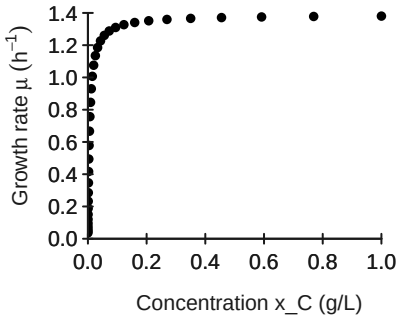
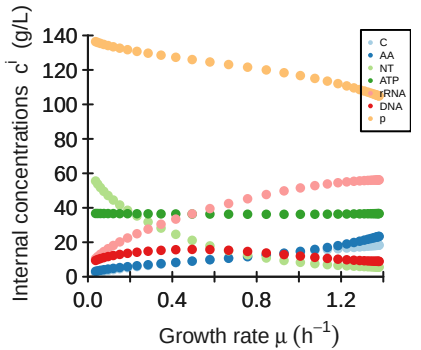
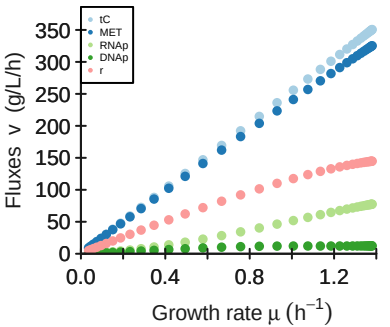
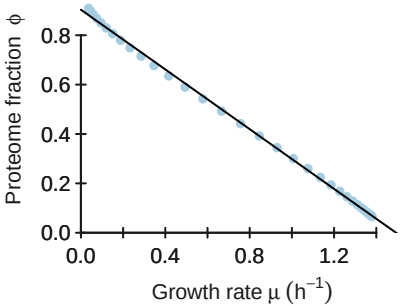


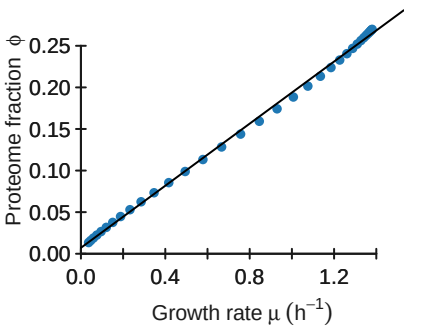




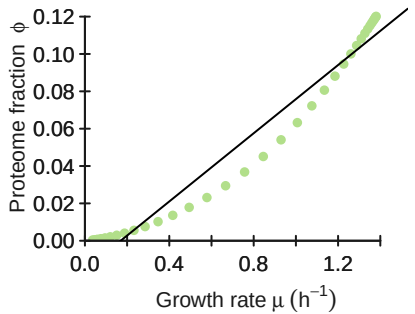
tC



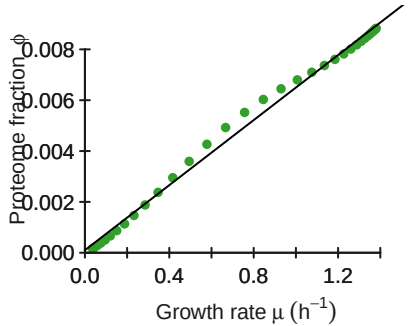
MET



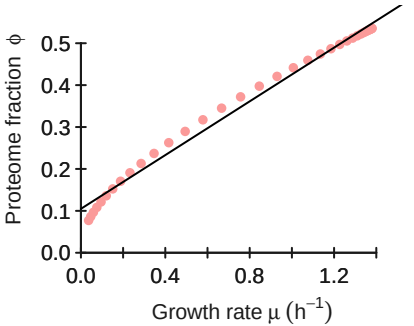
RNAp

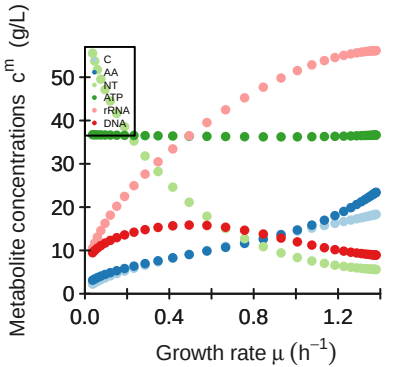


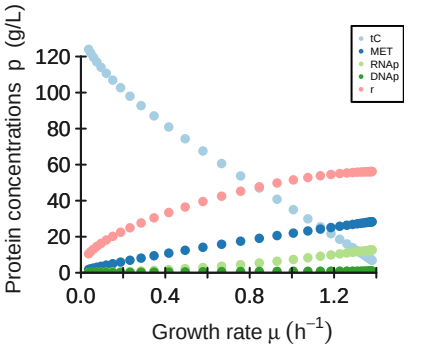
DNAp

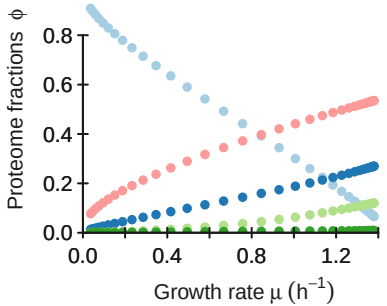


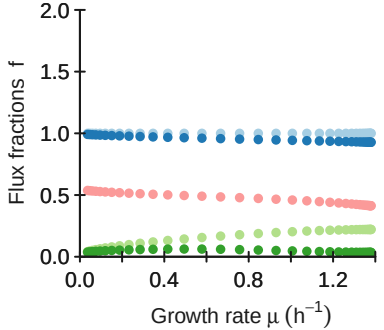
r

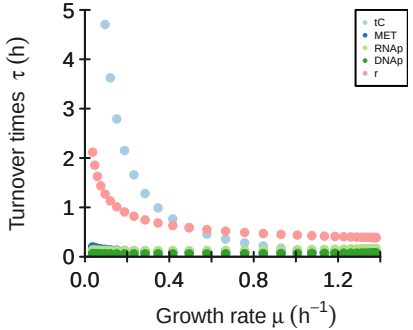


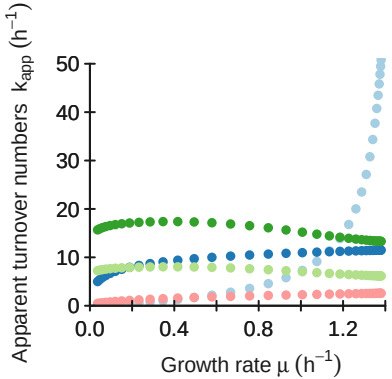


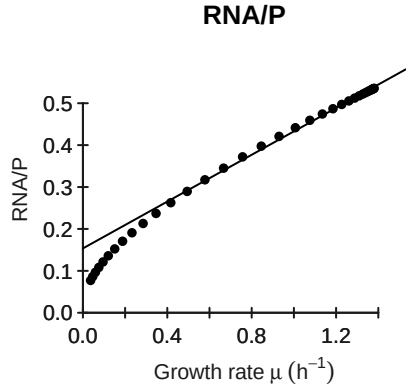


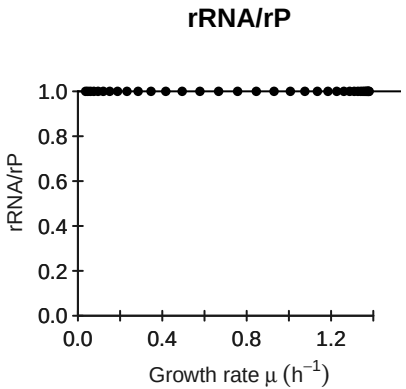

Proteome fractions ϕ
0.0
0.2
0.4
0.6
0.8
0.0
0.4
0.8
1.2
Growth rate μ (h−1)

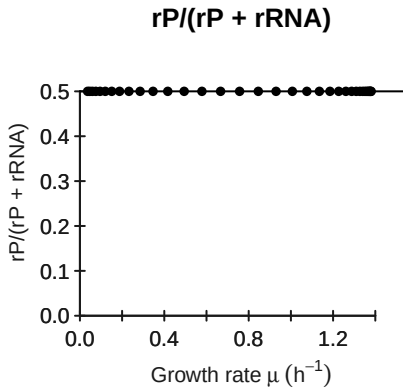

Flux fractions f
0.0
0.5
1.0
1.5
2.0
0.0
0.4
0.8
1.2
Growth rate μ (h−1)

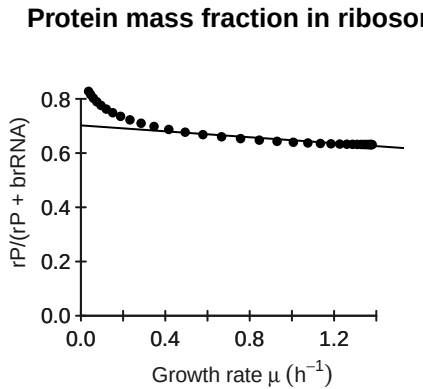

Turnover times τ (h)
0
1
2
3
4
5
0.0
0.4
0.8
1.2
Growth rate μ (h−1)
tC
MET
RNAp
DNAp
r

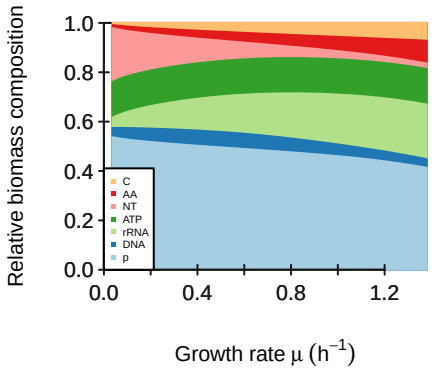

Apparent turnover numbers kapp (h−1)
0
10
20
30
40
50
0.0
0.4
0.8
1.2
Growth rate μ (h−1)

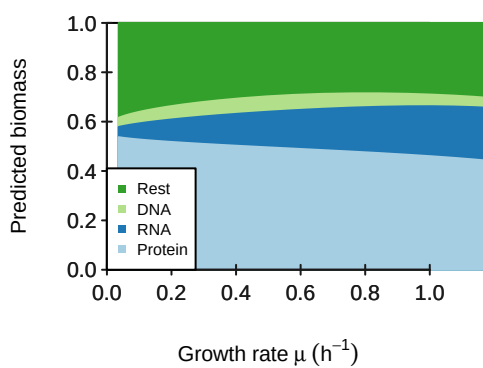

RNA/P
RNA/P
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.4
0.8
1.2
Growth rate μ (h−1)

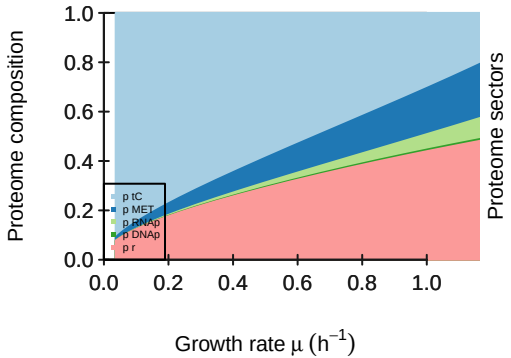

rRNA/rP
rRNA/rP
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.4
0.8
1.2
Growth rate μ (h−1)

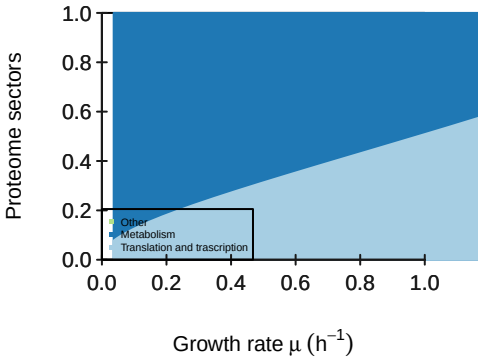

rP/(rP + rRNA)
rP/(rP + rRNA)
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.4
0.8
1.2
Growth rate μ (h−1)


Protein mass fraction in ribosome
rP/(rP + brRNA)
0.0
0.2
0.4
0.6
0.8
0.0
0.4
0.8
1.2
Growth rate μ (h−1)


Relative biomass composition
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.4
0.8
1.2
Growth rate μ (h−1)
C
AA
NT
ATP
rRNA
DNA
p


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


Proteome composition
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
p tC
p MET
p RNAp
p DNAp
p r
Growth rate μ (h−1)


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

keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

	tC	MET	RNAp	DNAp	r
C	1	−1	0	0	0
AA	0	0.5	0	0	−0.9
NT	0	0.3	−1	−1	0
ATP	0	0.2	0	0	−0.1
rRNA	0	0	1	0	0
DNA	0	0	0	1	0
p	0	0	0	0	1

K

	tC	MET	RNAp	DNAp	r
x_C	0.1	0	0	0	0
C	0	4	0	0	0
AA	0	0	0	0	4
NT	0	0	1	1	0
ATP	0	0	0	0	13
rRNA	0	0	0	0	0
DNA	0	0	0	0	0
p	0	0	0	0	0

KA

	tC	MET	RNAp	DNAp	r
x_C	0	0	0	0	0
C	0	0	0	0	0
AA	0	0	0	0	0
NT	0	0	0	0	0
ATP	0	0	0	0	0
rRNA	0	0	0	0	40
DNA	0	0	4	4	0
p	0	0	0	0	0

kcat

	tC	MET	RNAp	DNAp	r
kcatf	55.9	14	10.5	22.7	7
kcatb	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	0.065	0.352	0.12	0.003	0.46

average saturation input

3

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	0	0	0	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	0	0	0	0	0