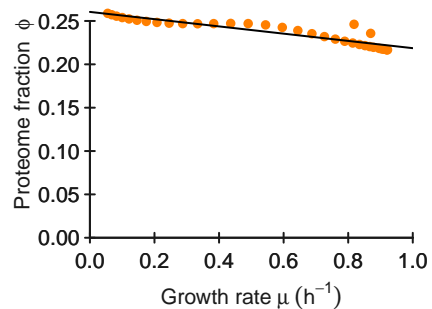
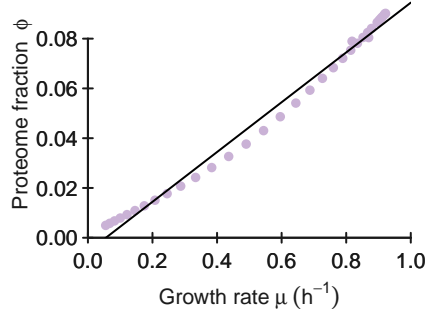


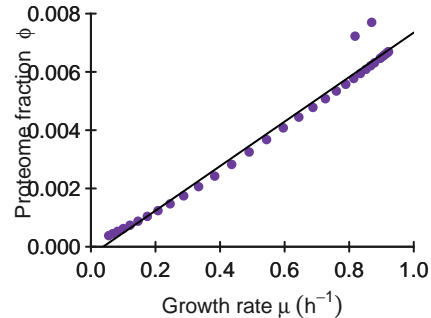
Maint



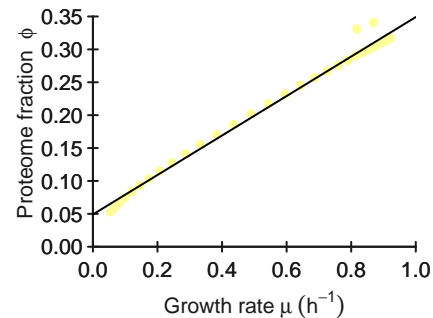
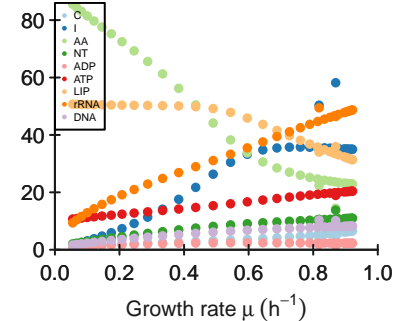
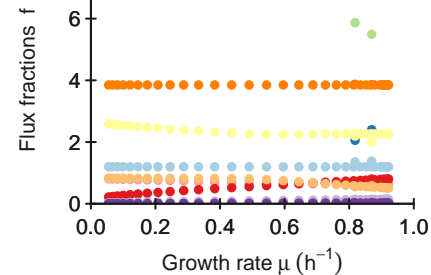
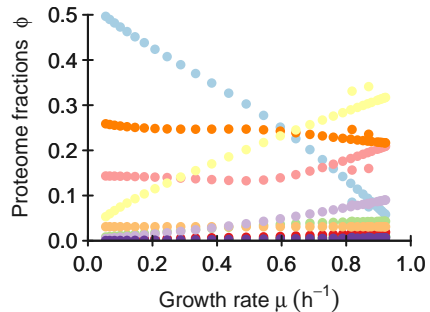
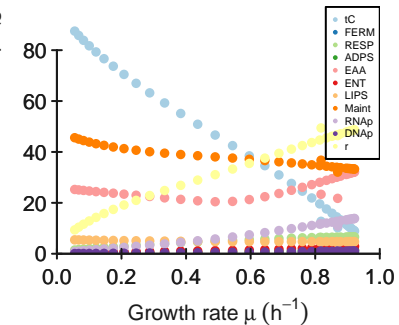
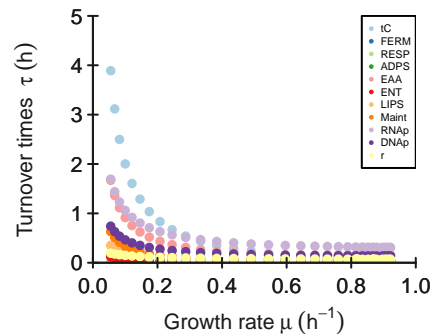
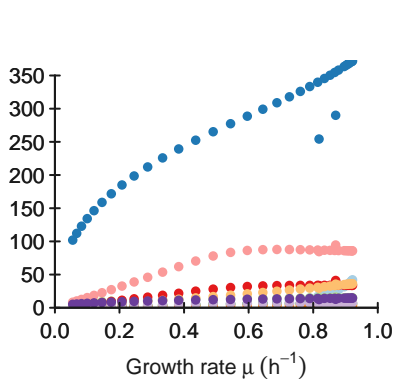
RNAP



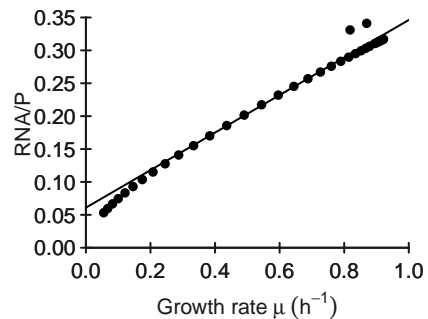
DNAP



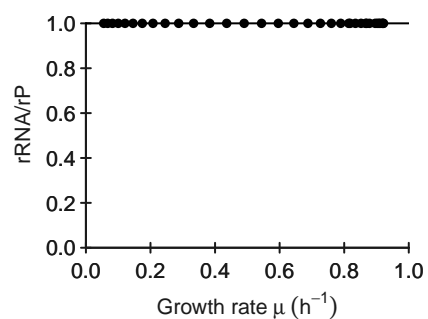
r

Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})

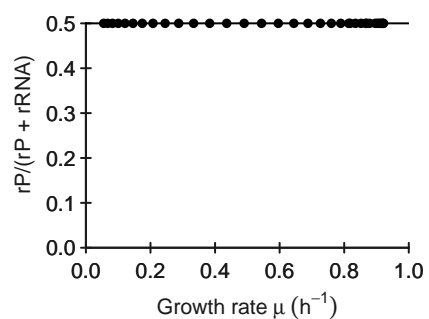
RNA/P



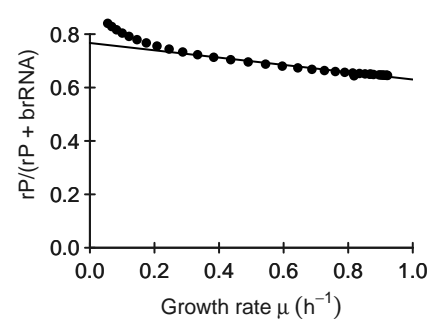
rRNA/rP



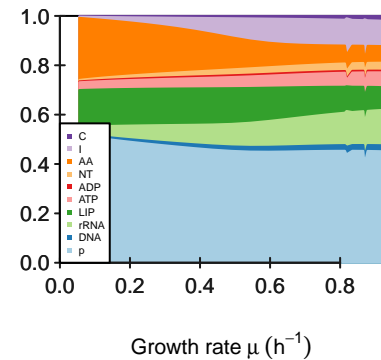
rP/(rP + rRNA)



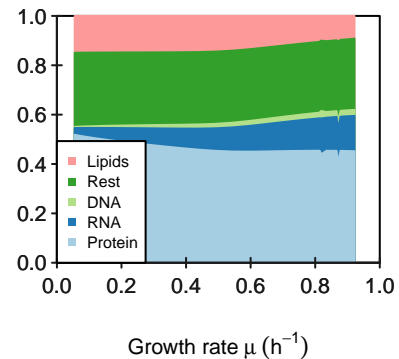
Protein mass fraction in ribosome



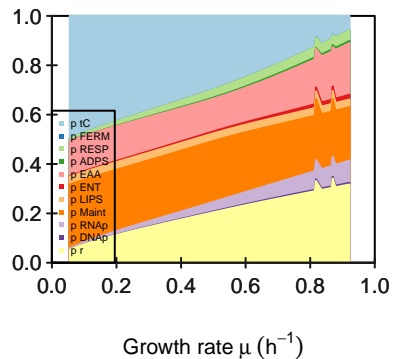
Relative biomass composition



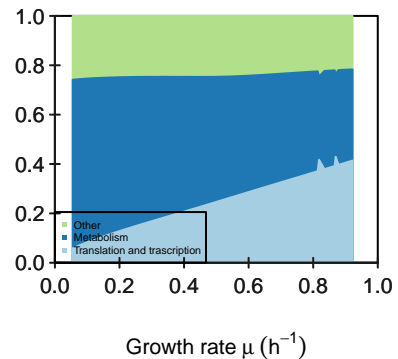
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

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	[,11] Inf
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phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	0.043	0.023	0.023	0.002	0.165	0.021	0.031	0.3036	0.0794	0.002	0.307

average saturation input

2

minimal phi constraint

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	0	0	0	0	0	0	0.031	0	0	0	0

minimal f constraint

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	0	0	0	0	0	0	0	3.85	0	0	0