Protein mass fraction in ribosome
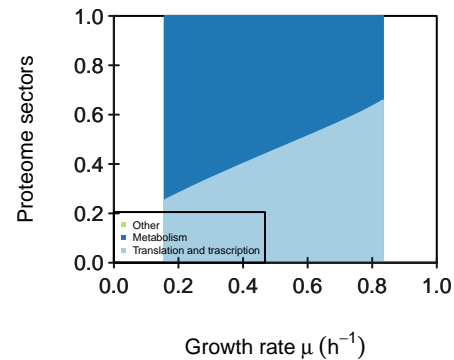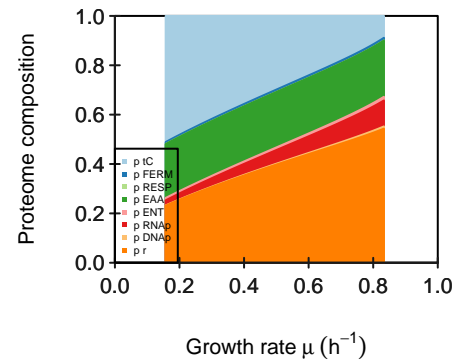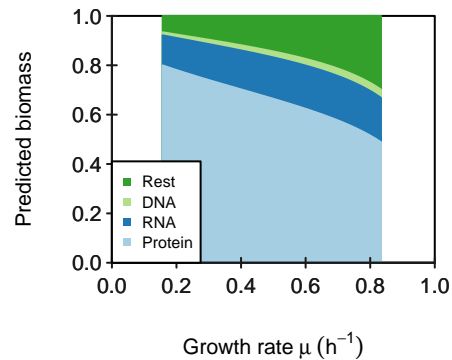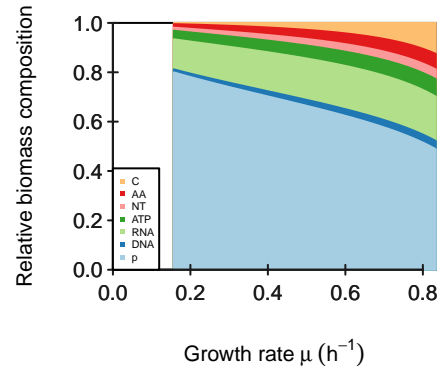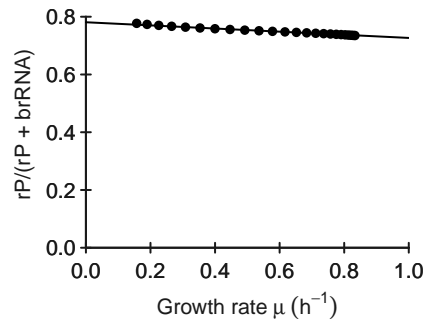
keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

	tC	FERM	RESP	EAA	ENT	RNAp	DNAp	r
C	1	−1	−1	−1	−0.45	0	0	0
AA	0	0	0	1	−0.45	0	0	−0.9
NT	0	0	0	0	1	−1	−1	0
ATP	0	0.5	1	0	−0.1	0	0	−0.1
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	1

K

	tC	FERM	RESP	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0
x_W	0	10	20	0	0	0	0	0
C	17	6	12	6	6	0	0	0
AA	0	0	0	11	4	0	0	4
NT	0	0	0	0	11	4	4	0
ATP	0	6	12	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	FERM	RESP	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
ATP	0	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	0	40
DNA	0	0	0	0	0	4	4	0
p	0	0	0	0	0	0	0	0

kcat

	tC	FERM	RESP	EAA	ENT	RNAp	DNAp	r
kcatf	29	80	8	7	48	6	13	4
kcatb	3	8	1	1	5	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]
[1,]	1643.33333333333	100	8	12.8333333333333	2.2	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]
[1,]	0.065	0.035	0.035	0.248	0.032	0.119	0.003	0.46

average saturation input

3

minimal phi constraint

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

minimal f constraint

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