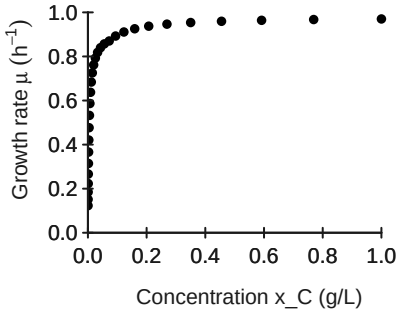
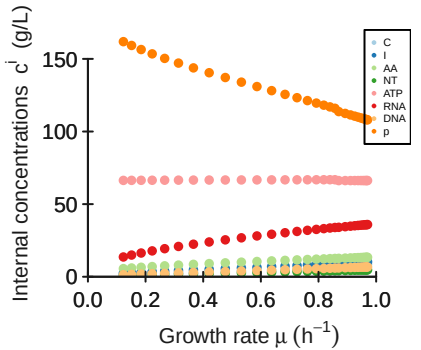
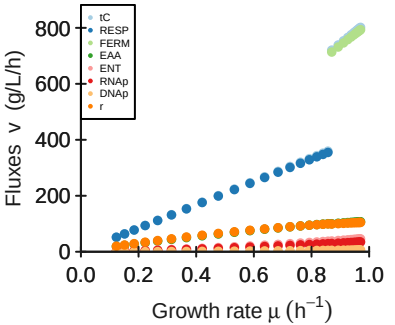
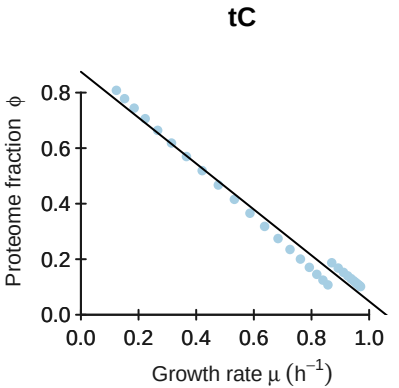
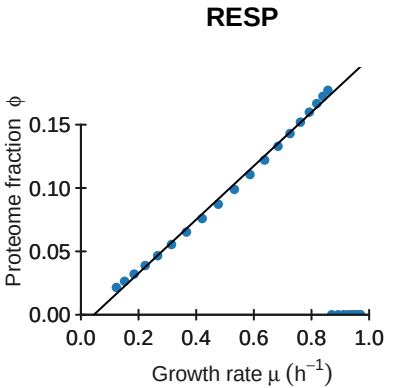
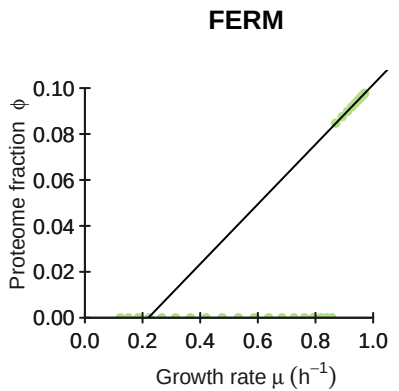

Growth rate μ (h^{-1})
Concentration x_C (g/L)

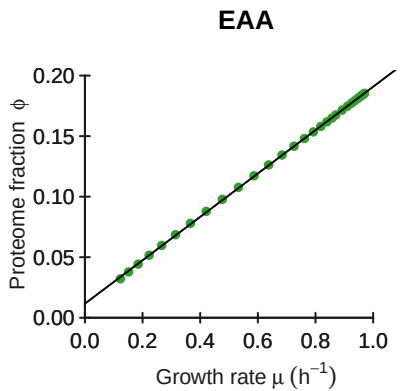

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
I
AA
NT
ATP
RNA
DNA
p

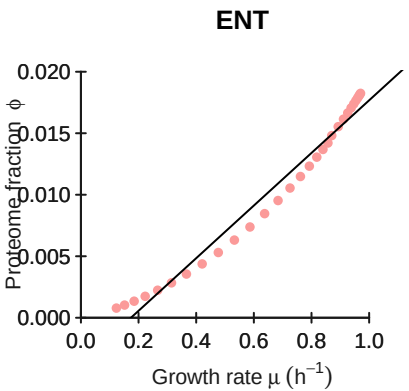

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
RESP
FERM
EAA
ENT
RNAp
DNAp
r

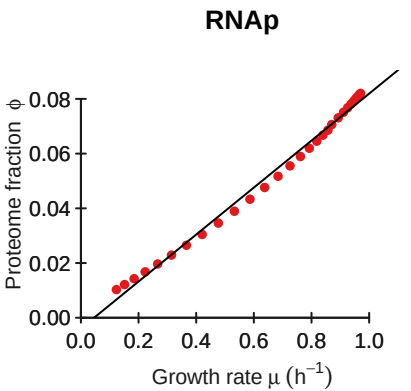

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

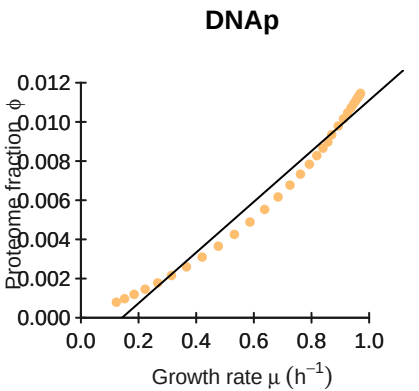

RESP
Proteome fraction ϕ
Growth rate μ (h^{-1})

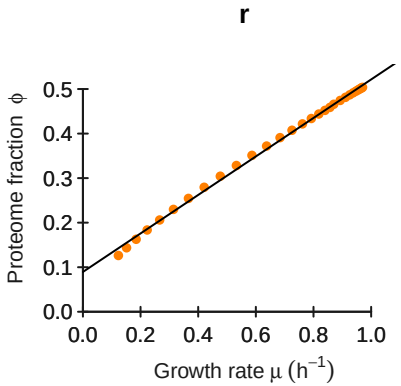

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

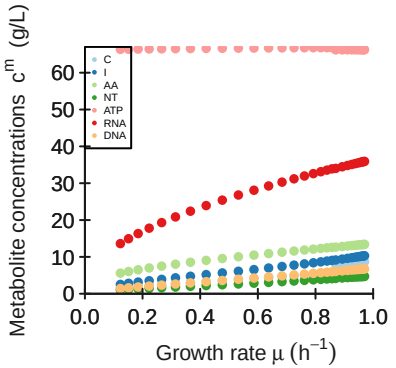

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

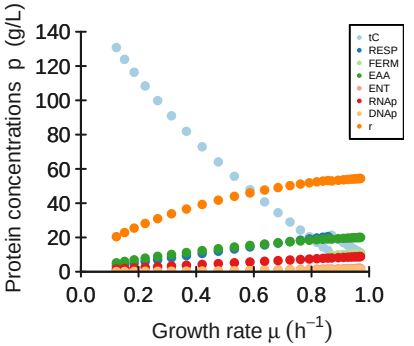

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

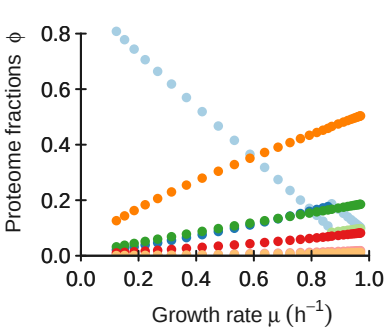

RNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

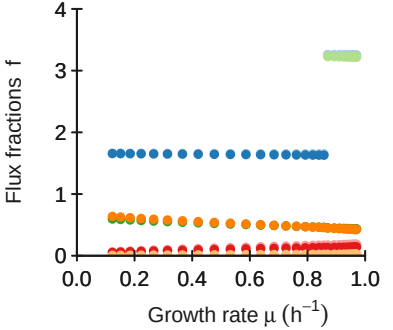

DNAp
Proteome fraction ϕ
Growth rate μ (h^{-1})

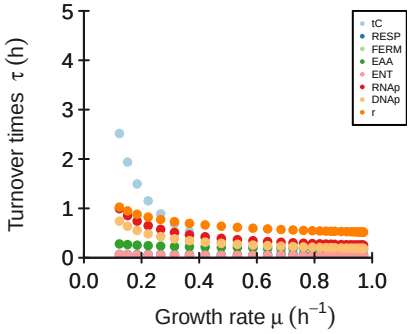

r
Proteome fraction ϕ
Growth rate μ (h−1)

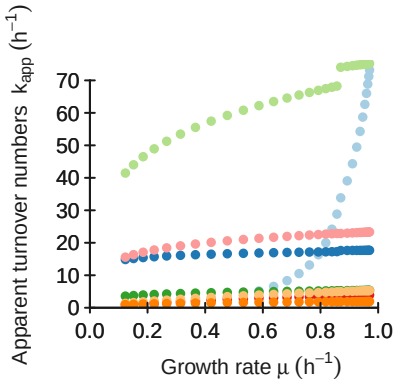

Metabolite concentrations cm (g/L)
C
I
AA
NT
ATP
RNA
DNA
Growth rate μ (h−1)

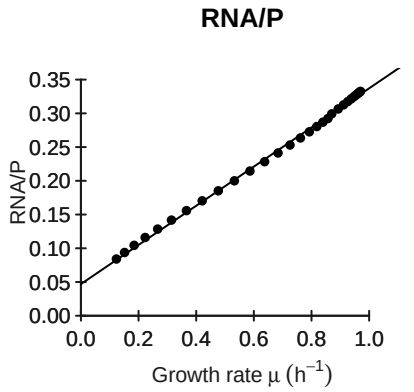

Protein concentrations p (g/L)
tC
RESP
FERM
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

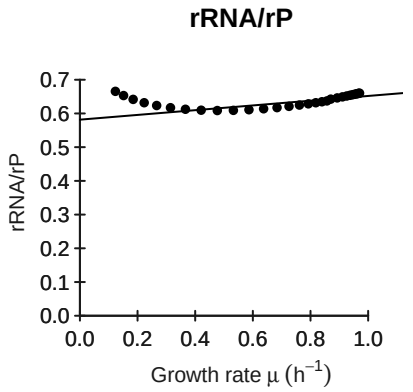

Proteome fractions ϕ
Growth rate μ (h−1)

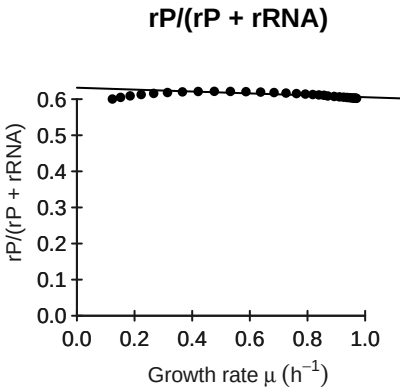

Flux fractions f
Growth rate μ (h−1)


Turnover times τ (h)
tC
RESP
FERM
EAA
ENT
RNAp
DNAp
r
Growth rate μ (h−1)

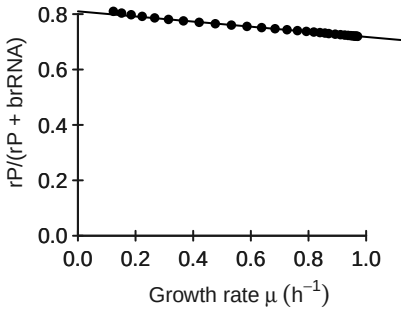

Apparent turnover numbers kapp (h−1)
Growth rate μ (h−1)

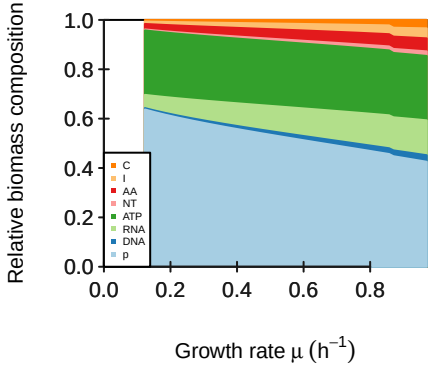

RNA/P
RNA/P
Growth rate μ (h−1)

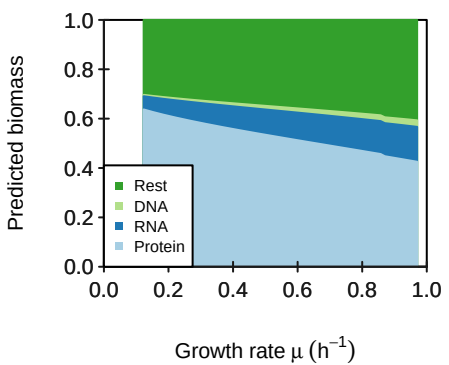

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

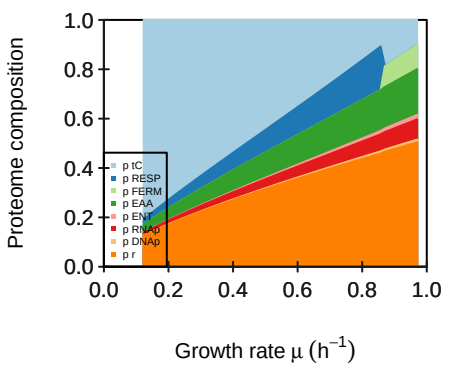

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)

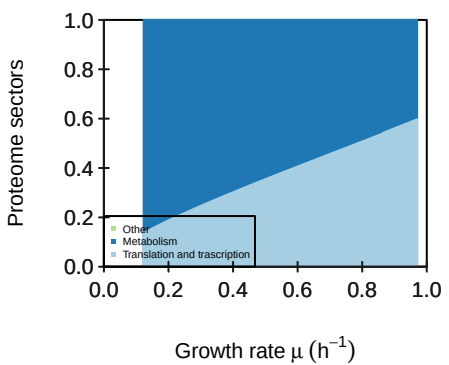
Protein mass fraction in ribosome











keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

	tC	RESP	FERM	EAA	ENT	RNAp	DNAp	r
C	1	−1	−1	0	0	0	0	0
I	0	0.4	0.2	−1	−0.9	0	0	0
AA	0	0	0	1	0	0	0	−0.9
NT	0	0	0	0	1	−1	−1	0
ATP	0	0.2	0.1	0	−0.1	0	0	−0.1
RNA	0	0	0	0	0	1	0	0
DNA	0	0	0	0	0	0	1	0
p	0	0	0	0	0	0	0	1

K

	tC	RESP	FERM	EAA	ENT	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0	0
C	0	0.4	2	0	0	0	0	0
I	0	0	0	2	2	0	0	0
AA	0	0	0	0	0	0	0	2
NT	0	0	0	0	0	1	1	0
ATP	0	0	0	0	22	0	0	22
RNA	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0
p	0	0	0	0	0	0	0	0

KA

	tC	RESP	FERM	EAA	ENT	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0	0
x_W	0	0	0	0	0	0	0	0
C	0	0	0	0	0	0	0	0
I	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0
RNA	0	0	0	0	0	0	0	25
DNA	0	0	0	0	0	4	4	0
p	0	0	0	0	0	0	0	0

kcat

	tC	RESP	FERM	EAA	ENT	RNAp	DNAp	r
kcatf	80.5	18.5	92.5	6.4	37.1	7.6	10.2	5
kcatb	0	0	0	0	0	0	0	0

Keq

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

phi input

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]
[1,]	0.06	0.065	0.004	0.248	0.035	0.119	0.003	0.461

average saturation input

3

minimal phi constraint

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

minimal f constraint

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