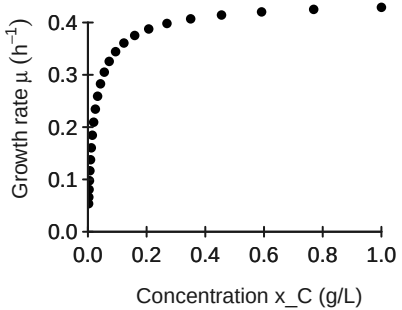
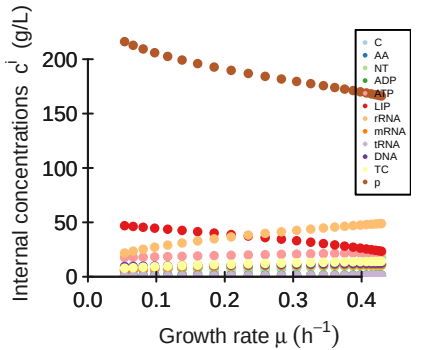
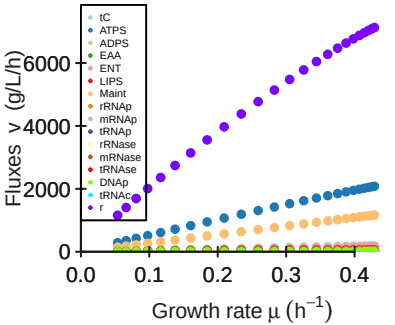
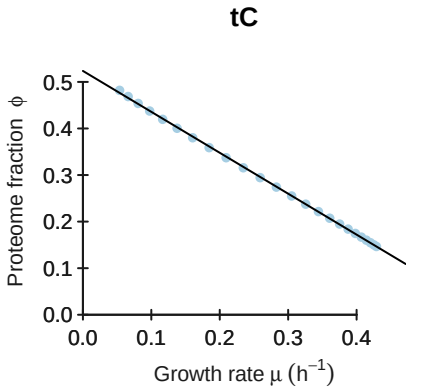
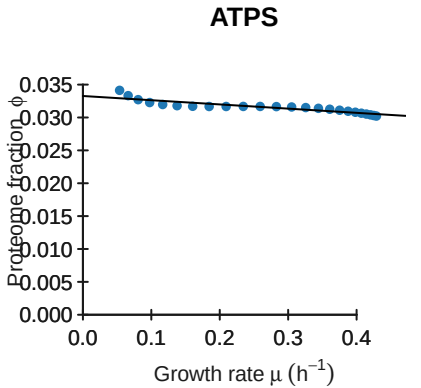
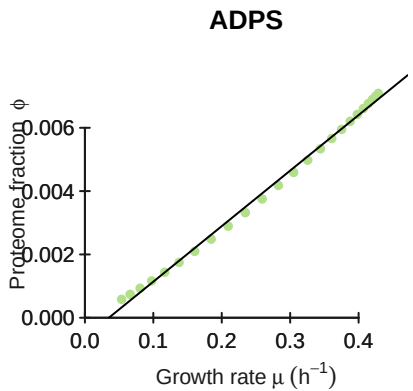

Growth rate μ (h^{-1})
Concentration x_C (g/L)

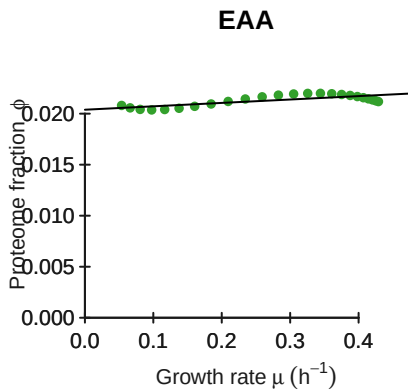

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
p

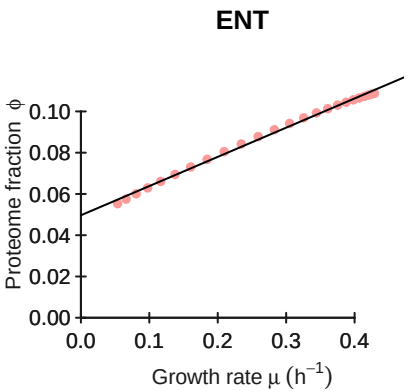

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r

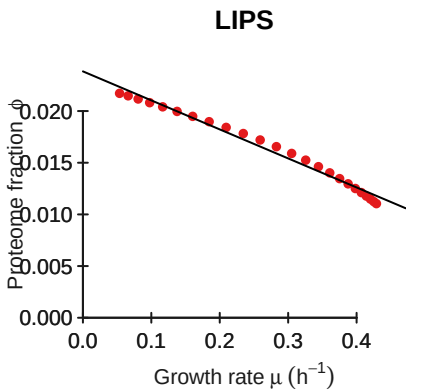

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

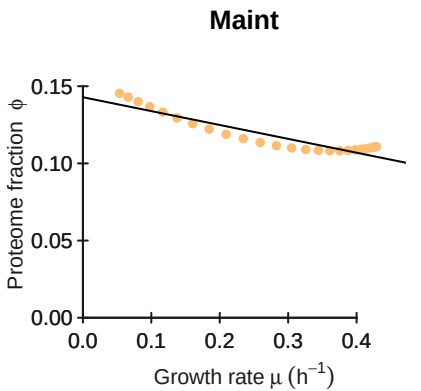

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

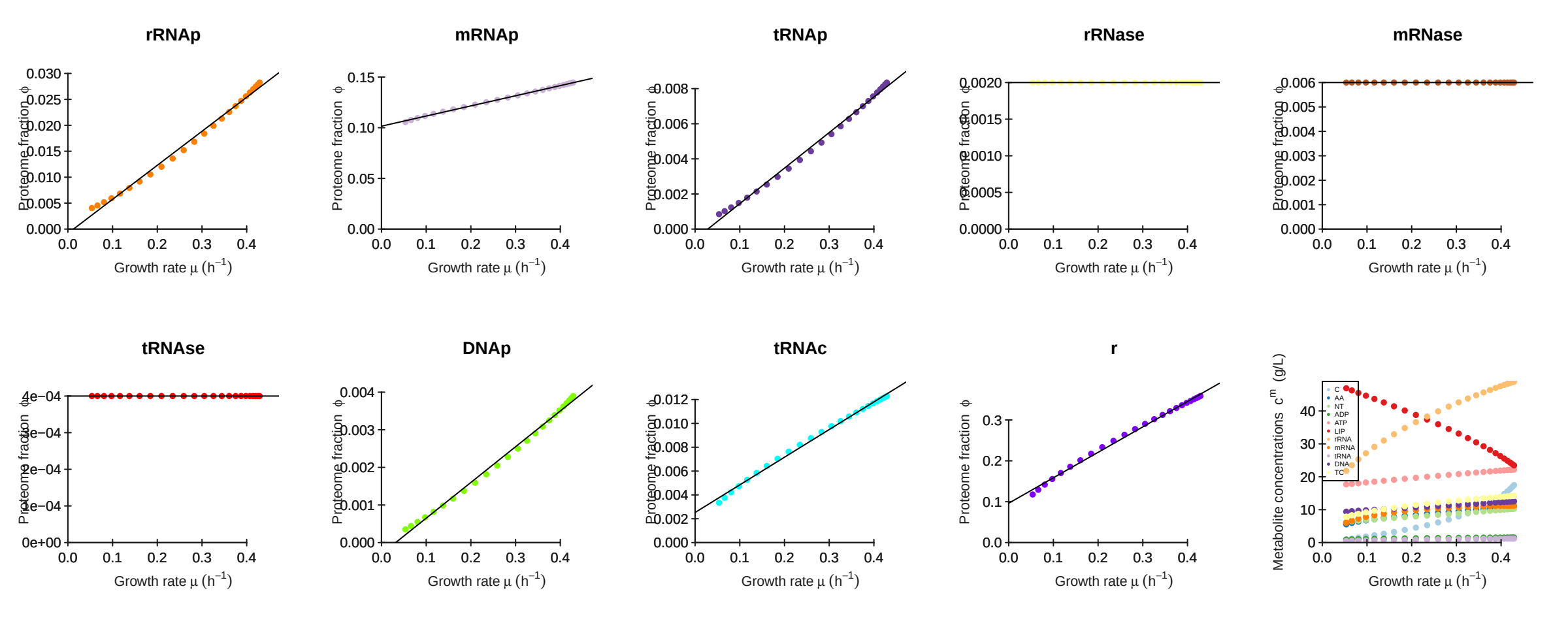

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

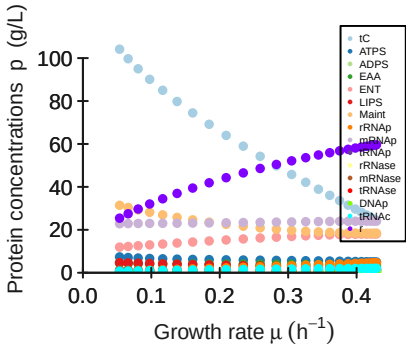

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

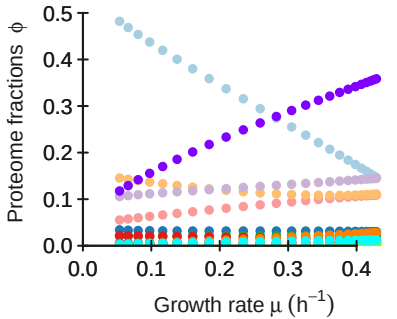

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

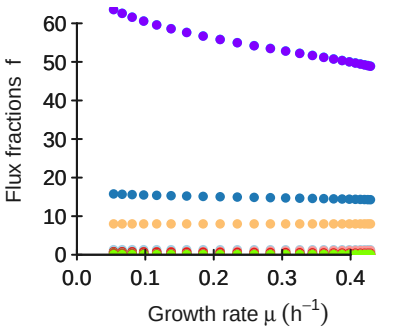

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

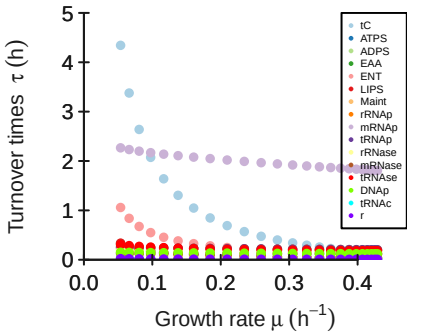

Maint
Proteome fraction ϕ
Growth rate μ (h^{-1})

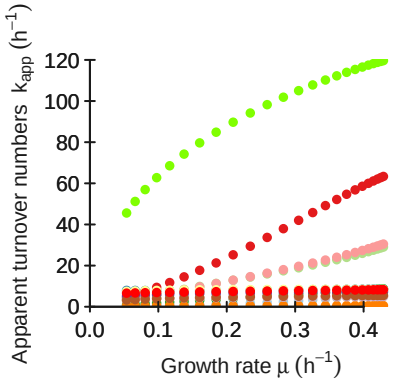

rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})
Metabolite concentrations c^{m} (g/L)
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC



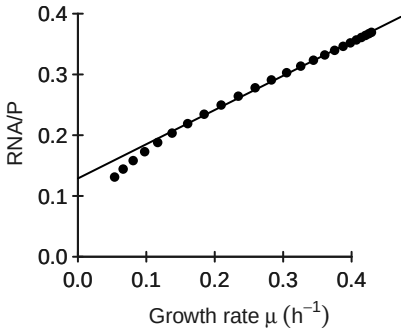




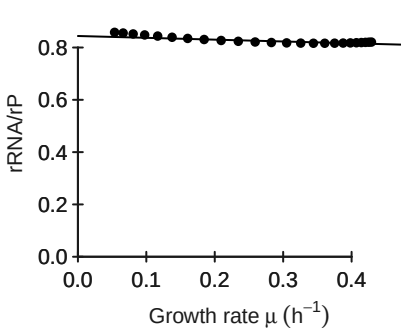




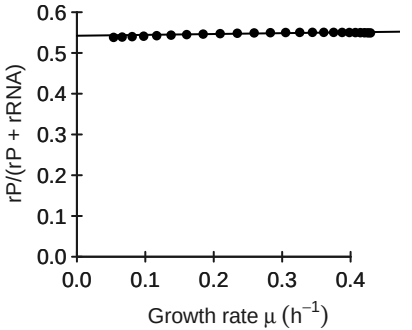
RNA/P



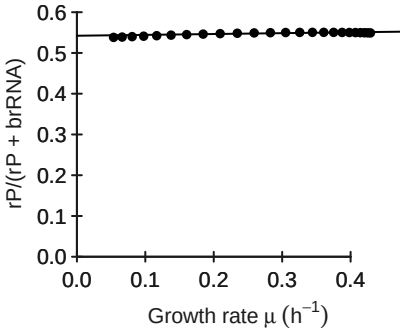
rRNA/rP

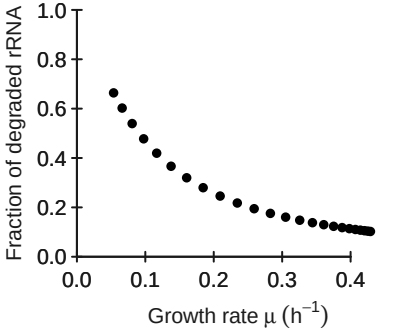


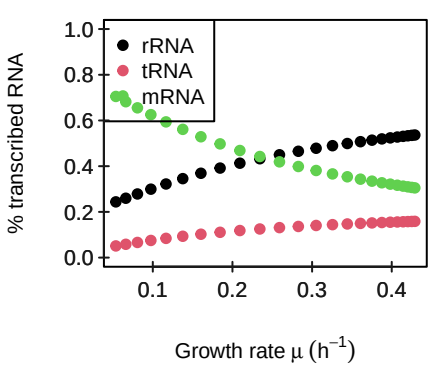
rP/(rP + rRNA)

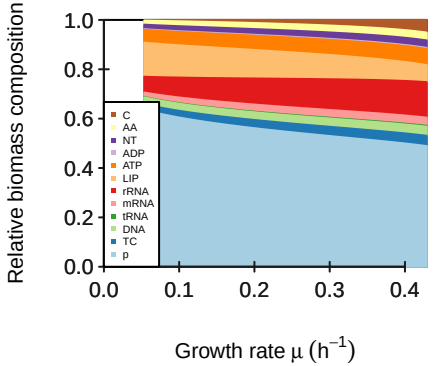


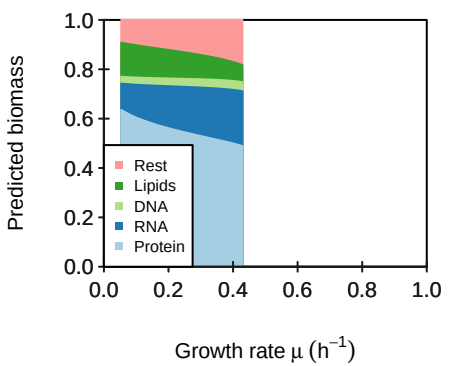
Protein mass fraction in ribosome

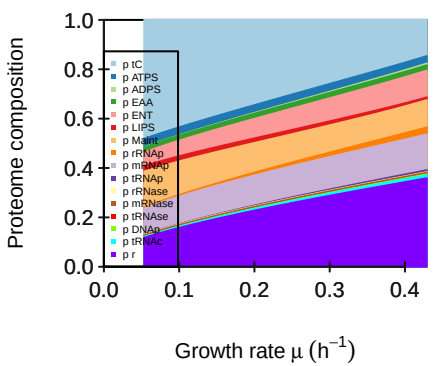


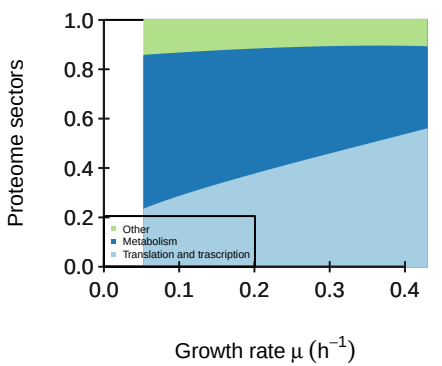



% transcribed RNA
rRNA
tRNA
mRNA
Growth rate μ (h−1)


Relative biomass composition
C
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
p tC
p ATPS
p ADPS
p EAA
p ENT
p LIPS
p Mainf
p rRNAp
p mRNAp
p tRNAp
p rRNase
p mRNase
p tRNAse
p DNAp
p tRNAc
p r
Growth rate μ (h−1)


Proteome sectors
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)

M

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

K

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_W	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	20	7	0	7	7	7	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	11	4	0	0	0	0	0	0	0	0	0	4	0
NT	0	0	3	0	7	0	0	3	3	3	0	0	0	3	0	0
ADP	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0
ATP	0	11	0	0	4	4	4	0	0	0	0	0	0	0	4	4
LIP	0	0	0	0	0	35	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	19	0	0	0	0	0
mRNA	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	1	0	1	0
DNA	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	3
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0.03	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
C	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
NT	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
ATP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	30	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	75
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	5	5	5	0	0	0	5	0	0
TC	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

kcat

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
kcatf	21	1171	16	54	21	58	77	9	1	9	10	10	10	15	10311	626
kcatb	2	117	2	5	2	6	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]
[1,]	2100	314.554334554335	2.66666666666667	16.9714285714286	0.65625	12.0833333333333	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]
[1,]	0.11	0.023	0.005	0.032	0.16	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

3

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
[1,]	0	0	0	0	0	0	0	0	0	0	0.002	0.006	4e−04	0	0	0

minimal f constraint

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