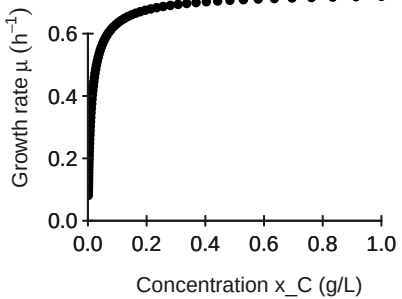
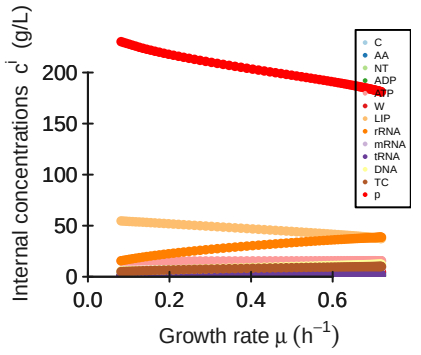
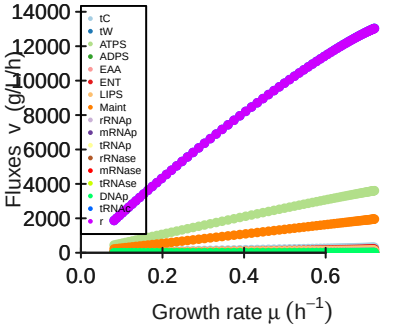
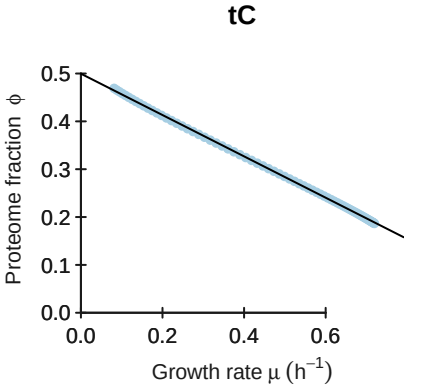
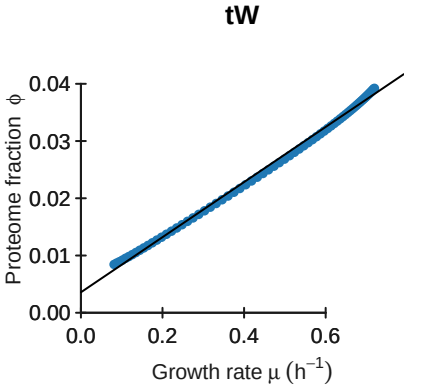
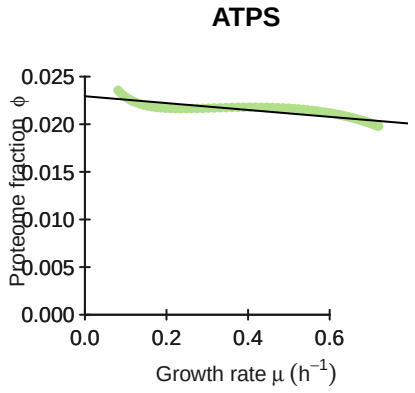

Growth rate μ (h^{-1})
0.0
0.2
0.4
0.6
0.0
0.2
0.4
0.6
0.8
1.0
Concentration x_C (g/L)

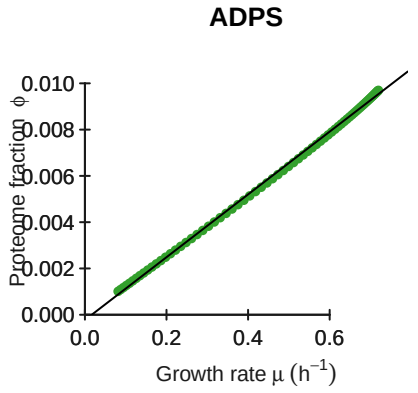

Internal concentrations c^i (g/L)
0
50
100
150
200
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
p

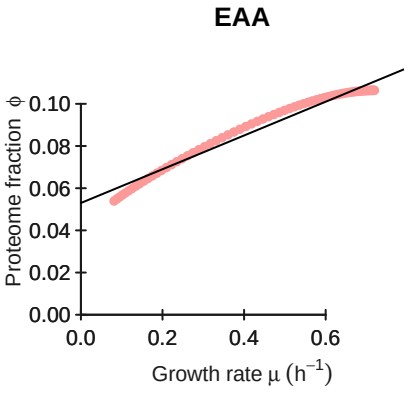

Fluxes v (g/L/h)
0
2000
4000
6000
8000
10000
12000
14000
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAse
r

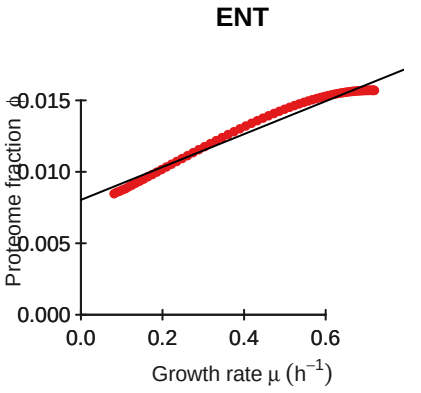

tC
Proteome fraction ϕ
0.0
0.1
0.2
0.3
0.4
0.5
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})

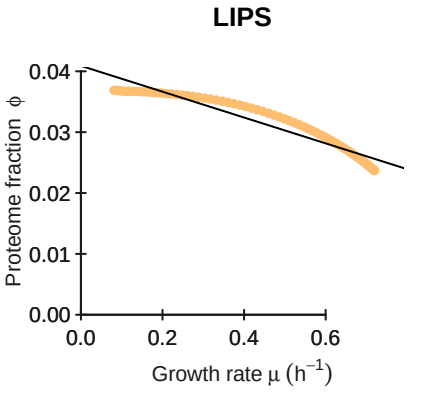

tW
Proteome fraction ϕ
0.00
0.01
0.02
0.03
0.04
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})

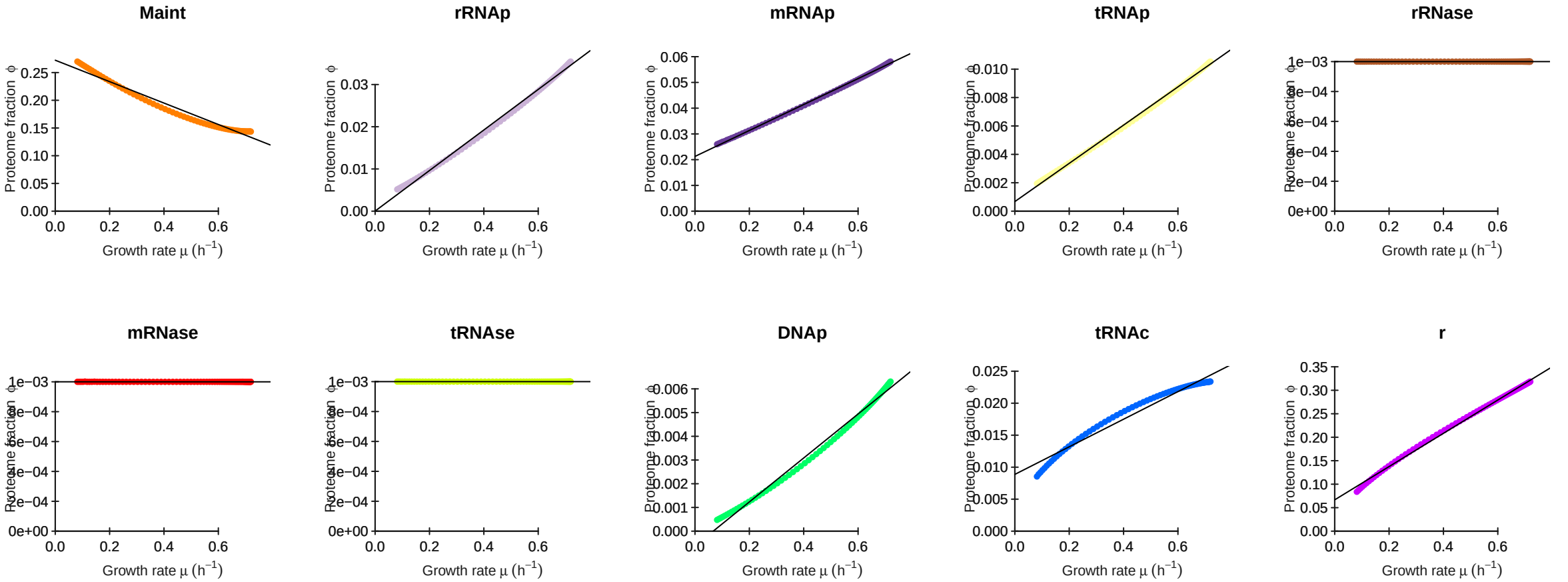

ATPS
Proteome fraction ϕ
0.000
0.005
0.010
0.015
0.020
0.025
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})

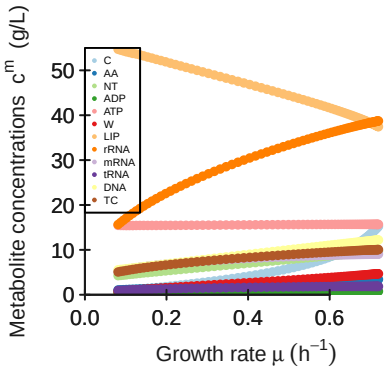

ADPS
Proteome fraction ϕ
0.000
0.002
0.004
0.006
0.008
0.010
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})

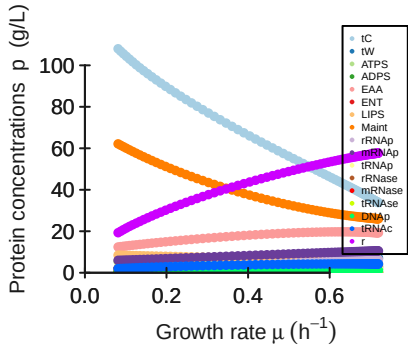

EAA
Proteome fraction ϕ
0.00
0.02
0.04
0.06
0.08
0.10
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})

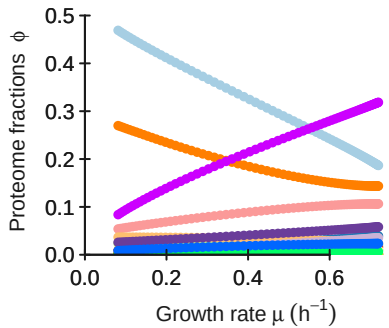

ENT
Proteome fraction ϕ
0.000
0.005
0.010
0.015
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})

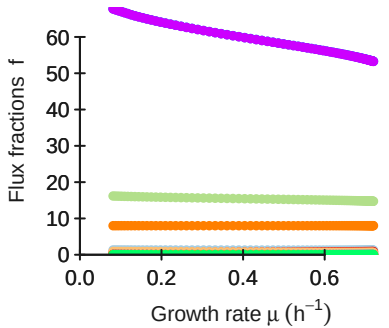

LIPS
Proteome fraction ϕ
0.00
0.01
0.02
0.03
0.04
0.0
0.2
0.4
0.6
Growth rate μ (h^{-1})

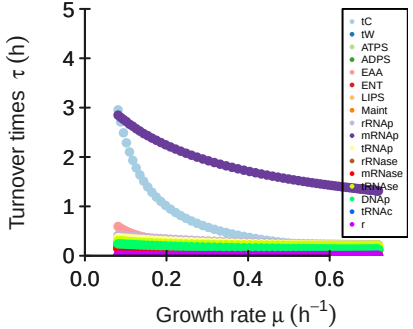

Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})

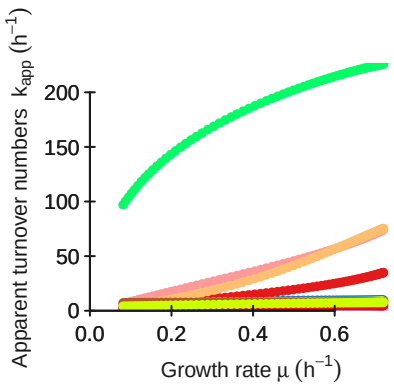

Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h^{-1})

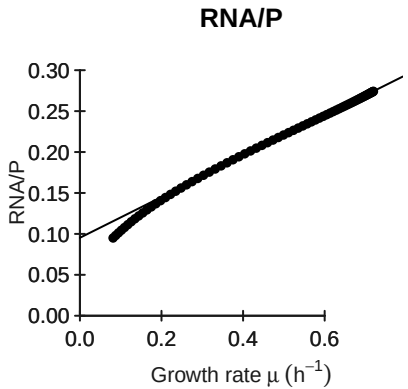

Protein concentrations p (g/L)
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

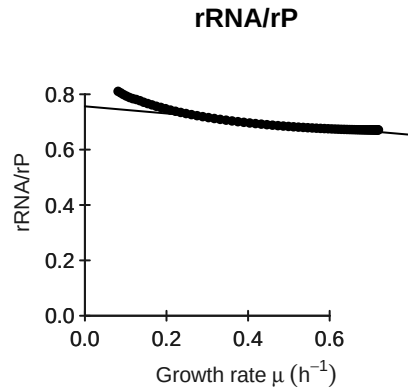

Proteome fractions ϕ
Growth rate μ (h^{-1})

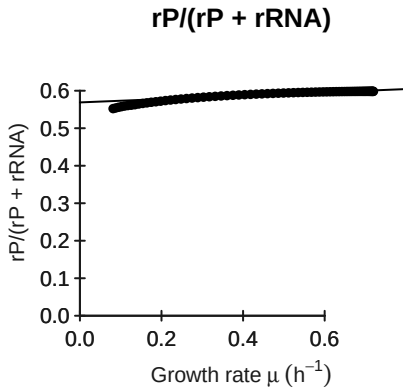

Flux fractions f
Growth rate μ (h^{-1})

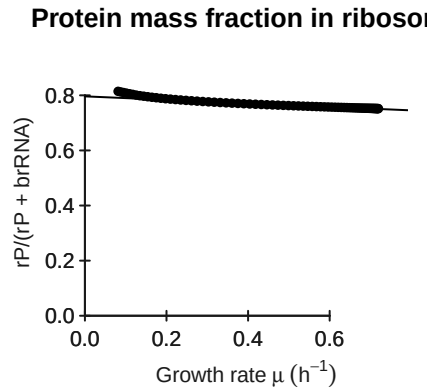

Turnover times τ (h)
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

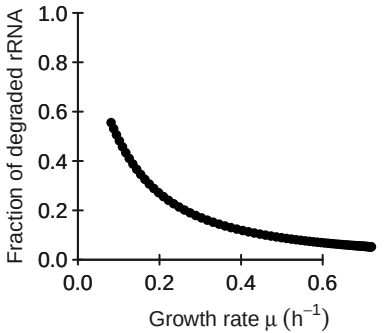

Apparent turnover numbers k_{app} (h^{-1})
Growth rate μ (h^{-1})

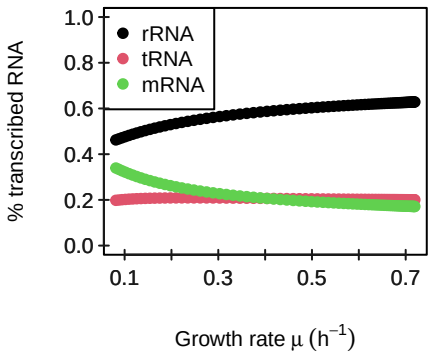

RNA/P
RNA/P
Growth rate μ (h^{-1})

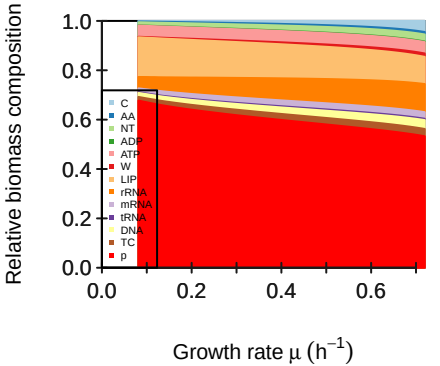

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

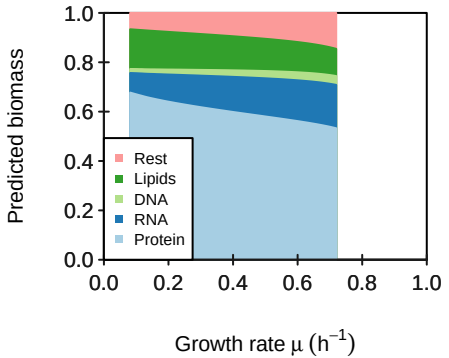

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})

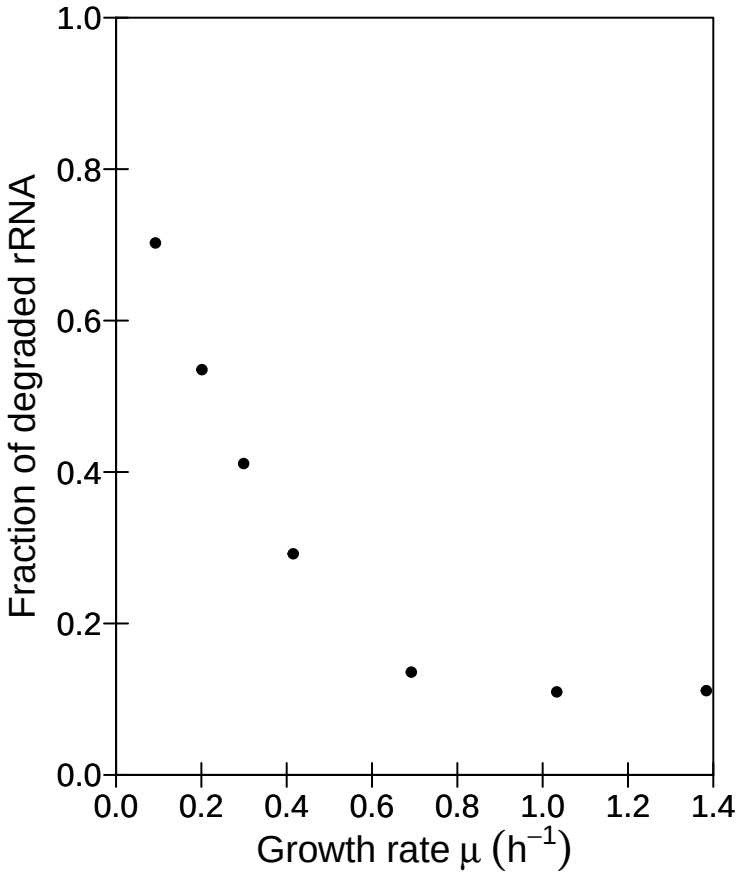

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})

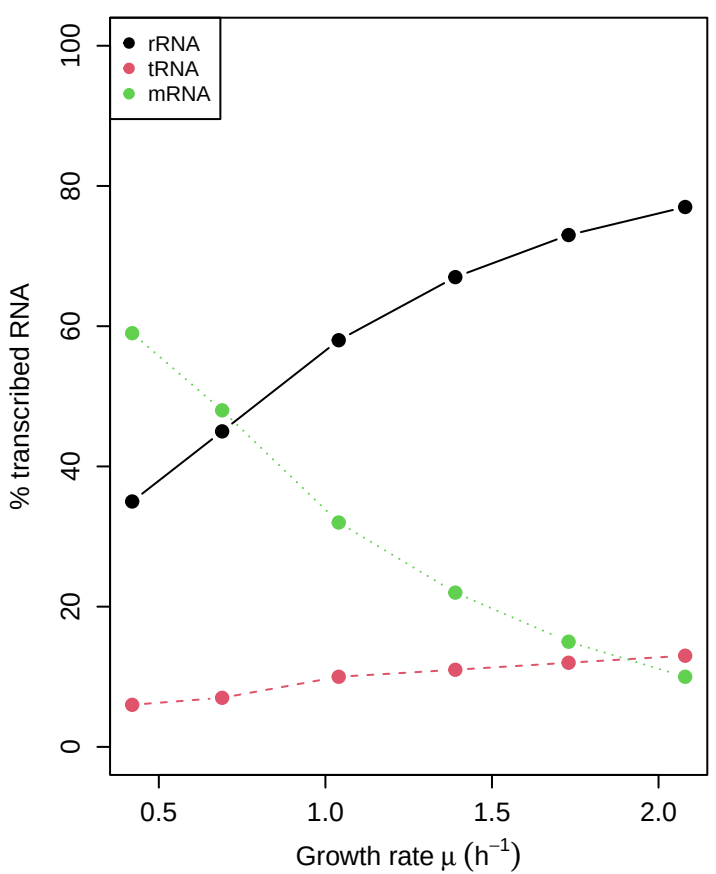

Fraction of degraded rRNA
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

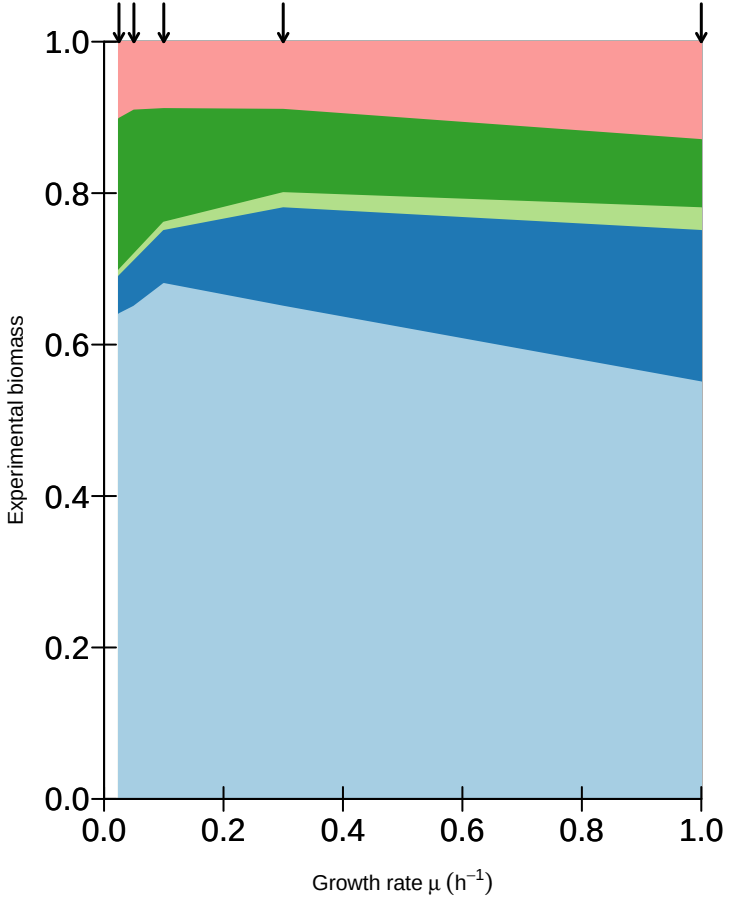

% transcribed RNA
rRNA
tRNA
mRNA
1.0
0.8
0.6
0.4
0.2
0.0
0.1
0.3
0.5
0.7
Growth rate μ (h−1)

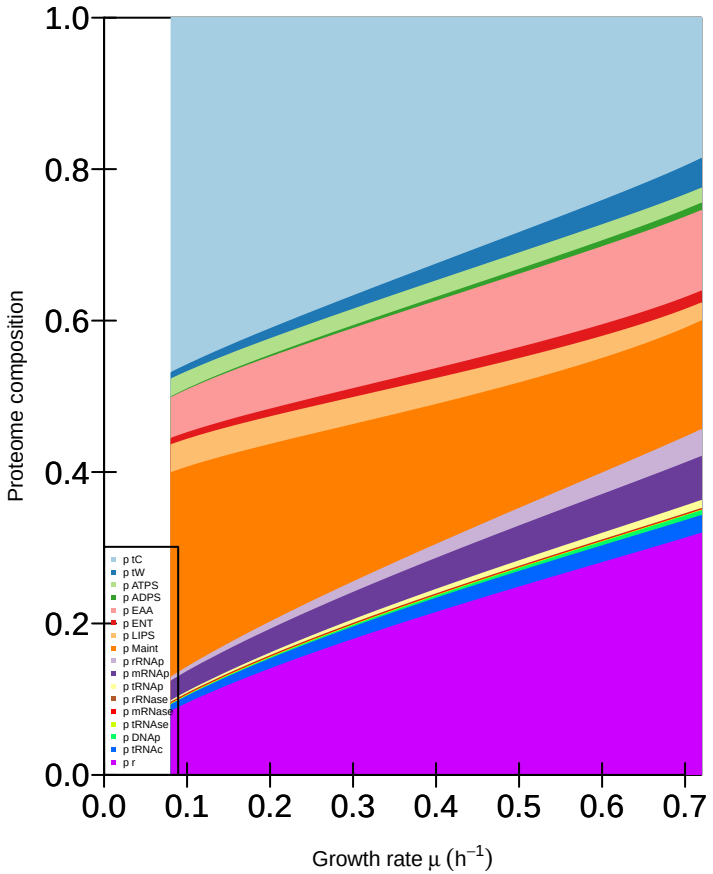

Relative biomass composition
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
p
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
Growth rate μ (h−1)

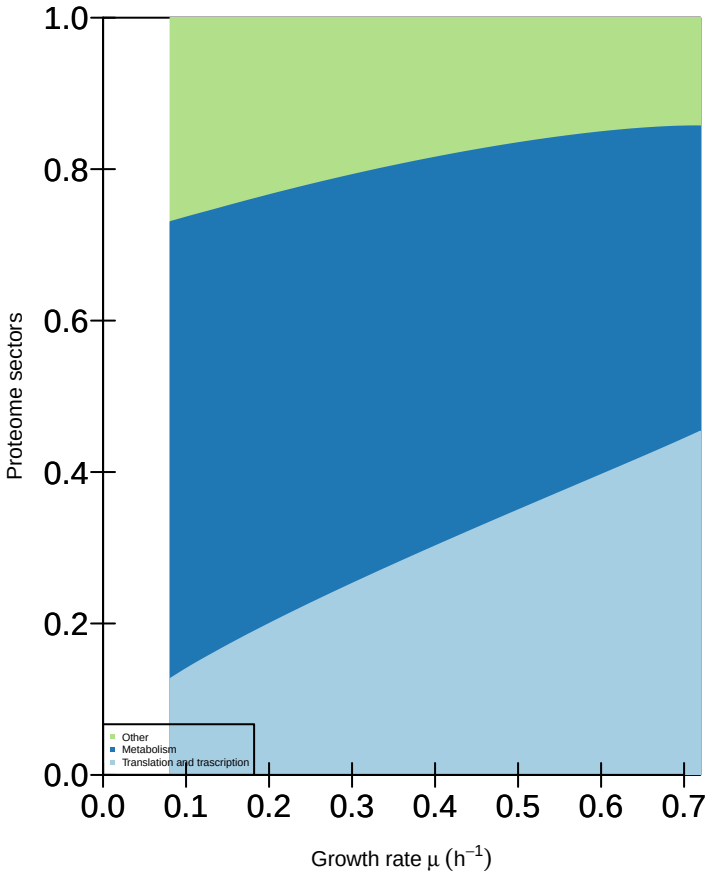

Predicted biomass
Rest
Lipids
DNA
RNA
Protein
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

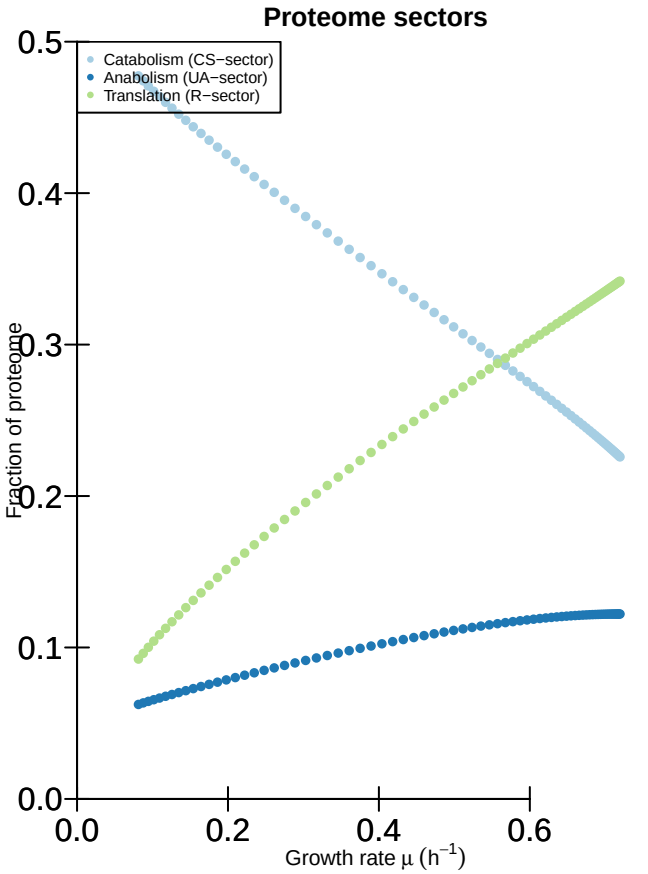

Fraction of degraded rRNA
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
Growth rate μ (h^{-1})


rRNA
tRNA
mRNA
% transcribed RNA
100
80
60
40
20
0
0.5
1.0
1.5
2.0
Growth rate μ (h^{-1})


Experimental biomass
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})


Proteome composition
Growth rate μ (h−1)
p tC
p tW
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


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


Proteome sectors
Fraction of proteome
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	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
C	1	0	−0.02	0	−1	−0.167	−0.18	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	1	−0.167	0	0	0	0	0	0	0	0	0	−0.01	0
NT	0	0	0	−1	0	0.334	0	0	−1	−1	−1	1	1	1	−1	0	0
ADP	0	0	−0.98	1	0	0.666	0.82	1	0	0	0	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	0	0	−0.05	−0.05
W	0	−1	0.02	0	0	0	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	0	0	0
rRNA	0	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	0	1	0	0	−1	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	1	0	0	−1	0	−0.94	0.94
DNA	0	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	0.95	−0.95
p	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

K

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0.0333333333333333	0	0	0	0	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	0	0	0	0
C	13	0	3.5	0	3.5	3.5	7	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	6	3	0	0	0	0	0	0	0	0	0	6	0
NT	0	0	0	2.5	0	5	0	0	2.5	5	1.66666666666667	0	0	0	2.5	0	0
ADP	0	0	0.333333333333333	1	0	0.5	0.5	0	0	0	0	0	0	0	0	0	0
ATP	0	0	7	0	0	2	2	2	0	0	0	0	0	0	0	2	2
W	0	2	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	17.5	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0
DNA	0	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	0	1.5
p	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	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0.025	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	0
C	0	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	0
NT	0	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	0
ATP	0	0	0	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	0	0	0
LIP	60	60	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	0	40
mRNA	0	0	0	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	0	0	0
DNA	0	0	0	0	0	0	0	0	9	9	9	0	0	0	8	0	0
TC	0	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	0

kcat

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
kcatf	26	36	2242	10	12	207	73	87	10	2	10	10	10	10	16	14679	792
kcatb	3	4	224	1	1	21	7	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]	[,17]
[1,]	3380	13.5	420.375	4	20.5714285714286	1.1734693877551	6.51785714285714	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]	[,17]
[1,]	0.089	0.021	0.027	0.005	0.165	0.023	0.031	0.2506	0.0426	0.0213	0.0071	0.002	0.006	4e−04	0.002	0.023	0.284

average saturation input

2

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
[1,]	0	0	0	0	0	0	0	0	0	0	0	0.001	0.001	0.001	0	0	0

minimal f constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
[1,]	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0