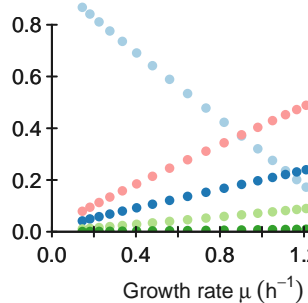
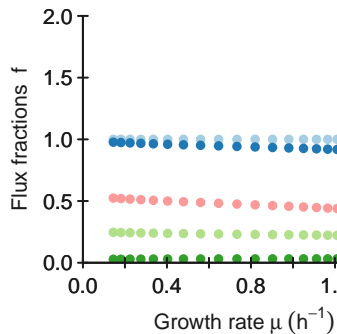
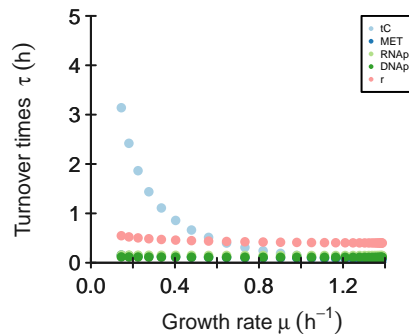
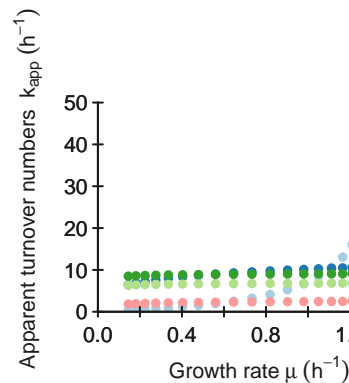
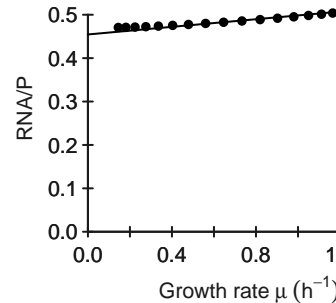
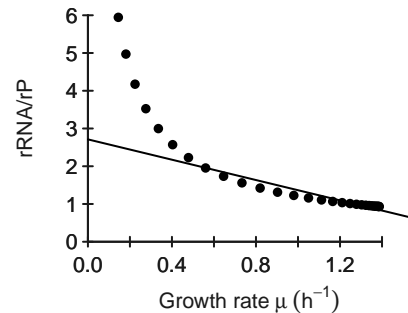


Proteome fractions ϕ Flux fractions f Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})

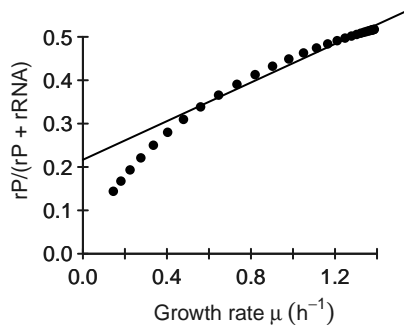
RNA/P



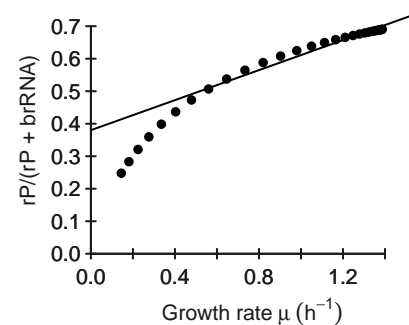
rRNA/rP



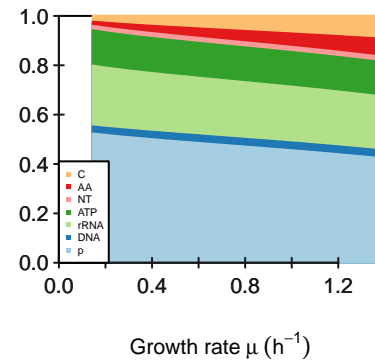
rP/(rP + rRNA)



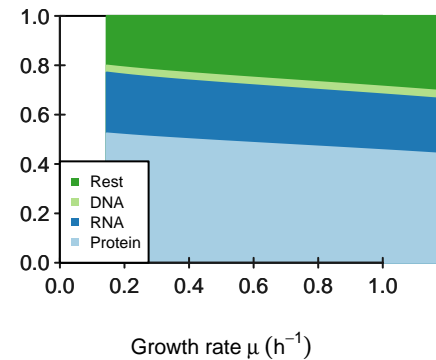
Protein mass fraction in ribosome



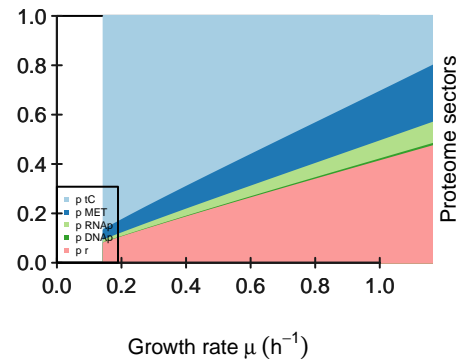
Relative biomass composition



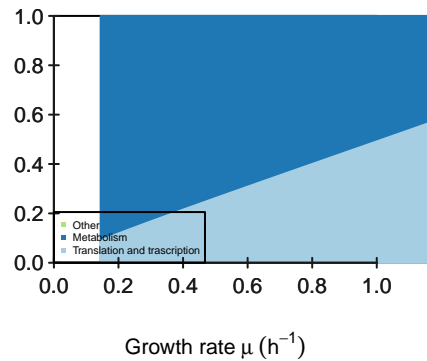
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

	tC	MET	RNAp	DNAp	r
C	1	-1	0	0	0
AA	0	0.5	0	0	-0.9
NT	0	0.3	-1	-1	0
ATP	0	0.2	0	0	-0.1
rRNA	0	0	1	0	0
DNA	0	0	0	1	0
p	0	0	0	0	1

K

	tC	MET	RNAp	DNAP	r
x_C	0.1	0	0	0	0
C	0	7	0	0	0
AA	0	0	0	0	3
NT	0	0	1	1	0
ATP	0	0	0	0	12
rRNA	0	0	0	0	0
DNA	0	0	0	0	0
p	0	0	0	0	0

KA

	tC	MET	RNAp	DNAp	r
x_C	0	0	0	0	0
C	0	0	0	0	0
AA	0	0	0	0	0
NT	0	0	0	0	0
ATP	0	0	0	0	0
rRNA	0	0	0	0	60
DNA	0	0	4	4	0
p	0	0	0	0	0

kcat

	tC	MET	RNAp	DNAp	r
kcatf	64.5	14.1	12.1	16.1	8.1
kcatb	0	0	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]
	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	0.065	0.352	0.12	0.003	0.46

average saturation input

3

minimal phi constraint

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

minimal f constraint

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