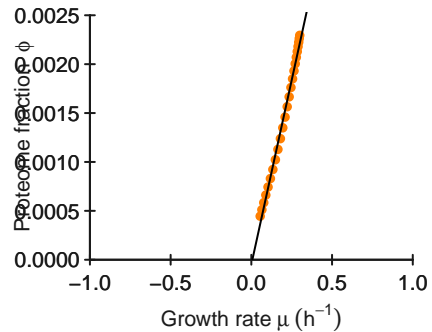
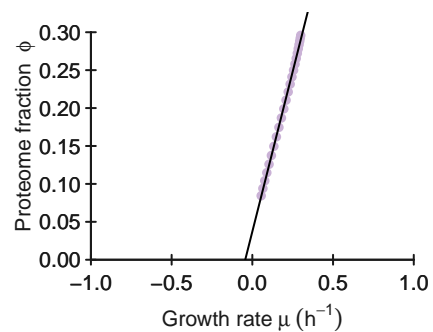
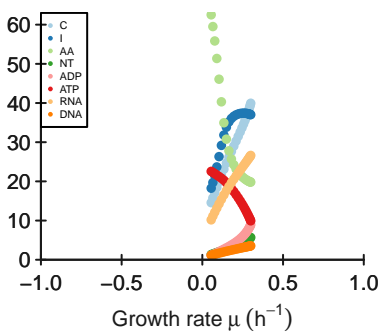
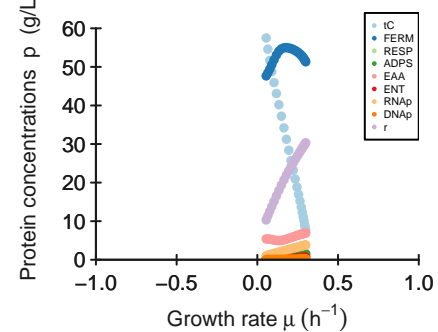
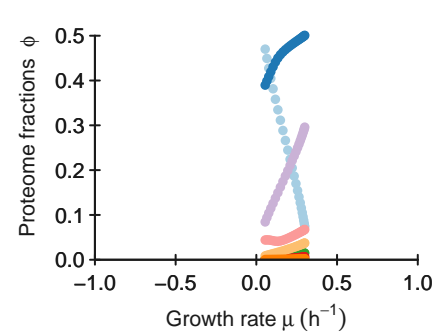
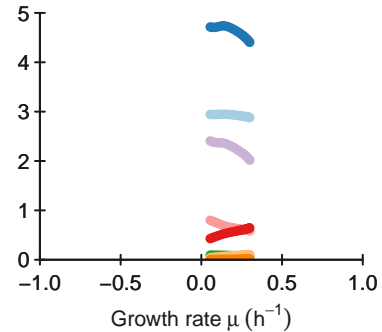
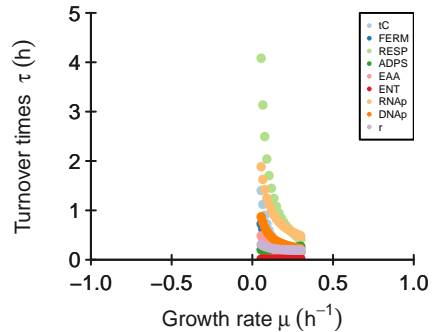
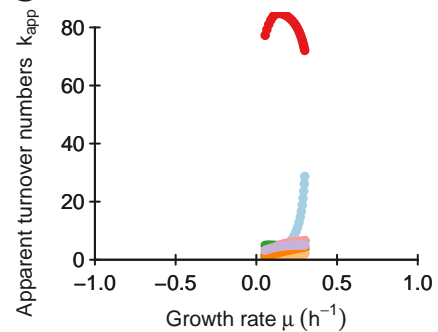
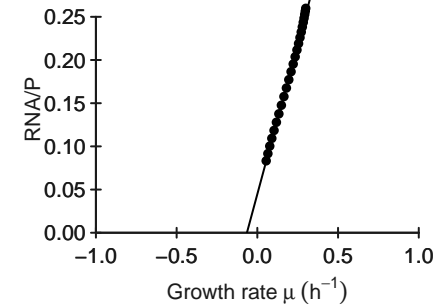
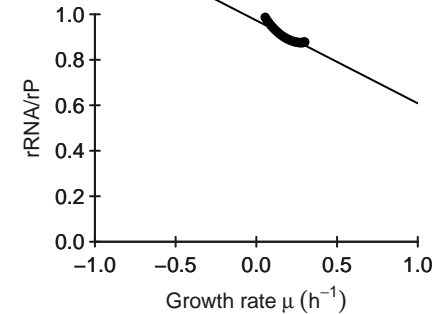
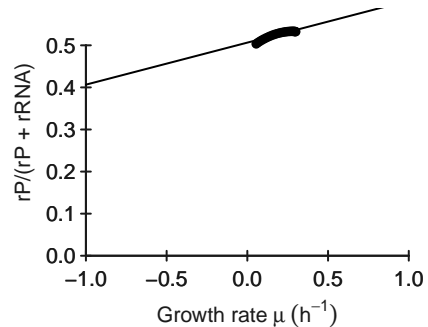
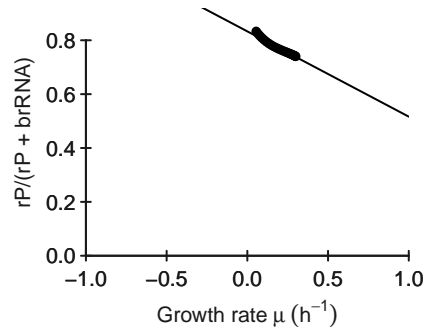


**DNAp****r**Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Flux fractions  $f$ Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )**RNA/P****rRNA/rP**

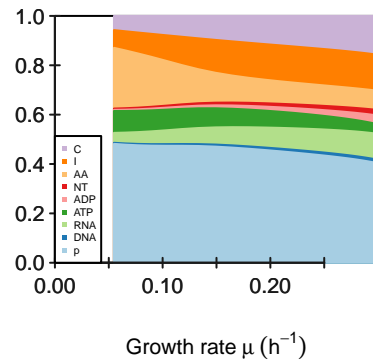
$rP/(rP + rRNA)$



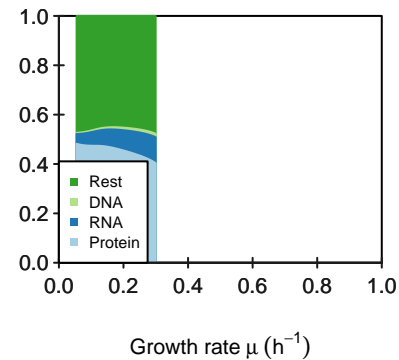
Protein mass fraction in ribosome



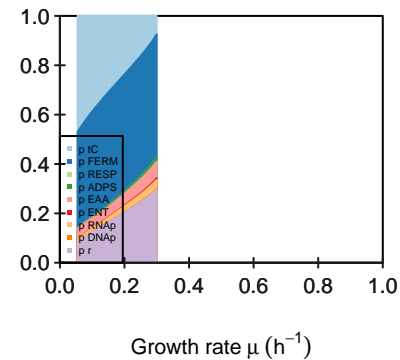
Relative biomass composition



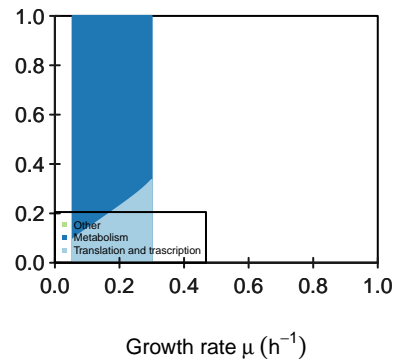
Predicted biomass



Proteome composition



Proteome sectors



```
keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant
```

## M

[illegible]





# kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	64	10	5	26	10	149	6	13	19
kcatb	6	1	1	3	1	15	0	0	0



Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
960	1322.222222222222	66.11111111111111	4.333333333333333	1.2962962962963	0.613168724279835	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**

3

### minimal phi constraint

[illegible]

