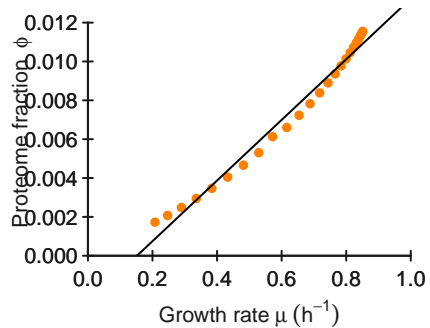
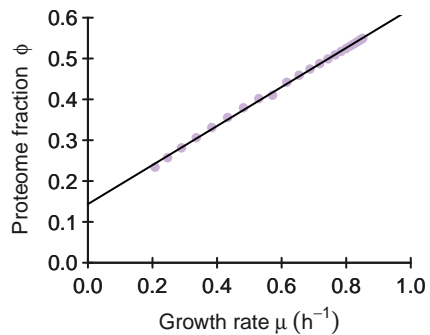


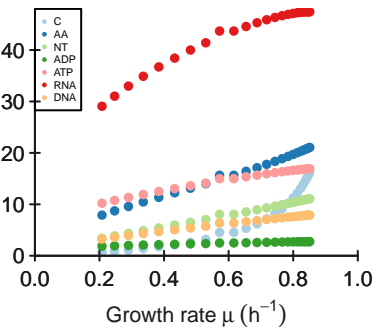
DNAP



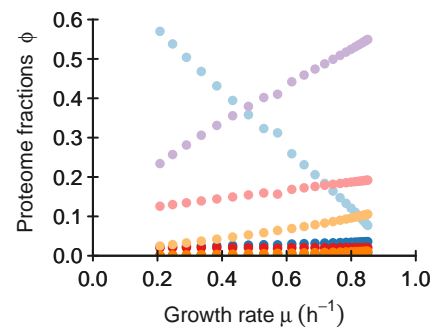
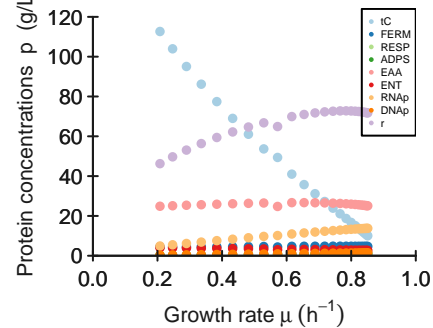
r



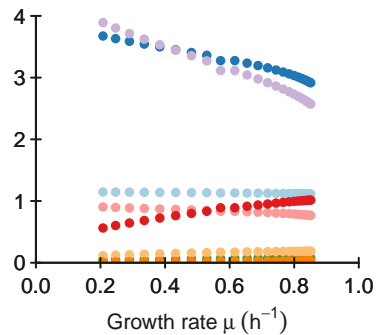
Metabolite concentrations c^m (g/L)



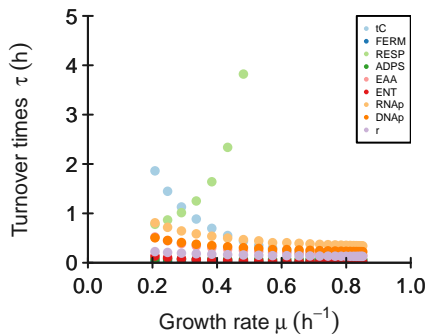
Protein concentrations p (g/L)



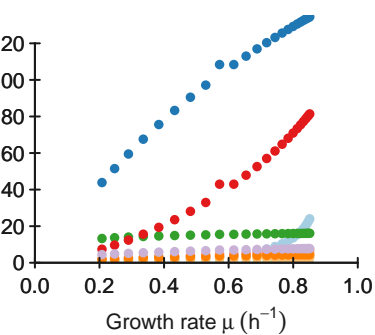
Flux fractions f



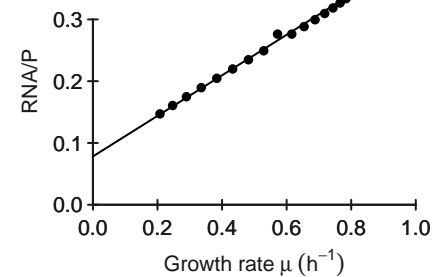
Turnover times τ (h)



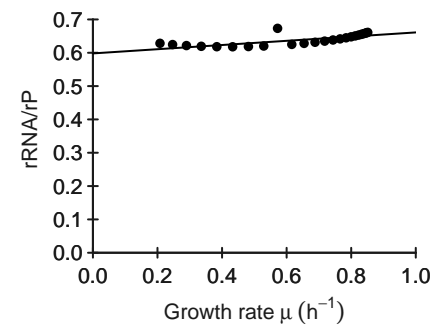
Apparent turnover numbers k_{app} (h^{-1})



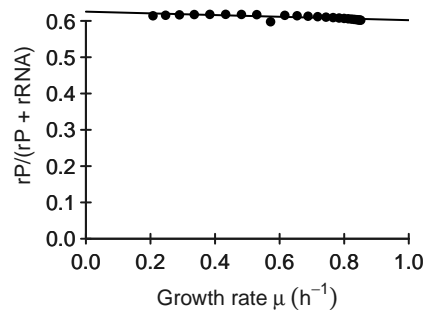
RNA/P



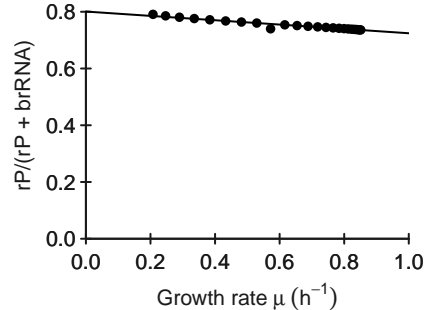
rRNA/rP



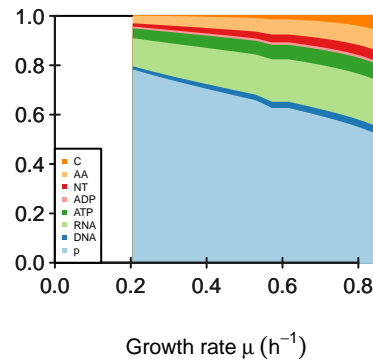
$rP/(rP + rRNA)$



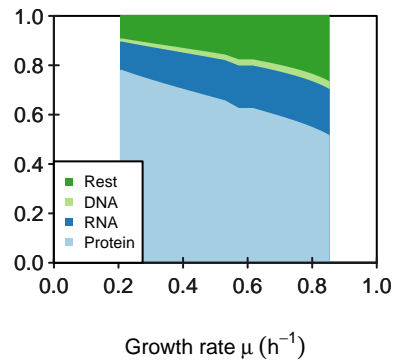
Protein mass fraction in ribosome



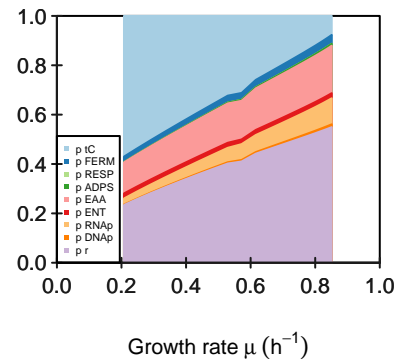
Relative biomass composition



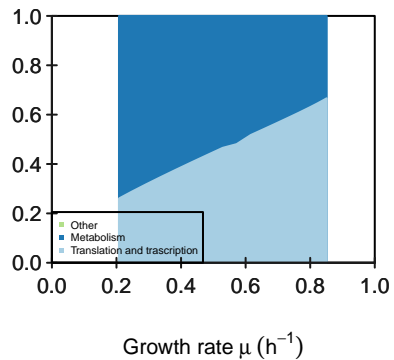
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

KA[illegible]

kcat

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
kcatf	29	200	150	18	8	153	6	13	19
kcatb	3	20	50	2	1	15	0	0	0

Keq

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]
1643.333333333333	2000	6	90	80	2.3375	Inf	Inf	Inf	

minimal phi constraint

[illegible]

minimal f constraint

[illegible]