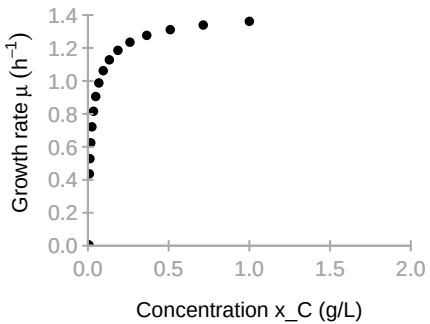
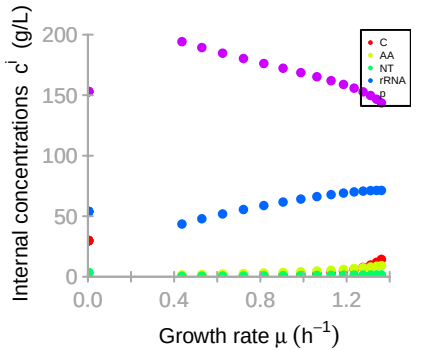
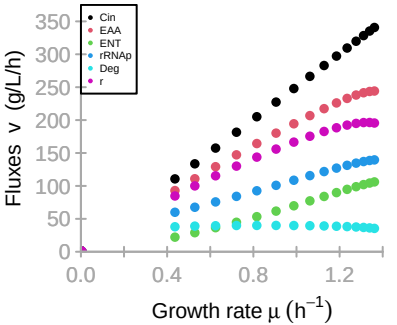
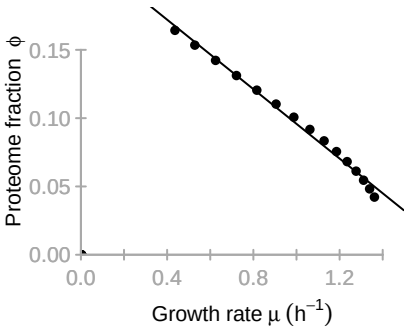


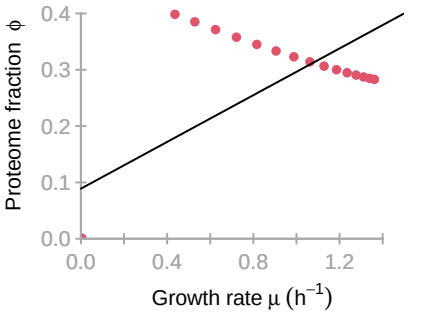




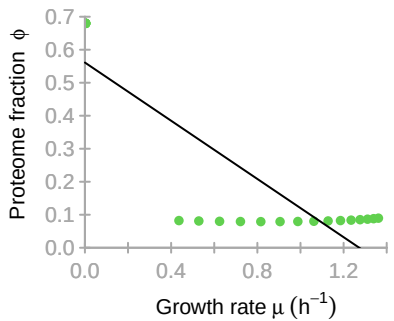
Cin



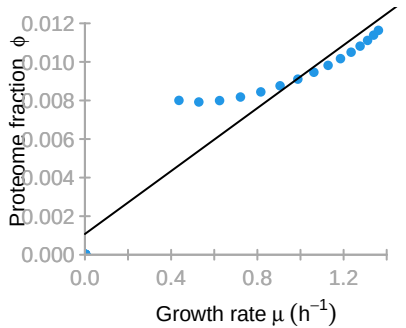
EAA



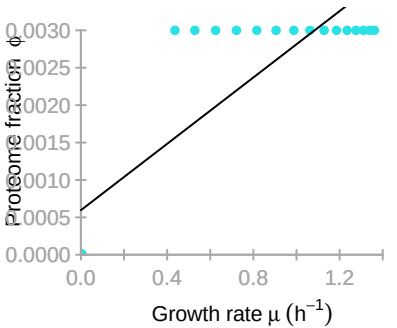
ENT



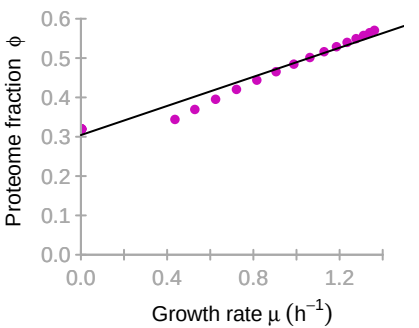
rRNAp

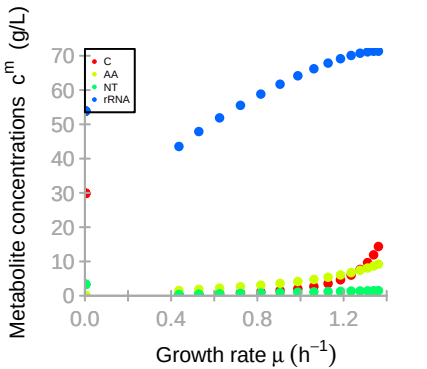


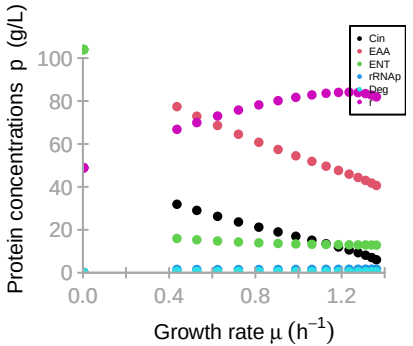
Deg

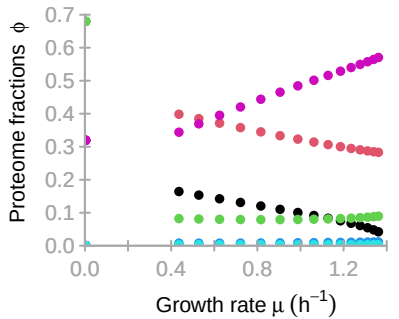


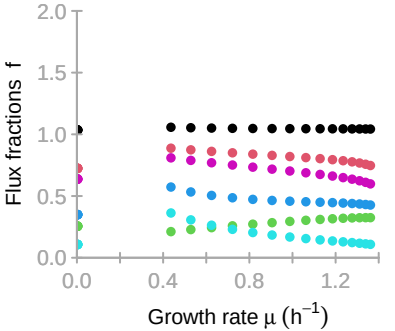
r

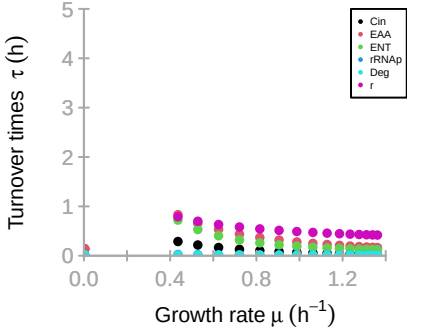


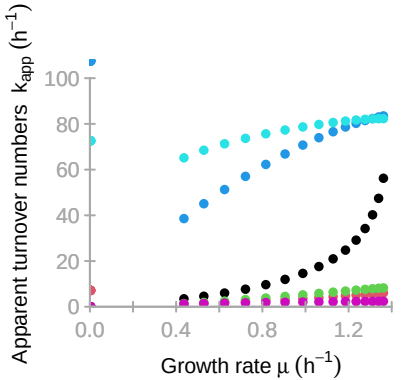




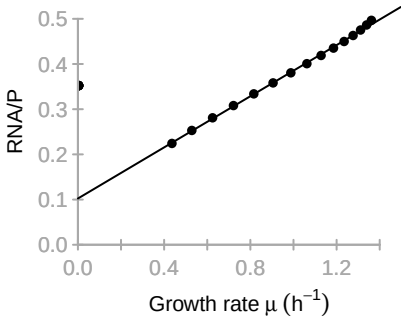




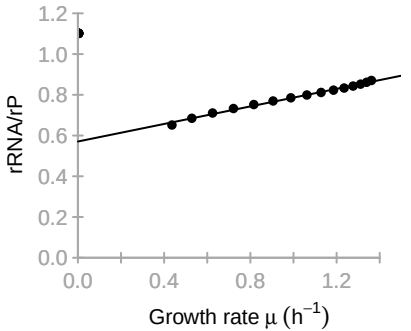




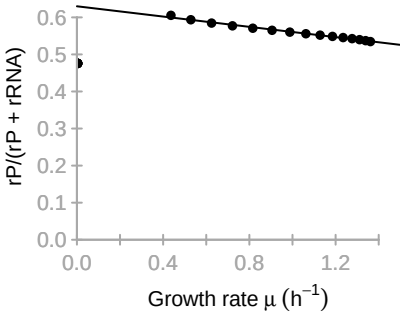
RNA/P



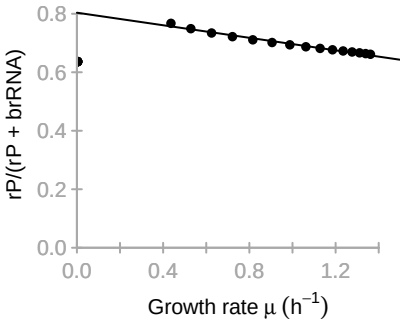
rRNA/rP

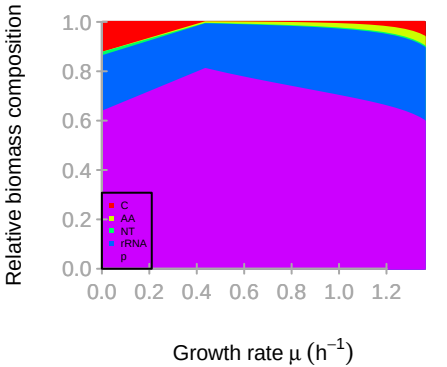


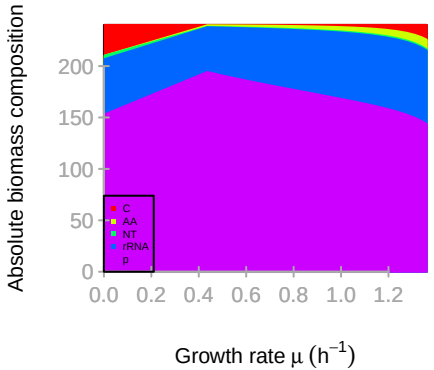
rP/(rP + rRNA)

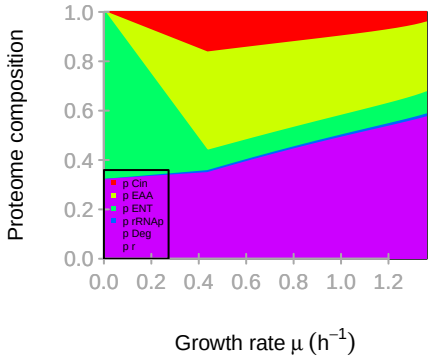


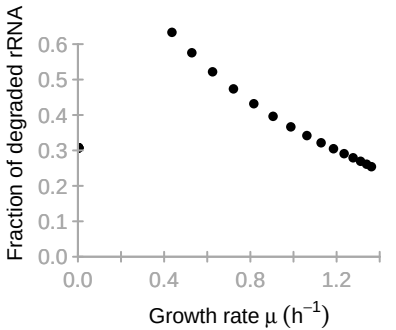
Protein mass fraction in ribosome






Absolute biomass composition
200
150
100
50
0
C
AA
NT
rRNA
p
0.0 0.2 0.4 0.6 0.8 1.0 1.2
Growth rate μ (h−1)


Proteome composition
1.0
0.8
0.6
0.4
0.2
0.0
p Cin
p EAA
p ENT
p rRNAp
p Deg
p r
0.0 0.2 0.4 0.6 0.8 1.0 1.2
Growth rate μ (h−1)


Fraction of degraded rRNA
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0 0.4 0.8 1.2
Growth rate μ (h−1)

M

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

K

	Cin	EAA	ENT	rRNAp	Deg	r
x_C	0.1	0	0	0	0	0
C	1	1	1	0	0	0
AA	0	5	1	0	0	1
NT	0	0	5	1	0	0
rRNA	0	0	0	0	50	0
p	0	0	0	0	0	0

KA

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

kcat

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]
kcatf	200	7.3846	9.8004	140	140	4.5
kcatb	40	1.47692	1.96008	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]
[1,]	50	25	25	Inf	Inf	Inf

minimal phi constraint

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

minimal f constraint

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