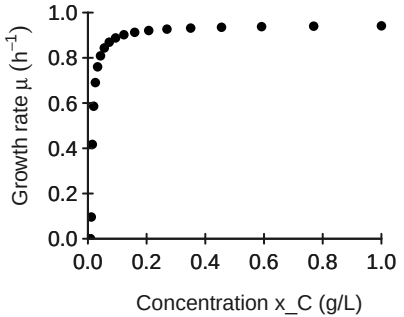
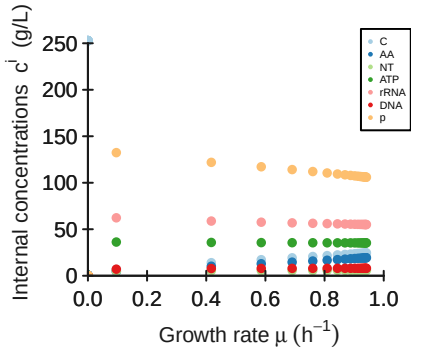
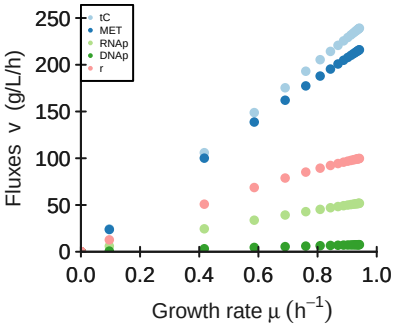
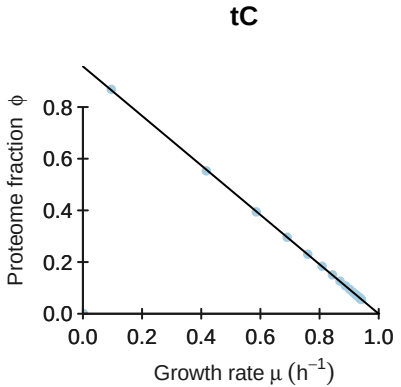
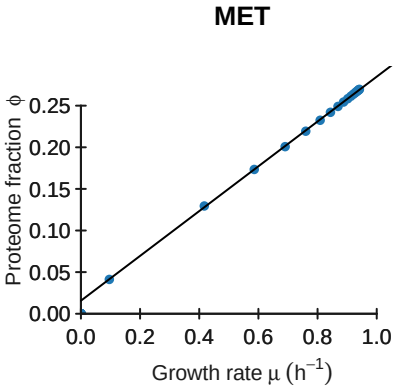
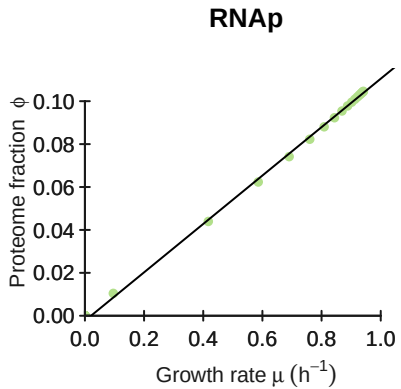

Growth rate μ (h^{-1})
Concentration x_C (g/L)

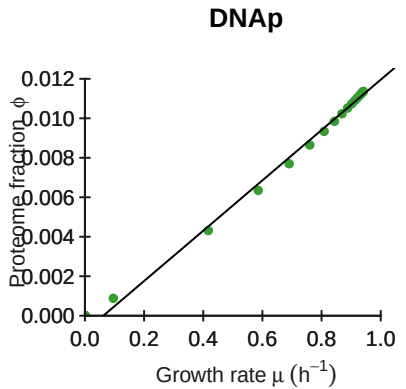

Internal concentrations c^{i} (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ATP
rRNA
DNA
p

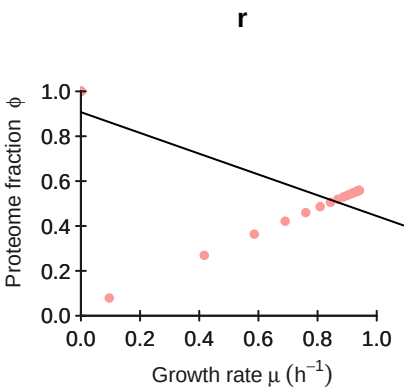

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
MET
RNAp
DNAp
r

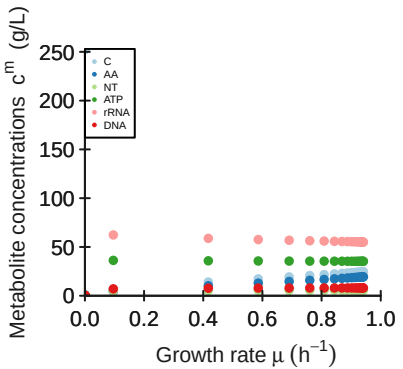

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

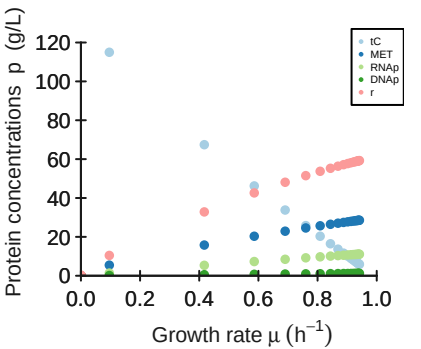

MET
Proteome fraction ϕ
Growth rate μ (h^{-1})

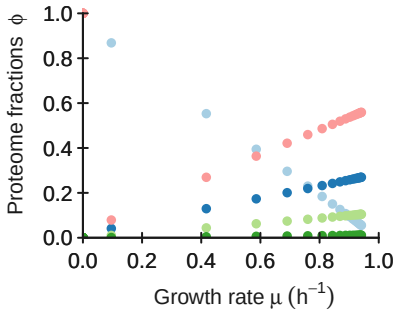

RNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

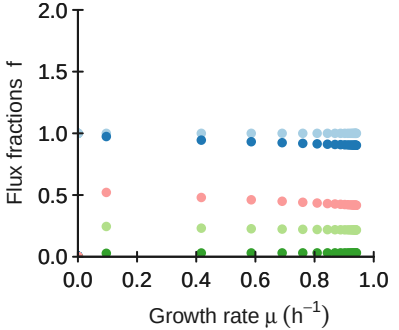

DNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

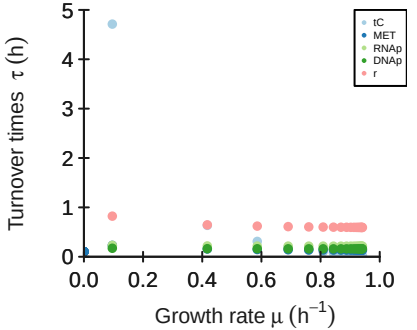

r
Proteome fraction ϕ
Growth rate μ (h^{-1})

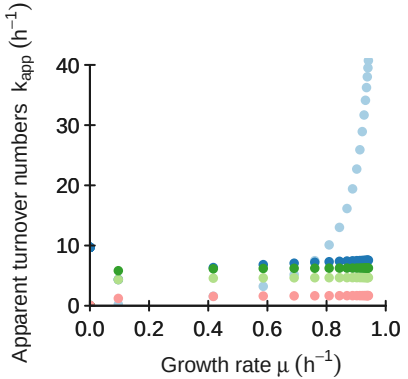

Metabolite concentrations c^{m} (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ATP
rRNA
DNA


Protein concentrations p (g/L)
Growth rate μ (h^{-1})
tC
MET
RNAp
DNAp
r

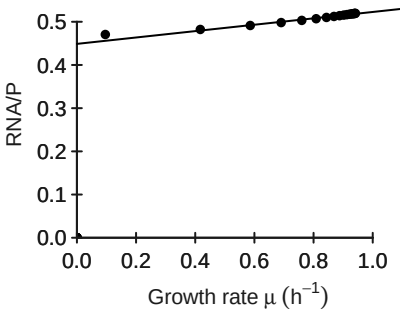




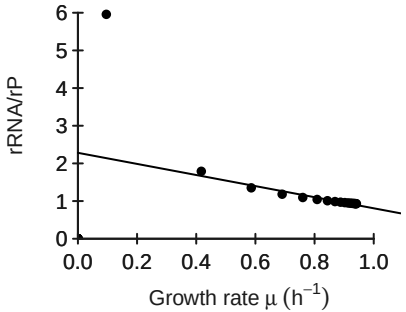




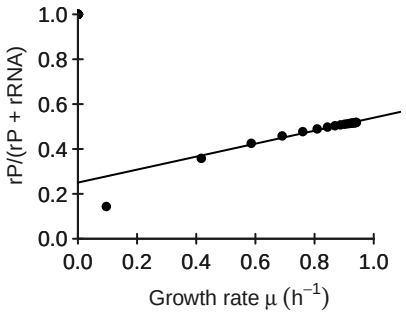
RNA/P



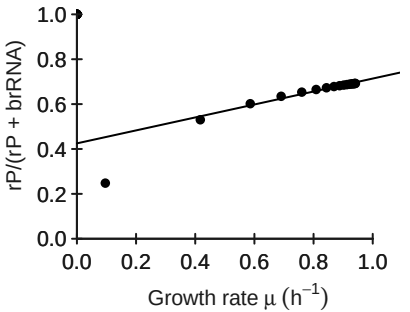
rRNA/rP

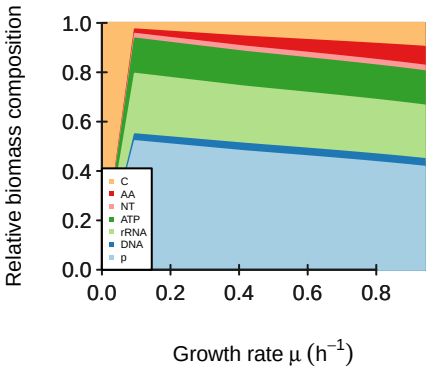


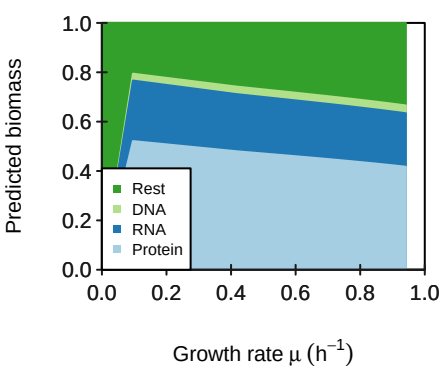
rP/(rP + rRNA)

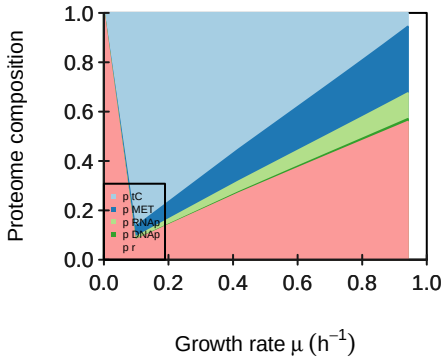


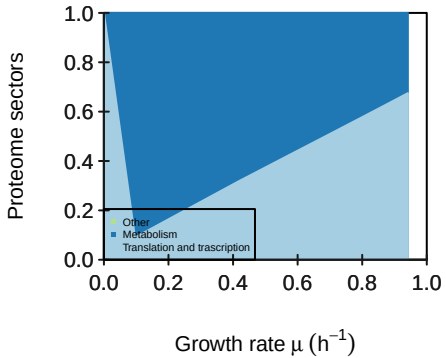
Protein mass fraction in ribosome








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	7	0	0	0
AA	0	0	0	0	3
NT	0	0	1	1	0
ATP	0	0	0	0	12
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	60
DNA	0	0	4	4	0
p	0	0	0	0	0

kcat

	tC	MET	RNAp	DNAp	r
kcatf	45.3	10	8.4	11.2	5.5
kcatb	5	1	1	1	1

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	90.6	1.42857142857143	8.4	11.2	0.152777777777778

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