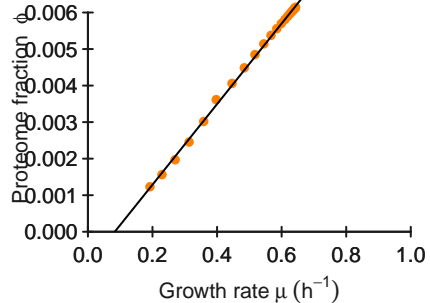
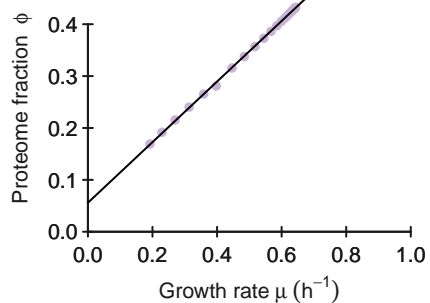


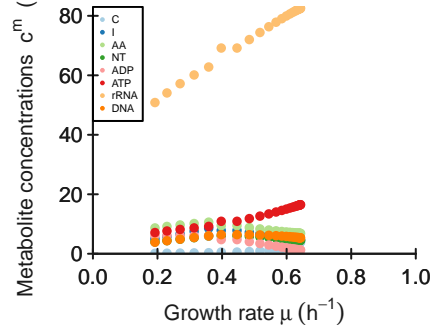
**DNAP**



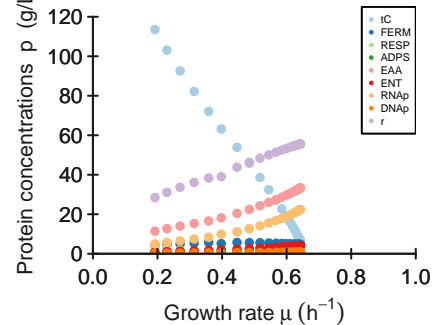
**r**



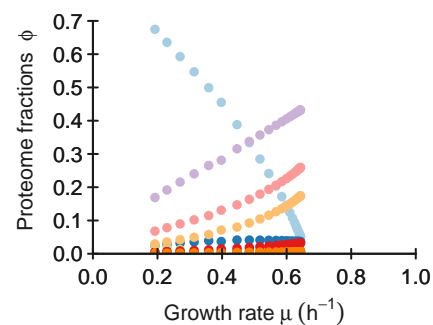
Metabolite concentrations  $c^m$  (g/L)



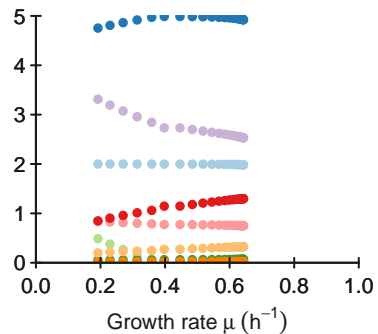
Protein concentrations  $p$  (g/L)



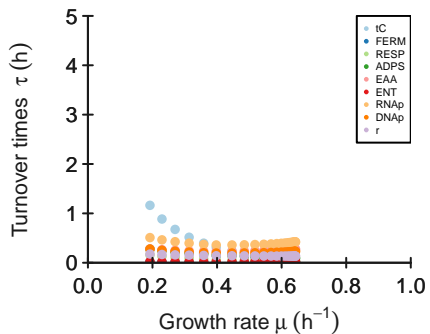
Proteome fractions  $\phi$



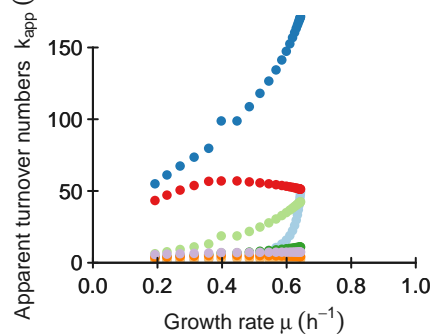
Flux fractions  $f$



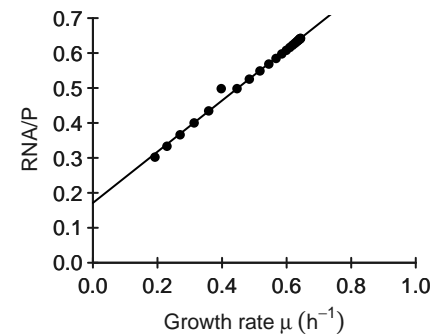
Turnover times  $\tau$  (h)



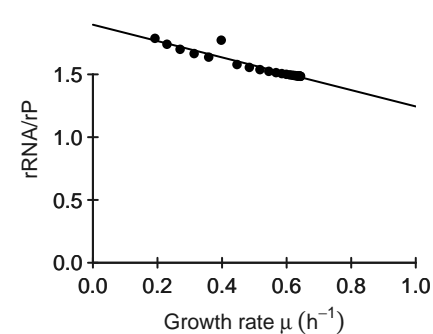
Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )



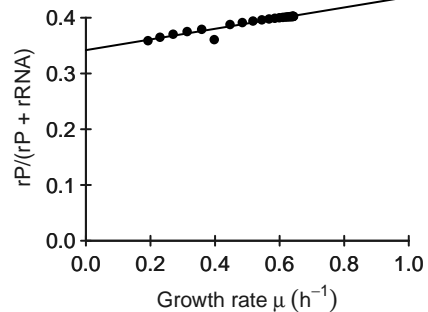
**RNA/P**



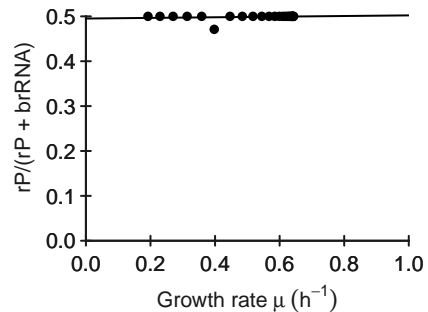
**rRNA/rP**



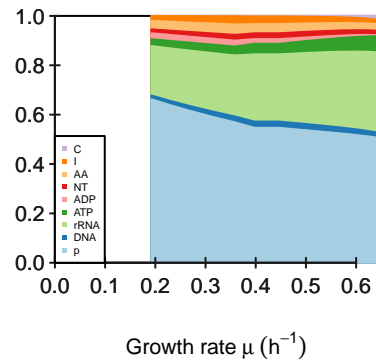
$rP/(rP + rRNA)$



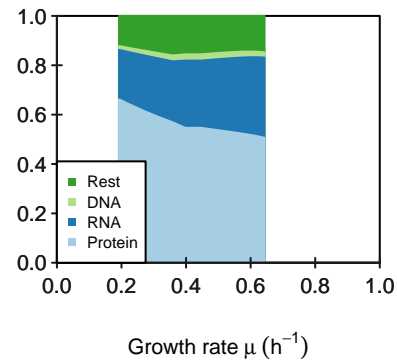
Protein mass fraction in ribosome



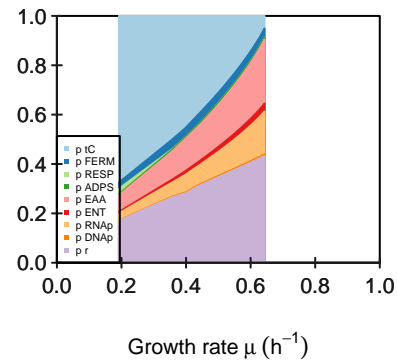
Relative biomass composition



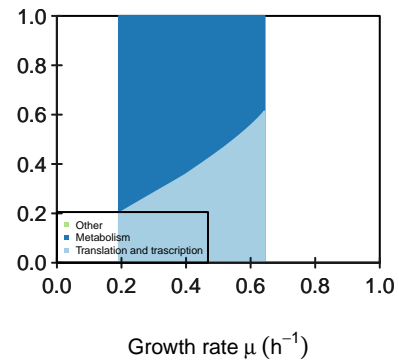
Predicted biomass



Proteome composition



Proteome sectors



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

# M

[illegible]

**K**

[illegible]



## kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	56	381	254	23	7	109	6	11	16
kcatb	6	38	25	2	1	11	0	0	0



Keq

[1,]	[1] 1306.66666666667	[2] 213.894736842105	[3] 216.746666666667	[4] 5.75	[5] 28	[6] 7.43181818181818	[7] Inf	[8] Inf	[9] 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**

5

### minimal phi constraint

[illegible]

### minimal f constraint

[illegible]