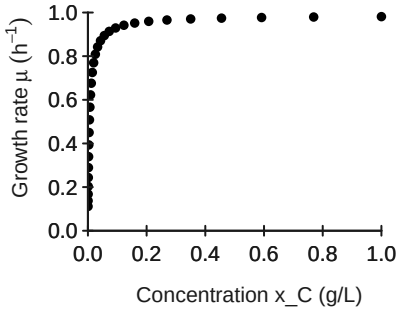
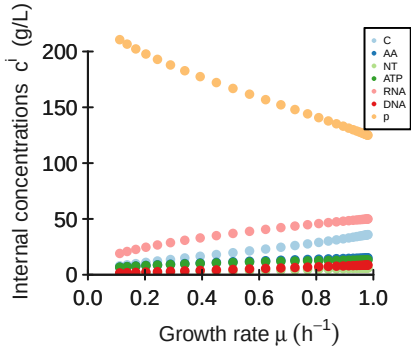
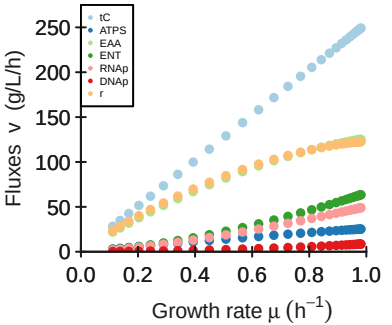
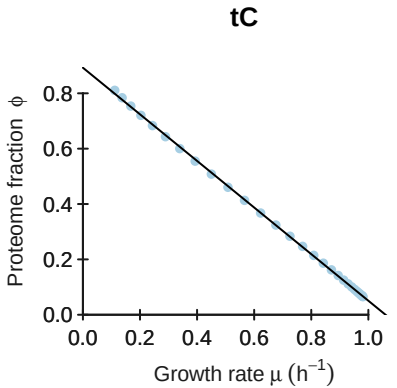
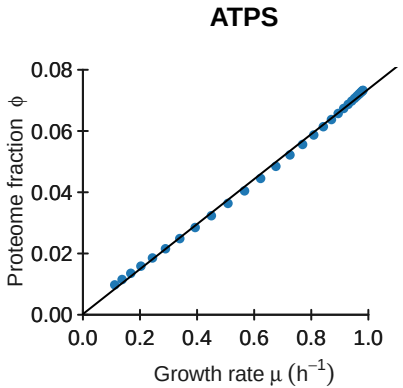
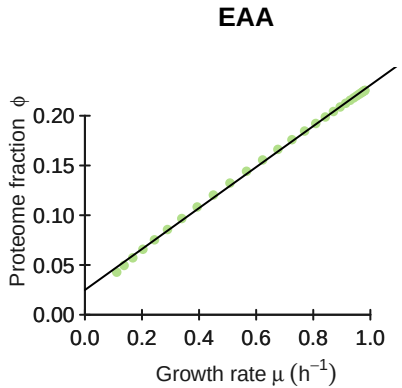

Growth rate μ (h$^{-1}$)
Concentration x_C (g/L)

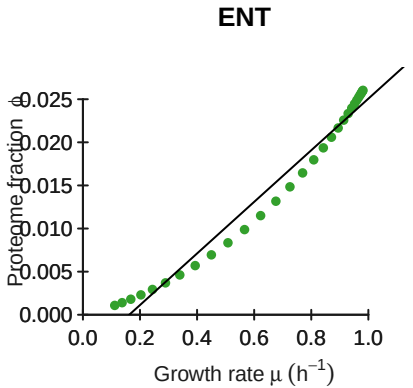

Internal concentrations c$^i$ (g/L)
Growth rate μ (h$^{-1}$)
C
AA
NT
ATP
RNA
DNA
p

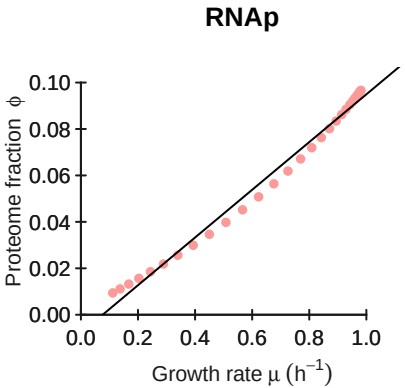

Fluxes v (g/L/h)
Growth rate μ (h$^{-1}$)
tC
ATPS
EAA
ENT
RNAp
DNAp
r

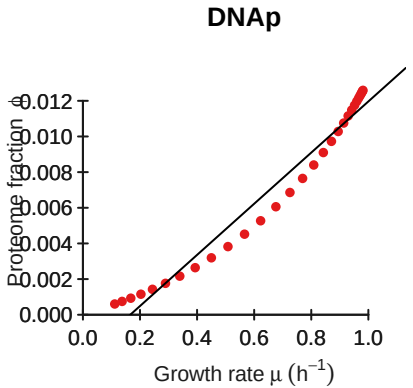

tC
Proteome fraction ϕ
Growth rate μ (h$^{-1}$)

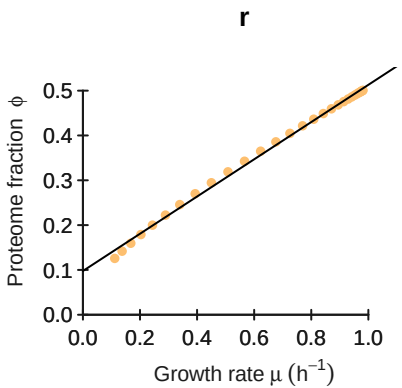

ATPS
Proteome fraction ϕ
Growth rate μ (h$^{-1}$)

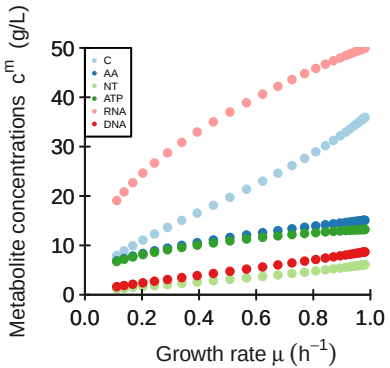

EAA
Proteome fraction ϕ
Growth rate μ (h$^{-1}$)

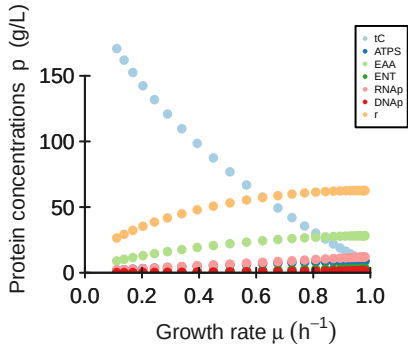

ENT
Proteome fraction ϕ
Growth rate μ (h$^{-1}$)

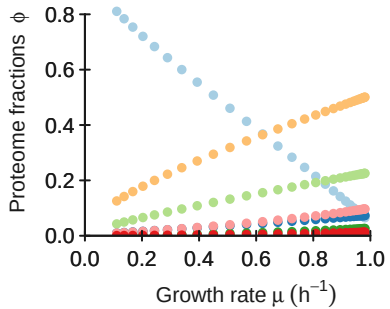

RNAp
Proteome fraction ϕ
Growth rate μ (h$^{-1}$)

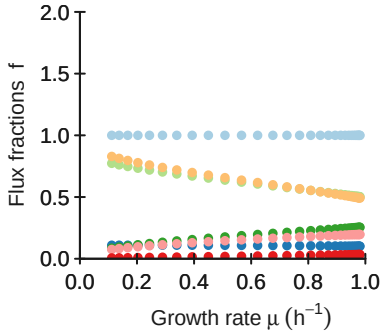

DNAp
Proteome fraction ϕ
Growth rate μ (h$^{-1}$)

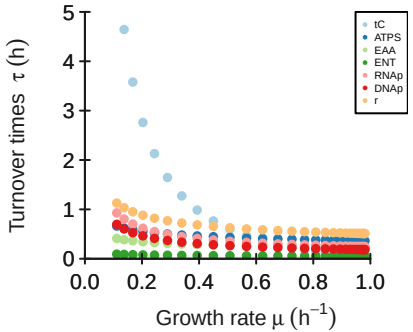

r
Proteome fraction ϕ
Growth rate μ (h$^{-1}$)

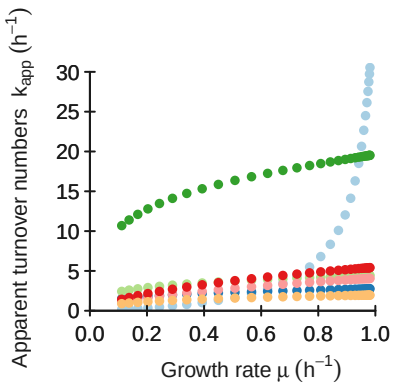

Metabolite concentrations $c^m$ (g/L)
C
AA
NT
ATP
RNA
DNA
Growth rate μ ($h^{-1}$)

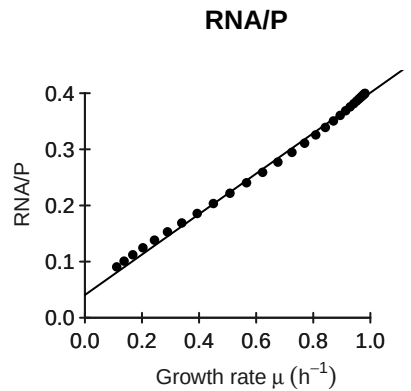

Protein concentrations p (g/L)
tC
ATPS
EAA
ENT
RNAp
DNAp
r
Growth rate μ ($h^{-1}$)

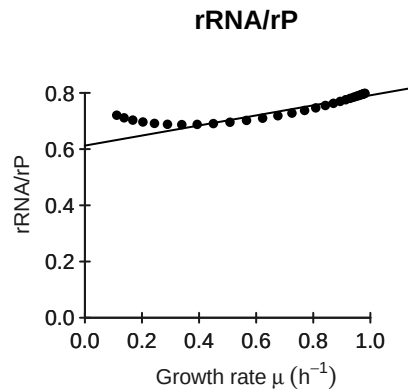

Proteome fractions ϕ
Growth rate μ ($h^{-1}$)

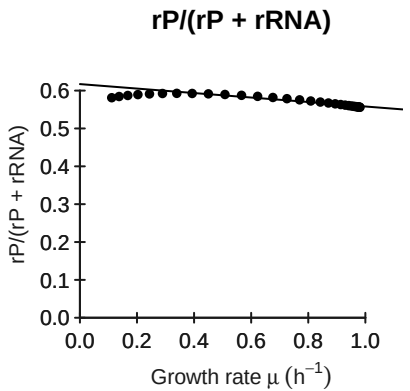

Flux fractions f
Growth rate μ ($h^{-1}$)

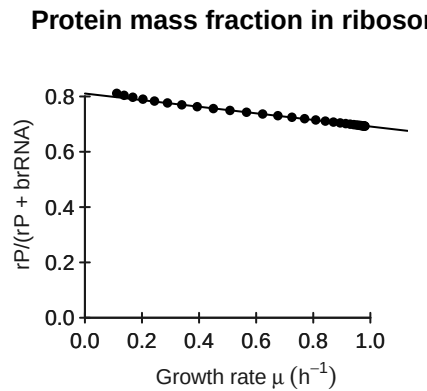

Turnover times τ (h)
tC
ATPS
EAA
ENT
RNAp
DNAp
r
Growth rate μ ($h^{-1}$)

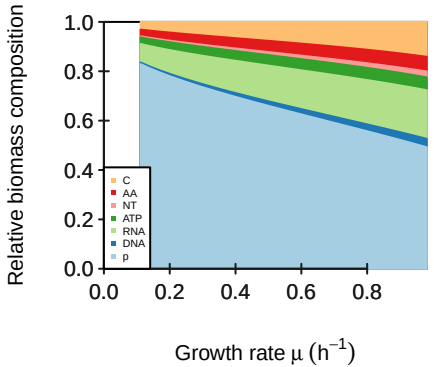

Apparent turnover numbers $k_{app}$ ($h^{-1}$)
Growth rate μ ($h^{-1}$)

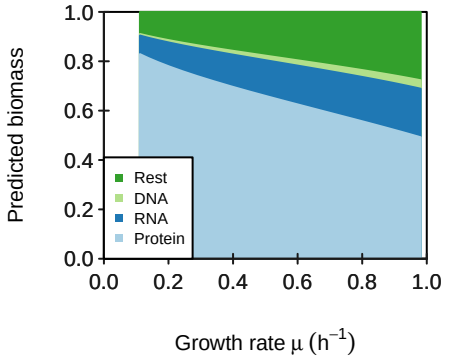

RNA/P
RNA/P
Growth rate μ ($h^{-1}$)

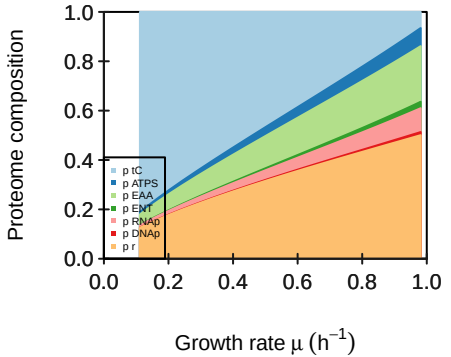

rRNA/rP
rRNA/rP
Growth rate μ ($h^{-1}$)

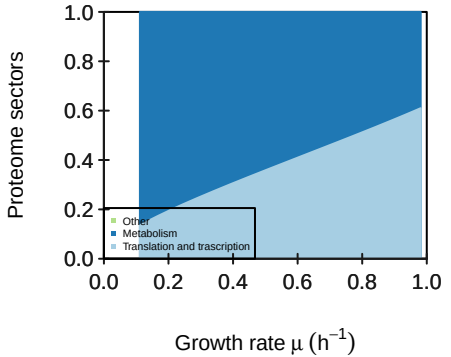

rP/(rP + rRNA)
rP/(rP + rRNA)
Growth rate μ ($h^{-1}$)


Protein mass fraction in ribosome
rP/(rP + brRNA)
Growth rate μ ($h^{-1}$)


Relative biomass composition
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
C
AA
NT
ATP
RNA
DNA
p
Growth rate μ (h−1)


Predicted biomass
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Rest
DNA
RNA
Protein
Growth rate μ (h−1)


Proteome composition
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
p tC
p ATPS
p EAA
p EMT
p RNAp
p DNAp
p r
Growth rate μ (h−1)


Proteome sectors
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Other
Metabolism
Translation and trascription
Growth rate μ (h−1)

keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

**M**

| | tC | ATPS | EAA | ENT | RNAp | DNAp | r |
|---|---|---|---|---|---|---|---|
| **C** | 1 | −1 | −1 | −1 | 0 | 0 | 0 |
| **AA** | 0 | 0 | 1 | 0 | 0 | 0 | −0.9 |
| **NT** | 0 | 0 | 0 | 1 | −1 | −1 | 0 |
| **ATP** | 0 | 1 | 0 | 0 | 0 | 0 | −0.1 |
| **RNA** | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| **DNA** | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| **p** | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

**K**

| | tC | ATPS | EAA | ENT | RNAp | DNAp | r |
|---|---|---|---|---|---|---|---|
| **x_C** | 0.1 | 0 | 0 | 0 | 0 | 0 | 0 |
| **C** | 0 | 11 | 11 | 11 | 0 | 0 | 0 |
| **AA** | 0 | 0 | 0 | 0 | 0 | 0 | 2 |
| **NT** | 0 | 0 | 0 | 0 | 1 | 1 | 0 |
| **ATP** | 0 | 0 | 0 | 0 | 0 | 0 | 2 |
| **RNA** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **DNA** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **p** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**KA**

| | tC | ATPS | EAA | ENT | RNAp | DNAp | r |
|---|---|---|---|---|---|---|---|
| **x_C** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **C** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **AA** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **NT** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **ATP** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **RNA** | 0 | 0 | 0 | 0 | 0 | 0 | 40 |
| **DNA** | 0 | 0 | 0 | 0 | 4 | 4 | 0 |
| **p** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

## kcat

| | tC | ATPS | EAA | ENT | RNAp | DNAp | r |
|---|---|---|---|---|---|---|---|
| **kcatf** | 33.6 | 3.6 | 5.8 | 25.5 | 6.9 | 9.2 | 4.6 |
| **kcatb** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Keq**

| | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] |
|---|---|---|---|---|---|---|---|
| **[1,]** | Inf | Inf | Inf | Inf | Inf | Inf | Inf |

**phi input**

| | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] |
|---|---|---|---|---|---|---|---|
| **[1,]** | 0.065 | 0.069 | 0.248 | 0.035 | 0.119 | 0.003 | 0.461 |

**average saturation input**

3

**minimal phi constraint**

| | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] |
|---|---|---|---|---|---|---|---|
| **[1,]** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**minimal f constraint**

| | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] |
|---|---|---|---|---|---|---|---|
| **[1,]** | 0 | 0 | 0 | 0 | 0 | 0 | 0 |