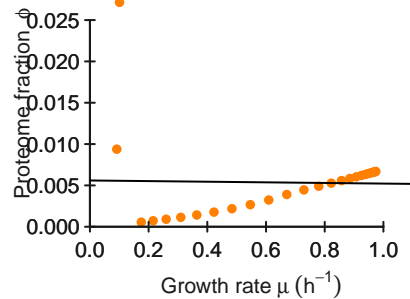
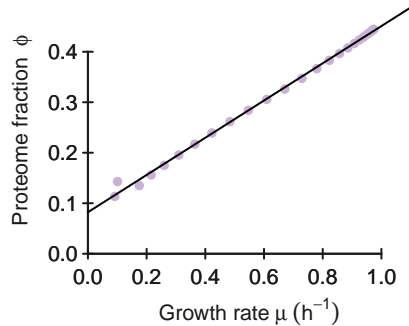


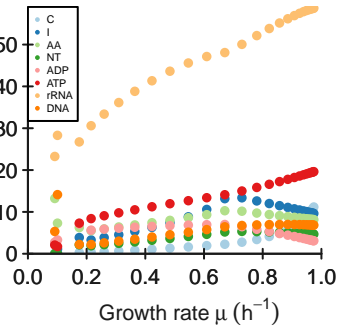
**DNAP**



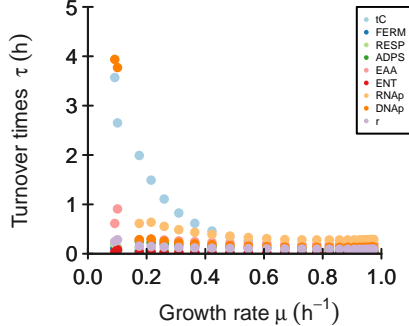
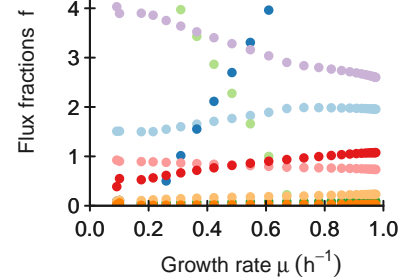
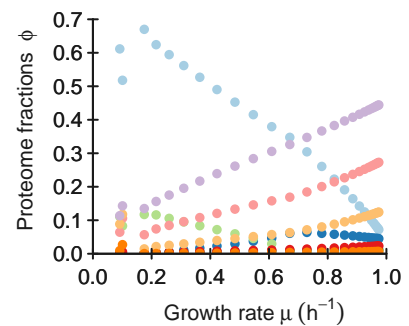
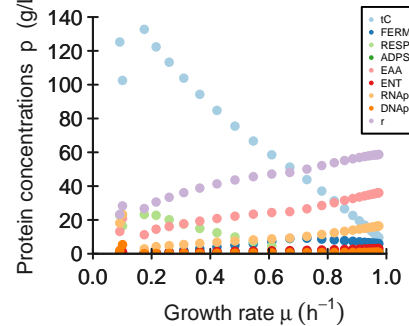
**r**



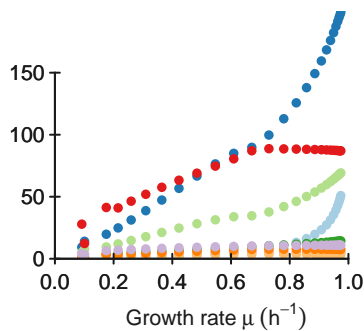
Metabolite concentrations  $c^m$  (g/L)



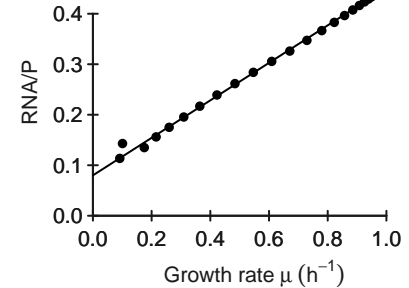
Protein concentrations  $p$  (g/L)



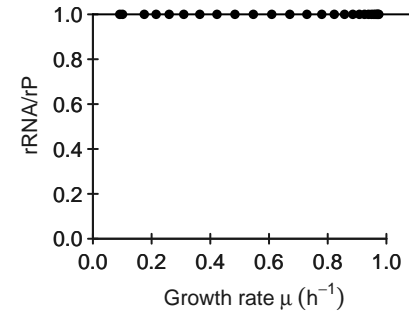
Apparent turnover numbers  $k_{app}$  ( $h^{-1}$ )



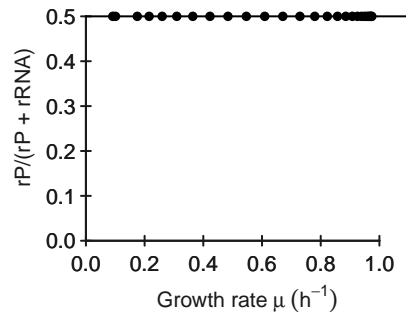
**RNA/P**



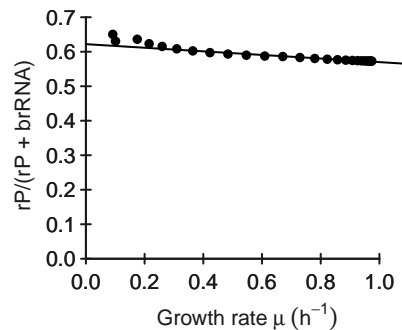
**rRNA/rP**



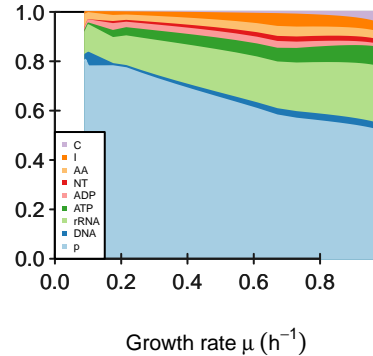
$rP/(rP + rRNA)$



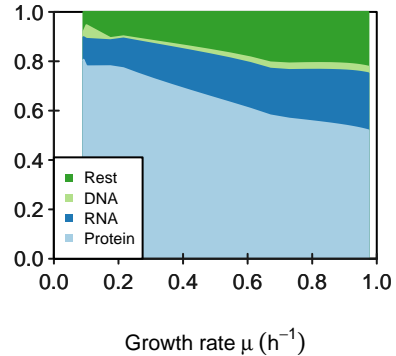
Protein mass fraction in ribosome



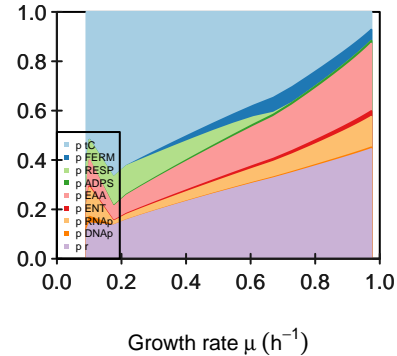
Relative biomass composition



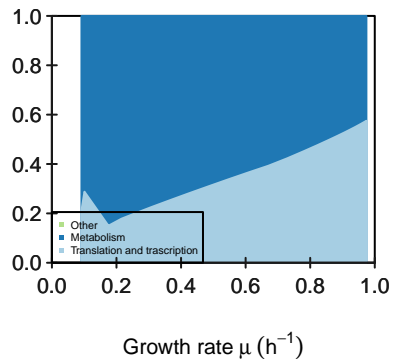
Predicted biomass



Proteome composition



Proteome sectors



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

# M

[illegible]





# kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	58.9	818.4	204.6	28.9	7.8	157.9	6.7	14.5	21.1
kcatb	6	82	20	3	1	16	0	0	0



## Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	2159.666666666667	598.829268292683	306.9	9.633333333333333	23.4	2.4671875	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 f constraint

[illegible]