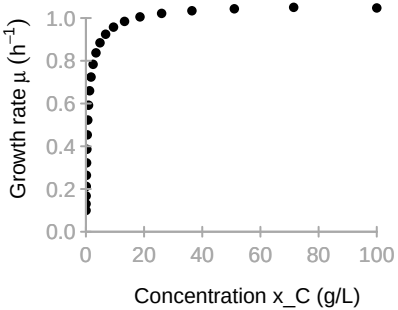
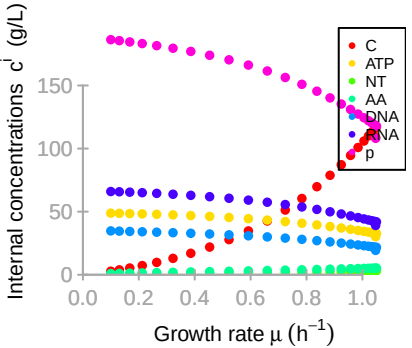
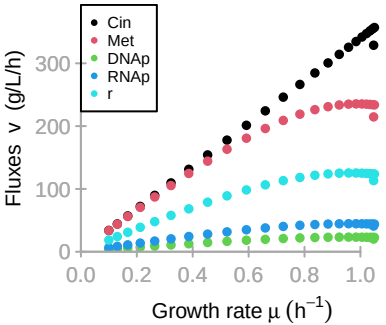
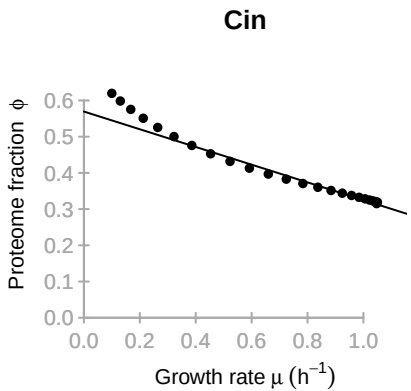
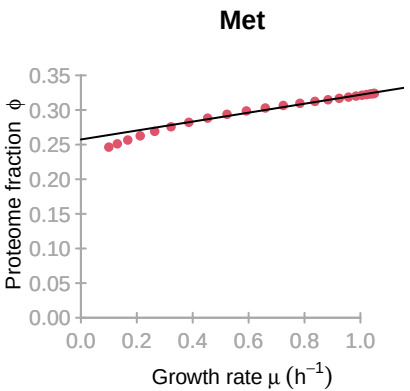
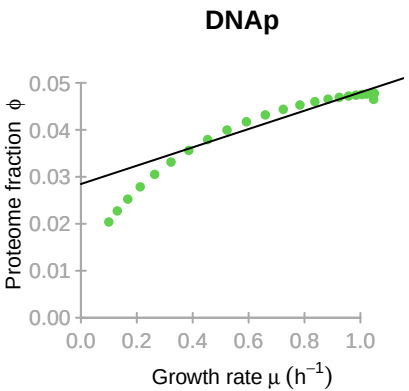

Growth rate μ (h^{-1})
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100
Concentration x_C (g/L)

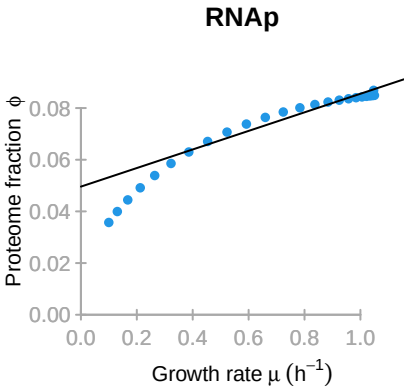

Internal concentrations c^{i} (g/L)
150
100
50
0
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})
C
ATP
NT
AA
DNA
RNA
p

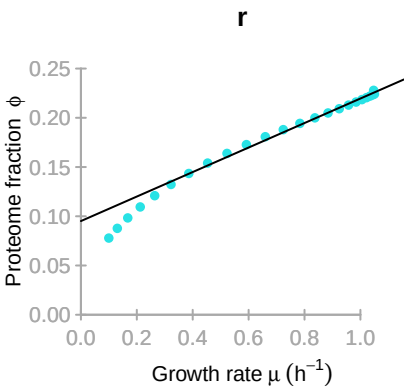

Fluxes v (g/L/h)
300
200
100
0
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})
Cin
Met
DNAp
RNAp
r

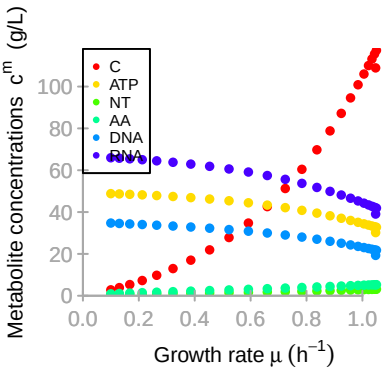

Cin
Proteome fraction ϕ
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})

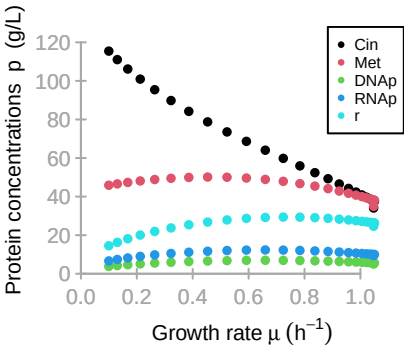

Met
Proteome fraction ϕ
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})

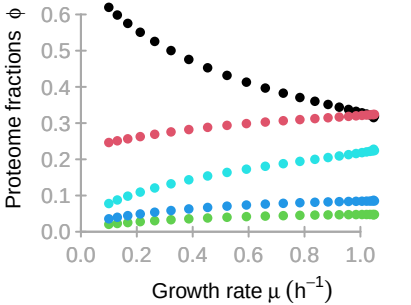

DNAp
Proteome fraction ϕ
0.05
0.04
0.03
0.02
0.01
0.00
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})

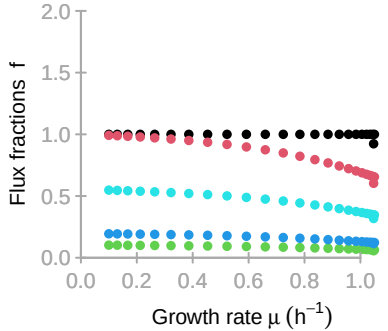

RNAp
Proteome fraction ϕ
0.00
0.02
0.04
0.06
0.08
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

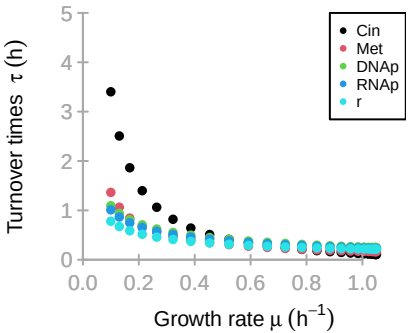

r
Proteome fraction ϕ
0.00
0.05
0.10
0.15
0.20
0.25
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)

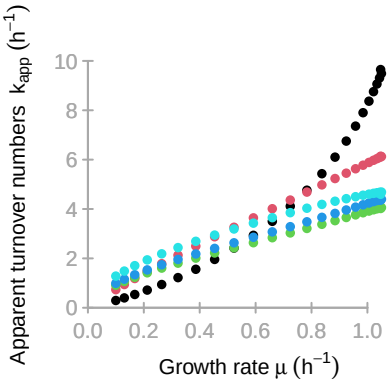

Metabolite concentrations cm (g/L)
C
ATP
NT
AA
DNA
RNA
0
20
40
60
80
100
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)


Protein concentrations p (g/L)
Cin
Met
DNAp
RNAp
r
0
20
40
60
80
100
120
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)


Proteome fractions ϕ
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)


Flux fractions f
0.0
0.5
1.0
1.5
2.0
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h−1)


Turnover times τ (h)
0
1
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})
Cin
Met
DNAp
RNAp
r


Apparent turnover numbers k_{app} (h^{-1})
0
2
4
6
8
10
0.0
0.2
0.4
0.6
0.8
1.0
Growth rate μ (h^{-1})

M

	Cin	Met	DNAp	RNAp	r
C	1	−1	0	0	0
ATP	0	0.2	0	0	−0.1
NT	0	0.3	−1	−1	0
AA	0	0.5	0	0	−0.9
DNA	0	0	1	0	0
RNA	0	0	0	1	0
p	0	0	0	0	1

K

	Cin	Met	DNAp	RNAp	r
[1,]	1	0	0	0	0
[2,]	50	1	0	0	0
[3,]	0	2	0	0	2
[4,]	0	3	5	5	0
[5,]	0	4	0	0	8
[6,]	0	0	0	0	0
[7,]	0	0	0	0	0
[8,]	0	0	0	0	0

KA

	Cin	Met	DNAp	RNAp	r
[1,]	0	0	0	0	0
[2,]	0	0	0	0	0
[3,]	0	0	0	0	0
[4,]	0	0	0	0	0
[5,]	0	0	0	0	0
[6,]	0	0	3	3	0
[7,]	0	0	0	0	5
[8,]	0	0	0	0	0

kcat

	[,1]	[,2]	[,3]	[,4]	[,5]
kcatf	10	11	12	13	14
kcatb	2	3	0	0	0

Keq

	[,1]	[,2]	[,3]	[,4]	[,5]
[1,]	250	88	Inf	Inf	Inf