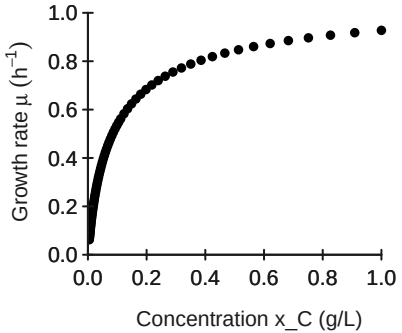
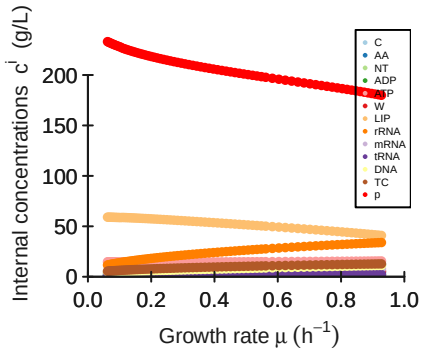
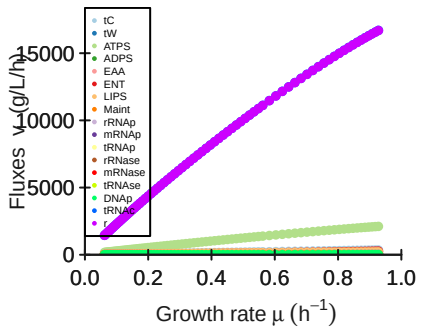
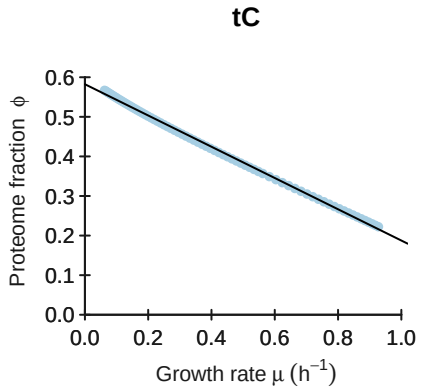
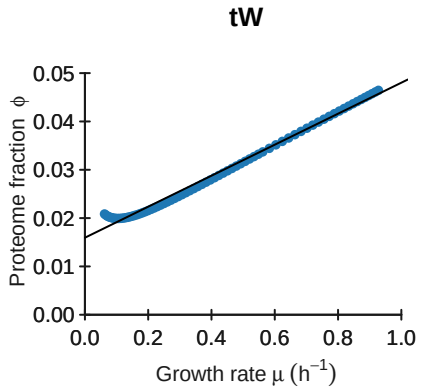
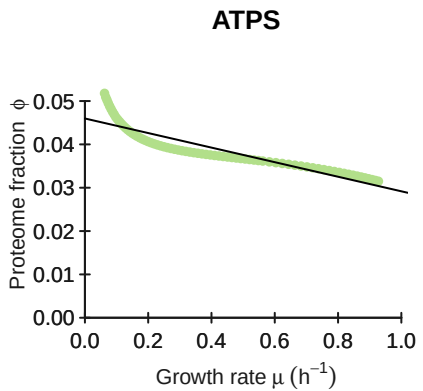

Growth rate μ (h^{-1})
Concentration x_C (g/L)

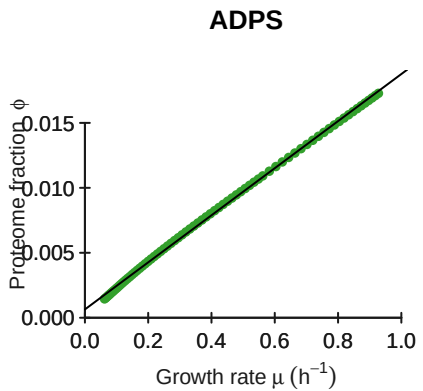

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
p

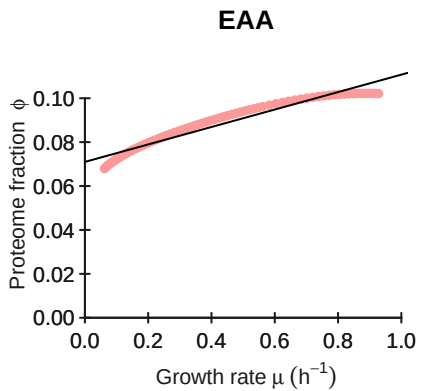

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNase
DNAp
tRNAse

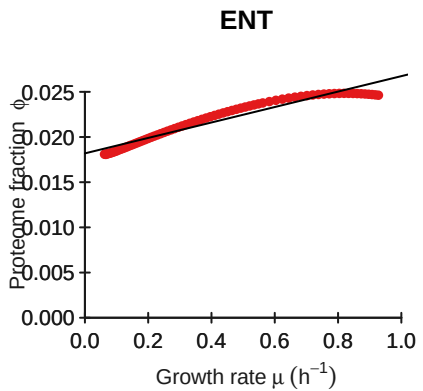

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

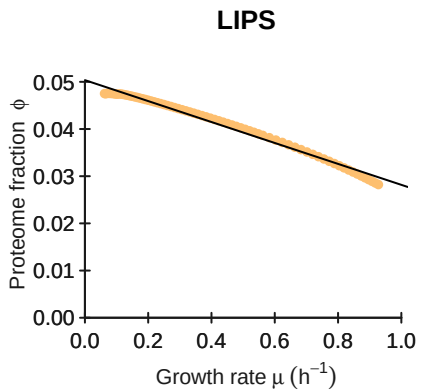

tW
Proteome fraction ϕ
Growth rate μ (h^{-1})

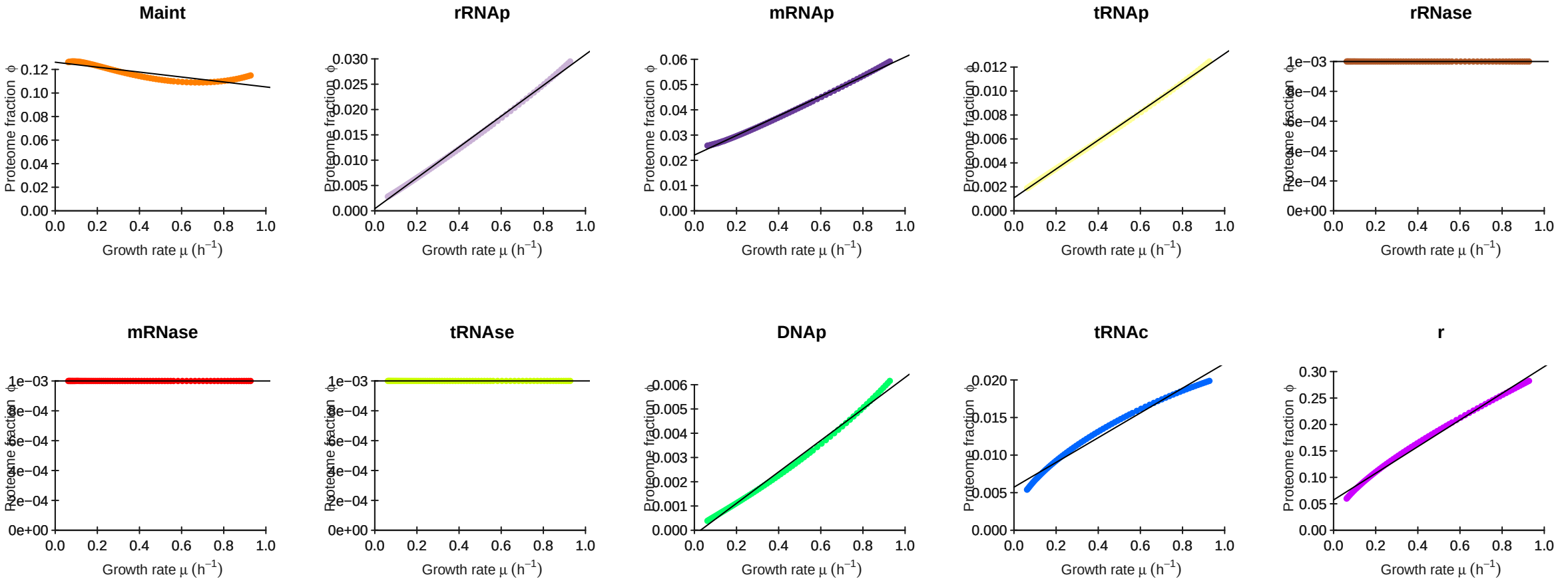

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

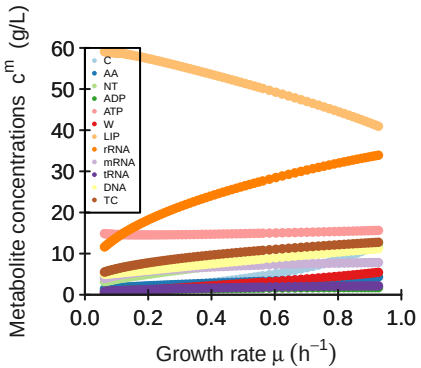

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

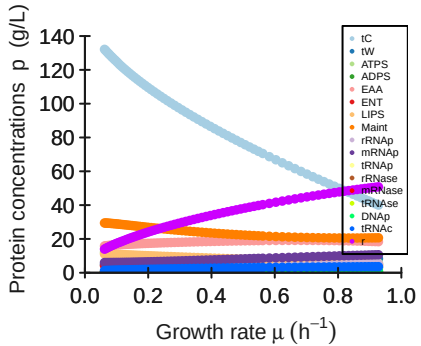

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

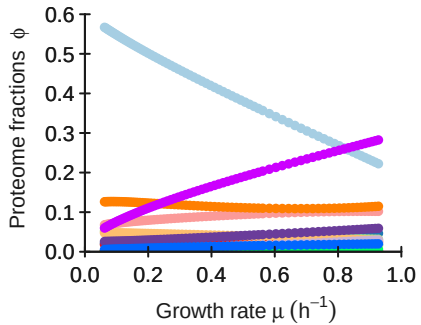

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

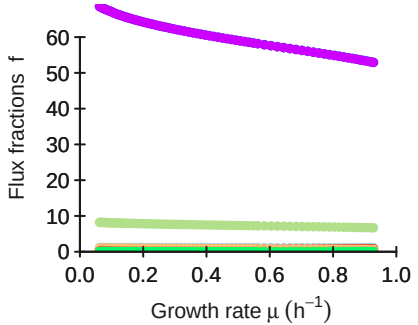

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

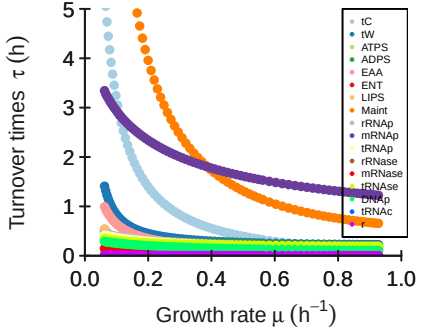

Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})

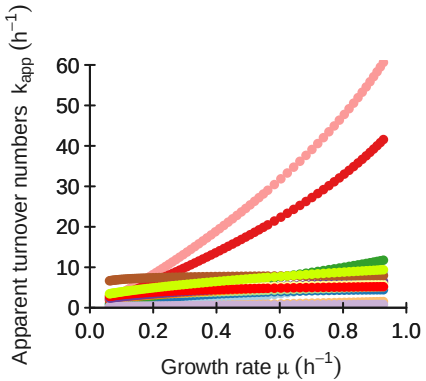

Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h^{-1})

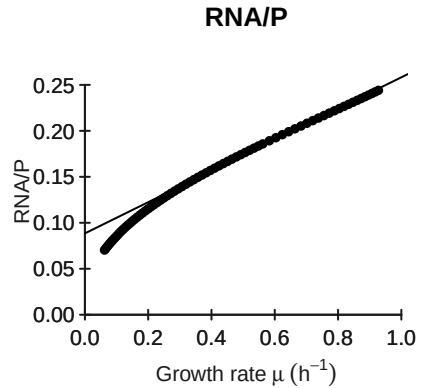

Protein concentrations p (g/L)
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

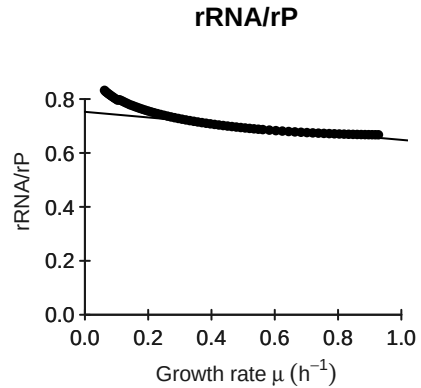

Proteome fractions ϕ
Growth rate μ (h^{-1})

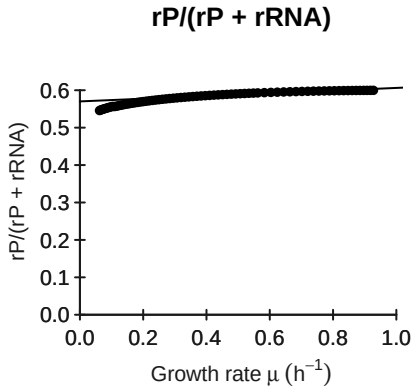

Flux fractions f
Growth rate μ (h^{-1})

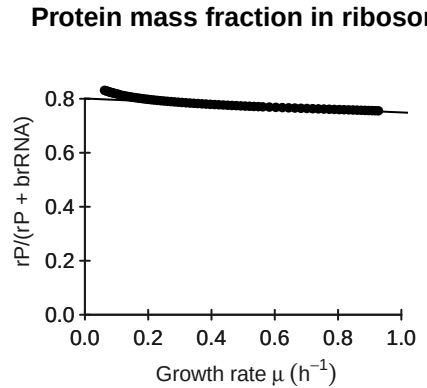

Turnover times τ (h)
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

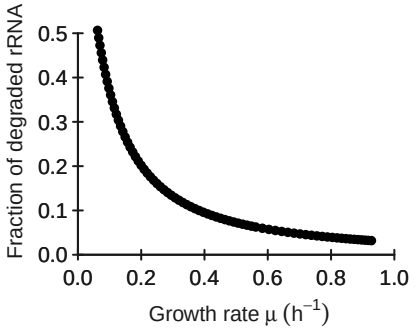

Apparent turnover numbers k_{app} (h^{-1})
Growth rate μ (h^{-1})

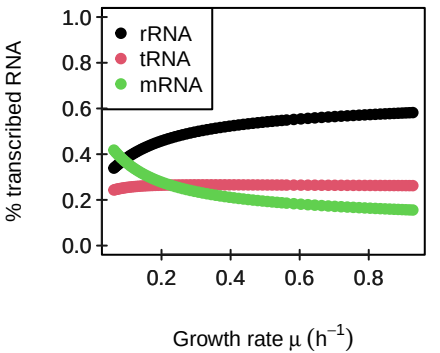

RNA/P
RNA/P
Growth rate μ (h^{-1})

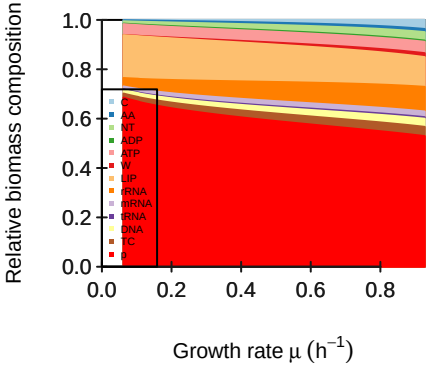

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

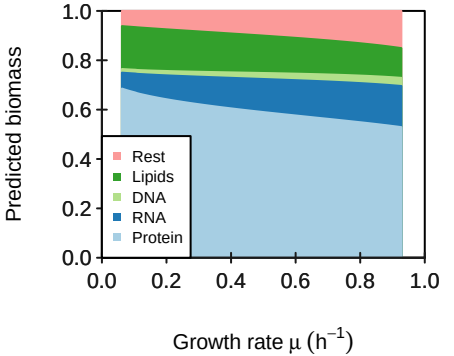

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})

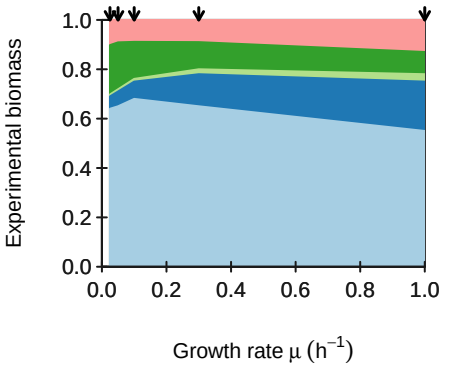

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})

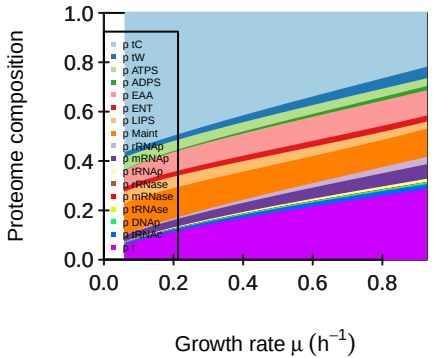


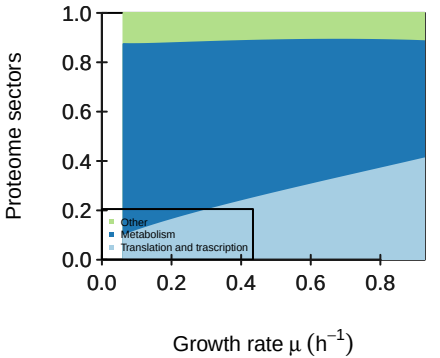




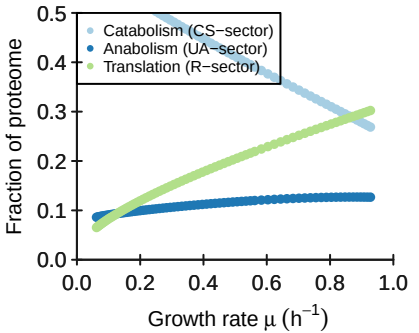








Proteome sectors



M

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
C	1	0	−0.02	0	−1	−0.167	−0.18	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	1	−0.167	0	0	0	0	0	0	0	0	0	−0.01	0
NT	0	0	0	−1	0	0.334	0	0	−1	−1	−1	1	1	1	−1	0	0
ADP	0	0	−0.98	1	0	0.666	0.82	1	0	0	0	0	0	0	0	0.05	0.05
ATP	0	0	0.98	0	0	−0.666	−0.82	−1	0	0	0	0	0	0	0	−0.05	−0.05
W	0	−1	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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	−0.94	0.94
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	0.95	−0.95
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

K

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0.3	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
C	11	0	6	0	6	6	6	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	11	6	0	0	0	0	0	0	0	0	0	6	0
NT	0	0	0	5	0	10	0	0	5	5	5	0	0	0	5	0	0
ADP	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0
ATP	0	0	5	0	0	3	3	3	0	0	0	0	0	0	0	3	3
W	0	3	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	29	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	25	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	2	0	2	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	3
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0.1	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	60	60	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	36
mRNA	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
DNA	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
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

kcat

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
kcatf	37	17	1717	12	20	301	97	2	15	2	16	10	10	10	23	25540	1379
kcatb	4	2	172	1	2	30	10	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,]	339.166666666667	8.5	49.9127906976744	2.4	18.3333333333333	0.929012345679012	15.6277777777778	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,]	0.089	0.021	0.027	0.005	0.165	0.023	0.031	0.2506	0.0426	0.0213	0.0071	0.002	0.006	4e−04	0.002	0.023	0.284

average saturation input

2

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	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]
[1,]	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0