





Proteome sectors 0.0 0.2 0.6 8.0 1.0 Growth rate μ (h⁻¹)

maintenance_fun constant

keep_ribosome_kcat FALSE keep_transport_kcat FALSE

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
С	1	1	-1	-1	0	0	Ō	Ō	0
I	0	0	0.8	0.6	-1	-0.9	0	0	0
AA	0	0	0	0	1	0	0	0	-0.8
NT	0	0	0	0	0	1	-1	-1	0
ATP	0	0	0.2	0.1	0	-0.1	0	0	-0.2
RNA	0	0	0	0	0	0	1	0	0
DNA	0	0	0	0	0	0	0	1	0
р	0	0	0	0	0	0	0	0	1

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	Ō	Ō	0
x_W	0	0.1	0	0	0	0	0	0	0
С	0	0	1.8	9	0	0	0	0	0
I	0	0	0	0	1	1	0	0	0
AA	0	0	0	0	0	0	0	0	1
NT	0	0	0	0	0	0	1	1	0
ATP	0	0	0	0	0	4	0	0	4
RNA	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0	0
р	0	0	0	0	0	0	0	0	0

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	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
x_C	0	0	0	0	0	0	Ō	Ō	0
x_W	0	0	0	0	0	0	0	0	0
С	0	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	0	0	25
DNA	0	0	0	0	0	0	4	4	0
р	0	0	0	0	0	0	0	0	0

kcat

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
kcatf	37.7	12.2	9.1	45.7	4.8	36.5	7.2	9.7	4.8
kcatb	0	0	0	0	0	0	0	0	0

Keq



phi input

[1,]	[,1] 0.06	[,2] 0.005	[,3] 0.065	[,4] 0.004	[,5] 0.248	[,6] 0.035	[,7] 0.119	[,8] 0.003	[,9 0.461

average saturation input

minimal phi constraint

[1,]

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
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