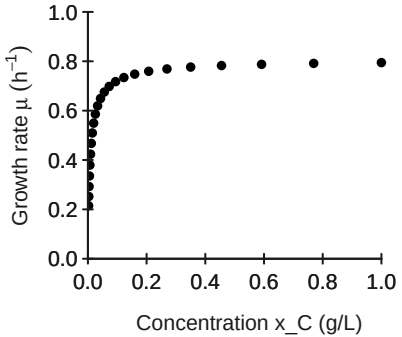
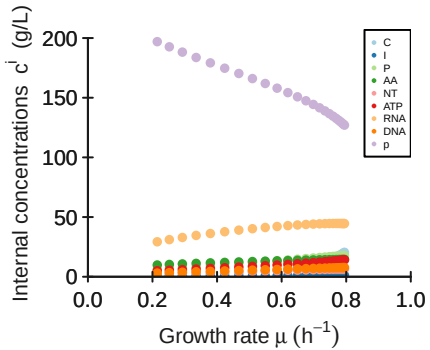
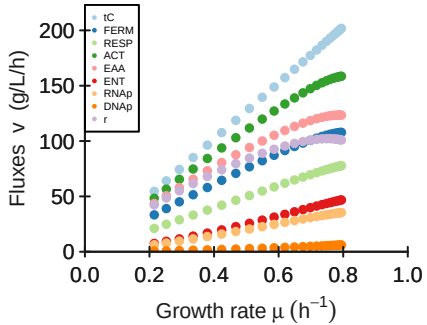
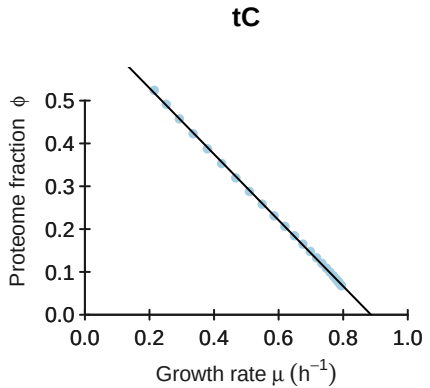
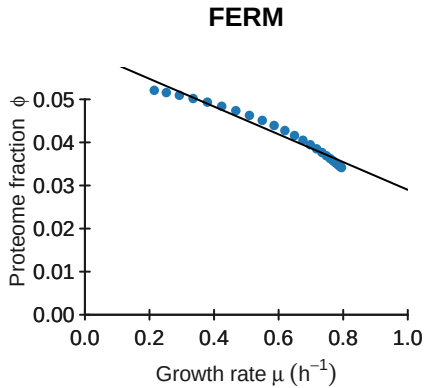
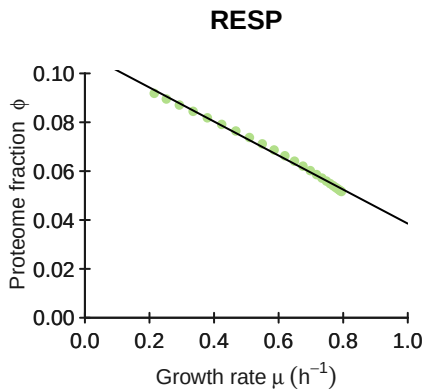

Growth rate μ (h^{-1})
Concentration x_C (g/L)

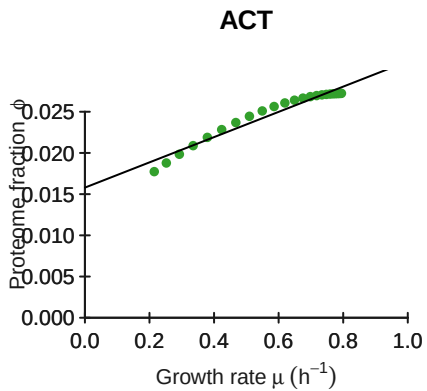

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
P
Pi
AA
NT
ATP
RNA
DNA
p

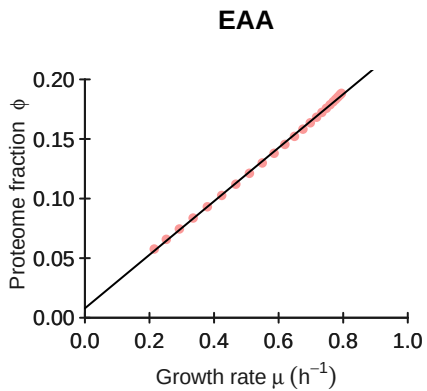

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
FERM
RESP
ACT
EAA
ENT
RNAp
DNAp
r

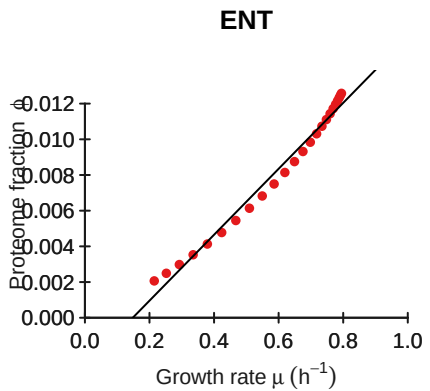

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

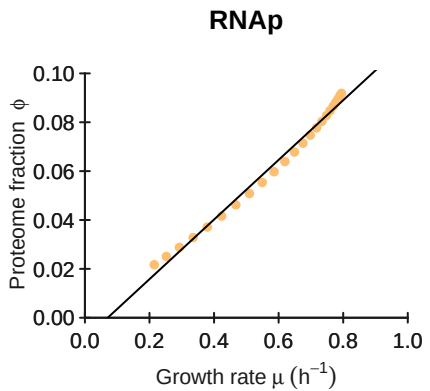

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

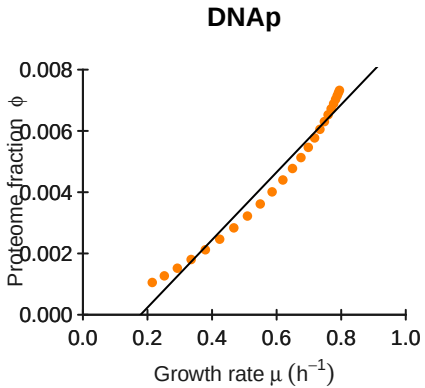

RESP
Proteome fraction ϕ
Growth rate μ (h^{-1})

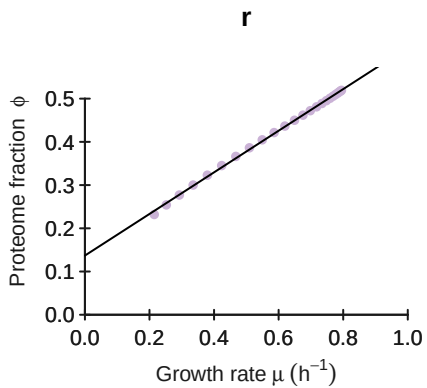

ACT
Proteome fraction ϕ
Growth rate μ (h^{-1})

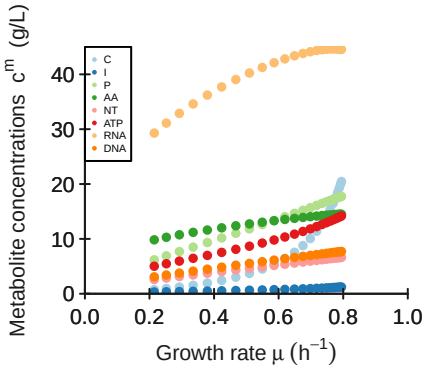

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

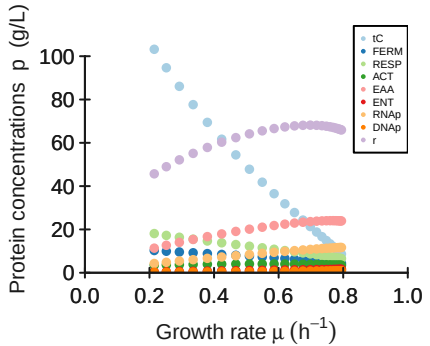

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

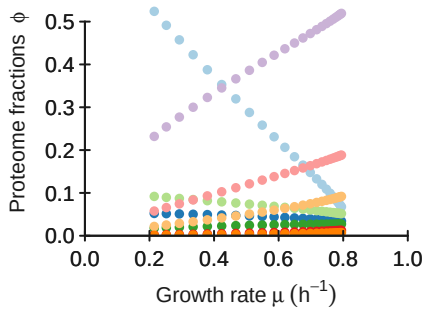

RNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

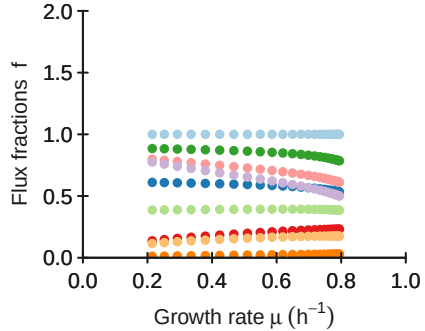

DNAp
Proteome fraction ϕ
Growth rate μ (h−1)

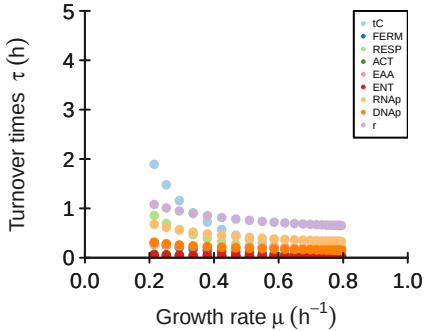

r
Proteome fraction ϕ
Growth rate μ (h−1)

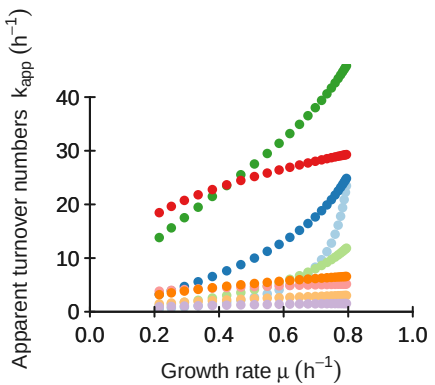

Metabolite concentrations cm (g/L)
C
I
P
AA
NT
ATP
RNA
DNA
Growth rate μ (h−1)

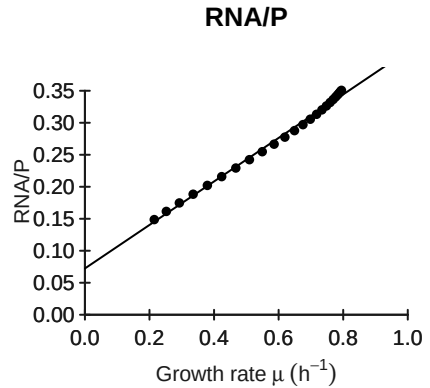

Protein concentrations p (g/L)
tC
FERM
RESP
ACT
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

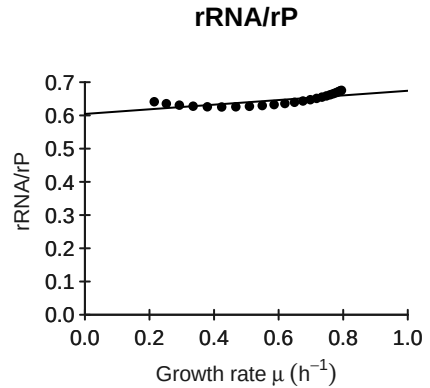

Proteome fractions ϕ
Growth rate μ (h−1)

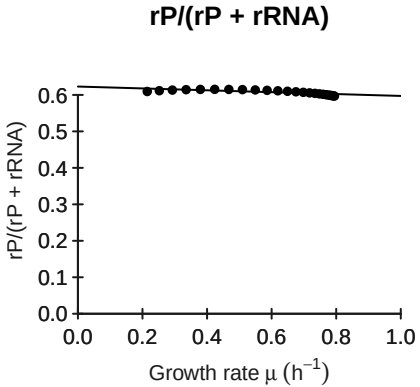

Flux fractions f
Growth rate μ (h−1)

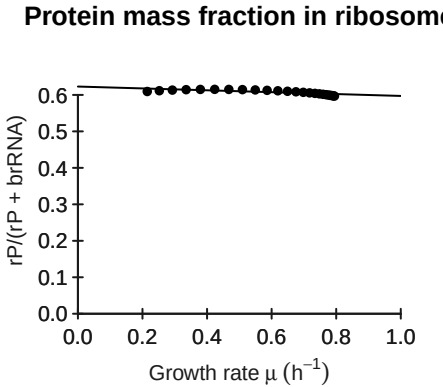

Turnover times τ (h)
tC
FERM
RESP
ACT
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

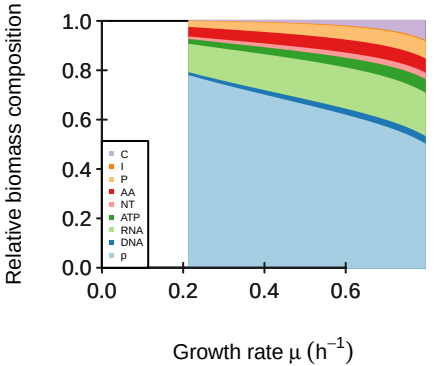

Apparent turnover numbers kapp (h−1)
Growth rate μ (h−1)

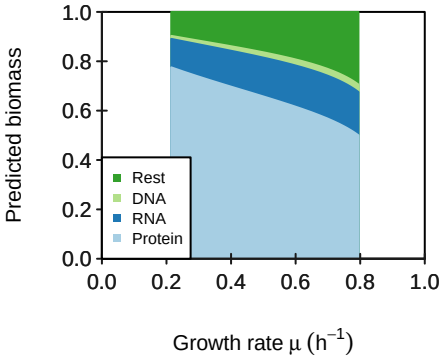

RNA/P
RNA/P
Growth rate μ (h−1)

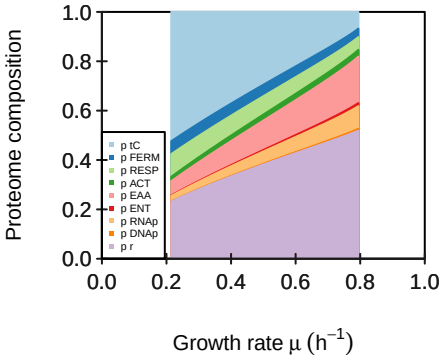

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

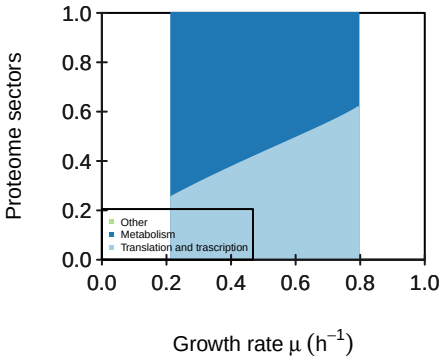

rP/(rP + rRNA)
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)


Protein mass fraction in ribosome
rP/(rP + brRNA)
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)


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


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


Proteome composition
0.0
0.2
0.4
0.6
0.8
1.0
p tC
p FERM
p RESP
p ACT
p EAA
p ENT
p RNAp
p DNAp
p r
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)


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

keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

	tC	FERM	RESP	ACT	EAA	ENT	RNAp	DNAp	r
C	1	−1	−1	0	0	0	0	0	0
I	0	0.6	0.2	−0.5	0	0	0	0	0
P	0	0	0	1	−1	−0.45	0	0	0
AA	0	0	0	0	1	−0.45	0	0	−0.9
NT	0	0	0	0	0	1	−1	−1	0
ATP	0	0.4	0.8	−0.5	0	−0.1	0	0	−0.1
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	FERM	RESP	ACT	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0	0
x_W	0	10	20	0	0	0	0	0	0
C	17	6	12	0	0	0	0	0	0
I	0	3	6	1	0	0	0	0	0
P	0	0	0	6	2	2	0	0	0
AA	0	0	0	0	8	3	0	0	3
NT	0	0	0	0	0	6	2	2	0
ATP	0	6	12	2	0	2	0	0	2
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	FERM	RESP	ACT	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
P	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	40
DNA	0	0	0	0	0	0	4	4	0
p	0	0	0	0	0	0	0	0	0

kcat

	tC	FERM	RESP	ACT	EAA	ENT	RNAp	DNAp	r
kcatf	29	61	30.5	115	7	45	6	13	4
kcatb	3	6	3	12	1	4	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	1643.33333333333	30.5	61	28.75	28	5.625	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	0.065	0.024	0.024	0.024	0.248	0.032	0.12	0.003	0.46

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