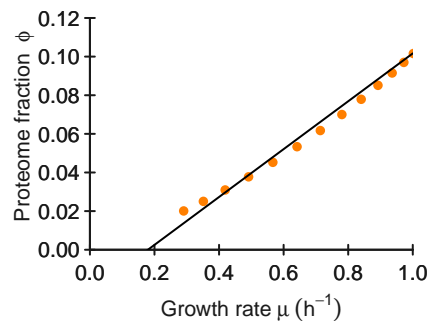
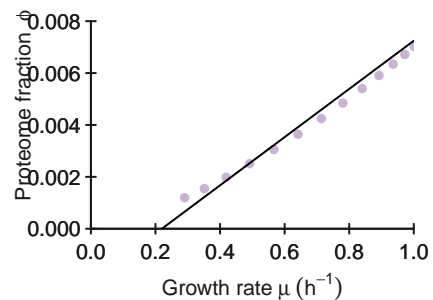


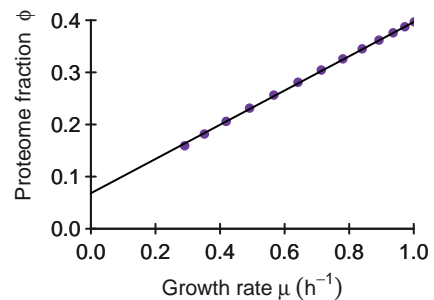
**RNAP**



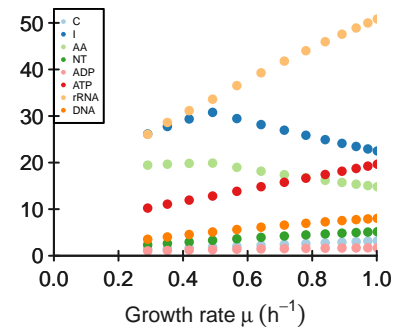
**DNAP**



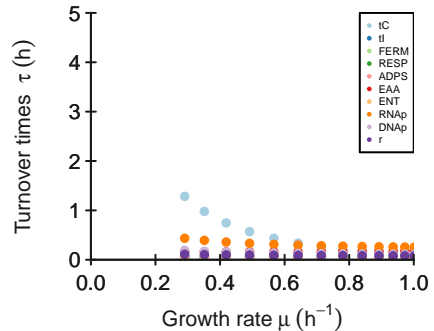
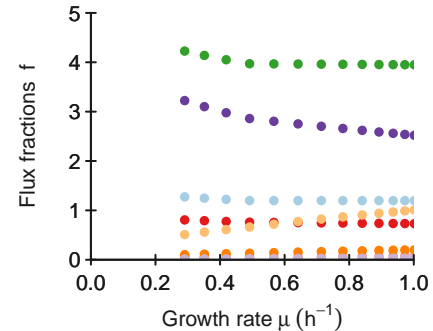
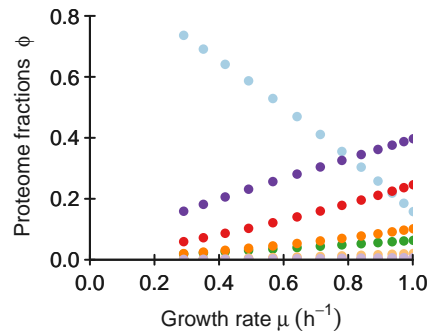
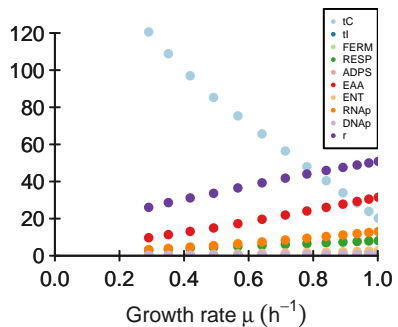
**r**



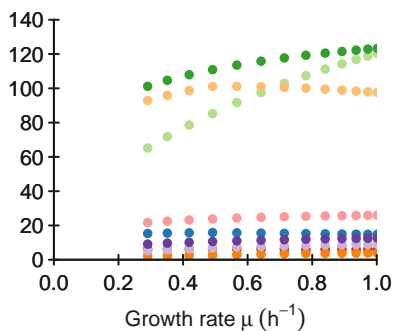
Metabolite concentrations  $c^m$  (g/L)



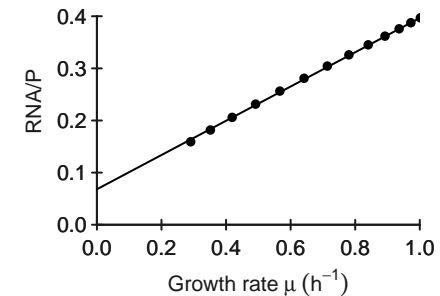
Protein concentrations  $p$  (g/L)

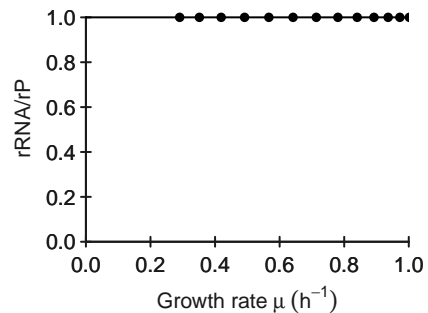
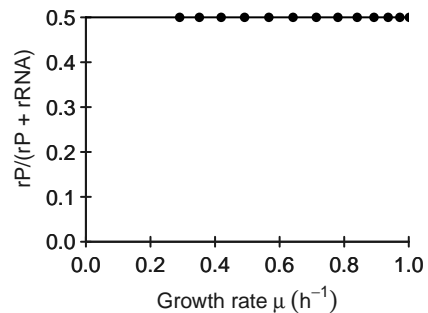
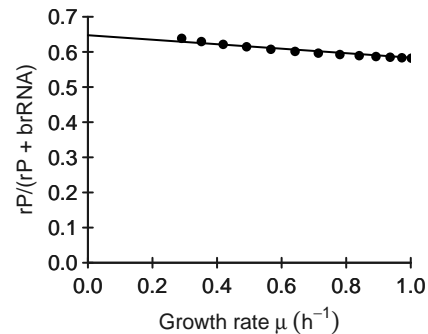
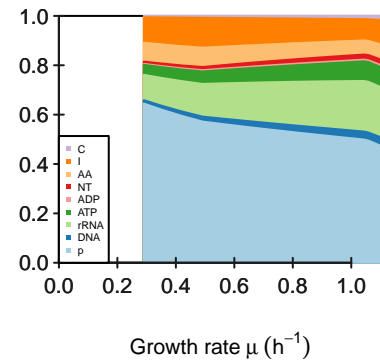
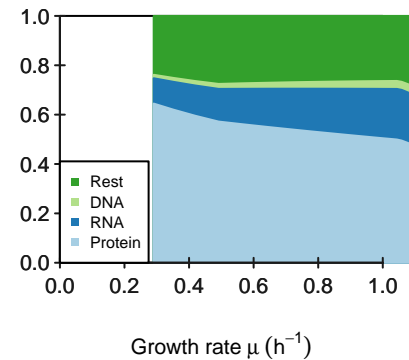
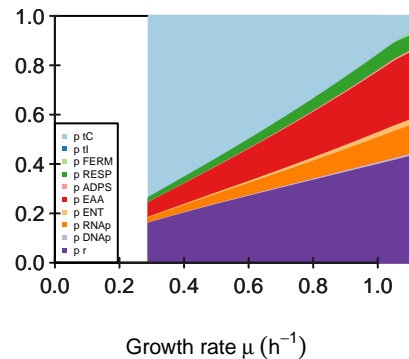
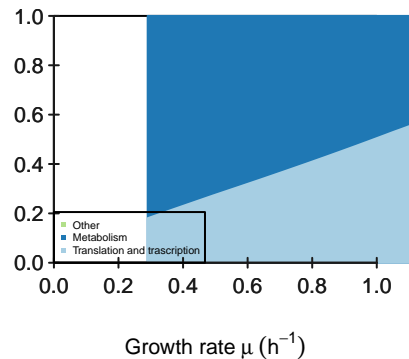


Apparent turnover numbers  $k_{app}$  ( $h^{-1}$ )



**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

[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
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## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
	0.06	0.005	0.035	0.035	0.003	0.248	0.032	0.119	0.003	0.46

**average saturation input**

3

### minimal phi constraint

[illegible]

### minimal f constraint

[illegible]