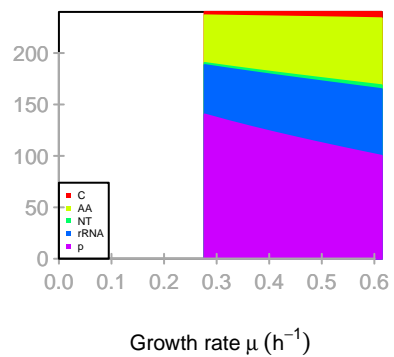
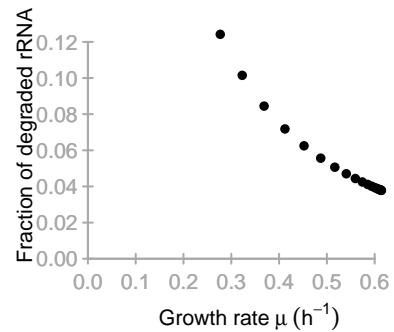
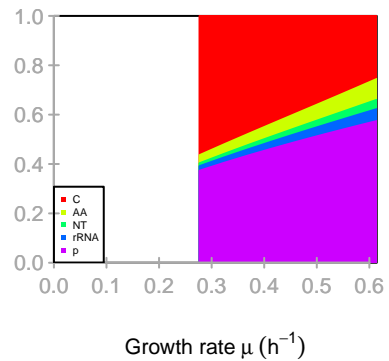


Absolute biomass composition



Proteome composition



**M**

	<b>Cin</b>	<b>EAA</b>	<b>ENT</b>	<b>rRNAp</b>	<b>Deg</b>	<b>r</b>
<b>C</b>	1	-1	-0.66	-0.05	0	0
<b>AA</b>	0	1	-0.34	0	0	-1
<b>NT</b>	0	0	1	-1	1	0
<b>rRNA</b>	0	0	0	0.95	-1	0
<b>p</b>	0	0	0	0	0	1

K

	Cin	EAA	ENT	rRNAp	Deg	r
x_C	0.01	0	0	0	0	0
C	0	1	1	1	0	0
AA	0	0	54	0	0	54
NT	0	0	0	2	0	0
rRNA	0	0	0	0	53	0
p	0	0	0	0	0	0

KA

	Cin	EAA	ENT	rRNAp	Deg	r
x_C	0	0	0	0	0	0
C	0	0	0	0	0	0
AA	0	0	0	0	0	0
NT	0	0	0	0	0	0
rRNA	0	0	0	0	0	100
p	0	0	0	0	0	0

**kcat**

	<b>Cin</b>	<b>EAA</b>	<b>ENT</b>	<b>rRNAp</b>	<b>Deg</b>	<b>r</b>
<b>kcatf</b>	6	16	25	16	10	5
<b>kcatb</b>	0	0	0	0	0	0

**Keq**

<b>[1,]</b>	<b>[,1]</b>	<b>[,2]</b>	<b>[,3]</b>	<b>[,4]</b>	<b>[,5]</b>	<b>[,6]</b>
	Inf	Inf	Inf	Inf	Inf	Inf



**phi input**

<b>[1,]</b>	<b>[,1]</b>	<b>[,2]</b>	<b>[,3]</b>	<b>[,4]</b>	<b>[,5]</b>	<b>[,6]</b>
	0.3	0.2	0.07	0.027	0.003	0.4

**average saturation input**

1

## minimal phi constraint

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]
	0	0	0	0	0.003	0

minimal f constraint

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