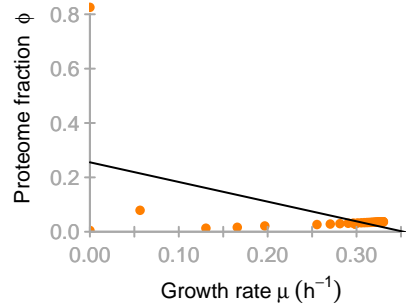
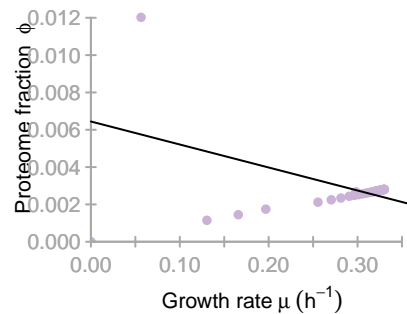
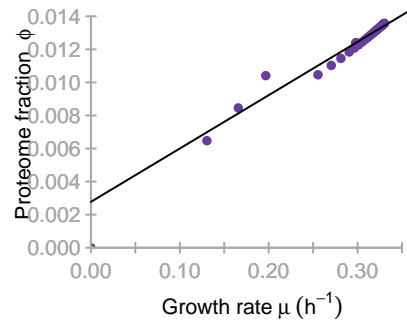
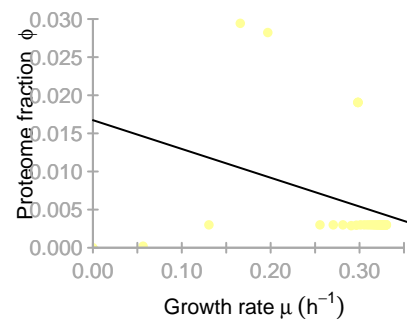
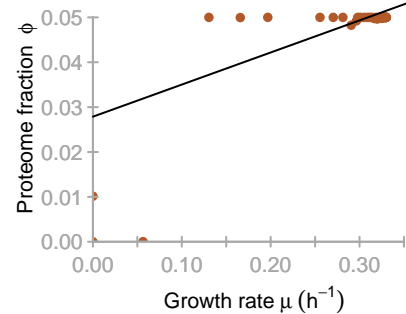
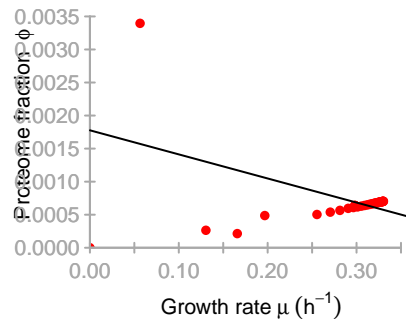
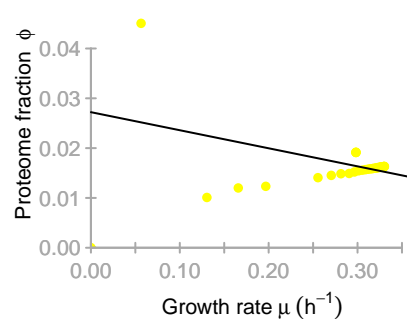
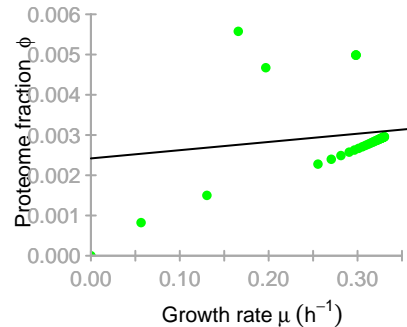
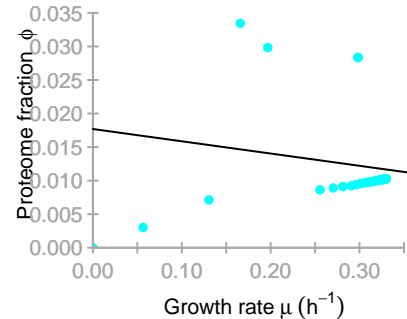
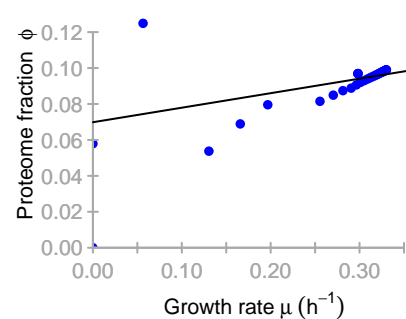
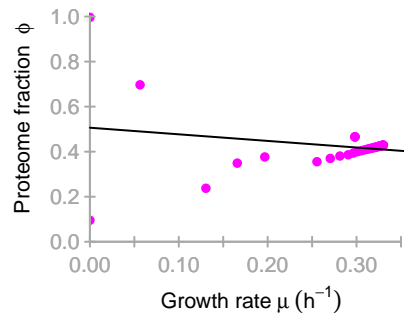
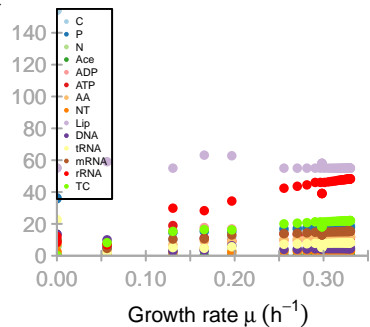
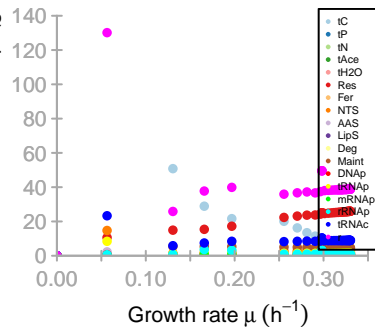
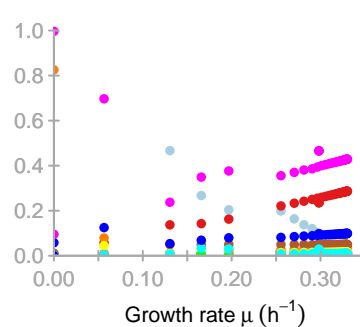
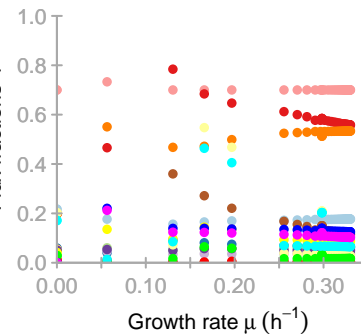
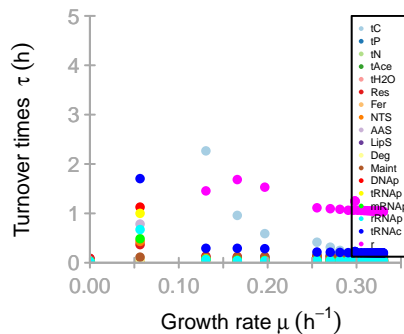
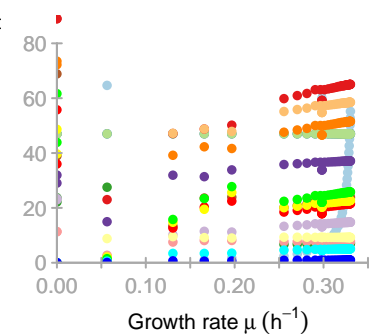
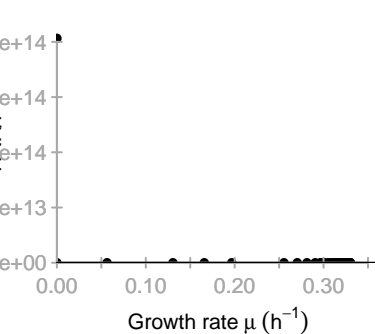


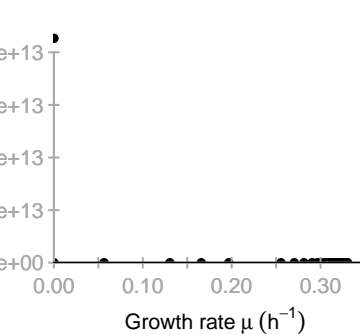
NTS**AAS****LipS****Deg****Maint****DNAp****tRNAp****mRNAp****rRNAp****tRNAc**

rMetabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f **RNA/P****rRNA/rP****rP/(rP + rRNA)**Apparent turnover numbers k_{app} (h^{-1})

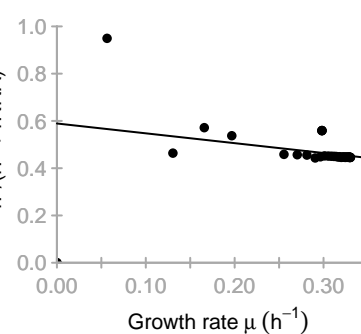
RNA/P



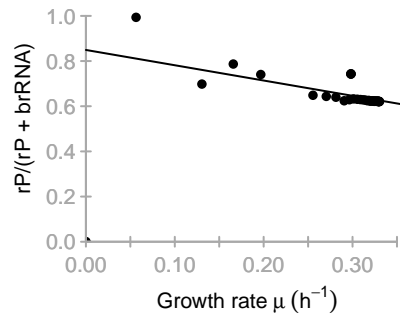
rRNA/rP



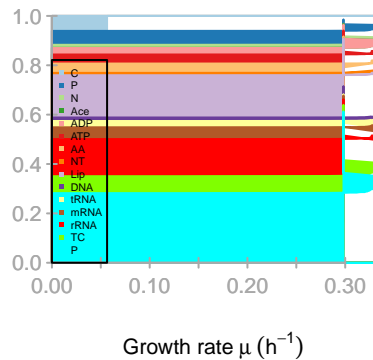
rP/(rP + rRNA)



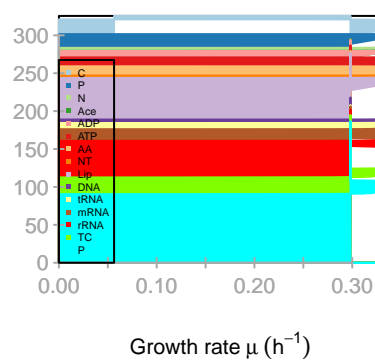
Protein mass fraction in ribosome



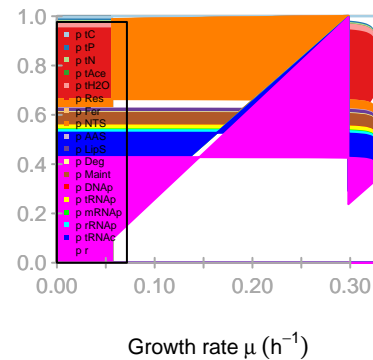
Relative biomass composition



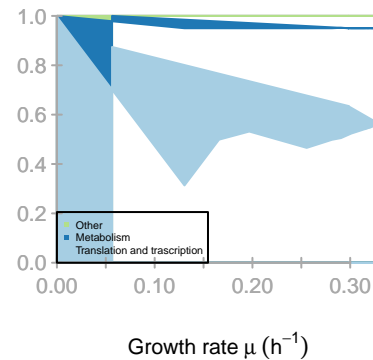
Absolute biomass composition



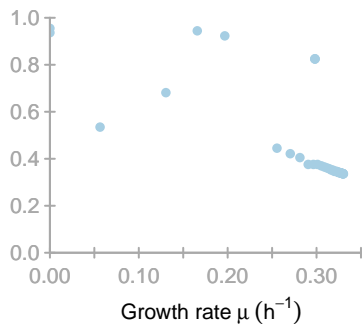
Proteome composition



Proteome sectors



Fraction of degraded rRNA



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	100	100	60	1000	20	100	100	100	40	50	10	200	136	96	136	20	4.55
kcatb	6	6	6	6	1	1	1	1	1	4	0	0	0	0	0	0	0	0

Keq

[1.]	[1] 16.6666666666667	[2] 16.6666666666667	[3] 16.6666666666667	[4] 10	[5] 100	[6] 0.16	[7] 33.3333333333333	[8] 20000	[9] 125	[10] 0.166666666666667	[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] 0.05	[,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] 0.05	[11] 0	[12] 0	[13] 0	[14] 0	[15] 0	[16] 0	[17] 0	[18] 0
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