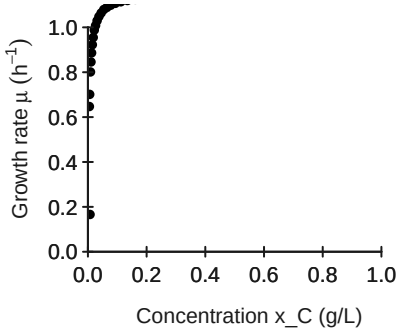
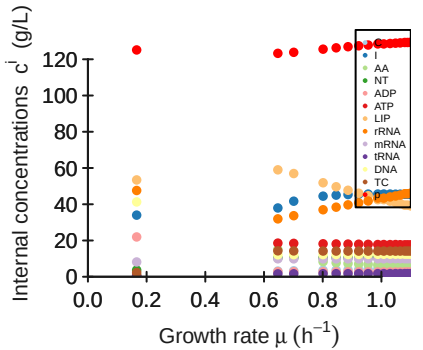
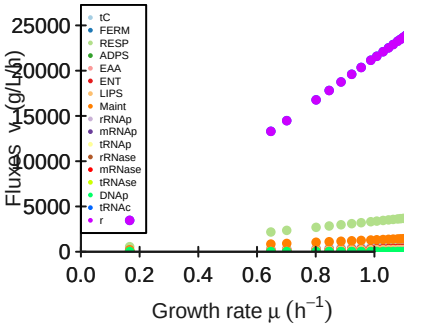
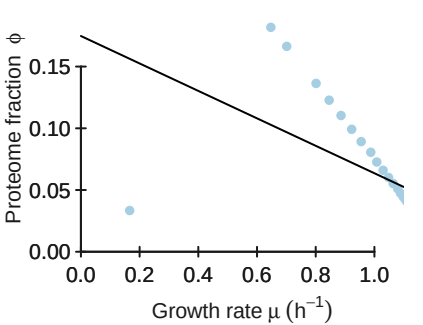


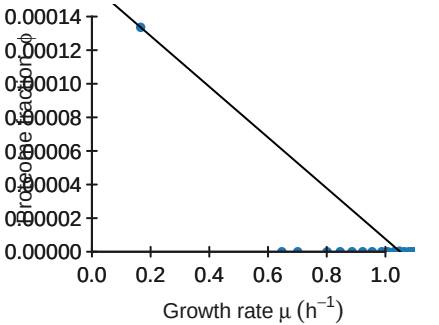




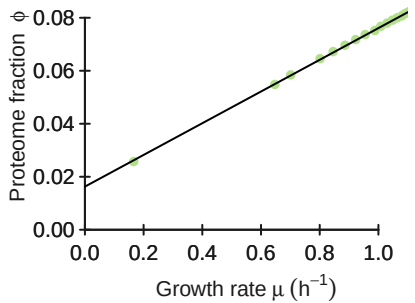
tC



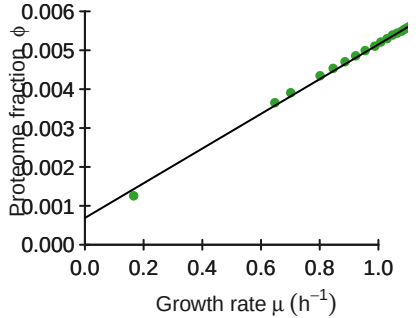
FERM



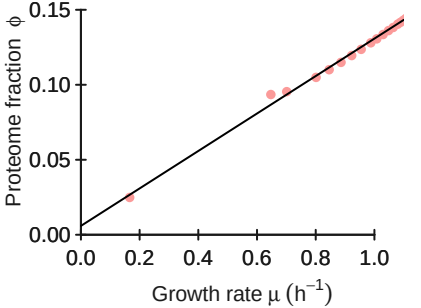
RESP



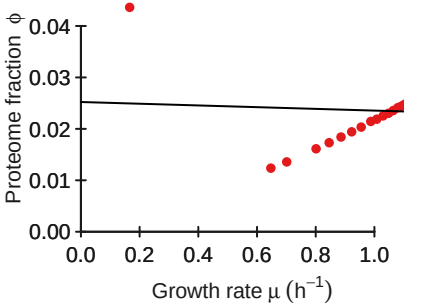
ADPS



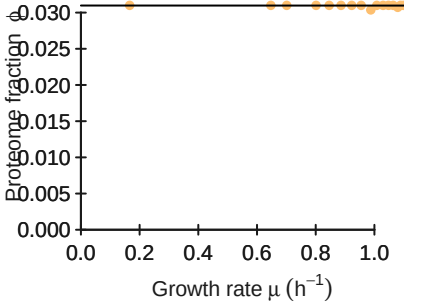
EAA

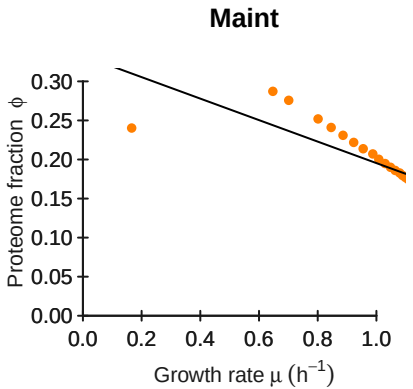


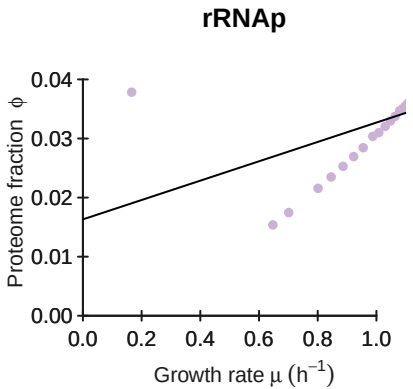
ENT

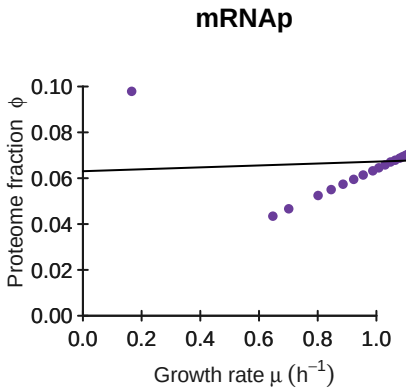


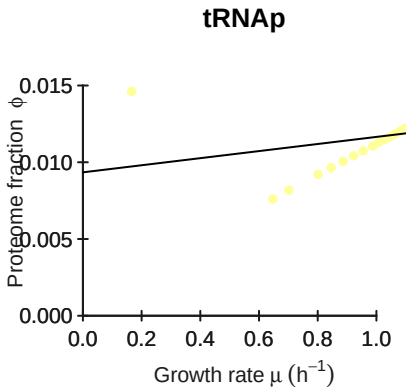
LIPS

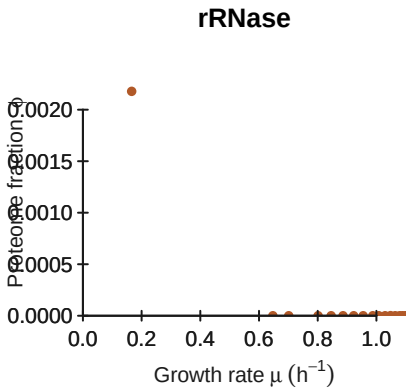


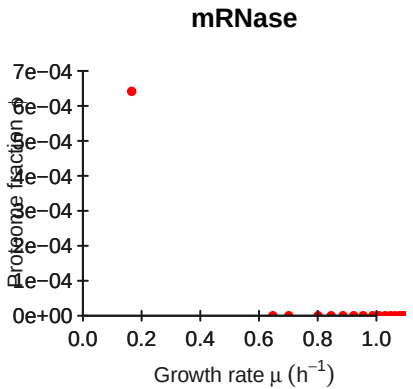

Maint
Proteome fraction ϕ
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

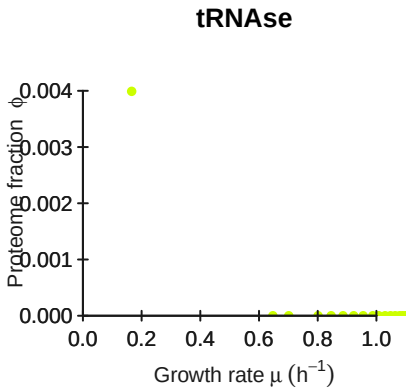

rRNAp
Proteome fraction ϕ
0.04
0.03
0.02
0.01
0.00
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

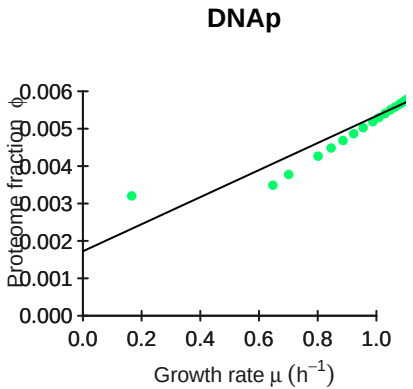

mRNAp
Proteome fraction ϕ
0.10
0.08
0.06
0.04
0.02
0.00
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

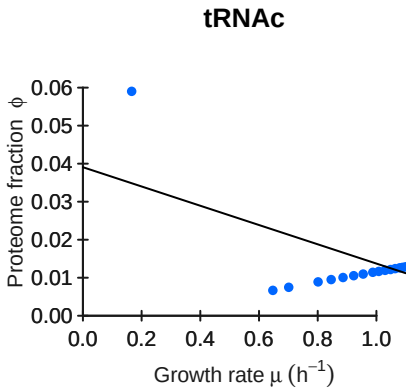

tRNAp
Proteome fraction ϕ
0.015
0.010
0.005
0.000
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

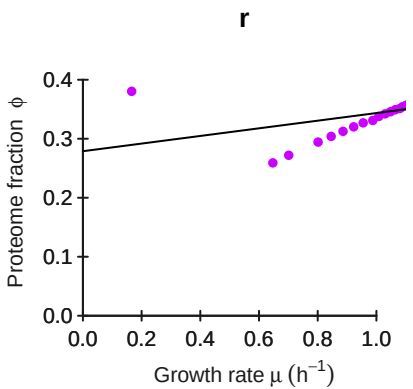

rRNase
Proteome fraction ϕ
0.0020
0.0015
0.0010
0.0005
0.0000
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

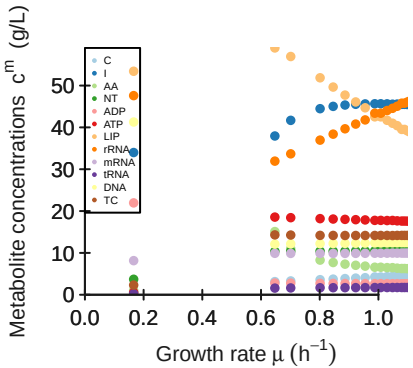

mRNase
Proteome fraction ϕ
7e−04
6e−04
5e−04
4e−04
3e−04
2e−04
1e−04
0e+00
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

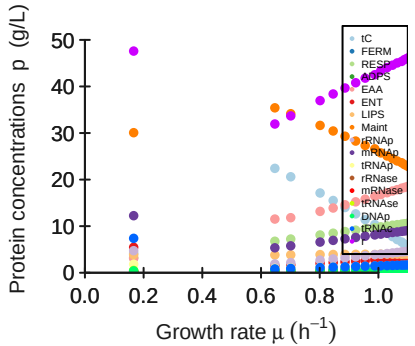

tRNAse
Proteome fraction ϕ
0.004
0.003
0.002
0.001
0.000
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

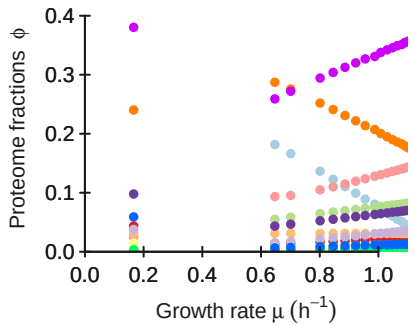

DNAp
Proteome fraction ϕ
0.006
0.005
0.004
0.003
0.002
0.001
0.000
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

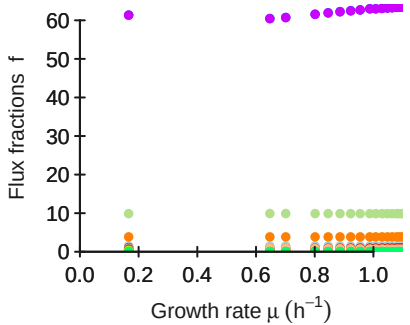

tRNAc
Proteome fraction ϕ
0.06
0.05
0.04
0.03
0.02
0.01
0.00
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

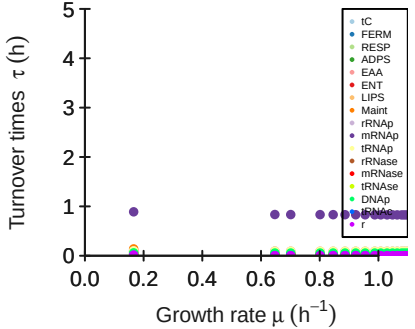

r
Proteome fraction ϕ
0.4
0.3
0.2
0.1
0.0
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

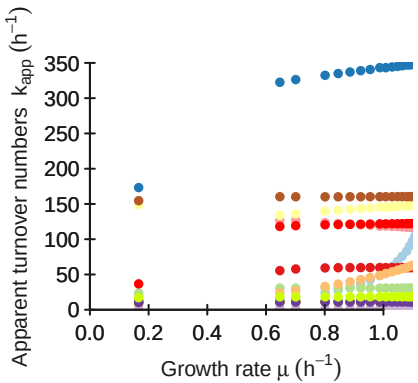

Metabolite concentrations c^m (g/L)
C
I
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h^{-1})

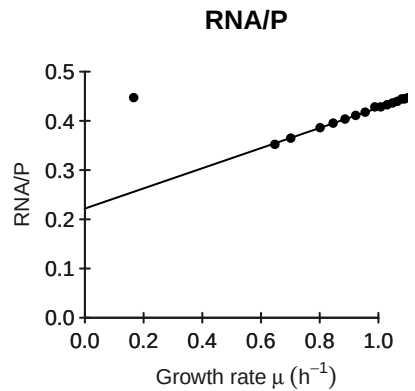

Protein concentrations p (g/L)
tC
FERM
RESP
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNAse
mRNAse
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

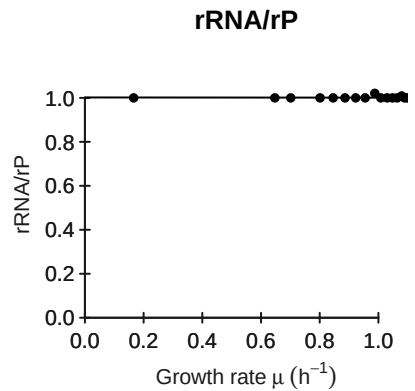

Proteome fractions ϕ
Growth rate μ (h^{-1})

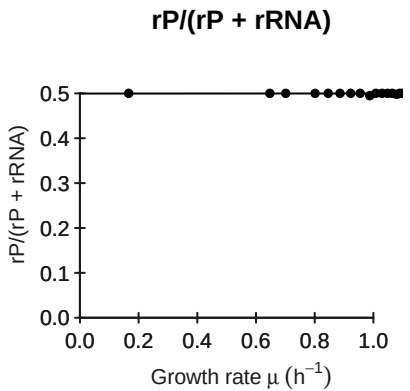

Flux fractions f
Growth rate μ (h^{-1})

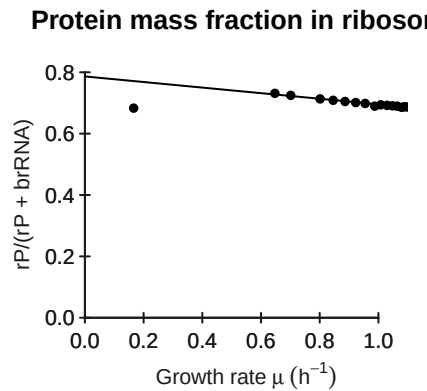

Turnover times τ (h)
tC
FERM
RESP
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNAse
mRNAse
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

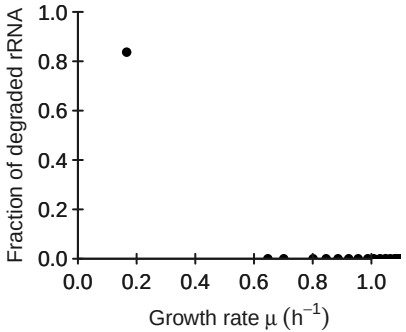

Apparent turnover numbers k_{app} (h^{-1})
Growth rate μ (h^{-1})

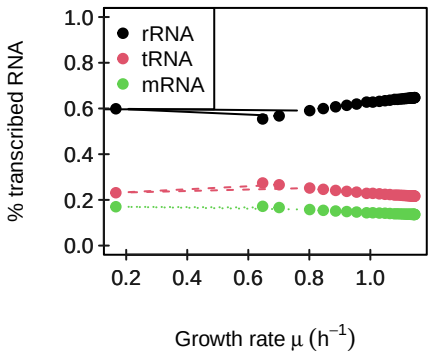

RNA/P
RNA/P
Growth rate μ (h^{-1})

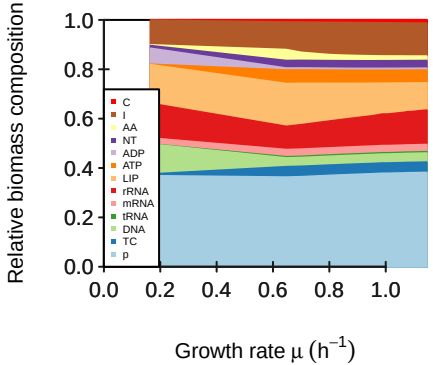

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

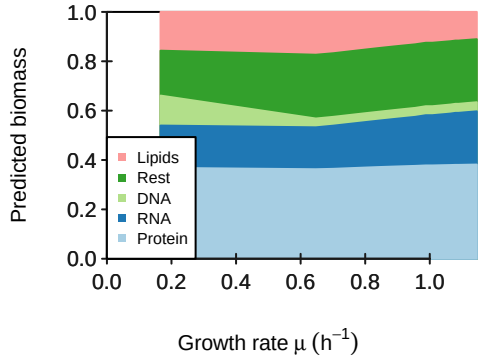

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})

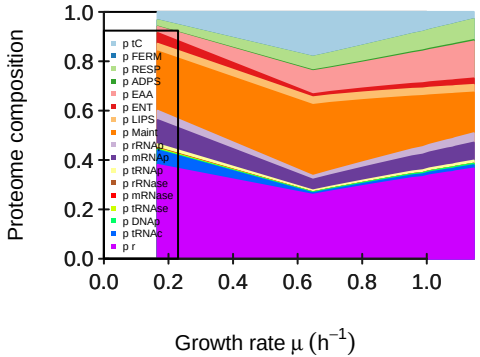

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})

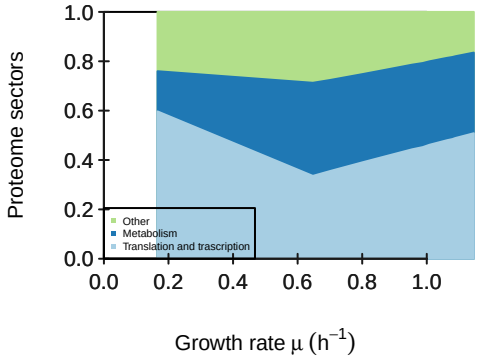

Fraction of degraded rRNA
1.0
0.8
0.6
0.4
0.2
0.0
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)


% transcribed RNA
rRNA
tRNA
mRNA
1.0
0.8
0.6
0.4
0.2
0.0
0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)


Relative biomass composition
C
I
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
p
1.0
0.8
0.6
0.4
0.2
0.0
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)


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


Proteome composition
p tC
p FERM
p RESP
p ADPS
p EAA
p ENT
p LIPS
p Maint
p rRNAse
p mRNAse
p tRNAse
p DNAp
p tRNAc
p r
1.0
0.8
0.6
0.4
0.2
0.0
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)


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

keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

	tC	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
C	1	−0.2	−0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0
I	0	0.1	0.1	0	−1	−0.17	−0.18	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	1	−0.17	0	0	0	0	0	0	0	0	0	−0.006	0
NT	0	0	0	−1	0	0.34	0	0	−1	−1	−1	1	1	1	−1	0	0
ADP	0	−0.8	−0.85	1	0	0.66	0.82	1	0	0	0	0	0	0	0	0.026	0.026
ATP	0	0.8	0.85	0	0	−0.66	−0.82	−1	0	0	0	0	0	0	0	−0.026	−0.026
LIP	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	1	0	0	−1	0	0	0	0	0
mRNA	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	1	0	0	−1	0	−0.968	0.968
DNA	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	0.974	−0.974
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.006

K

	tC	FERM	RESP	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
x_W	0	20	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	0	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
I	0	0	0	0	31	31	31	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	2	0
NT	0	0	0	2	0	0	0	0	2	2	2	0	0	0	2	0	0
ADP	0	1	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	2	2	2	0	0	0	0	0	0	0	2	2
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	0	0	14	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0
DNA	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	2
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0.01	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
I	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
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	0	0	0	0	0	0	0	55
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
tRNA	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	4	4	4	0	0	0	4	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	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
kcatf	159.9	3192	456	36.6	19.3	288.9	111.7	79	17.3	1.9	17.3	192.6	192.6	192.6	28.9	33090.6	2008.9
kcatb	0	0	0	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]	[,15]	[,16]	[,17]
[1,]	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	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,]	0.043	0.023	0.023	0.002	0.165	0.021	0.031	0.3036	0.0426	0.0213	0.0071	0.002	0.006	4e−04	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]	[,16]	[,17]
[1,]	0	0	0	0	0	0	0.031	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]	[,16]	[,17]
[1,]	0	0	0	0	0	0	0	3.85385	0	0	0	0	0	0	0	0	0