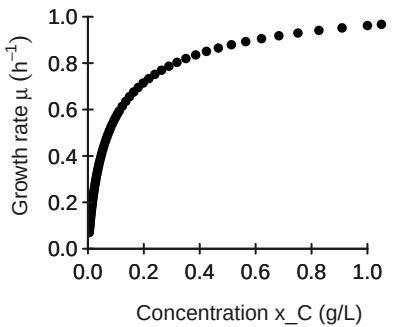
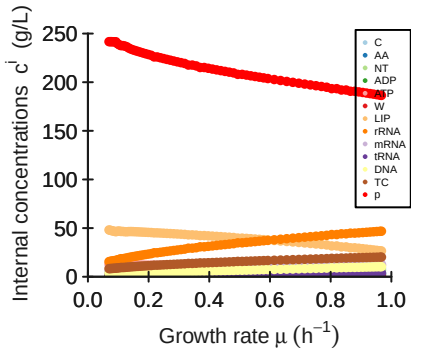
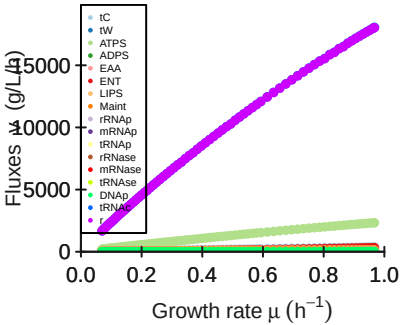
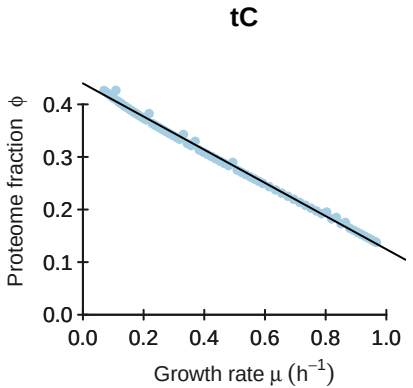
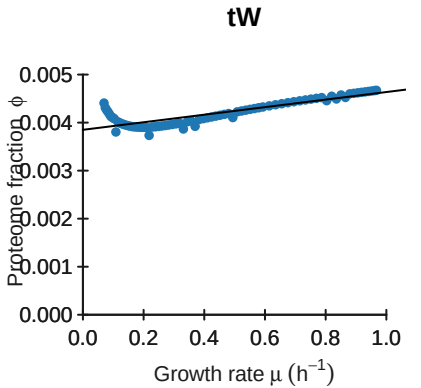
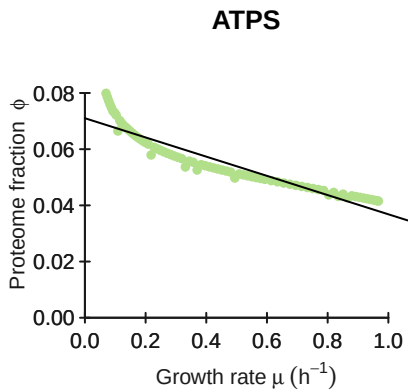

Growth rate μ (h^{-1})
Concentration x_C (g/L)

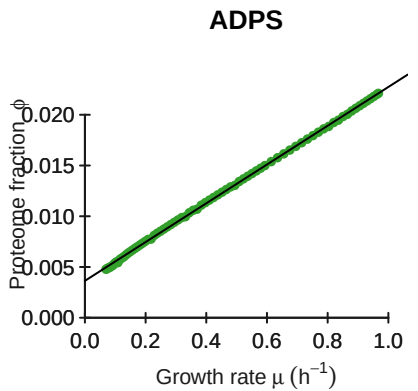

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
p

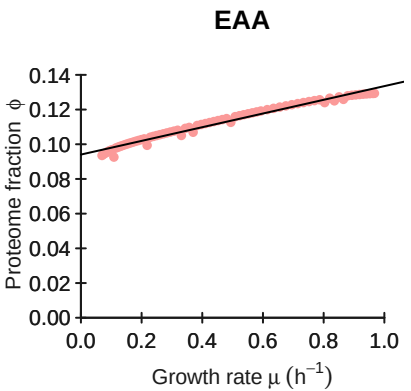

Fluxes v_i (g/L/h)
Growth rate μ (h^{-1})
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAse

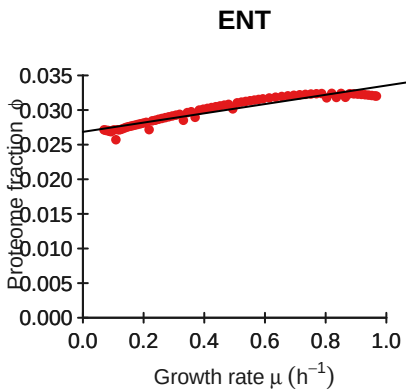

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

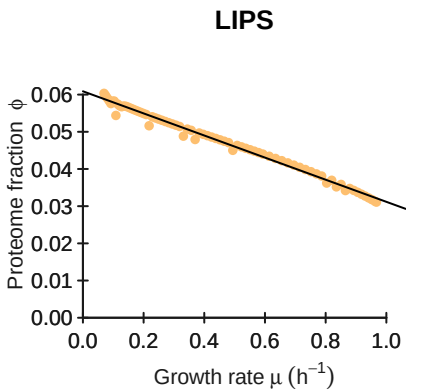

tW
Proteome fraction ϕ
Growth rate μ (h^{-1})

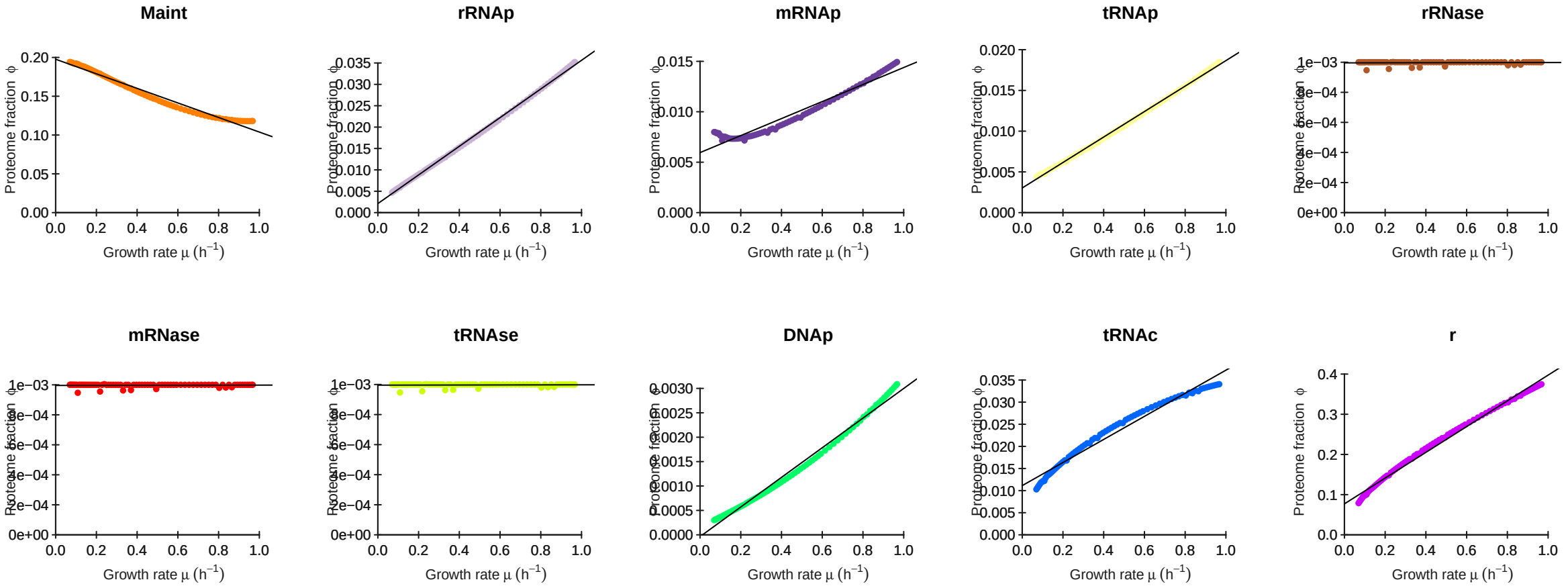

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

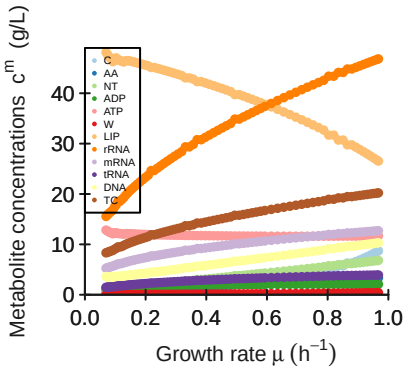

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

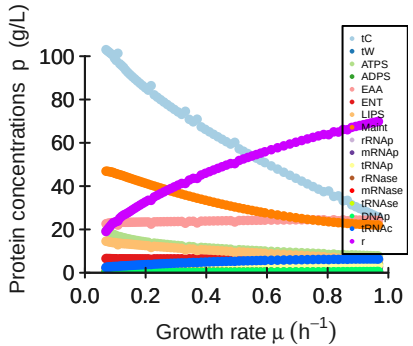

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

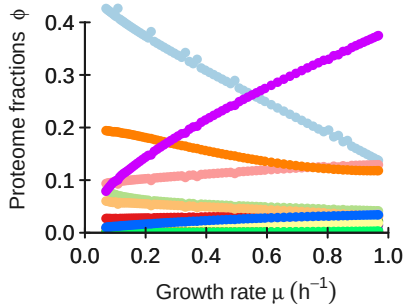

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

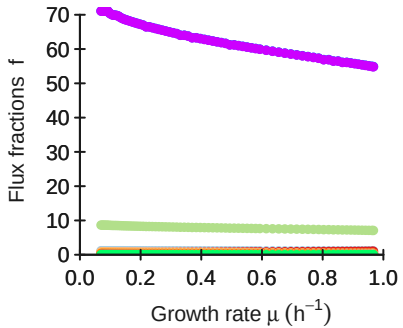

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

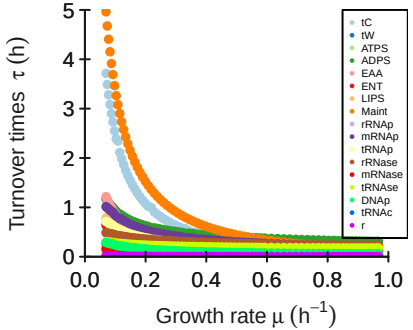

Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})

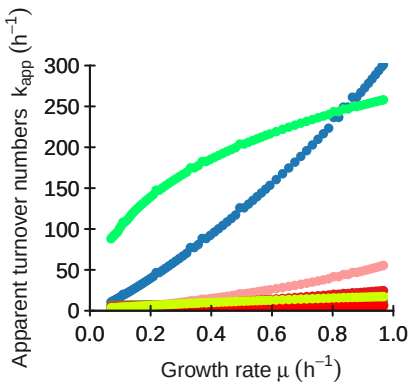




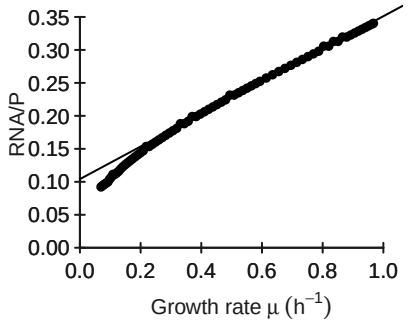




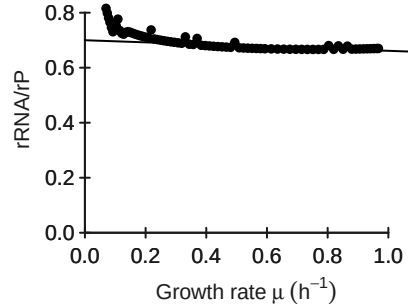




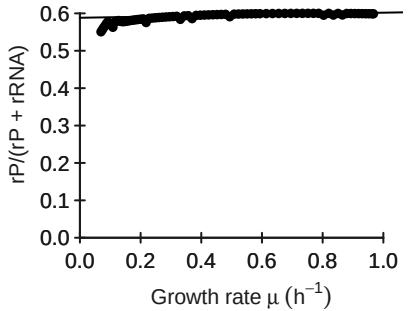
RNA/P



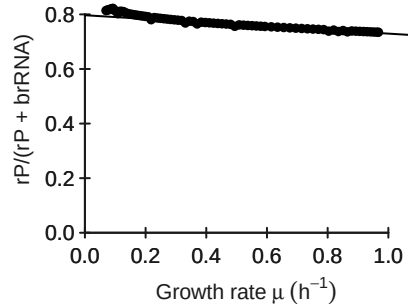
rRNA/rP

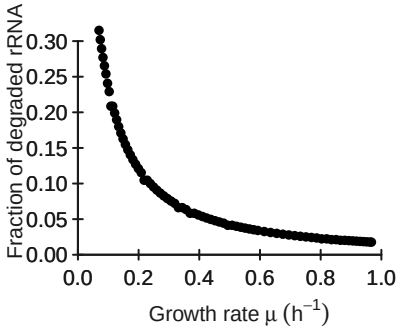


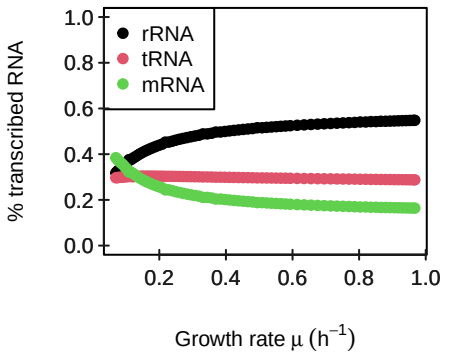
rP/(rP + rRNA)

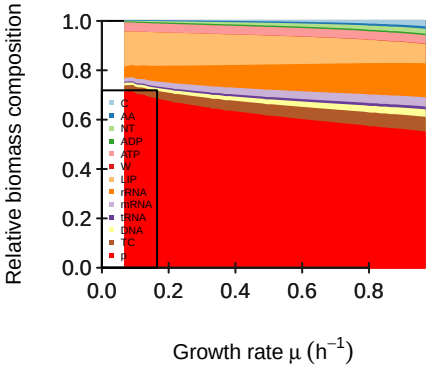


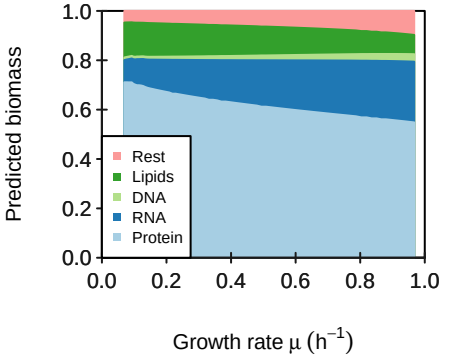
Protein mass fraction in ribosome

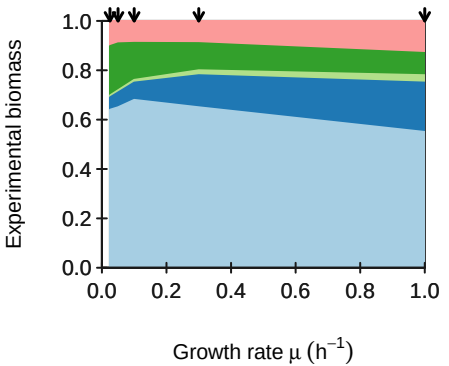


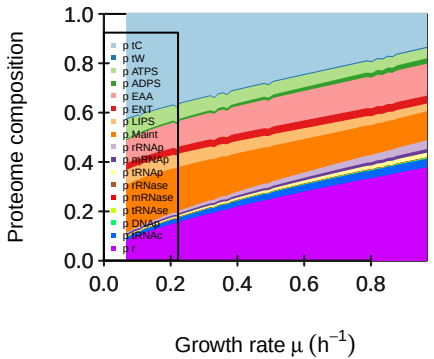


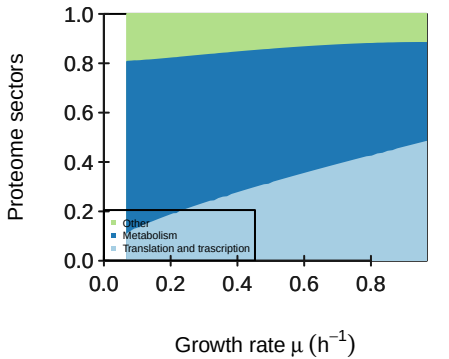




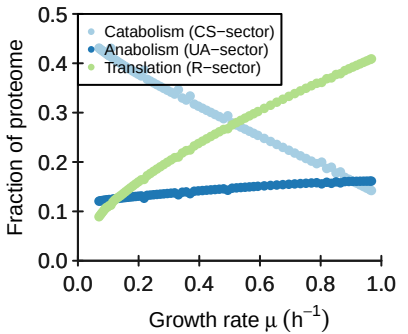








Proteome sectors



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	0.5	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	5	0	2	0	2	2	2	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	3	3	0	0	0	0	0	0	0	0	0	3	0
NT	0	0	0	1	0	2	0	0	2	2	2	0	0	0	2	0	0
ADP	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0
ATP	0	0	2	0	0	2	2	2	0	0	0	0	0	0	0	1	1
W	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	34	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	60	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	3	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	5
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	0.15	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	40
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
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	9	9	9	0	0	0	9	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

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
kcatf	120	1000	800	5	15	180	40	8	17	12	17	10	10	10	42	10306	750
kcatb	12	10	80	1	1	18	4	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,]	100	150	20	5	22.5	1.66666666666667	85	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

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	0.4	0	0	0	0	0	0	0	0	0