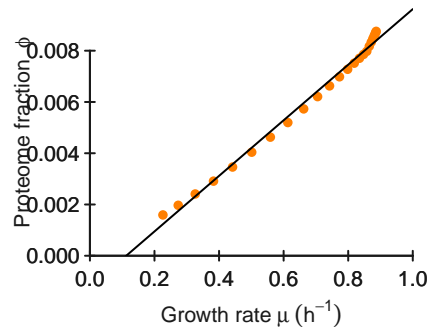
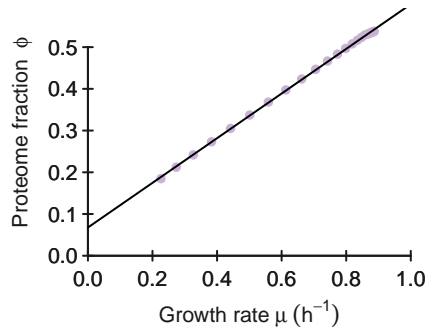


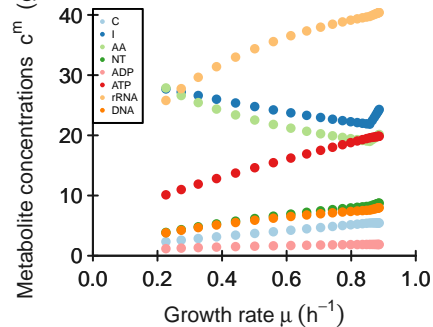
**DNAP**



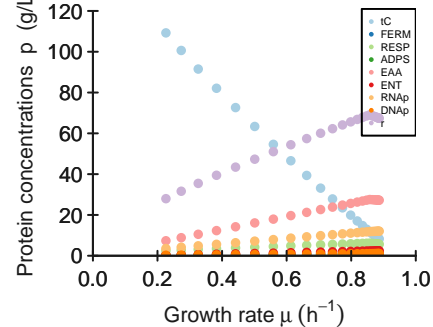
**r**



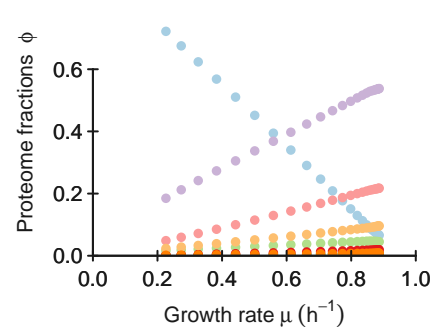
Metabolite concentrations  $c^m$  (g/L)



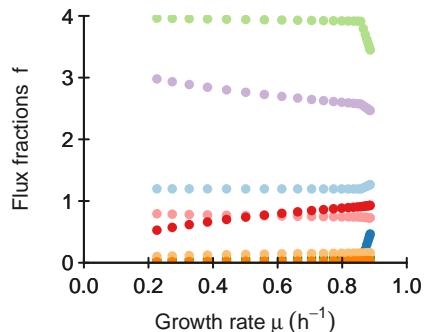
Protein concentrations  $p$  (g/L)



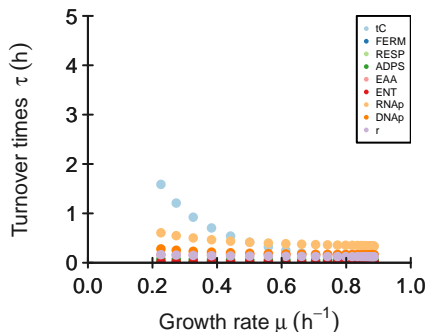
Proteome fractions  $\phi$



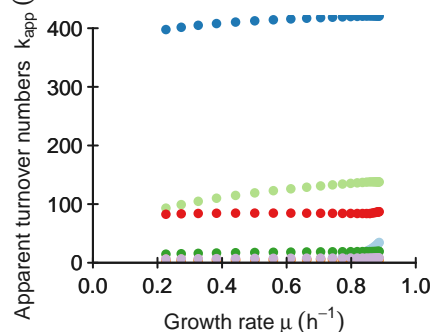
Flux fractions  $f$



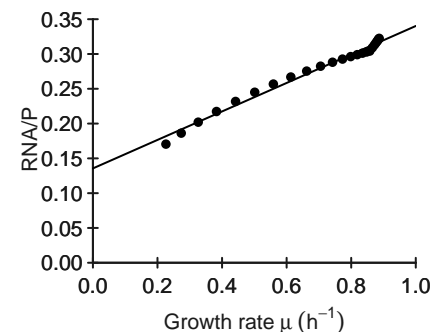
Turnover times  $\tau$  (h)



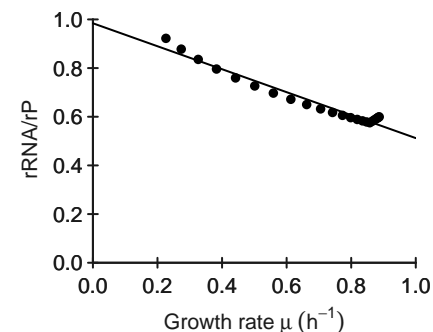
Apparent turnover numbers  $k_{app}$  ( $h^{-1}$ )



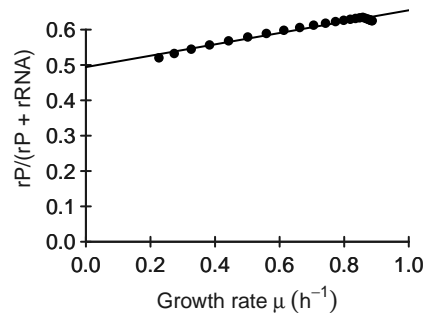
**RNA/P**



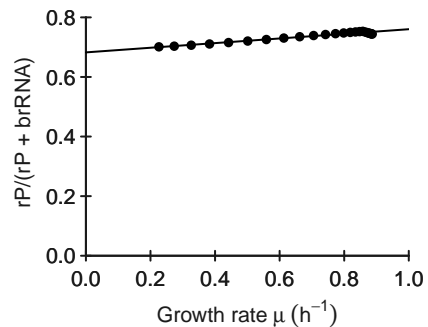
**rRNA/rP**



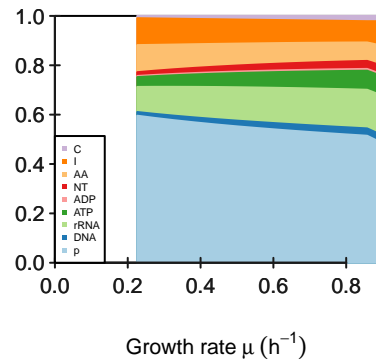
$rP/(rP + rRNA)$



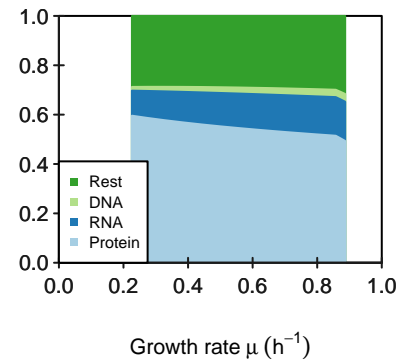
Protein mass fraction in ribosome



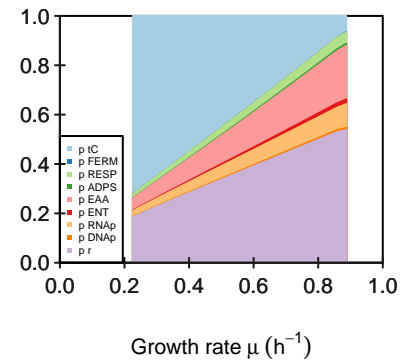
Relative biomass composition



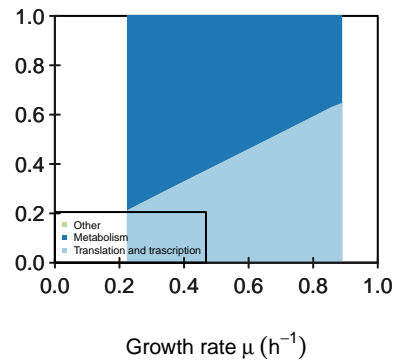
Predicted biomass



Proteome composition



Proteome sectors



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

# M

[illegible]

K

	tC		FERM		RESP	ADPS	EAA	ENT	RNAp	DNAP	r
x_C	0.1		0		0	0	0	0	0	0	0
x_W	0		0		0	0	0	0	0	0	0
C	0		0.2		2	0	0	0	0	0	0
I	0		0		0	0	8	8	0	0	0
AA	0		0		0	0	0	3	0	0	3
NT	0		0		0	3	0	0	3	3	0
ADP	0	0.0333333333333333		0.3333333333333333		0	0	0	0	0	0
ATP	0		0		0	0	0	3	0	0	3
rRNA	0		0		0	0	0	0	0	0	0
DNA	0		0		0	0	0	0	0	0	0
p	0		0		0	0	0	0	0	0	0







**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
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## 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]