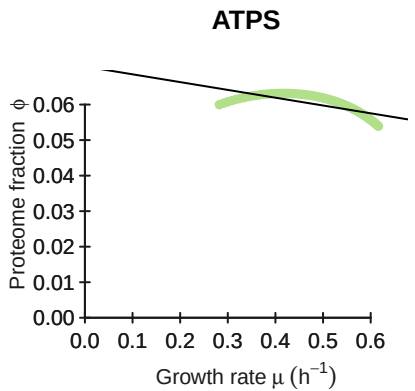

Growth rate μ (h⁻¹)
Concentration x_C (g/L)

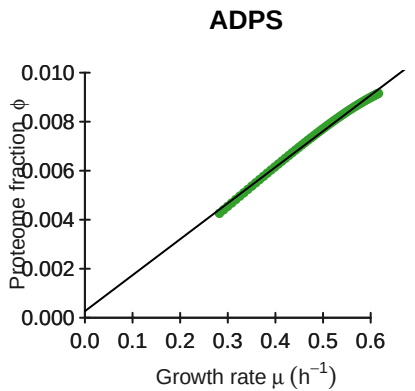

Internal concentrations c^i (g/L)
Growth rate μ (h⁻¹)
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
p

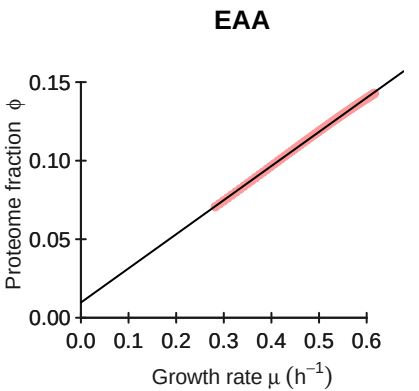

Fluxes v (g/L/h)
Growth rate μ (h⁻¹)
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

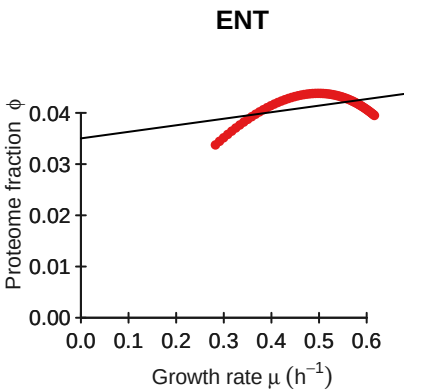

tC
Proteome fraction ϕ
Growth rate μ (h⁻¹)

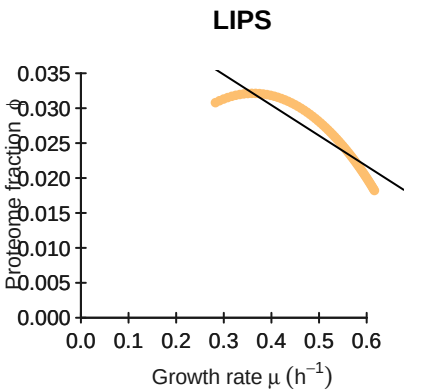

FERM
Proteome fraction ϕ
Growth rate μ (h⁻¹)

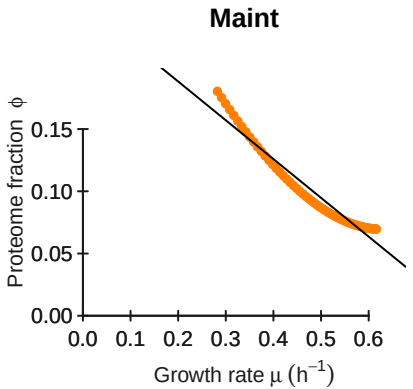

ATPS
Proteome fraction ϕ
Growth rate μ (h⁻¹)

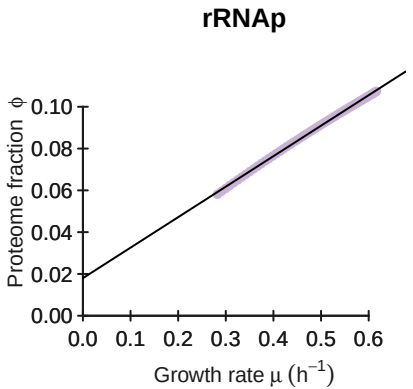

ADPS
Proteome fraction ϕ
Growth rate μ (h⁻¹)

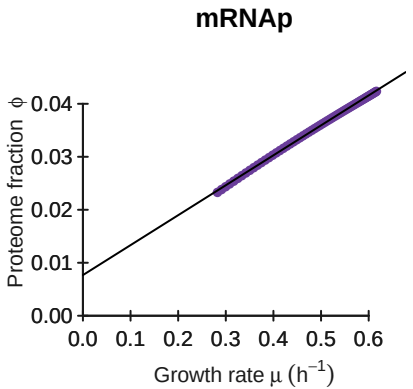

EAA
Proteome fraction ϕ
Growth rate μ (h⁻¹)

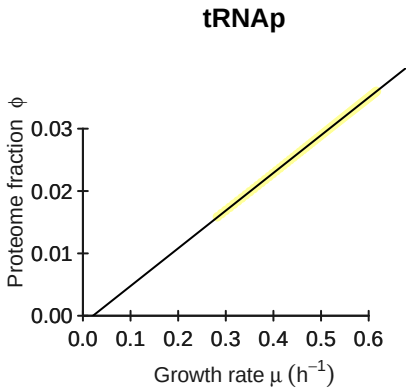

ENT
Proteome fraction ϕ
Growth rate μ (h⁻¹)

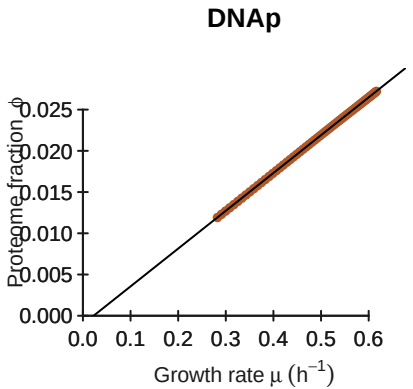

LIPS
Proteome fraction ϕ
Growth rate μ (h⁻¹)

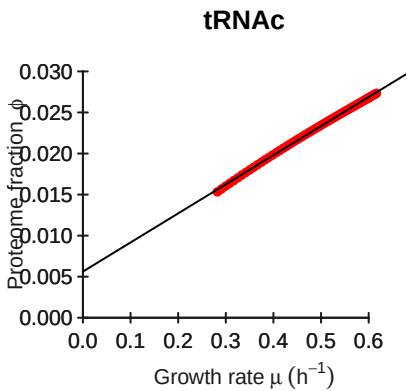

Maint
Proteome fraction ϕ
0.15
0.10
0.05
0.00
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

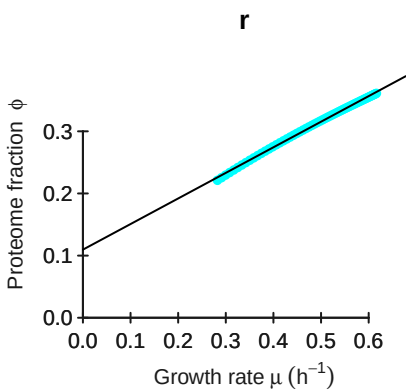

rRNAp
Proteome fraction ϕ
0.10
0.08
0.06
0.04
0.02
0.00
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

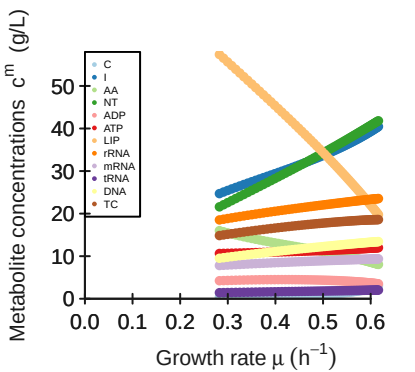

mRNAp
Proteome fraction ϕ
0.04
0.03
0.02
0.01
0.00
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

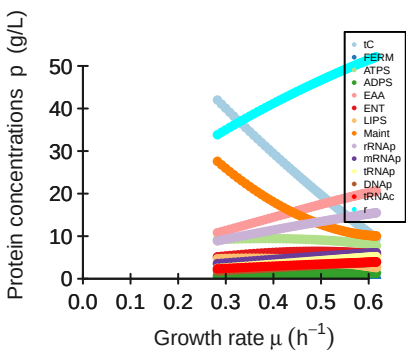

tRNAp
Proteome fraction ϕ
0.03
0.02
0.01
0.00
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

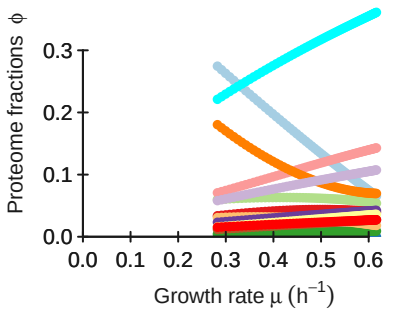

DNAp
Proteome fraction ϕ
0.025
0.020
0.015
0.010
0.005
0.000
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

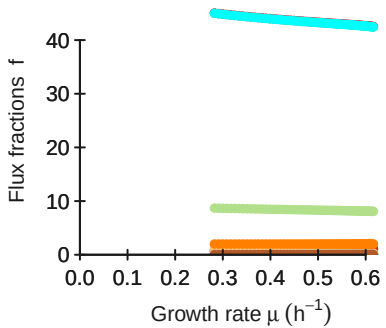

tRNAc
Proteome fraction ϕ
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

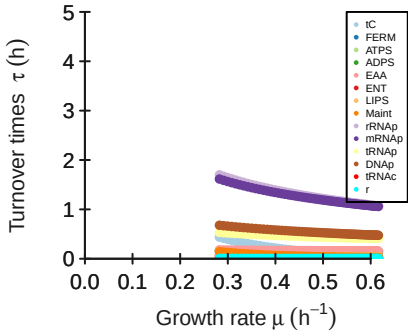

r
Proteome fraction ϕ
0.3
0.2
0.1
0.0
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

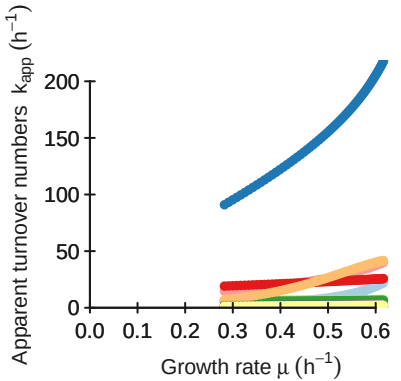

Metabolite concentrations cm (g/L)
C
I
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
50
40
30
20
10
0
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

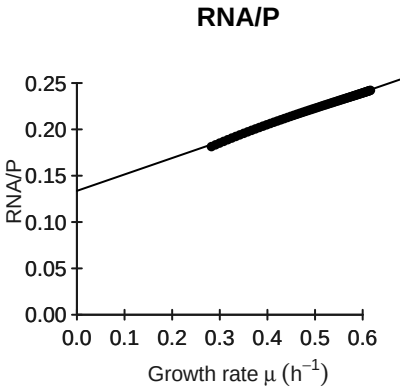

Protein concentrations p (g/L)
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r
50
40
30
20
10
0
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

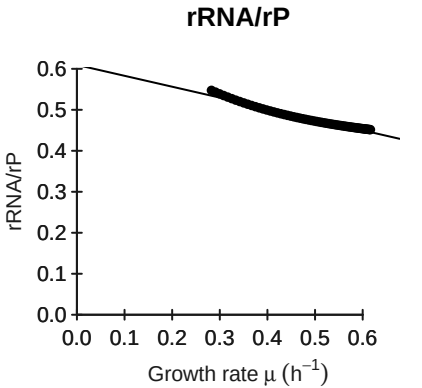

Proteome fractions ϕ
0.3
0.2
0.1
0.0
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h−1)

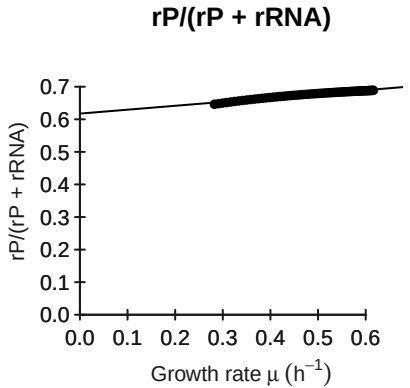

Flux fractions f
Growth rate μ (h⁻¹)

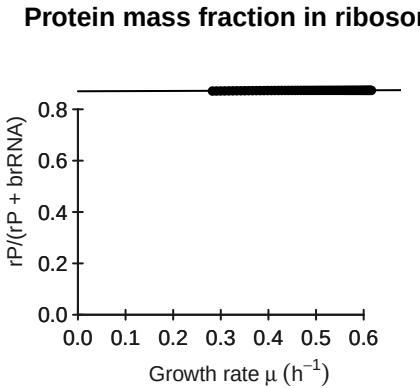

Turnover times τ (h)
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r
Growth rate μ (h⁻¹)

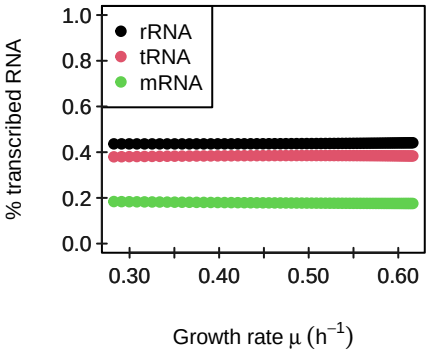

Apparent turnover numbers kapp (h⁻¹)
Growth rate μ (h⁻¹)

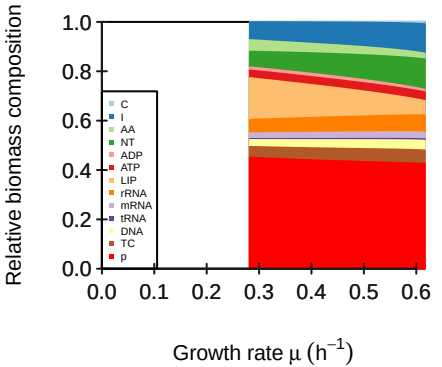

RNA/P
RNA/P
Growth rate μ (h⁻¹)

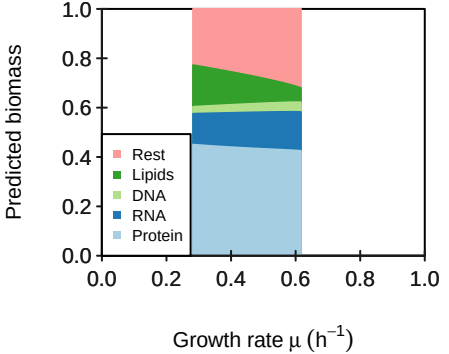

rRNA/rP
rRNA/rP
Growth rate μ (h⁻¹)

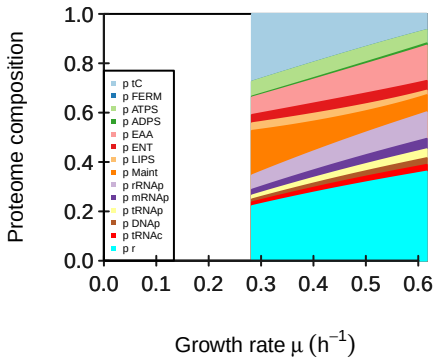

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h⁻¹)

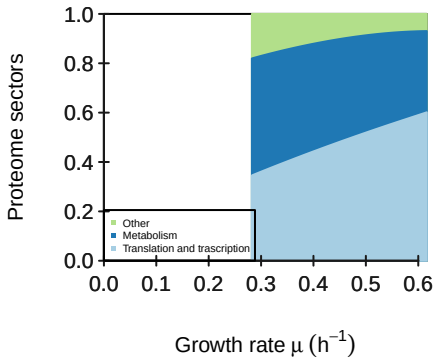

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h⁻¹)

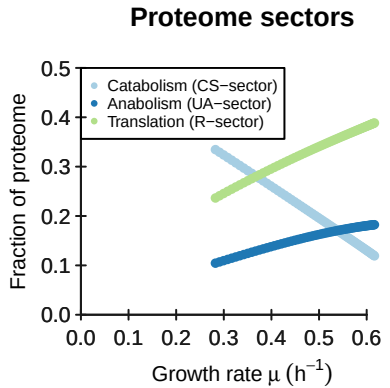

% transcribed RNA
rRNA
tRNA
mRNA
Growth rate μ (h⁻¹)


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


Predicted biomass
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 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h^{-1})
p tC
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


Proteome sectors
1.0
0.8
0.6
0.4
0.2
0.0
0.0 0.1 0.2 0.3 0.4 0.5 0.6
Growth rate μ (h^{-1})
Other
Metabolism
Translation and trascription


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

M

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
C	1	−0.2	−0.1	0	0	−0.167	0	0	0	0	0	0	0	0
I	0	0.1	0.1	0	−1	0	−0.18	0	0	0	0	0	0	0
AA	0	0	0	0	1	−0.167	0	0	0	0	0	0	−0.01	0
NT	0	0	0	−1	0	0.334	0	0	−1	−1	−1	−1	0	0
ADP	0	−0.8	−0.9	1	0	0.666	0.82	1	0	0	0	0	0.05	0.05
ATP	0	0.8	0.9	0	0	−0.666	−0.82	−1	0	0	0	0	−0.05	−0.05
LIP	0	0	0	0	0	0	0.18	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	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	1	0	−0.94	0.94
DNA	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	0.95	−0.95
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

K

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0
x_W	0	5	0	0	0	0	0	0	0	0	0	0	0	0
C	1	0.5	0.1	0	0	1	0	0	0	0	0	0	0	0
I	0	2	2	0	1	0	1	0	0	0	0	0	0	0
AA	0	0	0	0	3	1	0	0	0	0	0	0	1	0
NT	0	0	0	1	0	3	0	0	4	4	4	4	0	0
ADP	0	1	1	1	0	3	1	5	0	0	0	0	3	3
ATP	0	3	3	0	0	2	2	1	0	0	0	0	1	1
LIP	0	0	0	0	0	0	5	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	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	1	0	5	5
DNA	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	5	5
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	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
C	0	0	0	0	0	0	0	0	0	0	0	0	0	0
I	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
NT	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
ATP	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	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	50
mRNA	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
DNA	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
p	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]
kcatf	200	2000	500	8	7	78	33	50	5	3	5	8	10000	1000
kcatb	0	0	0	0	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]
[1,]	Inf	Inf	Inf	Inf	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]
[1,]	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]
[1,]	0	0	0	0	0	0	0	2	0	0	0	0	0	0