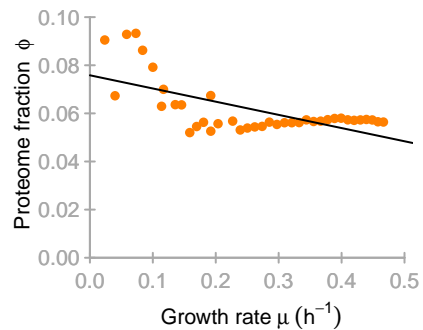
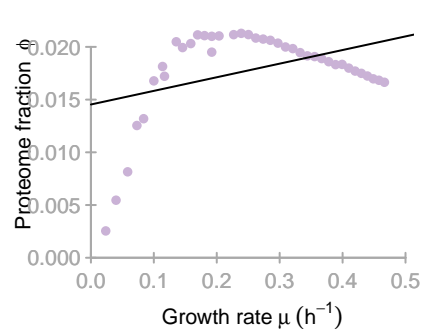
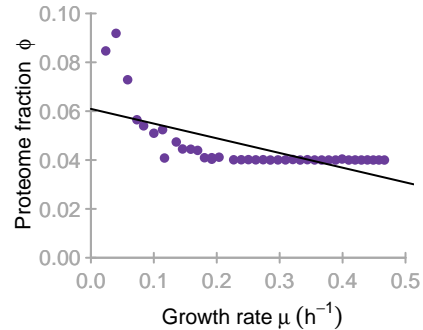
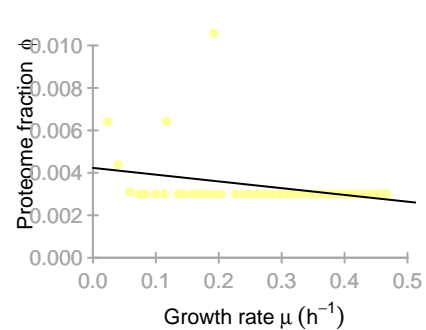
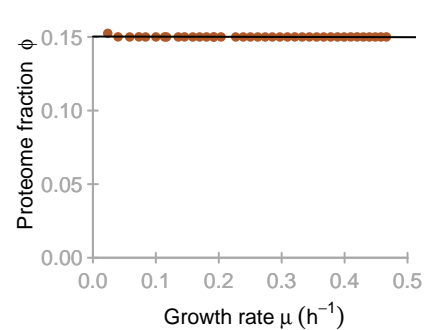
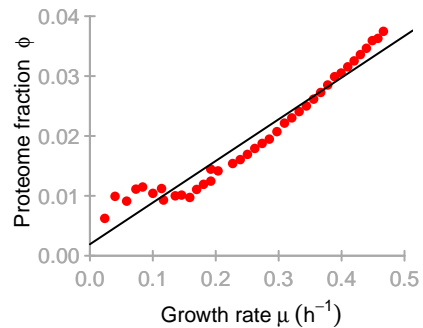
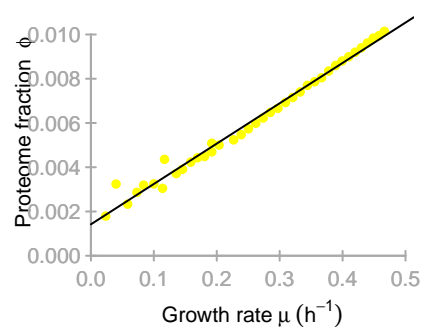
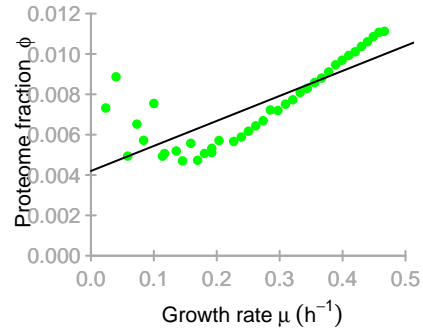
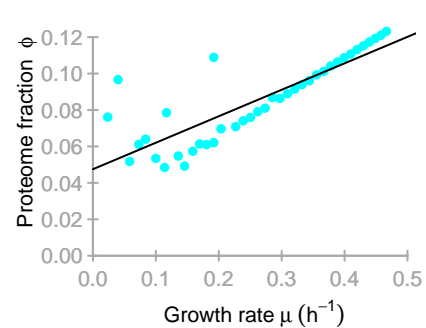
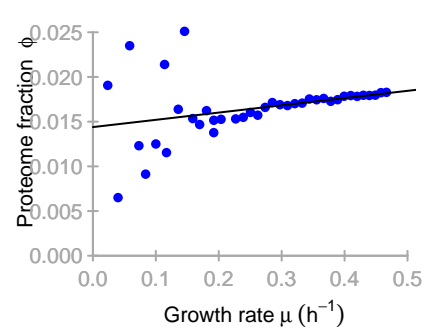
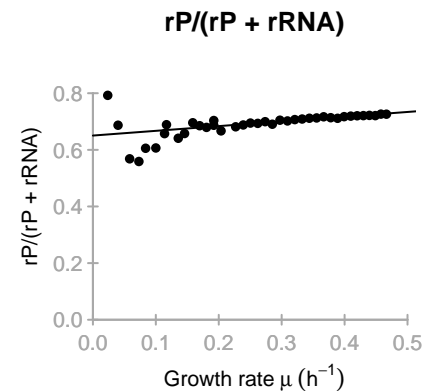
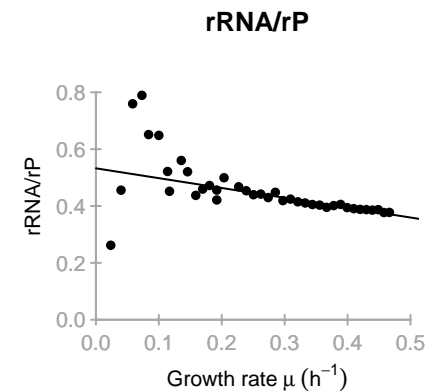
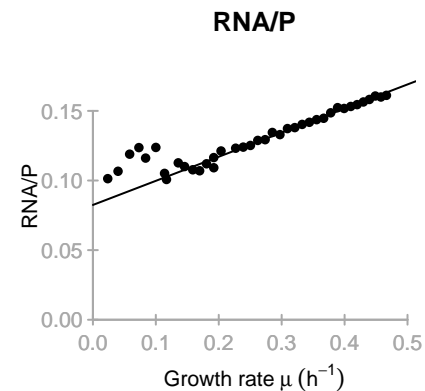
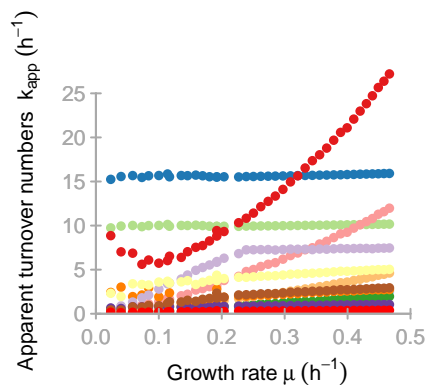
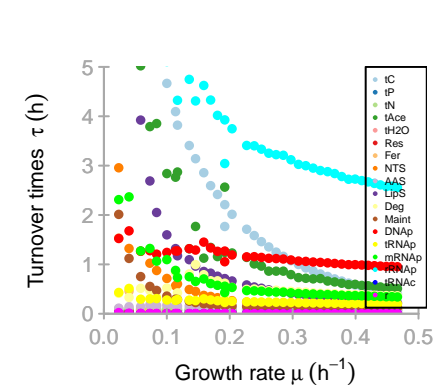
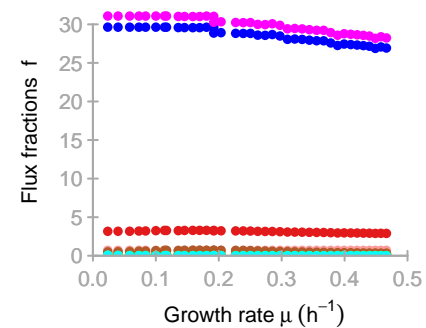
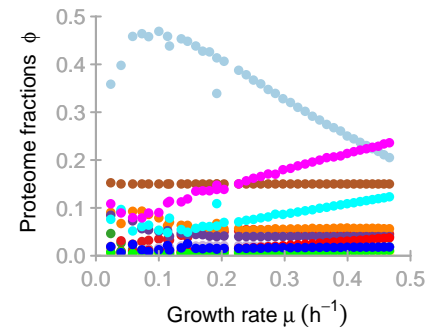
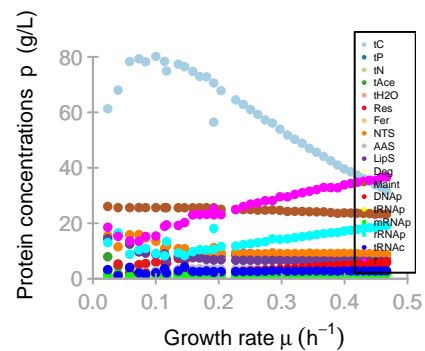
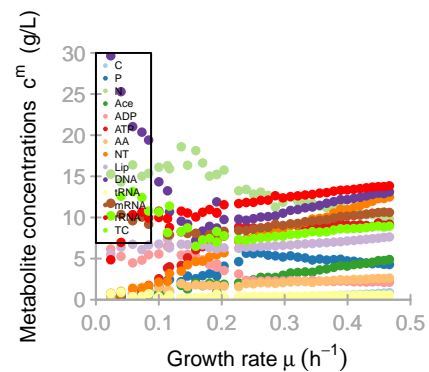
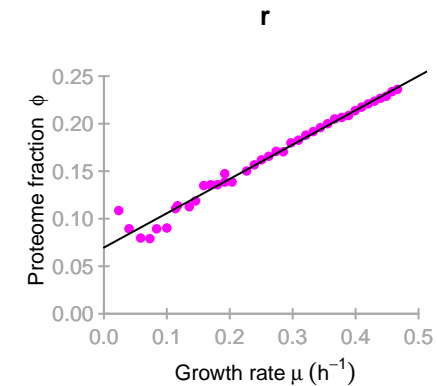
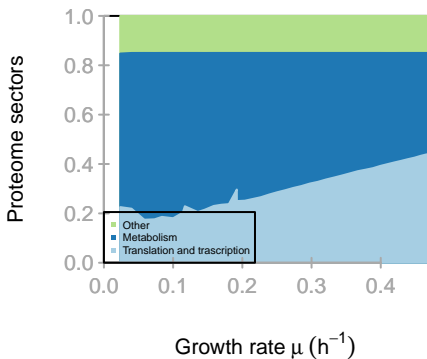
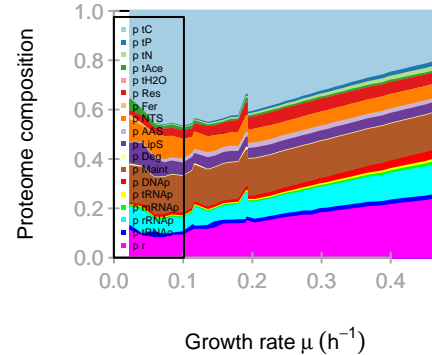
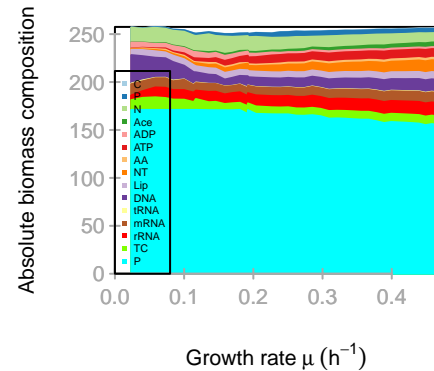
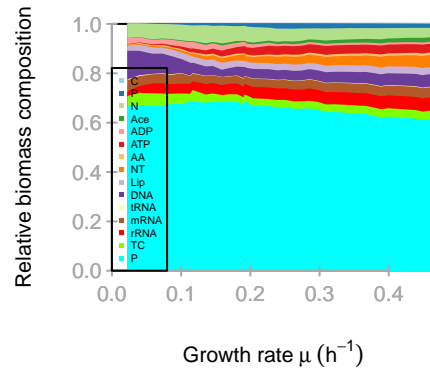
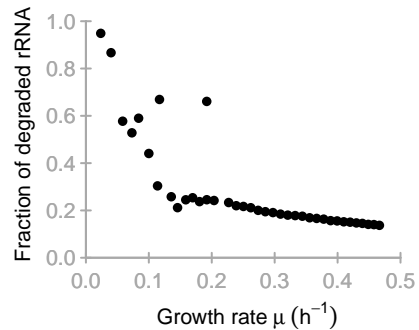
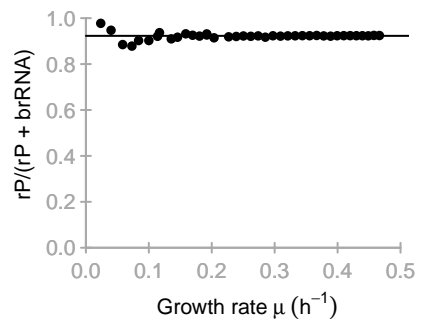


NTS**AAS****LipS****Deg****Maint****DNAP****tRNAp****mRNAp****rRNAp****tRNAc**



Protein mass fraction in ribosome



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	9	40	25	10	43852	1386	2772	75	76	26	10	10	2	10	10	1	61011	6400
kcatb	1	4	2	1	4385	139	277	8	8	3	0	0	0	0	0	0	0	0

Keq

[1,]	[,1] 9	[,2] 10	[,3] 12.5	[,4] 6.666666666666667	[,5] 10.0004561003421	[,6] 133564.532374101	[,7] 134046.714801444	[,8] 0.010498320268757	[,9] 9.5	[,10] 0.00970511384845092	[,11] Inf	[,12] Inf	[,13] Inf	[,14] Inf	[,15] Inf	[,16] Inf	[,17] Inf	
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phi input

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]	[10]	[11]	[12]	[13]	[14]	[15]	[16]	[17]	[18]
	0.0989	0.01	0.01	0.001	1e-04	0.1	0.15	0.05	0.05	0.02	0.01	0.15	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] 0.04	[,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	[11] 0	[12] 0	[13] 0	[14] 0	[15] 0	[16] 0	[17] 0	[18] 0
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