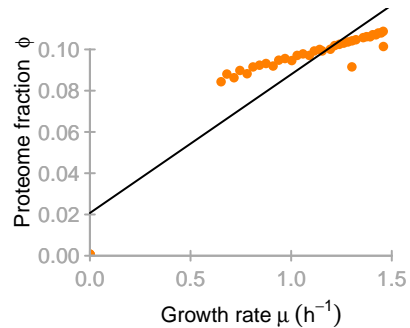
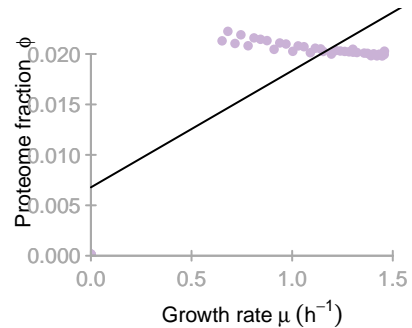
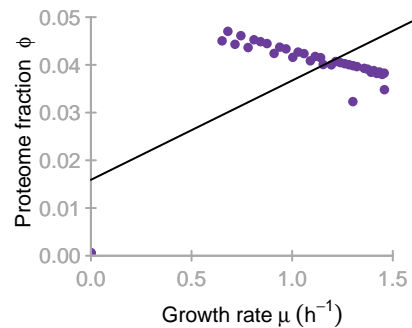
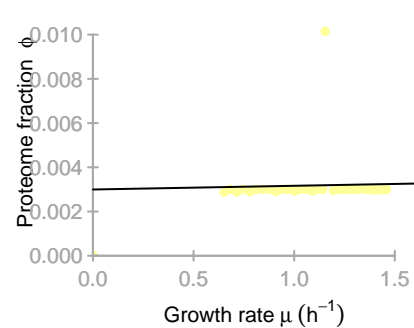
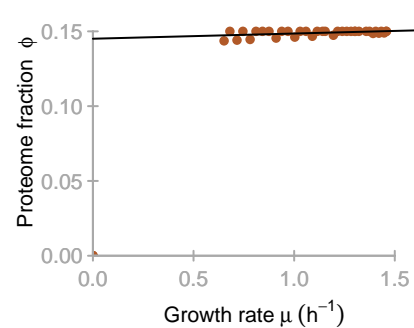
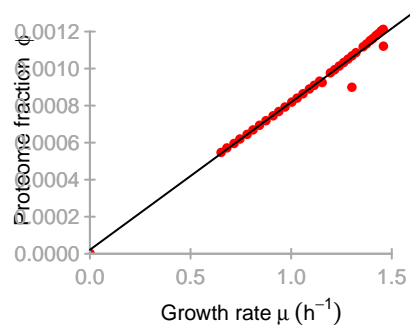
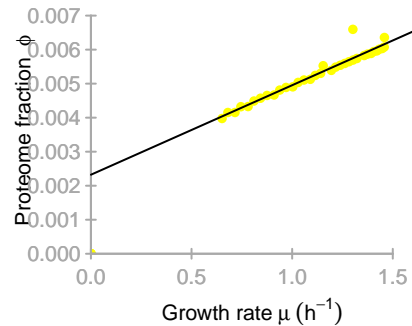
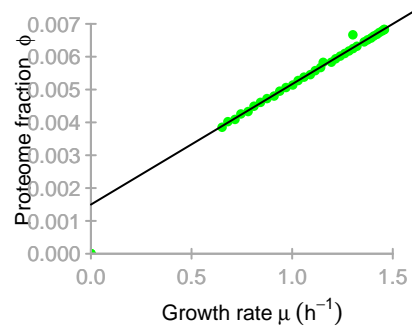
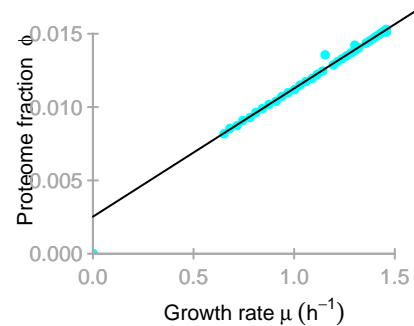
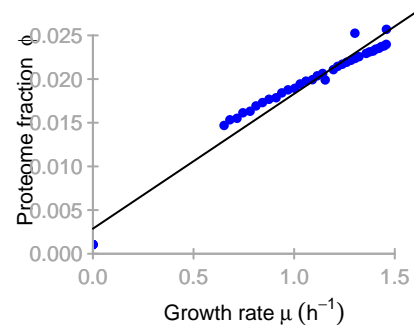
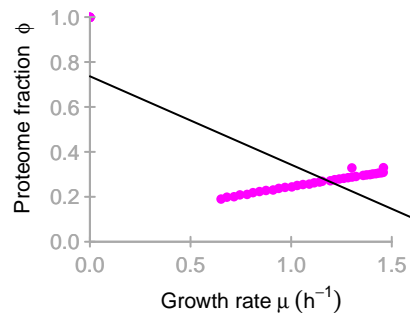
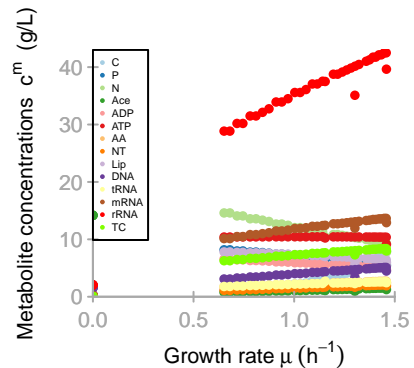
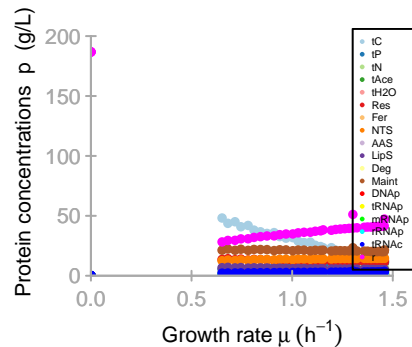
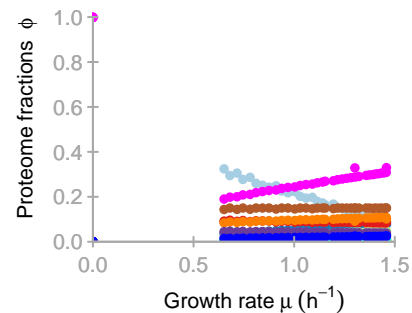
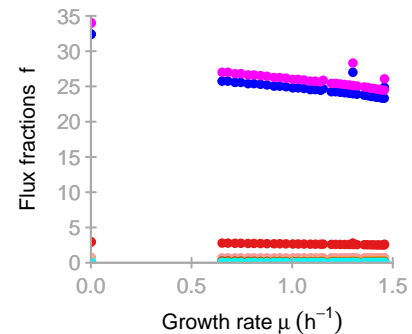
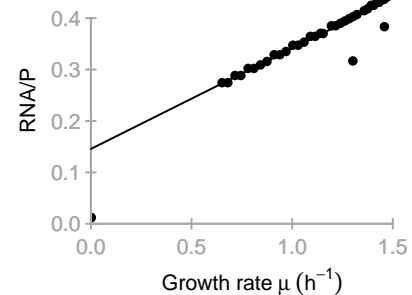
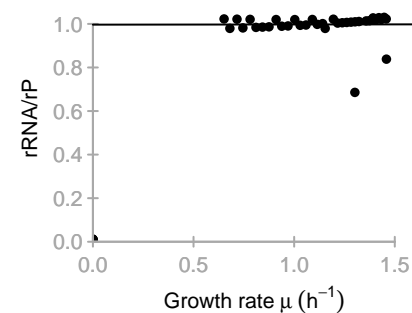
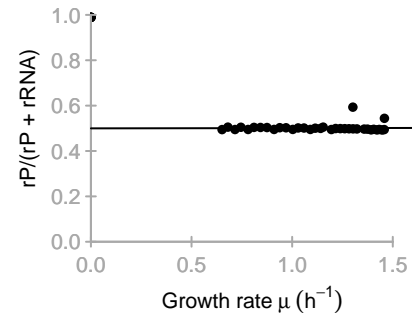
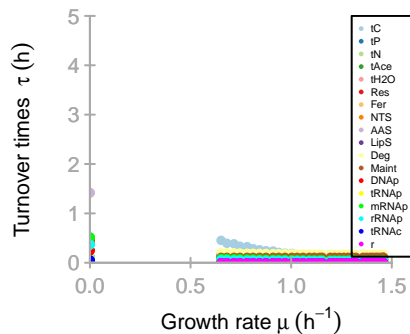
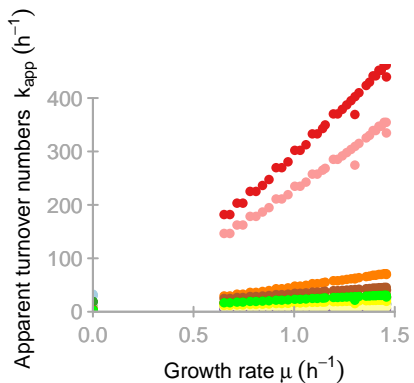
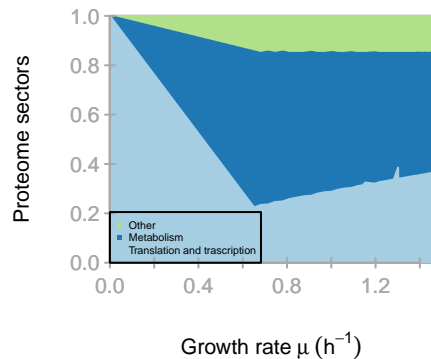
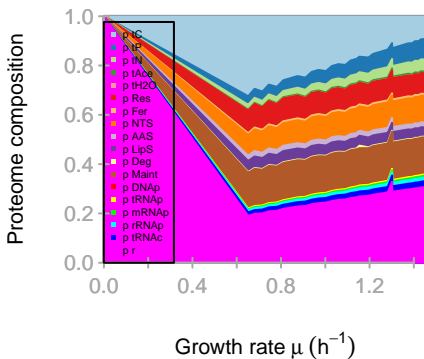
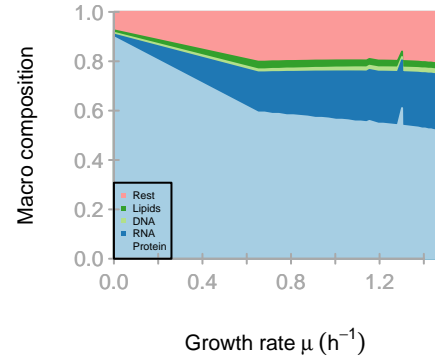
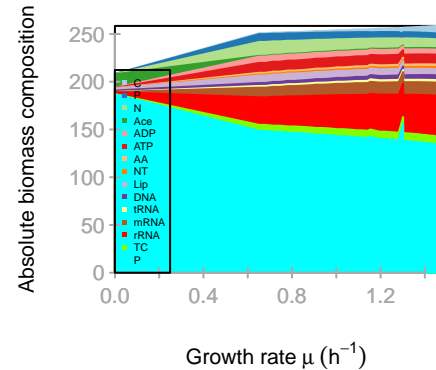
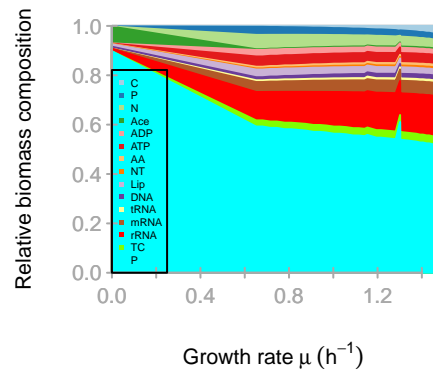
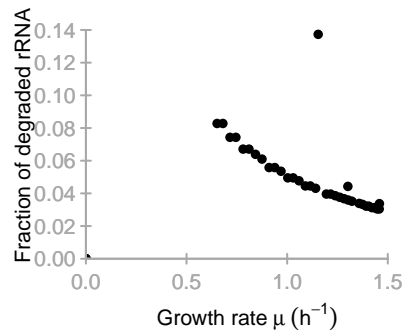
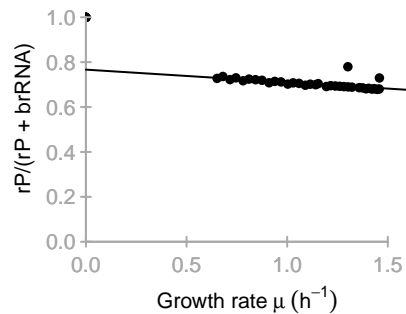


**NTS****AAS****LipS****Deg****Maint****DNAP****tRNAp****mRNAp****rRNAp****tRNAc**

**r**Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Flux fractions  $f$ **RNA/P****rRNA/rP****rP/(rP + rRNA)**Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )

## Protein mass fraction in ribosome



**M**

[illegible]

## K

[illegible]

**KA**[illegible]

# kcat

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]	[,18]
kcatf	100	40	40	40	40000	900	900	100	100	50	10	10	200	136	96	136	60000	6000
kcatb	10	4	4	2	4000	90	90	10	10	5	0	0	0	0	0	0	0	0



# Keq

[1,]	[,1] 100	[,2] 10	[,3] 10	[,4] 200	[,5] 10	[,6] 40000	[,7] 40000	[,8] 0.03125	[,9] 25	[,10] 0.3333333333333333	[,11] Inf	[,12] Inf	[,13] Inf	[,14] Inf	[,15] Inf	[,16] Inf	[,17] Inf	[,18] Inf
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## 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] 0.003	[,12] 0.15	[,13] 0	[,14] 0	[,15] 0	[,16] 0	[,17] 0	[,18] 0
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## minimal f constraint

[1,]	[,1] 0	[,2] 0	[,3] 0	[,4] 0	[,5] 0.7	[,6] 0	[,7] 0	[,8] 0	[,9] 0	[,10] 0.015	[,11] 0	[,12] 0	[,13] 0	[,14] 0	[,15] 0	[,16] 0	[,17] 0	[,18] 0
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