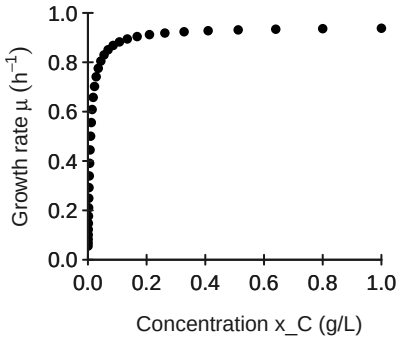
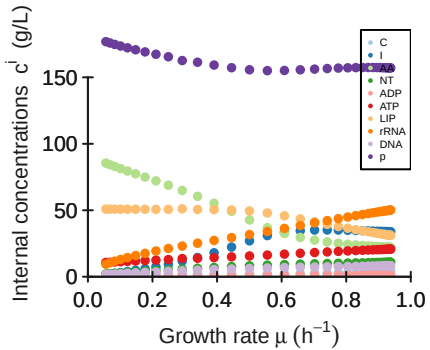
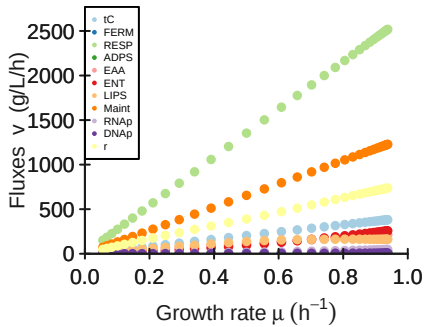
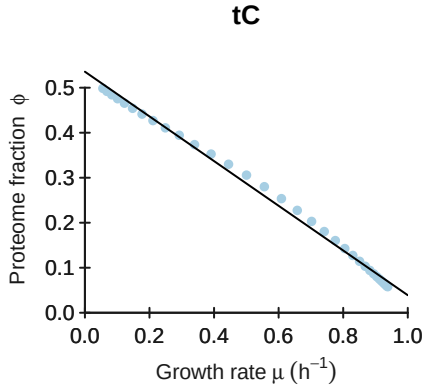
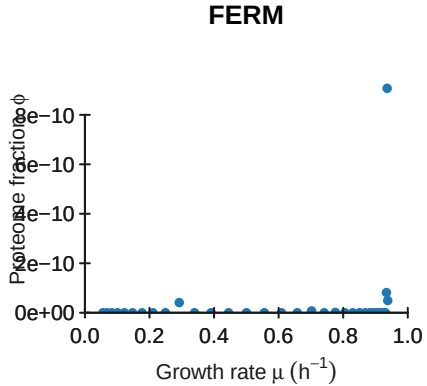
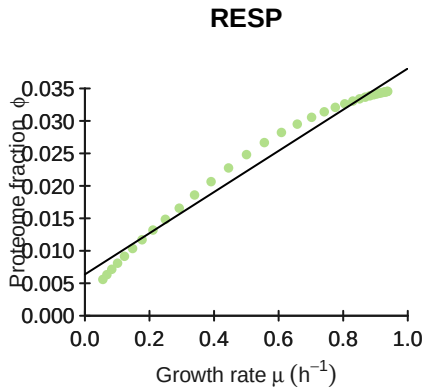

Growth rate μ (h^{-1})
Concentration x_C (g/L)

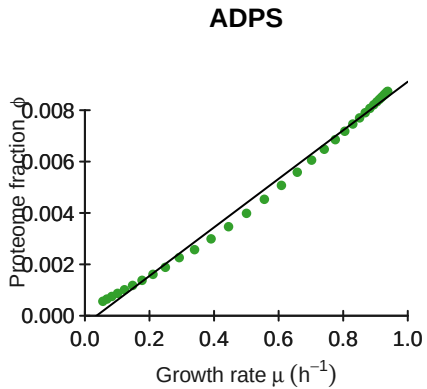

Internal concentrations c^i (g/L)
Growth rate μ (h^{-1})
C
I
AA
NT
ADP
ATP
LIP
rRNA
DNA
p

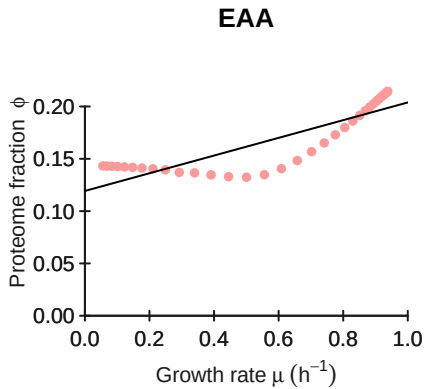

Fluxes v (g/L/h)
Growth rate μ (h^{-1})
tC
FERM
RESP
ADPS
EAA
ENT
LIPS
Maint
RNAp
DNAp
r

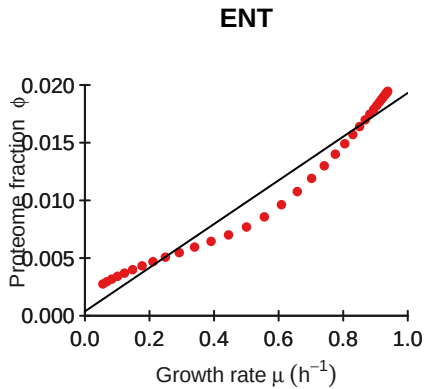

tC
Proteome fraction ϕ
Growth rate μ (h^{-1})

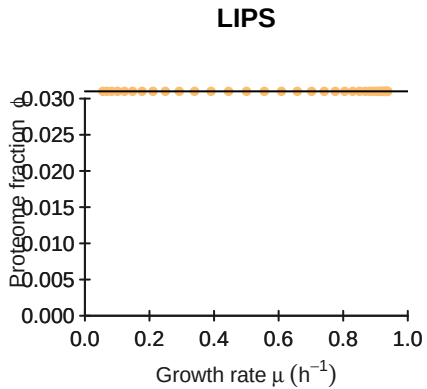

FERM
Proteome fraction ϕ
Growth rate μ (h^{-1})

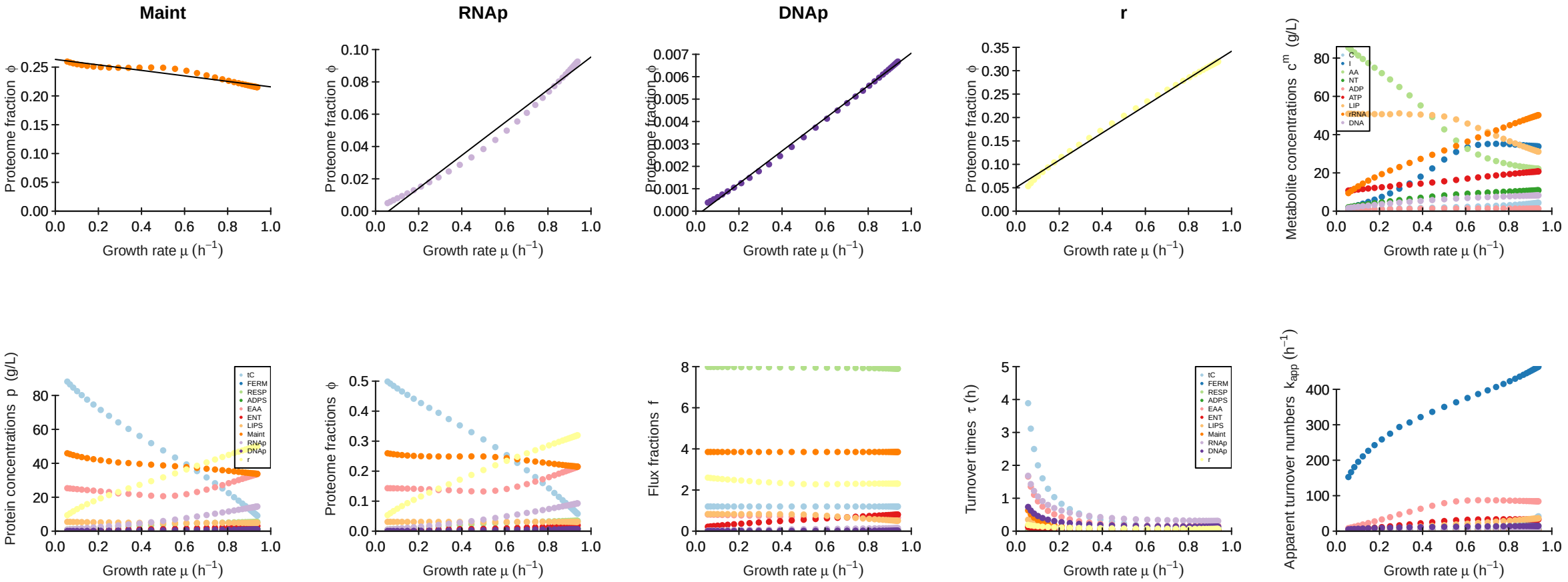

RESP
Proteome fraction ϕ
Growth rate μ (h^{-1})

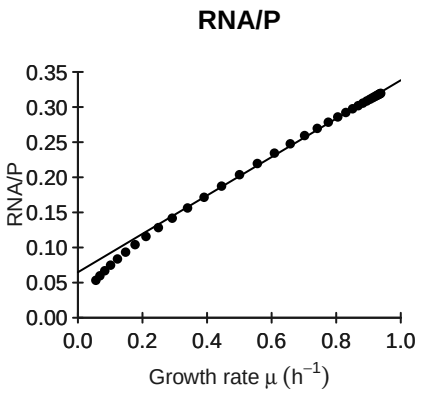

ADPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

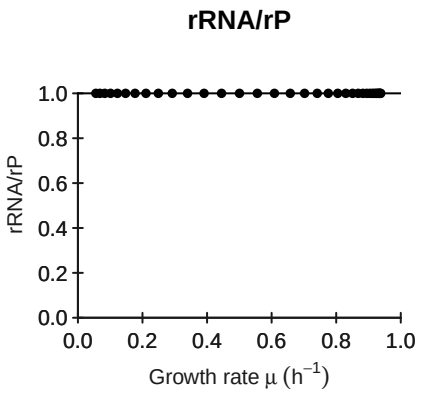

EAA
Proteome fraction ϕ
Growth rate μ (h^{-1})

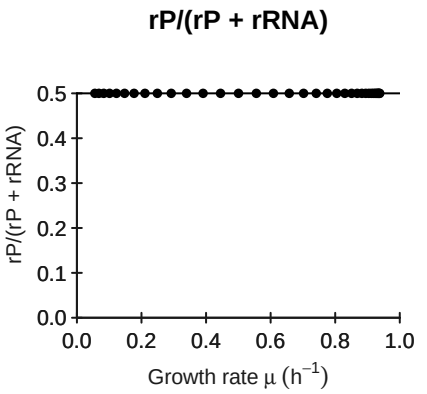

ENT
Proteome fraction ϕ
Growth rate μ (h^{-1})

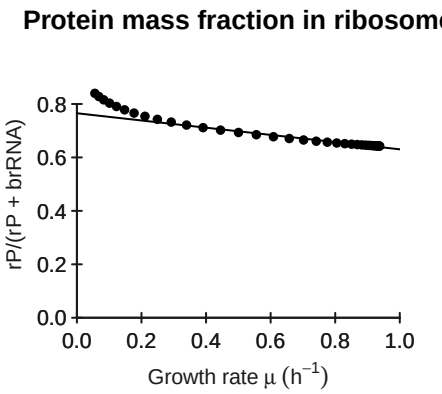

LIPS
Proteome fraction ϕ
Growth rate μ (h^{-1})

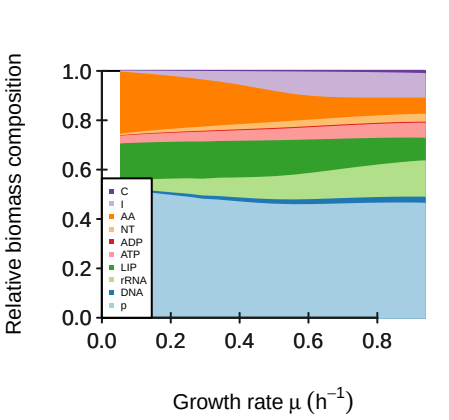

Maint
RNAp
DNAp
r
Proteome fraction ϕ
Growth rate μ (h^{-1})
Metabolite concentrations c^m (g/L)
C
I
AA
NT
ADP
ATP
LIP
rRNA
DNA
Protein concentrations p (g/L)
Proteome fractions ϕ
Flux fractions f
Turnover times τ (h)
Apparent turnover numbers k$_{app}$ (h^{-1})
tC
FERM
RESP
ADPS
EAA
ENT
LIPS
Maint
RNAp
DNAp
r

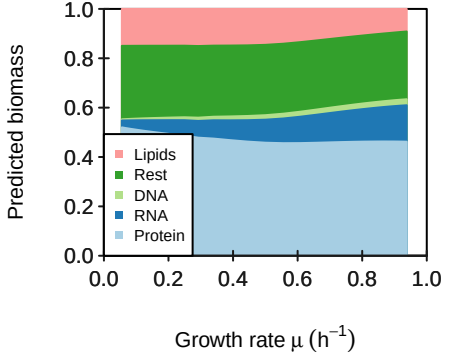

RNA/P
RNA/P
Growth rate μ (h−1)

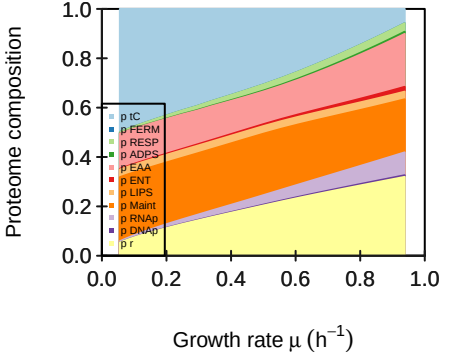

rRNA/rP
rRNA/rP
Growth rate μ (h−1)

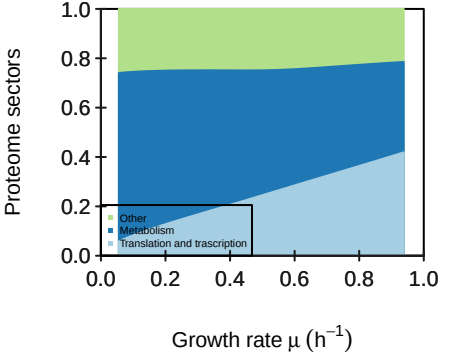

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ (h−1)


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


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


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


Proteome composition
p tC
p FERM
p RESP
p ADPS
p EAA
p ENT
p LIPS
p Maint
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	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
C	1	−0.225	−0.15	0	0	0	0	0	0	0	0
I	0	0.125	0.125	0	−1	−0.167	−0.18	0	0	0	0
AA	0	0	0	0	1	−0.167	0	0	0	0	−0.2
NT	0	0	0	−1	0	0.334	0	0	−1	−1	0
ADP	0	−0.775	−0.85	1	0	0.666	0.82	1	0	0	0.8
ATP	0	0.775	0.85	0	0	−0.666	−0.82	−1	0	0	−0.8
LIP	0	0	0	0	0	0	0.18	0	0	0	0
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	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
x_C	0.1	0	0	0	0	0	0	0	0	0	0
x_W	0	20	4	0	0	0	0	0	0	0	0
C	0	8	1.6	0	0	0	0	0	0	0	0
I	0	0	0	0	31	31	31	0	0	0	0
AA	0	0	0	0	0	5	0	0	0	0	5
NT	0	0	0	5	0	0	0	0	5	5	0
ADP	0	1	0.2	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	3	3	3	0	0	3
LIP	0	0	0	0	0	0	0	0	0	0	0
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	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
x_C	0	0	0	0	0	0	0	0.01	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
ADP	0	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0	0	0
LIP	10	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	40
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	FERM	RESP	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
kcatf	61	3650	730	22	12	226	73	42	7	16	37
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,]	0.043	0.023	0.023	0.002	0.165	0.021	0.031	0.3036	0.0794	0.002	0.307

average saturation input

2

minimal phi constraint

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
[1,]	0	0	0	0	0	0	0.031	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	3.85	0	0	0