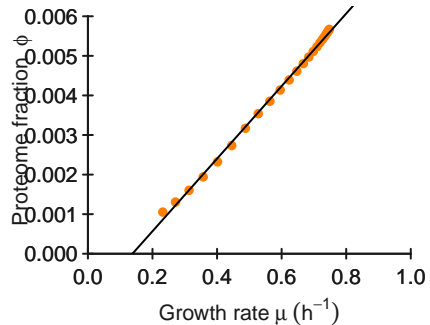
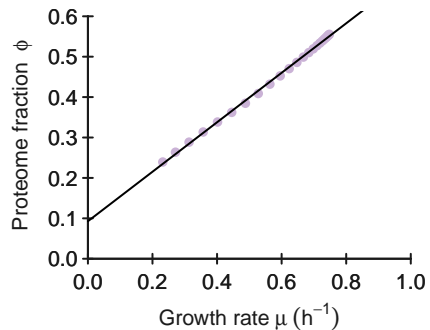


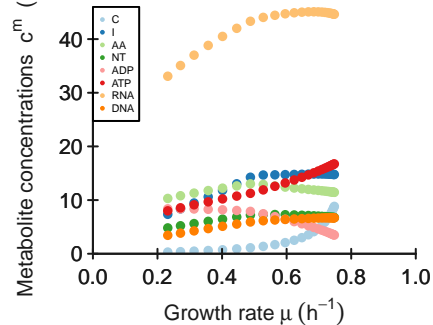
**DNAp**



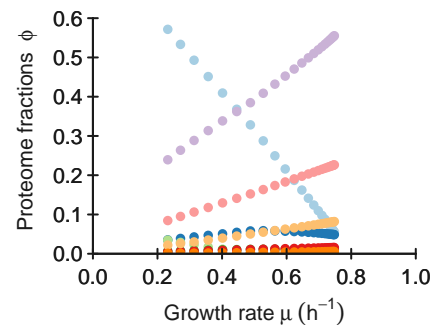
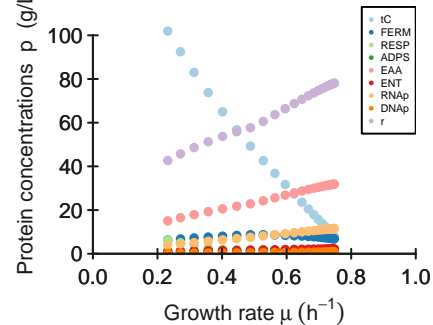
**r**



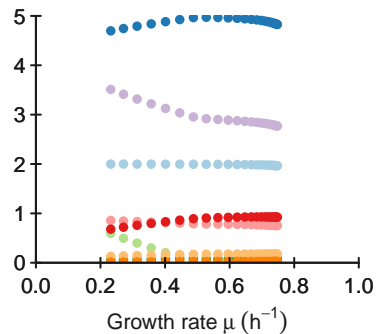
Metabolite concentrations  $c^m$  (g/L)



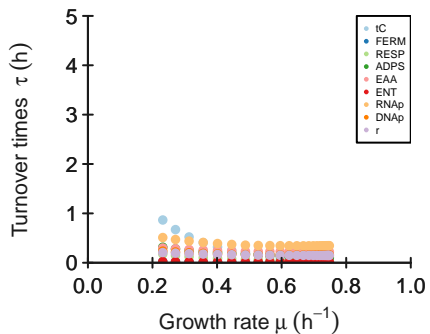
Protein concentrations  $p$  (g/L)



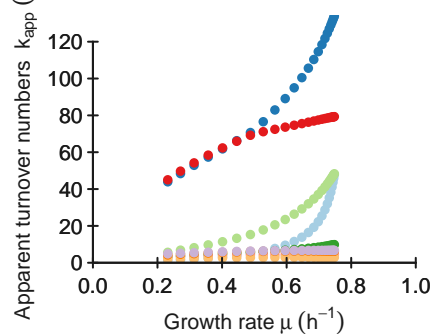
Flux fractions  $f$



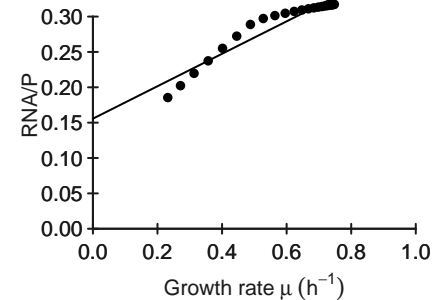
Turnover times  $\tau$  (h)



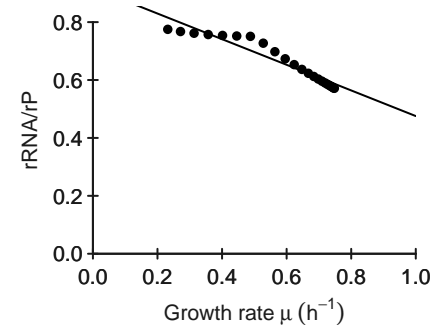
Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )



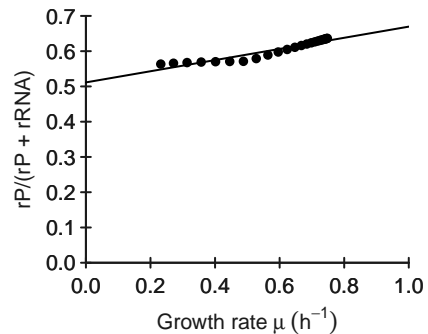
**RNA/P**



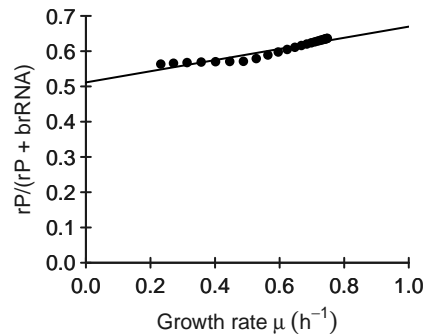
**rRNA/rP**



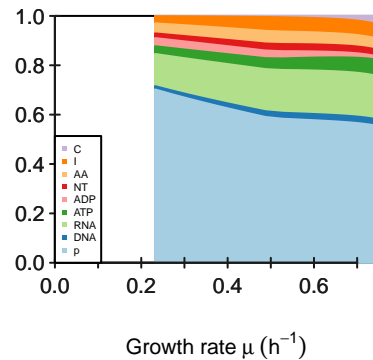
$rP/(rP + rRNA)$



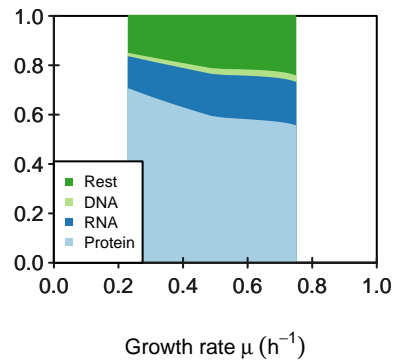
Protein mass fraction in ribosome



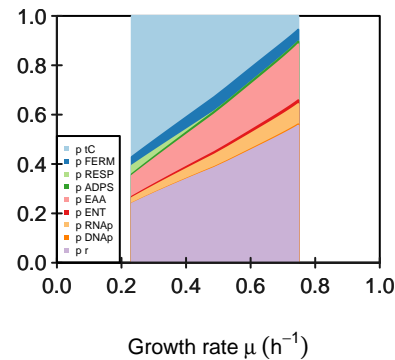
Relative biomass composition



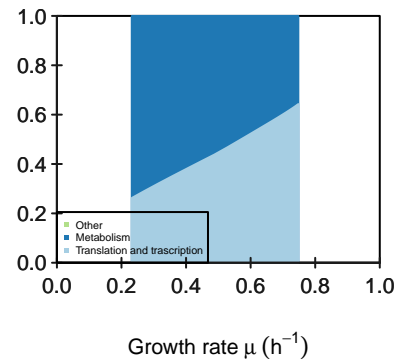
Predicted biomass



Proteome composition



Proteome sectors



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

**M**

[illegible]





## kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAP	r
kcatf	56	254	169.33333333333333	26	7	149	6	13	19
kcatb	6	25	17	3	1	15	0	0	0



## Keq

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]
	1306.66666666667	130.048	127.498039215686	4.33333333333333	18.6666666666667	2.20740740740741	Inf	Inf	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]