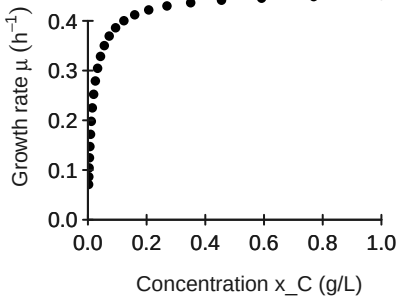
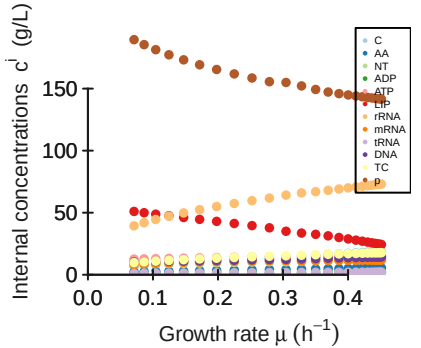
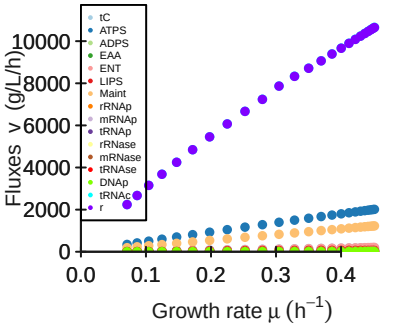
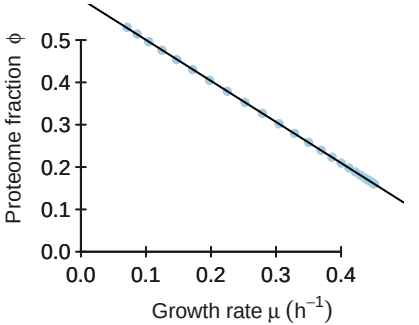


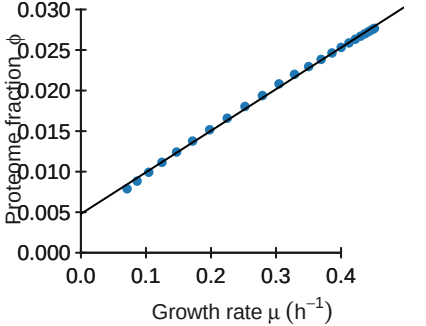




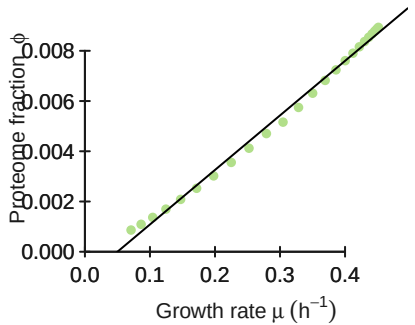
tC



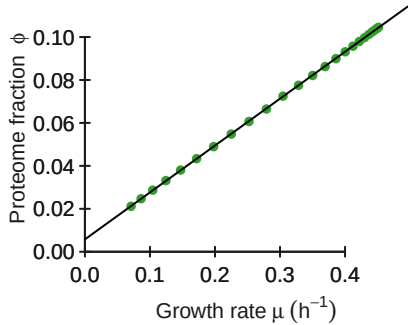
ATPS



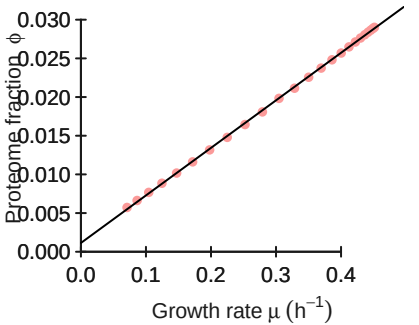
ADPS



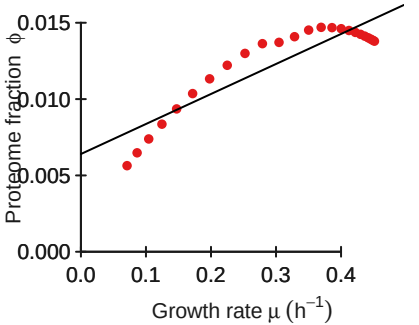
EAA



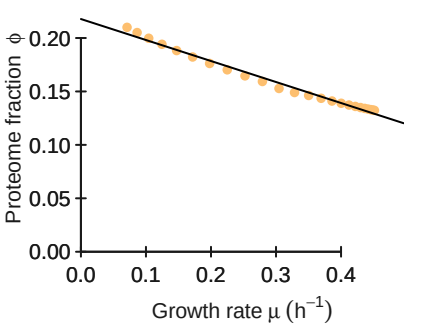
ENT

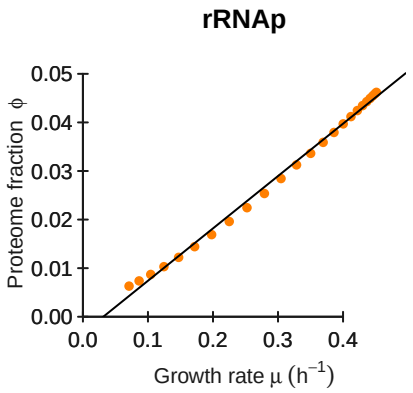


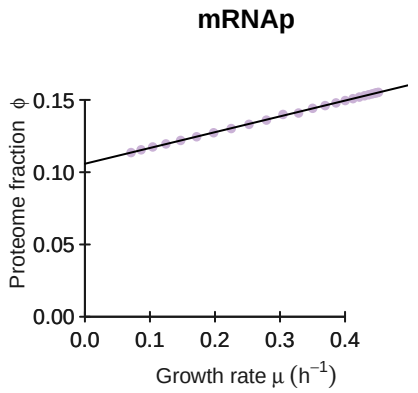
LIPS

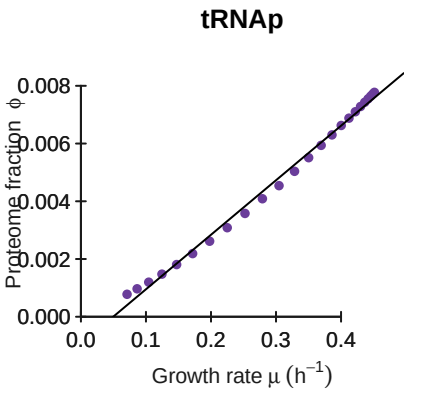


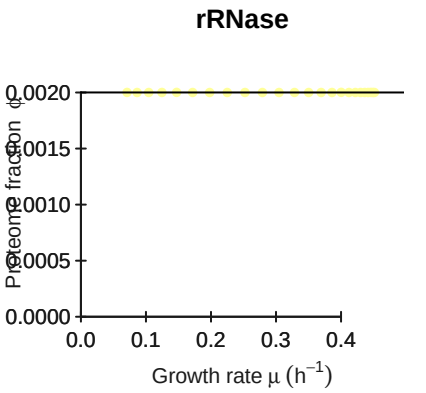
Maint

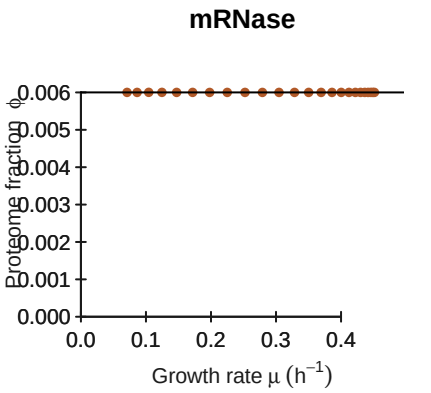


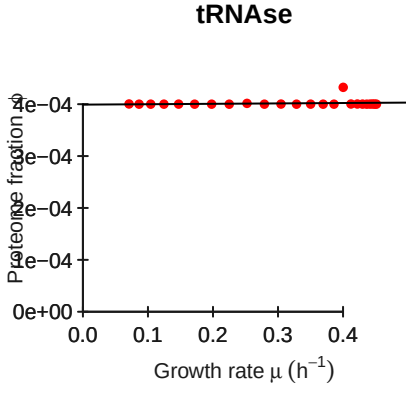

rRNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

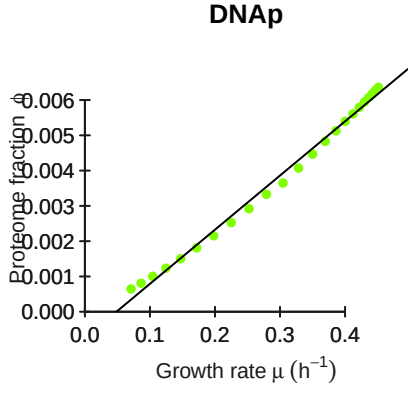

mRNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

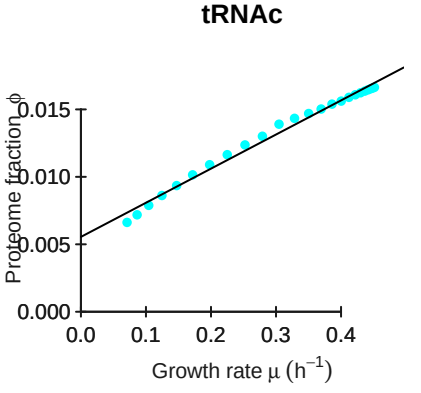

tRNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

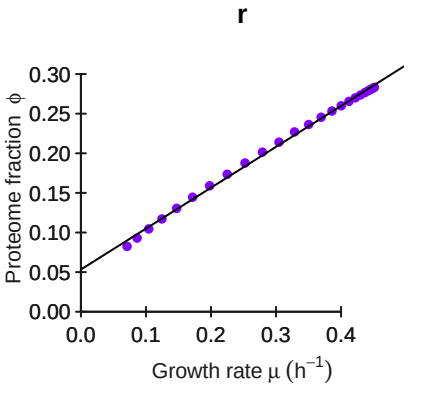

rRNase
Proteome fraction ϕ
Growth rate μ (h^{-1})

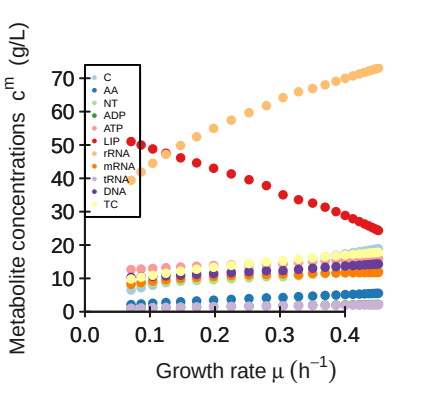

mRNase
Proteome fraction ϕ
Growth rate μ (h^{-1})

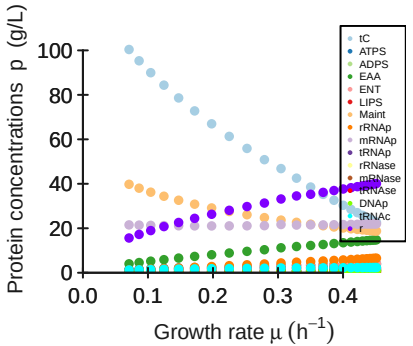

tRNAse
Proteome fraction ϕ
Growth rate μ (h^{-1})

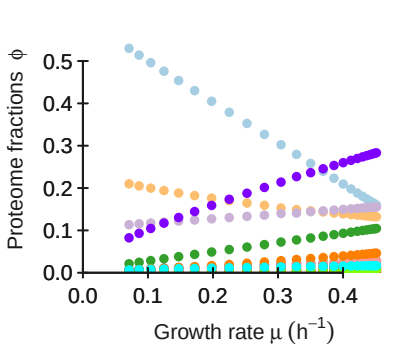

DNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

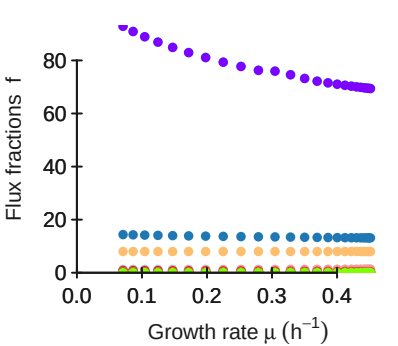

tRNAc
Proteome fraction ϕ
Growth rate μ (h^{-1})

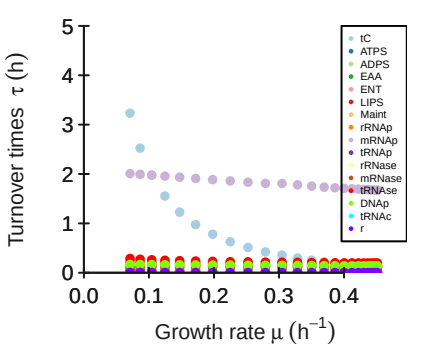

r
Proteome fraction ϕ
Growth rate μ (h^{-1})

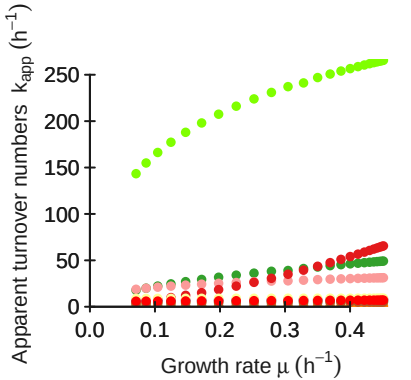

Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h^{-1})



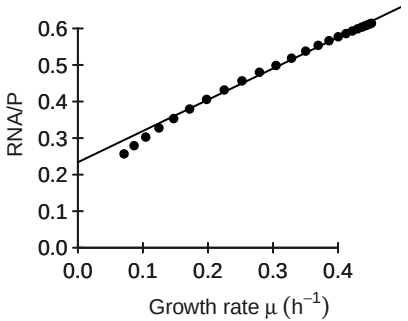




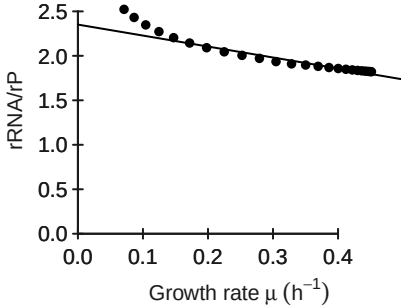




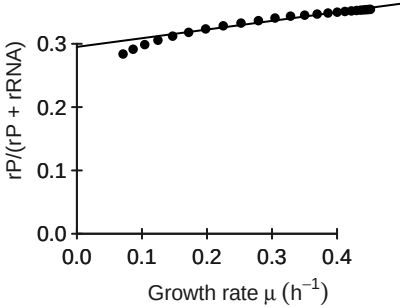
RNA/P



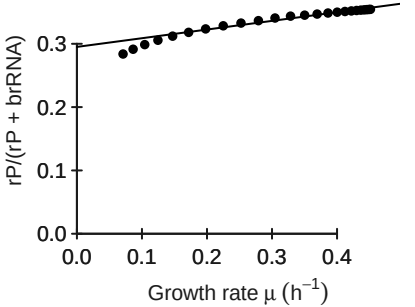
rRNA/rP

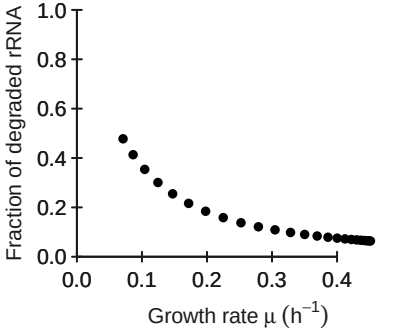


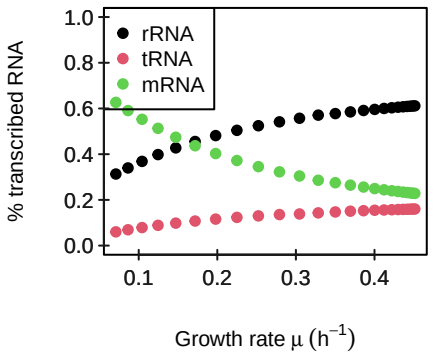
rP/(rP + rRNA)

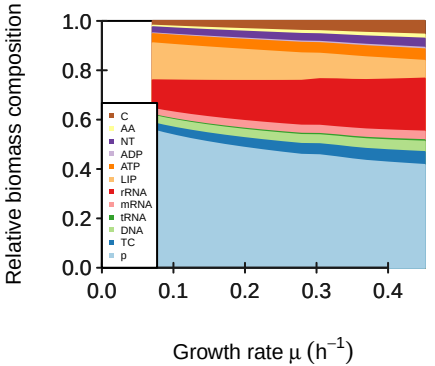


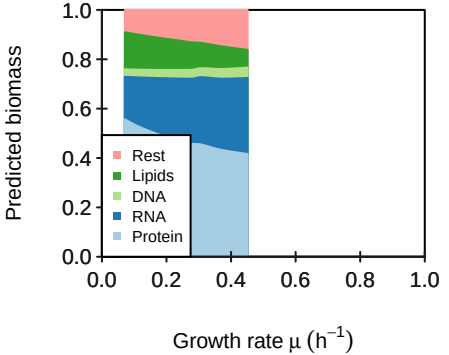
Protein mass fraction in ribosome

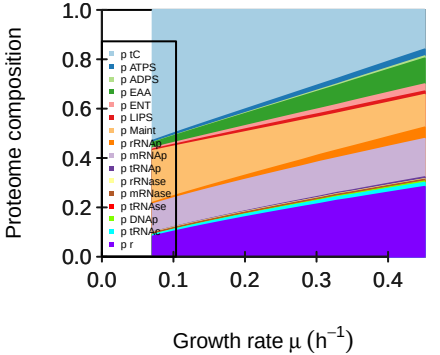


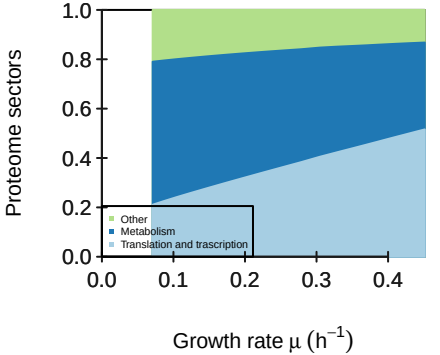



% transcribed RNA
rRNA
tRNA
mRNA
Growth rate μ (h−1)


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


Predicted biomass
Rest
Lipids
DNA
RNA
Protein
Growth rate μ (h−1)


Proteome composition
p tC
p ATPS
p ADPS
p EAA
p ENT
p LIPS
p Maint
p rRNAp
p mRNAp
p tRNAp
p rRNase
p mRNase
p tRNAse
p DNAp
p tRNAc
p r
Growth rate μ (h−1)


Proteome sectors
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)

M

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
C	1	−0.02	0	−1	−0.167	−0.18	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	1	−0.167	0	0	0	0	0	0	0	0	0	−0.006	0
NT	0	0	−1	0	0.334	0	0	−1	−1	−1	1	1	1	−1	0	0
ADP	0	−0.98	1	0	0.666	0.82	1	0	0	0	0	0	0	0	0.026	0.026
ATP	0	0.98	0	0	−0.666	−0.82	−1	0	0	0	0	0	0	0	−0.026	−0.026
LIP	0	0	0	0	0	0.18	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	1	0	0	−1	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	1	0	0	−1	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	1	0	0	−1	0	−0.968	0.968
DNA	0	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	0.974	−0.974
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.006

K

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_W	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
C	0	9	0	9	9	9	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	4	0	0	0	0	0	0	0	0	0	4	0
NT	0	0	3	0	0	0	0	3	3	3	0	0	0	3	0	0
ADP	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	2	2	2	0	0	0	0	0	0	0	2	2
LIP	0	0	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	19	0	0	0	0	0
mRNA	0	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	0	2	0	2	0
DNA	0	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	0	4
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0.03	0	0	0	0	0	0	0	0	0
x_W	0	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	0
AA	0	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	0
ADP	0	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	0
LIP	30	0	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	0	60
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	5	5	5	0	0	0	5	0	0
TC	0	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	0

kcat

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
kcatf	21	1105	8	10	141	52	76	9	1	14	10	10	10	12	17182	950
kcatb	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
[1,]	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
[1,]	0.11	0.023	0.005	0.165	0.023	0.031	0.2546	0.0426	0.0213	0.0071	0.002	0.006	4e−04	0.002	0.023	0.284

average saturation input

3

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
[1,]	0	0	0	0	0	0	0	0	0	0	0.002	0.006	4e−04	0	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
[1,]	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0