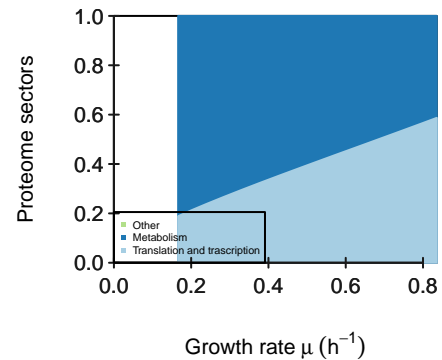
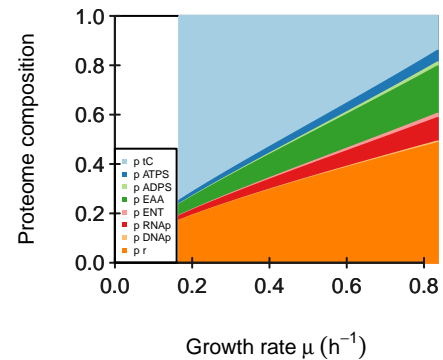
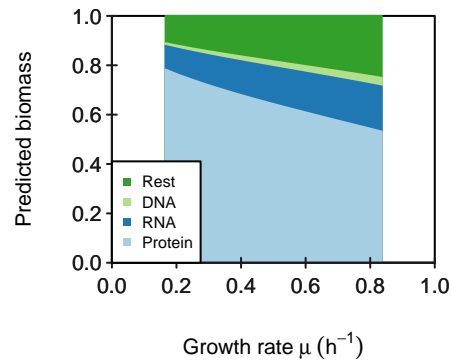
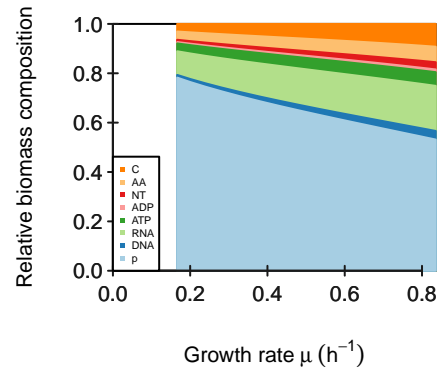
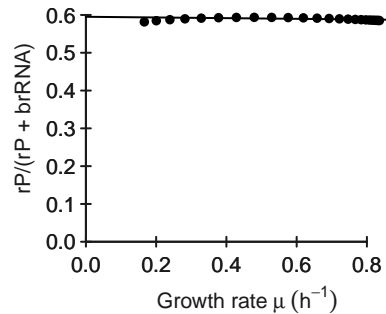


## Protein mass fraction in ribosome



**M**

	<b>tC</b>	<b>ATPS</b>	<b>ADPS</b>	<b>EAA</b>	<b>ENT</b>	<b>RNAp</b>	<b>DNAp</b>	<b>r</b>
<b>C</b>	1	-0.02	0	-1	-0.167	0	0	0
<b>AA</b>	0	0	0	1	-0.167	0	0	-0.2
<b>NT</b>	0	0	-1	0	0.334	-1	-1	0
<b>ADP</b>	0	-0.98	1	0	0.666	0	0	0.8
<b>ATP</b>	0	0.98	0	0	-0.666	0	0	-0.8
<b>RNA</b>	0	0	0	0	0	1	0	0
<b>DNA</b>	0	0	0	0	0	0	1	0
<b>p</b>	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	8	142	6	16	23
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]
	0.154	0.032	0.007	0.231	0.032	0.111	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