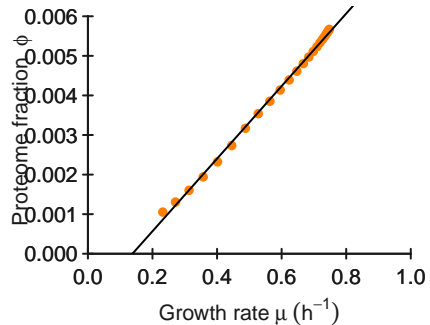
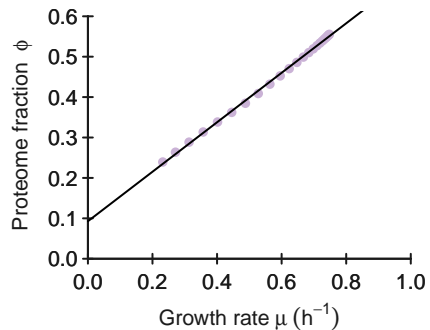


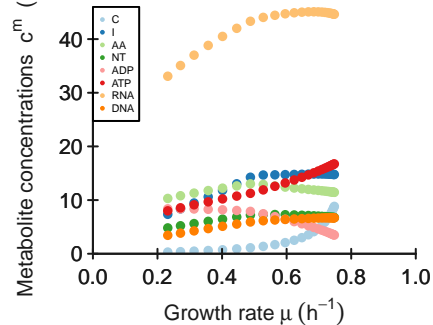
DNAP



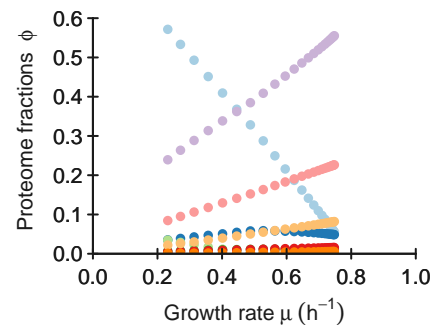
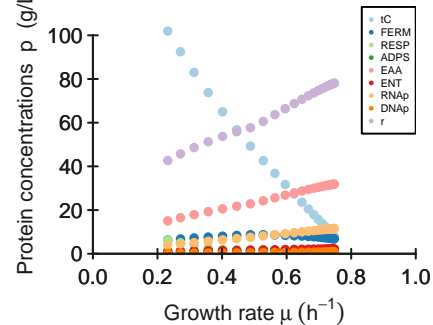
r



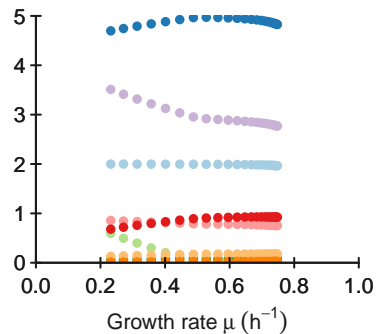
Metabolite concentrations c^m (g/L)



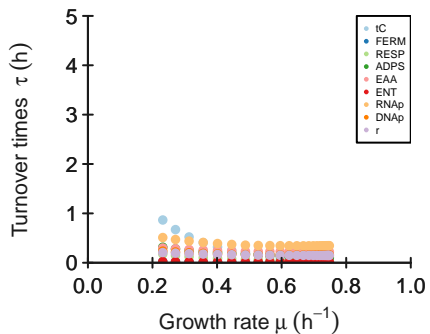
Protein concentrations p (g/L)



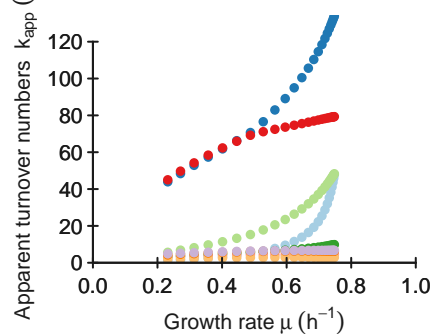
Flux fractions f



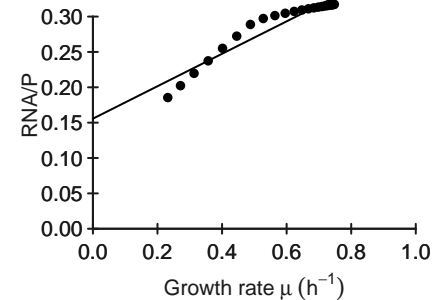
Turnover times τ (h)



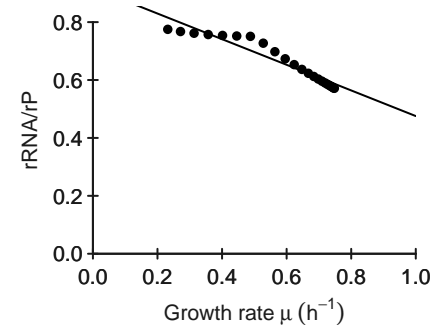
Apparent turnover numbers k_{app} (h^{-1})

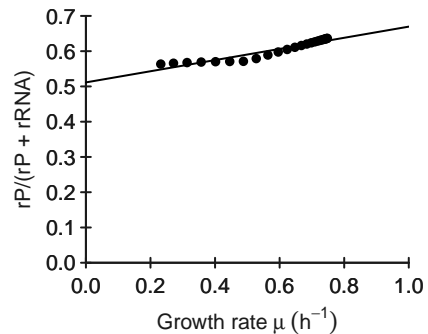
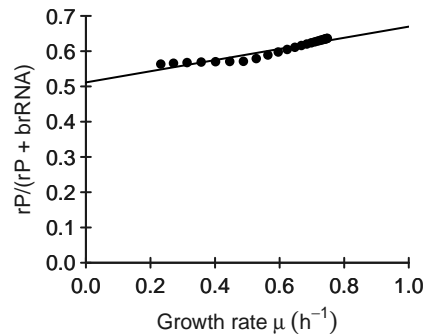


RNA/P

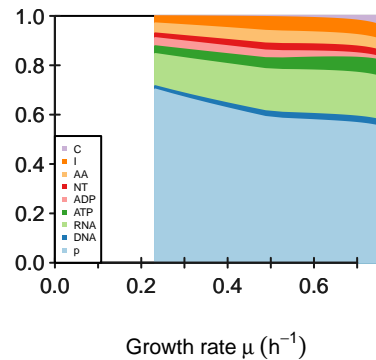


rRNA/rP

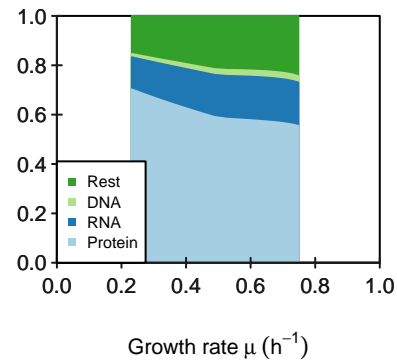


$rP/(rP + rRNA)$ **Protein mass fraction in ribosome**

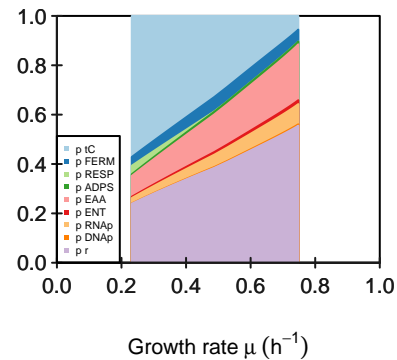
Relative biomass composition



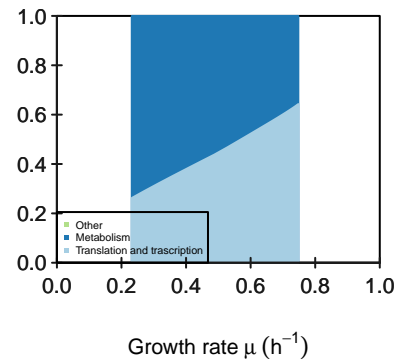
Predicted biomass



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	56	254	169.33333333333333	26	7	149	6	13	19
kcatb	6	25	17	3	1	15	0	0	0

Keq

[1,]	[1] 1306.66666666667	[2] 130.048	[3] 127.498039215686	[4] 4.33333333333333	[5] 18.6666666666667	[6] 2.20740740740741	[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

3

minimal f constraint

[illegible]