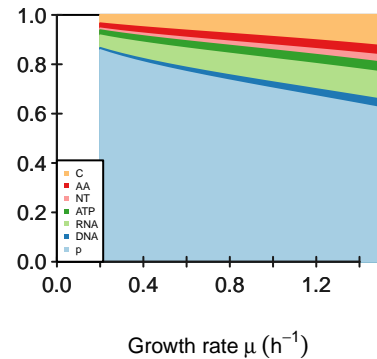
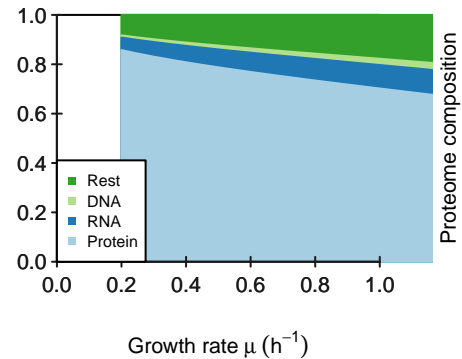


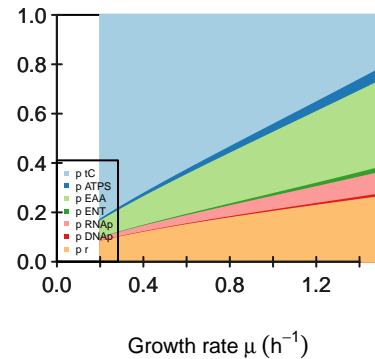
Relative biomass composition



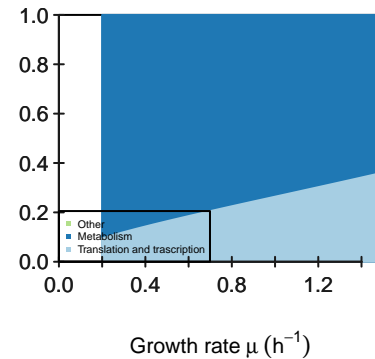
Predicted biomass



Proteome composition



Proteome sectors



M

	tC	ATPS	EAA	ENT	RNAp	DNAp	r
C	1	-1	-1	-1	0	0	0
AA	0	0	1	0	0	0	-0.9
NT	0	0	0	1	-1	-1	0
ATP	0	1	0	0	0	0	-0.1
RNA	0	0	0	0	1	0	0
DNA	0	0	0	0	0	1	0
p	0	0	0	0	0	0	1

K

	tC	ATPS	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0
C	0	7	7	7	0	0	0
AA	0	0	0	0	0	0	2
NT	0	0	0	0	2	2	0
ATP	0	0	0	0	0	0	2
RNA	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0

KA

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

kcat

	tC	ATPS	EAA	ENT	RNAp	DNAp	r
kcatf	12	6	5	25	6	16	23
kcatb	0	0	0	0	0	0	0

Keq

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

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
	0.155	0.032	0.233	0.032	0.112	0.003	0.433

average saturation input

3

minimal phi constraint

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

minimal f constraint

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