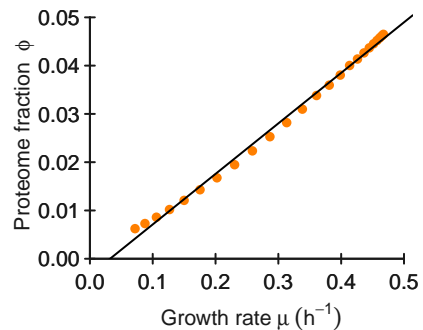
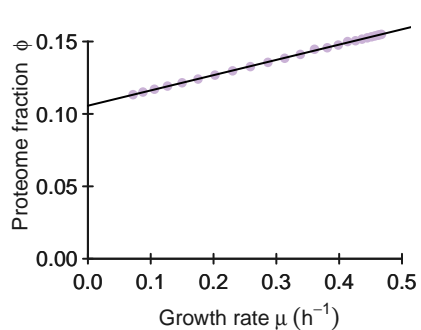
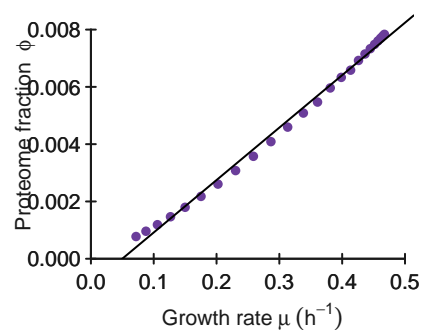
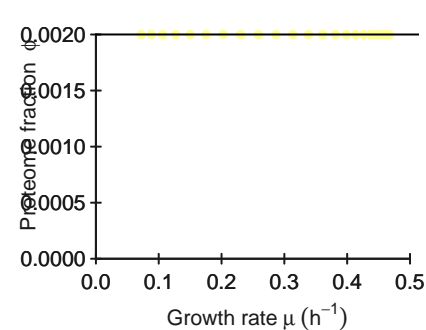
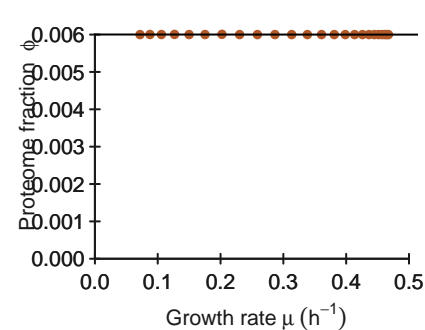
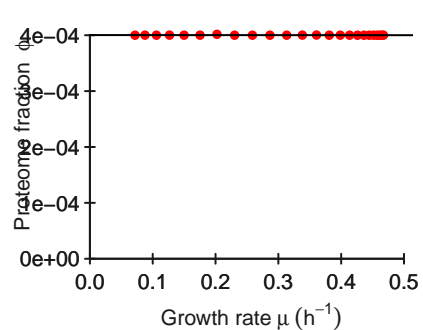
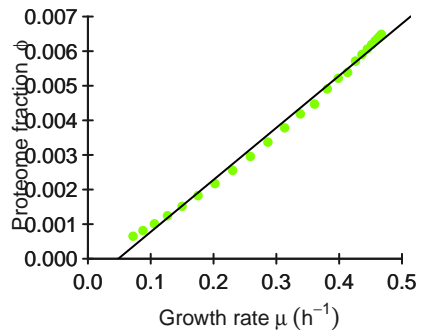
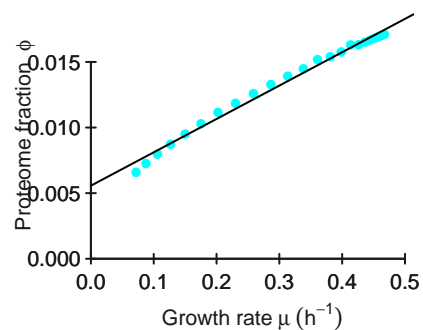
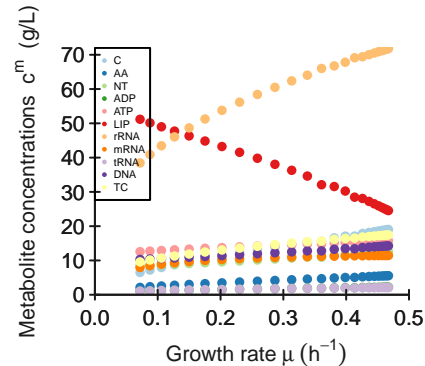
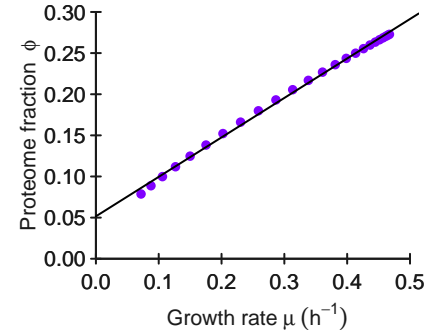
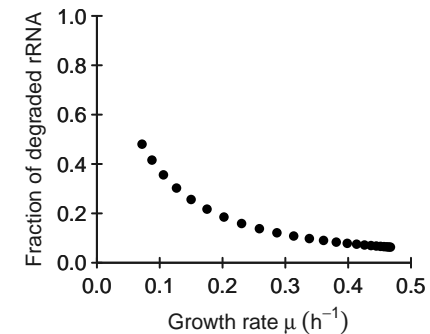
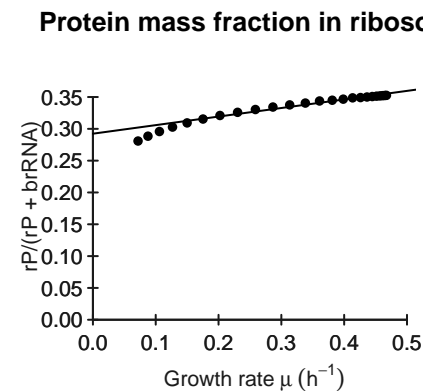
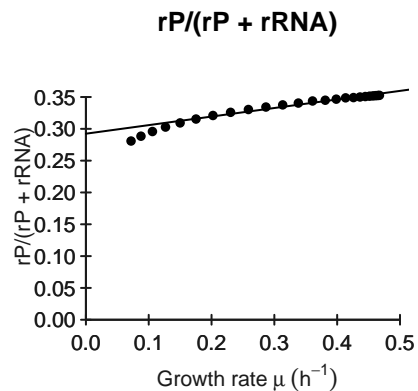
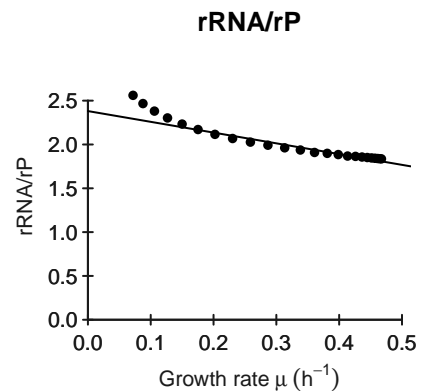
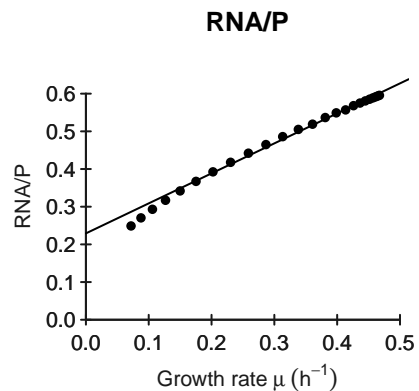
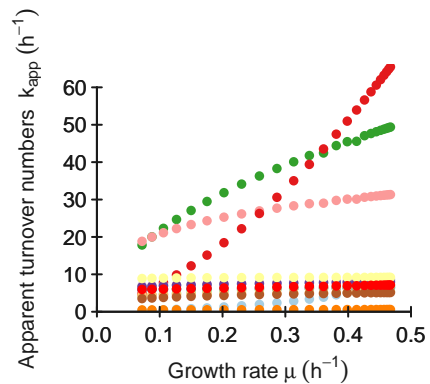
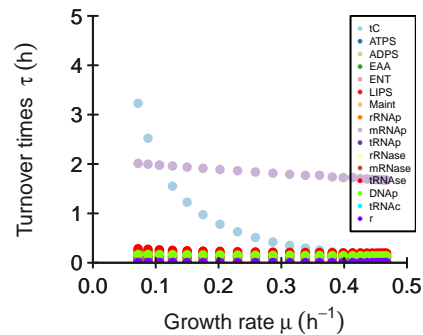
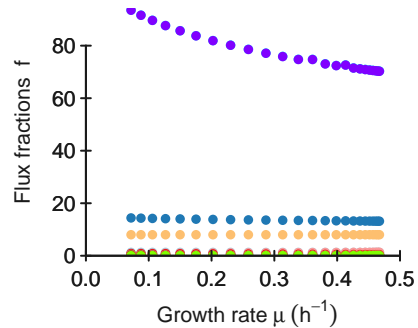
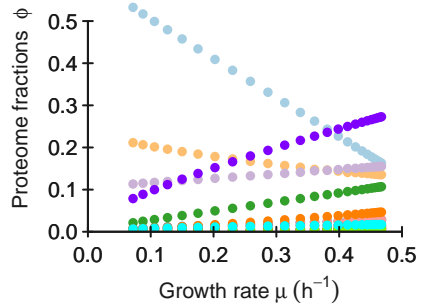
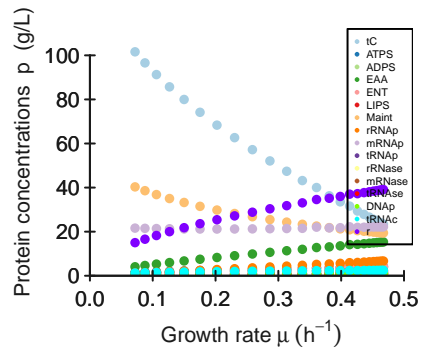
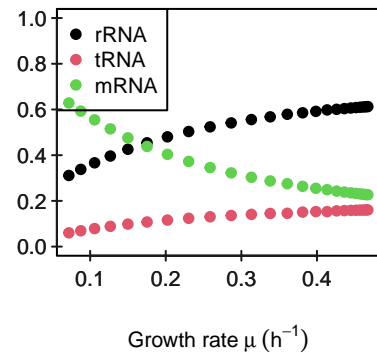


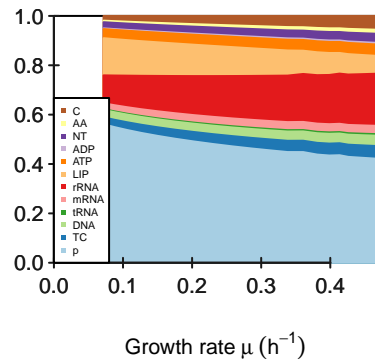
**rRNAp****mRNAp****tRNAp****rRNase****mRNase****tRNase****DNAp****tRNAc****r**



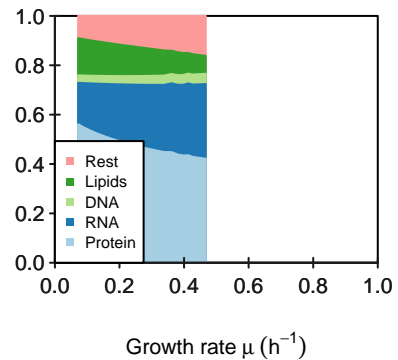
% transcribed RNA



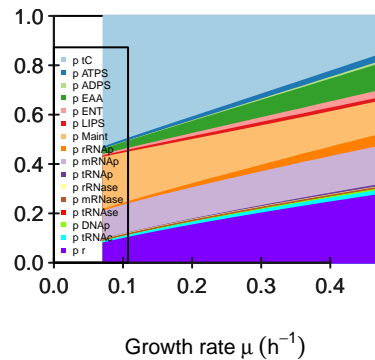
Relative biomass composition



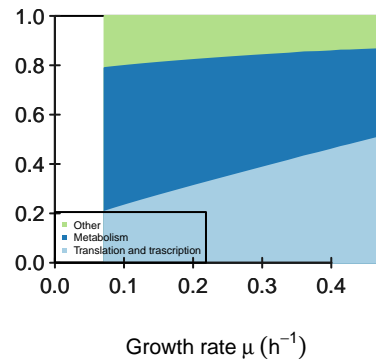
Predicted biomass



Proteome composition



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]
	0.11	0.023	0.005	0.165	0.023	0.031	0.2546	0.0426	0.0213	0.0071	0.002	0.006	4e-04	0.002	0.023	0.284

**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] 0.002	[,12] 0.006	[,13] 4e-04	[,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] 8	[,8] 0	[,9] 0	[,10] 0	[,11] 0	[,12] 0	[,13] 0	[,14] 0	[,15] 0	[,16] 0
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