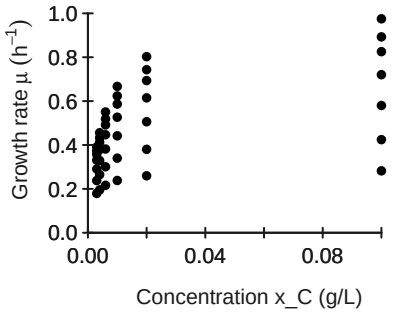
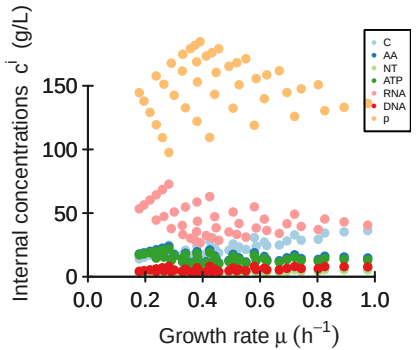
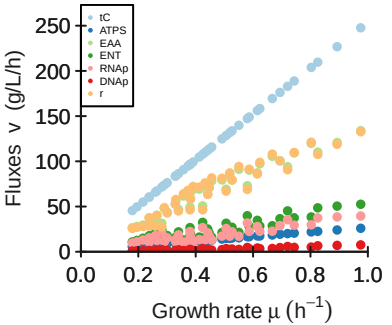
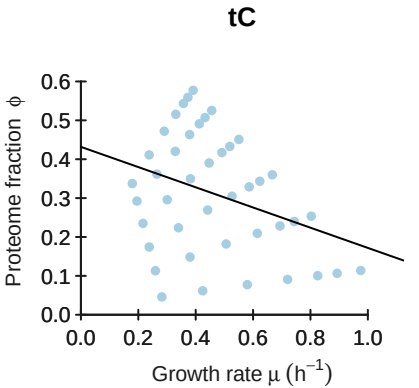
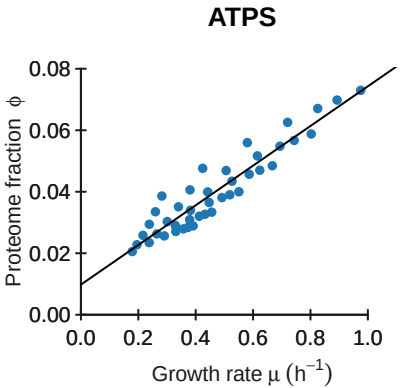
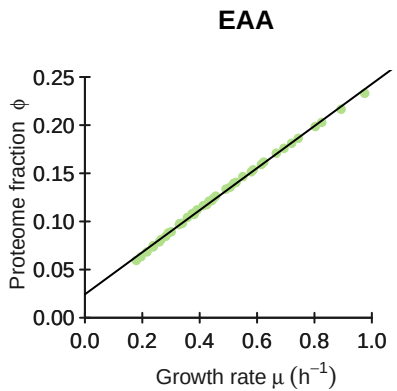

Growth rate μ (h^{-1})
Concentration x_C (g/L)

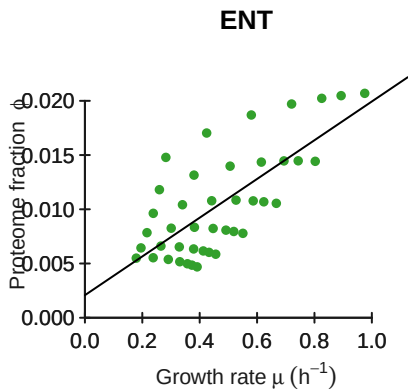

Internal concentrations c^i (g/L)
C
AA
NT
ATP
RNA
DNA
p
Growth rate μ (h^{-1})

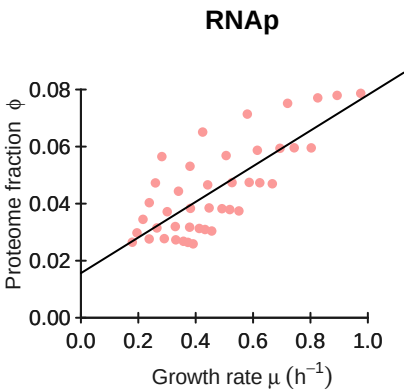

Fluxes v (g/L/h)
tC
ATPS
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h^{-1})

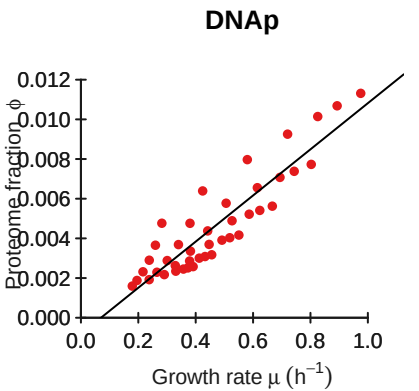

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

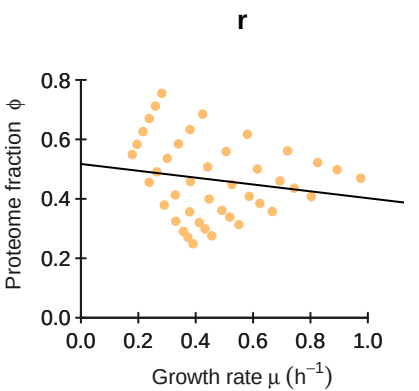

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

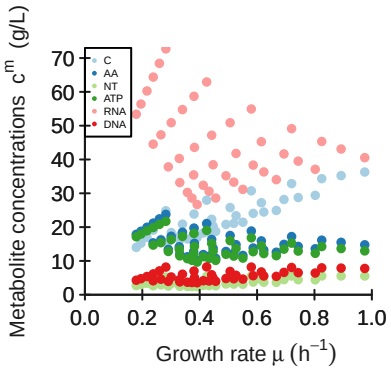

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

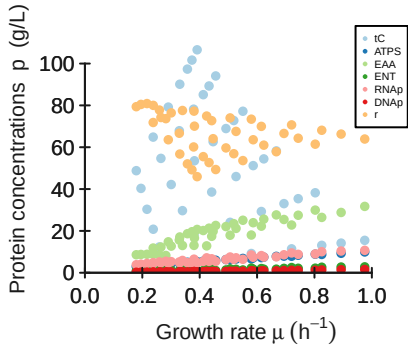

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

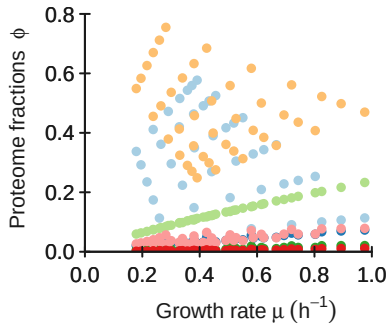

RNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

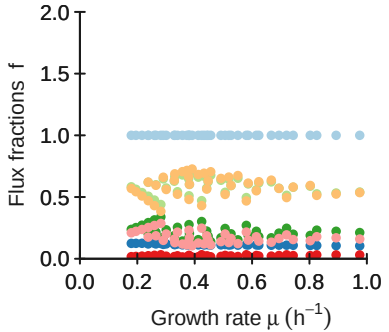

DNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

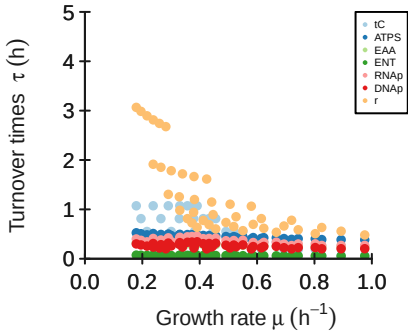

r
Proteome fraction ϕ
Growth rate μ (h^{-1})

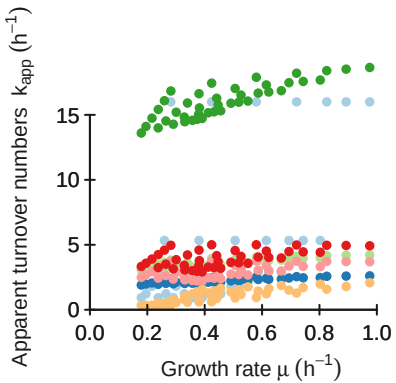

Metabolite concentrations c^m (g/L)
C
AA
NT
ATP
RNA
DNA
Growth rate μ (h^{-1})

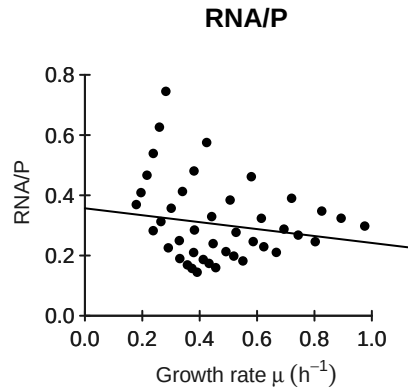

Protein concentrations p (g/L)
tC
ATPS
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h^{-1})

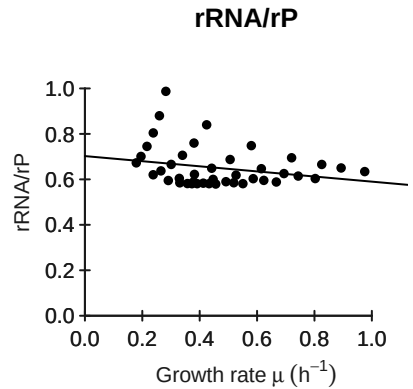

Proteome fractions ϕ
Growth rate μ (h^{-1})

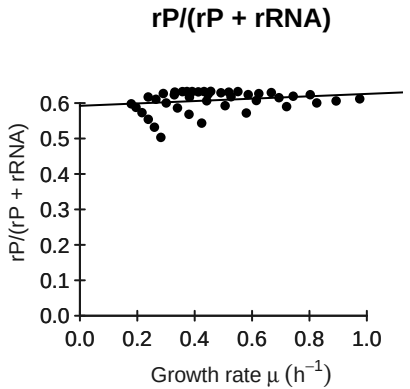

Flux fractions f
Growth rate μ (h^{-1})

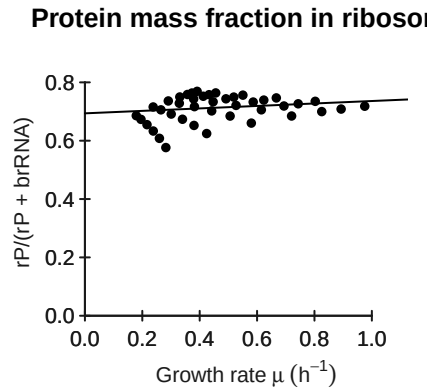

Turnover times τ (h)
tC
ATPS
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h^{-1})

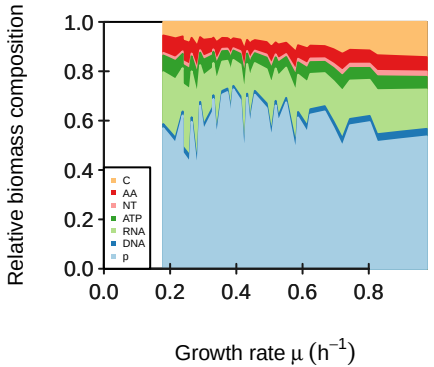

Apparent turnover numbers k_{app} (h^{-1})
Growth rate μ (h^{-1})

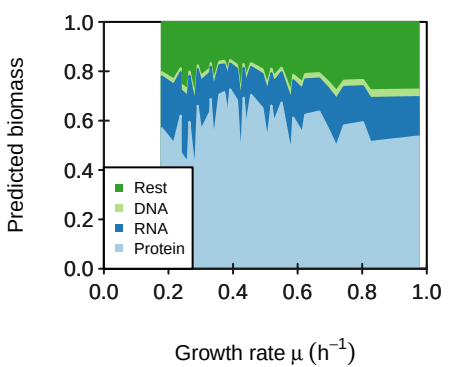

RNA/P
RNA/P
Growth rate μ (h^{-1})

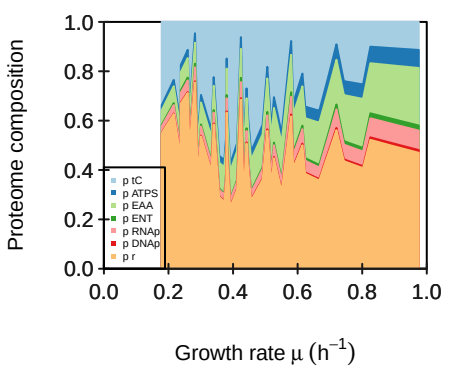

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

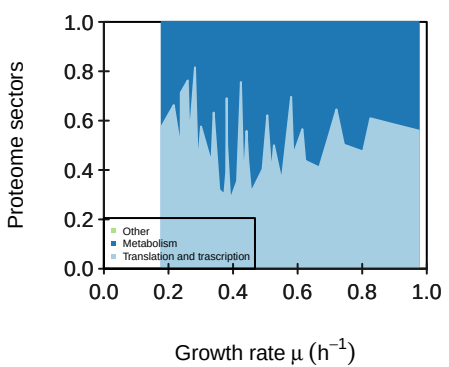

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})


Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})


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


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


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 ATPS
p EAA
p ENT
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	ATPS	EAA	ENT	RNAp	DNAp	r
C	1	−1	−1	−1	0	0	0
AA	0	0	1	0	0	0	−0.9
NT	0	0	0	1	−1	−1	0
ATP	0	1	0	0	0	0	−0.1
RNA	0	0	0	0	1	0	0
DNA	0	0	0	0	0	1	0
p	0	0	0	0	0	0	1

K

	tC	ATPS	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0
C	0	11	11	11	0	0	0
AA	0	0	0	0	0	0	2
NT	0	0	0	0	1	1	0
ATP	0	0	0	0	0	0	2
RNA	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0

KA

	tC	ATPS	EAA	ENT	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	25
DNA	0	0	0	0	4	4	0
p	0	0	0	0	0	0	0

kcat

	tC	ATPS	EAA	ENT	RNAp	DNAp	r
kcatf	32	3.4	5.5	24.3	6.6	8.8	4.4
kcatb	0	0	0	0	0	0	0

Keq

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

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
[1,]	0.065	0.069	0.248	0.035	0.119	0.003	0.461

average saturation input

3

minimal phi constraint

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

minimal f constraint

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