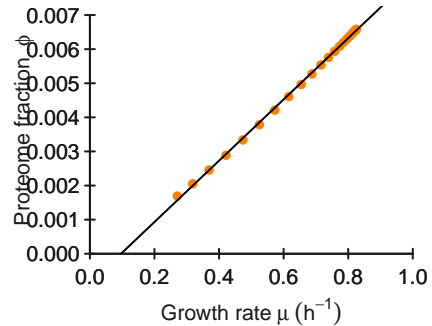
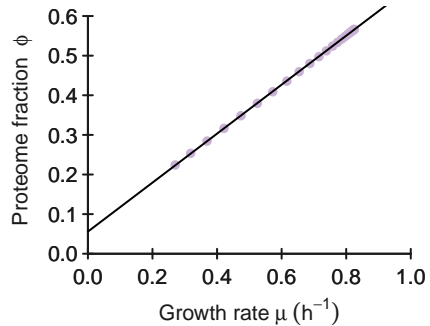
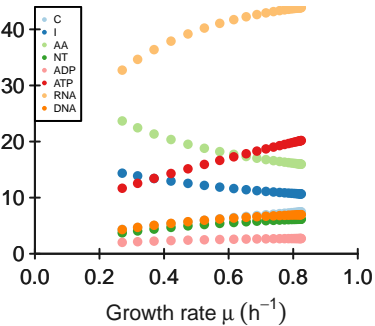
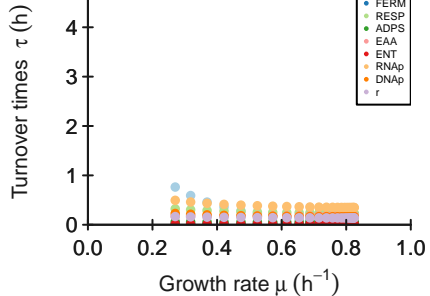
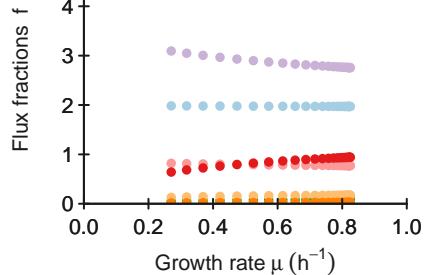
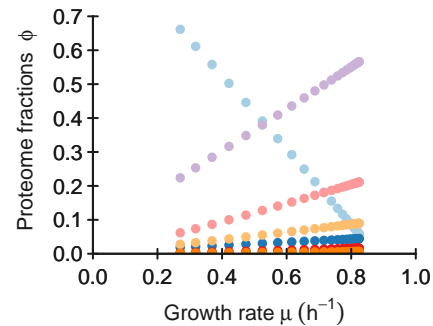
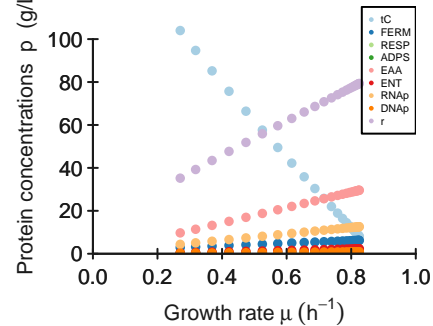
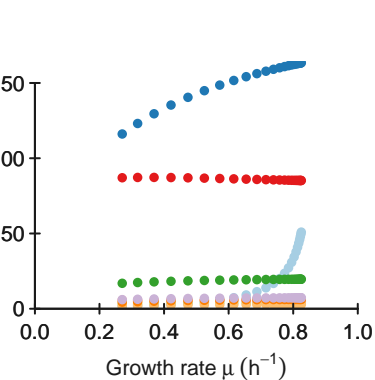
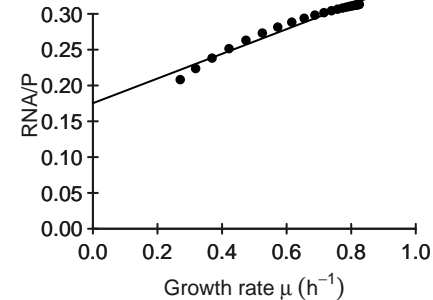
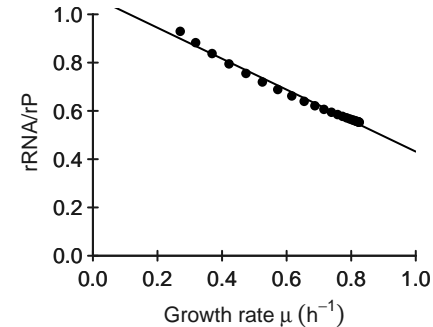
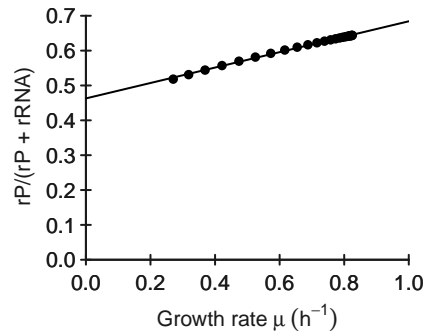
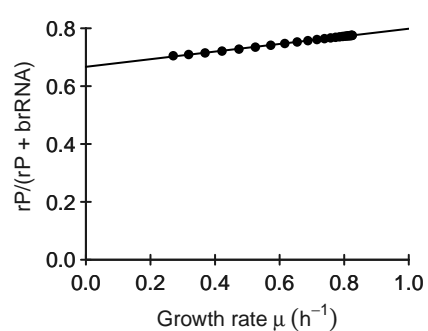
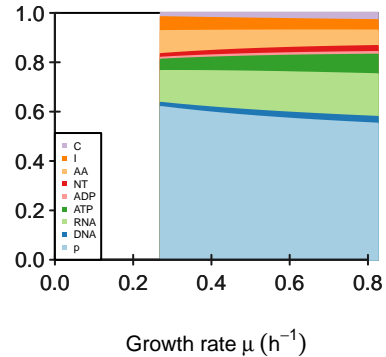
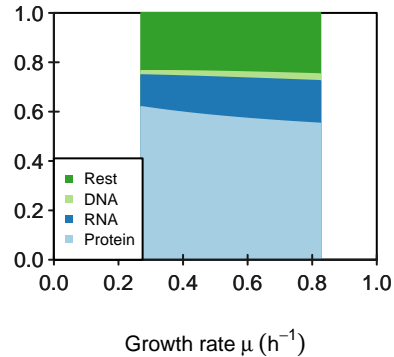
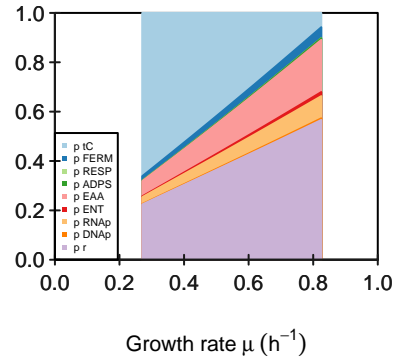
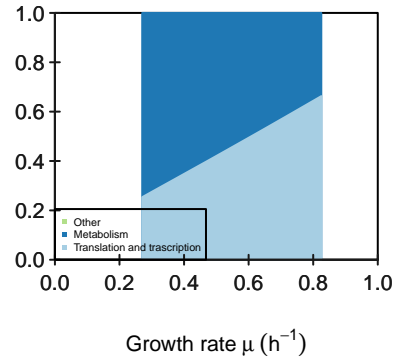


DNAp**r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Apparent turnover numbers k_{app} (h^{-1})**RNA/P****rRNA/rP**

$rP/(rP + rRNA)$ **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

kcat[illegible]

Keq

[1,]	[,1] Inf	[,2] Inf	[,3] Inf	[,4] Inf	[,5] Inf	[,6] Inf	[,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 phi constraint

[illegible]

minimal f constraint

[illegible]