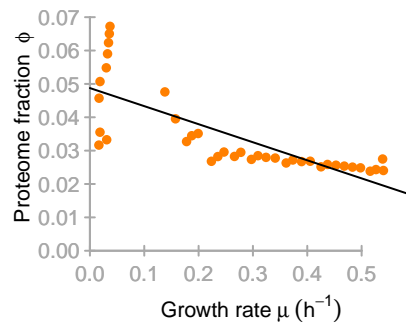
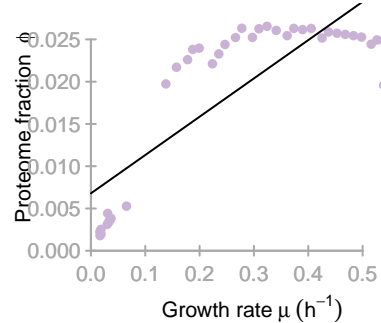
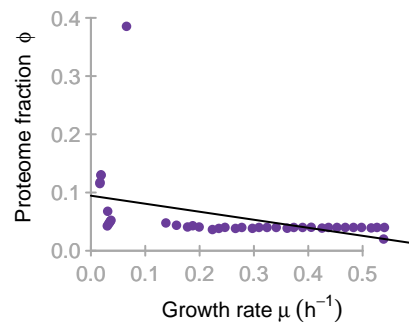
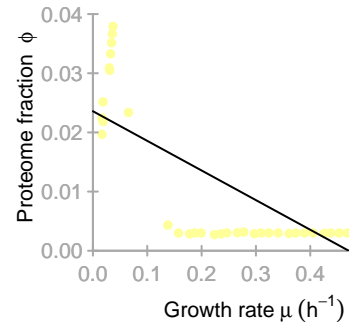
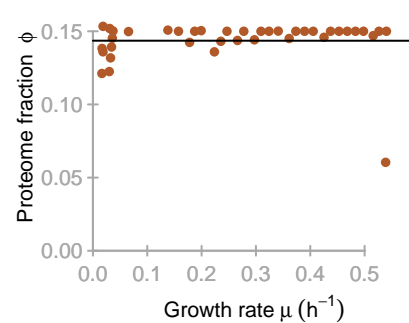
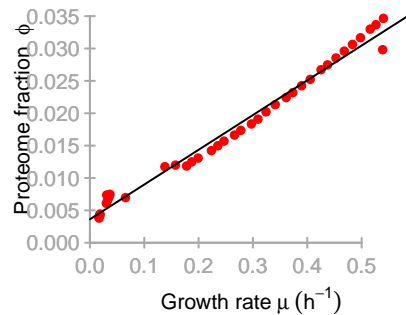
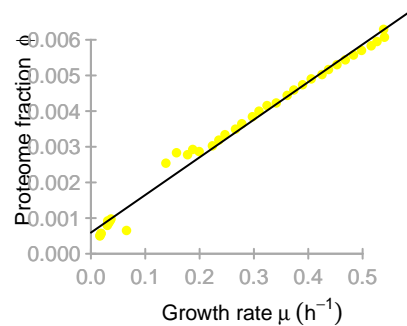
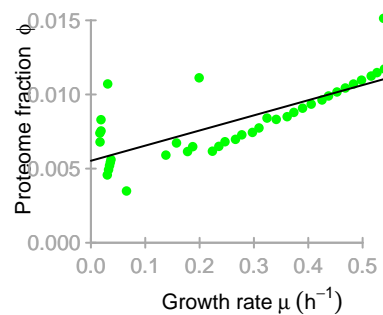
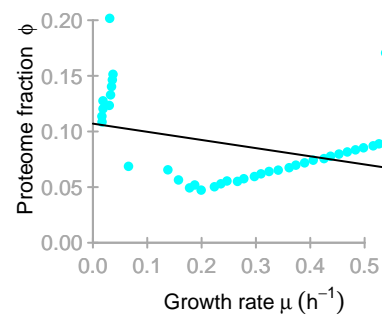
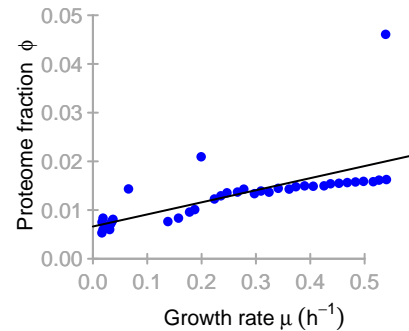
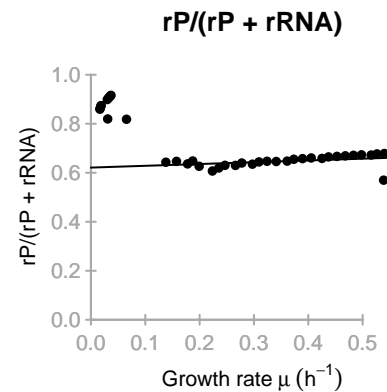
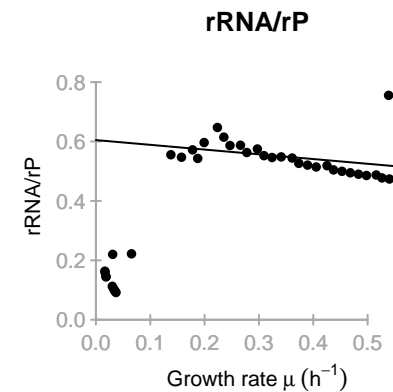
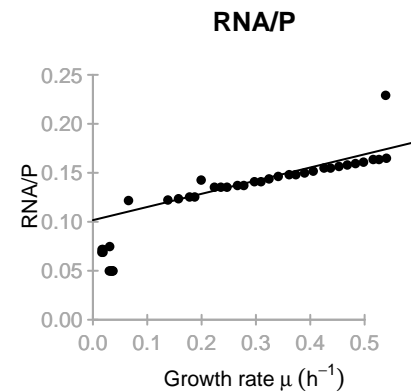
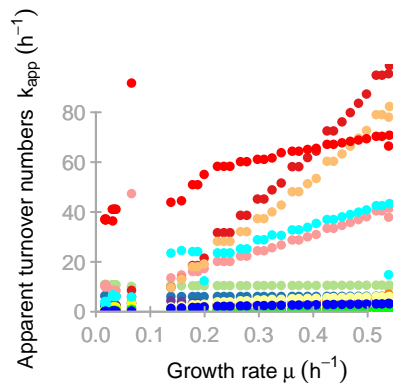
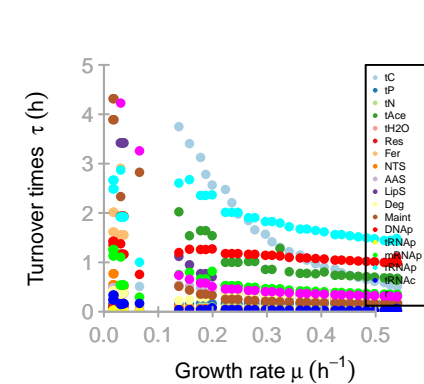
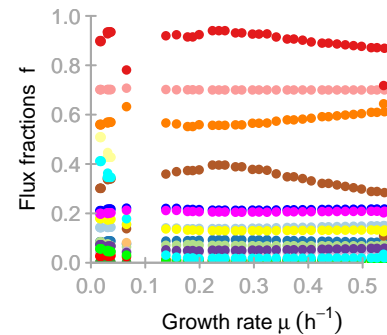
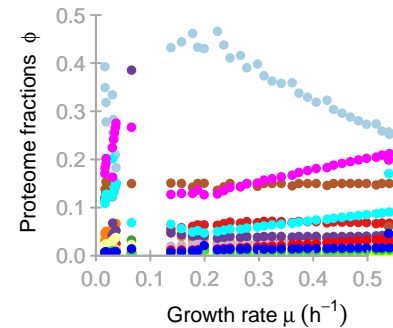
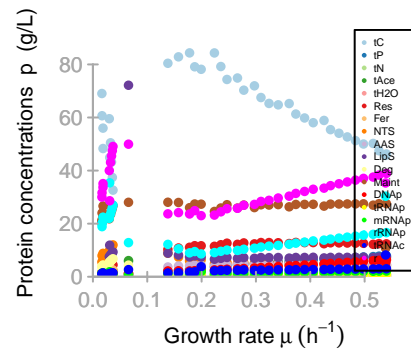
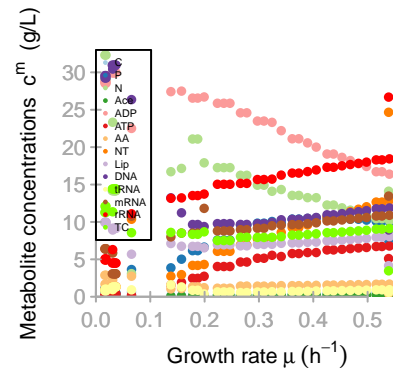
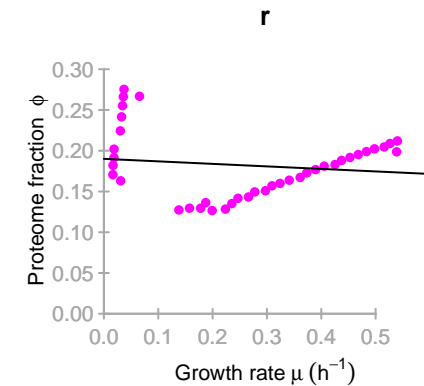
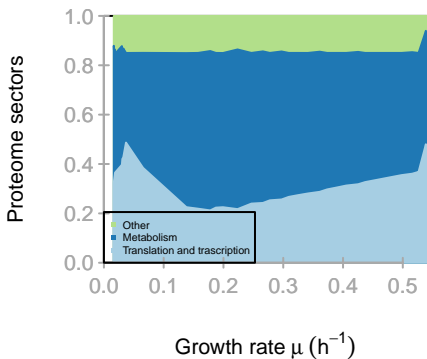
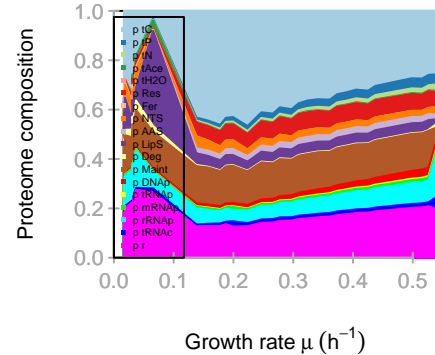
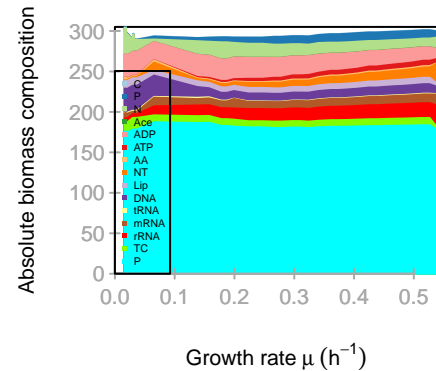
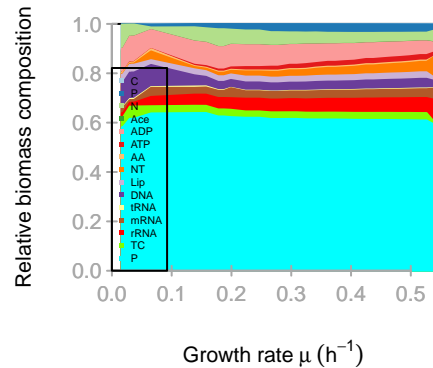
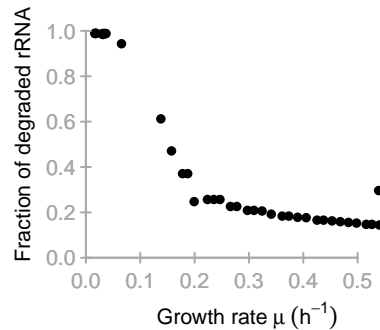
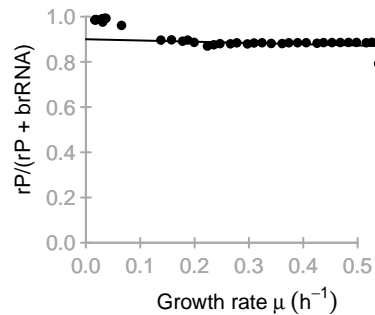


**NTS****AAS****LipS****Deg****Maint****DNAP****tRNAp****mRNAp****rRNAp****tRNAc**



## 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	7	16	27	10	47926	182	364	842	20	36	10	10	2	150	10	2	200	20
kcatb	1	2	3	1	4793	18	36	84	2	4	0	0	0	0	0	0	0	0



# Keq

[1,]	[,1] 7	[,2] 8	[,3] 9	[,4] 100	9.99916544961402	[,5] 1820	[,6] 45500	0.0556878306878307	[,8]	[,9] 10	[,10] 0.02	[,11] Inf	[,12] Inf	[,13] Inf	[,14] Inf	[,15] Inf	[,16] Inf	[,17] Inf	[,18] 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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