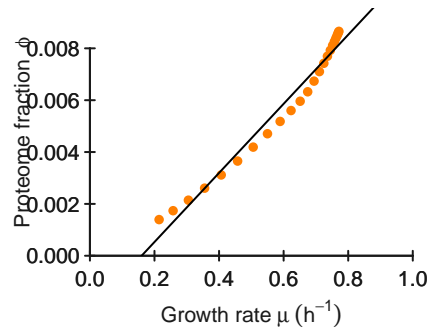
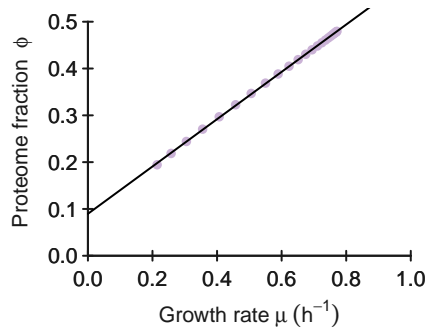


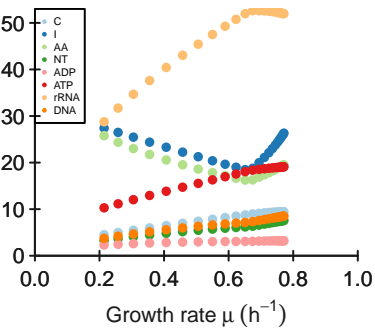
**DNAp**



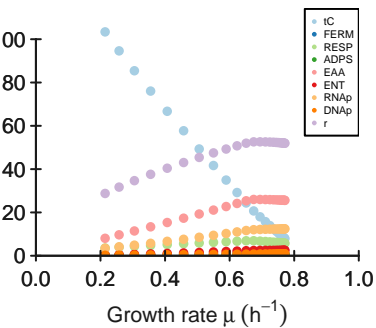
**r**



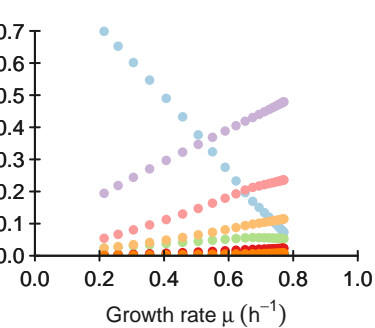
Metabolite concentrations  $c^m$  (g/L)



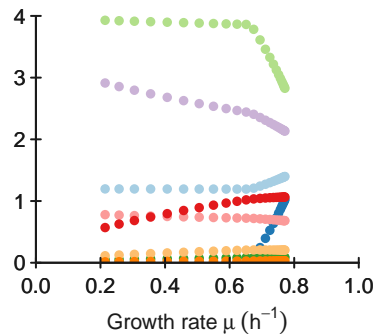
Protein concentrations  $p$  (g/L)



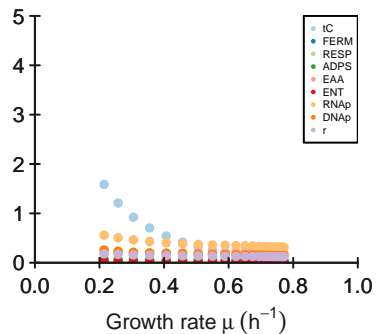
Proteome fractions  $\phi$



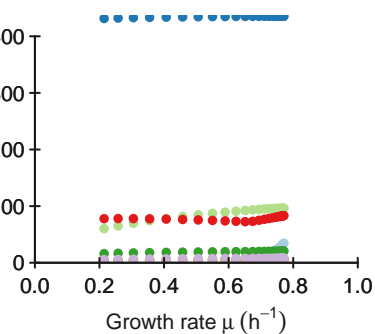
Flux fractions  $f$



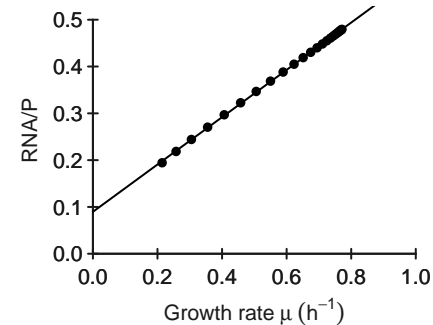
Turnover times  $\tau$  (h)



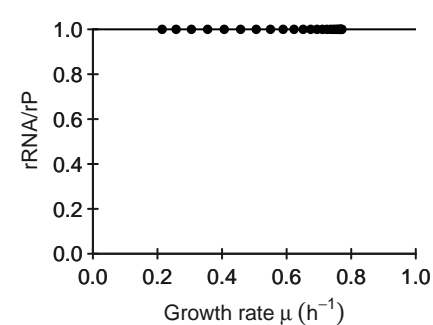
Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )



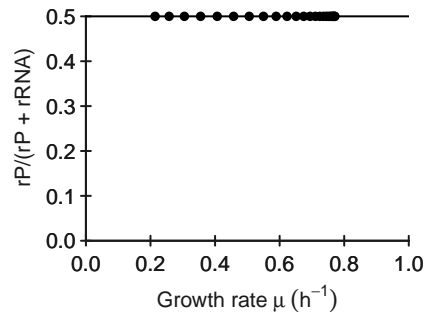
**RNA/P**



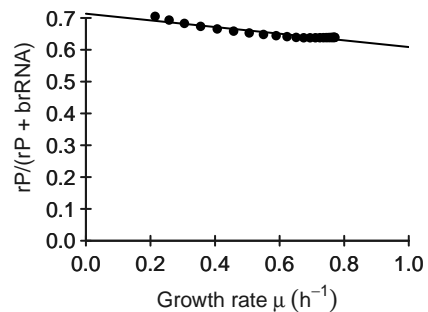
**rRNA/rP**



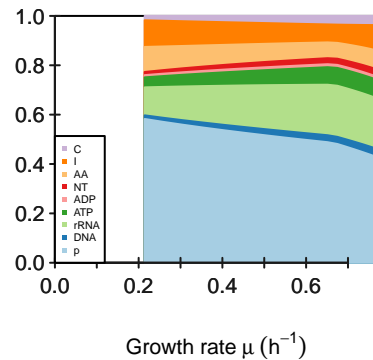
$rP/(rP + rRNA)$



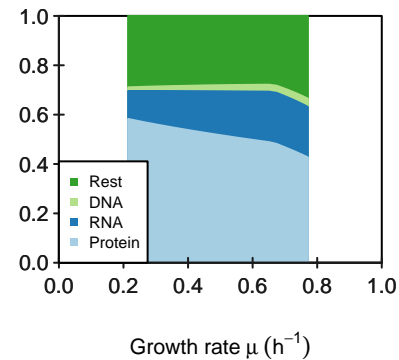
Protein mass fraction in ribosome



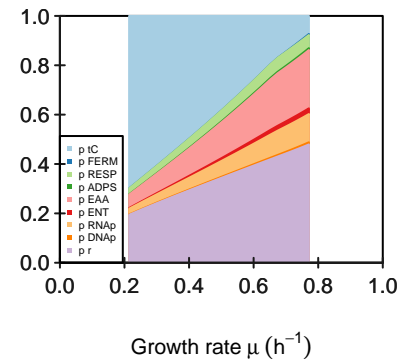
Relative biomass composition



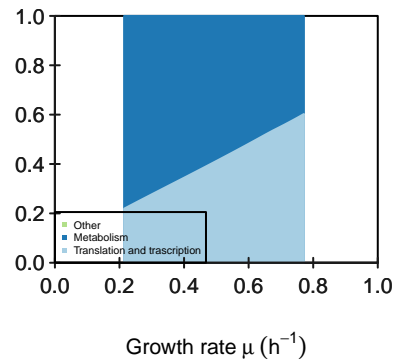
Predicted biomass



Proteome composition



Proteome sectors



```
keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant
```

M

[illegible]

**K**

[illegible]



**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
-------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------

## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.065	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]