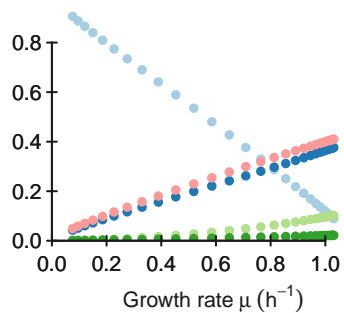
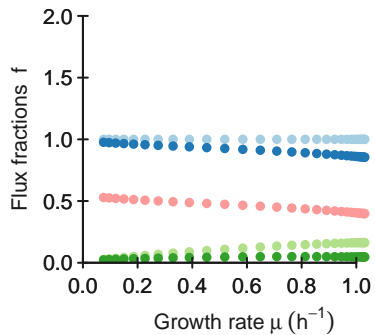
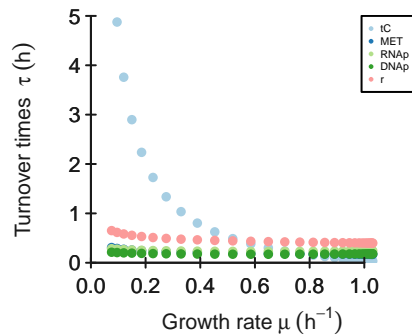
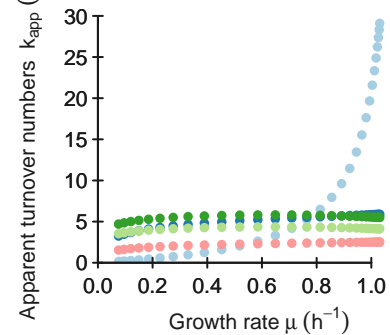
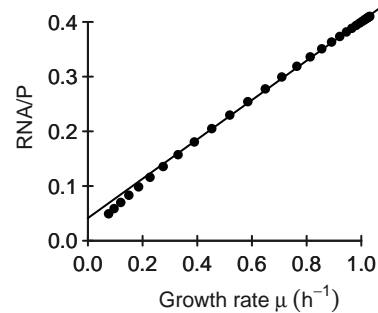
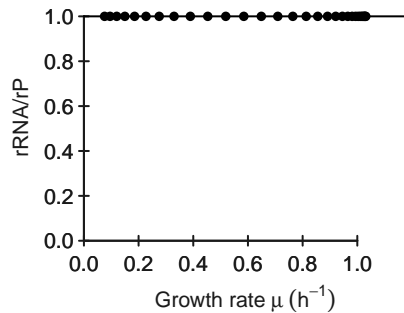


Proteome fractions  $\phi$ Flux fractions  $f$ Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{\text{app}}$  ( $\text{h}^{-1}$ )

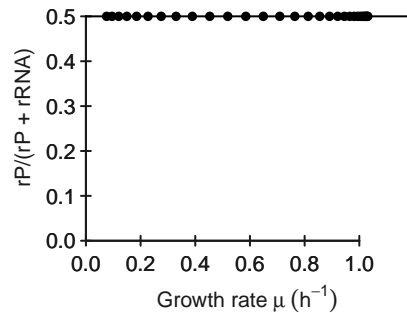
RNA/P



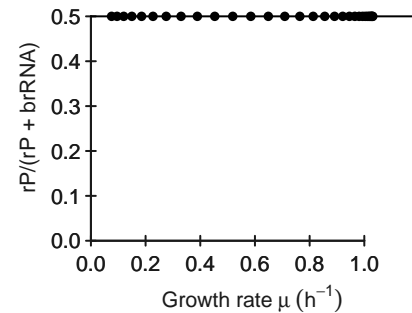
rRNA/rP



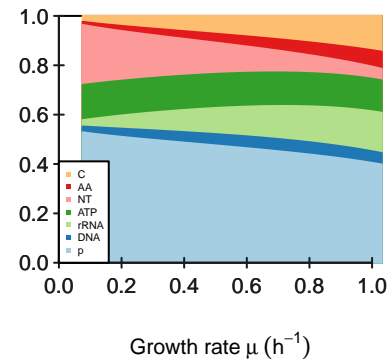
rP/(rP + rRNA)



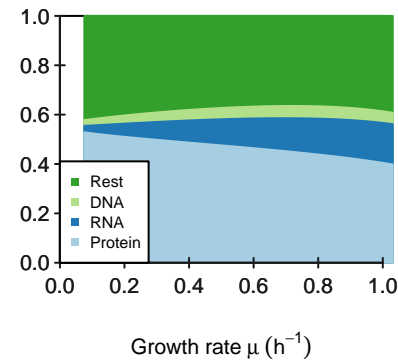
Protein mass fraction in ribosome



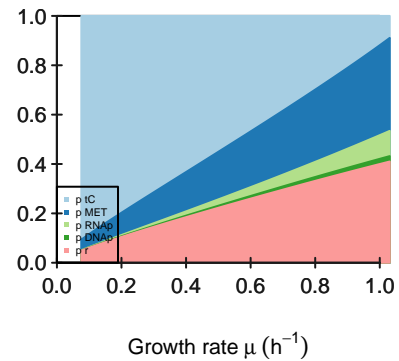
Relative biomass composition



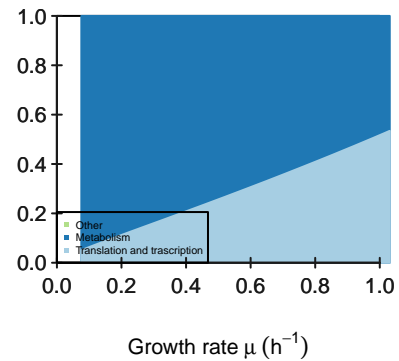
Predicted biomass



Proteome composition



Proteome sectors



keep\_ribosome\_kcat FALSE  
keep\_transport\_kcat FALSE  
maintenance\_fun constant

**M**

	<b>tC</b>	<b>MET</b>	<b>RNAp</b>	<b>DNAp</b>	<b>r</b>
<b>C</b>	1	-1	0	0	0
<b>AA</b>	0	0.5	0	0	-0.9
<b>NT</b>	0	0.3	-1	-1	0
<b>ATP</b>	0	0.2	0	0	-0.1
<b>rRNA</b>	0	0	1	0	0
<b>DNA</b>	0	0	0	1	0
<b>p</b>	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	0
DNA	0	0	4	4	0
p	0	0	0	0	0

**kcat**

	<b>tC</b>	<b>MET</b>	<b>RNAp</b>	<b>DNAp</b>	<b>r</b>
<b>kcatf</b>	32	7	6	8	4
<b>kcatb</b>	0	0	0	0	0



Keq

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

**phi input**

	<b>[,1]</b>	<b>[,2]</b>	<b>[,3]</b>	<b>[,4]</b>	<b>[,5]</b>
<b>[1,]</b>	0.065	0.352	0.12	0.003	0.46

**average saturation input**

3

minimal phi constraint

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

minimal f constraint

	<b>[1,]</b>	<b>[,1]</b>	<b>[,2]</b>	<b>[,3]</b>	<b>[,4]</b>	<b>[,5]</b>
	0	0	0	0	0	