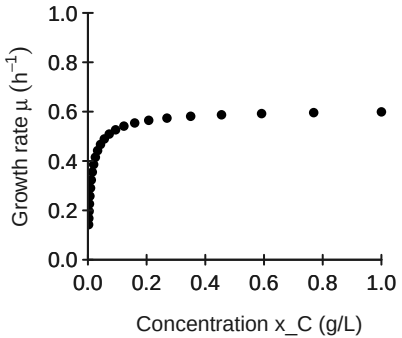
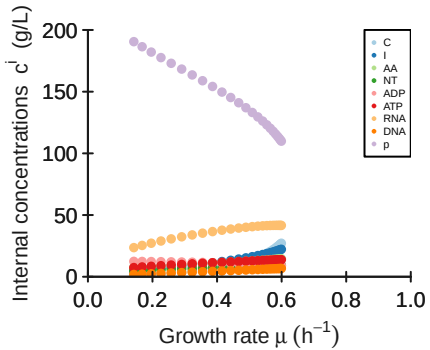
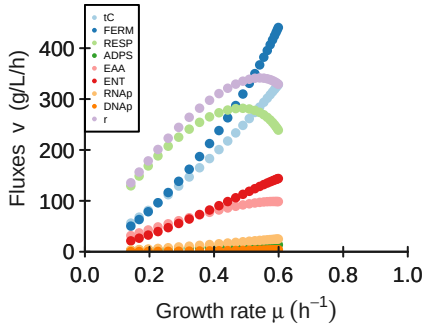
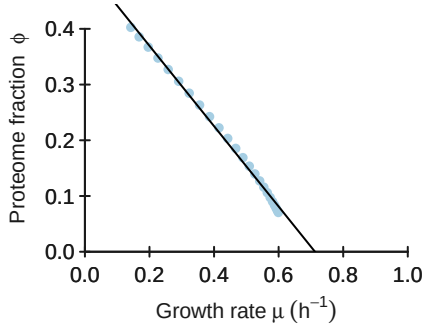


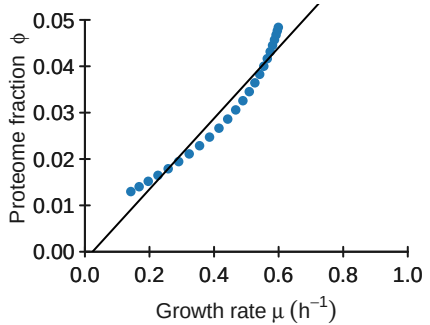




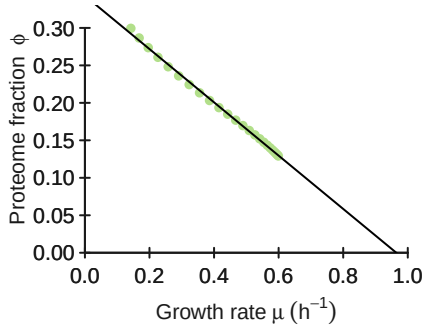
tC



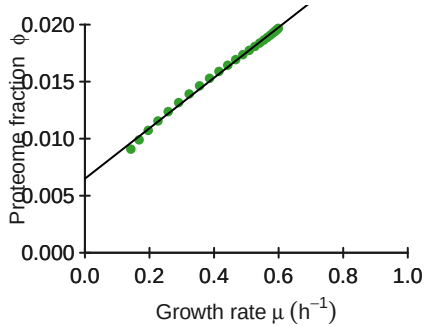
FERM



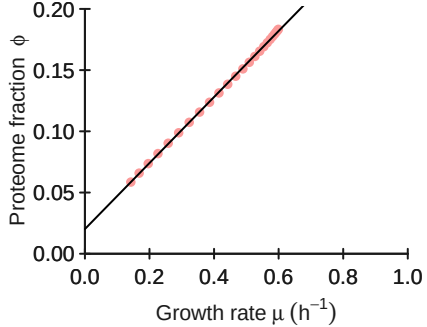
RESP



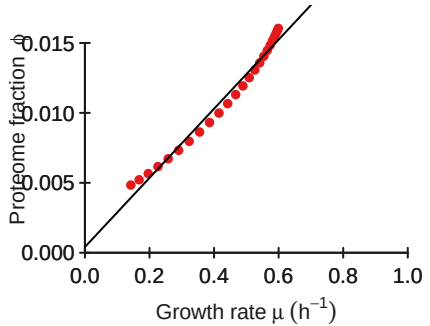
ADPS



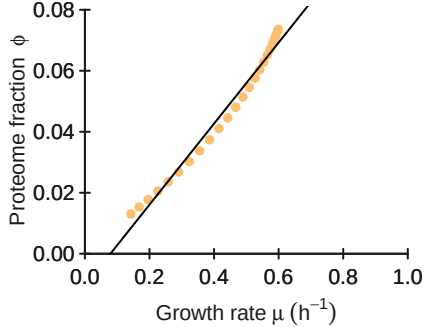
EAA

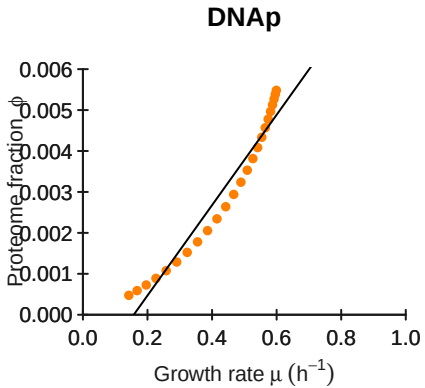


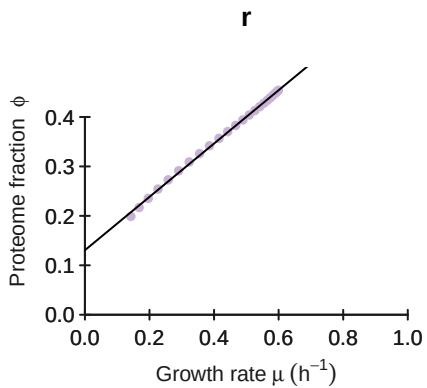
ENT

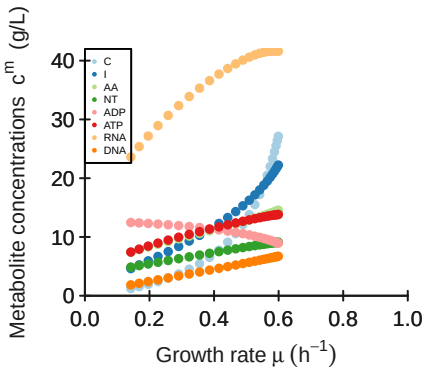


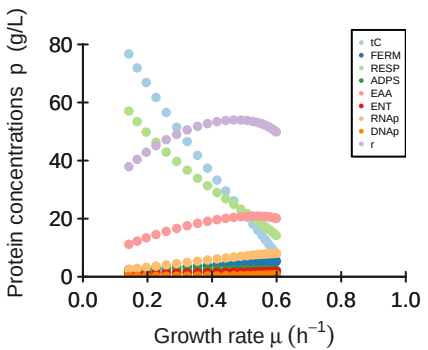
RNAp

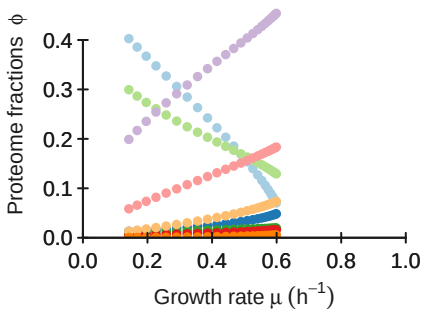


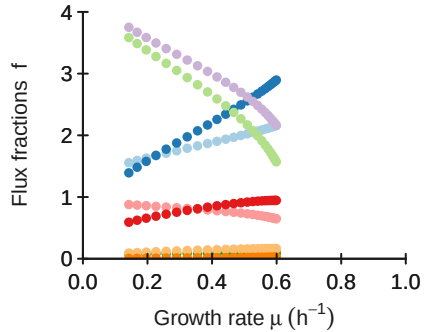

DNAp
Proteome fraction ϕ
Growth rate μ (h−1)

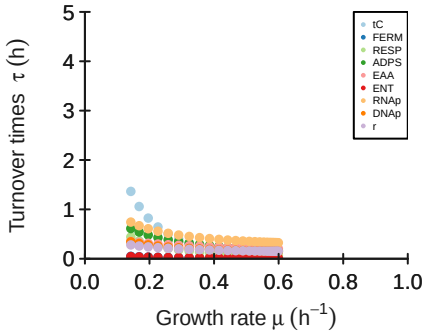

r
Proteome fraction ϕ
Growth rate μ (h−1)

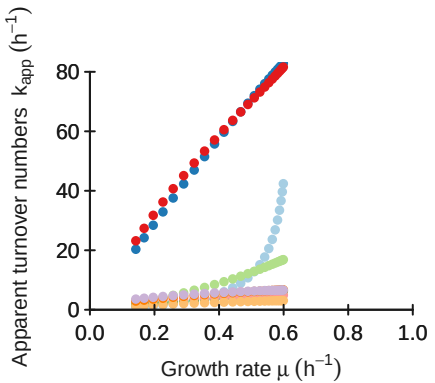

Metabolite concentrations cm (g/L)
C
I
AA
NT
ADP
ATP
RNA
DNA
Growth rate μ (h−1)

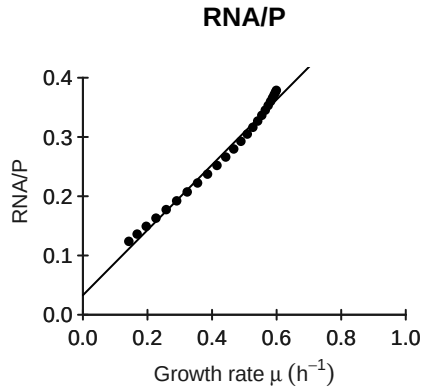

Protein concentrations p (g/L)
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

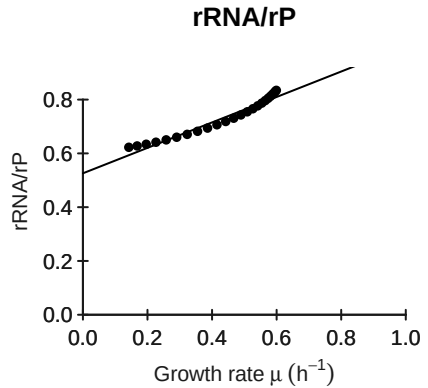

Proteome fractions ϕ
Growth rate μ (h−1)

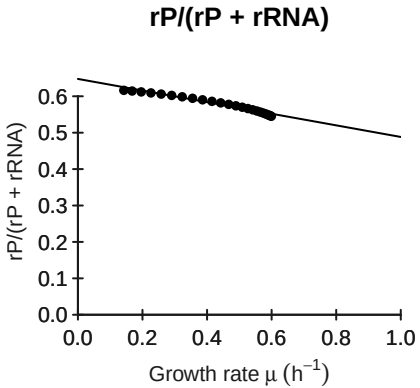

Flux fractions f
Growth rate μ (h−1)

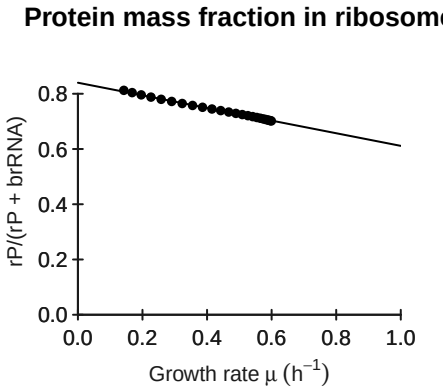

Turnover times τ (h)
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

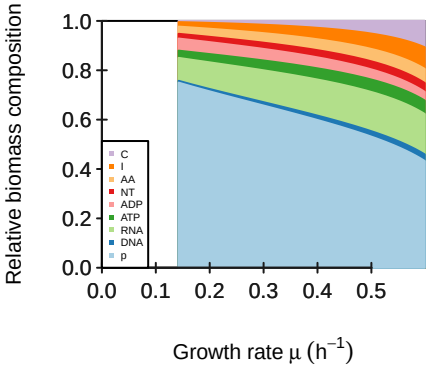

Apparent turnover numbers kapp (h−1)
Growth rate μ (h−1)

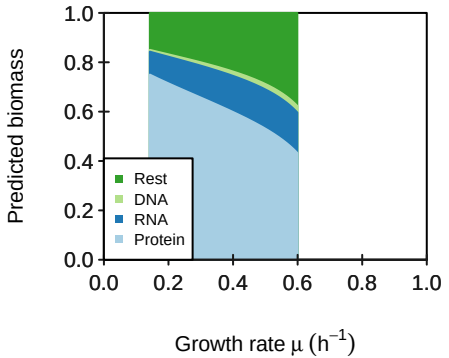

RNA/P
RNA/P
Growth rate μ (h−1)

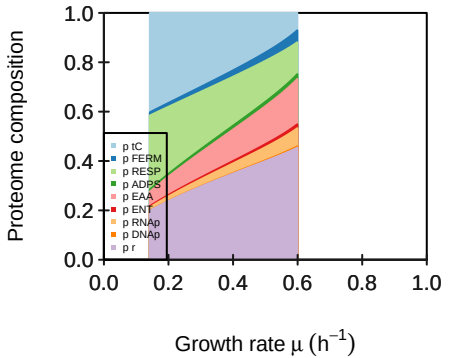

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

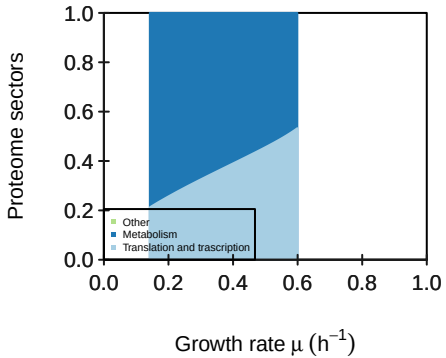

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


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


Relative biomass composition
C
I
AA
NT
ADP
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 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	−0.6	−0.2	0	0	0	0	0	0
I	0	0.2	0.2	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	−0.4	−0.8	1	0	0.666	0	0	0.8
ATP	0	0.4	0.8	0	0	−0.666	0	0	−0.8
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	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	30	0	0	0	0	0	0
C	14	5	15	0	0	0	0	0	0
I	0	8	24	0	3	3	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	1	3	1	0	1	0	0	0
ATP	0	8	24	0	0	3	0	0	3
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	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
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	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	56	125	41.6666666666667	26	7	149	6	13	19
kcatb	6	12	4	3	1	15	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	1306.66666666667	1333.33333333333	133.333333333333	4.33333333333333	18.6666666666667	2.20740740740741	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