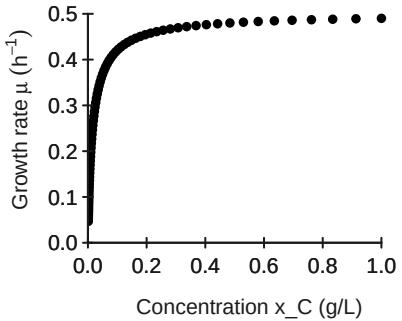
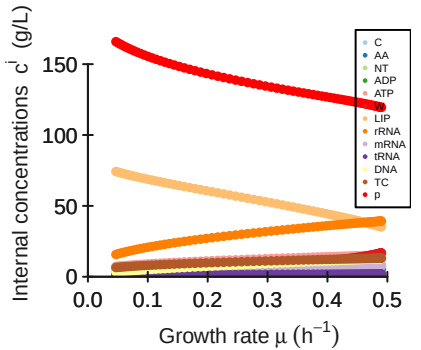
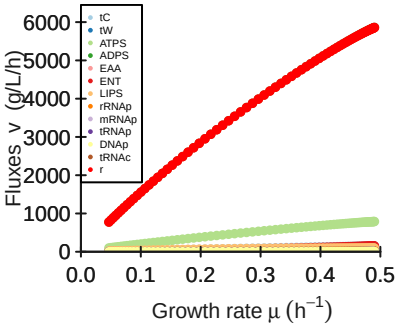
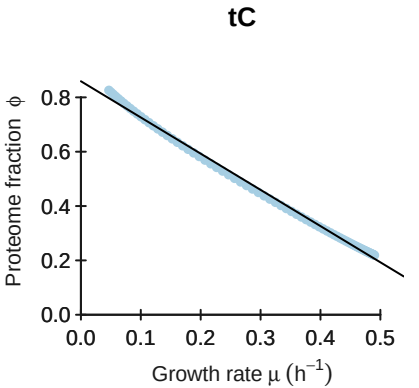
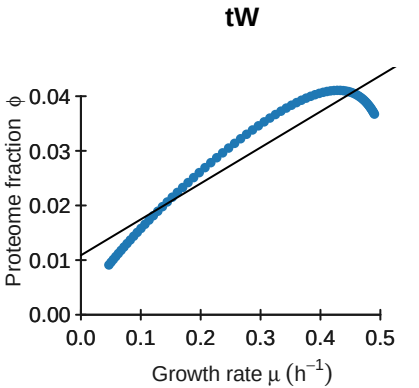
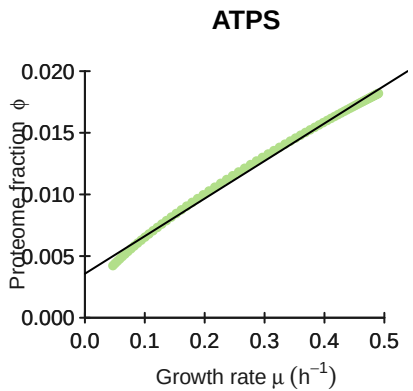

Growth rate μ (h^{-1})
Concentration x_C (g/L)

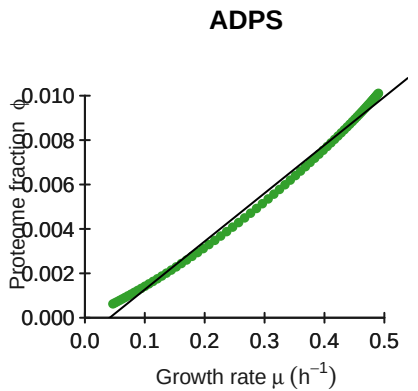

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
LIP
rRNA
mRNA
tRNA
DNA
TC
p

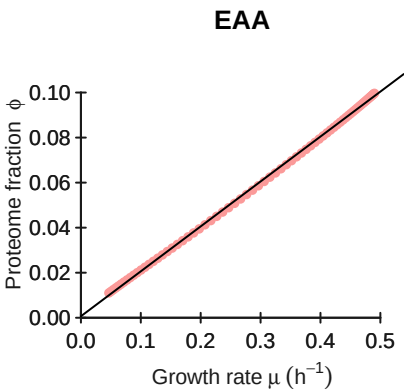

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

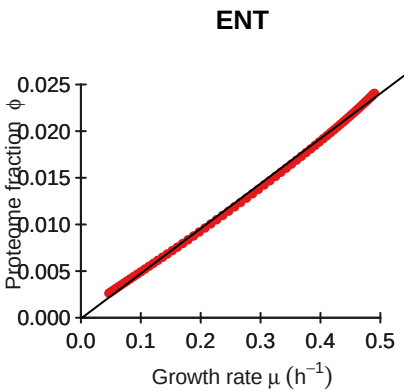

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

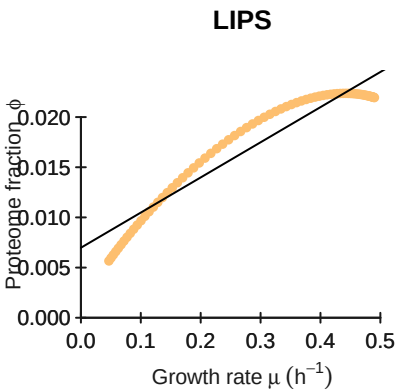

tW
Proteome fraction ϕ
Growth rate μ (h^{-1})

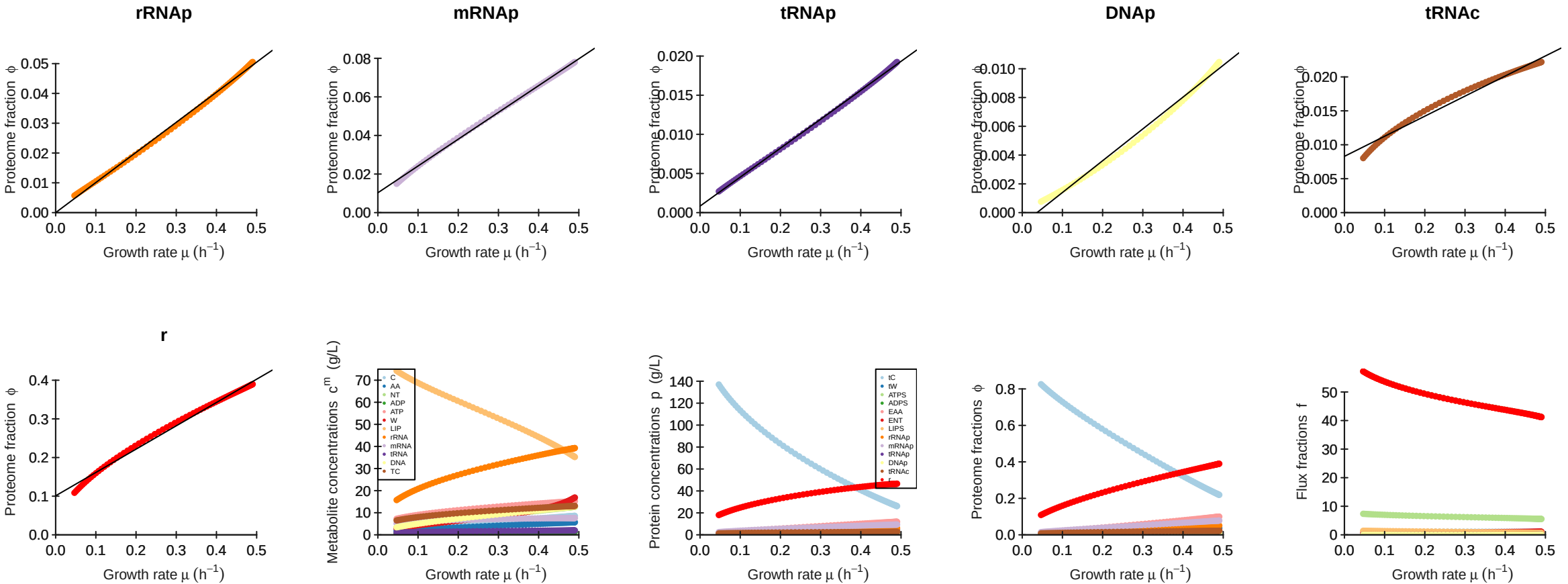

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

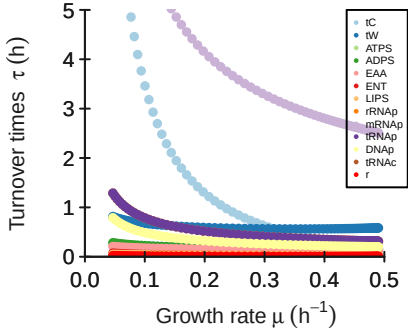

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

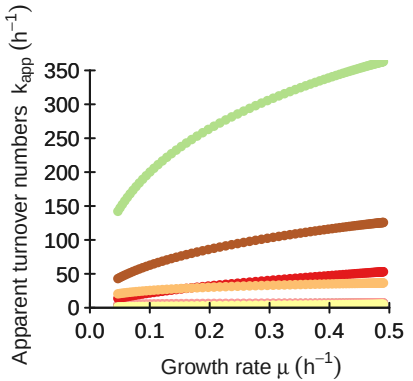

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})


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

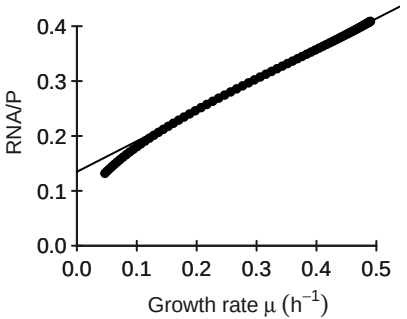

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})


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
W
LIP
rRNA
mRNA
tRNA
DNA
TC
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

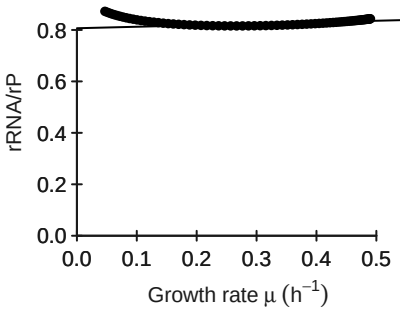




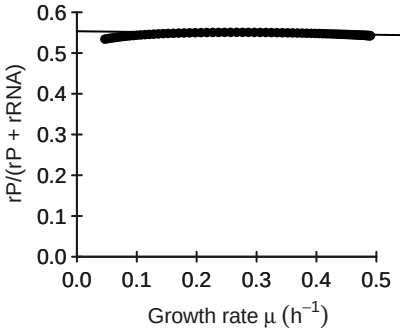
RNA/P



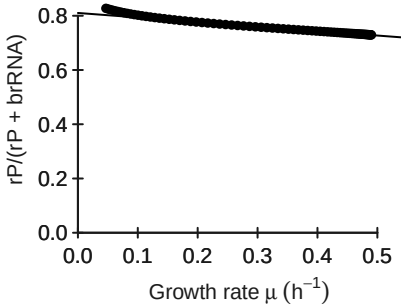
rRNA/rP

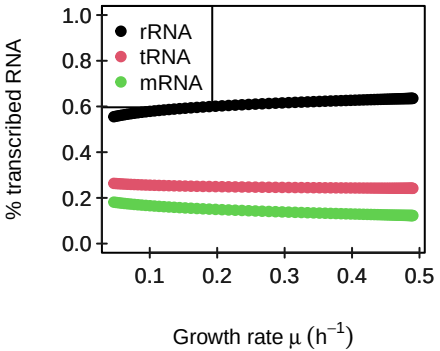


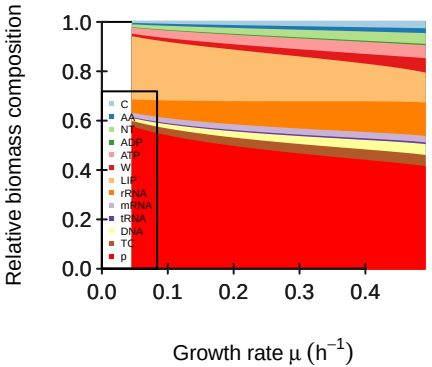
rP/(rP + rRNA)

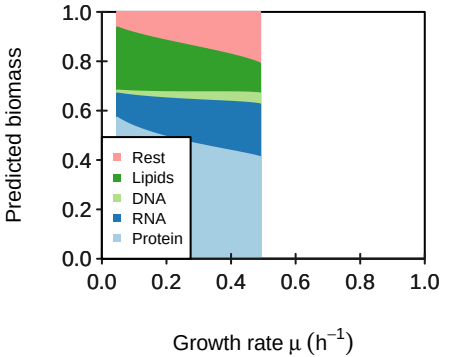


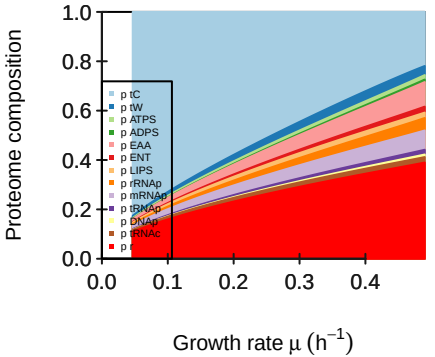
Protein mass fraction in ribosome

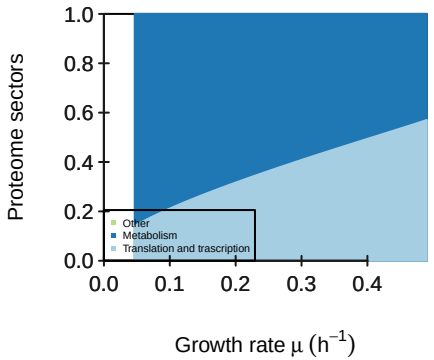


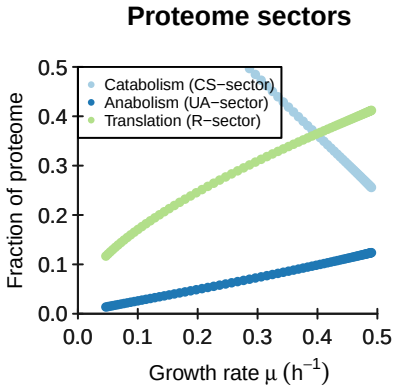









Proteome sectors
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.1
0.2
0.3
0.4
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)


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	tW	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
C	1	0	−0.02	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	−0.98	1	0	0.666	0.82	0	0	0	0	0.05	0.05
ATP	0	0	0.98	0	0	−0.666	−0.82	0	0	0	0	−0.05	−0.05
W	0	−1	0.02	0	0	0	0	0	0	0	0	0	0
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	tW	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0.1	0	0	0	0	0	0	0	0	0	0	0	0
x_W	0	3	0	0	0	0	0	0	0	0	0	0	0
C	0	0	2	0	2	2	2	0	0	0	0	0	0
AA	0	0	0	0	0	6	0	0	0	0	0	6	0
NT	0	0	0	6	0	0	0	6	6	6	6	0	0
ADP	0	0	1	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	3	3	0	0	0	0	3	3
W	0	5	0	0	0	0	0	0	0	0	0	0	0
LIP	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
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	2	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	3
p	0	0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	tW	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
W	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	60	60	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	9	9	9	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	tW	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
kcatf	17	6	747	10	9	161	54	8	1	8	12	10877	587
kcatb	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]
[1,]	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	
0.0364372469635628	0.0067476383265857	0.222672064777328	0.0310391363022942	0.0418353576248313	0.0574898785425101	0.0287449392712551	0.00958164642375169	0.002699055

average saturation input

2

minimal phi constraint

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