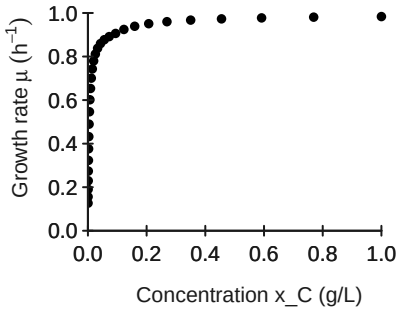
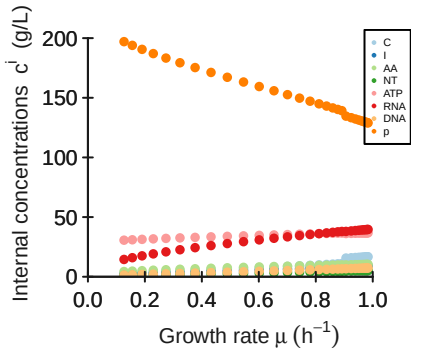
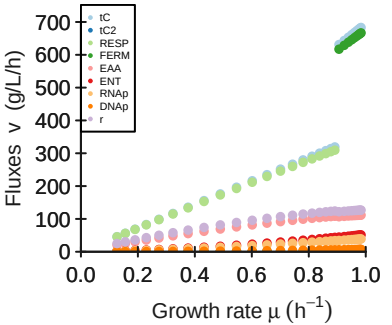
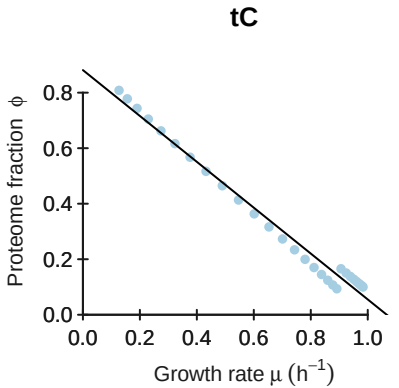
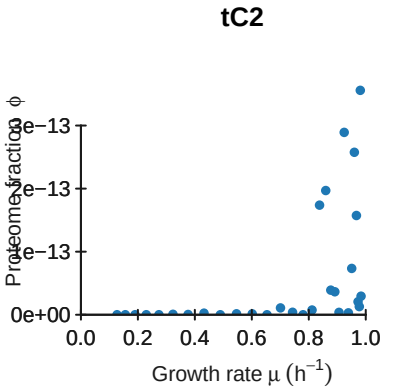
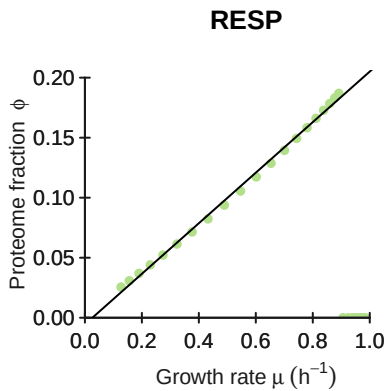

Growth rate μ (h^{-1})
Concentration x_C (g/L)

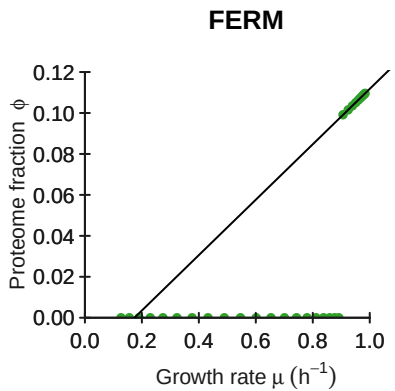

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
I
AA
NT
ATP
RNA
DNA
p

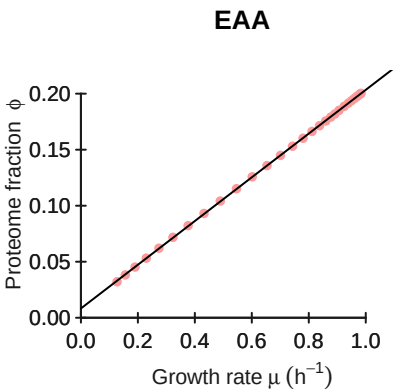

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
tC2
RESP
FERM
EAA
ENT
RNAp
DNAp
r

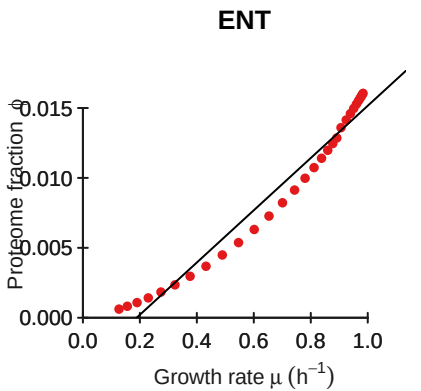

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

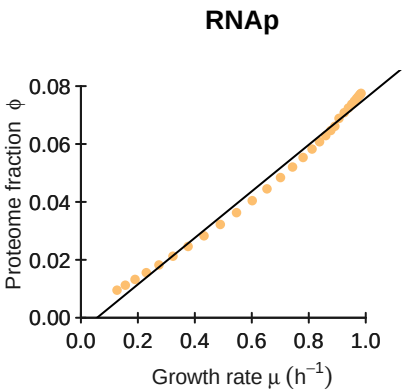

tC2
Proteome fraction ϕ
Growth rate μ (h^{-1})

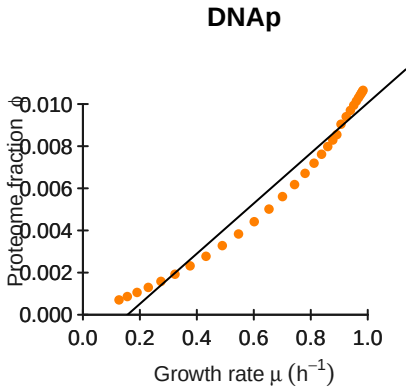

RESP
Proteome fraction ϕ
Growth rate μ (h^{-1})

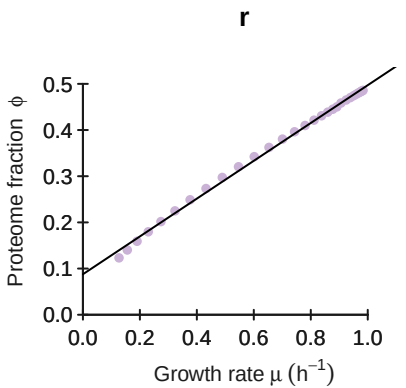

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

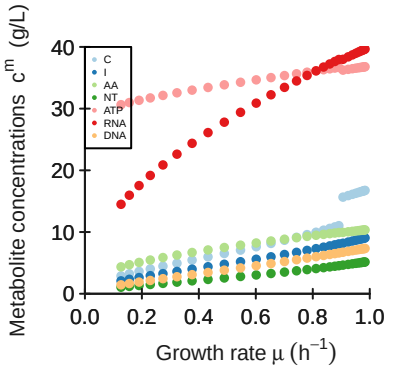

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

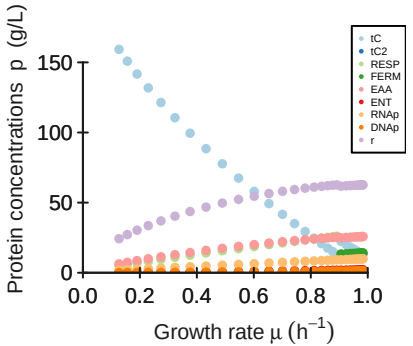

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

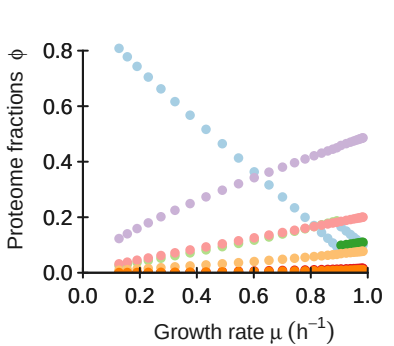

RNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

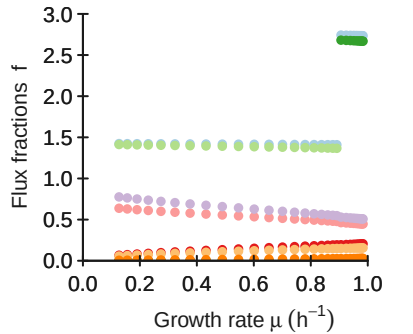

DNAp
Proteome fraction ϕ
0.000
0.002
0.004
0.006
0.008
0.010
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

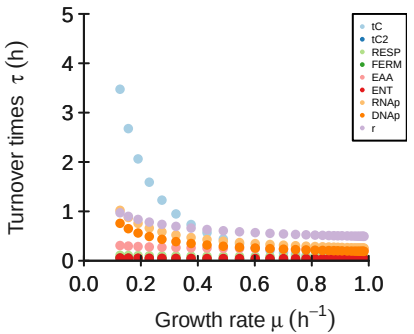

r
Proteome fraction ϕ
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

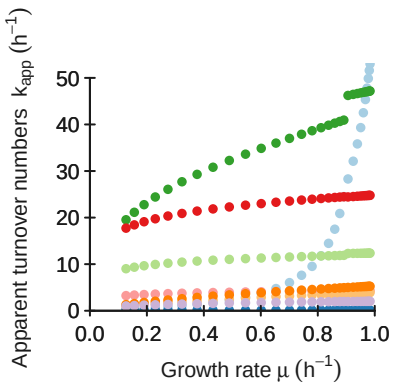

Metabolite concentrations cm (g/L)
C
I
AA
NT
ATP
RNA
DNA
0
10
20
30
40
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

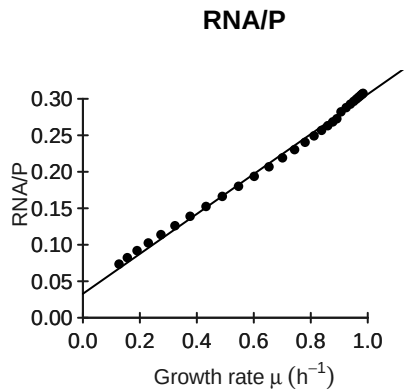

Protein concentrations p (g/L)
tC
tC2
RESP
FERM
EAA
ENT
RNAp
DNAp
r
0
50
100
150
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

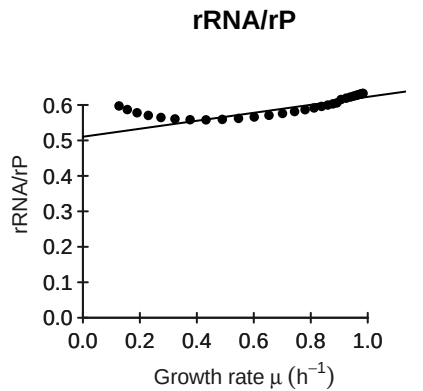

Proteome fractions ϕ
0.0
0.2
0.4
0.6
0.8
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

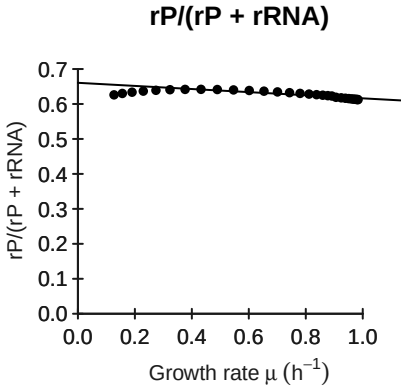

Flux fractions f
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

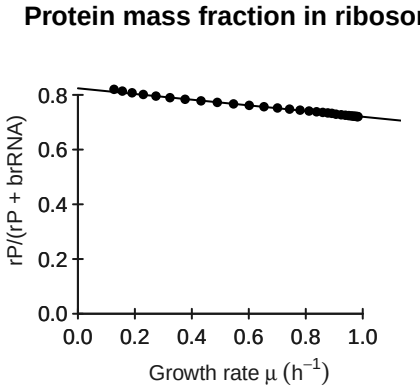

Turnover times τ (h)
tC
tC2
RESP
FERM
EAA
ENT
RNAp
DNAp
r
0
1
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

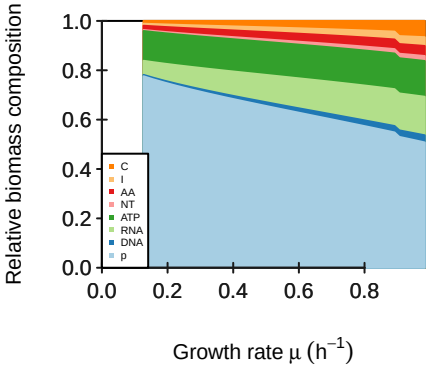

Apparent turnover numbers kapp (h−1)
0
10
20
30
40
50
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

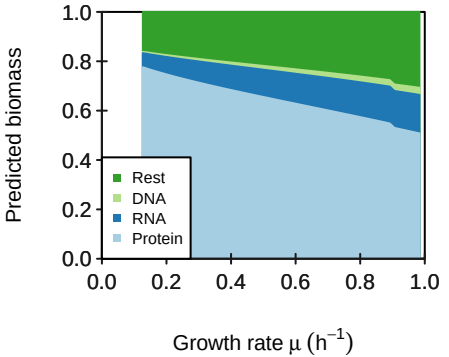

RNA/P
RNA/P
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

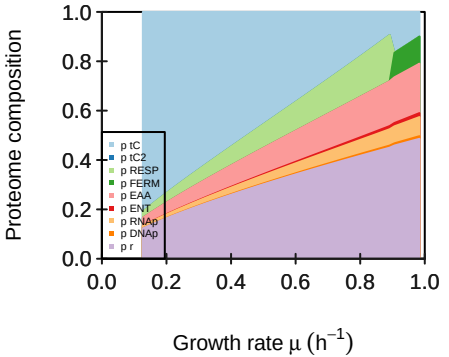

rRNA/rP
rRNA/rP
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

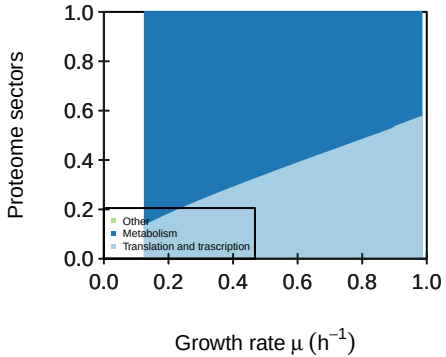

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h−1)


Relative biomass composition
C
I
AA
NT
ATP
RNA
DNA
p
Growth rate μ (h−1)


Predicted biomass
Rest
DNA
RNA
Protein
Growth rate μ (h−1)


Proteome composition
p tC
p tC2
p RESP
p FERM
p EAA
p ENT
p RNAp
p DNAp
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	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
C	1	1	−1	−1	0	0	0	0	0
I	0	0	0.5	0.25	−1	−0.9	0	0	0
AA	0	0	0	0	1	0	0	0	−0.8
NT	0	0	0	0	0	1	−1	−1	0
ATP	0	0	0.2	0.1	0	−0.1	0	0	−0.2
RNA	0	0	0	0	0	0	1	0	0
DNA	0	0	0	0	0	0	0	1	0
p	0	0	0	0	0	0	0	0	1

K

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0	0
x_W	0	0.1	0	0	0	0	0	0	0
C	0	0	1.4	7	0	0	0	0	0
I	0	0	0	0	1	1	0	0	0
AA	0	0	0	0	0	0	0	0	1
NT	0	0	0	0	0	0	1	1	0
ATP	0	0	0	0	0	12	0	0	12
RNA	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0	0	0

KA

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	0	0	25
DNA	0	0	0	0	0	0	4	4	0
p	0	0	0	0	0	0	0	0	0

kcat

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
kcatf	58.3	12.2	13.4	66.9	4.8	36.5	7.2	9.7	4.8
kcatb	0	0	0	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	0.06	0.005	0.065	0.004	0.248	0.035	0.119	0.003	0.461

average saturation input

3

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	0	0	0	0	0	0	0	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	0	0	0	0	0	0	0	0	0