Panel 1 (left): Relative biomass composition vs Growth rate μ (h⁻¹)
Legend: C, AA, NT, ATP, RNA, DNA, p

Panel 2: Predicted biomass vs Growth rate μ (h⁻¹)
Legend: Rest, DNA, RNA, Protein

Panel 3: Proteome composition vs Growth rate μ (h⁻¹)
Legend: p tC, p EAA, p ENT, p ATPS, p RNAp, p DNAp, p r

Panel 4 (right): Proteome sectors vs Growth rate μ (h⁻¹)
Legend: Other, Metabolism, Translation and trascription

M

	tC	EAA	ENT	ATPS	RNAp	DNAp	r
C	1	−1	−1	−1	0	0	0
AA	0	1	0	0	0	0	−0.9
NT	0	0	1	0	−1	−1	0
ATP	0	0	0	1	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	EAA	ENT	ATPS	RNAp	DNAp	r
x_C	1	0	0	0	0	0	0
C	21	7	7	7	0	0	0
AA	0	6	0	0	0	0	2
NT	0	0	6	0	2	2	0
ATP	0	0	0	6	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	EAA	ENT	ATPS	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	75
DNA	0	0	0	0	5	5	0
p	0	0	0	0	0	0	0

kcat

	tC	EAA	ENT	ATPS	RNAp	DNAp	r
kcatf	12	39	18	1	6	16	4
kcatb	1	4	2	1	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
[1,]	252	8.35714285714286	7.71428571428571	0.857142857142857	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]
[1,]	0.15	0.032	0.045	0.23	0.11	0.003	0.43

3

minimal phi constraint

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

minimal f constraint

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