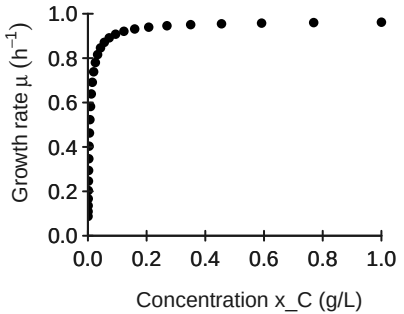
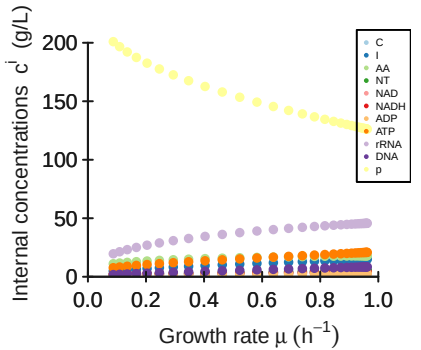
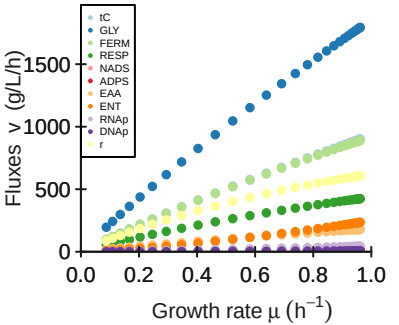
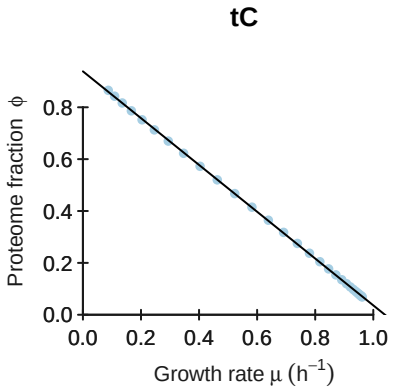
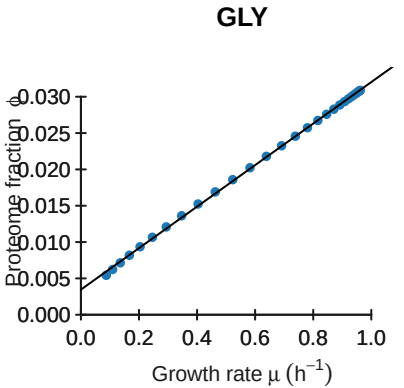
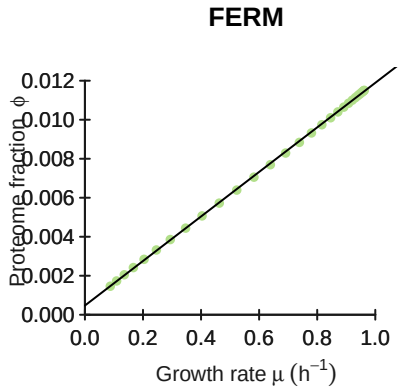

Growth rate μ (h^{-1})
Concentration x_C (g/L)

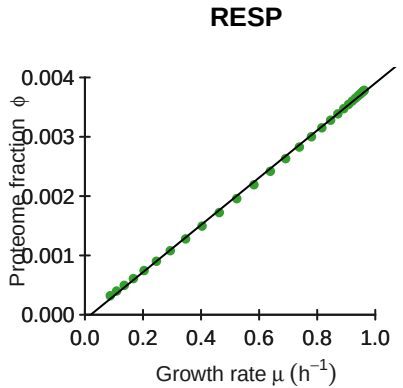

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
I
AA
NT
NAD
NADH
ADP
ATP
rRNA
DNA
p

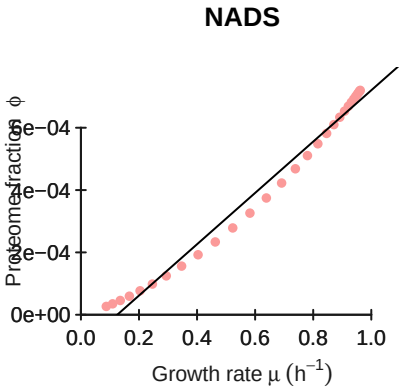

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
GLY
FERM
RESP
NADS
ADPS
EAA
ENT
RNAp
DNAp
r

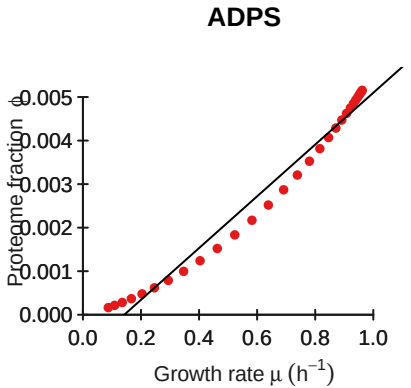

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

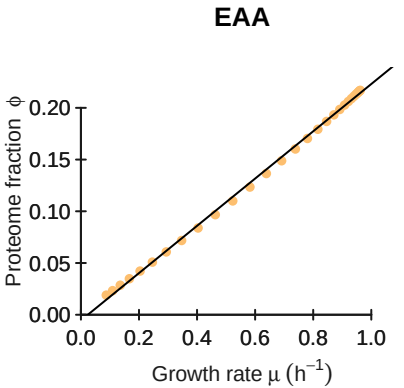

GLY
Proteome fraction ϕ
Growth rate μ (h^{-1})

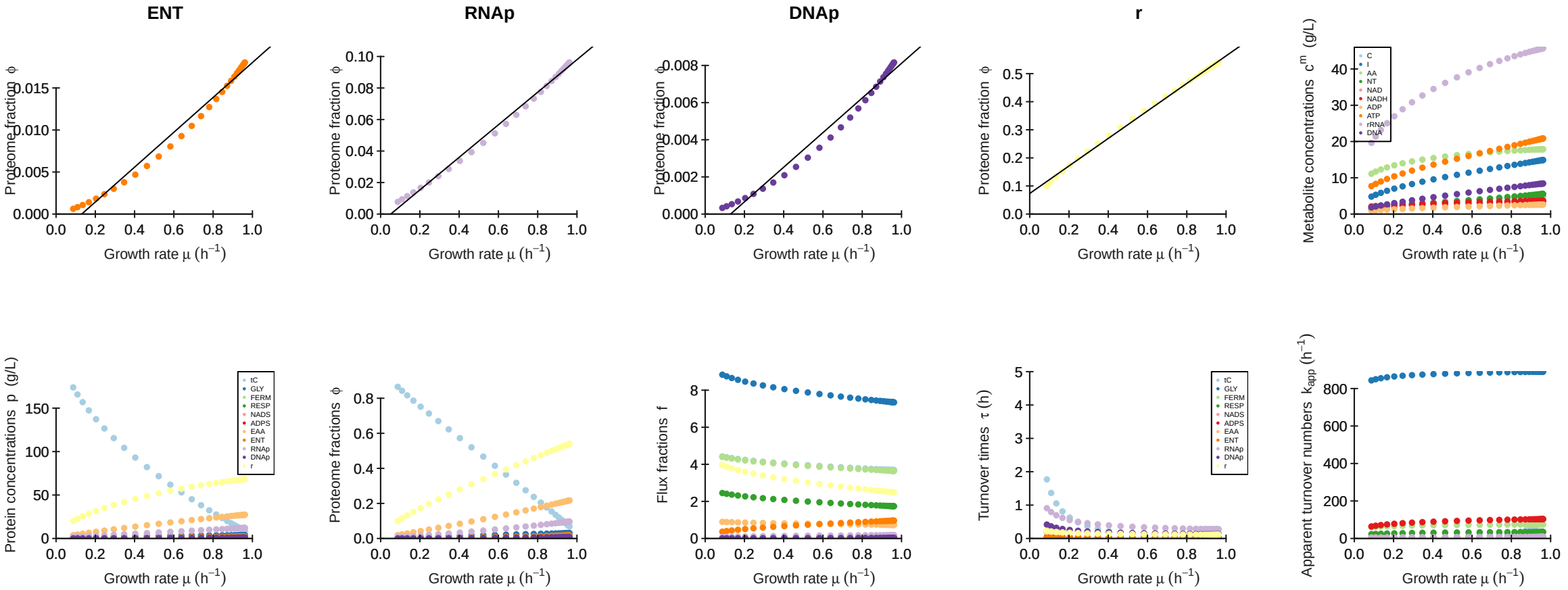

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

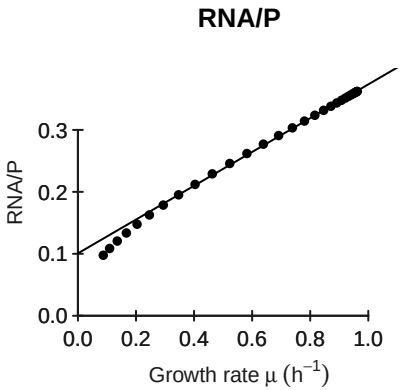

RESP
Proteome fraction ϕ
Growth rate μ (h^{-1})

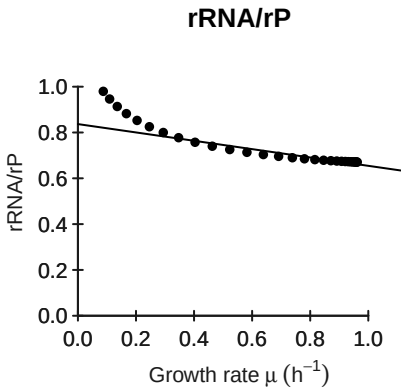

NADS
Proteome fraction ϕ
Growth rate μ (h^{-1})

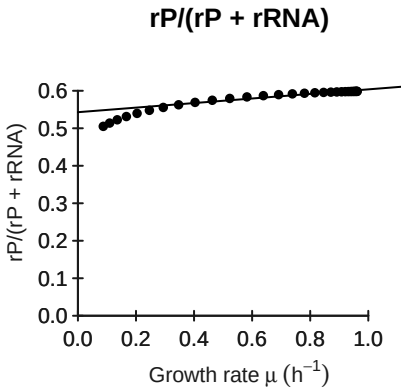

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

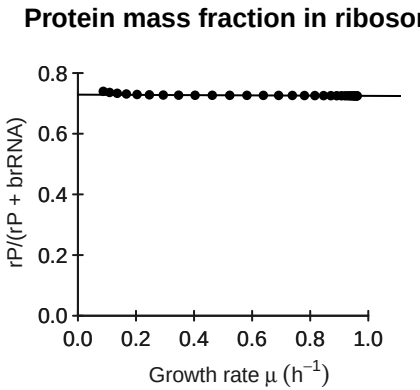

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

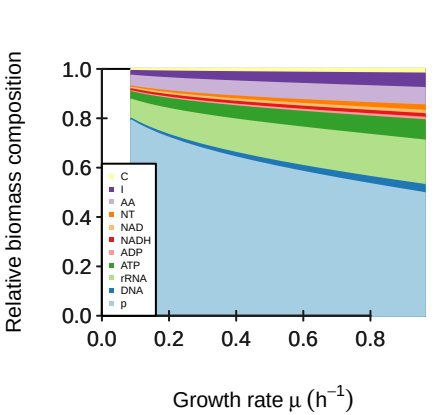

ENT
RNAp
DNAp
r
Proteome fraction ϕ
Growth rate μ (h−1)
Metabolite concentrations cm (g/L)
C
I
AA
NT
NAD
NADH
ADP
ATP
rRNA
DNA
Protein concentrations p (g/L)
Proteome fractions ϕ
Flux fractions f
Turnover times τ (h)
Apparent turnover numbers kapp (h−1)
tC
GLY
FERM
RESP
NADS
ADPS
EAA
ENT
RNAp
DNAp
r

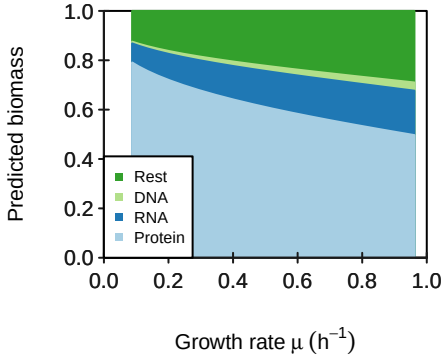

RNA/P
RNA/P
Growth rate μ (h−1)

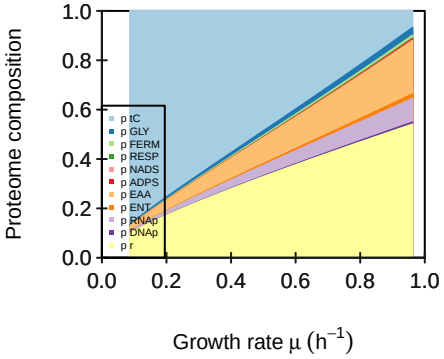

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

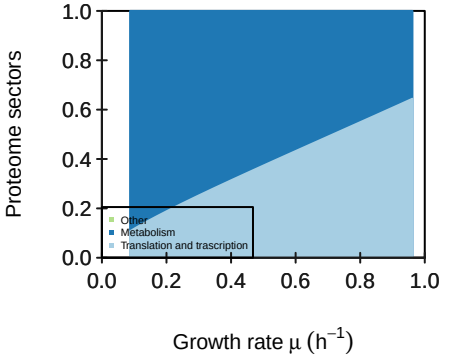

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ (h−1)


Relative biomass composition
C
I
AA
NT
NAD
NADH
ADP
ATP
rRNA
DNA
p
Growth rate μ (h−1)


Predicted biomass
Rest
DNA
RNA
Protein
Growth rate μ (h−1)


Proteome composition
p tC
p GLY
p FERM
p RESP
p NADS
p ADPS
p EAA
p ENT
p RNAp
p DNAp
p r
Growth rate μ (h−1)


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

keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

	tC	GLY	FERM	RESP	NADS	ADPS	EAA	ENT	RNAp	DNAp	r
C	1	−0.5	0	0	0	0	0	0	0	0	0
I	0	0.5	−0.5	−0.5	−1	0	−1	−0.17	0	0	0
AA	0	0	0	0	0	0	1	−0.17	0	0	−0.2
NT	0	0	0	0	0	−1	0	0.34	−1	−1	0
NAD	0	−0.25	0.5	0	1	0	0	0	0	0	0
NADH	0	0.25	−0.5	0	0	0	0	0	0	0	0
ADP	0	−0.25	0	−0.5	0	1	0	0.66	0	0	0.8
ATP	0	0.25	0	0.5	0	0	0	−0.66	0	0	−0.8
rRNA	0	0	0	0	0	0	0	0	1	0	0
DNA	0	0	0	0	0	0	0	0	0	1	0
p	0	0	0	0	0	0	0	0	0	0	0.2

K

	tC	GLY	FERM	RESP	NADS	ADPS	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0	0	0	0
x_W	0	0	10	2	0	0	0	0	0	0	0
C	0	2	0	0	0	0	0	0	0	0	0
I	0	0	2	0.4	2	0	2	2	0	0	0
AA	0	0	0	0	0	0	0	2	0	0	2
NT	0	0	0	0	0	1	0	0	1	1	0
NAD	0	1	0	0	0	0	0	0	0	0	0
NADH	0	0	6	1.2	0	0	0	0	0	0	0
ADP	0	1	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	3	0	0	3
rRNA	0	0	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0	0	0	0	0

KA

	tC	GLY	FERM	RESP	NADS	ADPS	EAA	ENT	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0	0	0	0
NAD	0	0	0	0	0	0	0	0	0	0	0
NADH	0	0	0	0	0	0	0	0	0	0	0
ADP	0	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	35
DNA	0	0	0	0	0	0	0	0	4	4	0
p	0	0	0	0	0	0	0	0	0	0	0

kcat

	tC	GLY	FERM	RESP	NADS	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	114.4	1169.7	1827	913.5	85	41	7.4	149.1	6.3	13.7	20
kcatb	0	0	0	0	0	0	0	0	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
[1,]	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf	Inf

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
[1,]	0.065	0.03	0.005	0.034	0.002	0.002	0.248	0.032	0.119	0.003	0.46

average saturation input

3

minimal phi constraint

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