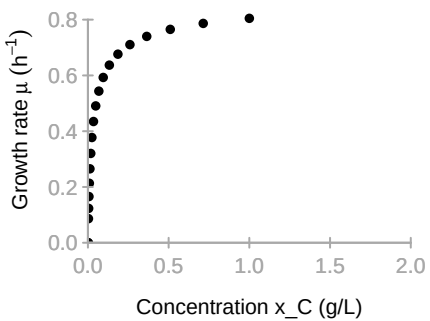
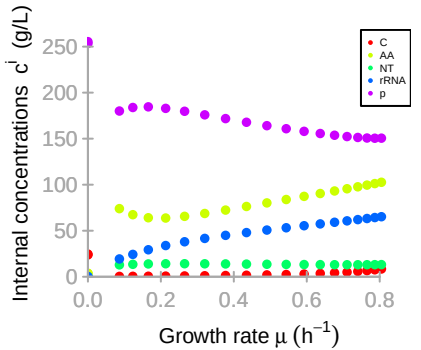
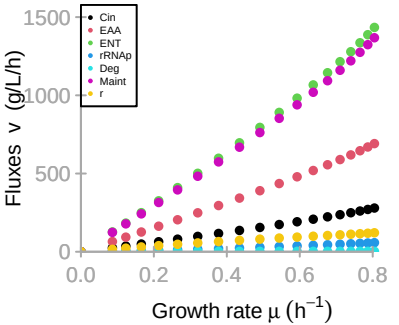
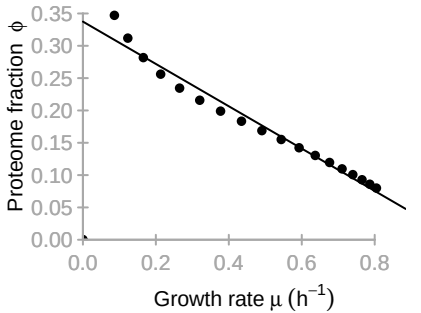


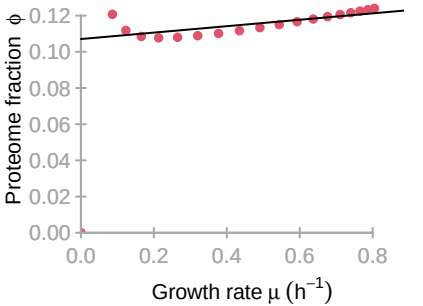




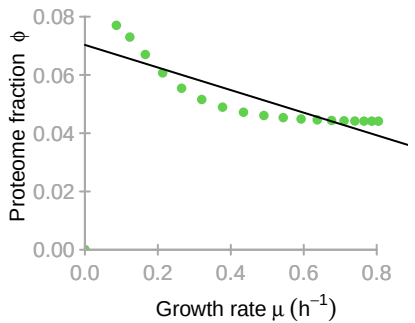
Cin



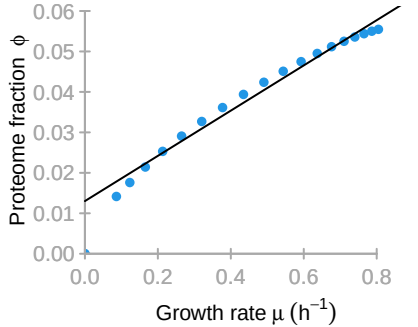
EAA



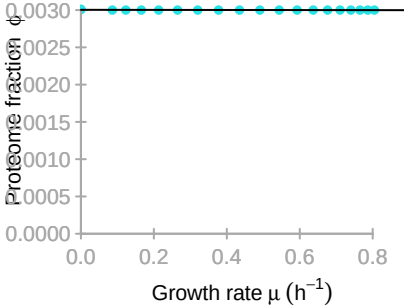
ENT



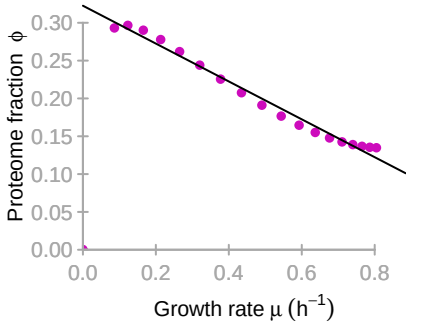
rRNAp



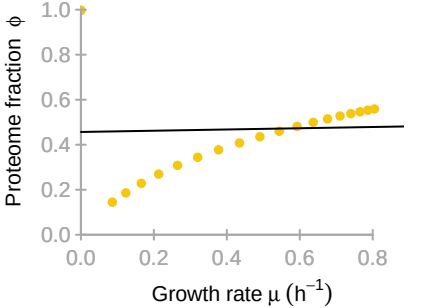
Deg

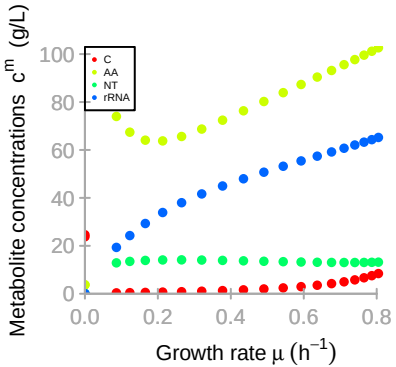


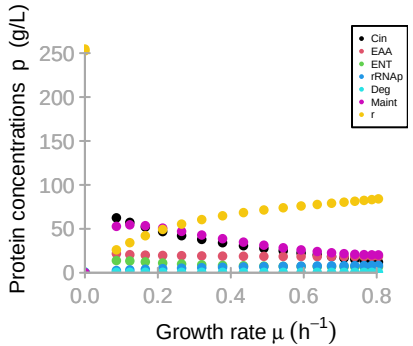
Maint

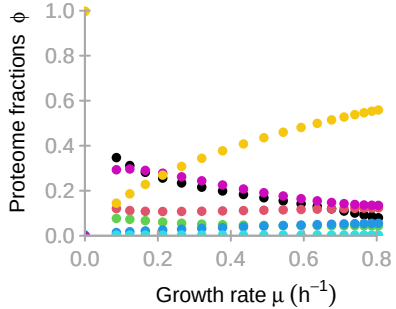


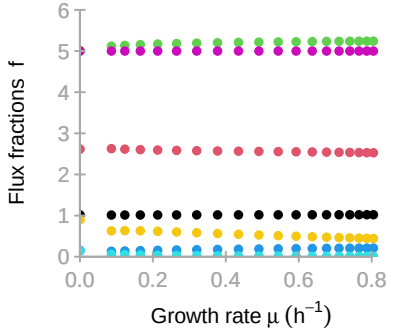
r

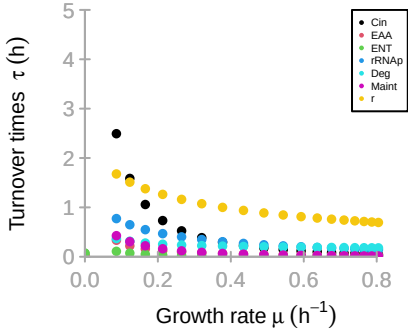


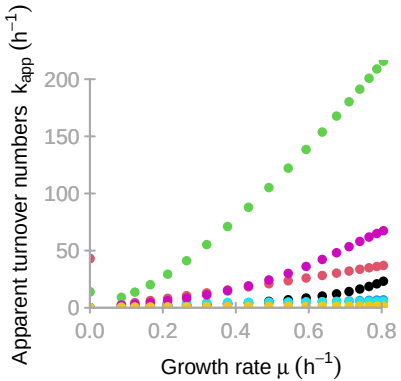

Metabolite concentrations c^m (g/L)
C
AA
NT
rRNA
Growth rate μ (h^{-1})

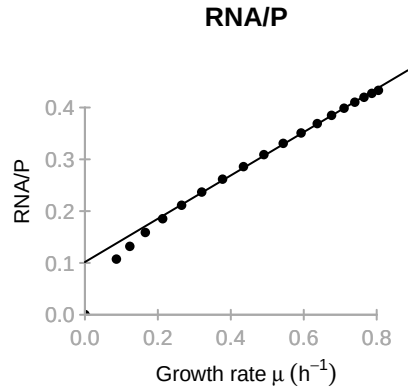

Protein concentrations p (g/L)
Cin
EAA
ENT
rRNAp
Deg
Maint
r
Growth rate μ (h^{-1})

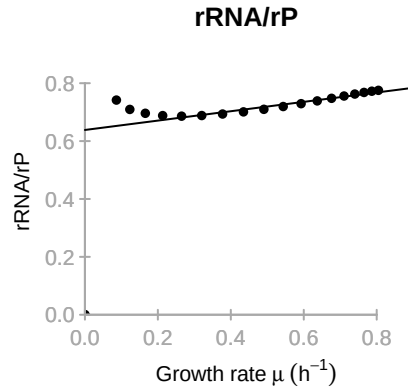

Proteome fractions ϕ
Growth rate μ (h^{-1})

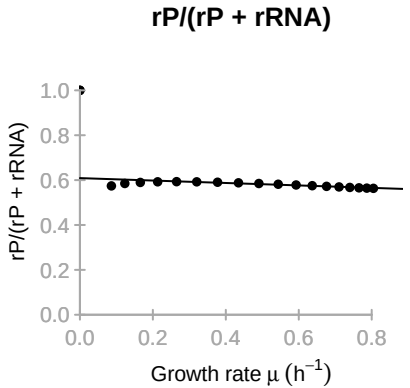

Flux fractions f
Growth rate μ (h^{-1})

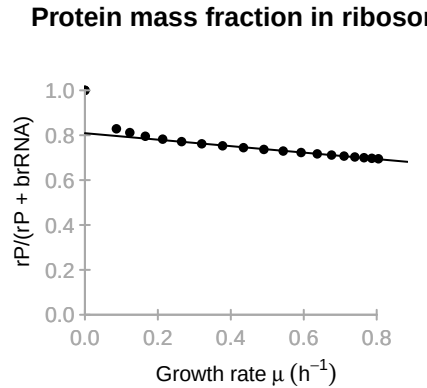

Turnover times τ (h)
Cin
EAA
ENT
rRNAp
Deg
Maint
r
Growth rate μ (h^{-1})

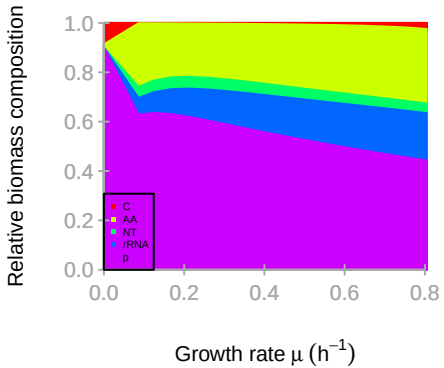

Apparent turnover numbers k_{app} (h^{-1})
Growth rate μ (h^{-1})

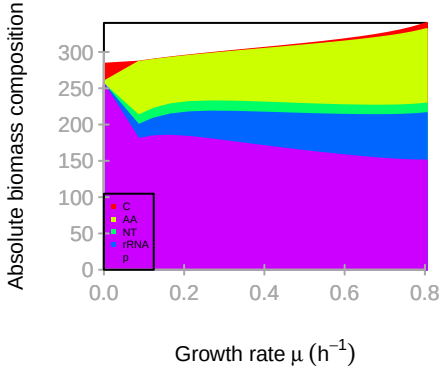

RNA/P
RNA/P
Growth rate μ (h^{-1})

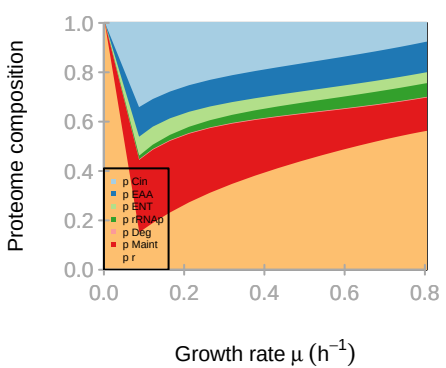

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

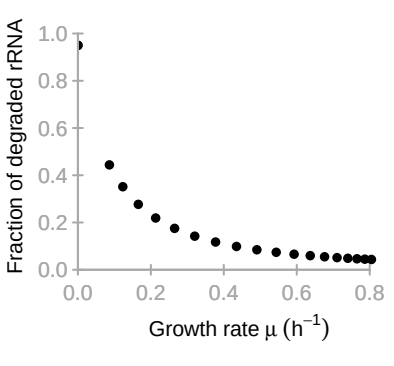

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})


Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})


Relative biomass composition
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
C
AA
NT
rRNA
p
Growth rate μ (h−1)


Absolute biomass composition
300
250
200
150
100
50
0
0.0
0.2
0.4
0.6
0.8
C
AA
NT
rRNA
p
Growth rate μ (h−1)


Proteome composition
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
p Cin
p EAA
p ENT
p rRNAp
p Deg
p Maint
p r
Growth rate μ (h−1)


Fraction of degraded rRNA
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
Growth rate μ (h−1)

M

	Cin	EAA	ENT	rRNAp	Deg	Maint	r
C	1	−1	−0.66	−0.05	0	1	0
AA	0	1	−0.34	0	0	0	−1
NT	0	0	1	−1	1	−1	0
rRNA	0	0	0	0.95	−1	0	0
p	0	0	0	0	0	0	1

K

	Cin	EAA	ENT	rRNAp	Deg	Maint	r
x_C	0.1	0	0	0	0	0	0
C	2	2	2	2	0	0	0
AA	0	0	99	0	0	0	99
NT	0	0	0	3	0	3	0
rRNA	0	0	0	52	52	0	0
p	0	0	0	0	0	0	0

KA

	Cin	EAA	ENT	rRNAp	Deg	Maint	r
x_C	0	0	0	0	0	0.1	0
C	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	50
p	0	0	0	0	0	0	0

kcat

	Cin	EAA	ENT	rRNAp	Deg	Maint	r
kcatf	37	47	537	11	10	91	5
kcatb	4	5	54	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
[1,]	185	4.7	0.0502244668911336	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
[1,]	0.05	0.2	0.07	0.027	0.003	0.2	0.4

average saturation input

1

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
[1,]	0	0	0	0	0.003	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
[1,]	0	0	0	0	0	5	0