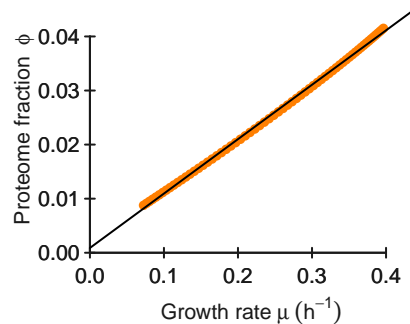
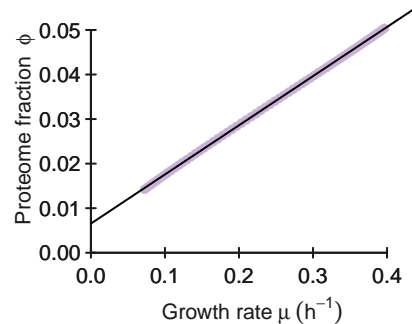
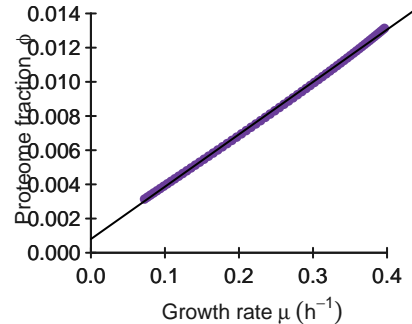
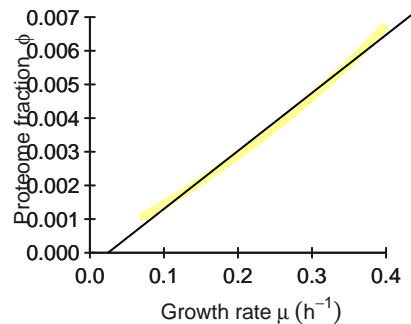
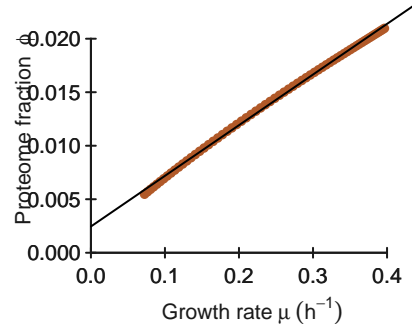
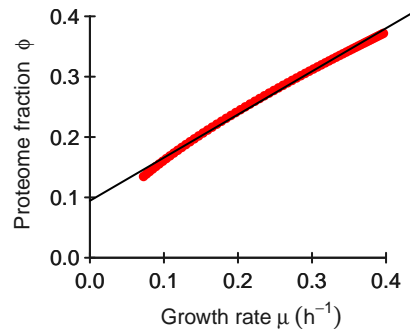
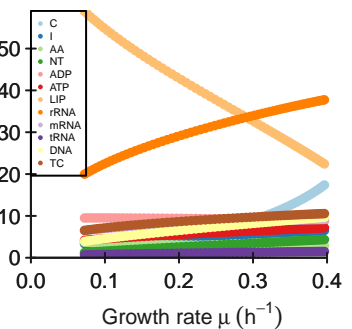
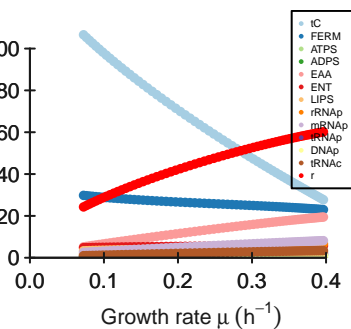
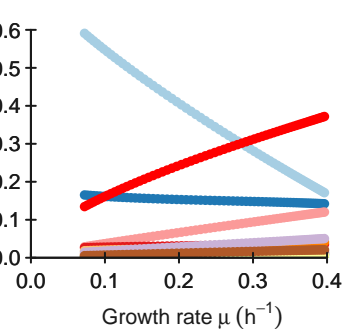
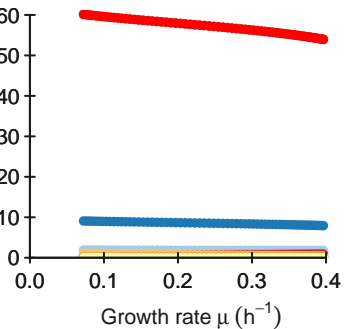
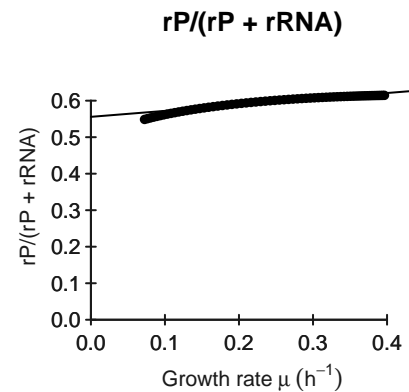
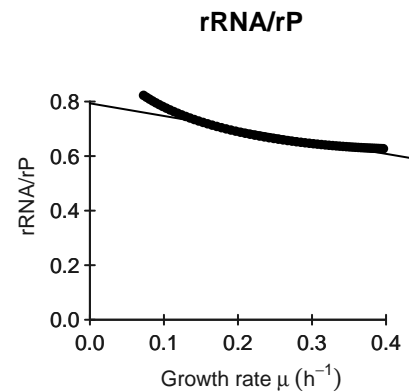
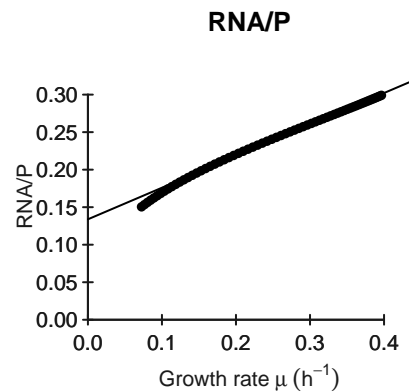
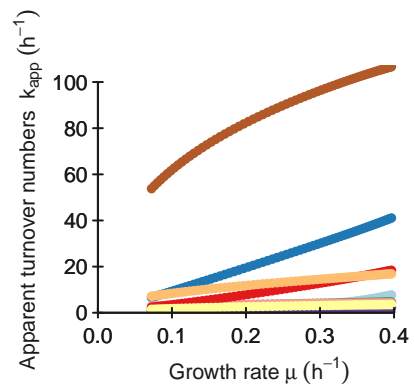
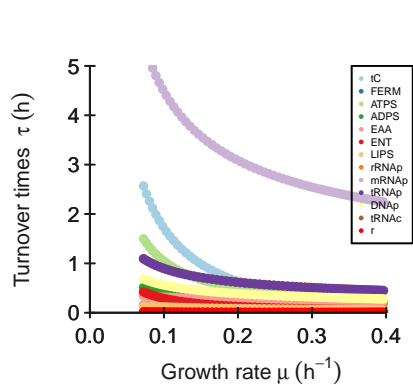
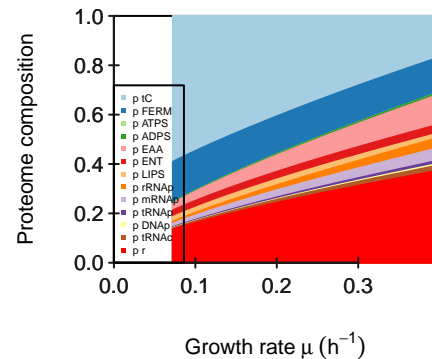
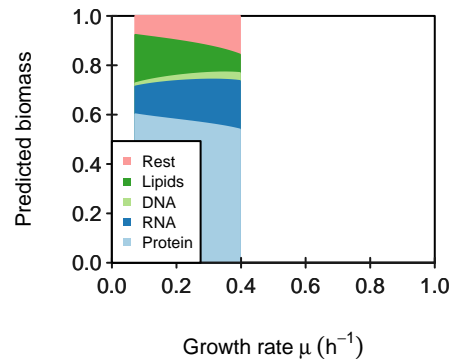
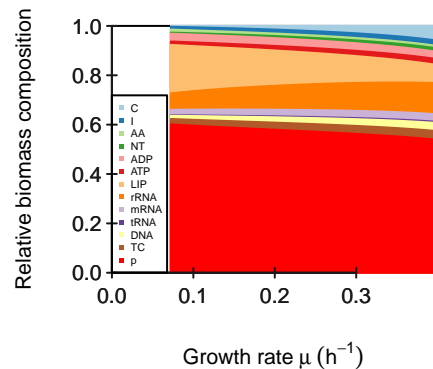
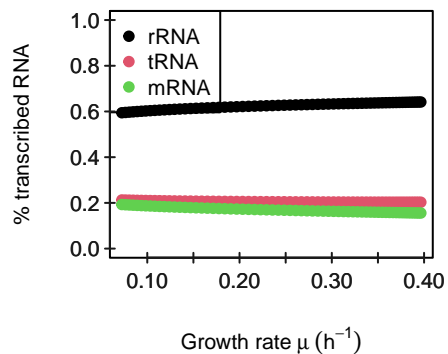
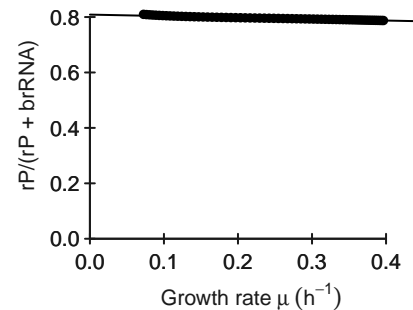


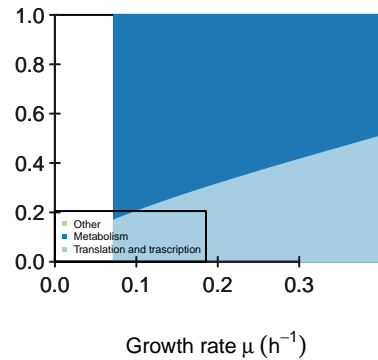
rRNAp**mRNAp****tRNAp****DNAp****tRNAc****r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f 



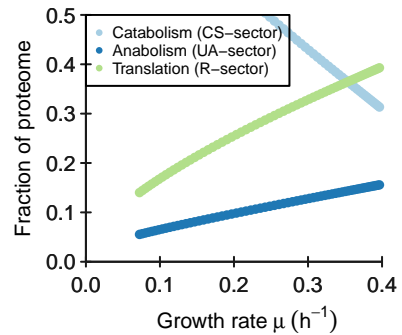
Protein mass fraction in ribosome



Proteome sectors



Proteome sectors



M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
kcatf	54	100	10	8	7	78	33	5	1	5	8	7350	446
kcatb	5	10	1	1	1	8	3	0	0	0	0	0	0

Keq

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phi input

0.0364656381486676	0.00701262272089762	0.231416549789621	0.032258064516129	0.0434782608695652	0.0597475455820477	0.0298737727910238	0.00995792426367462	0.002805046
[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	

average saturation input

3

minimal phi constraint

[illegible]

minimal f constraint

[illegible]