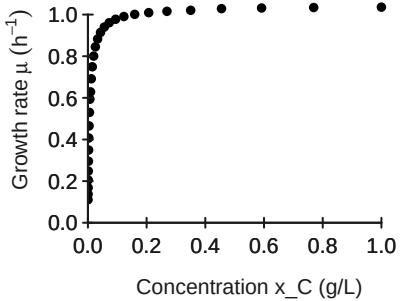
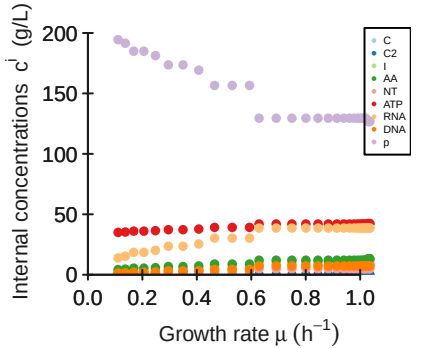
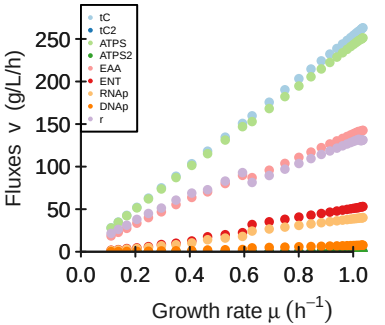
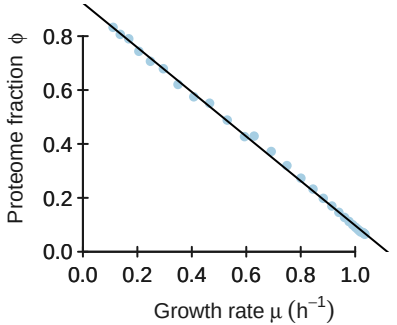


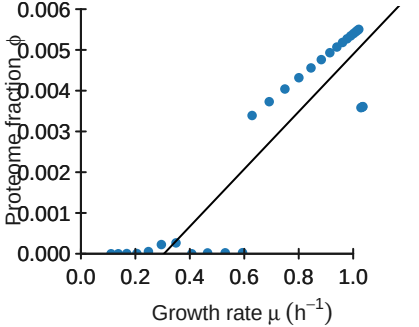




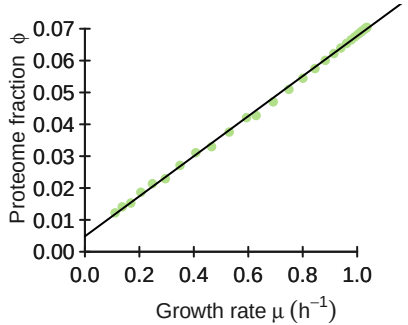
tC



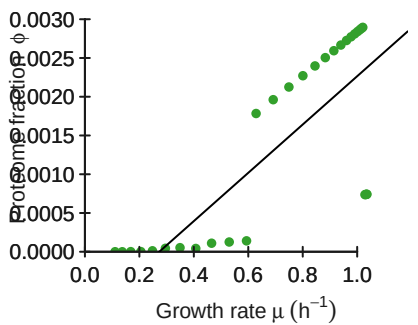
tC2



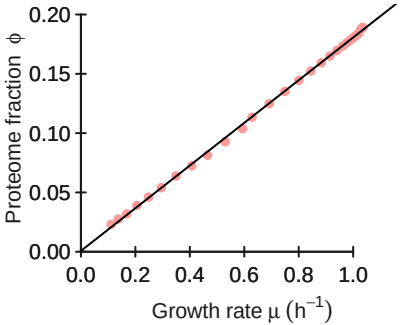
ATPS



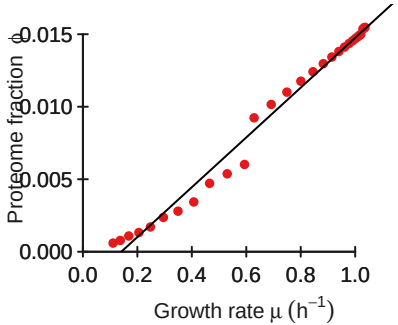
ATPS2



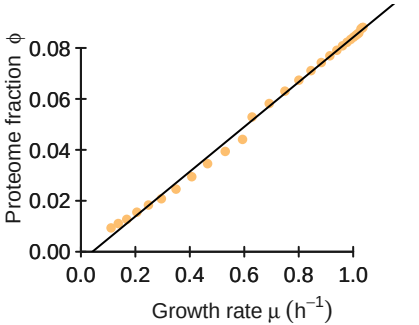
EAA

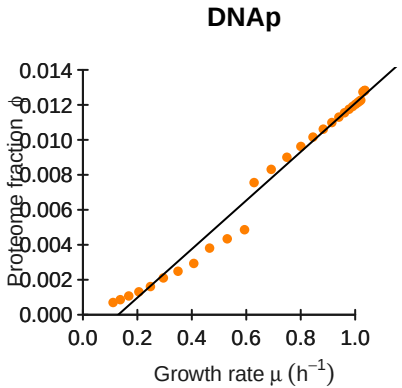


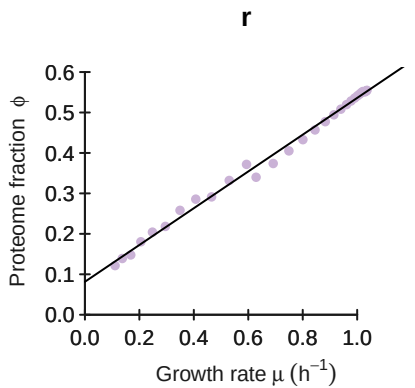
ENT

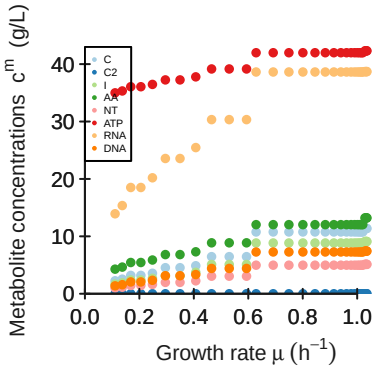


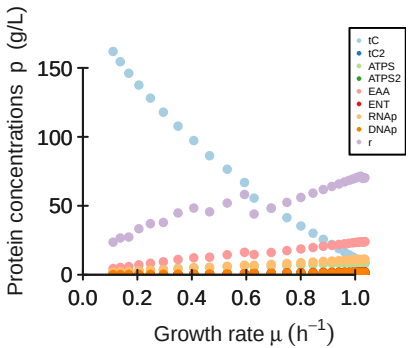
RNAp

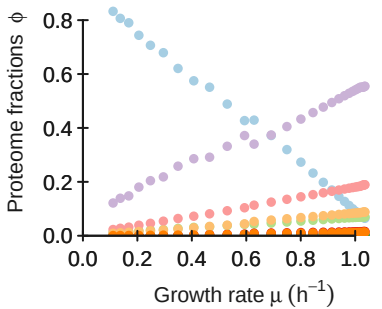


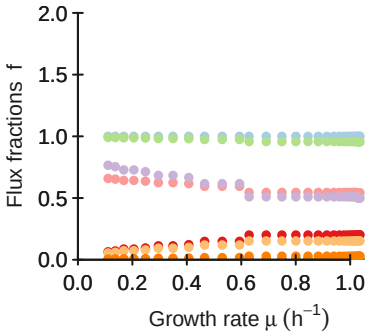

DNAp
Proteome fraction ϕ
Growth rate μ (h−1)

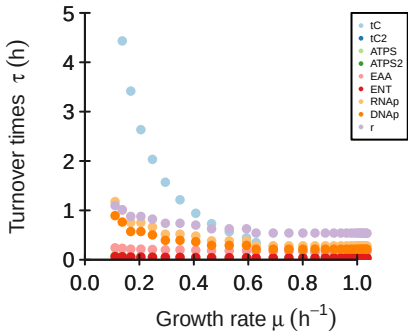

r
Proteome fraction ϕ
Growth rate μ (h−1)

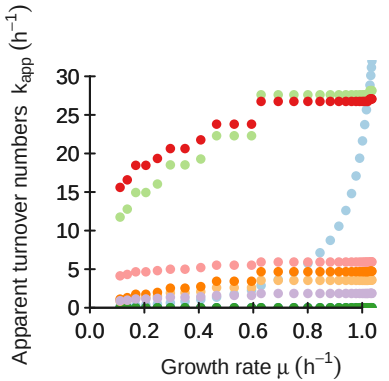

Metabolite concentrations cm (g/L)
C
C2
I
AA
NT
ATP
RNA
DNA
Growth rate μ (h−1)

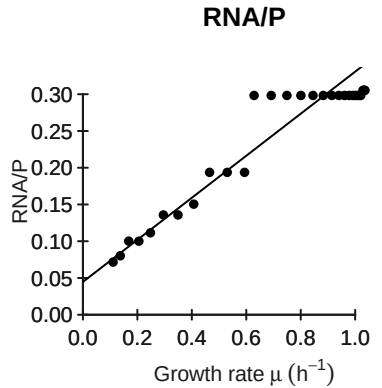

Protein concentrations p (g/L)
tC
tC2
ATPS
ATPS2
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

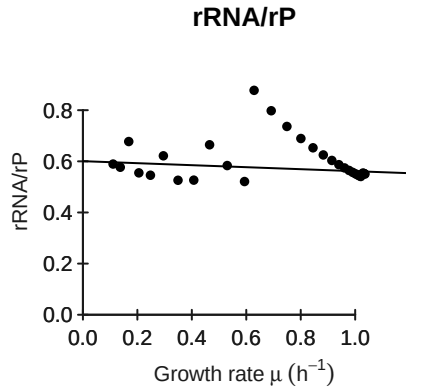

Proteome fractions ϕ
Growth rate μ (h−1)

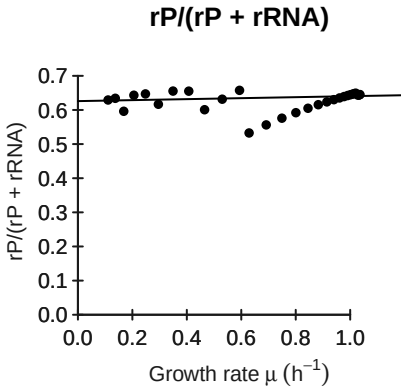

Flux fractions f
Growth rate μ (h−1)

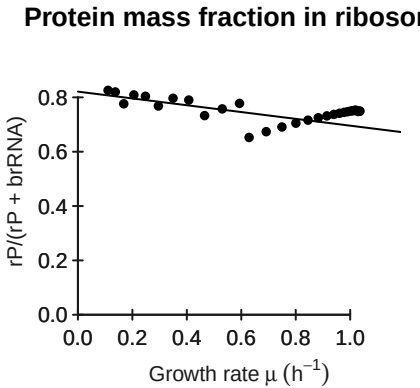

Turnover times τ (h)
tC
tC2
ATPS
ATPS2
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

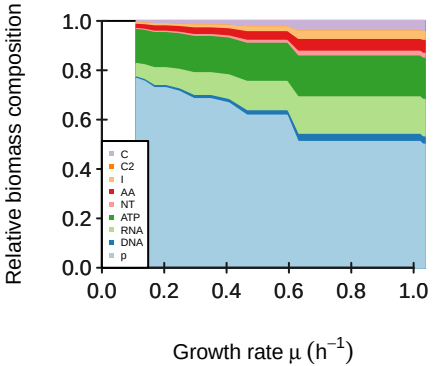

Apparent turnover numbers kapp (h−1)
Growth rate μ (h−1)

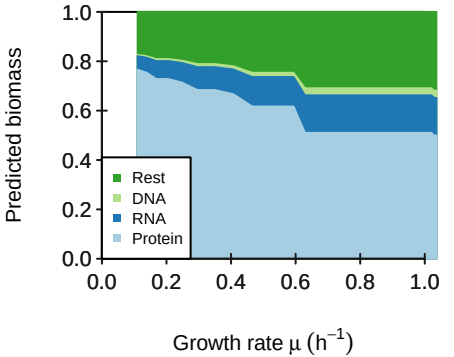

RNA/P
RNA/P
Growth rate μ (h−1)

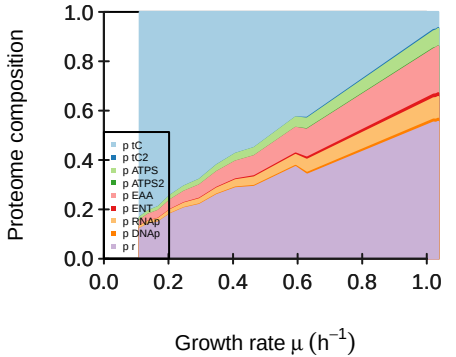

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

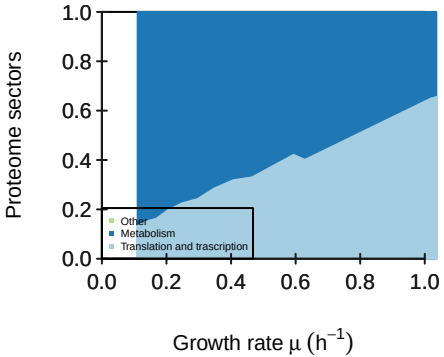

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


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


Relative biomass composition
C
C2
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 ATPS
p ATPS2
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	ATPS	ATPS2	EAA	ENT	RNAp	DNAp	r
C	1	0	−1	0	0	0	0	0	0
C2	0	1	0	−1	0	0	0	0	0
I	0	0	0.7	0.7	−1	−0.45	0	0	0
AA	0	0	0	0	1	−0.45	0	0	−0.8
NT	0	0	0	0	0	1	−1	−1	0
ATP	0	0	0.3	0.3	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	ATPS	ATPS2	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0	0
x_C2	0	0.1	0	0	0	0	0	0	0
C	0	0	6	0	0	0	0	0	0
C2	0	0	0	1	0	0	0	0	0
I	0	0	0	0	1	1	0	0	0
AA	0	0	0	0	0	1	0	0	1
NT	0	0	0	0	0	0	1	1	0
ATP	0	0	0	0	0	14	0	0	14
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	ATPS	ATPS2	EAA	ENT	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0	0	0
x_C2	0	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0	0
C2	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	ATPS	ATPS2	EAA	ENT	RNAp	DNAp	r
kcatf	35.2	11	43	11	6.6	43	6.6	8.7	4.4
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,]	0.065	0.001	0.067	0.001	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