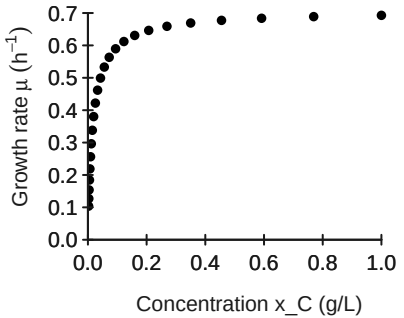
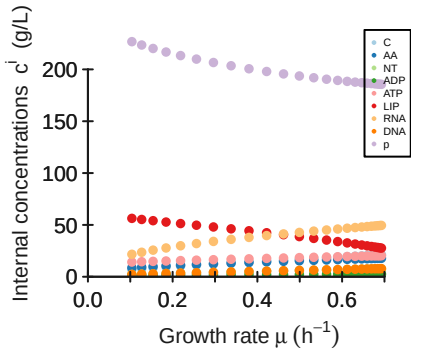
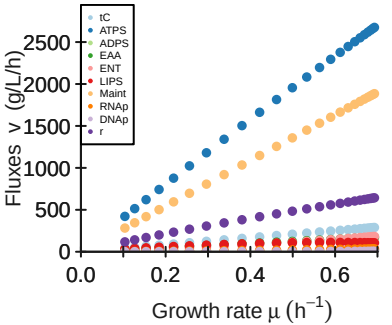
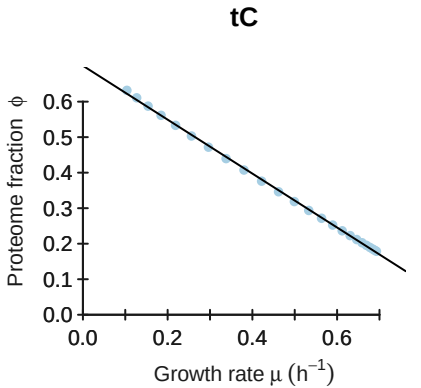
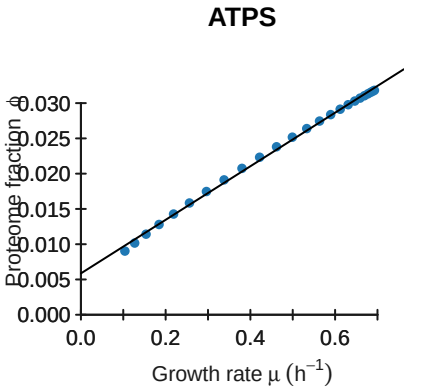
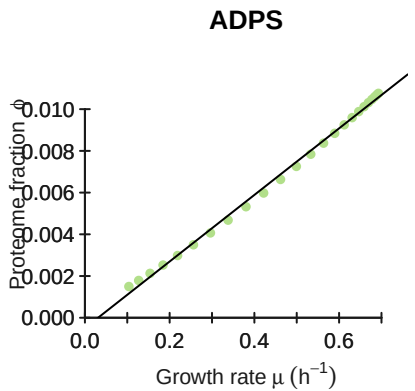

Growth rate μ (h^{-1})
Concentration x_C (g/L)

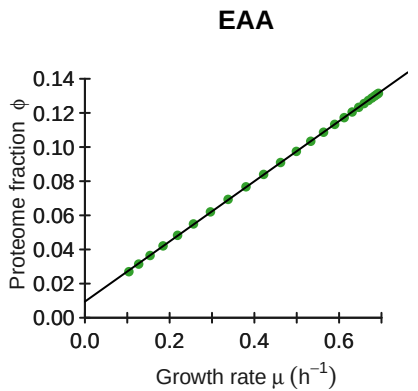

Internal concentrations c^{i} (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
LIP
RNA
DNA
p

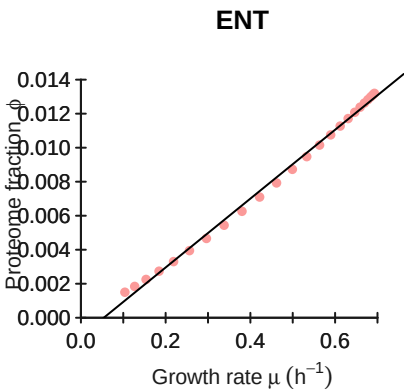

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
ATPS
ADPS
EAA
ENT
LIPS
Maint
RNAp
DNAp
r

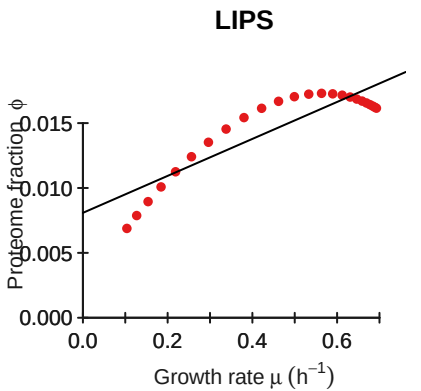

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

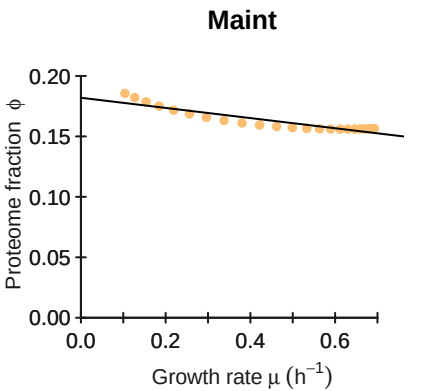

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

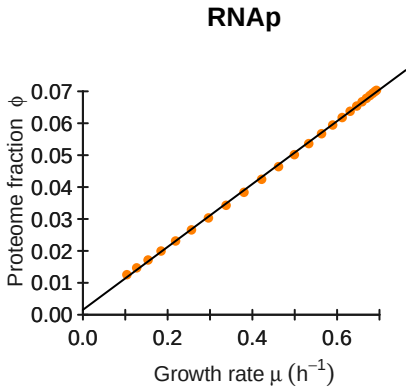

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

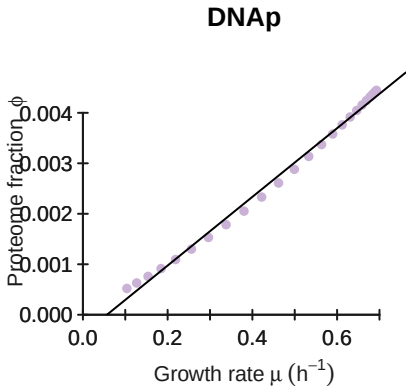

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

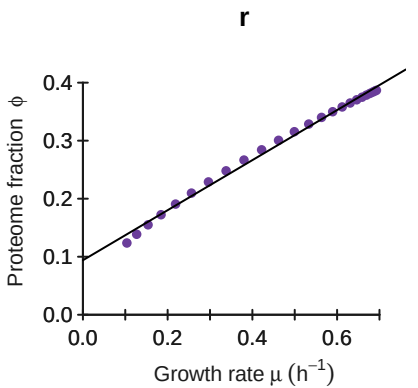

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

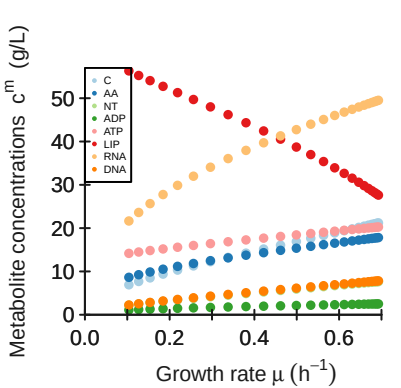

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

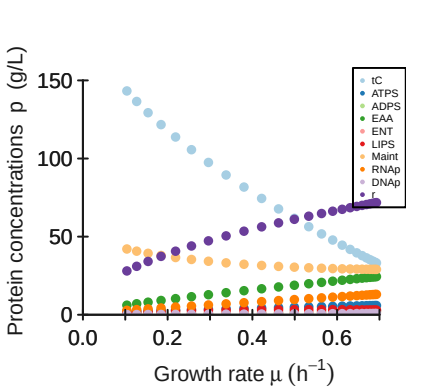

Maint
Proteome fraction ϕ
Growth rate μ (h^{-1})

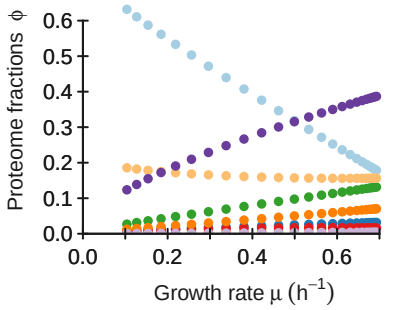

RNAp
Proteome fraction ϕ
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0.07
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

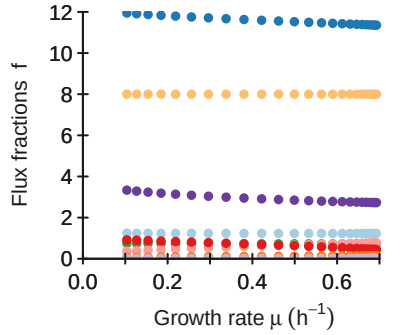

DNAp
Proteome fraction ϕ
0.000
0.001
0.002
0.003
0.004
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

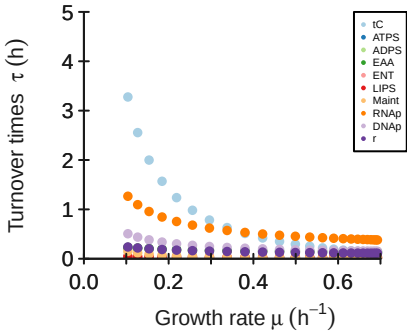

r
Proteome fraction ϕ
0.0
0.1
0.2
0.3
0.4
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

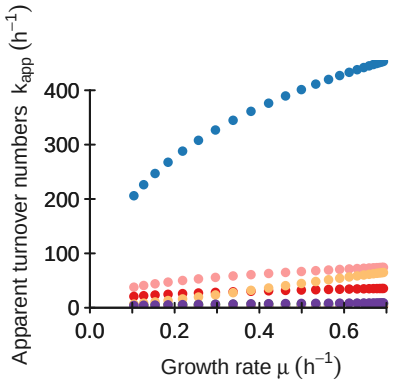

Metabolite concentrations cm (g/L)
0
10
20
30
40
50
0.0
0.2
0.4
0.6
Growth rate μ (h−1)
C
AA
NT
ADP
ATP
LIP
RNA
DNA

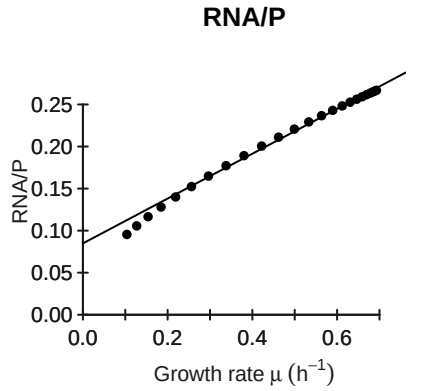

Protein concentrations p (g/L)
0
50
100
150
0.0
0.2
0.4
0.6
Growth rate μ (h−1)
tC
ATPS
ADPS
EAA
ENT
LIPS
Maint
RNAp
DNAp
r

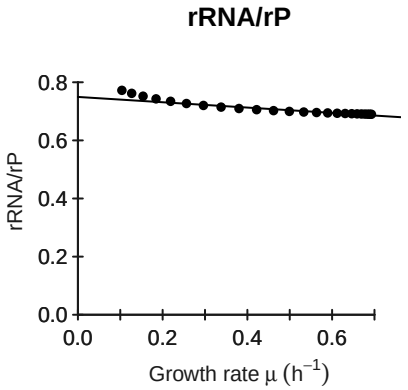

Proteome fractions ϕ
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

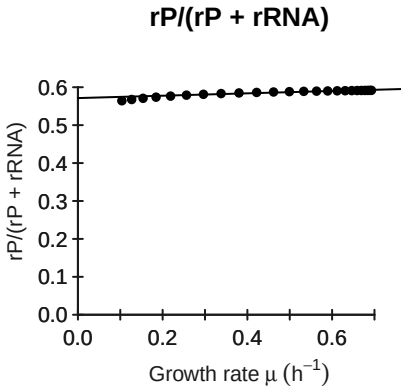

Flux fractions f
0
2
4
6
8
10
12
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

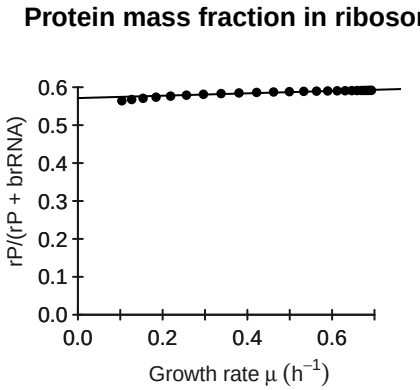

Turnover times τ (h)
0
1
2
3
4
5
0.0
0.2
0.4
0.6
Growth rate μ (h−1)
tC
ATPS
ADPS
EAA
ENT
LIPS
Maint
RNAp
DNAp
r

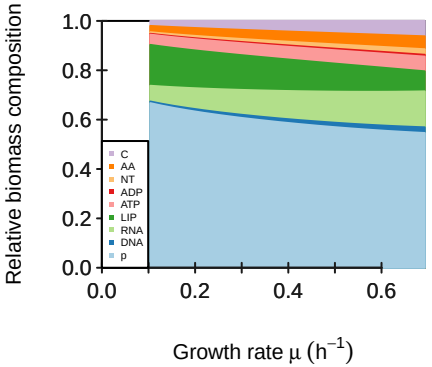

Apparent turnover numbers kapp (h−1)
0
100
200
300
400
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

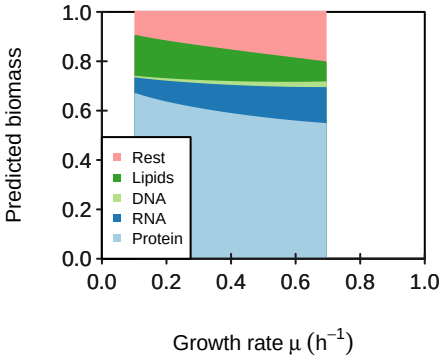

RNA/P
RNA/P
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

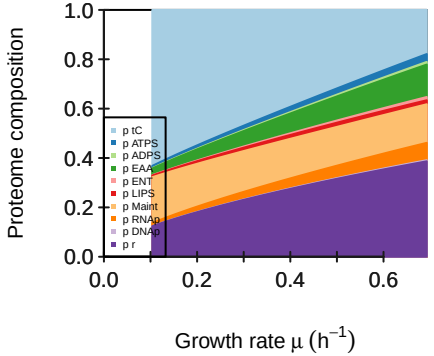

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

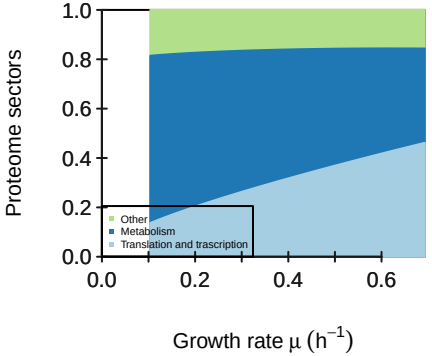

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


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


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


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


Proteome composition
p tC
p ATPS
p ADPS
p EAA
p ENT
p LIPS
p Maint
p RNAp
p DNAp
p r
Growth rate μ (h−1)


Proteome sectors
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)

M

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
C	1	−0.02	0	−1	−0.167	−0.18	0	0	0	0
AA	0	0	0	1	−0.167	0	0	0	0	−0.2
NT	0	0	−1	0	0.334	0	0	−1	−1	0
ADP	0	−0.98	1	0	0.666	0.82	1	0	0	0.8
ATP	0	0.98	0	0	−0.666	−0.82	−1	0	0	−0.8
LIP	0	0	0	0	0	0.18	0	0	0	0
RNA	0	0	0	0	0	0	0	1	0	0
DNA	0	0	0	0	0	0	0	0	1	0
p	0	0	0	0	0	0	0	0	0	0.2

K

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0	0	0
x_W	0	20	0	0	0	0	0	0	0	0
C	0	9	0	9	9	9	0	0	0	0
AA	0	0	0	0	3	0	0	0	0	3
NT	0	0	3	0	0	0	0	3	3	0
ADP	0	1	0	0	0	0	0	0	0	0
ATP	0	0	0	0	3	3	3	0	0	3
LIP	0	0	0	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0	0	0	0

KA

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0.02	0	0	0
x_W	0	0	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0	0	0
ADP	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0	0
LIP	30	0	0	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	0	0	0	70
DNA	0	0	0	0	0	0	0	5	5	0
p	0	0	0	0	0	0	0	0	0	0

kcat

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
kcatf	20	903	11	10	142	58	76	6	15	29
kcatb	0	0	0	0	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	0.11	0.023	0.005	0.165	0.023	0.031	0.2546	0.0794	0.002	0.307

average saturation input

3

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	0	0	0	0	0	0	0	0	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	0	0	0	0	0	0	8	0	0	0