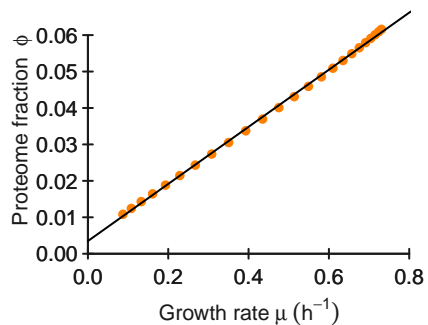
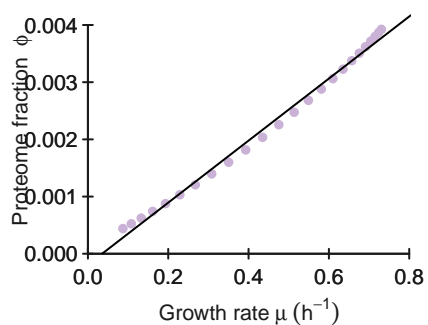


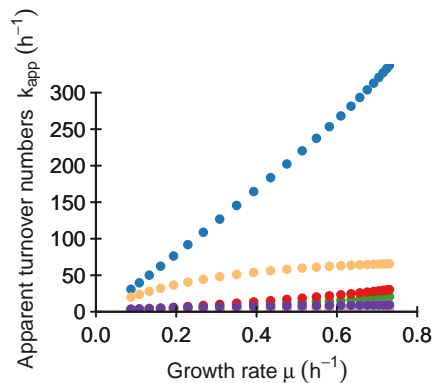
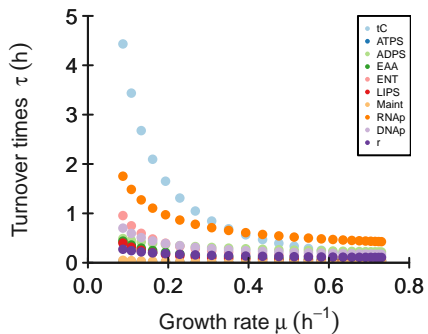
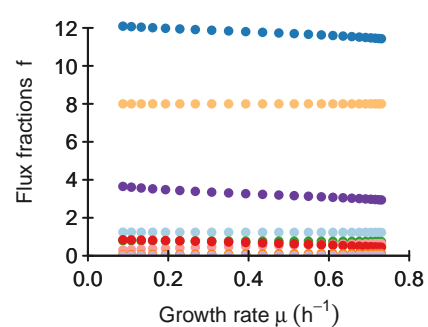
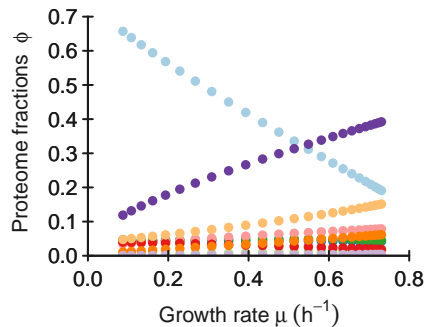
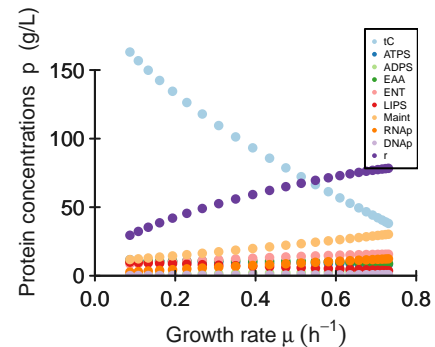
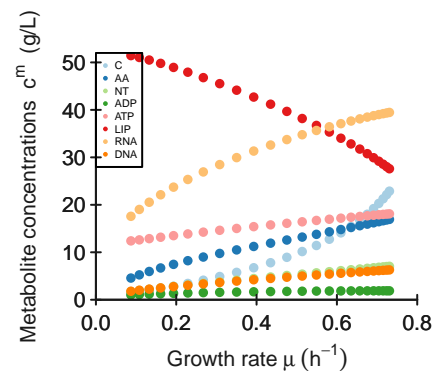
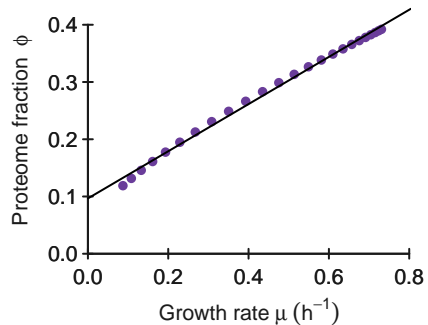
**RNAp**



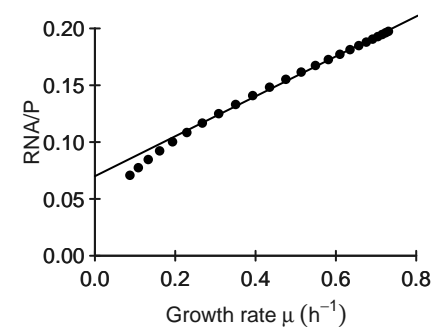
**DNAp**



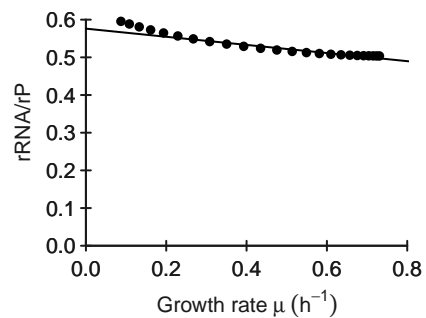
**r**



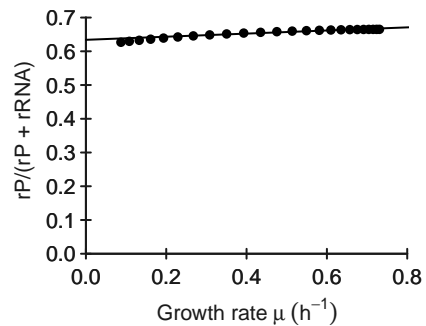
**RNA/P**



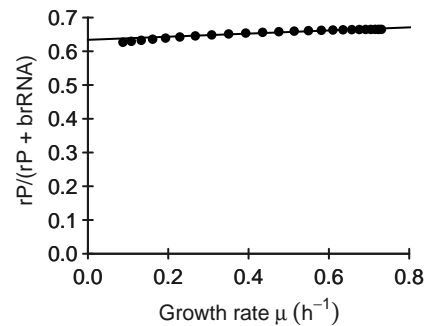
rRNA/rP



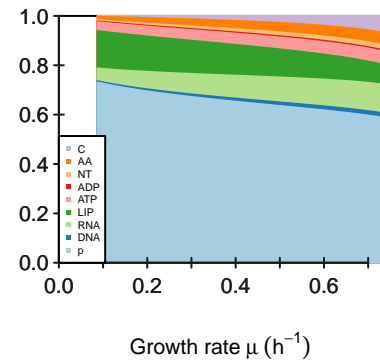
rP/(rP + rRNA)



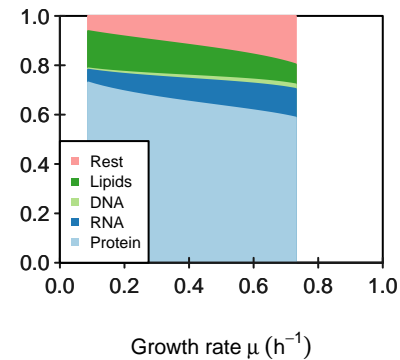
Protein mass fraction in ribosome



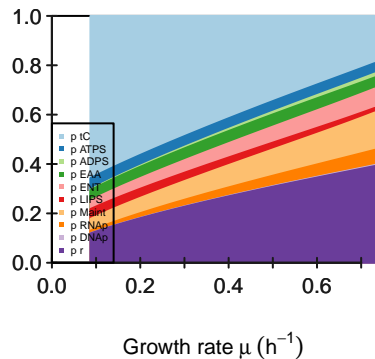
Relative biomass composition



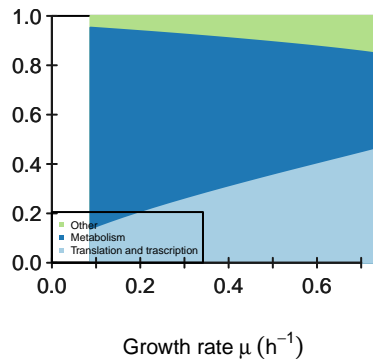
Predicted biomass



Proteome composition



Proteome sectors



**M**

[illegible]

**K**

[illegible]

**KA**[illegible]

# kcat

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
kcatf	20	903	11	53	20	58	77	6	15	29
kcatb	2	90	1	5	2	6	0	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
2600	156.074074074074	3.66666666666667	8.24444444444444	0.864197530864197	12.5308641975309	Inf	Inf	Inf	Inf	



## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
	0.11	0.023	0.005	0.032	0.16	0.031	0.2506	0.0794	0.002	0.307

**average saturation input**

3

### minimal phi constraint

[illegible]

minimal f constraint

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
	0	0	0	0	0	0	8	0	0	0