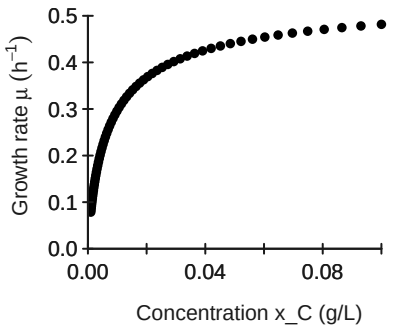
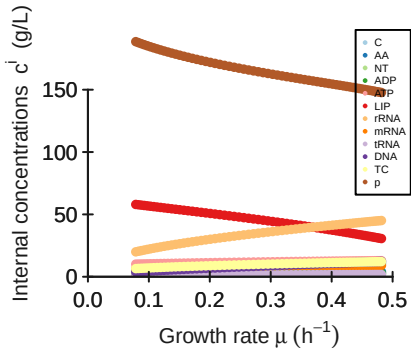
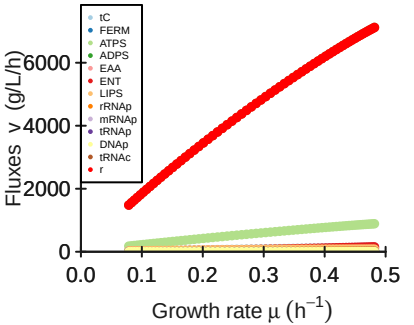
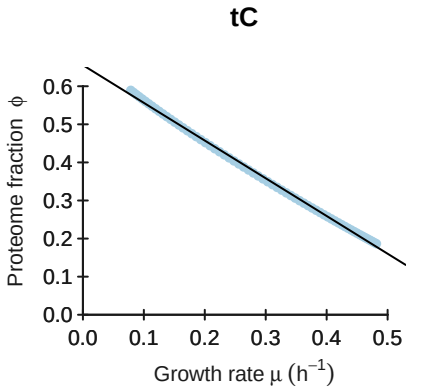
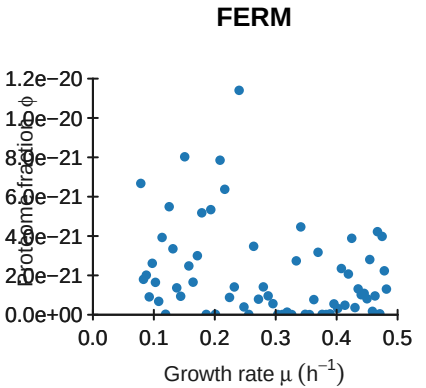
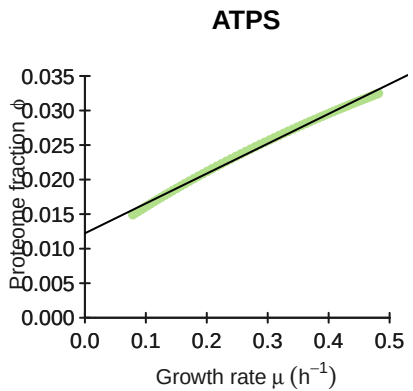

Growth rate μ (h^{-1})
Concentration x_C (g/L)

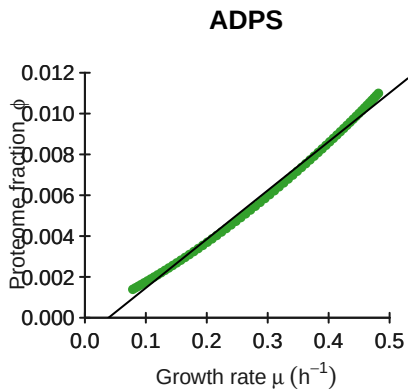

Internal concentrations c^i (g/L)
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
p
Growth rate μ (h^{-1})

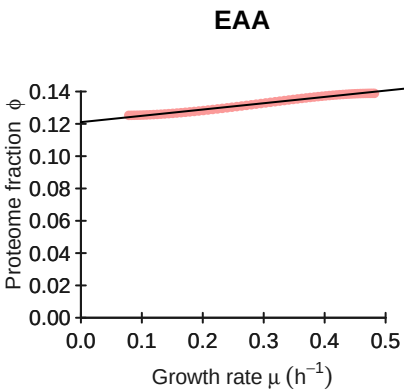

Fluxes v (g/L/h)
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r
Growth rate μ (h^{-1})

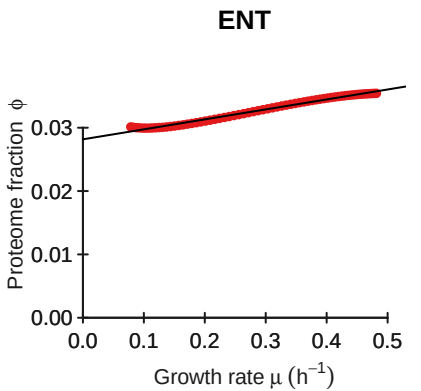

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

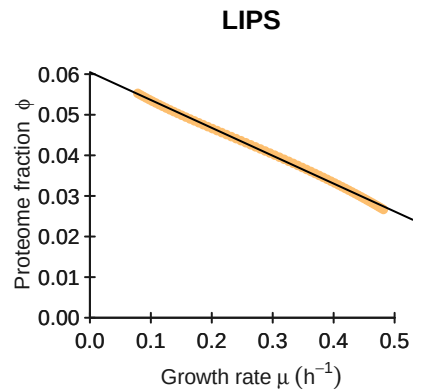

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

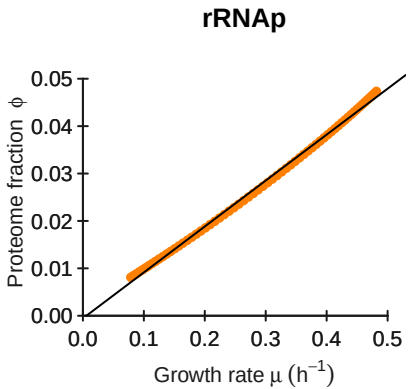

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

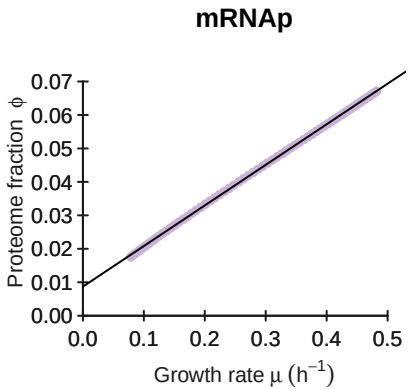

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

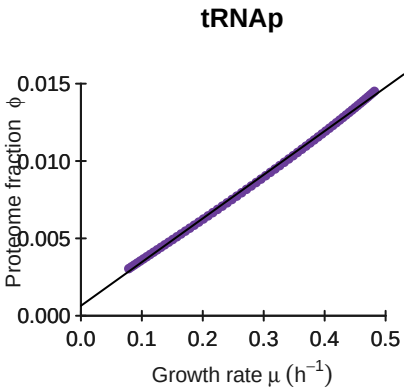

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

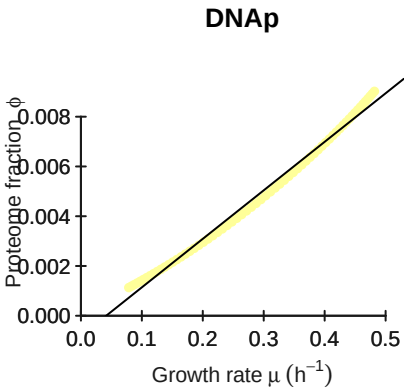

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

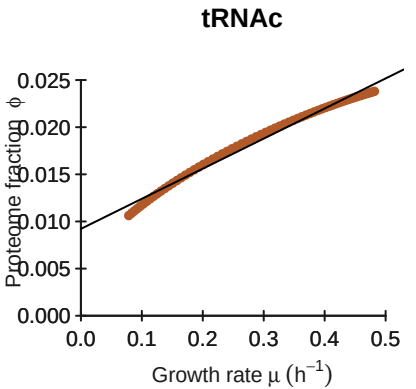

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

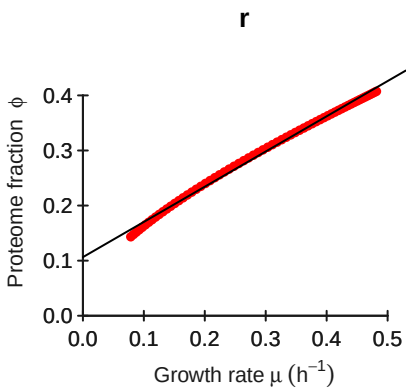

rRNAp
Proteome fraction ϕ
Growth rate μ (h−1)

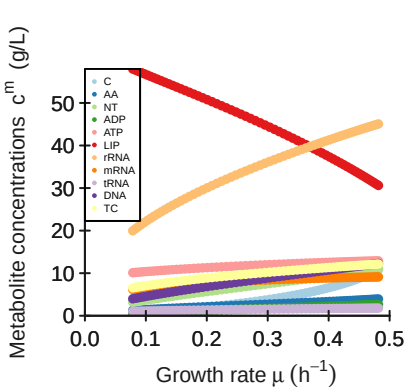

mRNAp
Proteome fraction ϕ
Growth rate μ (h−1)

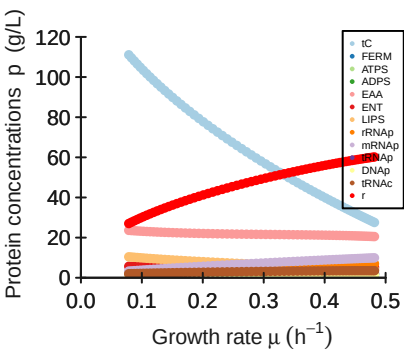

tRNAp
Proteome fraction ϕ
Growth rate μ (h−1)

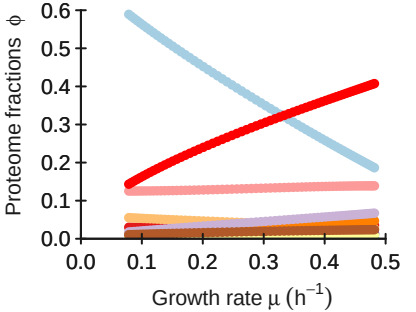

DNAp
Proteome fraction ϕ
Growth rate μ (h−1)

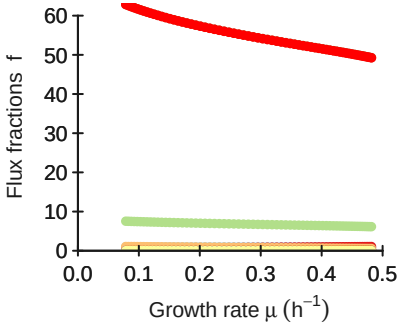

tRNAc
Proteome fraction ϕ
Growth rate μ (h−1)

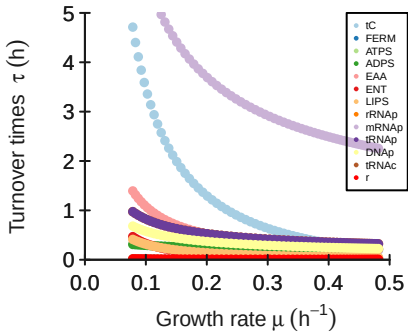

r
Proteome fraction ϕ
Growth rate μ (h−1)

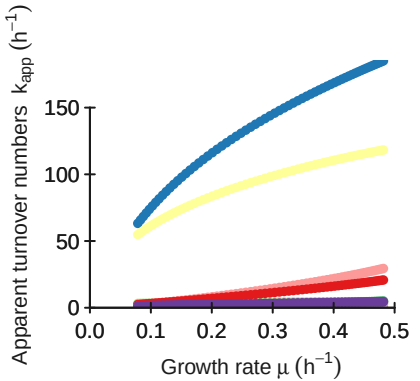

Metabolite concentrations cm (g/L)
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h−1)

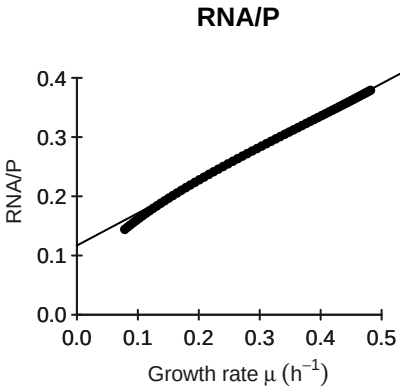

Protein concentrations p (g/L)
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r
Growth rate μ (h−1)

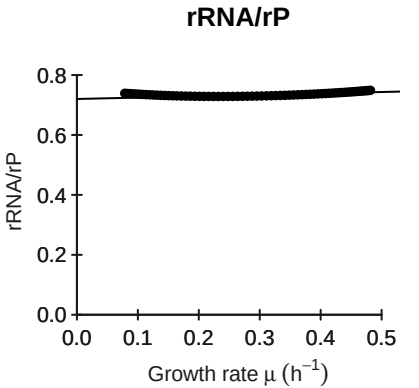

Proteome fractions ϕ
Growth rate μ (h−1)

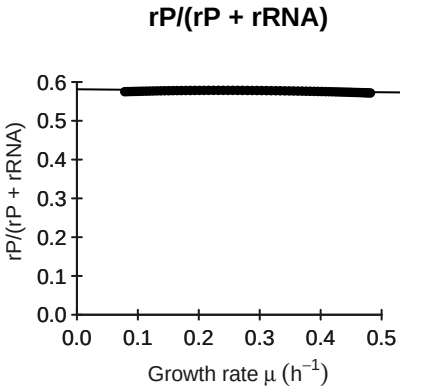

Flux fractions f
Growth rate μ (h−1)

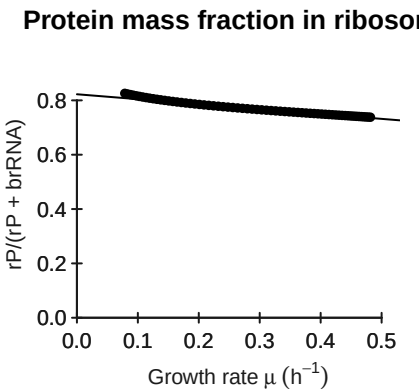

Turnover times τ (h)
Growth rate μ (h⁻¹)
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

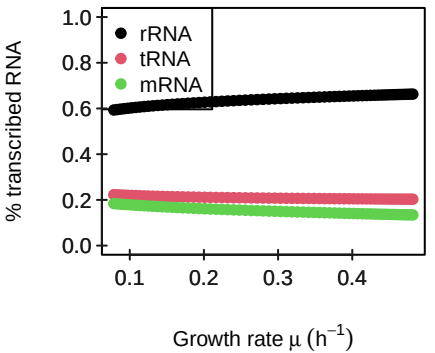

Apparent turnover numbers kapp (h⁻¹)
Growth rate μ (h⁻¹)

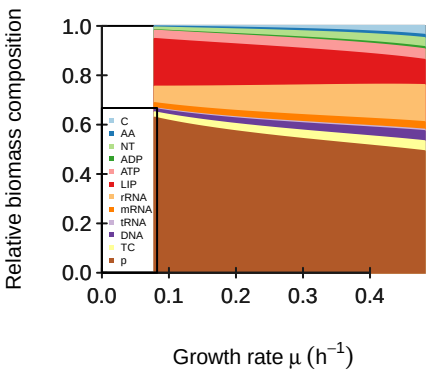

RNA/P
RNA/P
Growth rate μ (h⁻¹)

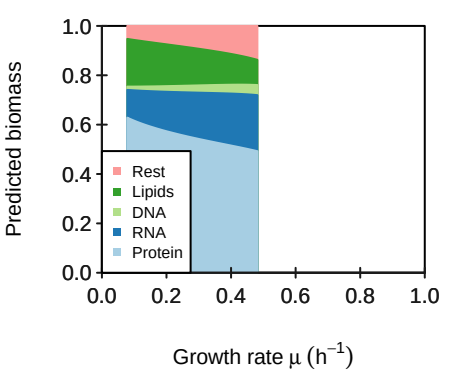

rRNA/rP
rRNA/rP
Growth rate μ (h⁻¹)

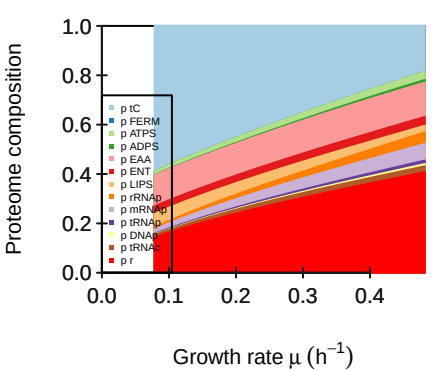

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h⁻¹)

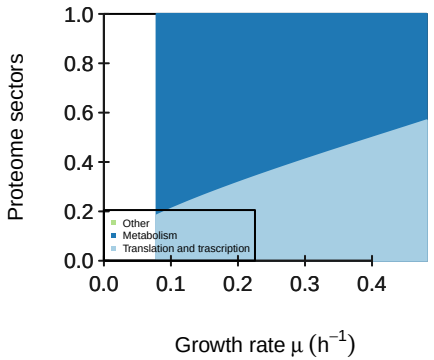

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h⁻¹)

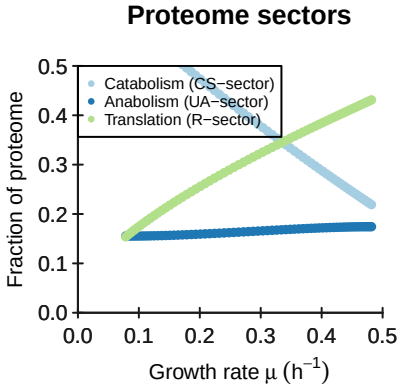

% transcribed RNA
rRNA
tRNA
mRNA
Growth rate μ (h⁻¹)


Relative biomass composition
C
AA
NT
ADP
ATP
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 FERM
p ATPS
p ADPS
p EAA
p ENT
p LIPS
p rRNAp
p mRNAp
p tRNAp
p DNAp
p tRNAc
p r
Growth rate μ (h⁻¹)


Proteome sectors
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.1
0.2
0.3
0.4
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)


Proteome sectors
Fraction of proteome
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.1
0.2
0.3
0.4
0.5
Catabolism (CS−sector)
Anabolism (UA−sector)
Translation (R−sector)
Growth rate μ (h−1)

M

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
C	1	−0.2	0	0	−1	−0.167	−0.18	0	0	0	0	0	0
AA	0	0	0	0	1	−0.167	0	0	0	0	0	−0.01	0
NT	0	0	0	−1	0	0.334	0	−1	−1	−1	−1	0	0
ADP	0	−0.8	−1	1	0	0.666	0.82	0	0	0	0	0.05	0.05
ATP	0	0.8	1	0	0	−0.666	−0.82	0	0	0	0	−0.05	−0.05
LIP	0	0	0	0	0	0	0.18	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	1	0	0	0	0
tRNA	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	1	0	0
TC	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	0.01

K

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0.05	0	0	0	0	0	0	0	0	0	0	0	0
x_W	0	5	4.5	0	0	0	0	0	0	0	0	0	0
C	13	5	4.5	0	5	5	5	0	0	0	0	0	0
AA	0	0	0	0	11	4	0	0	0	0	0	4	0
NT	0	0	0	4	0	11	0	4	4	4	4	0	0
ADP	0	1	0.9	2	0	2	2	0	0	0	0	0	0
ATP	0	6	5.4	0	0	2	2	0	0	0	0	2	2
LIP	0	0	0	0	0	0	30	0	0	0	0	0	0
rRNA	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
tRNA	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
TC	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

KA

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0	0	0	0	0	0
x_W	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
AA	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
ADP	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
LIP	60	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	50
mRNA	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
DNA	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
p	0	0	0	0	0	0	0	0	0	0	0	0	0

kcat

	tC	FERM	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
kcatf	31	4330	433	9	8	109	41	7	1	7	10	7351	446
kcatb	3	433	43	1	1	11	4	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]
[1,]	2686.66666666667	60	60.4186046511628	4.5	17.6	5.45	61.5	Inf	Inf	Inf	Inf	Inf	Inf

phi input

[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	
0.0364656381486676	0.00701262272089762	0.231416549789621	0.032258064516129	0.0434782608695652	0.0597475455820477	0.0298737727910238	0.00995792426367462	0.00280504

average saturation input

3

minimal phi constraint

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