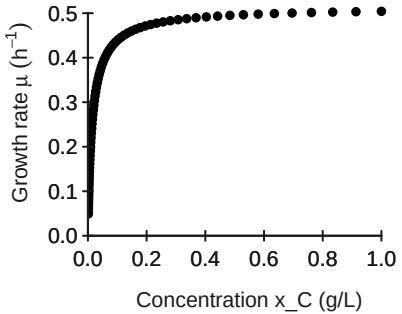
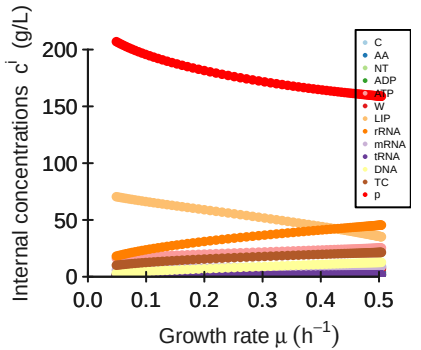
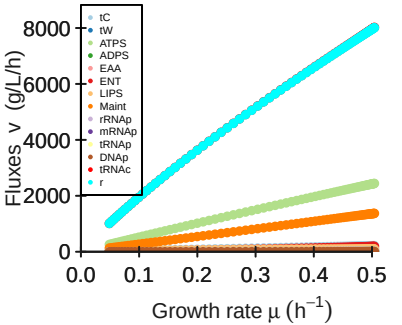
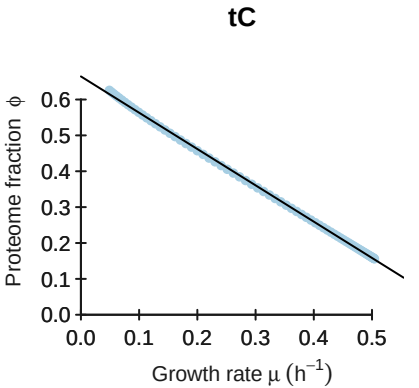
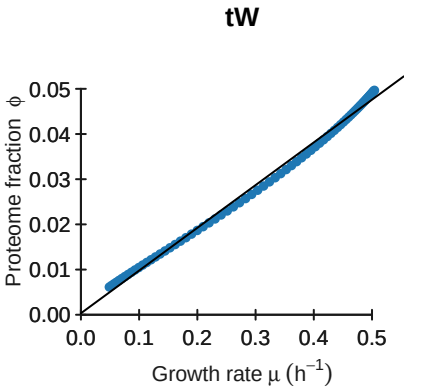
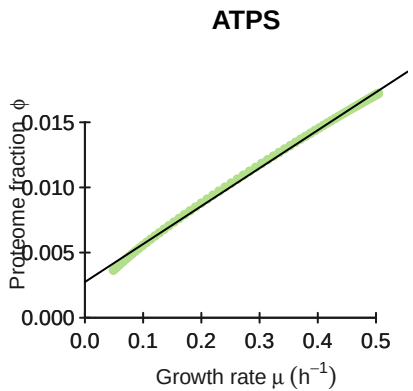

Growth rate μ (h^{-1})
Concentration x_C (g/L)

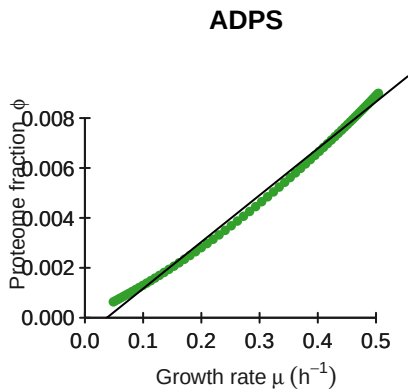

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
p

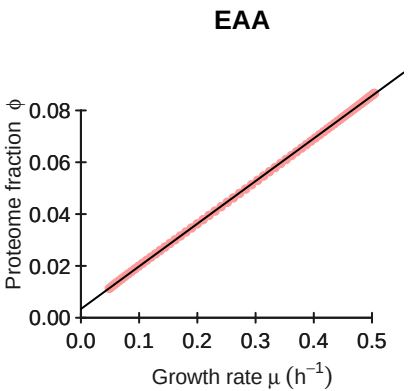

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
DNAp
tRNAc
r

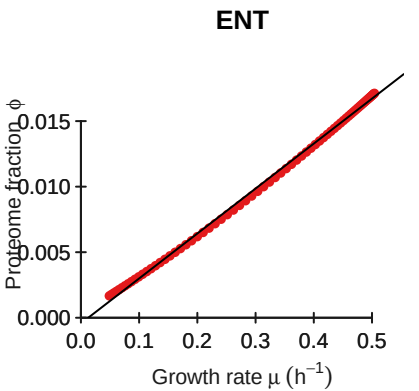

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

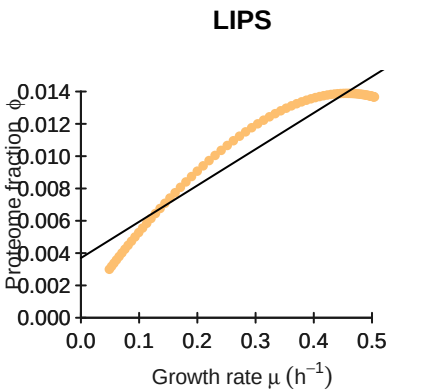

tW
Proteome fraction ϕ
Growth rate μ (h^{-1})

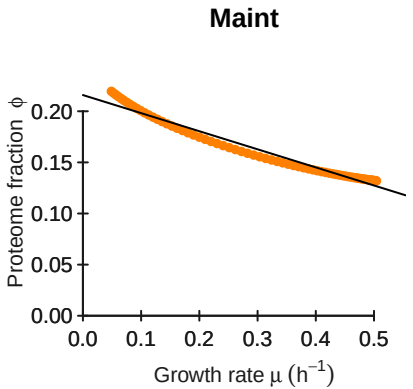

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

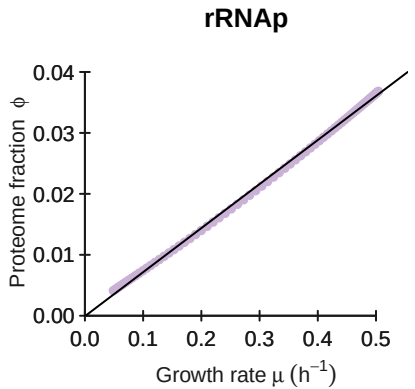

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

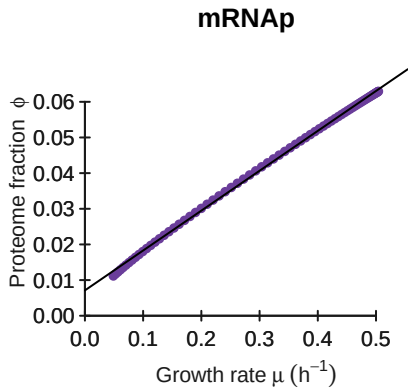

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

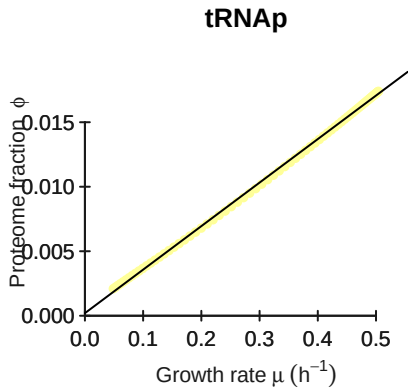

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

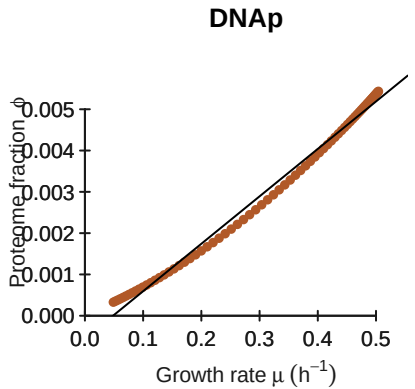

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

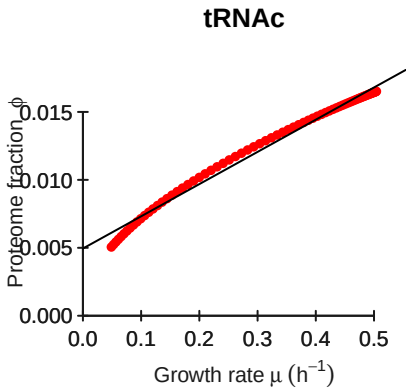

Maint
Proteome fraction ϕ
Growth rate μ (h^{-1})

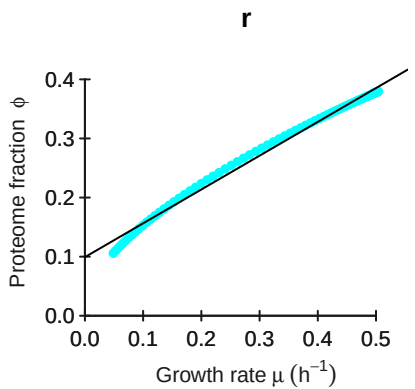

rRNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

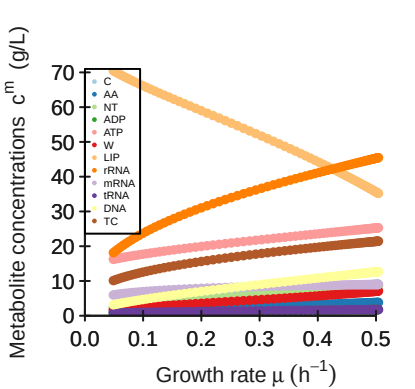

mRNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

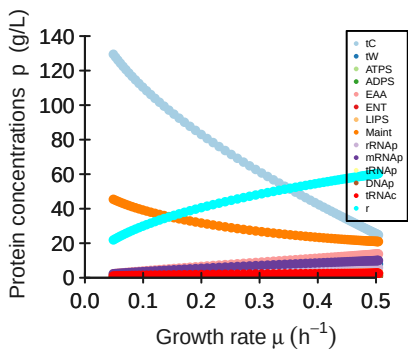

tRNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

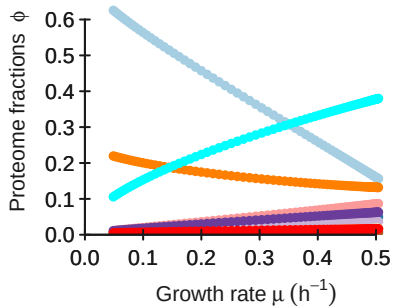

DNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

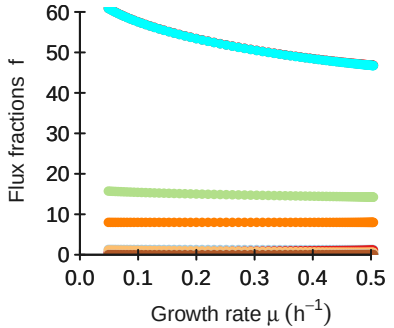

tRNAc
Proteome fraction ϕ
Growth rate μ (h^{-1})

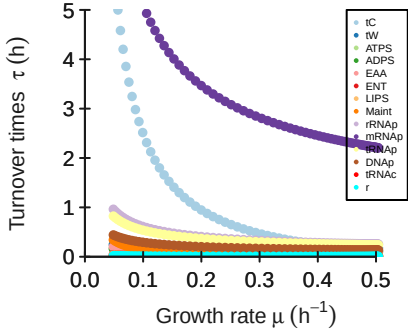

r
Proteome fraction ϕ
Growth rate μ (h^{-1})

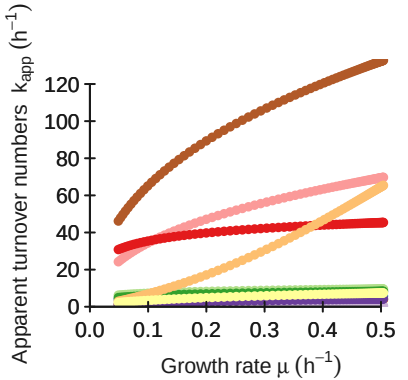

Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h^{-1})


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

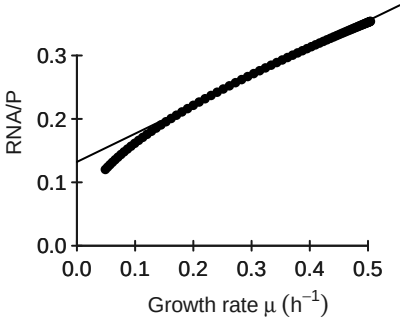

Proteome fractions ϕ
Growth rate μ (h^{-1})



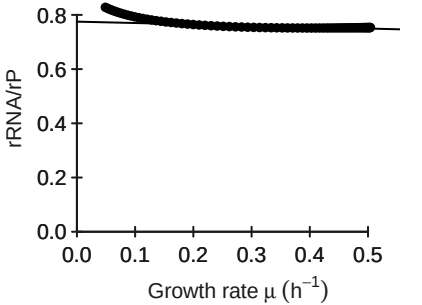




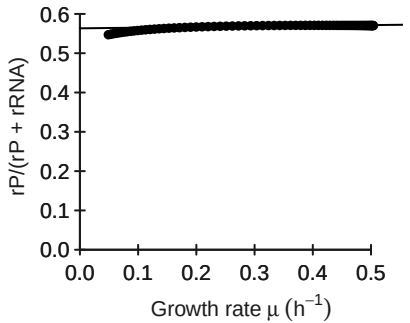
RNA/P



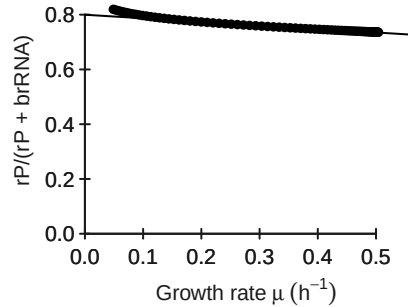
rRNA/rP

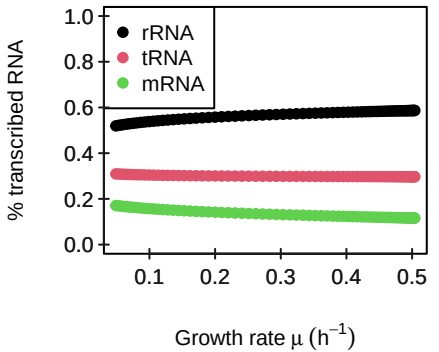


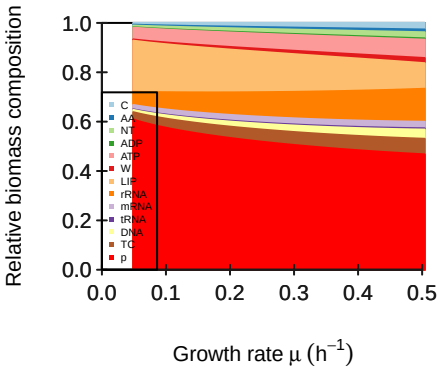
rP/(rP + rRNA)

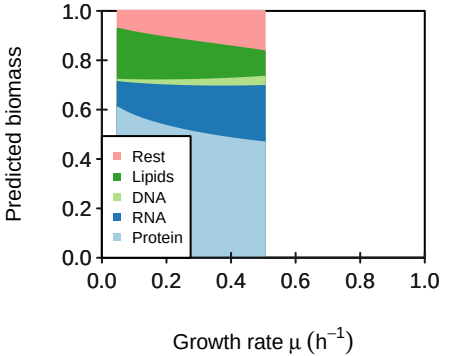


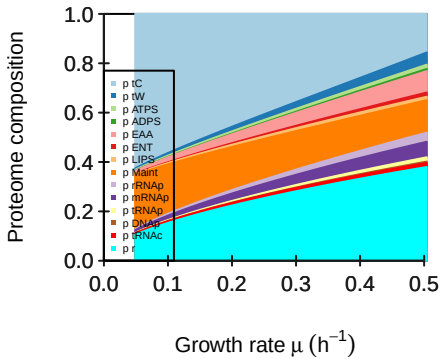
Protein mass fraction in ribosome

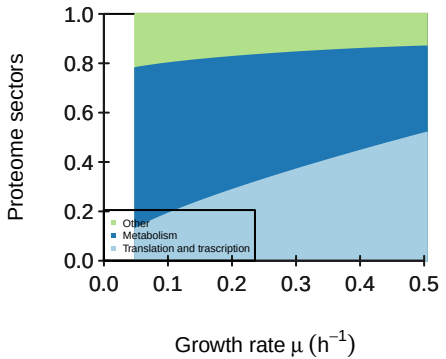


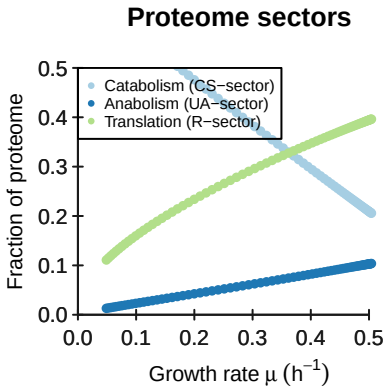







Proteome composition
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.1
0.2
0.3
0.4
0.5
Growth rate μ (h^{-1})
p tC
p tW
p ATPS
p ADPS
p EAA
p ENT
p UPS
p Maint
p rRNAp
p mRNAp
p tRNAp
p DNAp
p tRNAc


Proteome sectors
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.1
0.2
0.3
0.4
0.5
Growth rate μ (h^{-1})
Other
Metabolism
Translation and trascription


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
Growth rate μ (h^{-1})
Catabolism (CS−sector)
Anabolism (UA−sector)
Translation (R−sector)

M

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
C	1	0	−0.02	0	−1	−0.167	−0.18	0	0	0	0	0	0	0
AA	0	0	0	0	1	−0.167	0	0	0	0	0	0	−0.01	0
NT	0	0	0	−1	0	0.334	0	0	−1	−1	−1	−1	0	0
ADP	0	0	−0.98	1	0	0.666	0.82	1	0	0	0	0	0.05	0.05
ATP	0	0	0.98	0	0	−0.666	−0.82	−1	0	0	0	0	−0.05	−0.05
W	0	−1	0.02	0	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	0
rRNA	0	0	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	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	1	0	−0.94	0.94
DNA	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	0.95	−0.95
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

K

tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc
0	0	0	0	0	0	0	0	0	0	0	0
2.93678333333333	0	0	0	0	0	0	0	0	0	0	0
0	1.70125	0	2.98843333333333	1.66073333333333	1.62021666666667	0	0	0	0	0	0
0	0	0	0	2.66073333333333	0	0	0	0	0	0	2.54853333333333
0	0	2.15583333333333	0	0	0	0	2.90383333333333	2.45191666666667	2.1496	2.03428333333333	0
0	1.20125	0	0	0	0	0	0	0	0	0	0
0	0	0	0	2.16073333333333	2.12021666666667	3	0	0	0	0	2.04853333333333
3.43678333333333	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	1.54853333333333
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0.025	0	0	0	0	0	0
x_W	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
AA	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
ADP	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
W	0	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	0
rRNA	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	3
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DNA	0	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	0
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0

kcat

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
kcatf	26	23	1775	12	11	152	58	75	9	1	9	15	10310	626
kcatb	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]
[1,]	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]
[1,]	0.089	0.021	0.027	0.005	0.165	0.023	0.031	0.259	0.0426	0.0213	0.0071	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]
[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]	[,14]
[1,]	0	0	0	0	0	0	0	8	0	0	0	0	0	0