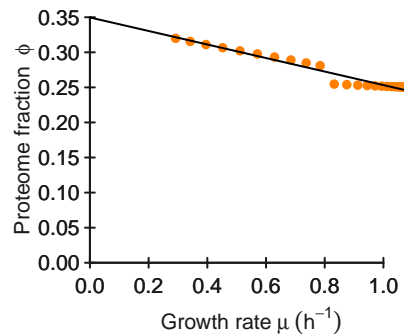
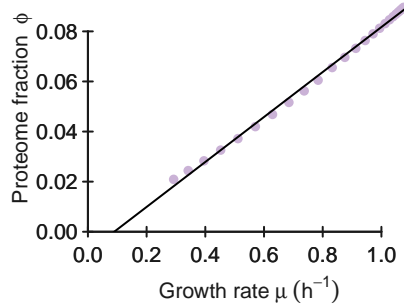


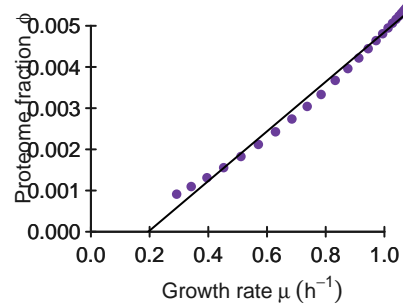
Maint



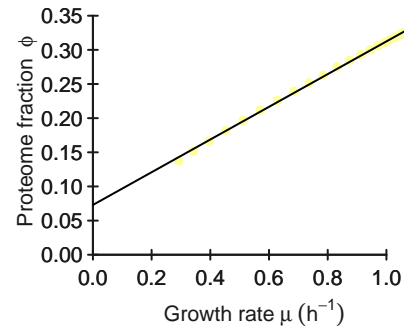
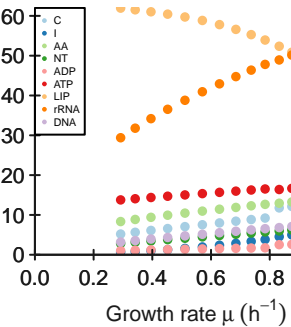
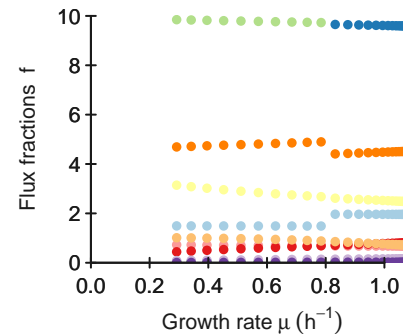
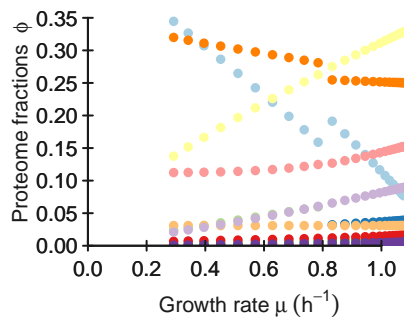
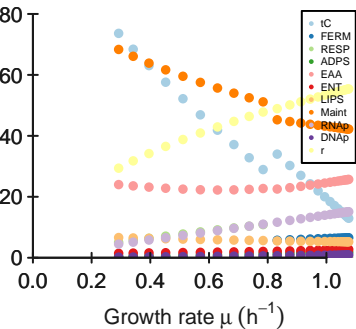
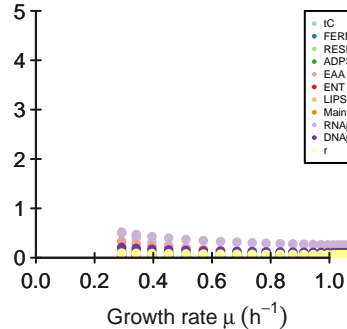
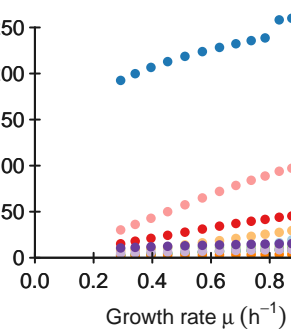
RNAP



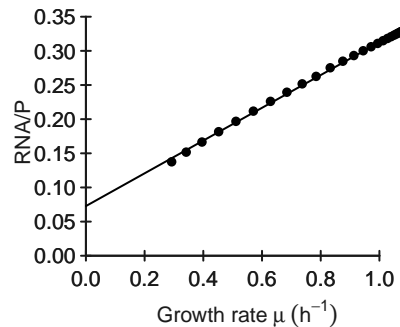
DNAP



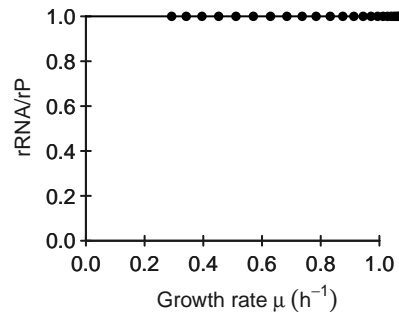
r

Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )

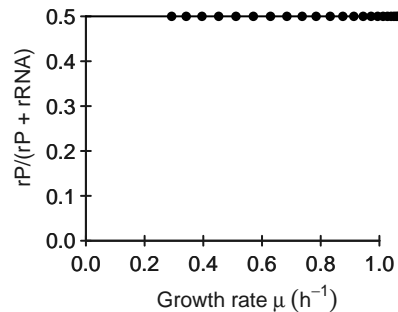
RNA/P



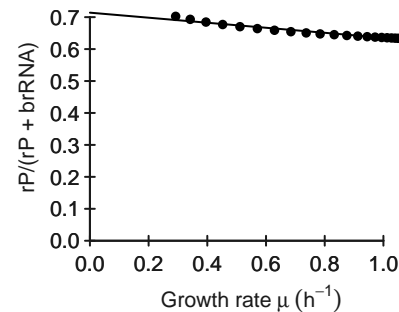
rRNA/rP



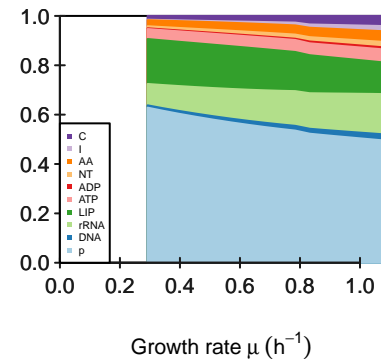
rP/(rP + rRNA)



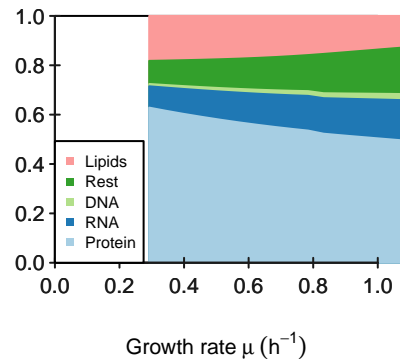
Protein mass fraction in ribosome



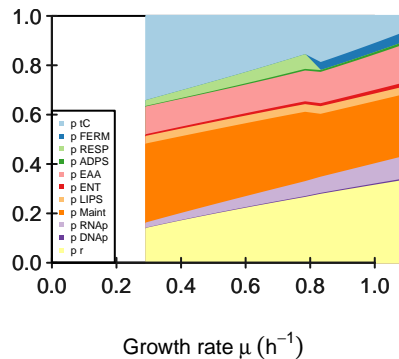
Relative biomass composition



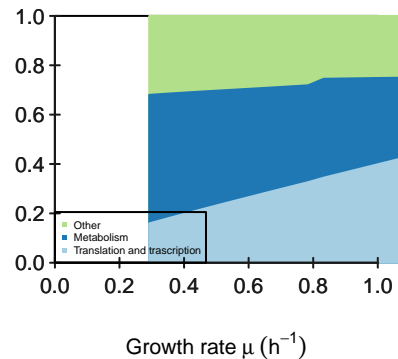
Predicted biomass



Proteome composition



Proteome sectors



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

M

[illegible]

**K**

[illegible]

**KA**[illegible]

**kcat**[illegible]



**Keq**

<b>[1,]</b>	<b>[,1]</b> Inf	<b>[,2]</b> Inf	<b>[,3]</b> Inf	<b>[,4]</b> Inf	<b>[,5]</b> Inf	<b>[,6]</b> Inf	<b>[,7]</b> Inf	<b>[,8]</b> Inf	<b>[,9]</b> Inf	<b>[,10]</b> Inf	<b>[,11]</b> Inf
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## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	0.043	0.023	0.023	0.002	0.165	0.021	0.031	0.3036	0.0794	0.002	0.307

**average saturation input**

3

## minimal phi constraint

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	0	0	0	0	0	0	0.031	0	0	0	0

## minimal f constraint

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	0	0	0	0	0	0	0	3.85	0	0	0