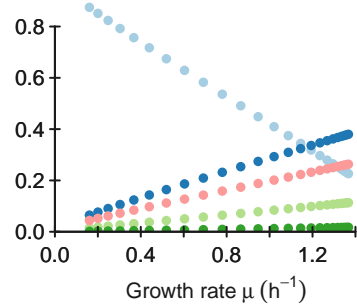
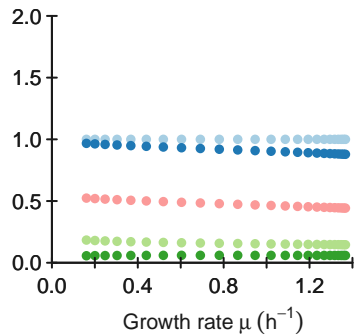
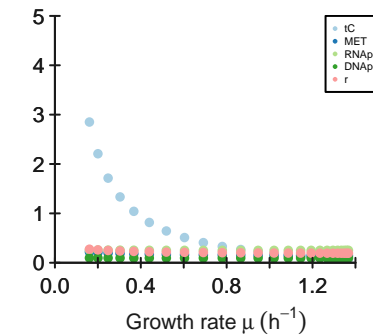
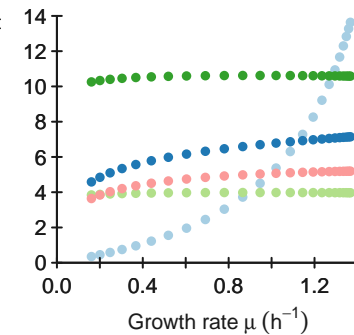
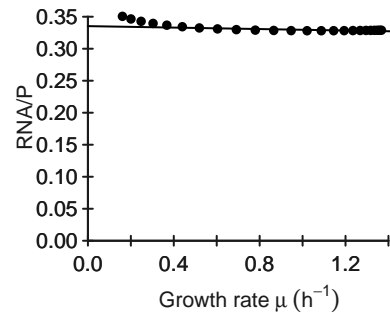
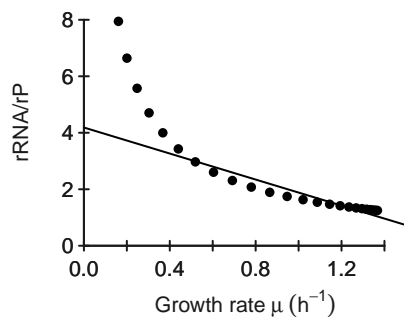


Proteome fractions ϕ Flux fractions f Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})

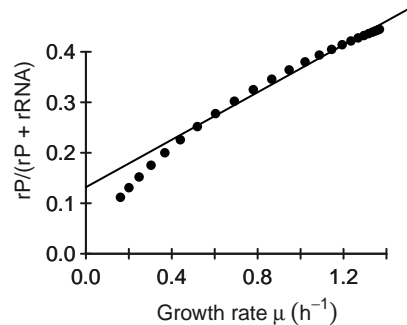
RNA/P



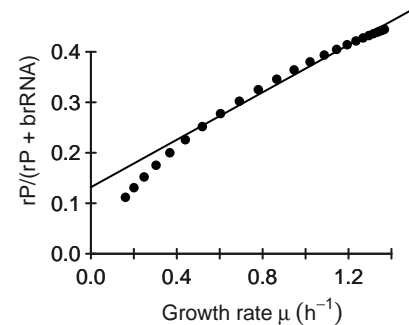
rRNA/rP



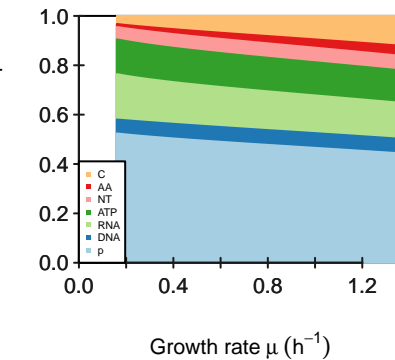
rP/(rP + rRNA)



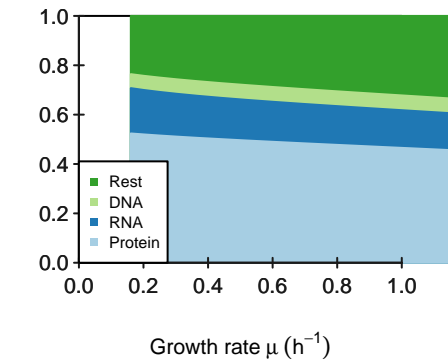
Protein mass fraction in ribosome



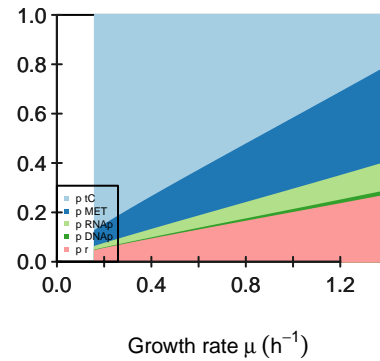
Relative biomass composition



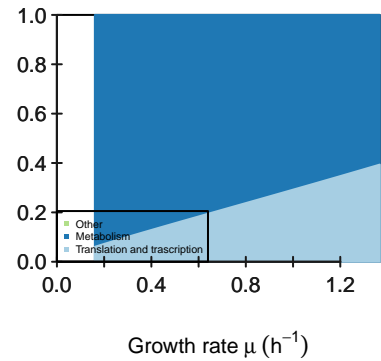
Predicted biomass



Proteome composition



Proteome sectors



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
RNA	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	8	0	0	0
AA	0	0	0	0	4
NT	0	0	2	2	0
ATP	0	0	0	0	12
RNA	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
RNA	0	0	0	0	50
DNA	0	0	5	5	0
p	0	0	0	0	0

kcat

	tC	MET	RNAp	DNAp	r
kcatf	15	9	6	16	23
kcatb	0	0	0	0	0

Keq

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

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]
	0.15	0.307	0.11	0.003	0.43

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	