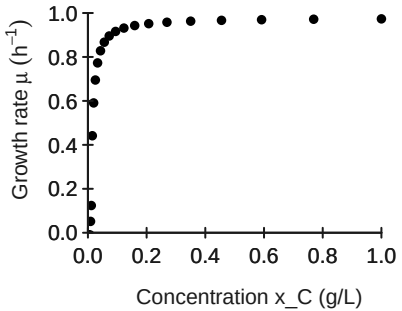
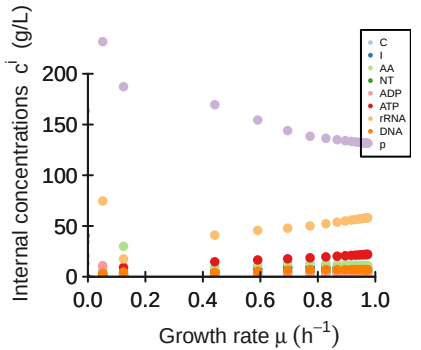
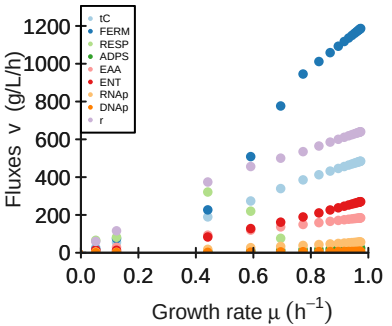
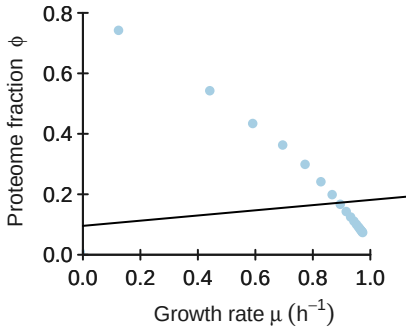


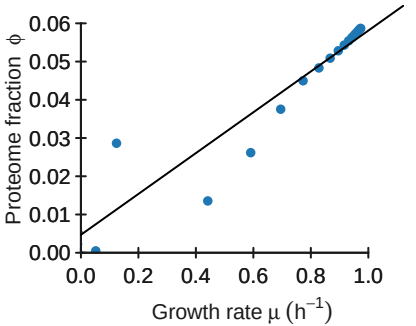




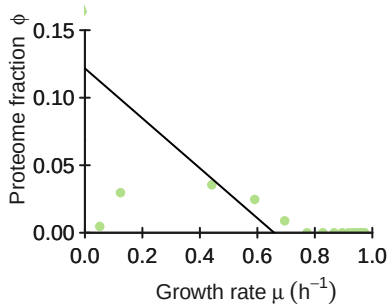
tC



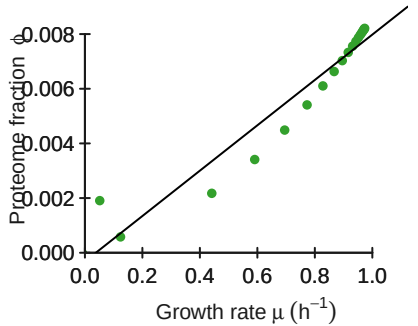
FERM



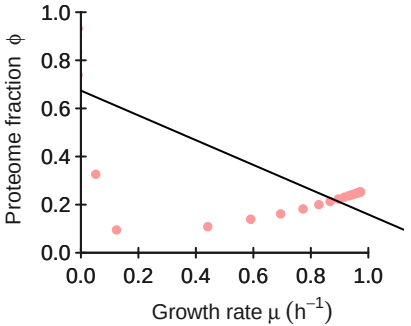
RESP



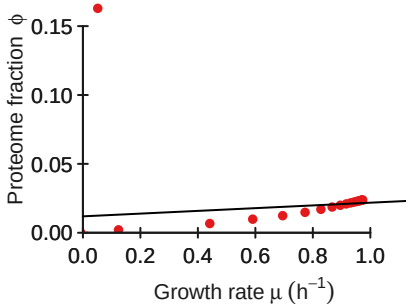
ADPS



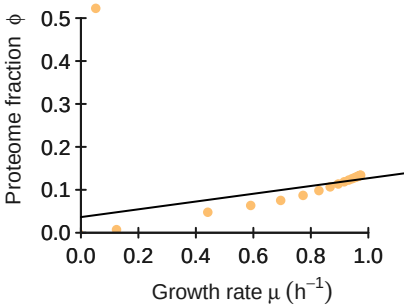
EAA

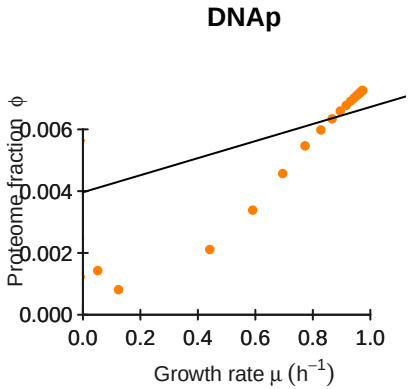


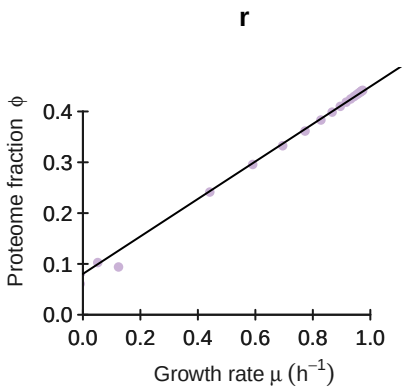
ENT

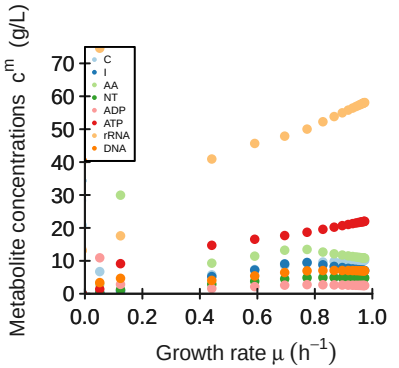


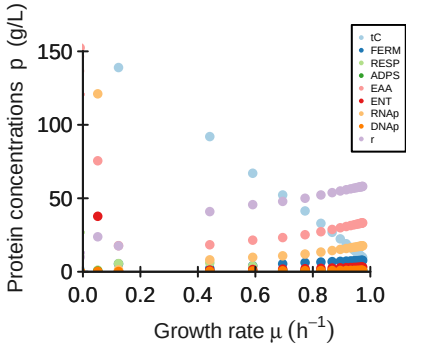
RNAp

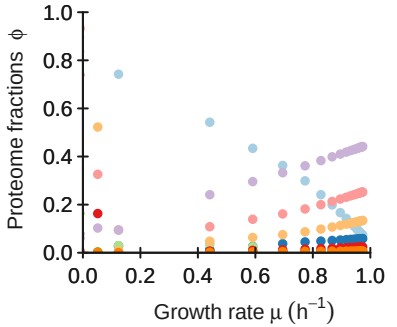


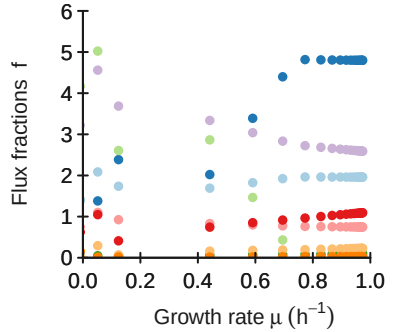

DNAp
Proteome fraction ϕ
0.000
0.002
0.004
0.006
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

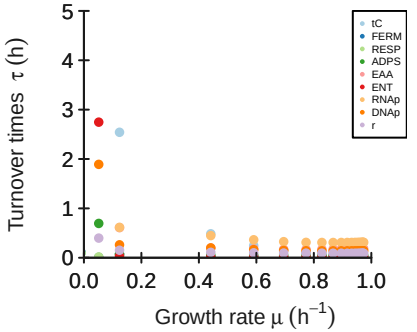

r
Proteome fraction ϕ
0.0
0.1
0.2
0.3
0.4
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

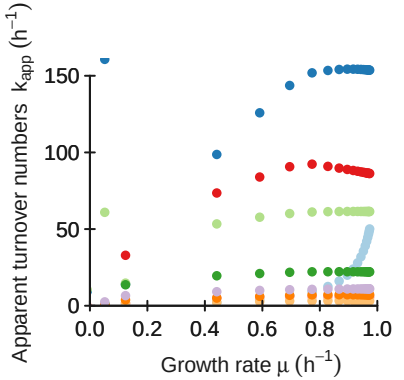

Metabolite concentrations cm (g/L)
C
I
AA
NT
ADP
ATP
rRNA
DNA
0 10 20 30 40 50 60 70
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

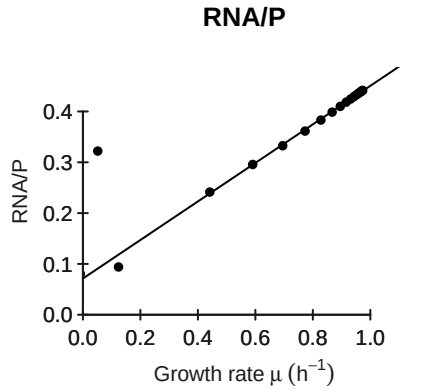

Protein concentrations p (g/L)
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
0 50 100 150
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

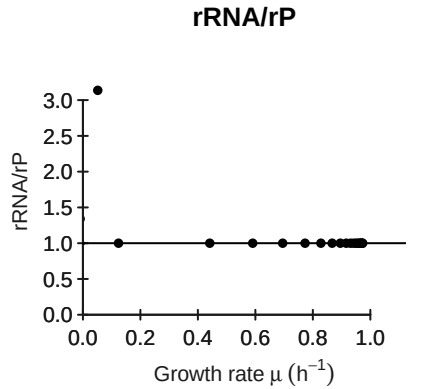

Proteome fractions ϕ
0.0 0.2 0.4 0.6 0.8 1.0
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

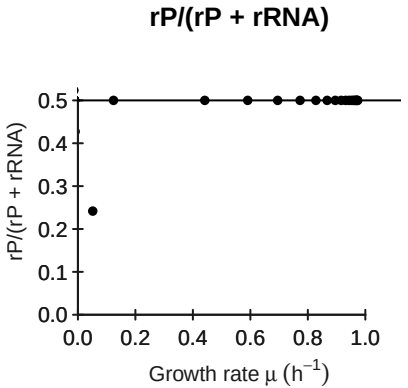

Flux fractions f
0 1 2 3 4 5 6
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

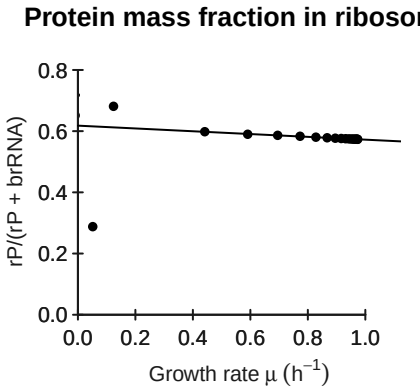

Turnover times τ (h)
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
0 1 2 3 4 5
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

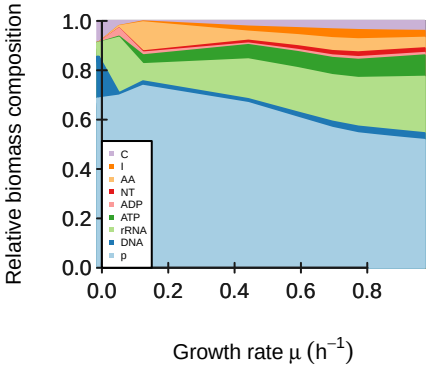

Apparent turnover numbers kapp (h−1)
0 50 100 150
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

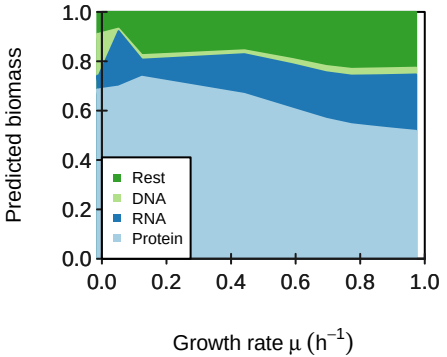

RNA/P
RNA/P
0.0 0.1 0.2 0.3 0.4
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

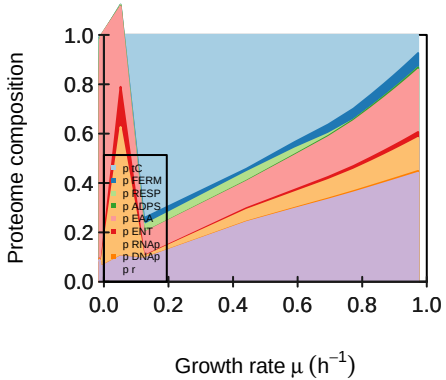

rRNA/rP
rRNA/rP
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

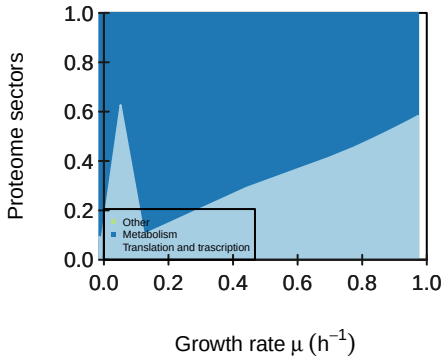

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


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


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


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


Proteome composition
p TC
p FERM
p RESP
p ADPS
p AAA
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	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
C	1	−0.4	−0.3	0	0	0	0	0	0
I	0	0.2	0.2	0	−1	−0.17	0	0	0
AA	0	0	0	0	1	−0.17	0	0	−0.2
NT	0	0	0	−1	0	0.34	−1	−1	0
ADP	0	−0.6	−0.7	1	0	0.66	0	0	0.8
ATP	0	0.6	0.7	0	0	−0.66	0	0	−0.8
rRNA	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	0.2

K

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0	0
x_W	0	10	2	0	0	0	0	0	0
C	0	8	1.6	0	0	0	0	0	0
I	0	0	0	0	2	2	0	0	0
AA	0	0	0	0	0	2	0	0	2
NT	0	0	0	1	0	0	1	1	0
ADP	0	1	0.2	0	0	0	0	0	0
ATP	0	0	0	0	0	3	0	0	3
rRNA	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	GLY	RESP	ADPS	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
ADP	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	20
DNA	0	0	0	0	0	0	4	4	0
p	0	0	0	0	0	0	0	0	0

kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	55.7	384.1	76.8	27.3	7.4	149.1	6.3	13.7	20
kcatb	6	38	8	3	1	15	1	1	2

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	92.8333333333333	12.6348684210526	60	9.1	3.7	0.828333333333333	6.3	13.7	1.66666666666667

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	0.065	0.035	0.035	0.003	0.248	0.032	0.119	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