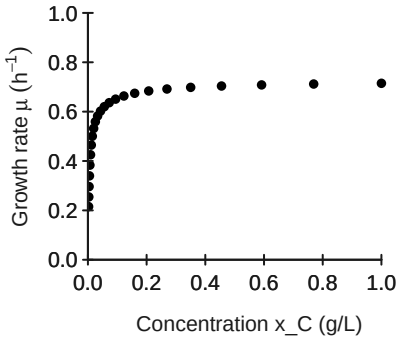
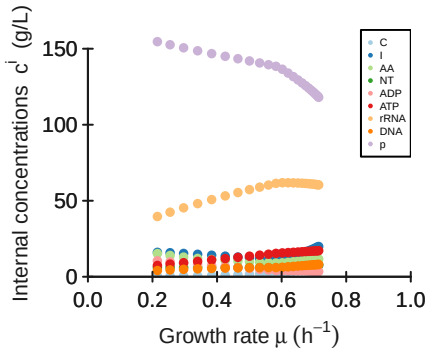
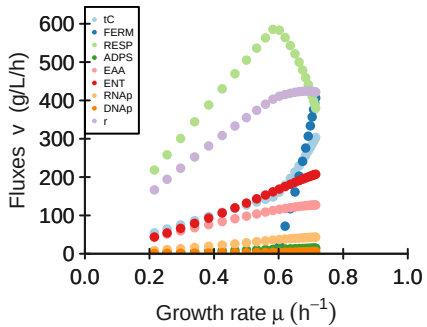
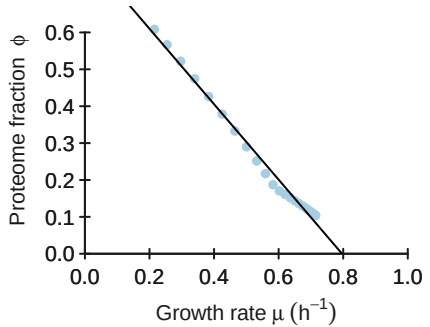


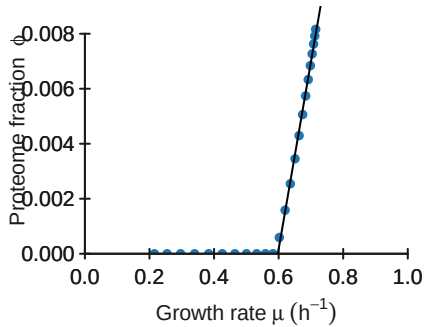




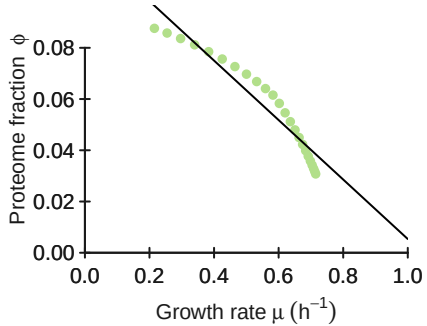
tC



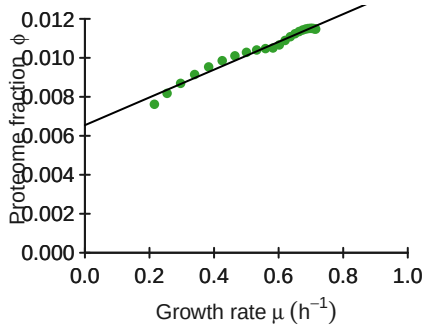
FERM



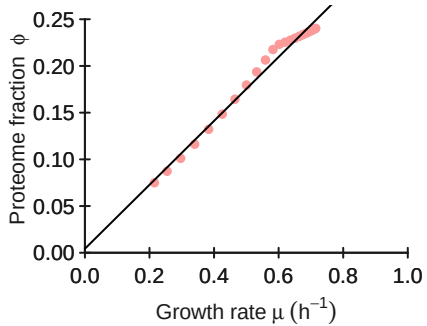
RESP



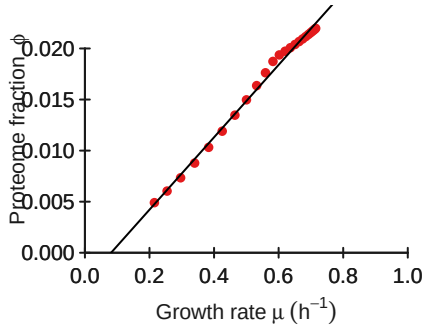
ADPS



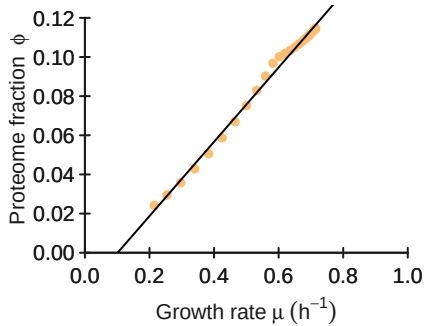
EAA

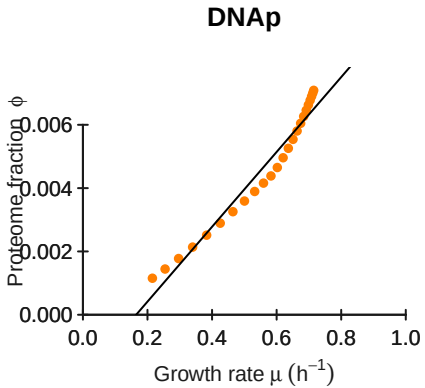


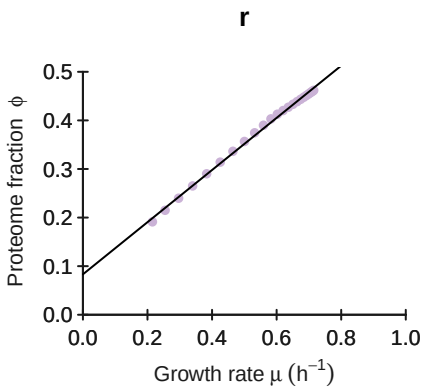
ENT

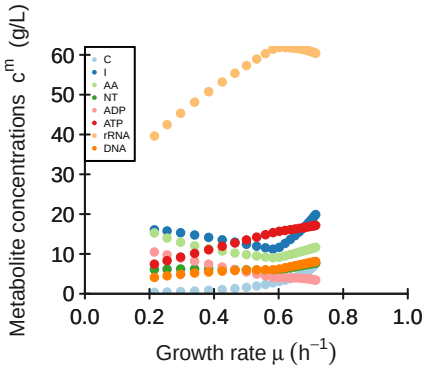


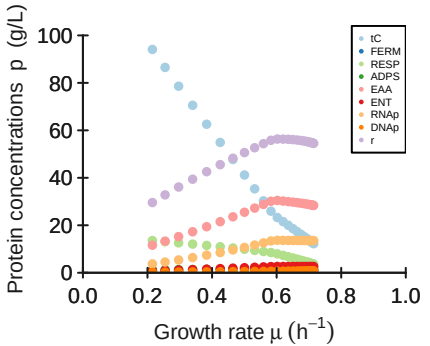
RNAp

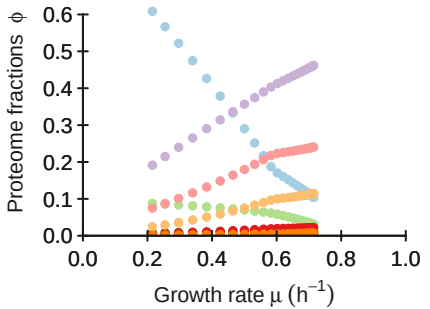


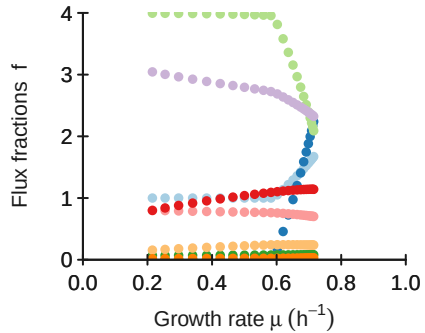

DNAp
Proteome fraction ϕ
0.000
0.002
0.004
0.006
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

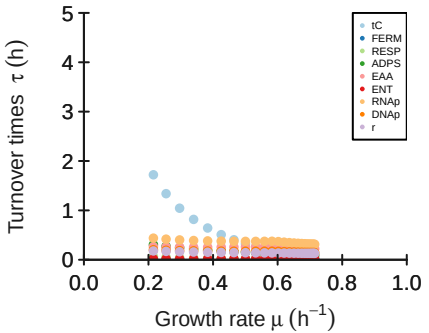

r
Proteome fraction ϕ
0.0 0.1 0.2 0.3 0.4 0.5
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

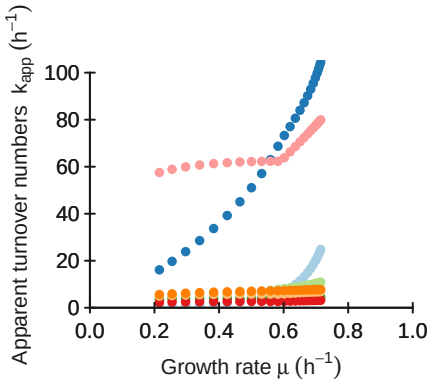

Metabolite concentrations cm (g/L)
0 10 20 30 40 50 60
C
I
AA
NT
ADP
ATP
rRNA
DNA
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

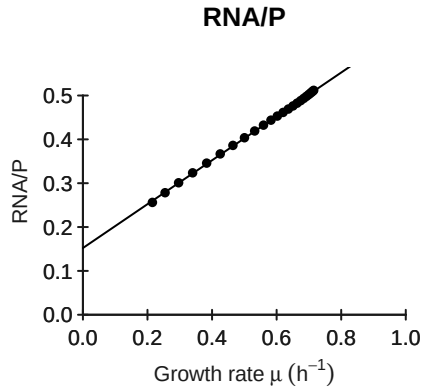

Protein concentrations p (g/L)
0 20 40 60 80 100
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

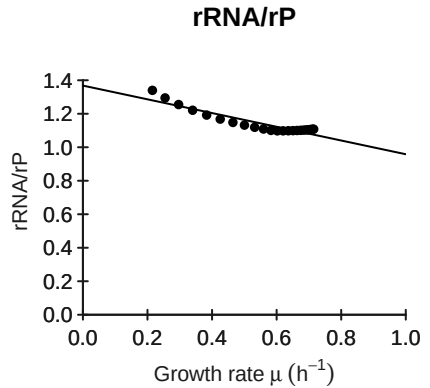

Proteome fractions ϕ
0.0 0.1 0.2 0.3 0.4 0.5 0.6
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

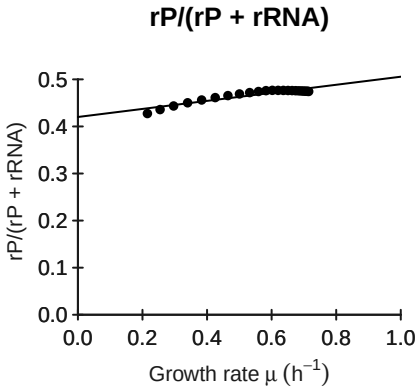

Flux fractions f
0 1 2 3 4
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

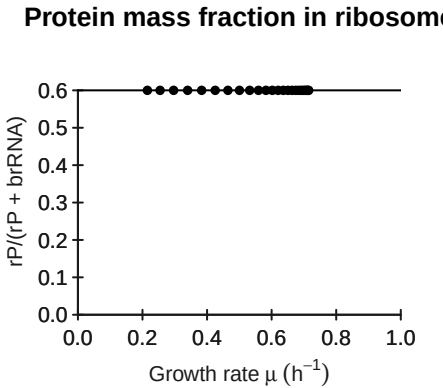

Turnover times τ (h)
0 1 2 3 4 5
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

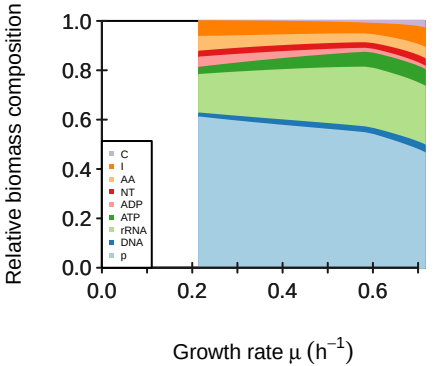

Apparent turnover numbers kapp (h−1)
0 20 40 60 80 100
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

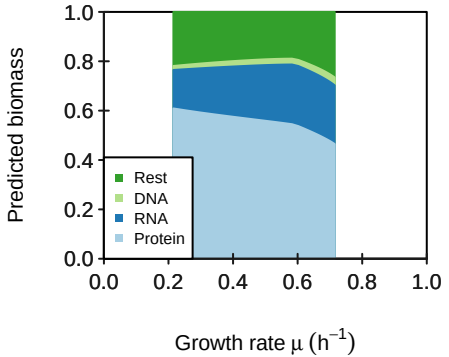

RNA/P
RNA/P
0.0 0.1 0.2 0.3 0.4 0.5
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

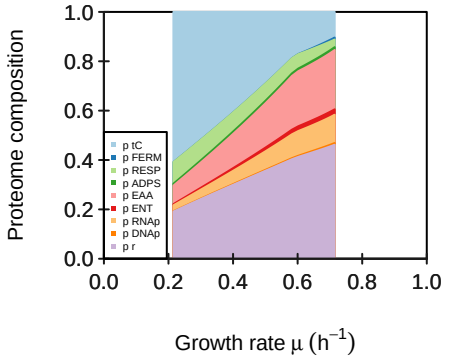

rRNA/rP
rRNA/rP
0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4
0.0 0.2 0.4 0.6 0.8 1.0
Growth rate μ (h−1)

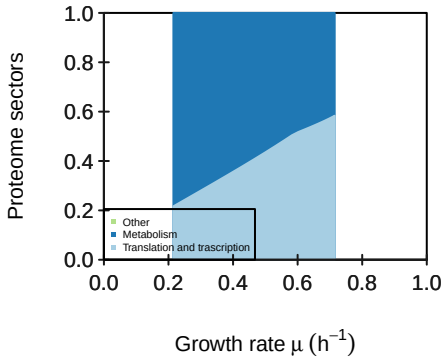

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


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 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	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
C	1	−0.5	−0.25	0	0	0	0	0	0
I	0	0.2	0.25	0	−1	−0.167	0	0	0
AA	0	0	0	0	1	−0.167	0	0	−0.2
NT	0	0	0	−1	0	0.334	−1	−1	0
ADP	0	−0.5	−0.75	1	0	0.666	0	0	0.8
ATP	0	0.5	0.75	0	0	−0.666	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	0	0	0	0	0	0	0	0
C	12	2	4	0	0	0	0	0	0
I	0	5	10	0	4	4	0	0	0
AA	0	0	0	0	8	3	0	0	3
NT	0	0	0	2	0	6	2	2	0
ADP	0	0.5	1	1	0	1	0	0	0
ATP	0	4	8	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	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	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	29	1095	365	26	7	149	6	13	19
kcatb	3	110	36	3	1	15	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	1160	199.090909090909	202.777777777778	4.33333333333333	14	1.65555555555556	Inf	Inf	Inf

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