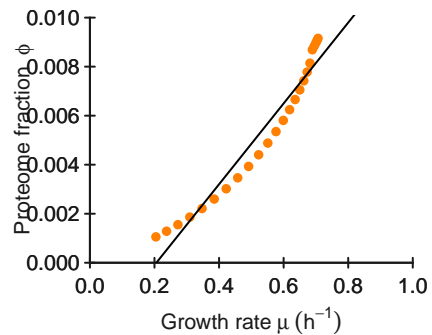
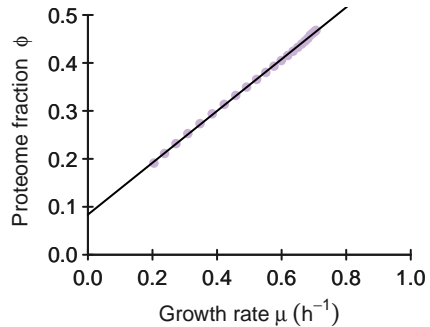
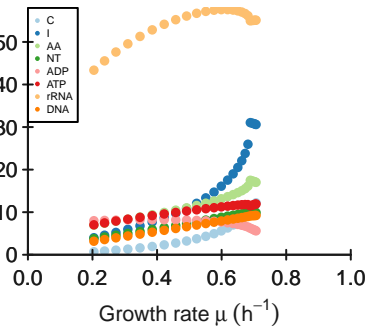
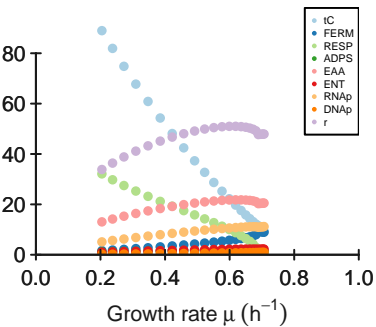
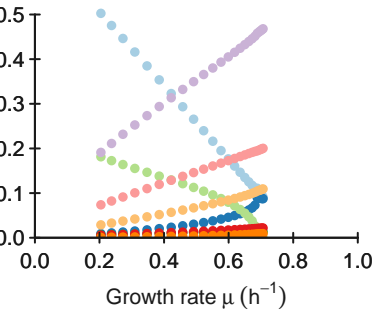
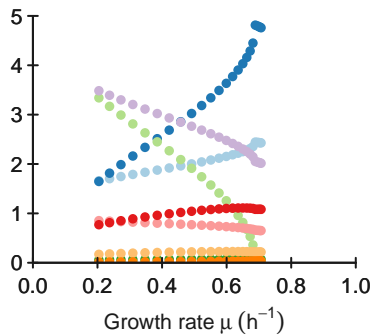
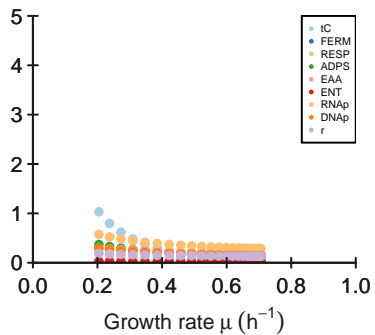
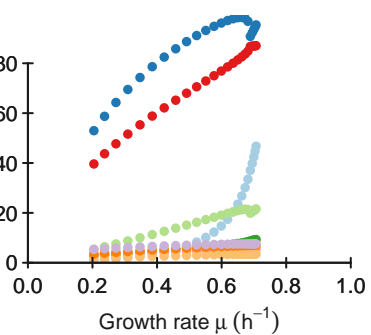
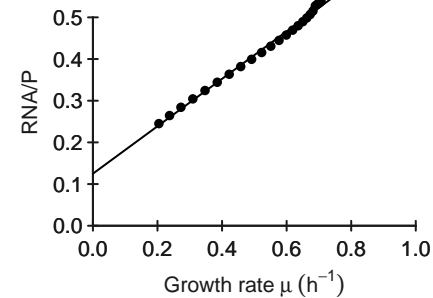
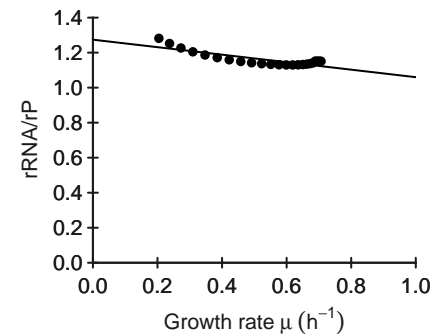
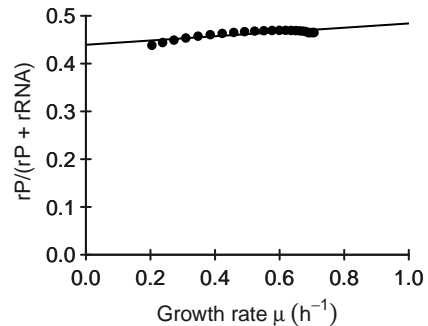
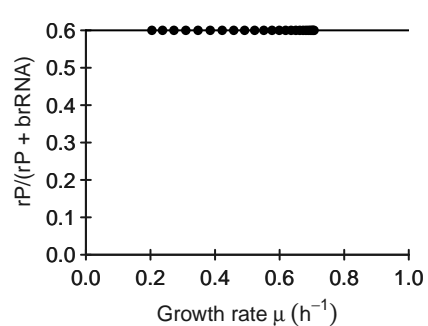


**DNAp****r**Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Flux fractions  $f$ Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )**RNA/P****rRNA/rP**

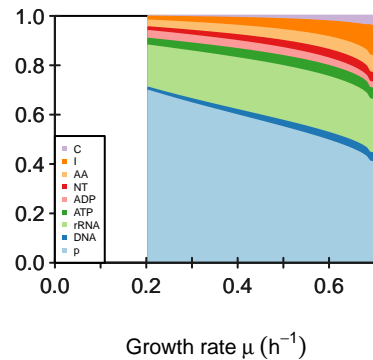
$rP/(rP + rRNA)$



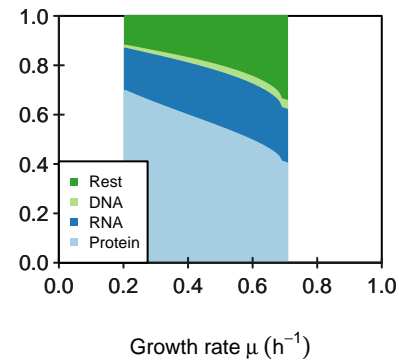
Protein mass fraction in ribosome



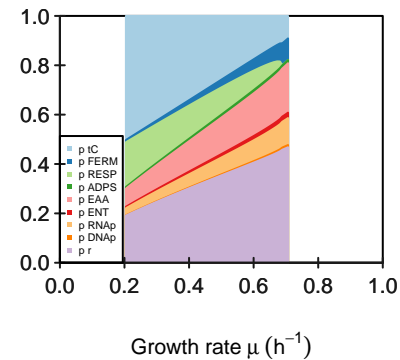
Relative biomass composition



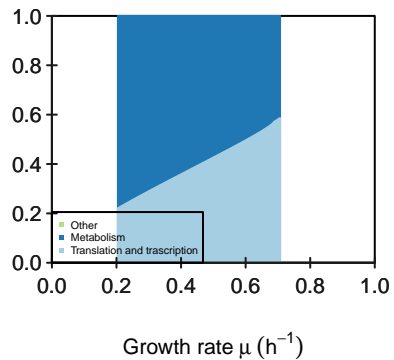
Predicted biomass



Proteome composition



Proteome sectors



keep\_ribosome\_kcat FALSE  
keep\_transport\_kcat FALSE  
maintenance\_fun constant

**M**

[illegible]

**K**

[illegible]



## kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAP	r
kcatf	56	148	49.33333333333333	24	7	123	6	12	17
kcatb	6	15	5	2	1	12	0	0	0



## Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	1306.66666666667	157.866666666667	157.866666666667	6	28	7.6875	Inf	Inf	Inf

## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.065	0.035	0.035	0.003	0.248	0.032	0.119	0.003	0.46

**average saturation input**

4

### minimal phi constraint

[illegible]

### minimal f constraint

[illegible]