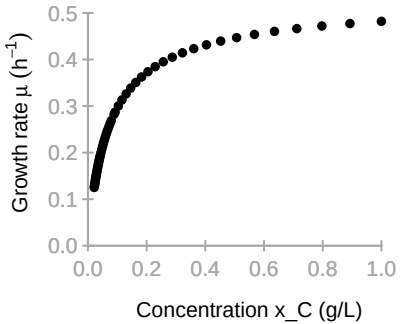
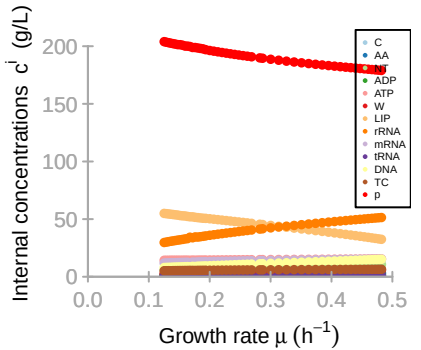
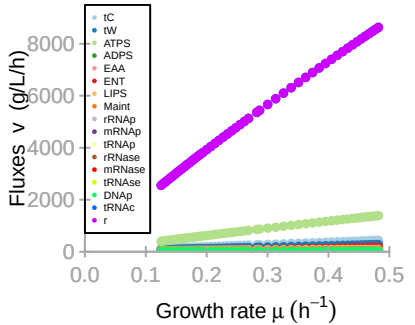
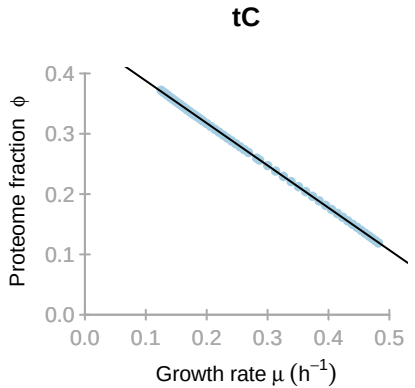
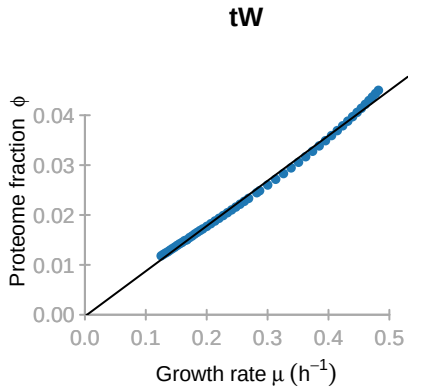
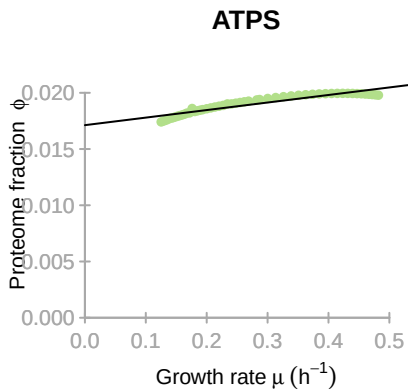

Growth rate μ (h^{-1})
Concentration x_C (g/L)

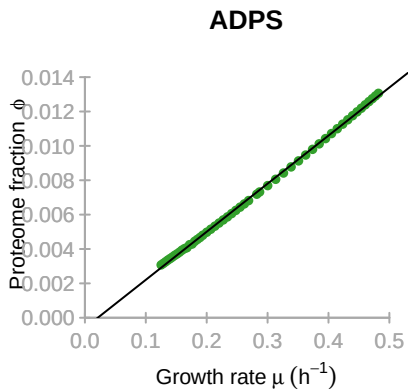

Internal concentrations c^i (g/L)
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
p
Growth rate μ (h^{-1})

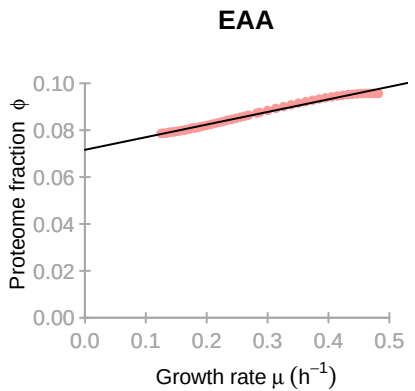

Fluxes v (g/L/h)
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

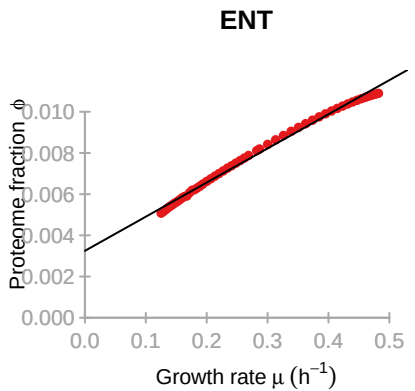

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

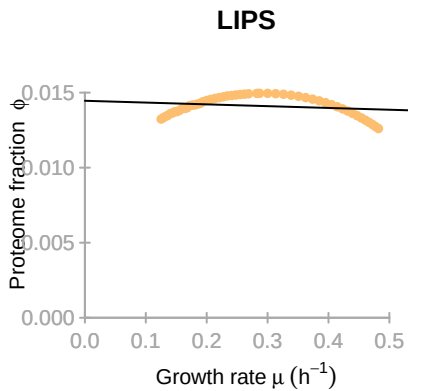

tW
Proteome fraction ϕ
Growth rate μ (h^{-1})

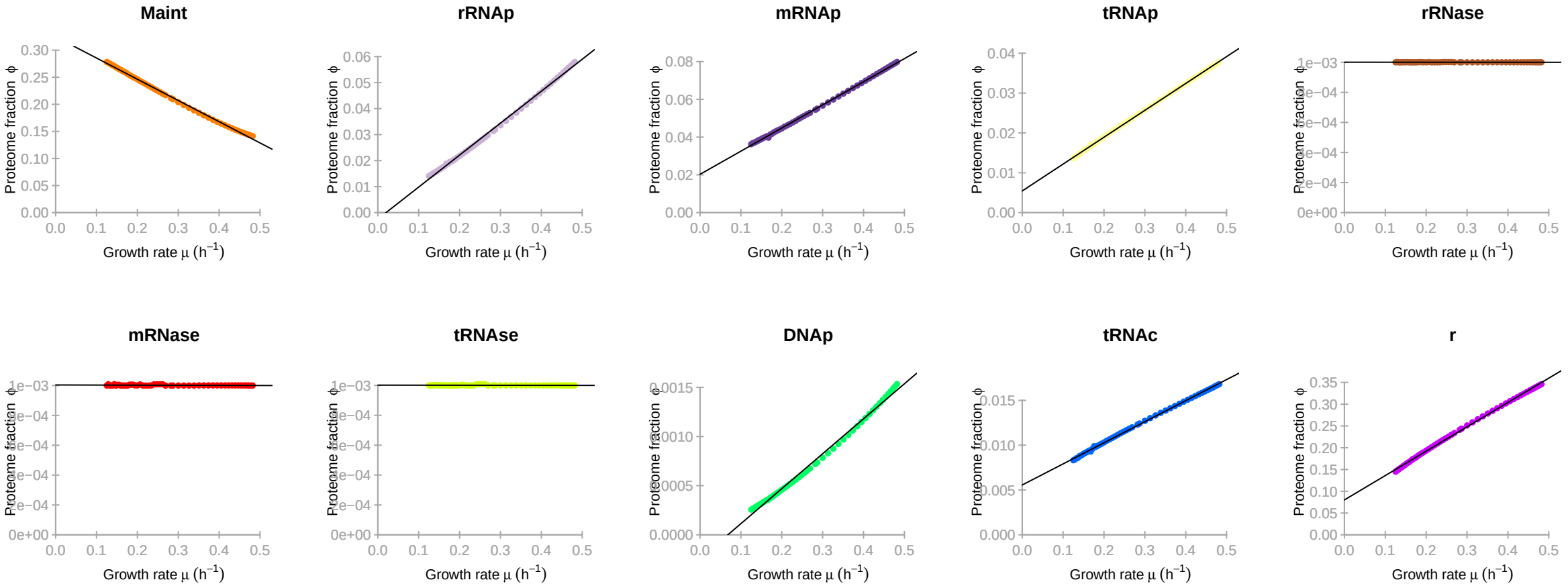

ATPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

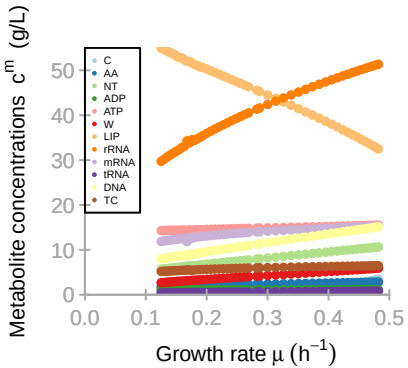

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

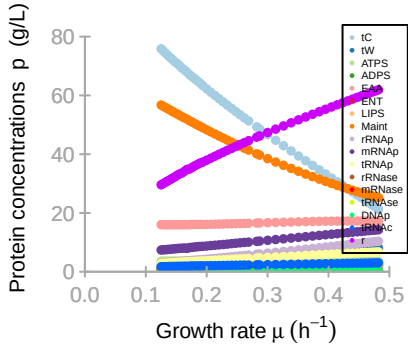

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

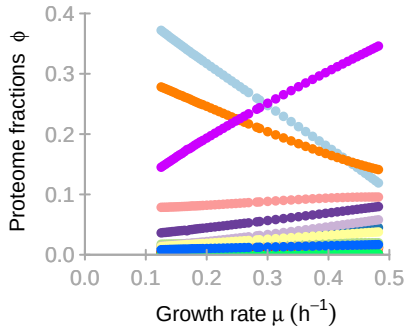

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

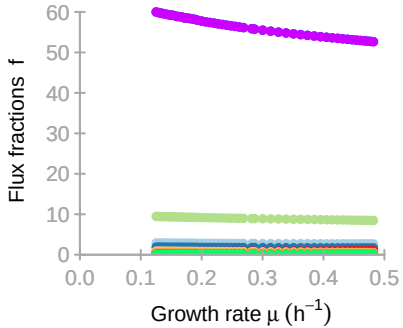

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

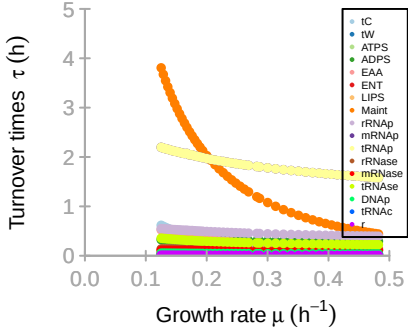

Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Proteome fraction ϕ
Growth rate μ (h^{-1})

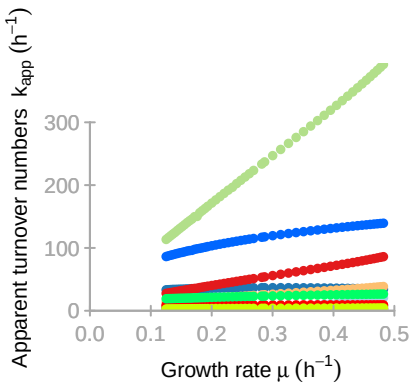

Metabolite concentrations c^m (g/L)
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
Growth rate μ (h^{-1})

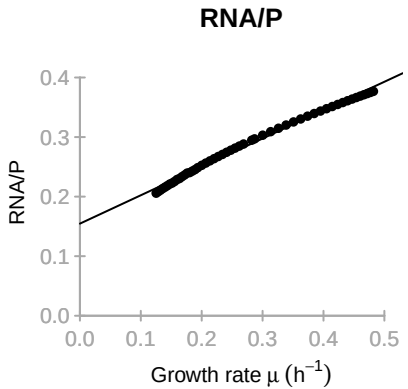

Protein concentrations p (g/L)
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

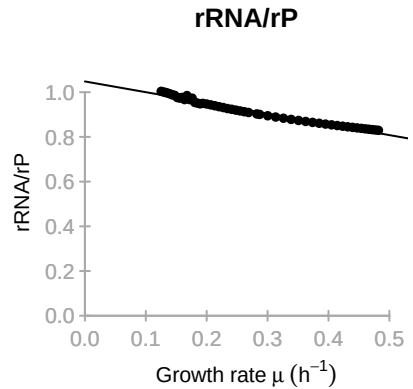

Proteome fractions ϕ
Growth rate μ (h^{-1})

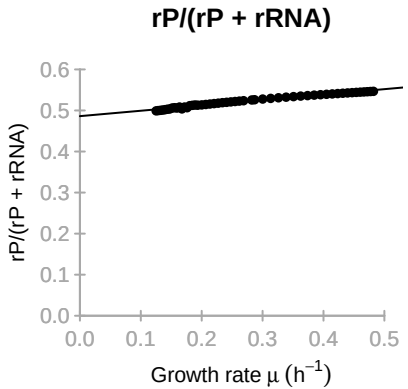

Flux fractions f
Growth rate μ (h^{-1})

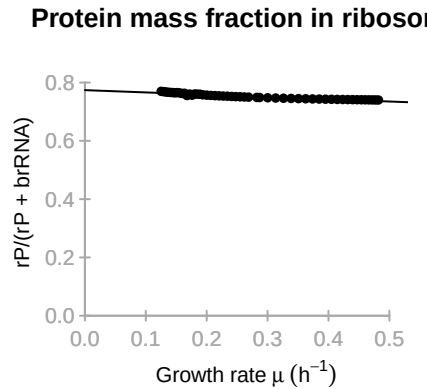

Turnover times τ (h)
tC
tW
ATPS
ADPS
EAA
ENT
LIPS
Maint
rRNAp
mRNAp
tRNAp
rRNase
mRNase
tRNAse
DNAp
tRNAc
r
Growth rate μ (h^{-1})

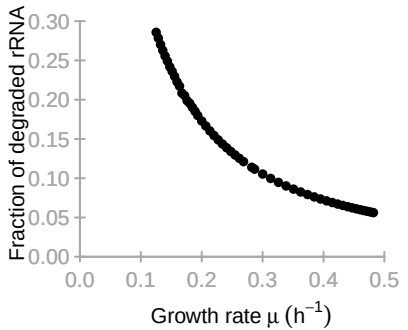

Apparent turnover numbers k_{app} (h^{-1})
Growth rate μ (h^{-1})

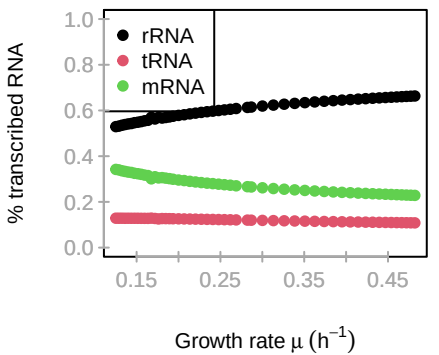

RNA/P
RNA/P
Growth rate μ (h^{-1})

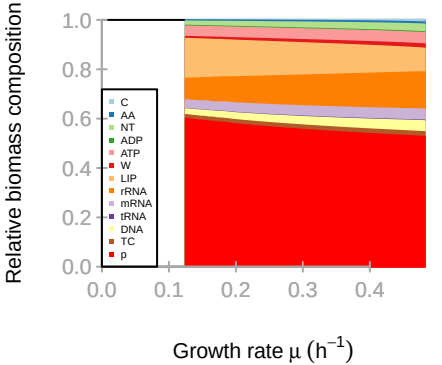

rRNA/rP
rRNA/rP
Growth rate μ (h^{-1})

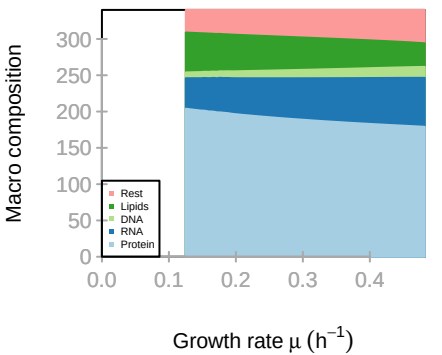

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h^{-1})

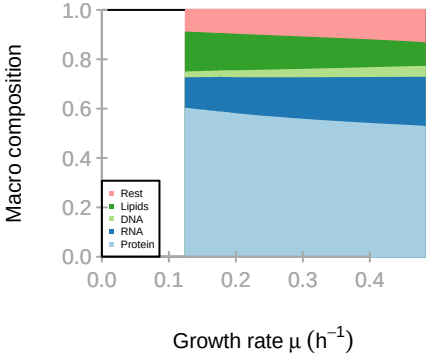

Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h^{-1})

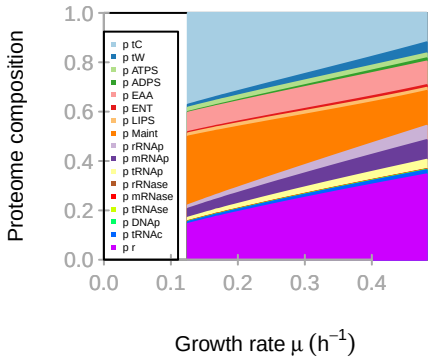

Fraction of degraded rRNA
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.0
0.1
0.2
0.3
0.4
0.5
Growth rate μ (h−1)

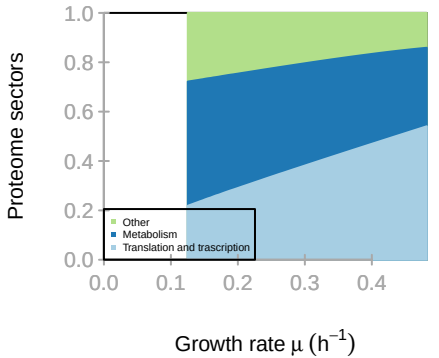

% transcribed RNA
rRNA
tRNA
mRNA
0.0
0.2
0.4
0.6
0.8
1.0
0.15
0.25
0.35
0.45
Growth rate μ (h−1)

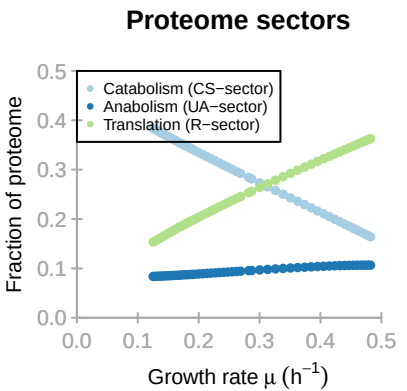

Relative biomass composition
C
AA
NT
ADP
ATP
W
LIP
rRNA
mRNA
tRNA
DNA
TC
p
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.1
0.2
0.3
0.4
Growth rate μ (h−1)


Macro composition
Rest
Lipids
DNA
RNA
Protein
0
50
100
150
200
250
300
0.0
0.1
0.2
0.3
0.4
Growth rate μ (h−1)


Macro composition
Rest
Lipids
DNA
RNA
Protein
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.1
0.2
0.3
0.4
Growth rate μ (h−1)


Proteome composition
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
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.1
0.2
0.3
0.4
Growth rate μ (h−1)


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


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

M

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	rRNase	mRNase	tRNAse	DNAp	tRNAc	r
C	1	0	−0.2	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	−0.8	1	0	0.666	0.82	1	0	0	0	0	0	0	0	0.05	0.05
ATP	0	0	0.8	0	0	−0.666	−0.82	−1	0	0	0	0	0	0	0	−0.05	−0.05
W	0	−1	0.2	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	0.5	0	0	0	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	0	0	0	0
C	5	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
NT	0	0	0	1	0	0	0	0	2	2	2	0	0	0	2	0	0
ADP	0	0	1	2	0	0	0	2	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	2	2
W	0	2	0	0	0	0	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	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0	0	0
mRNA	0	0	0	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	0	0	0	1	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	2	1
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	0.2	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	50	50	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	70
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7
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	5	5	5	0	0	0	5	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

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]	[,17]
kcatf	100	120	968	4	9	160	53	3	4	1	1	10	10	10	42	10306	626
kcatb	10	12	97	1	1	16	5	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,]	100	5	9.97938144329897	8	9	10	10.6	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

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	0.35	0	0	0	0	0	0	0	0	0