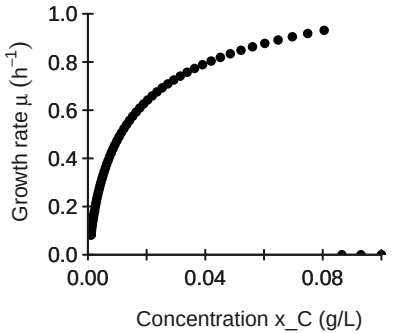
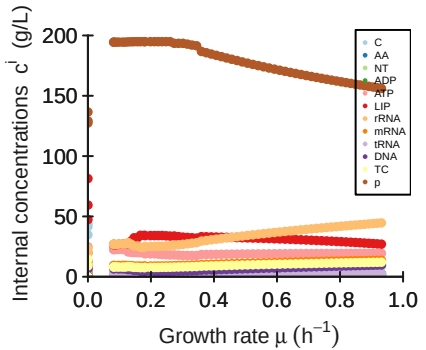
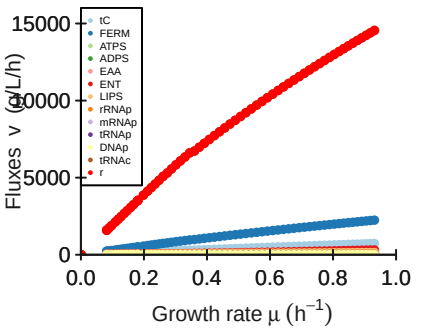
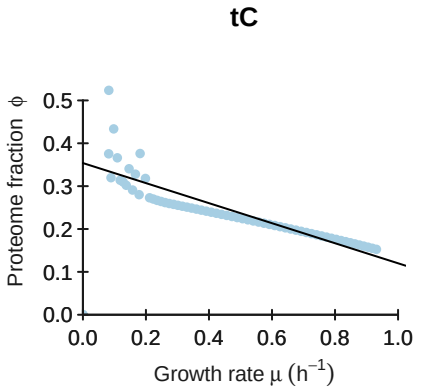
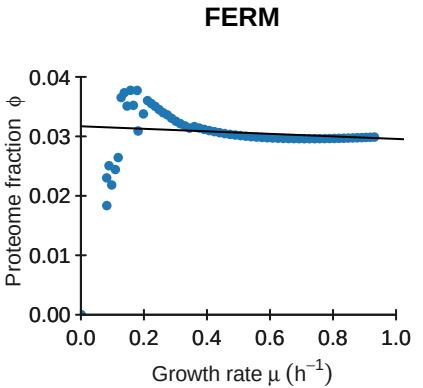
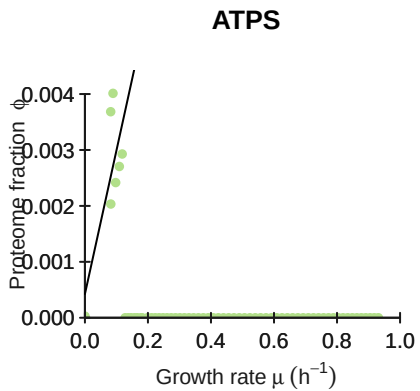

Growth rate μ (h^{-1})
Concentration x_C (g/L)

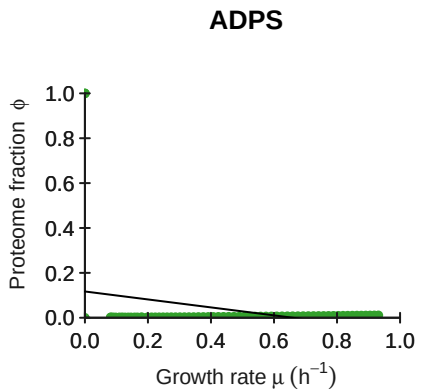

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
p

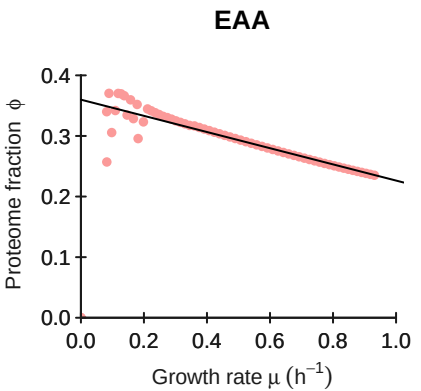

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

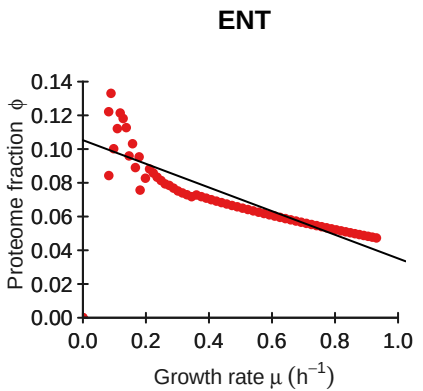

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

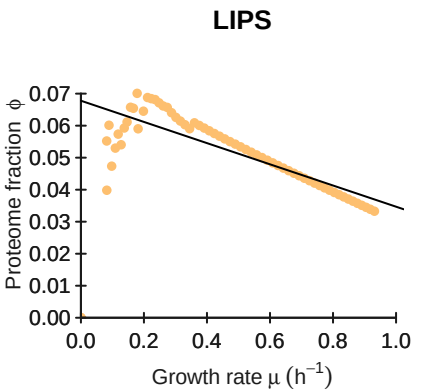

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

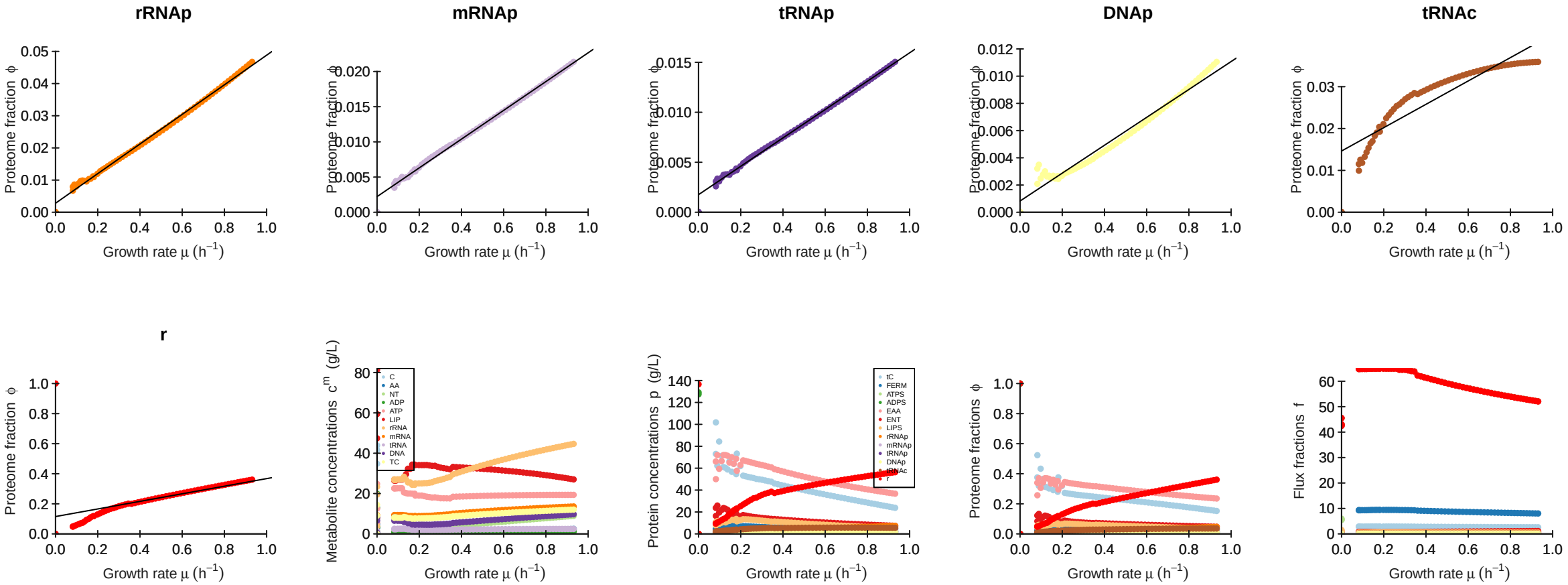

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

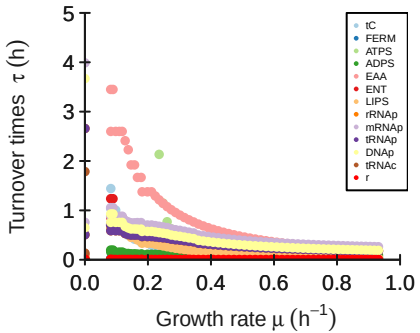

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

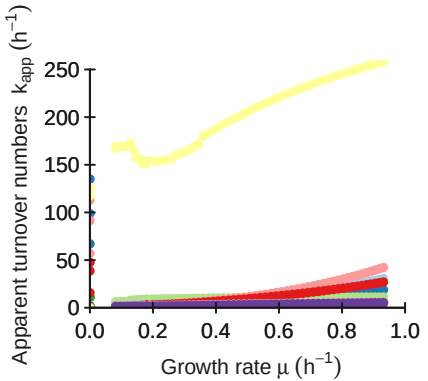

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})


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

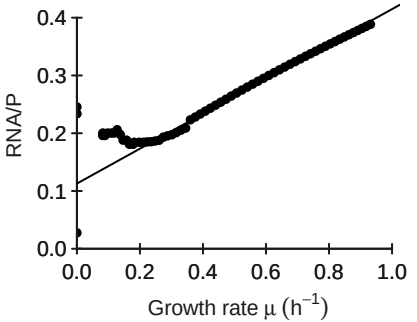

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})


rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})
Metabolite concentrations c^m (g/L)
Protein concentrations p (g/L)
Proteome fractions ϕ
Flux fractions f
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
tC
FERM
ATPS
ADPS
EAA
ENT
LIPS
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

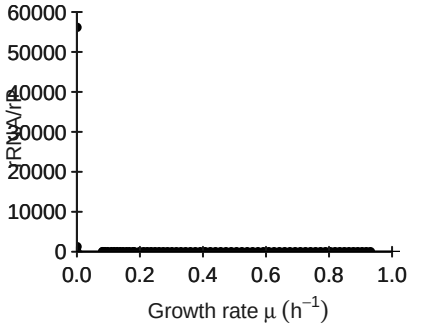




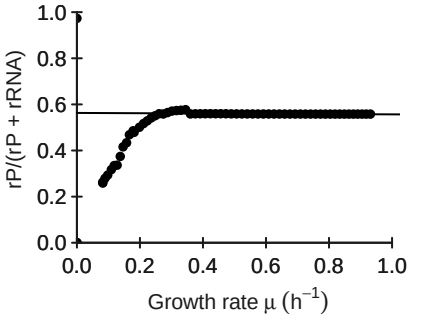
RNA/P



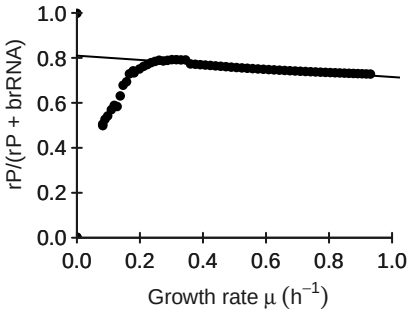
rRNA/rP

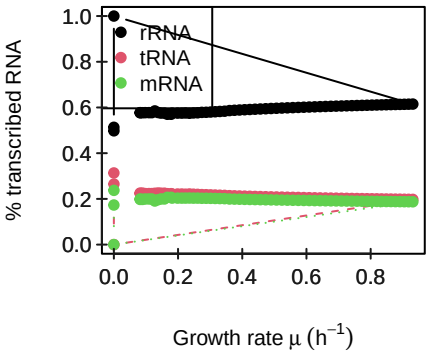


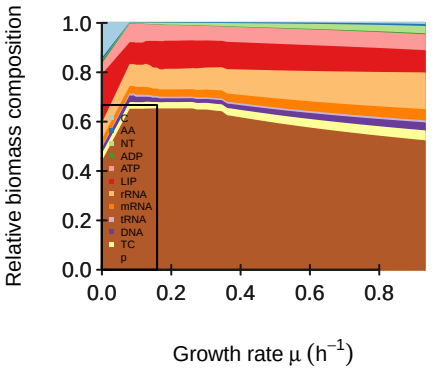
rP/(rP + rRNA)

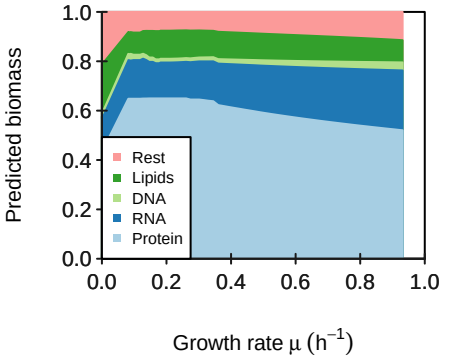


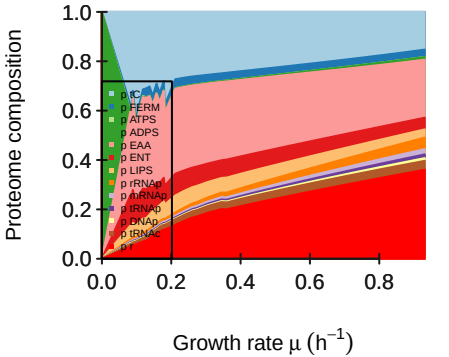
Protein mass fraction in ribosome

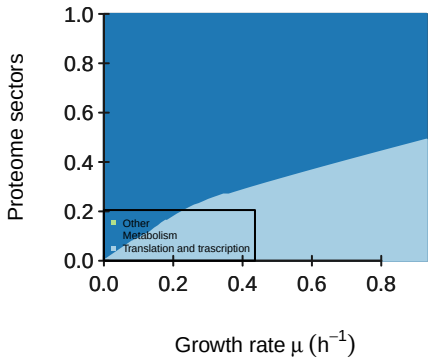


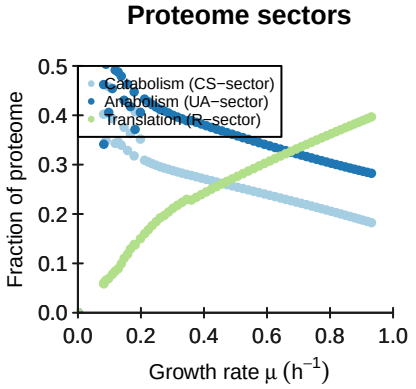









Proteome sectors
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)


Proteome sectors
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Catabolism (CS−sector)
Anabolism (UA−sector)
Translation (R−sector)
Fraction of proteome
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	0	0	0	0	0	0	0	0	0	0	0
C	0.5	0.1	1	0	2	2	2	0	0	0	0	0	0
AA	0	0	0	0	5	3	0	0	0	0	0	6	0
NT	0	0	0	1	0	10	0	4	4	4	6	0	0
ADP	0	1	1	1	0	1	1	0	0	0	0	0	0
ATP	0	5	5	0	0	3	3	0	0	0	0	3	3
LIP	0	0	0	0	0	0	15	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

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]
kcatf	700	1000	150	14	12	220	73	15	10	15	16	15000	900
kcatb	70	100	15	1	1	22	7	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]
[1,]	100	2500	50	14	30	5.55555555555556	26.0714285714286	Inf	Inf	Inf	Inf	Inf	Inf

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