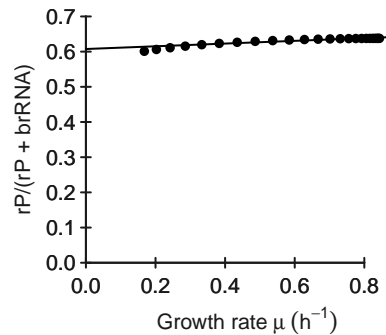
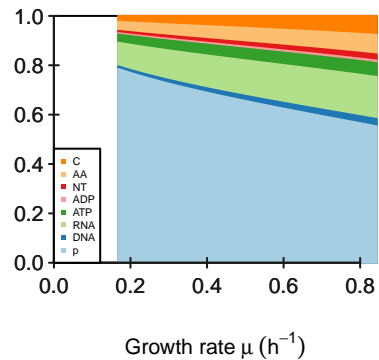


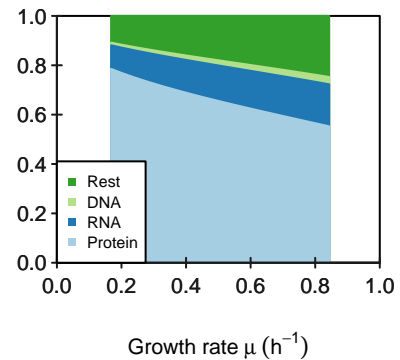
Protein mass fraction in ribosome



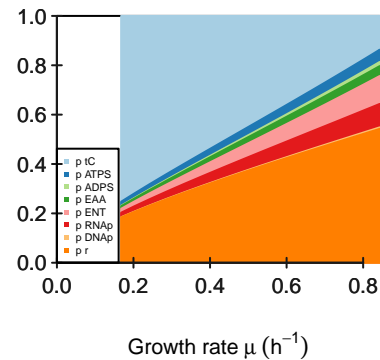
Relative biomass composition



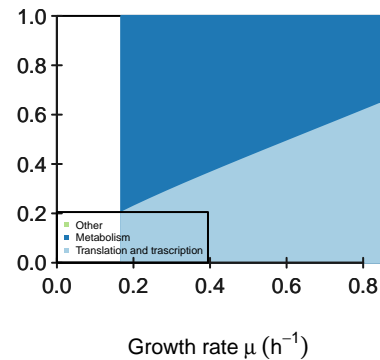
Predicted biomass



Proteome composition



Proteome sectors



**M**

	tC	ATPS	ADPS	EAA	ENT	RNAp	DNAp	r
C	1	-0.02	0	-1	-0.167	0	0	0
AA	0	0	0	1	-0.167	0	0	-0.2
NT	0	0	-1	0	0.334	-1	-1	0
ADP	0	-0.98	1	0	0.666	0	0	0.8
ATP	0	0.98	0	0	-0.666	0	0	-0.8
RNA	0	0	0	0	0	1	0	0
DNA	0	0	0	0	0	0	1	0
p	0	0	0	0	0	0	0	0.2

K

	tC	ATPS	ADPS	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0
x_W	0	20	0	0	0	0	0	0
C	0	7	0	7	7	0	0	0
AA	0	0	0	0	2	0	0	2
NT	0	0	2	0	0	2	2	0
ADP	0	1	0	0	0	0	0	0
ATP	0	0	0	0	2	0	0	2
RNA	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0	0

KA

	tC	ATPS	ADPS	EAA	ENT	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0
ADP	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	0	50
DNA	0	0	0	0	0	5	5	0
p	0	0	0	0	0	0	0	0

## kcat

	tC	ATPS	ADPS	EAA	ENT	RNAp	DNAP	r
kcatf	13	169	8	40	20	6	16	21
kcatb	0	0	0	0	0	0	0	0

**Keq**

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]
	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf



## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]
	0.15	0.032	0.007	0.045	0.223	0.11	0.003	0.43

**average saturation input**

3

### minimal phi constraint

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

### minimal f constraint

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