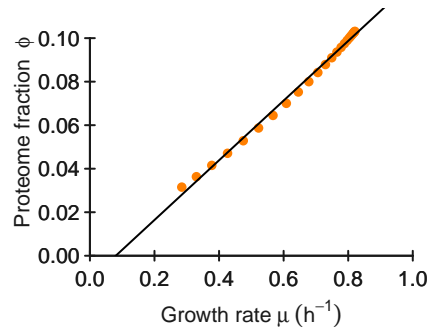
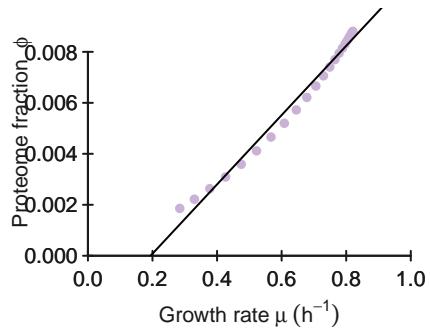


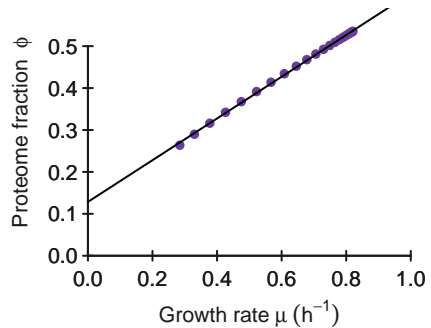
**RNAP**



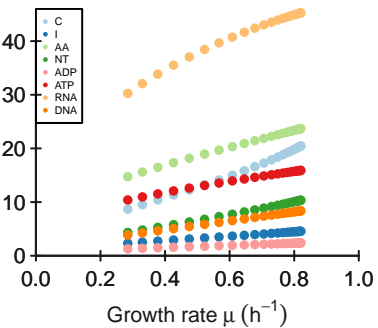
**DNAP**



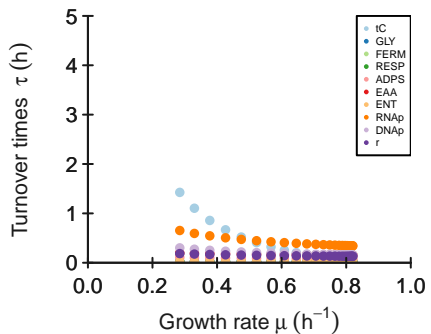
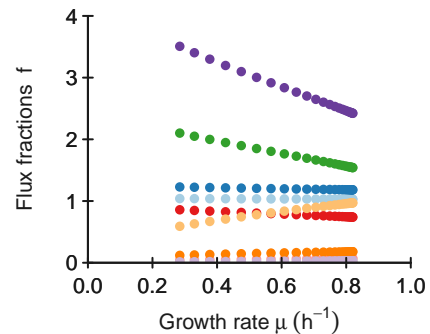
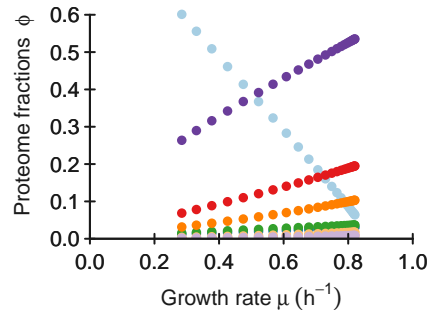
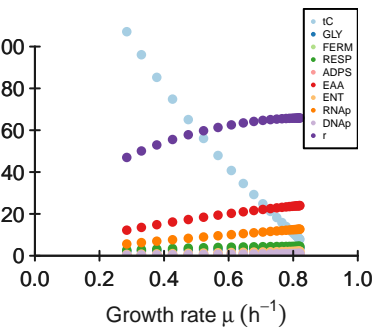
**r**



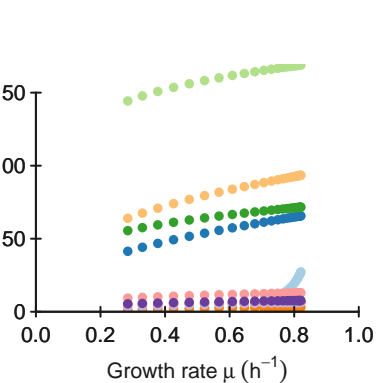
Metabolite concentrations  $c^m$  (g/L)



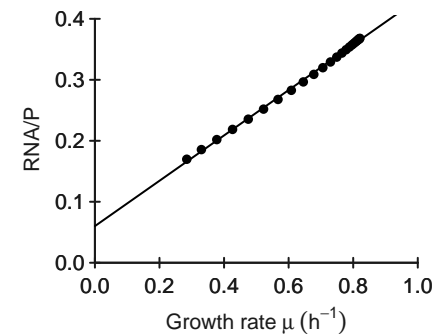
Protein concentrations  $p$  (g/L)



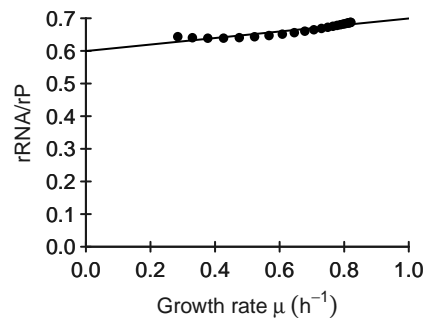
Apparent turnover numbers  $k_{app}$  ( $h^{-1}$ )



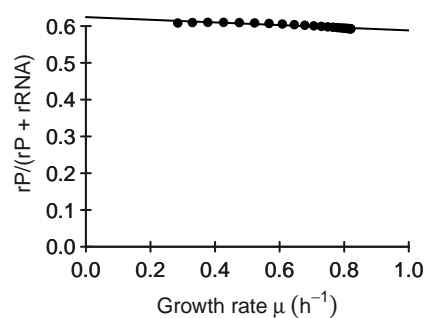
**RNA/P**



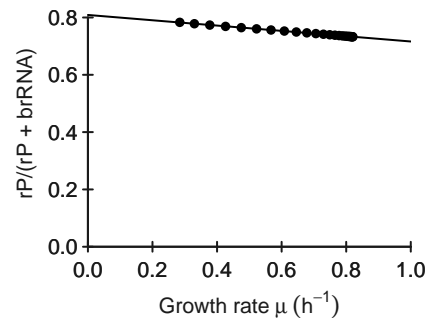
rRNA/rP



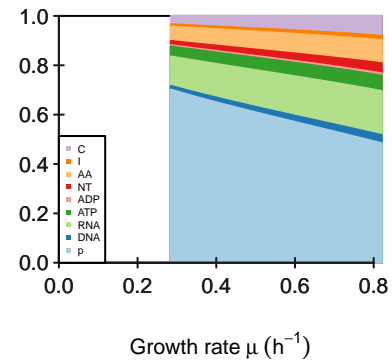
rP/(rP + rRNA)



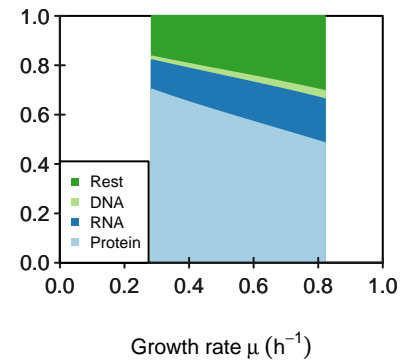
Protein mass fraction in ribosome



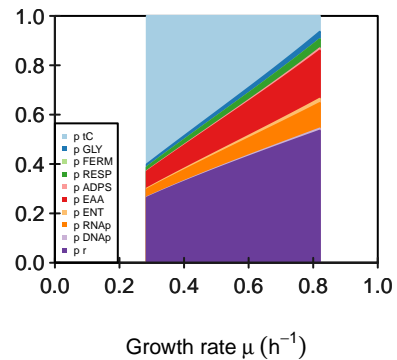
Relative biomass composition



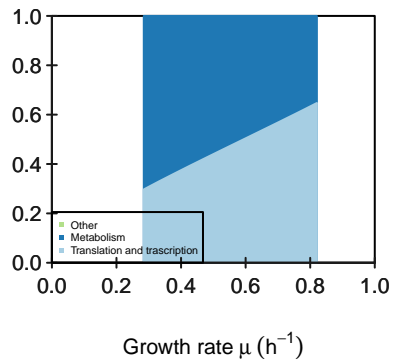
Predicted biomass



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]
	0.065	0.03	0.005	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]