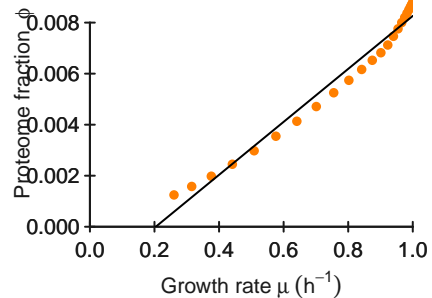
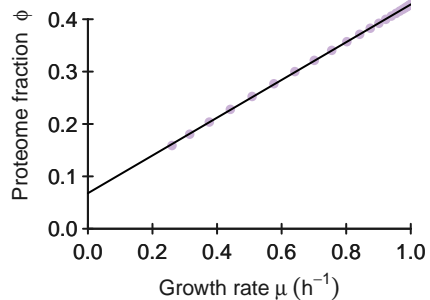


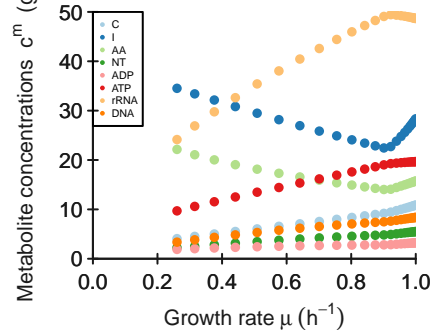
DNAP



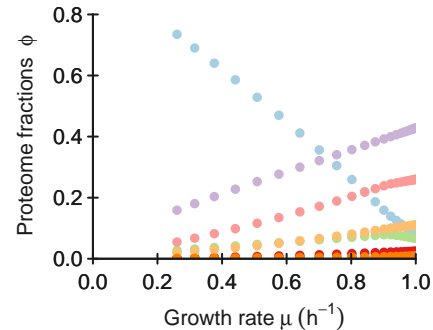
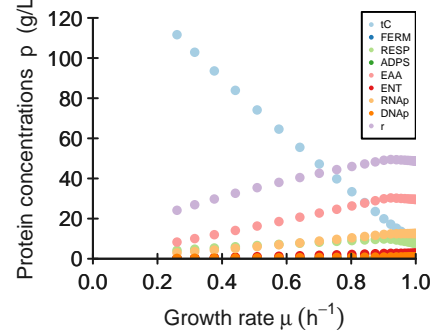
r



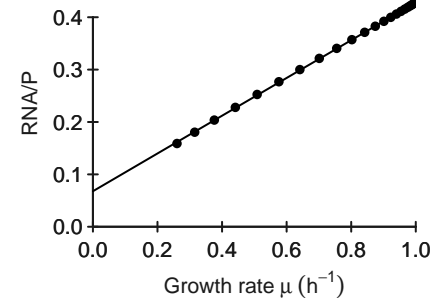
Metabolite concentrations c^m (g/L)



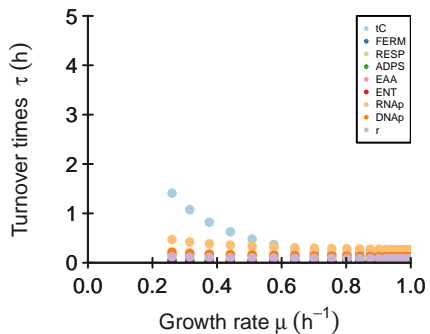
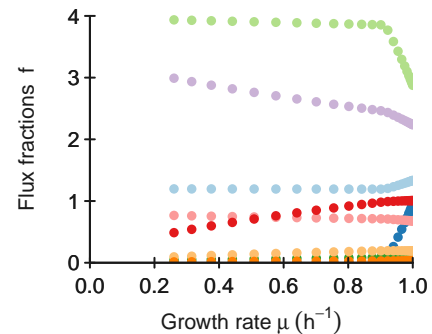
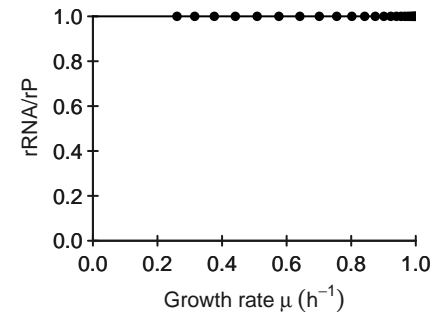
Protein concentrations p (g/L)



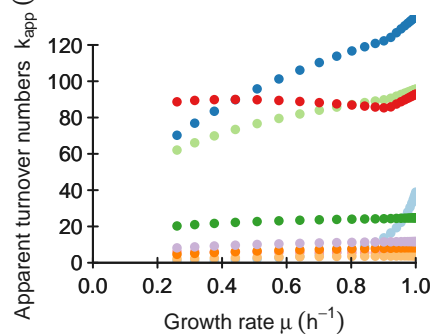
RNA/P



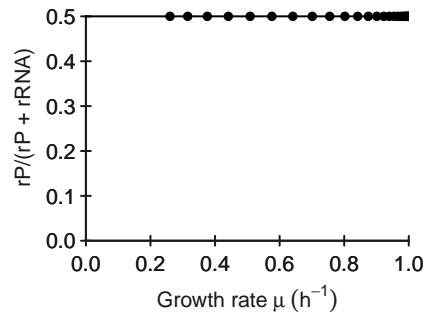
rRNA/rP



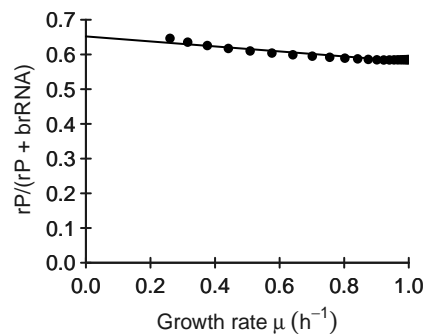
Apparent turnover numbers k_{app} (h^{-1})



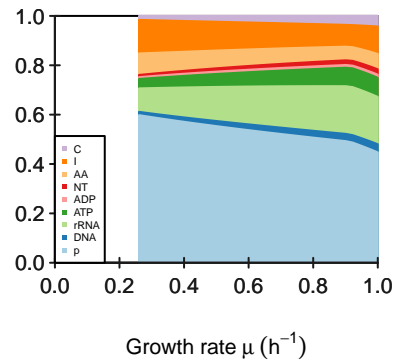
$rP/(rP + rRNA)$



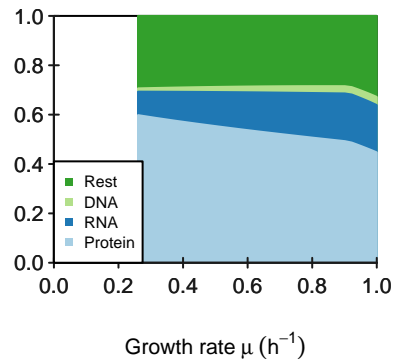
Protein mass fraction in ribosome



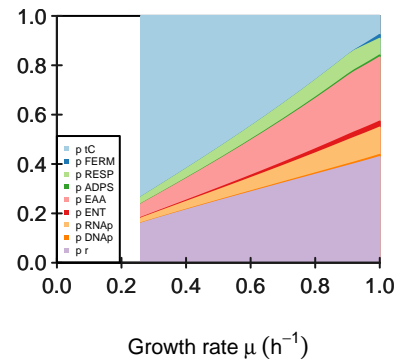
Relative biomass composition



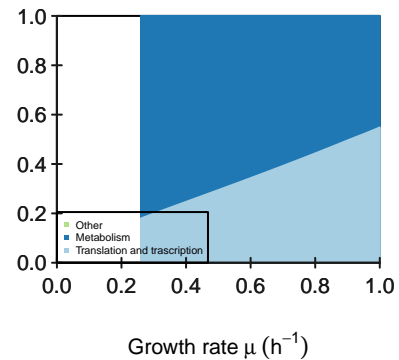
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

KA[illegible]

kcat

tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	2'
12.7810207028360	291.9617026912840	145.9808513456420	29.27122469141410	7.880714339996110	163.2433684713480	6.754898005710950	14.63561234570710	2'

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]