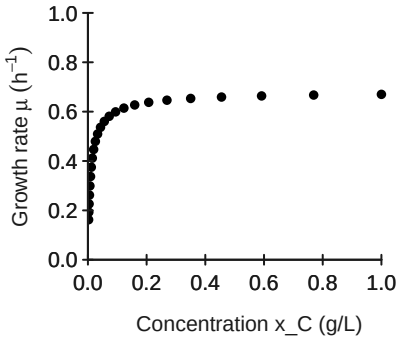
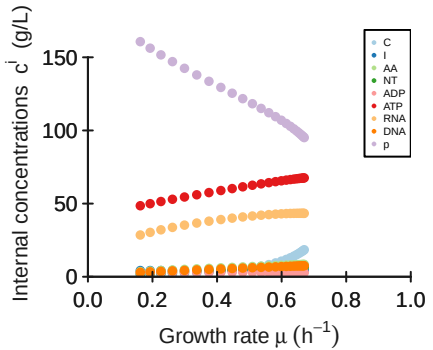
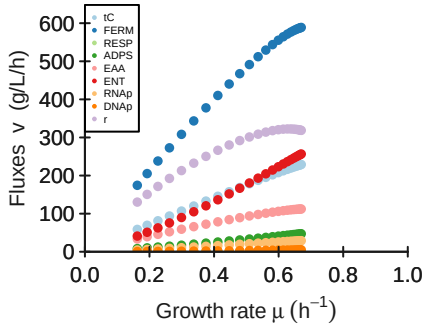
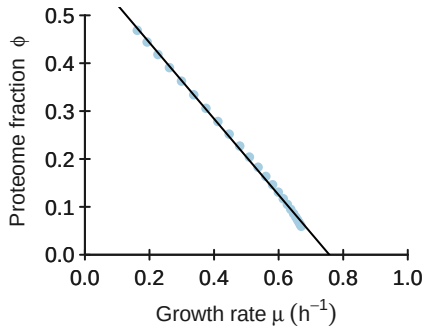


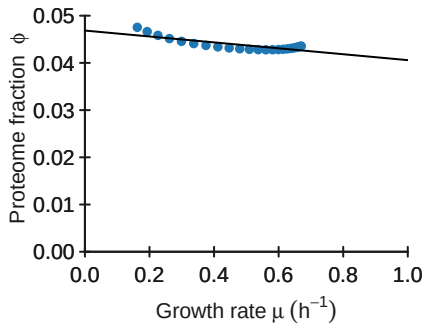




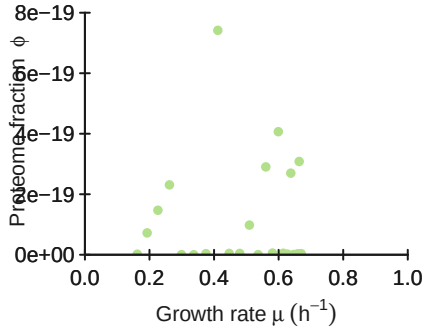
tC



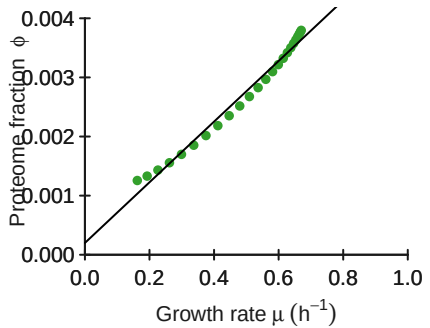
FERM



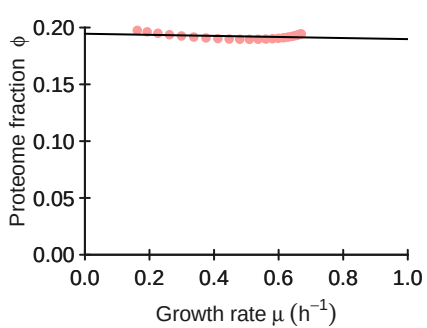
RESP



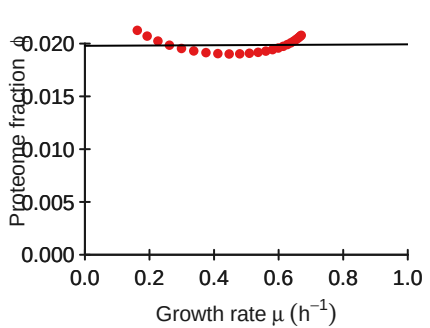
ADPS



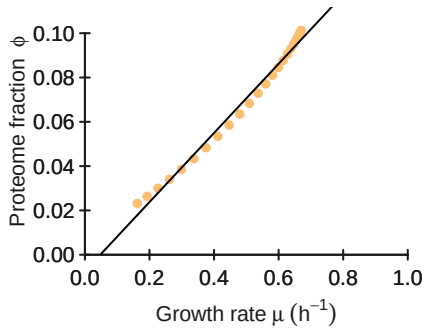
EAA

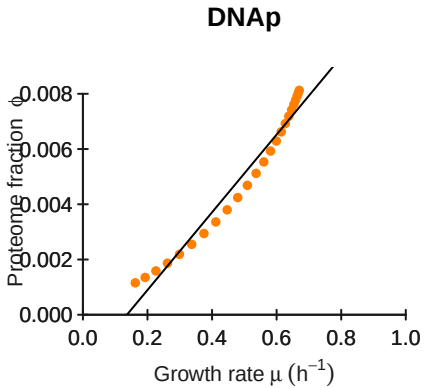


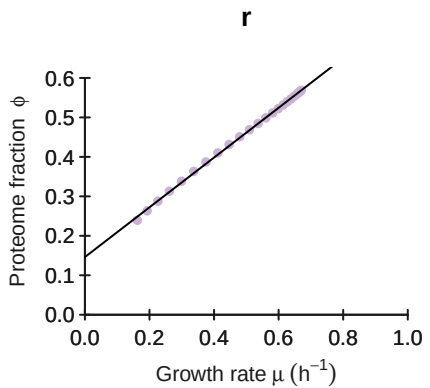
ENT

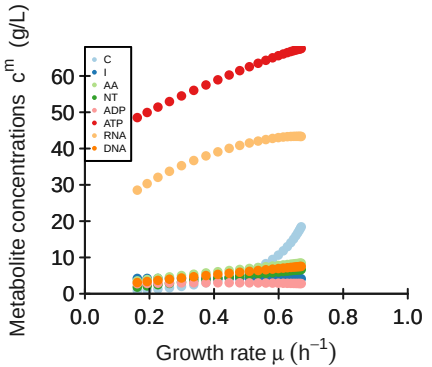


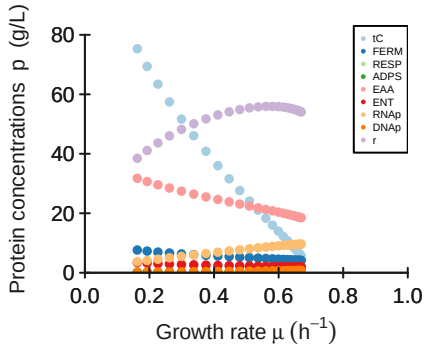
RNAp

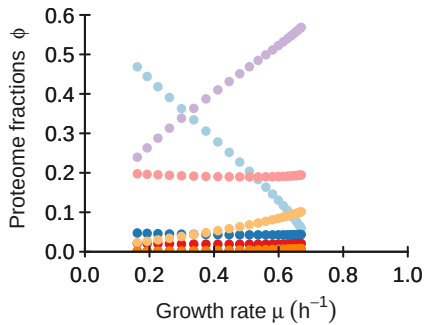


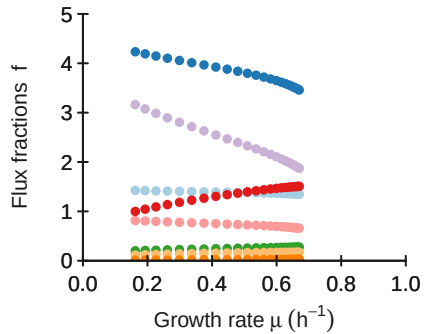

DNAp
Proteome fraction ϕ
0.000
0.002
0.004
0.006
0.008
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

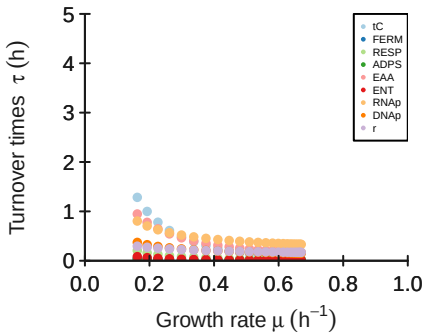

r
Proteome fraction ϕ
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

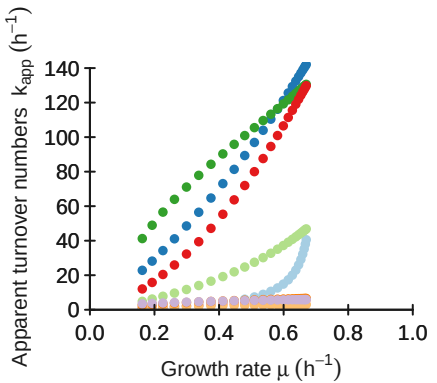

Metabolite concentrations cm (g/L)
C
I
AA
NT
ADP
ATP
RNA
DNA
0
10
20
30
40
50
60
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

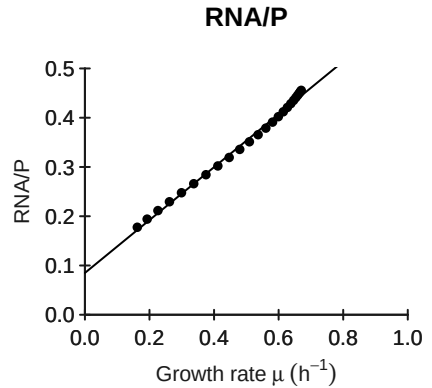

Protein concentrations p (g/L)
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
0
20
40
60
80
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

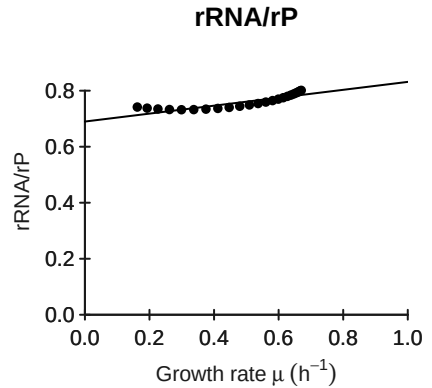

Proteome fractions ϕ
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

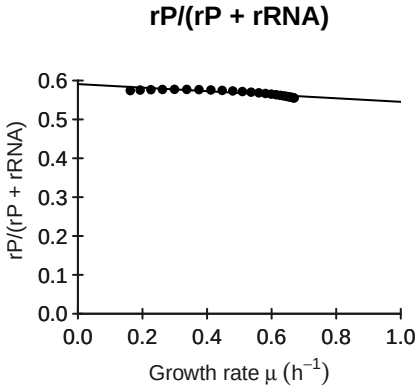

Flux fractions f
0
1
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

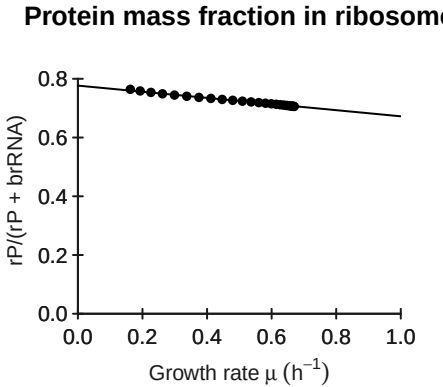

Turnover times τ (h)
tC
FERM
RESP
ADPS
EAA
ENT
RNAp
DNAp
r
0
1
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

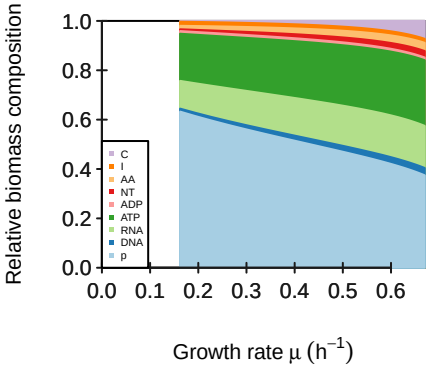

Apparent turnover numbers kapp (h−1)
0
20
40
60
80
100
120
140
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

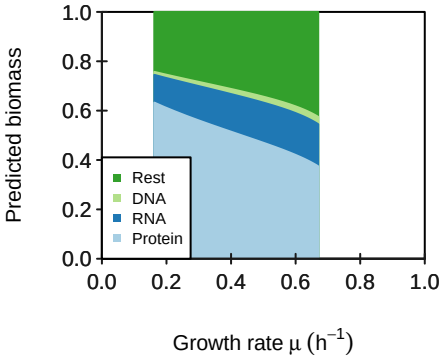

RNA/P
RNA/P
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

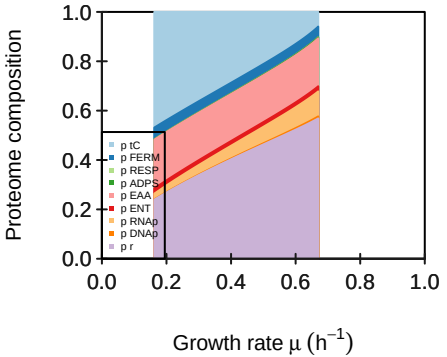

rRNA/rP
rRNA/rP
0.0
0.2
0.4
0.6
0.8
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

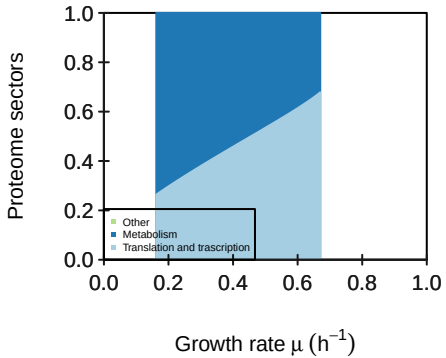

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


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


Relative biomass composition
C
I
AA
NT
ADP
ATP
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	−0.2	−0.1	0	−0.5	−0.167	0	0	0
I	0	0.1	0.1	0	−0.5	0	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	−0.8	−0.9	1	0	0.666	0	0	0.8
ATP	0	0.8	0.9	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	20	0	0	0	0	0	0
C	10	4	8	0	4	4	0	0	0
I	0	6	12	0	2	0	0	0	0
AA	0	0	0	0	6	2	0	0	2
NT	0	0	0	2	0	4	2	2	0
ADP	0	1	2	1	0	1	0	0	0
ATP	0	70	140	0	0	24	0	0	24
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	53	260	130	306	12	289	6	13	19
kcatb	5	26	13	31	1	29	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	1060	10500	1050	4.93548387096774	9	0.207614942528736	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