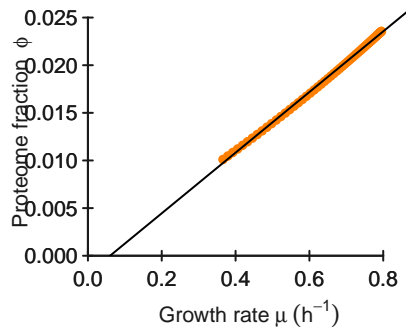
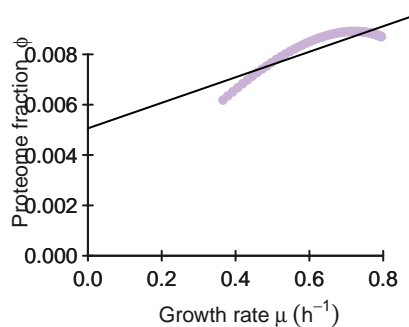
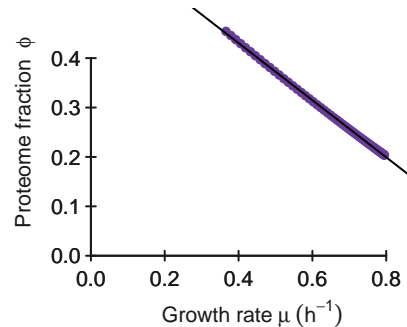
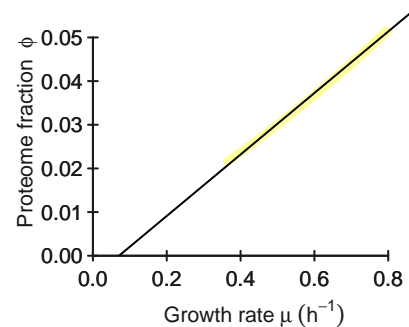
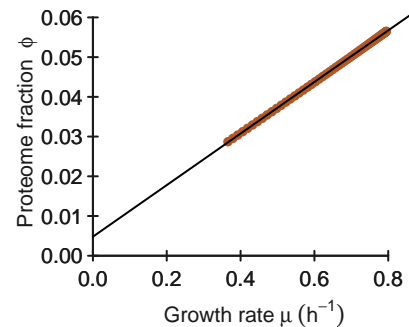
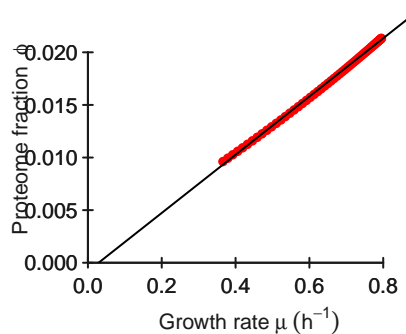
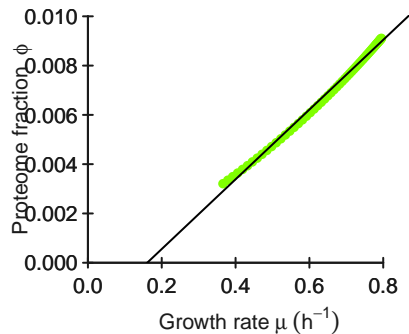
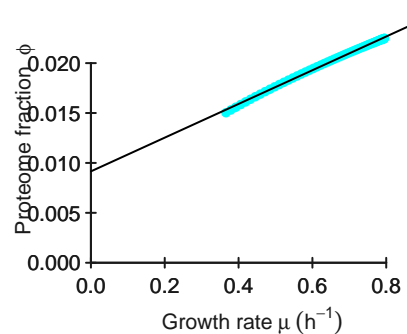
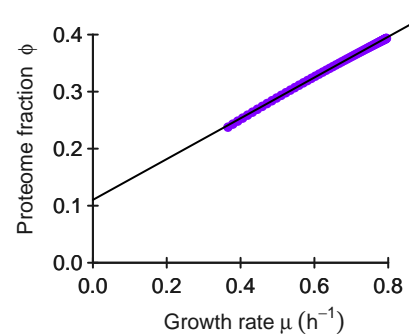
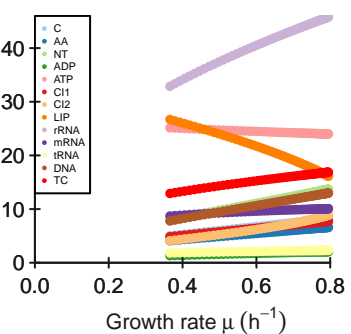
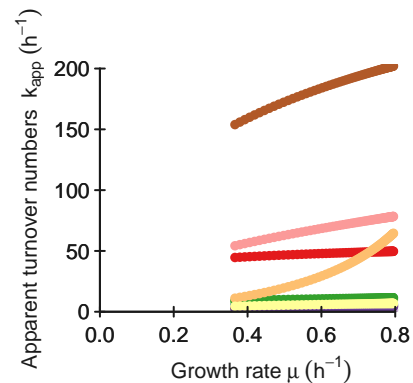
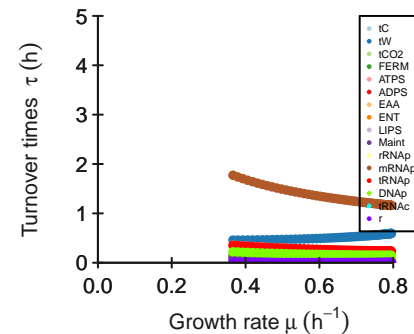
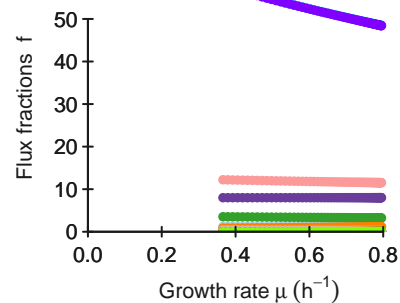
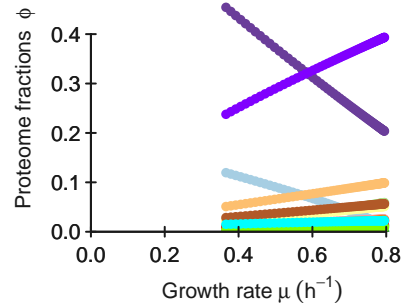
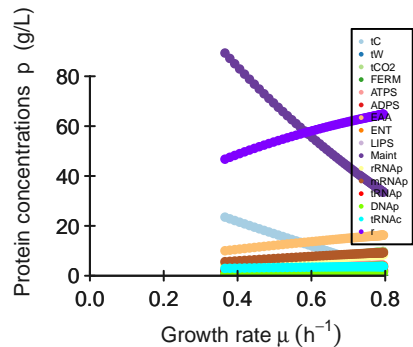
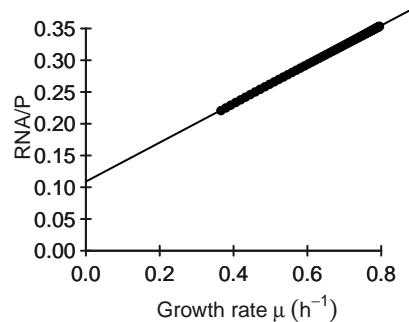


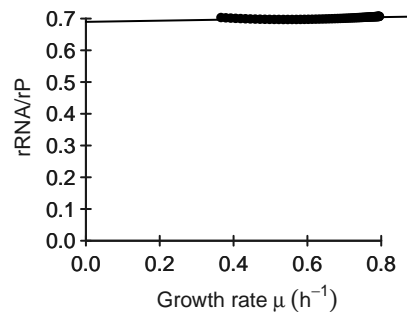
ENT**LIPS****Maint****rRNAp****mRNAp****tRNAp****DNAp****tRNAc****r****Metabolite concentrations c^m (g/L)**



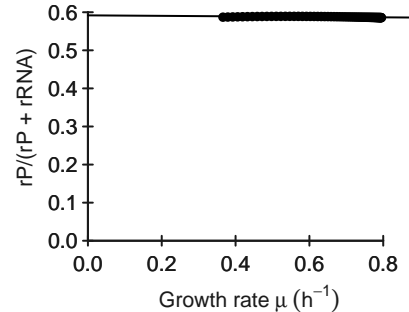
RNA/P



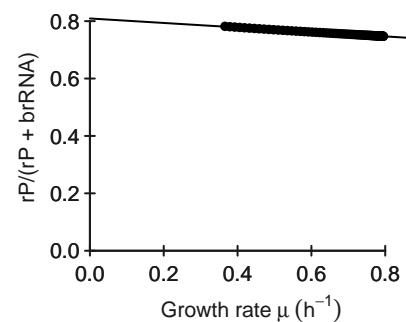
rRNA/rP



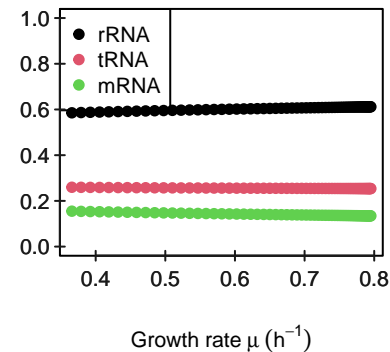
rP/(rP + rRNA)



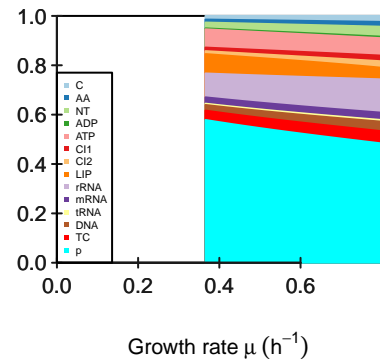
Protein mass fraction in ribosome



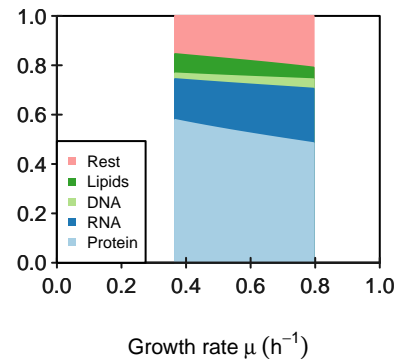
% transcribed RNA



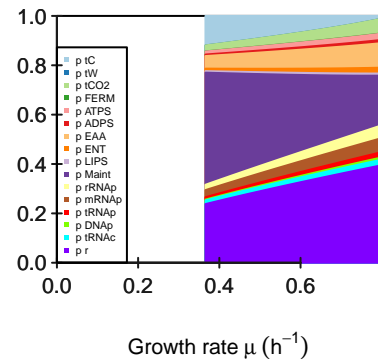
Relative biomass composition



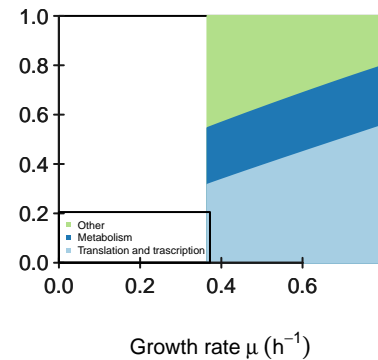
Predicted biomass



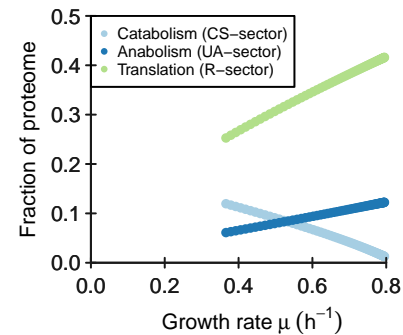
Proteome composition



Proteome sectors



Proteome sectors



M

[illegible]

K

[illegible]

KA[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	[,12] Inf	[,13] Inf	[,14] Inf	[,15] Inf	[,16] Inf
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phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
	0.002	0.02	0.01	0.041	0.046	0.005	0.165	0.023	0.031	0.277	0.0426	0.0213	0.0071	0.002	0.023	0.284

average saturation input

2

minimal phi constraint

[1,]	[.1] 0	[.2] 0	[.3] 0	[.4] 0	[.5] 0	[.6] 0	[.7] 0	[.8] 0	[.9] 0	[.10] 0	[.11] 0	[.12] 0	[.13] 0	[.14] 0	[.15] 0	[.16] 0
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minimal f constraint

[1,]	[,1] 0	[,2] 0	[,3] 0	[,4] 0	[,5] 0	[,6] 0	[,7] 0	[,8] 0	[,9] 0	[,10] 8	[,11] 0	[,12] 0	[,13] 0	[,14] 0	[,15] 0	[,16] 0
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