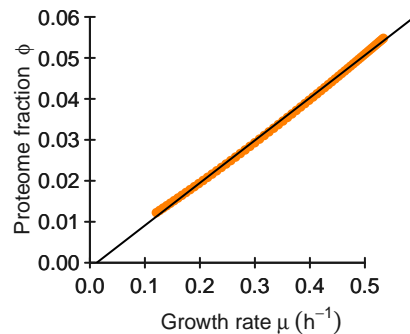
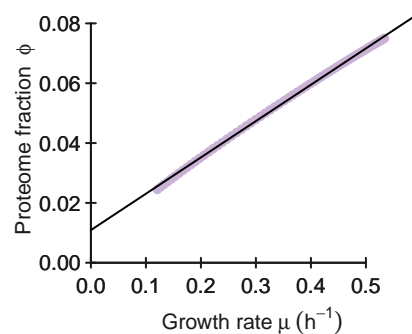
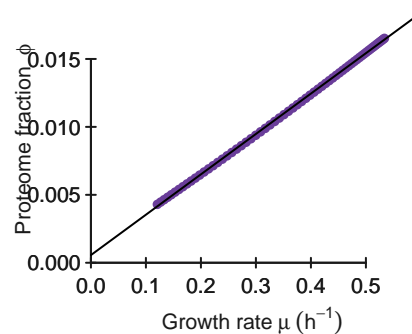
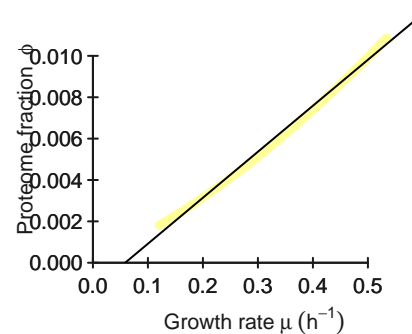
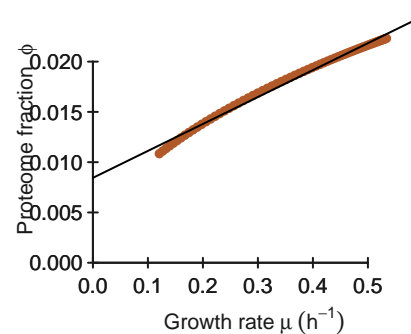
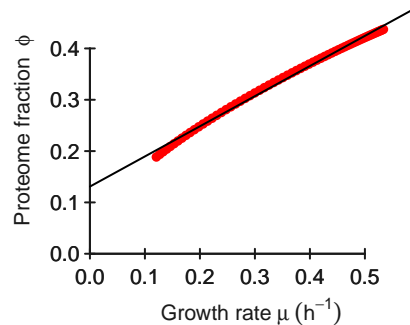
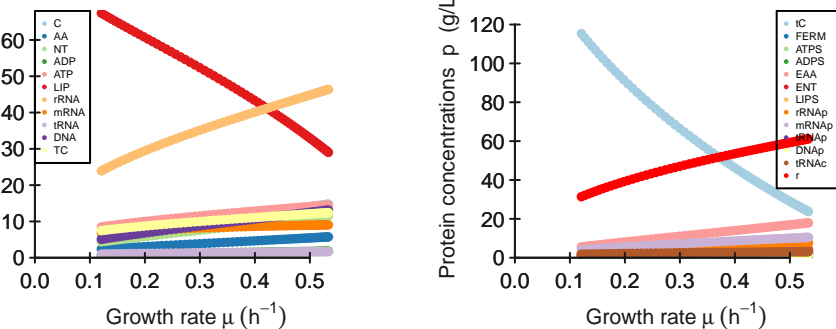
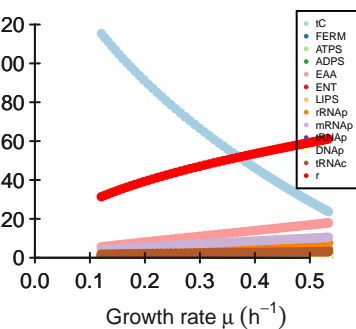
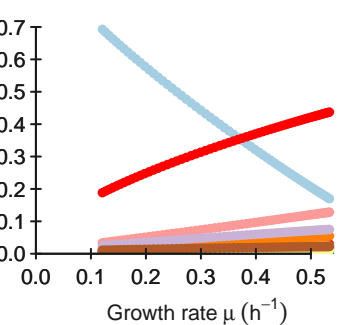
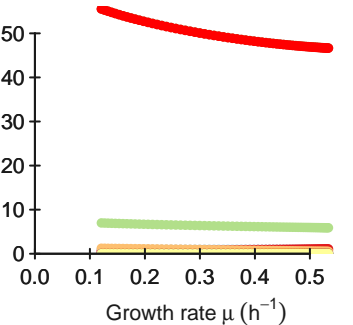
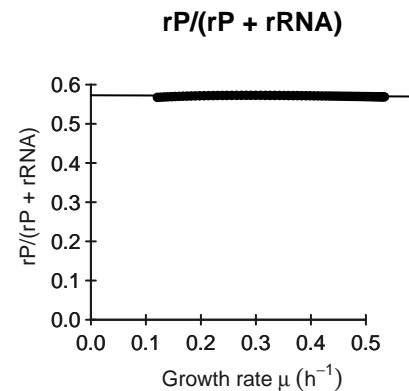
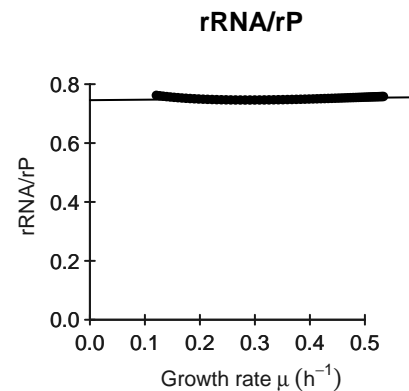
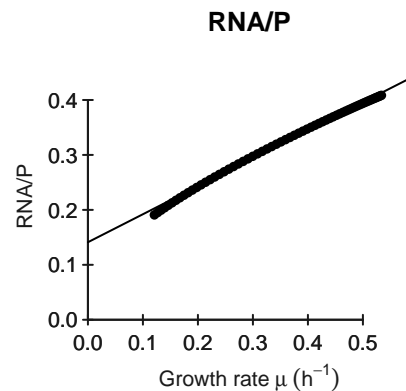
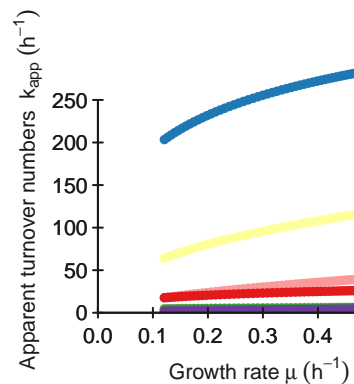
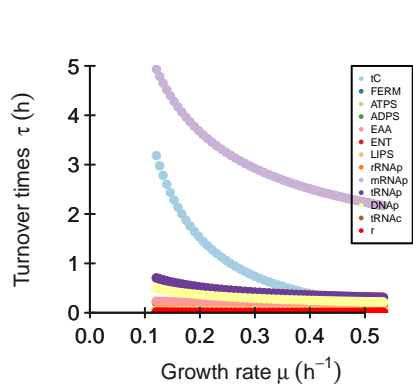
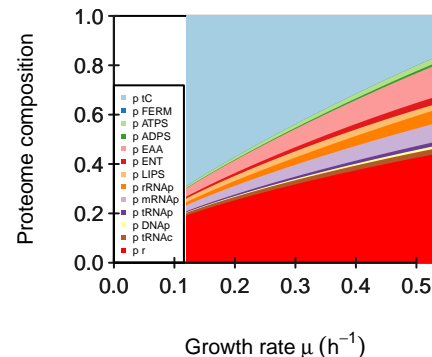
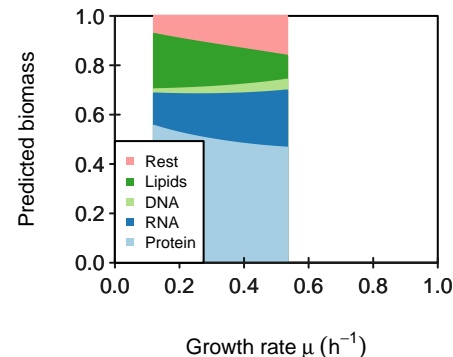
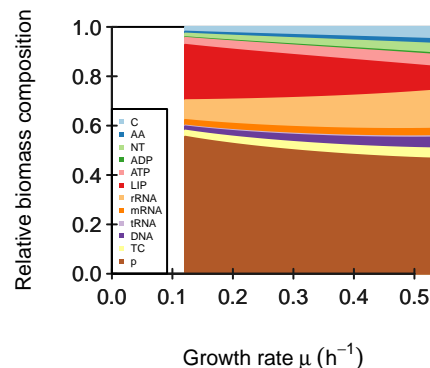
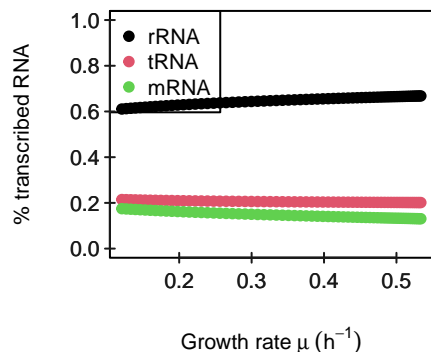
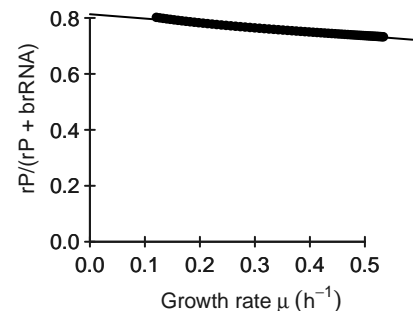


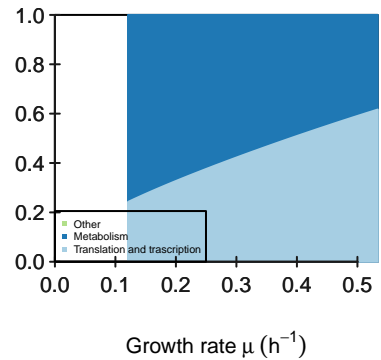
rRNAp**mRNAp****tRNAp****DNAp****tRNAc****r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f 



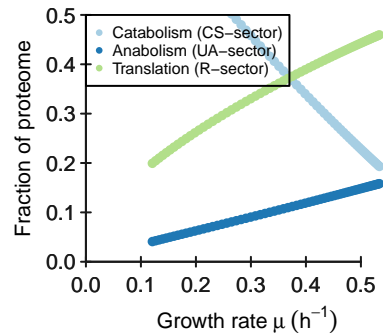
Protein mass fraction in ribosome



Proteome sectors



Proteome sectors



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	[,12] Inf	[,13] Inf
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phi input

0.0364656381486676	0.00701262272089762	0.231416549789621	0.032258064516129	0.0434782608695652	0.0597475455820477	0.0298737727910238	0.00995792426367462	0.002805046
[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	

average saturation input

3

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
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minimal f constraint

[illegible]