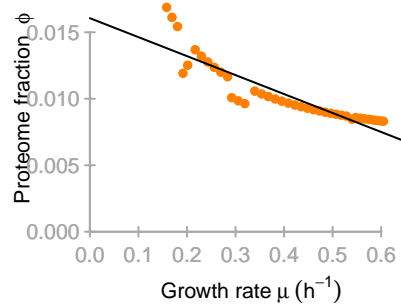
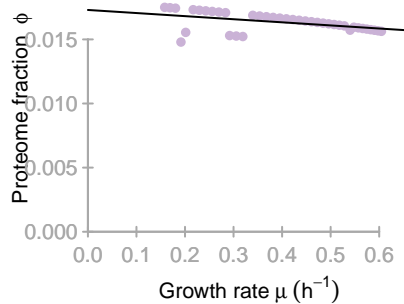
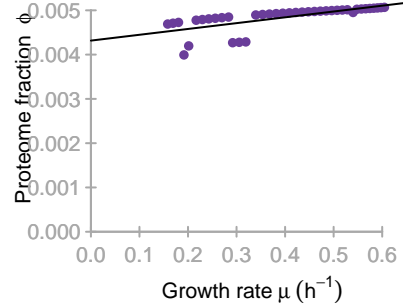
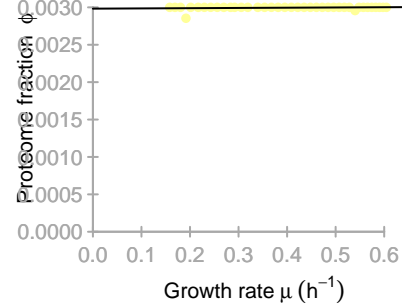
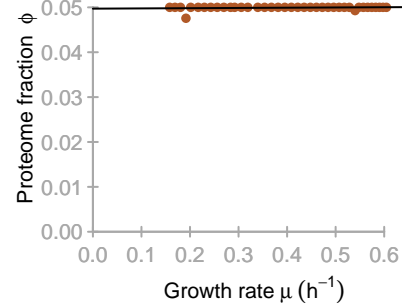
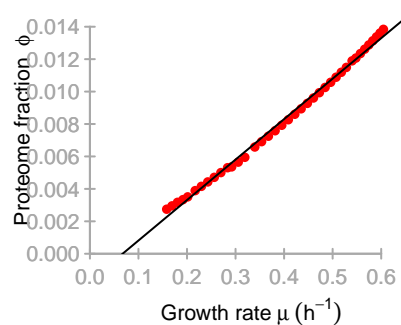
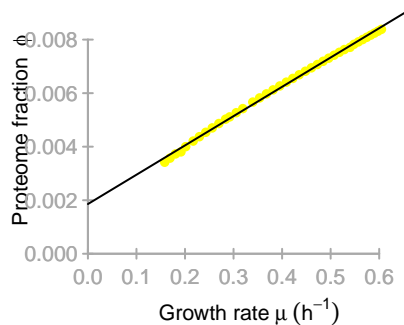
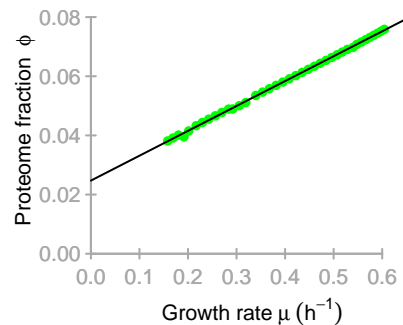
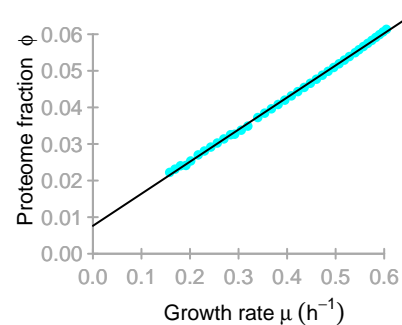
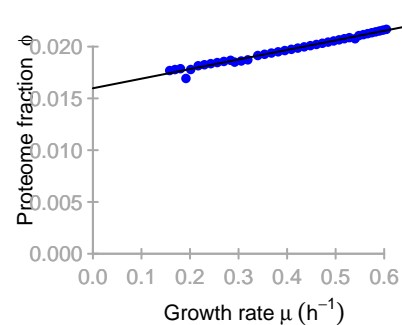
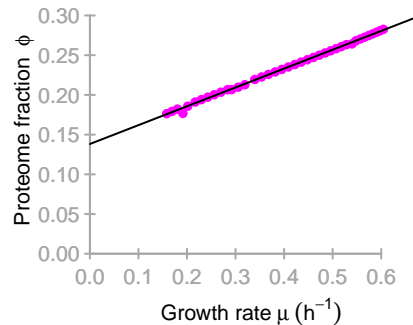
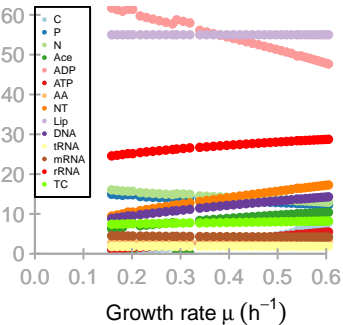
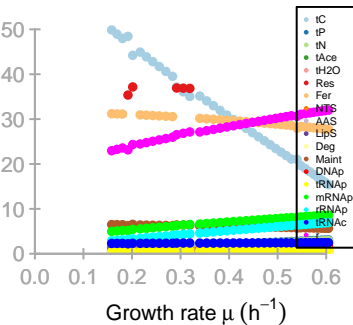
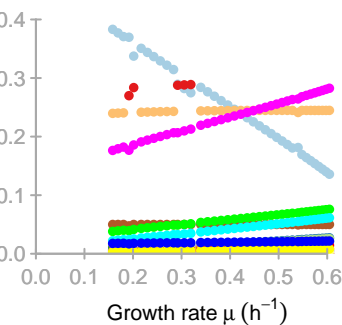
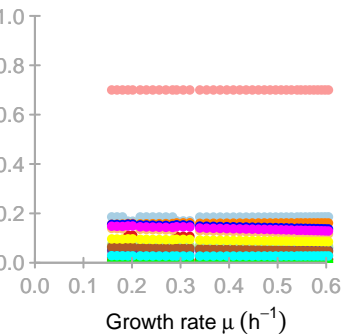
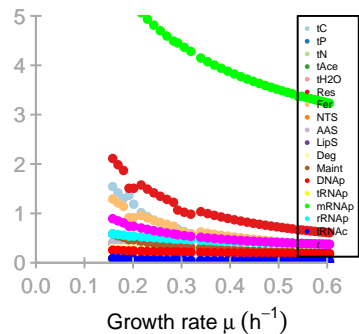
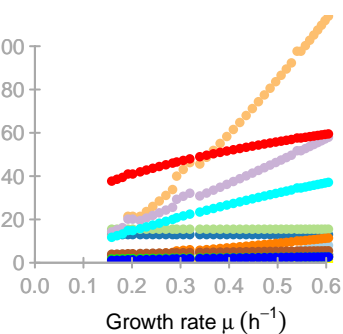
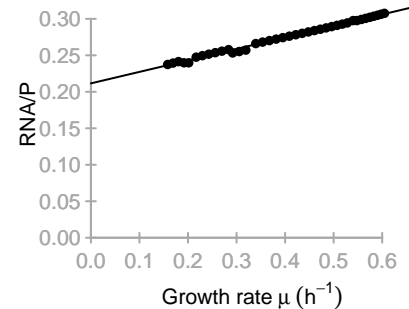
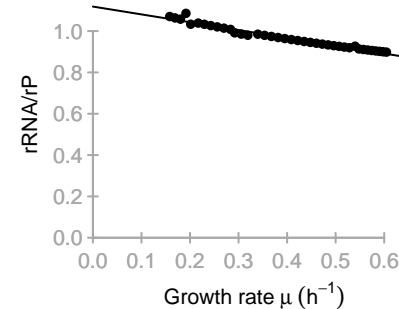
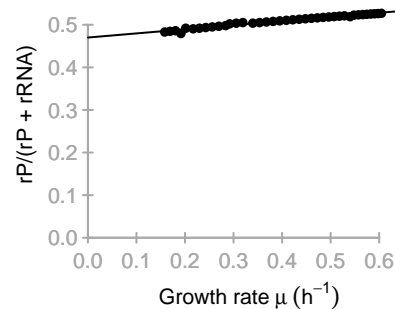
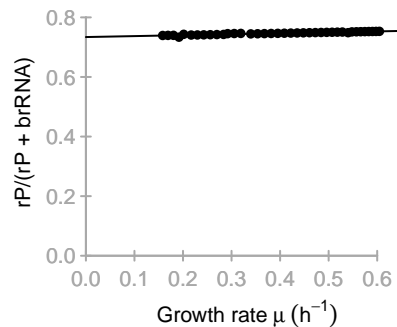


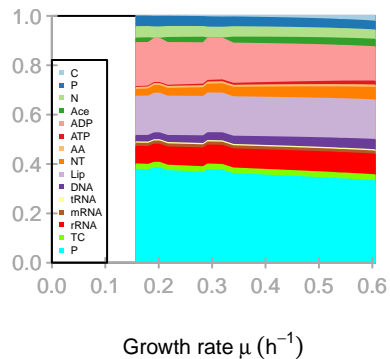
NTS**AAS****LipS****Deg****Maint****DNAp****tRNAp****mRNAp****rRNAp****tRNAc**

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

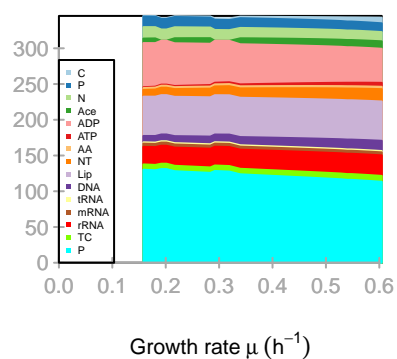
Protein mass fraction in ribosome



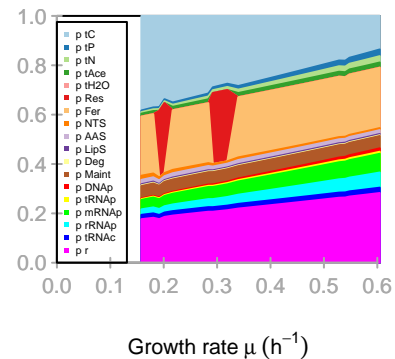
Relative biomass composition



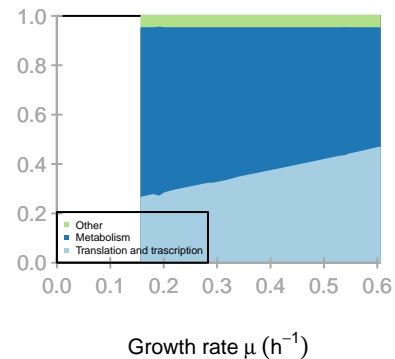
Absolute biomass composition



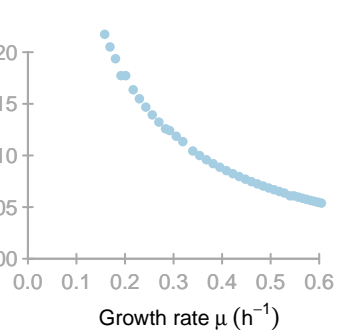
Proteome composition



Proteome sectors



Fraction of degraded rRNA



M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	tP	tN	tAce	tH2O	Res	Fer	NTS	AAS	LipS	Deg	Maint	DNAP	tRNAp	mRNAp	rRNAp	tRNAc	r
kcatf	22	29	35	11	41625	10	20	323	21	118	10	10	11	152	1	7	201	20
kcatb	2	3	4	1	4162	1	2	32	2	12	0	0	0	0	0	0	0	0

Keq

[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
44	9.666666666666667	8.75	0.7333333333333333	10.001201345507	7.0602089251377e-05	0.000694830461367426	33.1201171875	3.9375	33.80208333333333	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

[1,]	0.04889999999999999	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]	[,18]
		0.01	0.01	0.001	1e-04	0.1	0.15	0.05	0.05	0.02	0.01	0.2	0.01	0.01	0.01	0.02	0.05	0.25	

average saturation input

1

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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