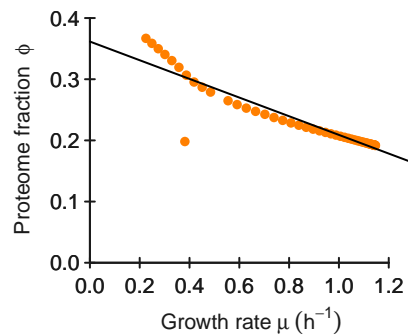
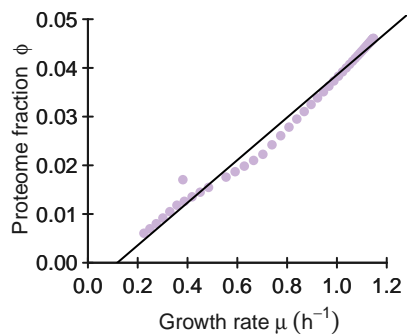
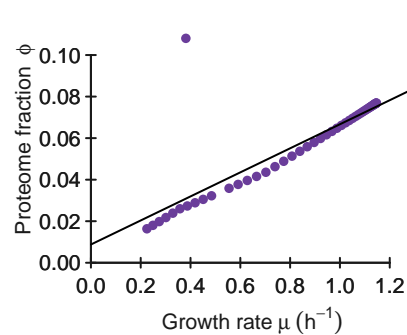
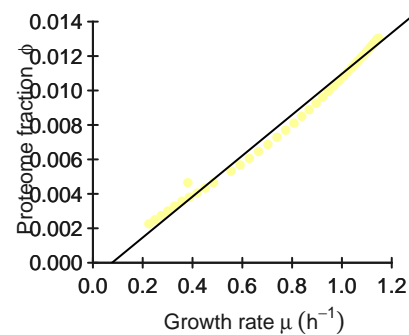
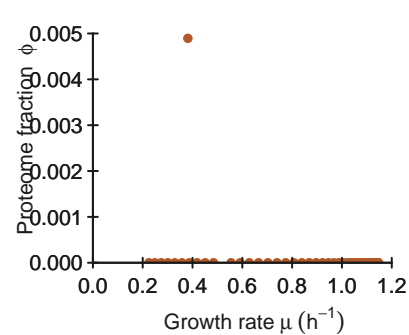
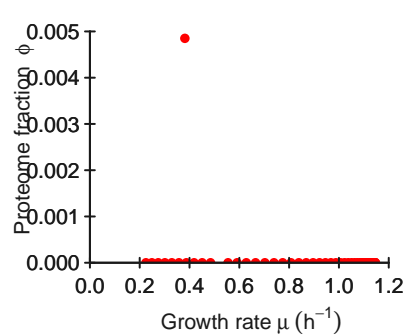
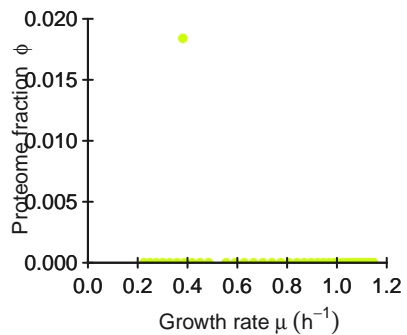
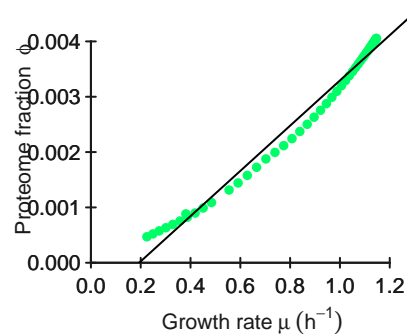
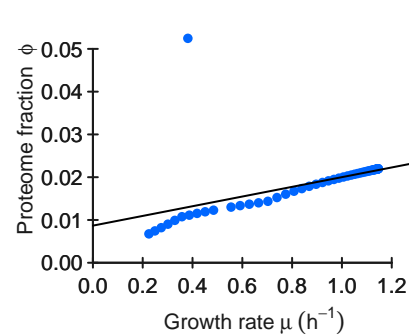
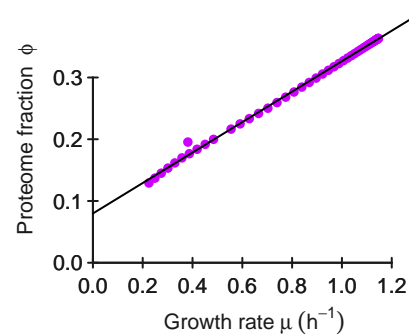
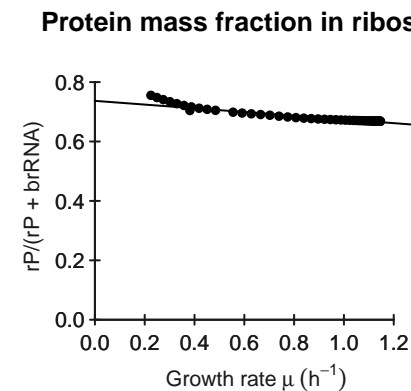
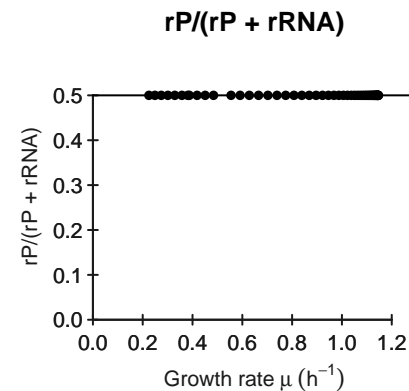
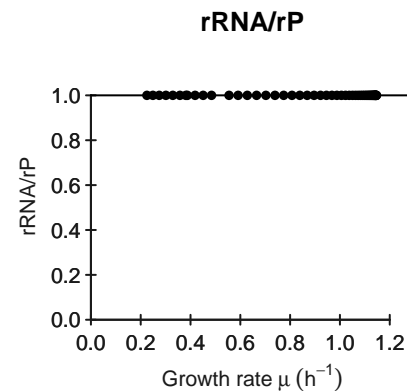
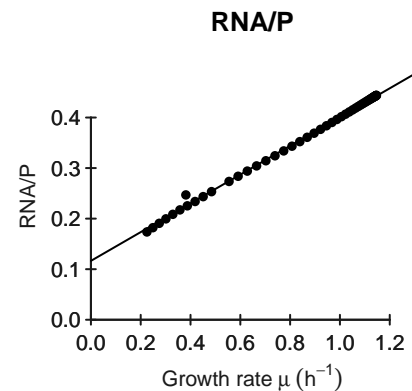
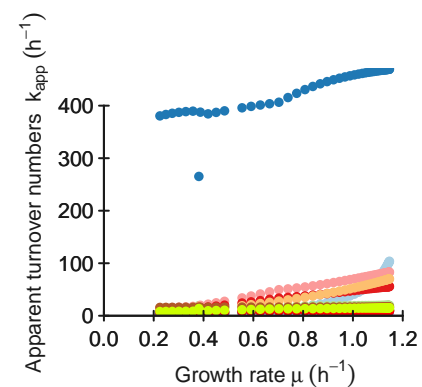
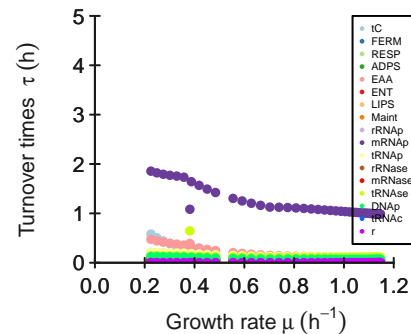
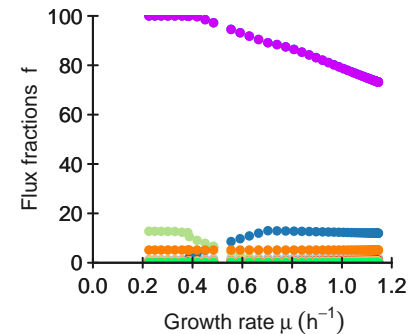
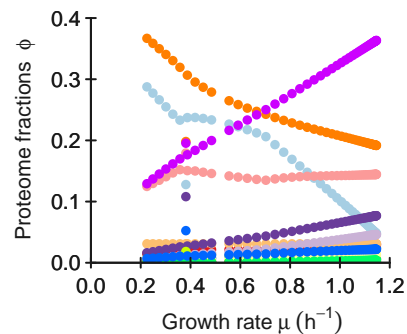
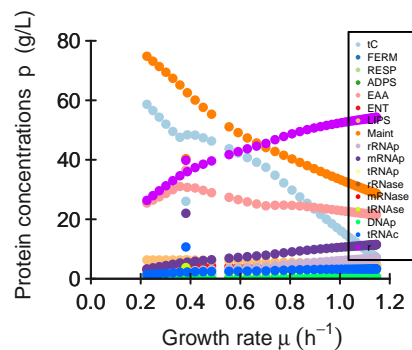
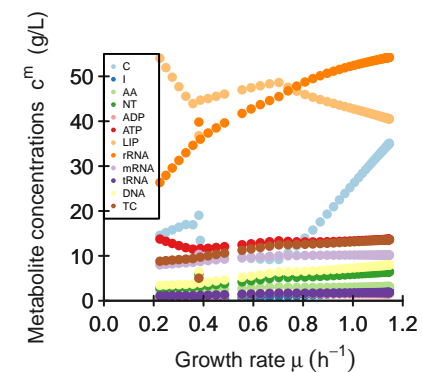
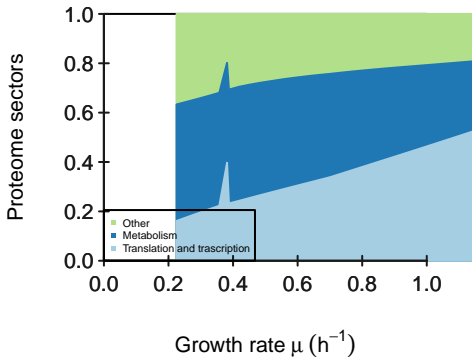
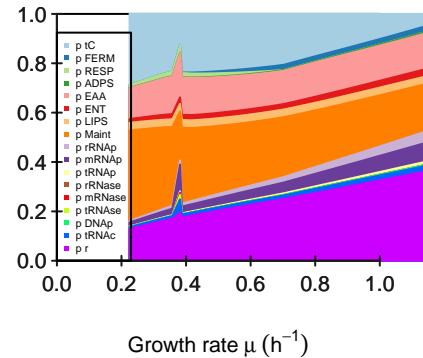
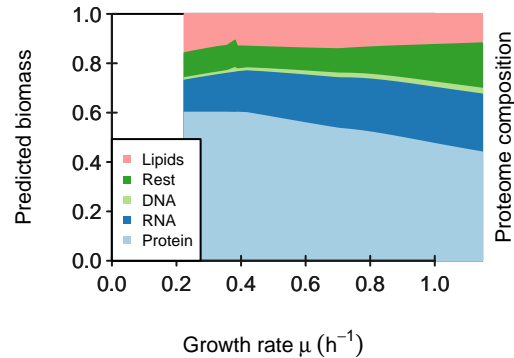
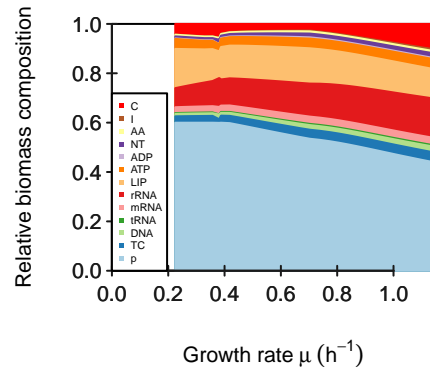
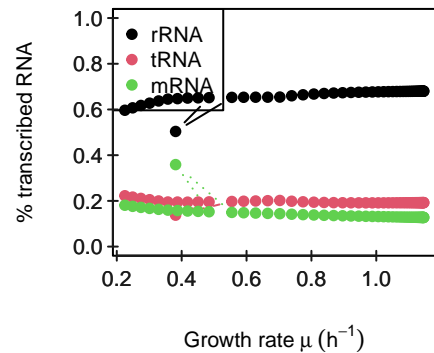
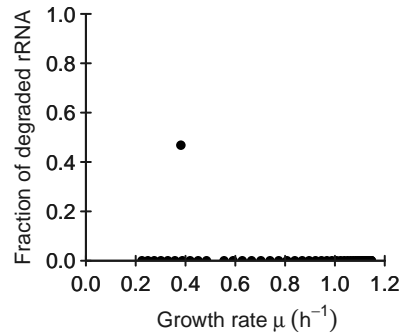


Maint**rRNAp****mRNAp****tRNAp****rRNase****mRNase****tRNase****DNAp****tRNAc****r**





keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

K

[illegible]

KA[illegible]

kcat

kcatf	tC	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNase	DNAp	tRNAc	r
kcatb	108.9 0	2807.8 0	561.6 0	25.7 0	19.8 0	279.1 0	114.8 0	81.2 0	17.8 0	2 0	17.8 0	19.8 0	19.8 0	19.8 0	29.7 0	34010.8 0	2064.8 0

Keq

[1,]	[,1] Inf	[,2] Inf	[,3] Inf	[,4] Inf	[,5] Inf	[,6] Inf	[,7] Inf	[,8] Inf	[,9] Inf	[,10] Inf	[,11] Inf	[,12] Inf	[,13] Inf	[,14] Inf	[,15] Inf	[,16] Inf	[,17] Inf
------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	-------------	--------------	--------------	--------------	--------------	--------------	--------------	--------------	--------------

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
	0.043	0.023	0.023	0.002	0.165	0.021	0.031	0.3036	0.0426	0.0213	0.0071	0.002	0.006	4e-04	0.002	0.023	0.284

average saturation input

3

minimal phi constraint

[1,]	[,1] 0	[,2] 0	[,3] 0	[,4] 0	[,5] 0	[,6] 0	[,7] 0.031	[,8] 0	[,9] 0	[,10] 0	[,11] 0	[,12] 0	[,13] 0	[,14] 0	[,15] 0	[,16] 0	[,17] 0
------	-----------	-----------	-----------	-----------	-----------	-----------	---------------	-----------	-----------	------------	------------	------------	------------	------------	------------	------------	------------

