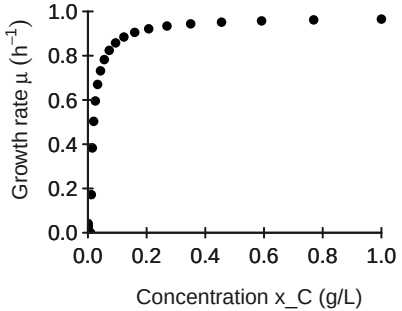
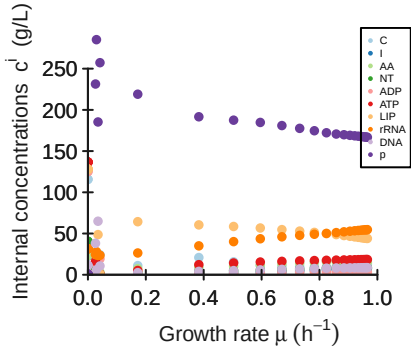
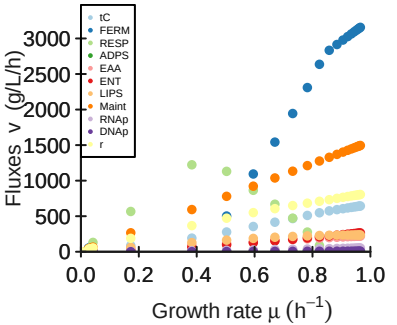
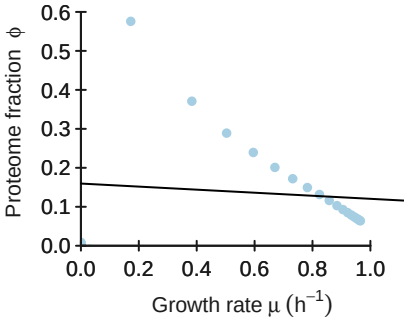


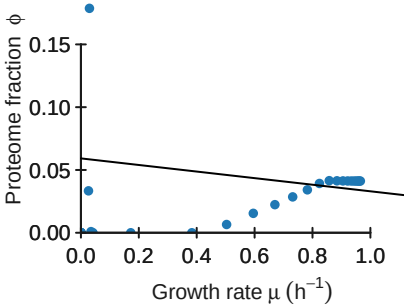




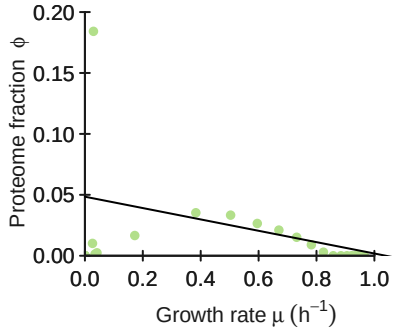
tC



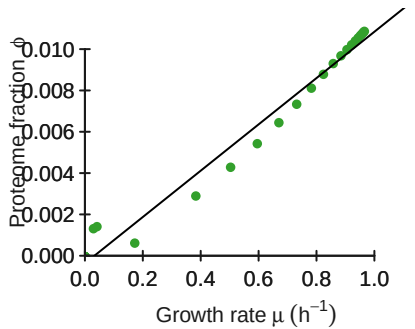
FERM



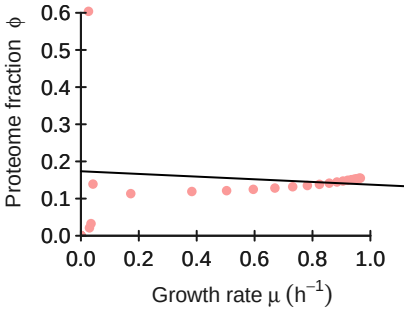
RESP



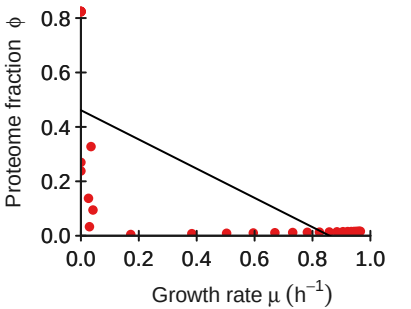
ADPS



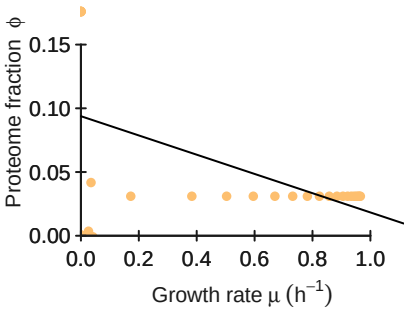
EAA

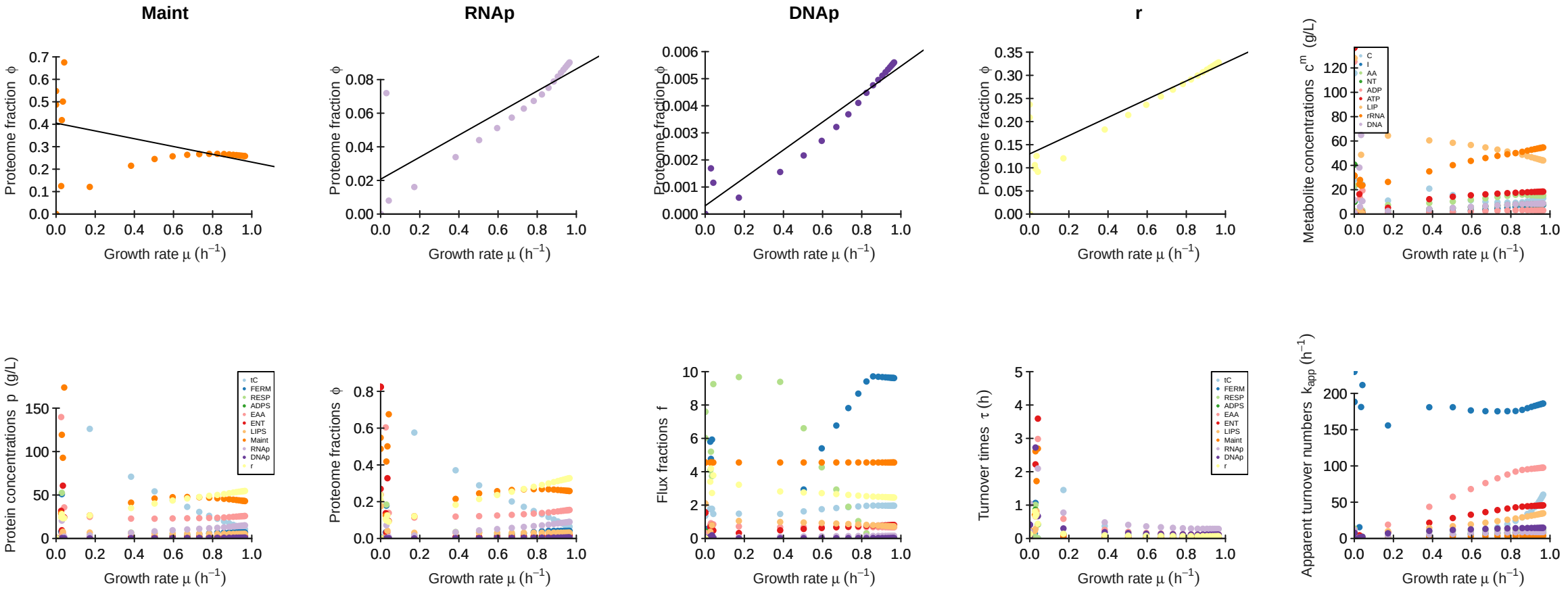


ENT

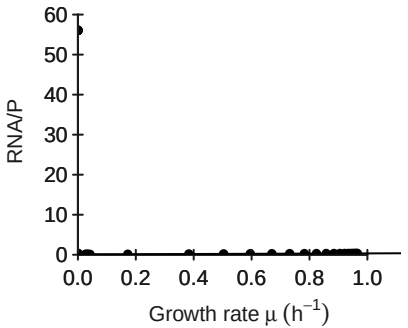


LIPS

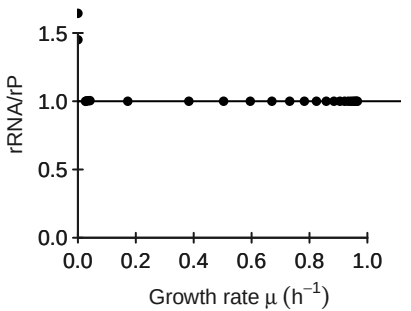



Maint
RNAp
DNAp
r
Proteome fraction ϕ
Growth rate μ (h^{-1})
Metabolite concentrations c^m (g/L)
C
I
AA
NT
ADP
ATP
LIP
rRNA
DNA
Protein concentrations p (g/L)
Proteome fractions ϕ
Flux fractions f
Turnover times τ (h)
Apparent turnover numbers k$_{app}$ (h^{-1})
tC
FERM
RESP
ADPS
EAA
ENT
LIPS
Maint
RNAp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

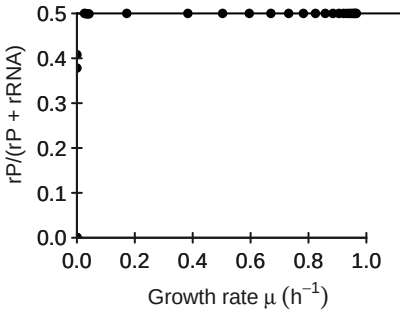
RNA/P



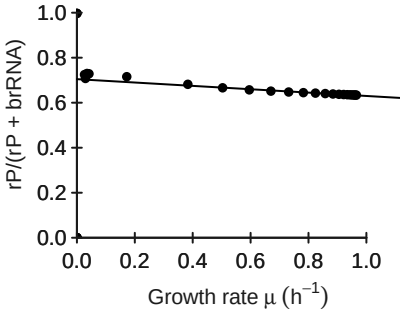
rRNA/rP

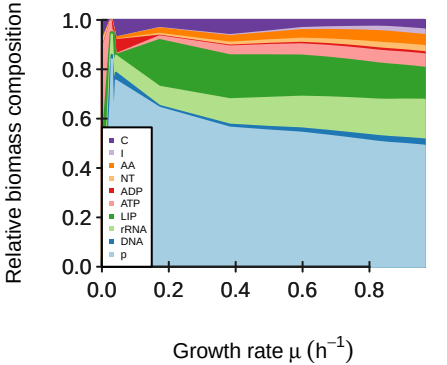


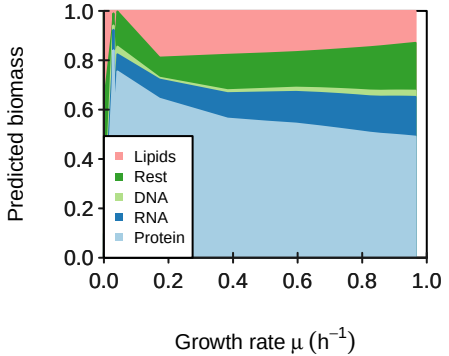
rP/(rP + rRNA)

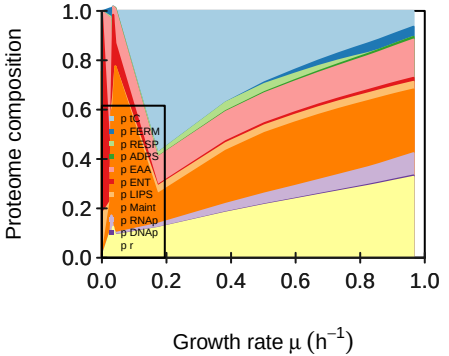


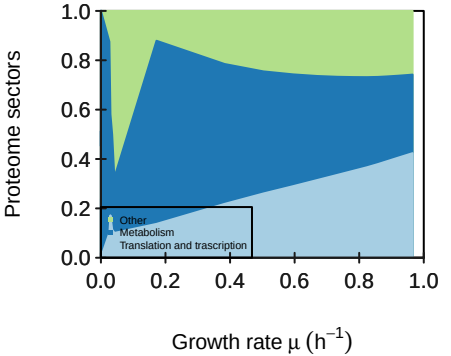
Protein mass fraction in ribosome











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	−0.2	−0.15	0	0	0	0	0	0	0	0
I	0	0.1	0.1	0	−1	−0.17	−0.18	0	0	0	0
AA	0	0	0	0	1	−0.17	0	0	0	0	−0.2
NT	0	0	0	−1	0	0.34	0	0	−1	−1	0
ADP	0	−0.8	−0.85	1	0	0.66	0.82	1	0	0	0.8
ATP	0	0.8	0.85	0	0	−0.66	−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	12	2.4	0	0	0	0	0	0	0	0
I	0	0	0	0	2	2	2	0	0	0	0
AA	0	0	0	0	0	2	0	0	0	0	2
NT	0	0	0	2	0	0	0	0	2	2	0
ADP	0	1	0.2	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	2	2	2	0	0	2
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	0.02	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	0	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	67.2	1174.1	234.9	14.4	11	154.3	63.9	39.7	6.6	16.6	32
kcatb	7	117	23	1	1	15	6	4	1	2	3

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
[1,]	96	16.7250712250712	85.1086956521739	7.2	5.5	1.28583333333333	2.6625	4.9625	3.3	4.15	2.66666666666667

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

3

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	4.55437091503269	0	0	0