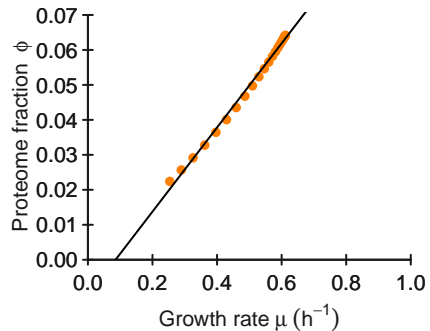
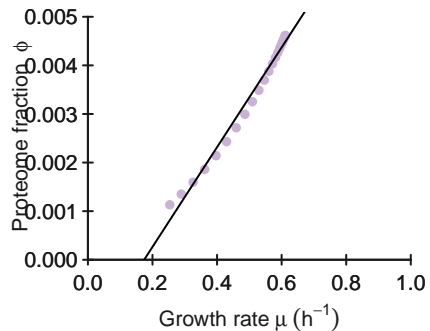


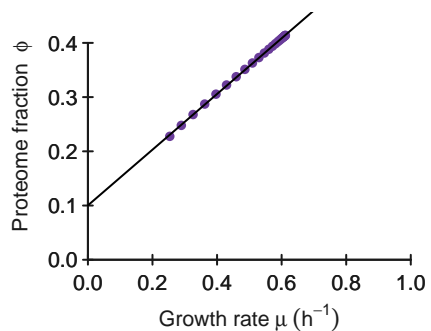
RNAP



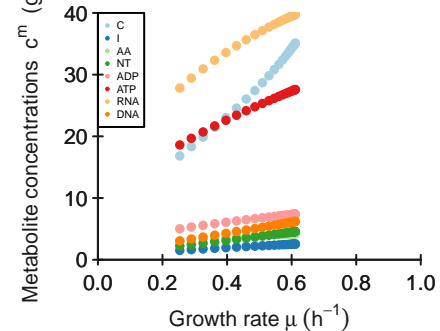
DNAP



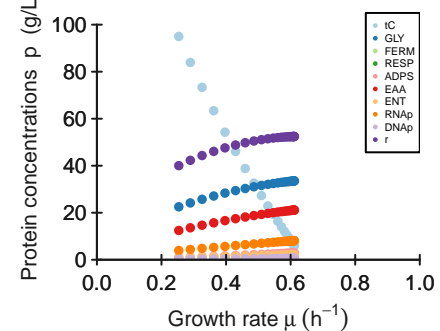
r



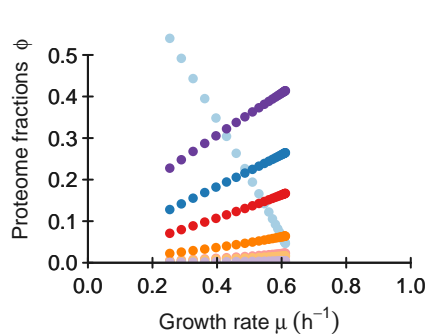
Metabolite concentrations c^m (g/L)



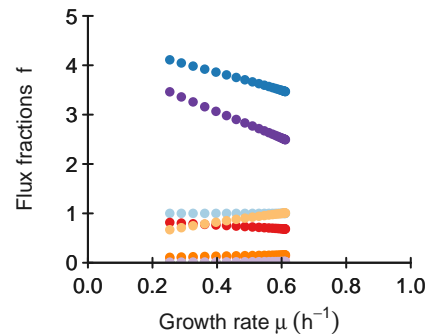
Protein concentrations p (g/L)



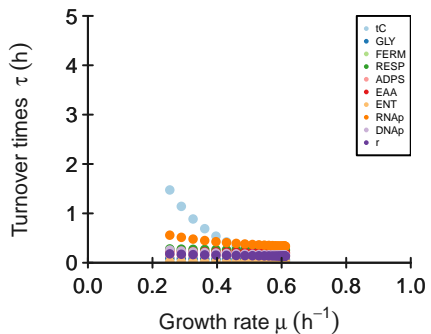
Proteome fractions ϕ



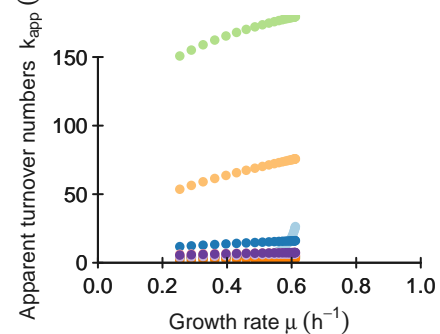
Flux fractions f



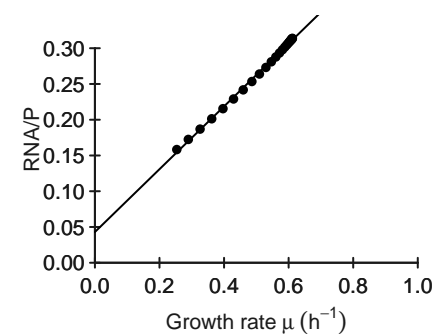
Turnover times τ (h)

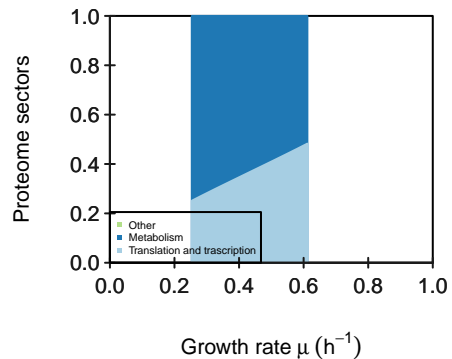
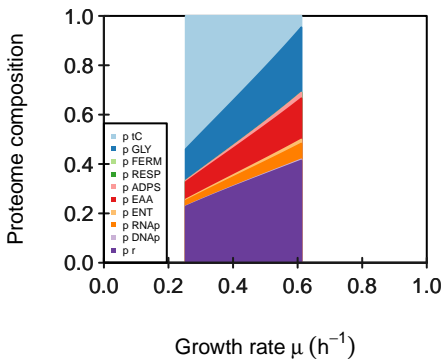
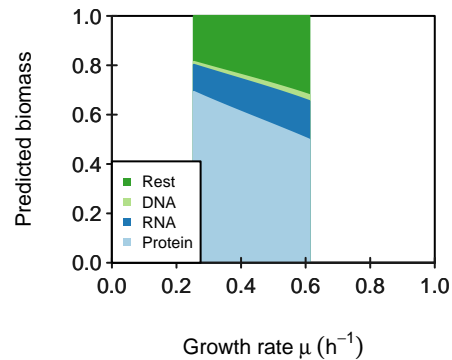
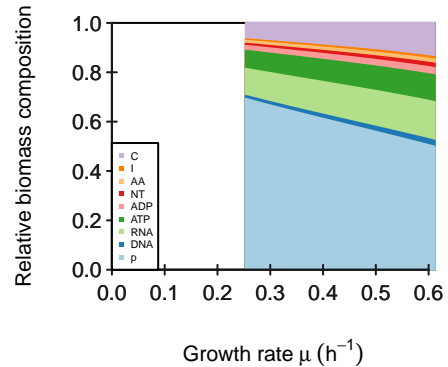
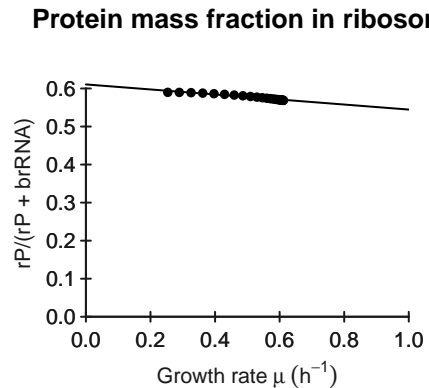
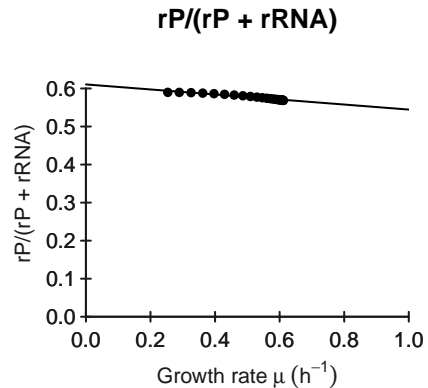
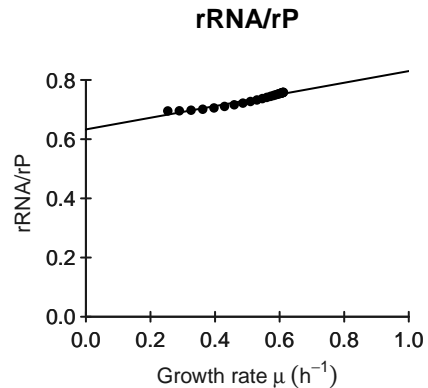


Apparent turnover numbers k_{app} (h^{-1})



RNA/P





keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

K

[illegible]

KA[illegible]

kcat[illegible]

Keq

[1,]	[,1] Inf	[,2] Inf	[,3] Inf	[,4] Inf	[,5] Inf	[,6] Inf	[,7] Inf	[,8] Inf	[,9] Inf	[,10] Inf
-------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	---------------------

phi input

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]	[10]
	0.065	0.03	0.005	0.035	0.003	0.248	0.032	0.119	0.003	0.46

average saturation input

3

minimal phi constraint

[illegible]

minimal f constraint

[illegible]