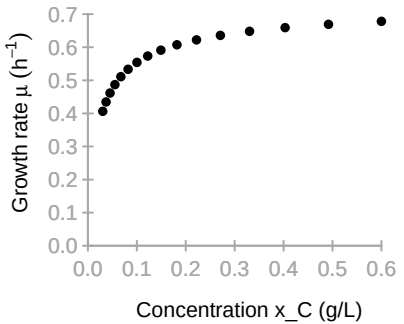
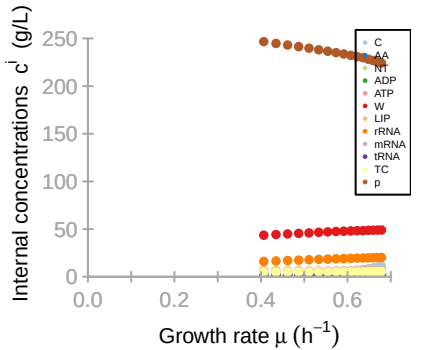
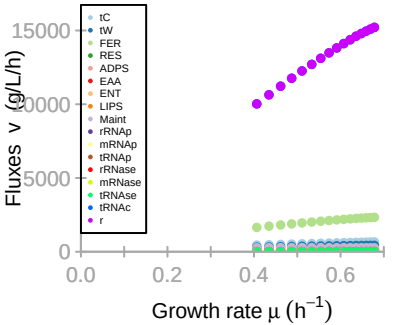
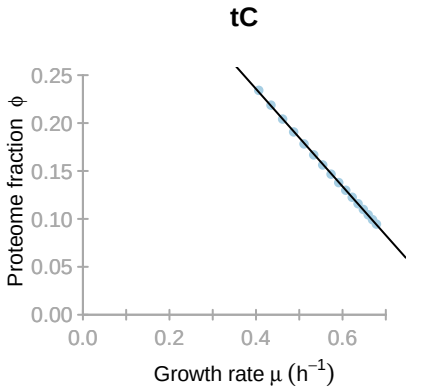
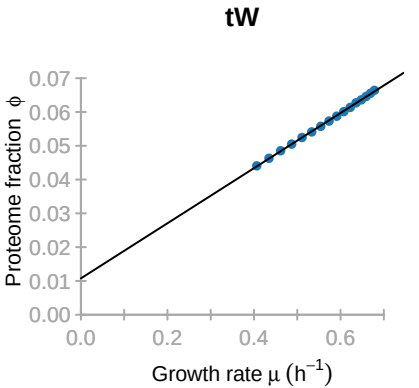
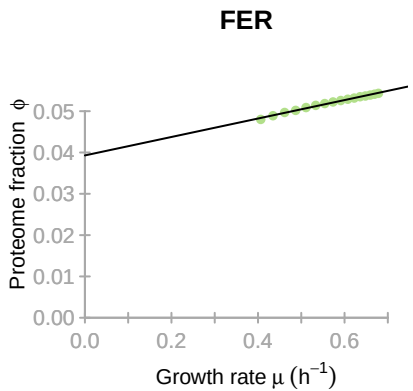

Growth rate μ (h−1)
Concentration x_C (g/L)

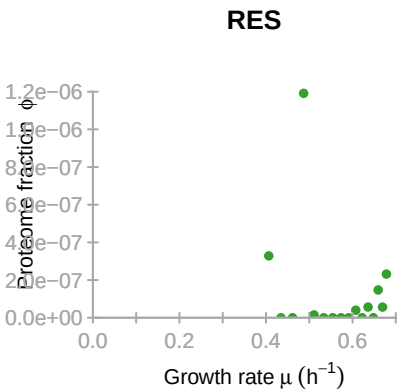

Internal concentrations ci (g/L)
Growth rate μ (h−1)
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
TC
p

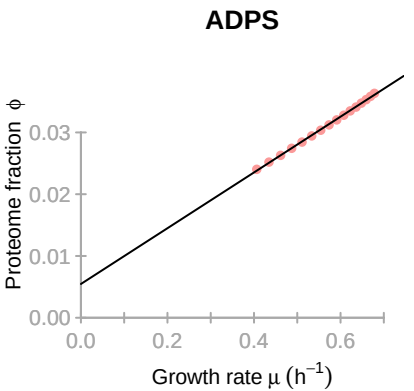

Fluxes v (g/L/h)
Growth rate μ (h−1)
tC
tW
FER
RES
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
tRNAc
r

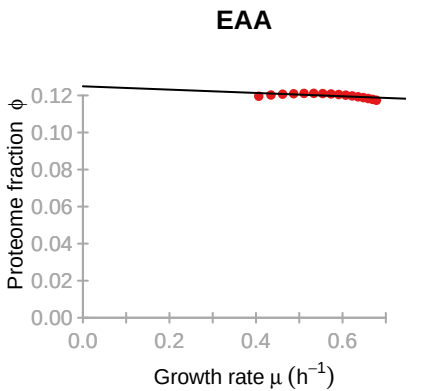

tC
Proteome fraction ϕ
Growth rate μ (h−1)

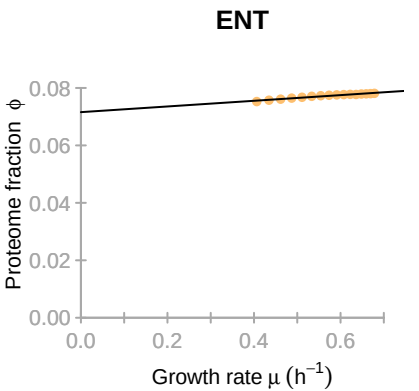

tW
Proteome fraction ϕ
Growth rate μ (h−1)

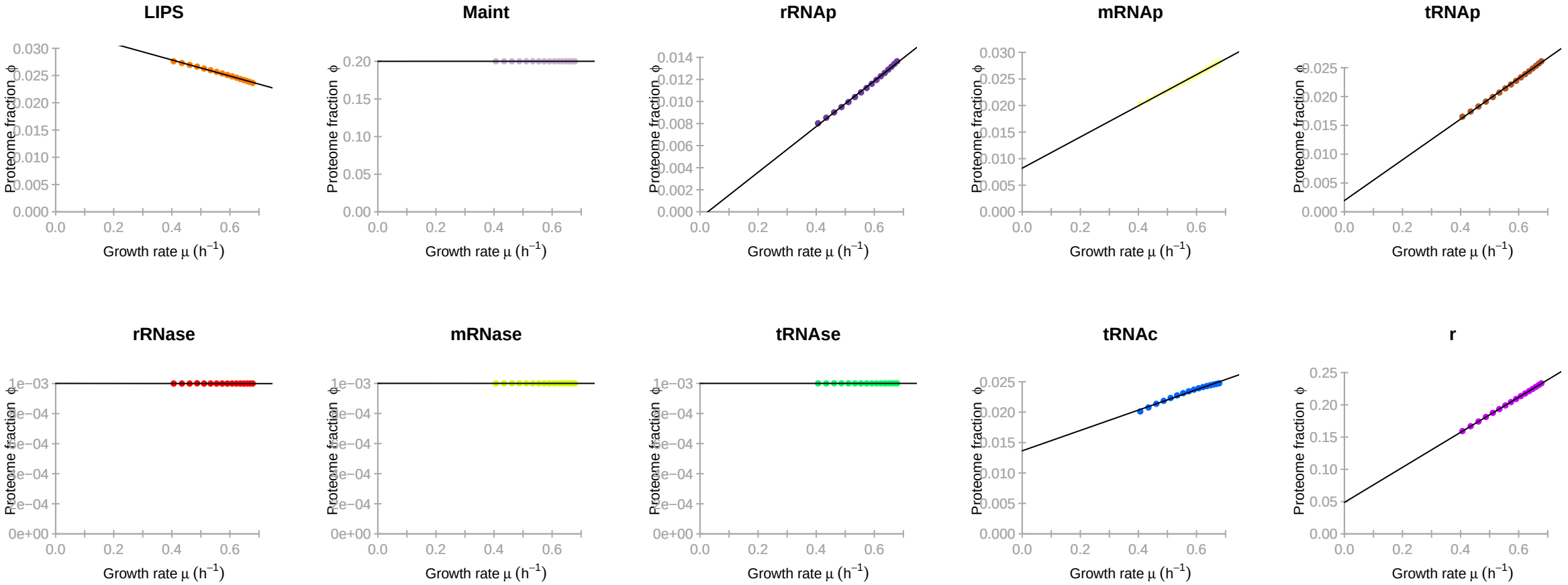

FER
Proteome fraction ϕ
Growth rate μ (h−1)

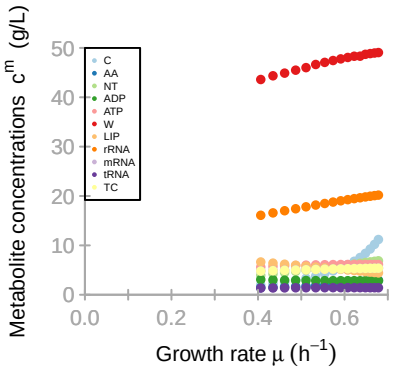

RES
Proteome fraction ϕ
Growth rate μ (h−1)

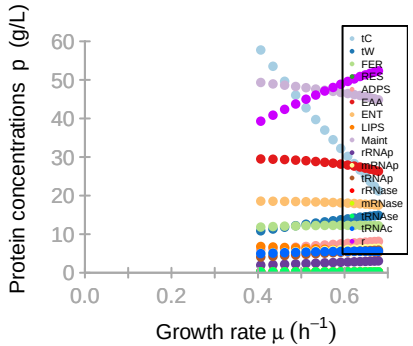

ADPS
Proteome fraction ϕ
Growth rate μ (h−1)

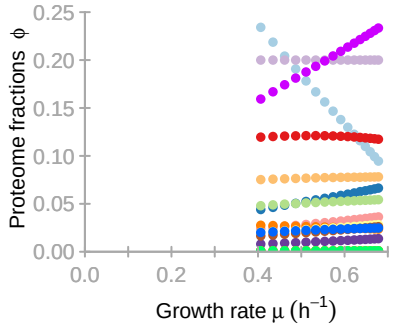

EAA
Proteome fraction ϕ
Growth rate μ (h−1)

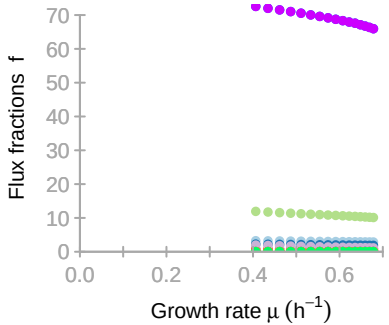

ENT
Proteome fraction ϕ
Growth rate μ (h−1)

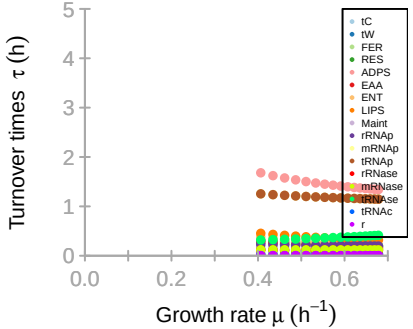

LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})

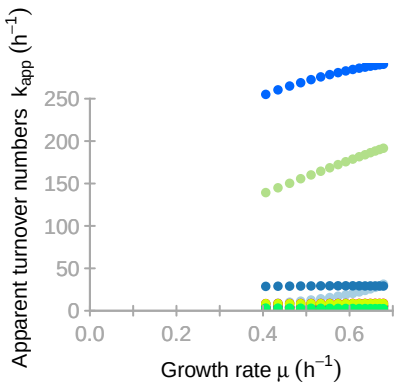

Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
TC
Growth rate μ (h^{-1})

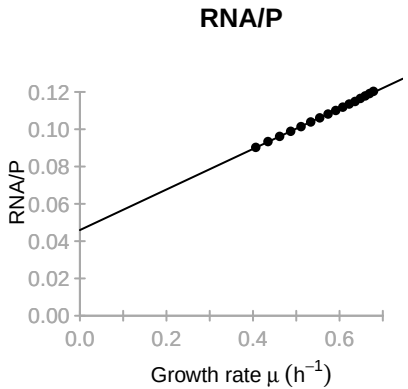

Protein concentrations p (g/L)
tC
tW
FER
RES
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
tRNAc
r
Growth rate μ (h^{-1})

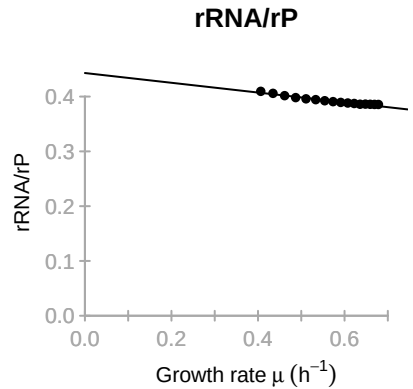

Proteome fractions ϕ
Growth rate μ (h^{-1})

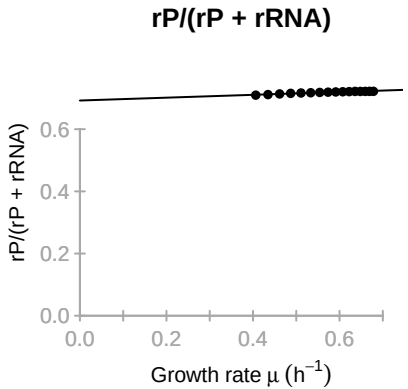

Flux fractions f
Growth rate μ (h^{-1})

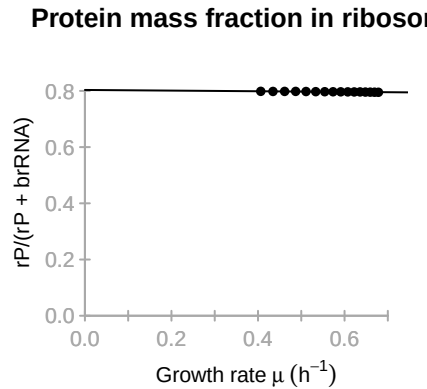

Turnover times τ (h)
tC
tW
FER
RES
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
tRNAc
r
Growth rate μ (h^{-1})

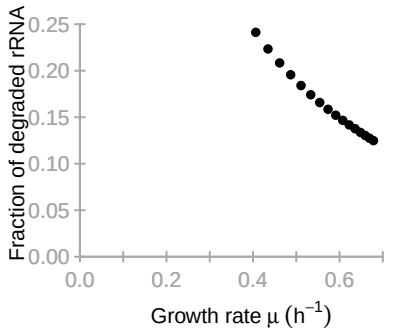

Apparent turnover numbers k_{app} (h^{-1})
Growth rate μ (h^{-1})

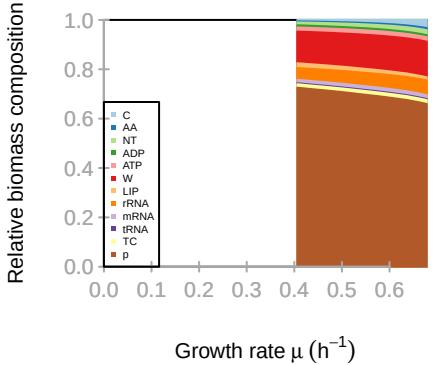

RNA/P
RNA/P
Growth rate μ (h^{-1})

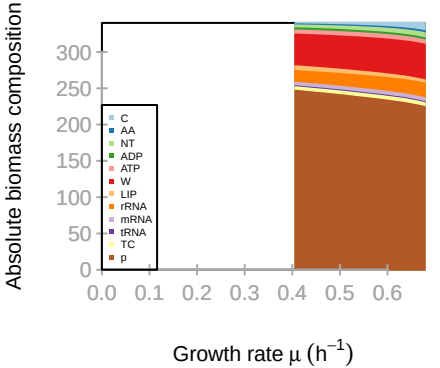

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

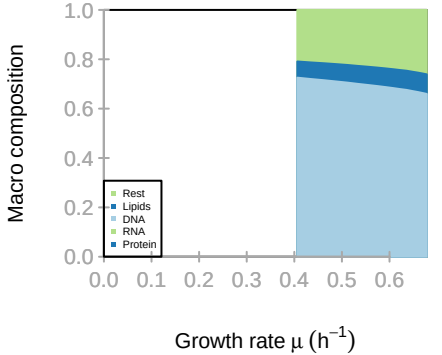

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})

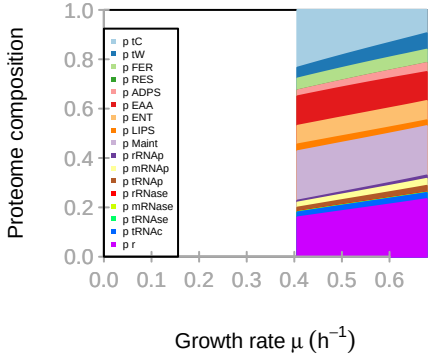

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})

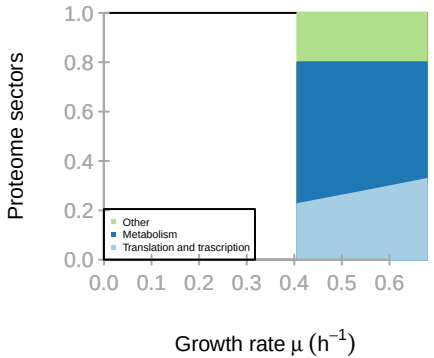

Fraction of degraded rRNA
0.25
0.20
0.15
0.10
0.05
0.00
0.0
0.2
0.4
0.6
Growth rate μ (h−1)


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


Absolute biomass composition
300
250
200
150
100
50
0
0.0 0.1 0.2 0.3 0.4 0.5 0.6
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
TC
p
Growth rate μ (h−1)


Macro 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
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
p tC
p tW
p FER
p RES
p ADPS
p EAA
p ENT
p LIPS
p Maint
p rRNAp
p mRNAp
p tRNAp
p rRNase
p mRNase
p tRNAse
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 0.1 0.2 0.3 0.4 0.5 0.6
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)

M

	tC	tW	FER	RES	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	tRNAc	r
C	1	0	−0.2	−0.02	0	−1	−0.167	−0.18	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	1	−0.167	0	0	0	0	0	0	0	0	−0.01	0
NT	0	0	0	0	−1	0	0.334	0	0	−1	−1	−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	0	0.05	0.05
ATP	0	0	0.8	0.98	0	0	−0.666	−0.82	−1	0	0	0	0	0	0	−0.05	−0.05
W	0	−1	0.2	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	0.18	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	1	0	0	−1	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	1	0	0	−1	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	1	0	0	−1	−0.94	0.94
TC	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	0.01

K

	tC	tW	FER	RES	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	tRNAc	r
x_C	0.1	0	0	0	0	0	0	0	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
C	3	0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0
NT	0	0	0	0	1	0	2	0	0	1	1	1	0	0	2	0	0
ADP	0	0	1	1	0	0	1	0	1	0	0	0	0	0	0	0	0
ATP	0	0	0	2	0	0	1	1	1	0	0	0	0	0	0	1	1
W	0	52	0	154	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	0	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	7	0	0	3	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	tW	FER	RES	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	tRNAc	r
x_C	0	0	0	0	0	0	0	0	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
C	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
NT	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
ATP	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
LIP	1	1	0	1	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	10
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
tRNA	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
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

kcat

	tC	tW	FER	RES	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	tRNAc	r
kcatf	73	82	283	10	1	9	10	4	10	8	1	1	10	10	10	7901	711
kcatb	7	8	28	1	1	1	1	1	1	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]
[1,]	312.857142857143	0.197115384615385	10.1071428571429	3080	1	9	20	4	10	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
[1,]	0.05	0.02	0.08	0.1	0.02	0.15	0.05	0.03	0.2	0.007	0.005	0.005	0.001	0.001	0.001	0.03	0.25

average saturation input

3

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
[1,]	0	0	0	0	0	0	0	0	0.2	0	0	0	0.001	0.001	0.001	0	0

minimal f constraint

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