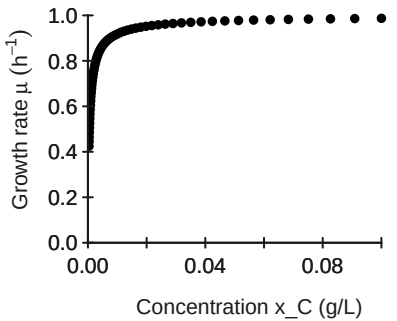
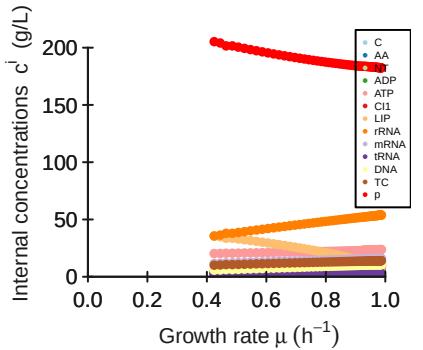
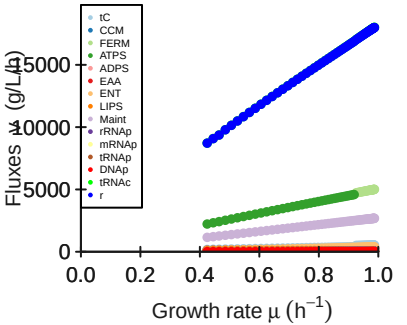
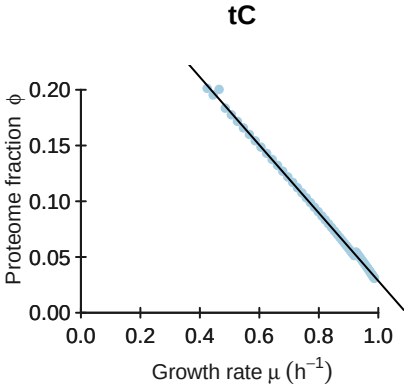
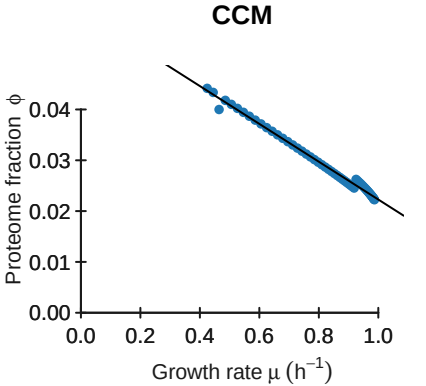
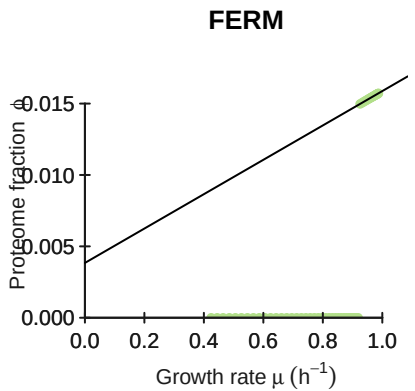

Growth rate μ (h^{-1})
Concentration x_C (g/L)

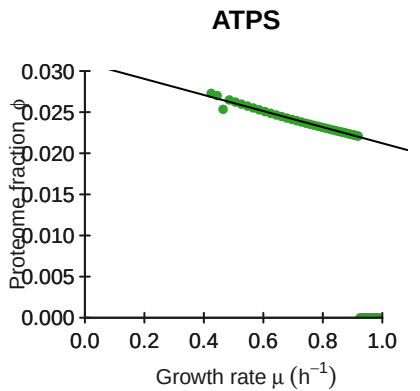

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
N
ADP
ATP
Cl1
LIP
rRNA
mRNA
tRNA
DNA
TC
p

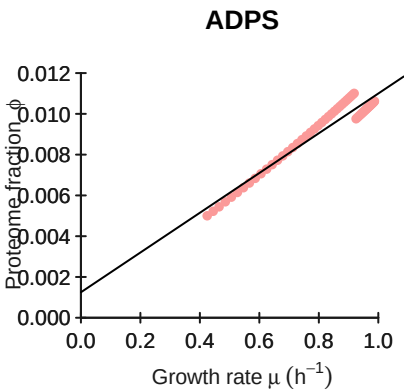

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
CCM
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

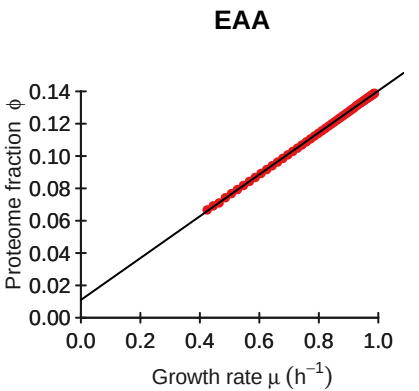

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

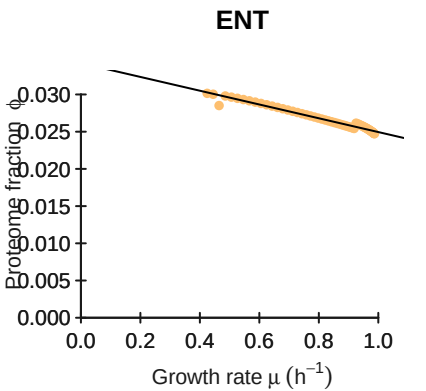

CCM
Proteome fraction ϕ
Growth rate μ (h^{-1})

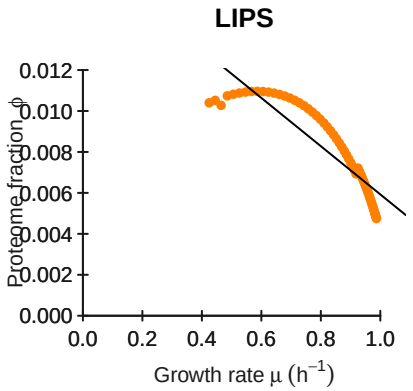

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

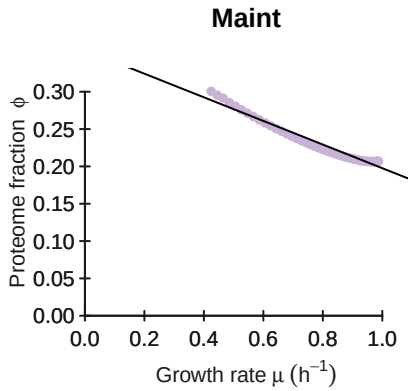

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

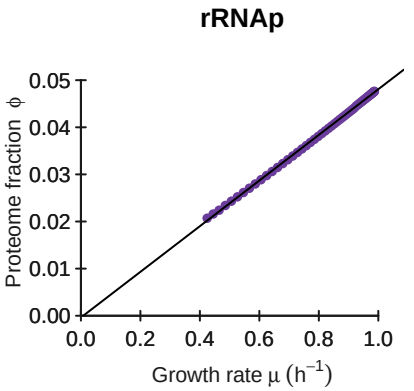

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

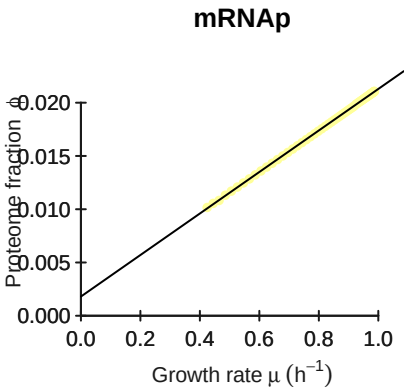

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

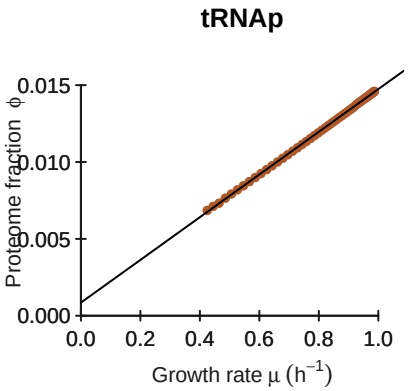

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

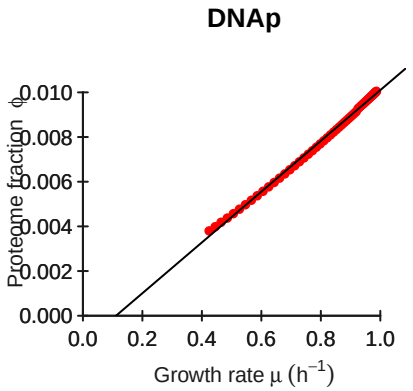

LIPS
Proteome fraction ϕ
Growth rate μ (h−1)

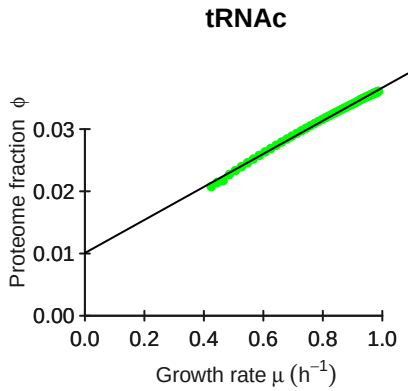

Maint
Proteome fraction ϕ
Growth rate μ (h−1)

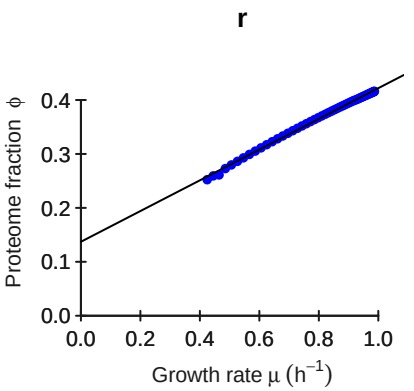

rRNAp
Proteome fraction ϕ
Growth rate μ (h−1)

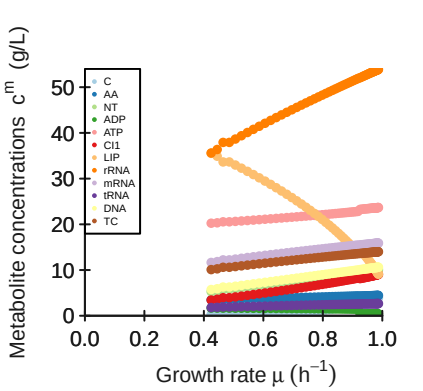

mRNAp
Proteome fraction ϕ
Growth rate μ (h−1)

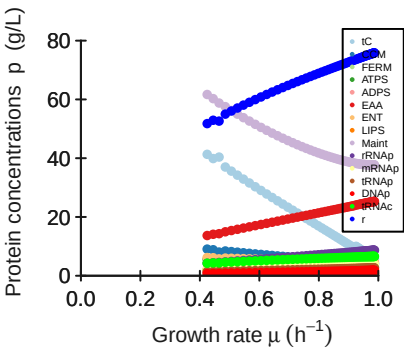

tRNAp
Proteome fraction ϕ
Growth rate μ (h−1)

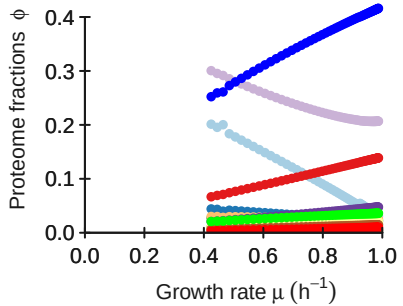

DNAp
Proteome fraction ϕ
Growth rate μ (h−1)

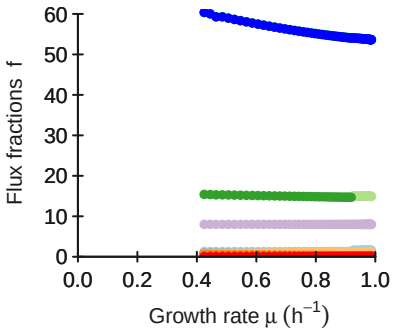

tRNAc
Proteome fraction ϕ
Growth rate μ (h−1)

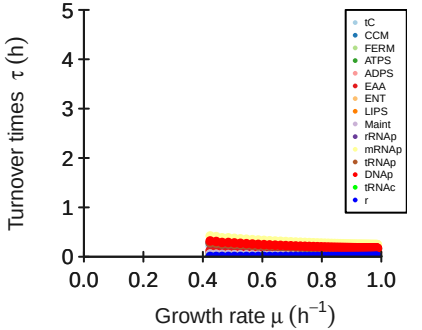

r
Proteome fraction ϕ
Growth rate μ (h−1)

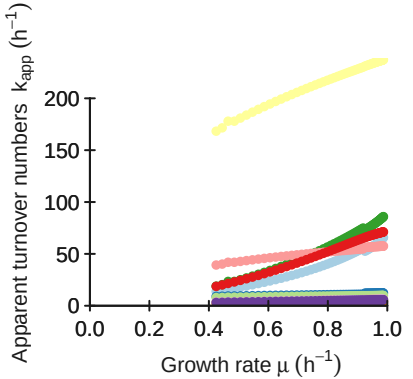

Metabolite concentrations cm (g/L)
C
AA
NT
ADP
ATP
Ci1
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h−1)

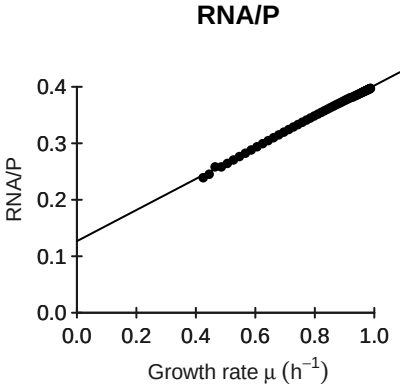

Protein concentrations p (g/L)
tC
M
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r
Growth rate μ (h−1)

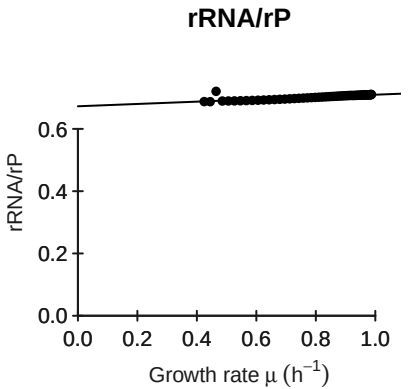

Proteome fractions ϕ
Growth rate μ (h−1)

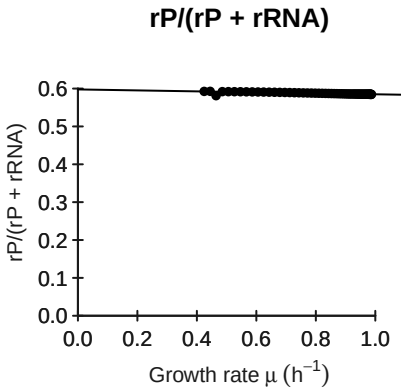

Flux fractions f
Growth rate μ (h−1)

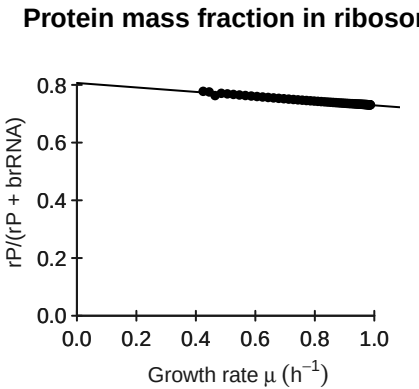

Turnover times τ (h)
Growth rate μ (h−1)
tC
CCM
FERM
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

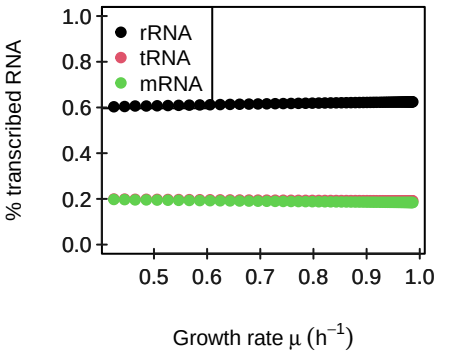

Apparent turnover numbers kapp (h−1)
Growth rate μ (h−1)

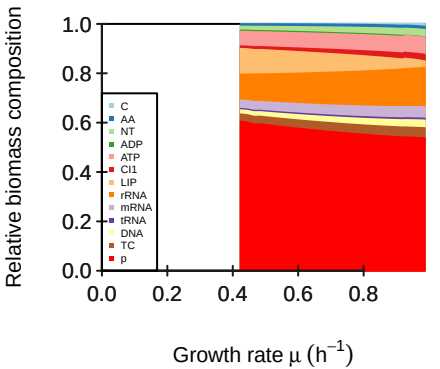

RNA/P
RNA/P
Growth rate μ (h−1)

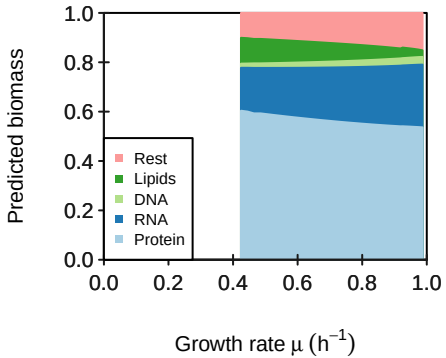

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

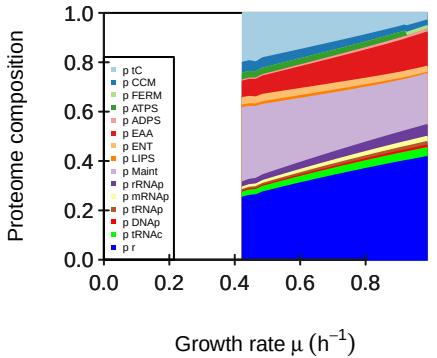

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)

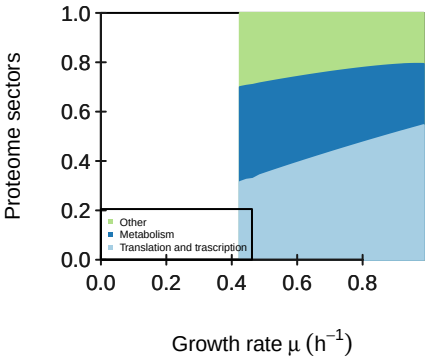

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h−1)


% transcribed RNA
rRNA
tRNA
mRNA
Growth rate μ (h−1)

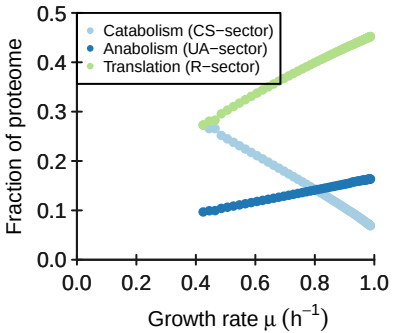

Relative biomass composition
C
AA
NT
ADP
ATP
CI1
LIP
rRNA
mRNA
tRNA
DNA
TC
p
Growth rate μ (h−1)







Proteome sectors



M

	tC	CCM	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
C	1	−1	−0.04	−0.019	0	0	−0.167	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	1	−0.167	0	0	0	0	0	0	−0.01	0
NT	0	0	0	0	−1	0	0.334	0	0	−1	−1	−1	−1	0	0
ADP	0	0	−0.96	−0.981	1	0	0.666	0.82	1	0	0	0	0	0.05	0.05
ATP	0	0	0.96	0.981	0	0	−0.666	−0.82	−1	0	0	0	0	−0.05	−0.05
CI1	0	1	0	0	0	−1	0	−0.18	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	0.18	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	1	0	−0.94	0.94
DNA	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0.95	−0.95
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

K

	tC	CCM	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0.02	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_W	0	0	10	10	0	0	0	0	0	0	0	0	0	0	0
C	5	1	0.05	0.5	0	0	1	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	5	1	0	0	0	0	0	0	6	0
NT	0	0	0	0	1	0	10	0	0	4	4	4	6	0	0
ADP	0	0	0.05	0.5	1	0	1	1	0	0	0	0	0	0	0
ATP	0	0	10	10	0	0	3	3	3	0	0	0	0	3	3
Cl1	0	10	0	0	0	1	0	1	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
DNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	CCM	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0	0.001	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ADP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cl1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	60	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0	0	8	8	8	8	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

kcat

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
kcatf	1000	100	2000	2000	14	12	150	73	81	15	10	15	16	10000	700
kcatb	100	10	200	200	1	1	15	7	0	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
[1,]	2500	100	4e+05	4000	14	60	33.3333333333333	52.1428571428571	Inf	Inf	Inf	Inf	Inf	Inf	Inf

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
[1,]	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
[1,]	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0