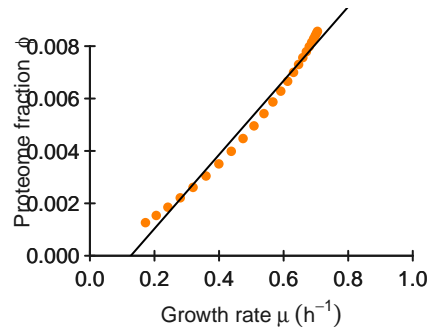
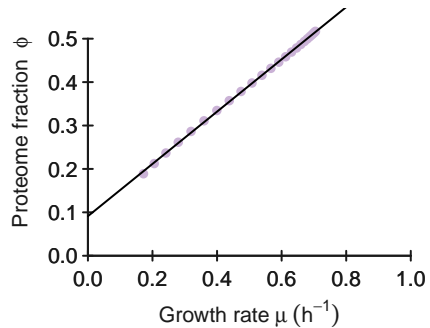


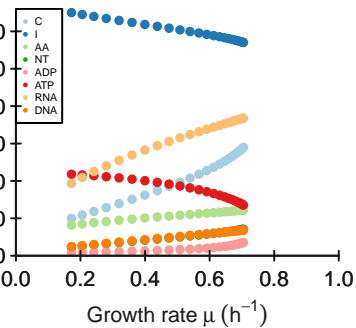
DNAp



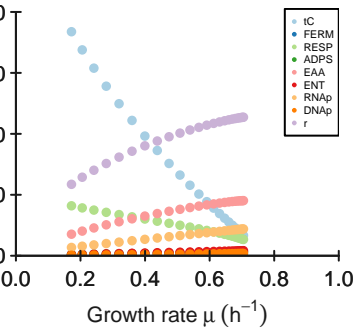
r



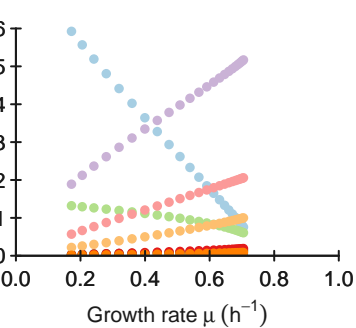
Metabolite concentrations c^m (g/L)



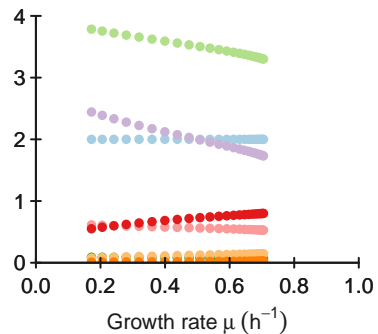
Protein concentrations p (g/L)



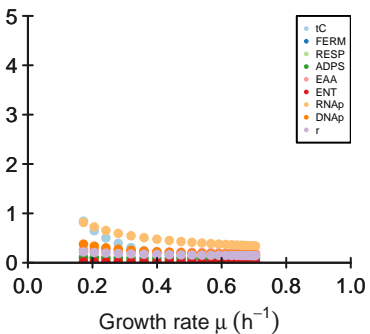
Proteome fractions ϕ



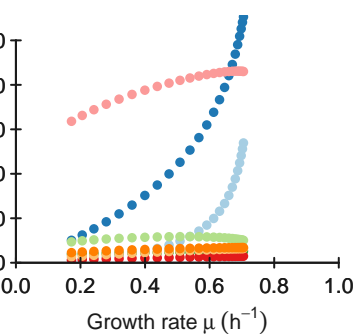
Flux fractions f



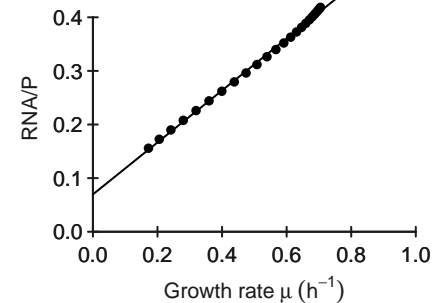
Turnover times τ (h)



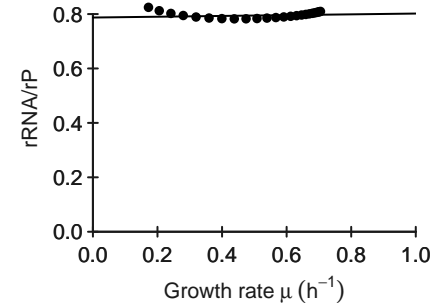
Apparent turnover numbers k_{app} (h^{-1})



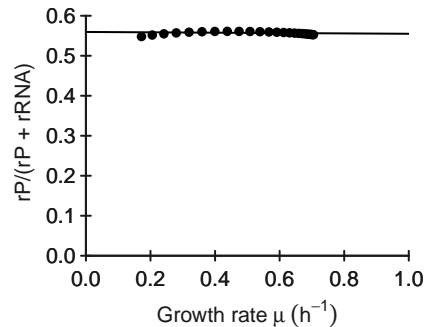
RNA/P



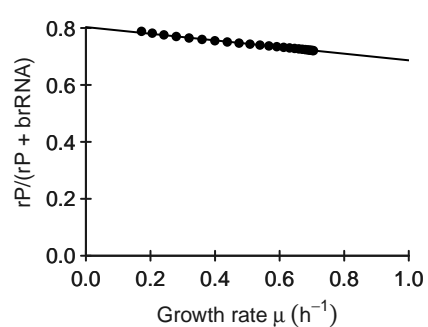
rRNA/rP



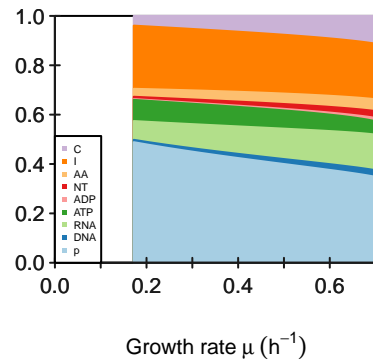
$rP/(rP + rRNA)$



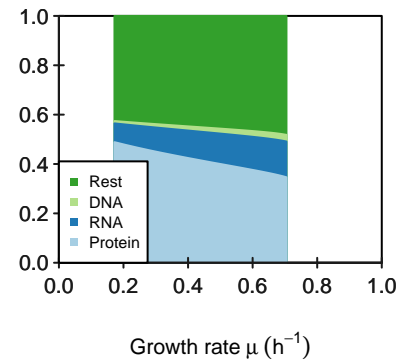
Protein mass fraction in ribosome



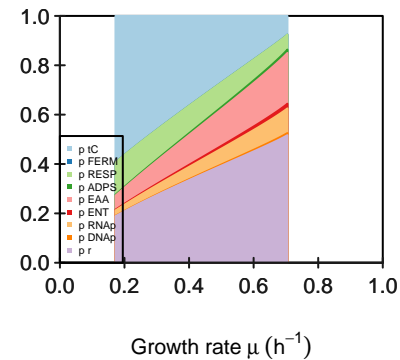
Relative biomass composition



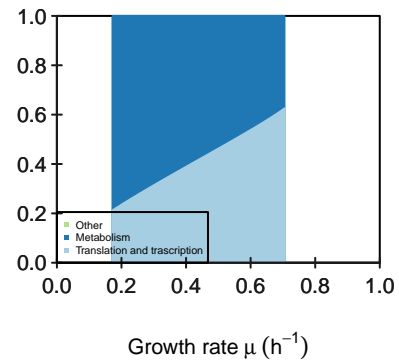
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	77	8920	446	26	10	149	6	13	19
kcatb	8	892	45	3	1	15	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
914.375	5228.57142857143	518.209523809524	4.33333333333333	0.408163265306122	1.41904761904762	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]

