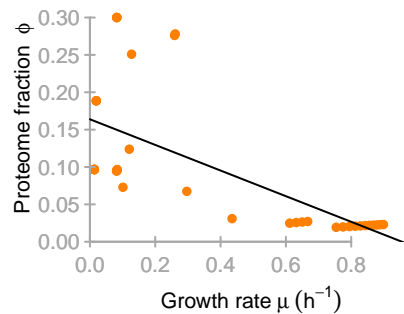
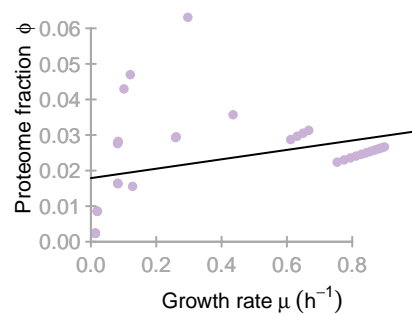
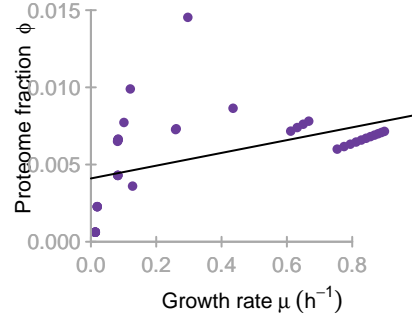
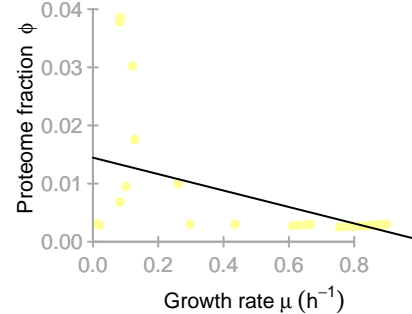
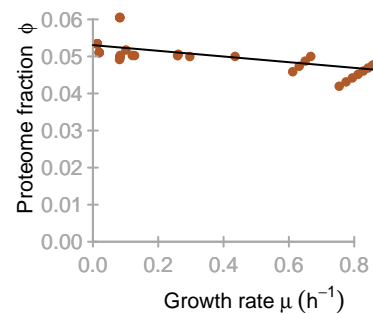
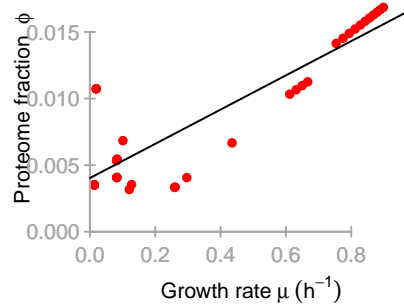
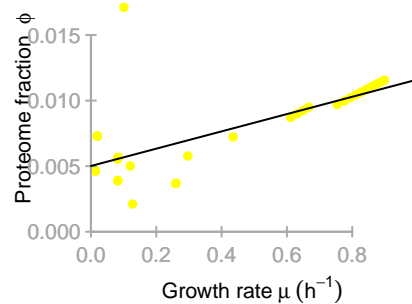
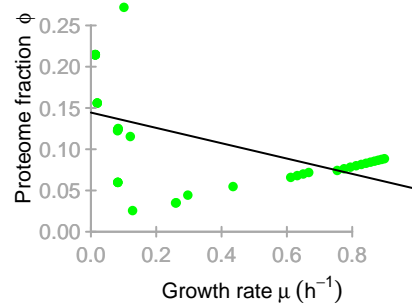
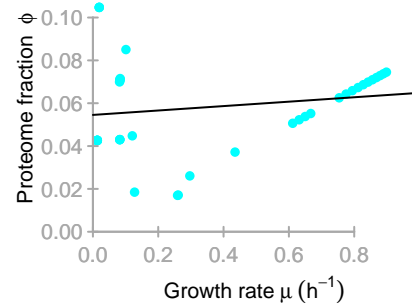
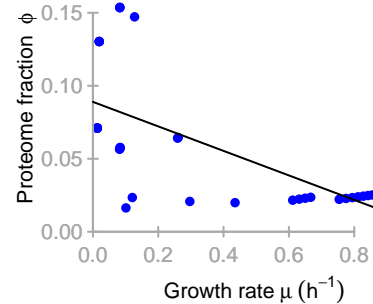
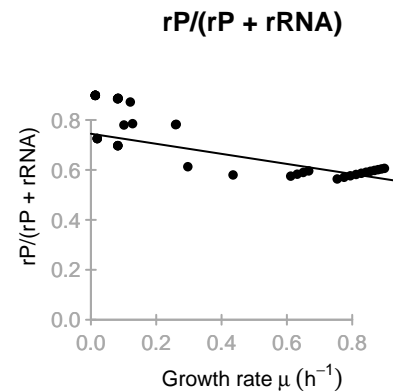
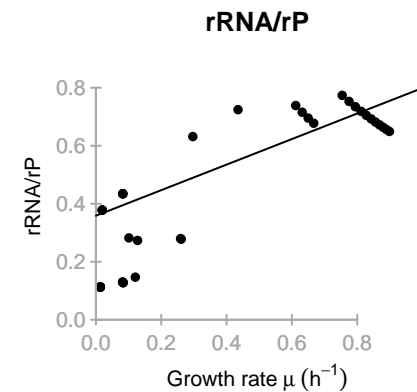
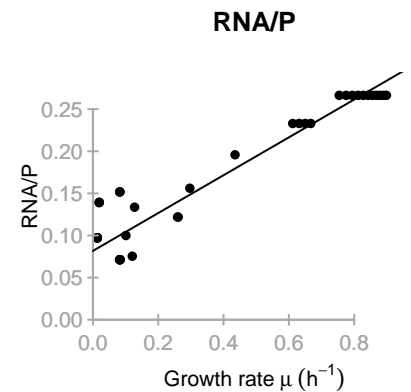
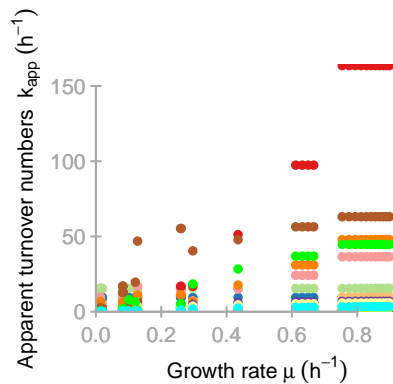
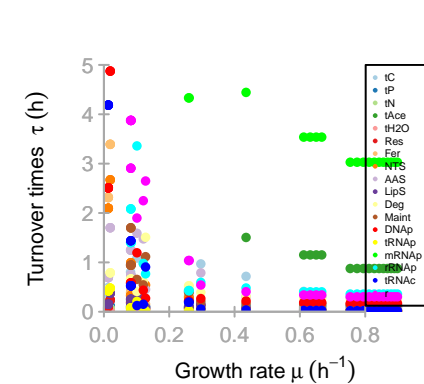
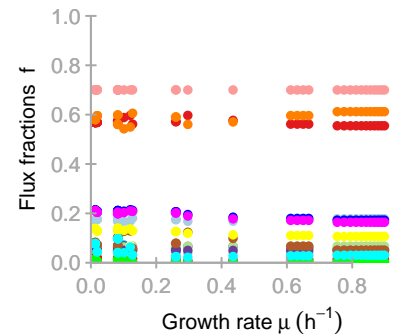
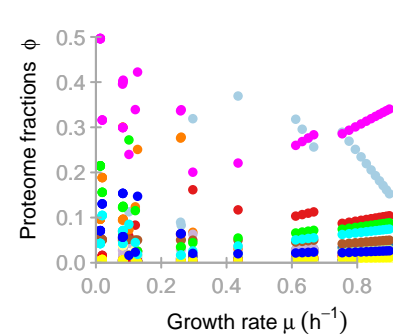
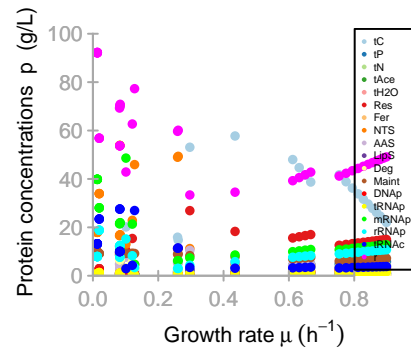
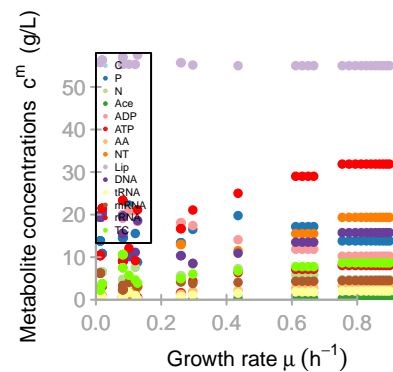
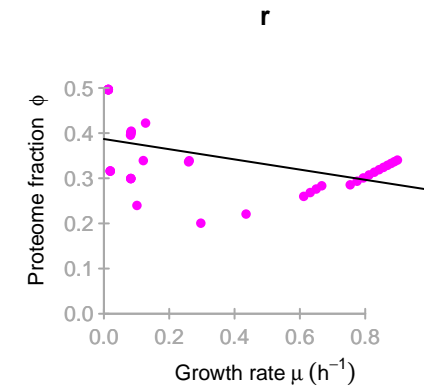
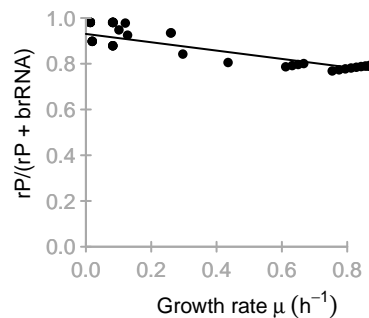


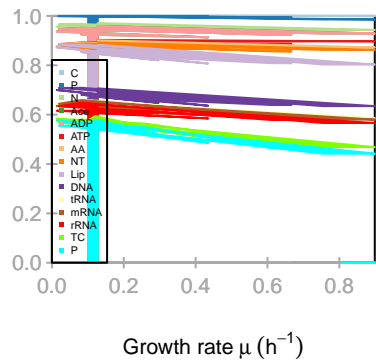
NTS**AAS****LipS****Deg****Maint****DNAP****tRNAp****mRNAp****rRNAp****tRNAc**



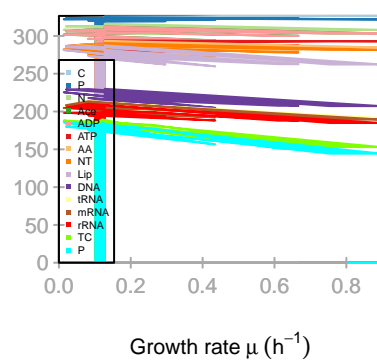
Protein mass fraction in ribosome



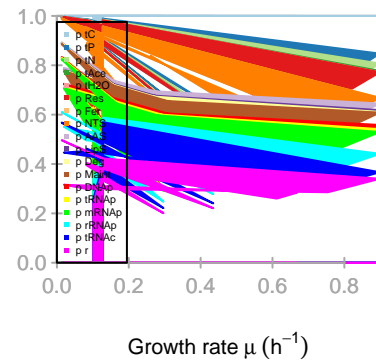
Relative biomass composition



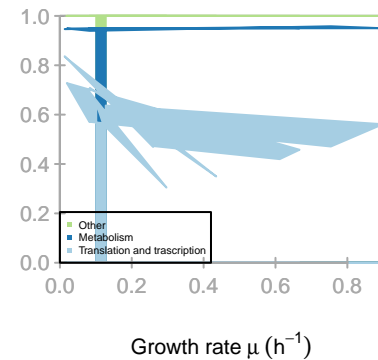
Absolute biomass composition



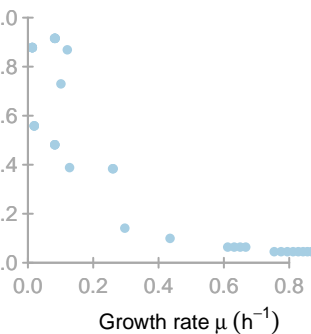
Proteome composition



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	21	21	35	10	43119	213	426	1026	21	118	10	10	11	152	1	7	201	20
kcatb	2	2	4	1	4312	21	43	103	2	12	0	0	0	0	0	0	0	0

Keq

[1.]	[,1] 31.5	[,2] 10.5	[,3] 8.75	[,4] 10	9.9997680890538	[,5]	139.919413919414	[,6]	5774.11627906977	[,7]	0.0802324322373408	[,8]	[,9] 10.5	[,10] 60.0925925925926	[,11] Inf	[,12] Inf	[,13] Inf	[,14] Inf	[,15] Inf	[,16] Inf	[,17] Inf	[,18] Inf
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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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