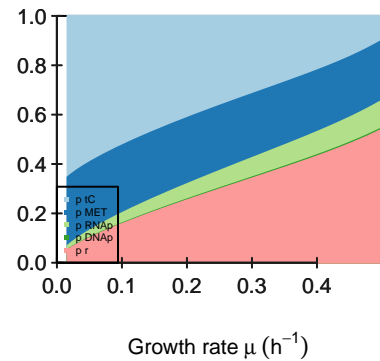
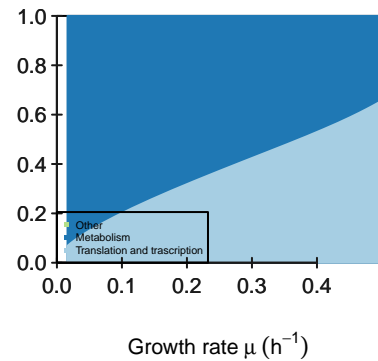


Proteome composition



Proteome sectors



**M**

	<b>tC</b>	<b>MET</b>	<b>RNAp</b>	<b>DNAP</b>	<b>r</b>
<b>C</b>	1	-1	0	0	0
<b>AA</b>	0	0.5	0	0	-0.9
<b>NT</b>	0	0.3	-1	-1	0
<b>ATP</b>	0	0.2	0	0	-0.1
<b>RNA</b>	0	0	1	0	0
<b>DNA</b>	0	0	0	1	0
<b>p</b>	0	0	0	0	1

K

	tC	MET	RNAp	DNAp	r
x_C	0.1	0	0	0	0
C	24	8	0	0	0
AA	0	12	0	0	4
NT	0	5	2	2	0
ATP	0	35	0	0	12
RNA	0	0	0	0	0
DNA	0	0	0	0	0
p	0	0	0	0	0

KA

	tC	MET	RNAp	DNAp	r
x_C	0	0	0	0	0
C	0	0	0	0	0
AA	0	0	0	0	0
NT	0	0	0	0	0
ATP	0	0	0	0	0
RNA	0	0	0	0	75
DNA	0	0	3	3	0
p	0	0	0	0	0

**kcat**

	<b>tC</b>	<b>MET</b>	<b>RNAp</b>	<b>DNAp</b>	<b>r</b>
<b>kcatf</b>	15	9	6	16	4
<b>kcatb</b>	2	1	0	0	0

Keq

	[1,]	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]		1800	2362.5	Inf	Inf	Inf



**phi input**

<b>[1,]</b>	<b>[,1]</b>	<b>[,2]</b>	<b>[,3]</b>	<b>[,4]</b>	<b>[,5]</b>
	0.15	0.307	0.11	0.003	0.43

**average saturation input**

3

minimal phi constraint

	<b>[1,]</b>	<b>[,1]</b>	<b>[,2]</b>	<b>[,3]</b>	<b>[,4]</b>	<b>[,5]</b>
	0	0	0	0	0	

minimal f constraint

	[1,]	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	0	0	0	0	0	