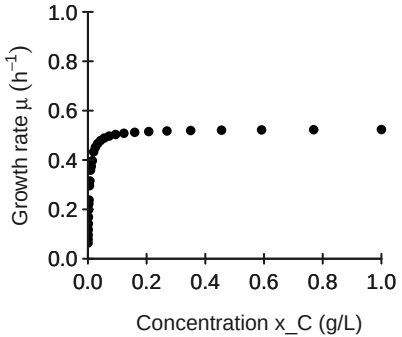
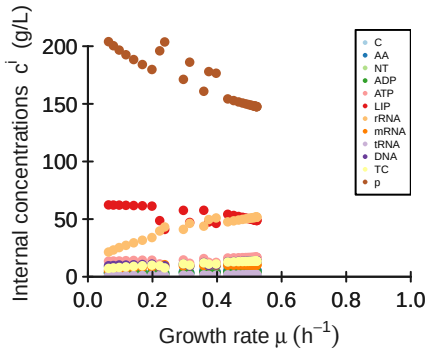
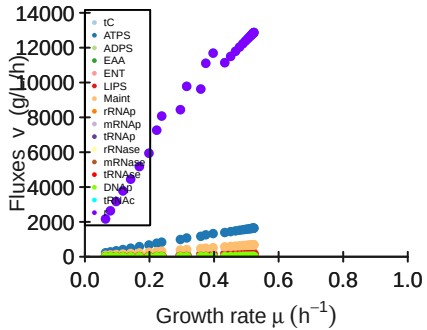
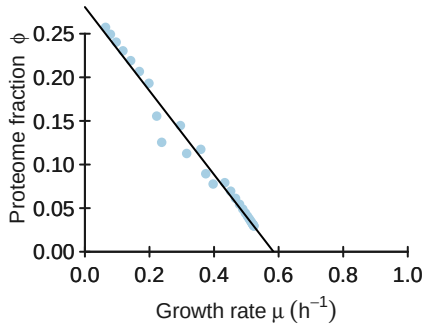


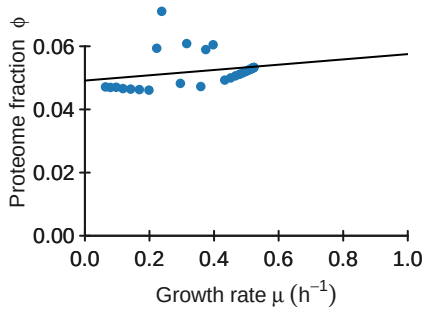




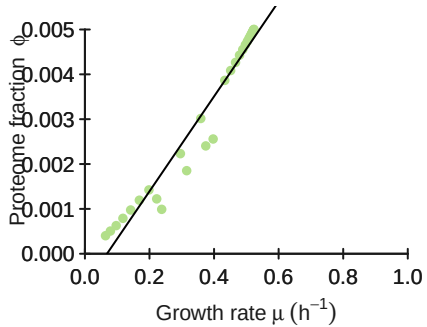
tC



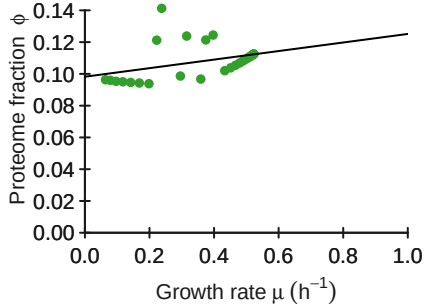
ATPS



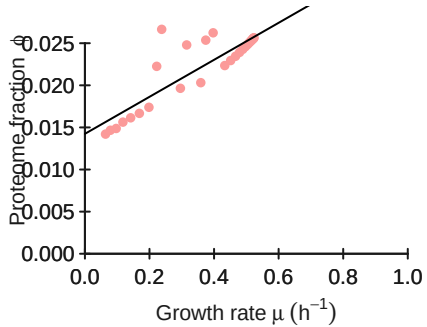
ADPS



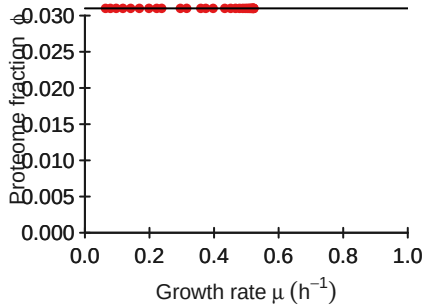
EAA



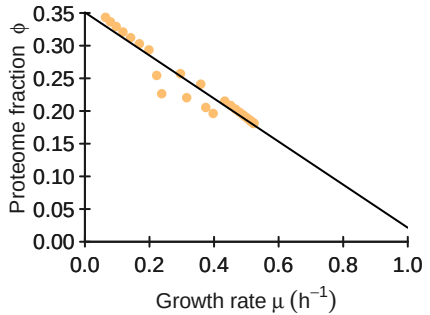
ENT

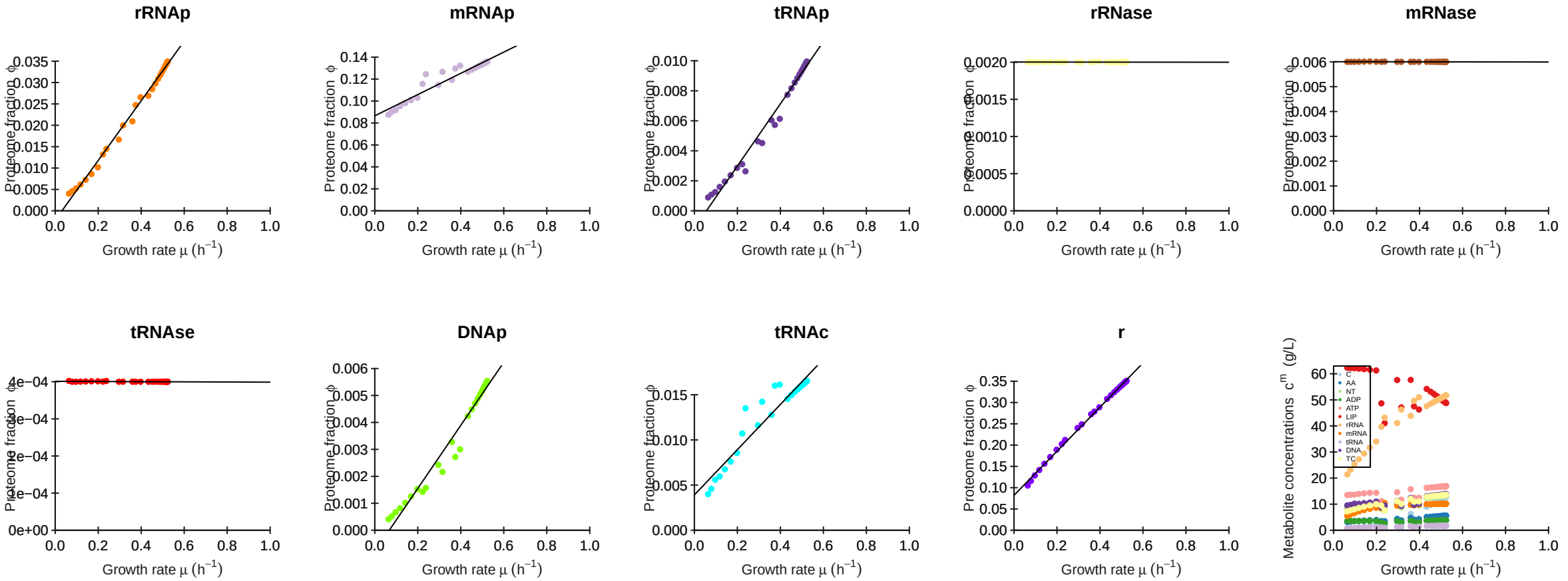


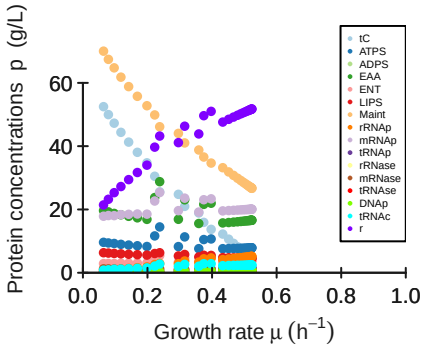
LIPS

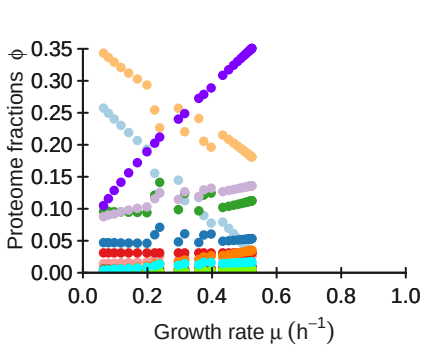


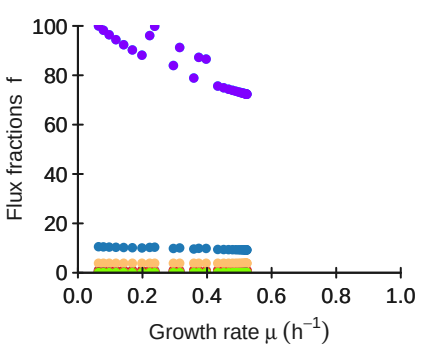
Maint

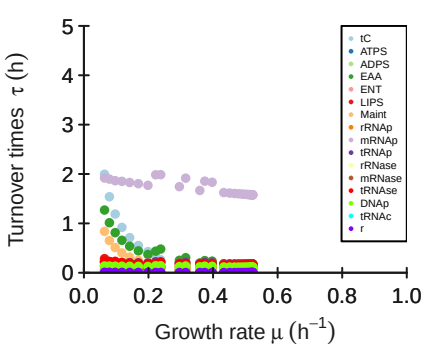


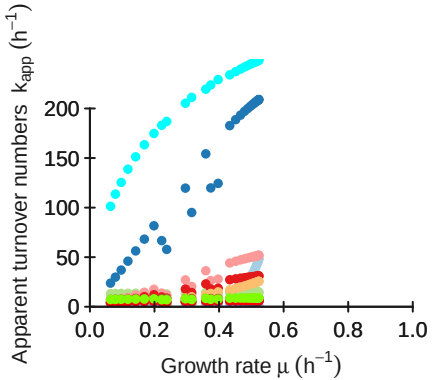

rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})
Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC

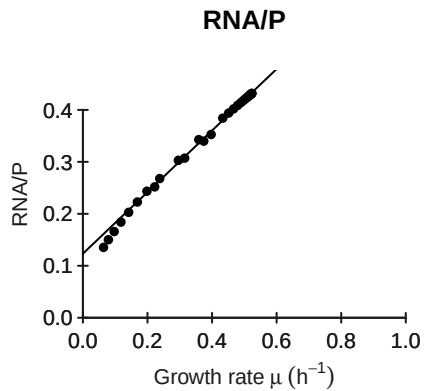

Protein concentrations p (g/L)
Growth rate μ (h^{-1})
tC
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r

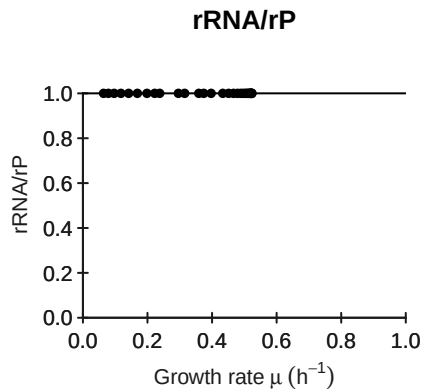

Proteome fractions ϕ
Growth rate μ (h^{-1})

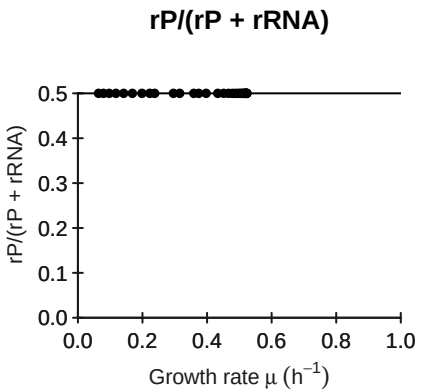

Flux fractions f
Growth rate μ (h^{-1})

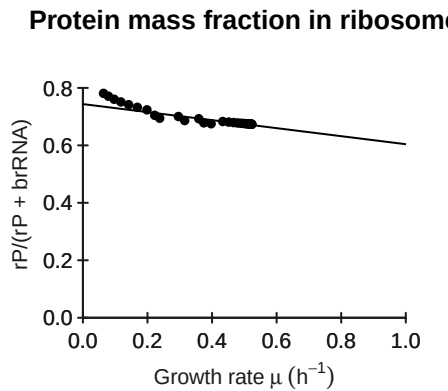

Turnover times τ (h)
Growth rate μ (h^{-1})
tC
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r

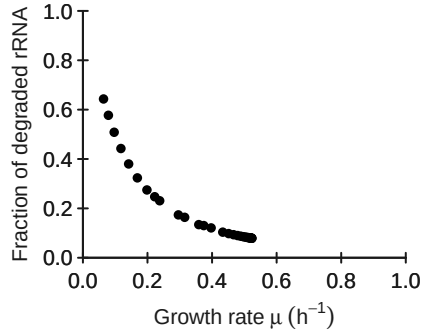

Apparent turnover numbers k$_{app}$ (h^{-1})
Growth rate μ (h^{-1})

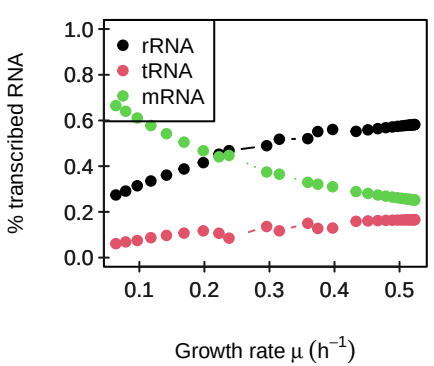

RNA/P
RNA/P
Growth rate μ (h^{-1})

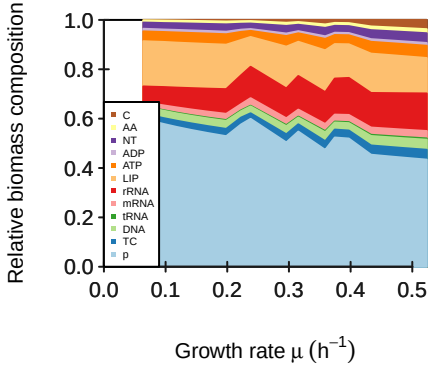

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

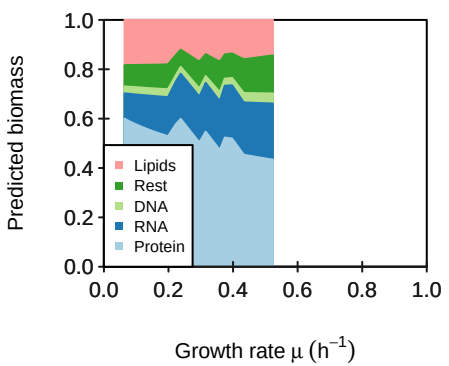

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})

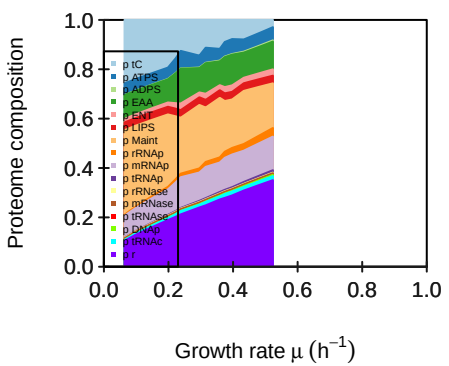

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})

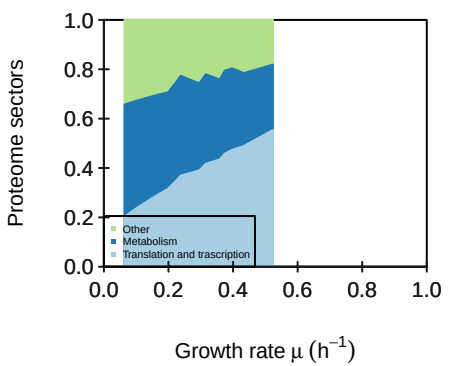

Fraction of degraded rRNA
Growth rate μ (h^{-1})


% 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
Lipids
Rest
DNA
RNA
Protein
Growth rate μ (h−1)


Proteome composition
p tC
p ATPS
p ADPS
p EAA
p ENT
p LIPS
p Maint
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)

keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

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	−0.006	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	0.026	0.026
ATP	0	0.98	0	0	−0.666	−0.82	−1	0	0	0	0	0	0	0	−0.026	−0.026
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	−0.968	0.968
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	0.974	−0.974
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.006

K

	tC	ATPS	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
x_W	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	0	6	0	6	6	6	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	3	0	0	0	0	0	0	0	0	0	3	0
NT	0	0	3	0	0	0	0	3	3	3	0	0	0	3	0	0
ADP	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP	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
rRNA	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	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	2
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	0.01	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
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	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	55
mRNA	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
DNA	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
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	51	387	18	10	131	51	29	9	1	9	10	10	10	14	14156	917
kcatb	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]
[1,]	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]
[1,]	0.043	0.046	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

4

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	0.031	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	3.85	0	0	0	0	0	0	0	0	0