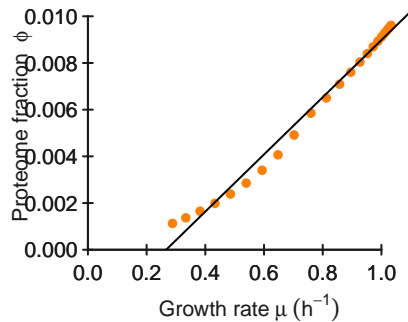
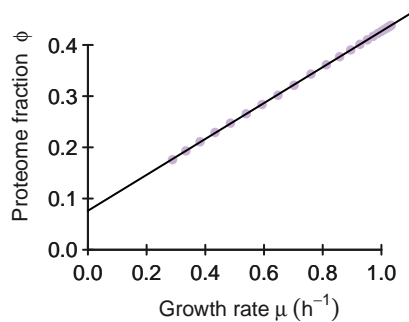


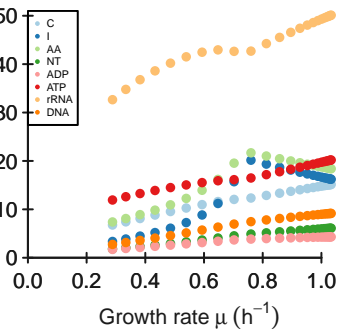
DNAp



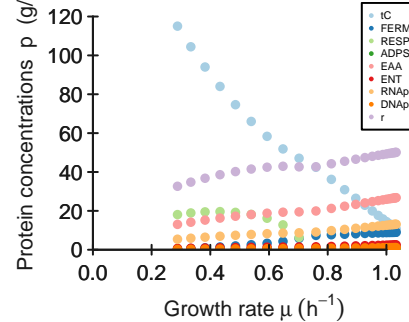
r



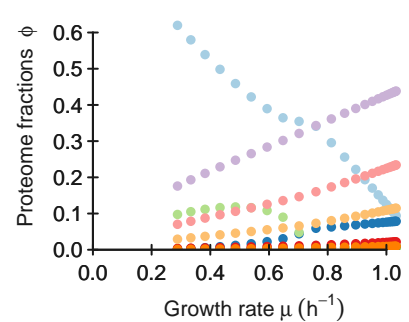
Metabolite concentrations c^m (g/L)



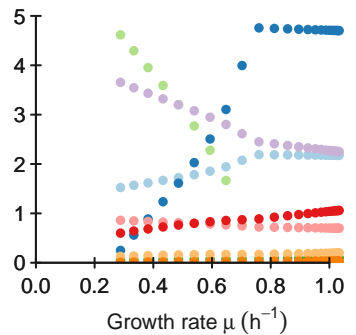
Protein concentrations p (g/L)



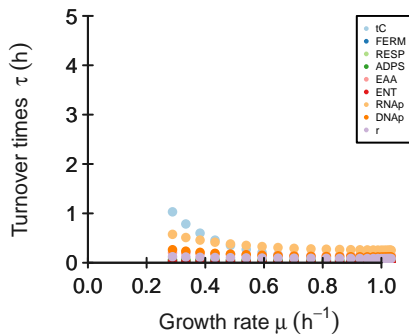
Proteome fractions ϕ



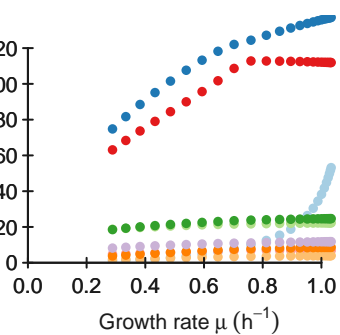
Flux fractions f



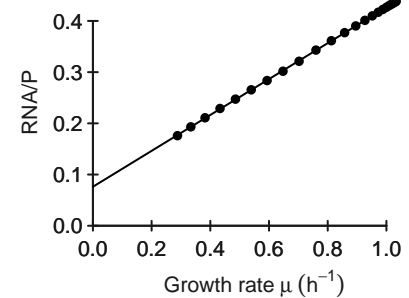
Turnover times τ (h)



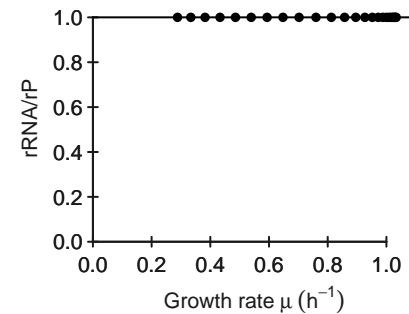
Apparent turnover numbers k_{app} (h^{-1})



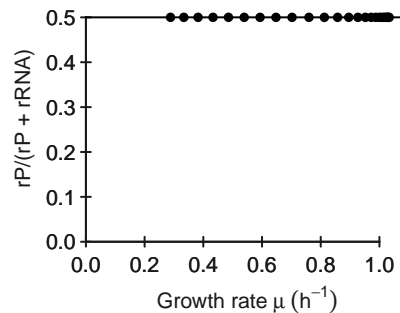
RNA/P



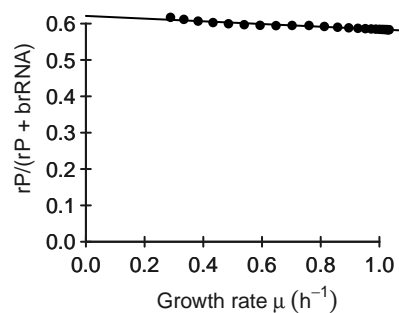
rRNA/rP



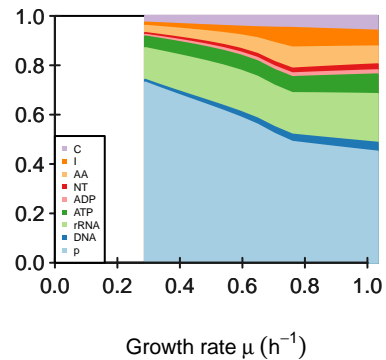
$rP/(rP + rRNA)$



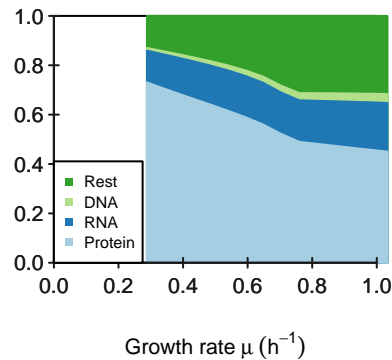
Protein mass fraction in ribosome



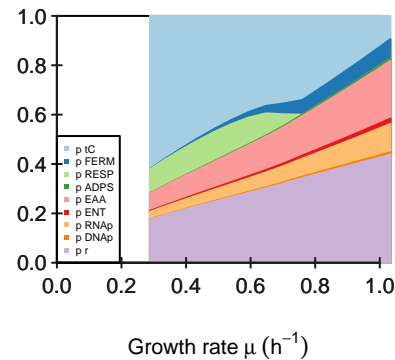
Relative biomass composition



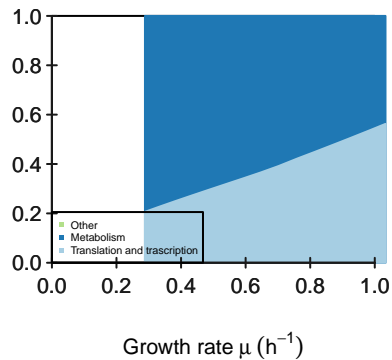
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

Keq

| | | | | | | | | | |
|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| [1,] | [,1] Inf | [,2] Inf | [,3] Inf | [,4] Inf | [,5] Inf | [,6] Inf | [,7] Inf | [,8] Inf | [,9] Inf |
|-------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|

phi input

| | | | | | | | | | |
|------|-------|-------|-------|-------|-------|-------|-------|-------|------|
| [1,] | [,1] | [,2] | [,3] | [,4] | [,5] | [,6] | [,7] | [,8] | [,9] |
| | 0.065 | 0.035 | 0.035 | 0.003 | 0.248 | 0.032 | 0.119 | 0.003 | 0.46 |

average saturation input

3

minimal phi constraint

[illegible]

