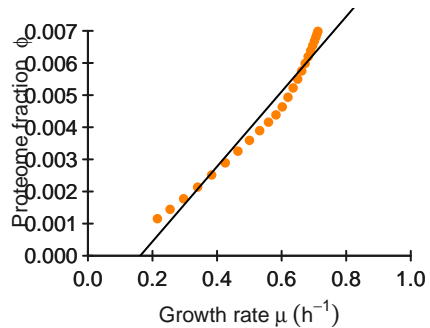
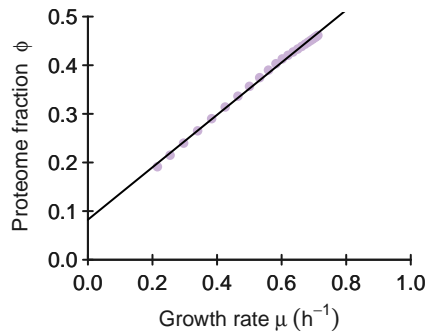
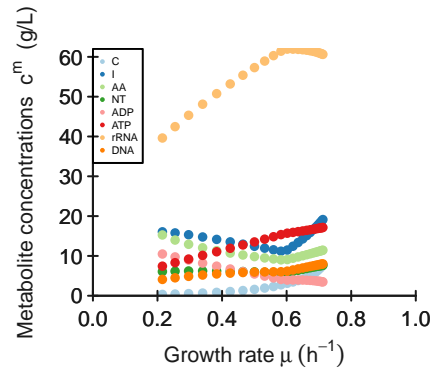
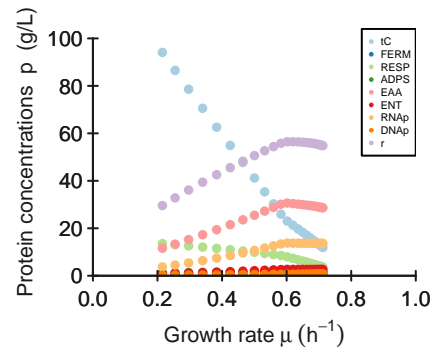
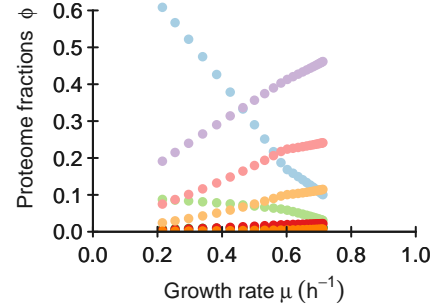
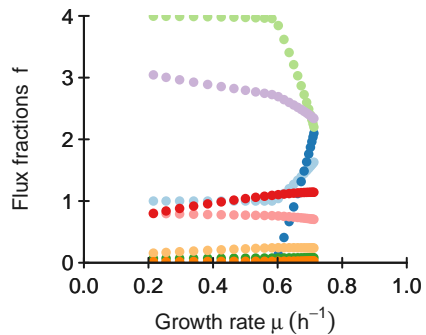
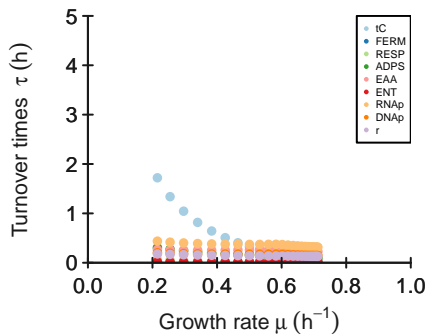
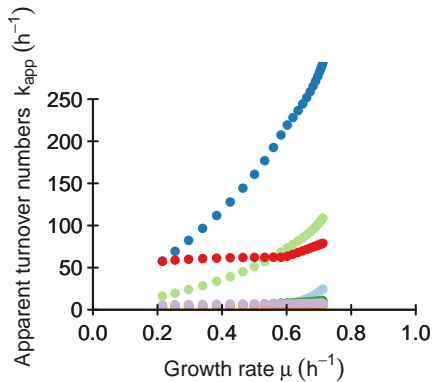
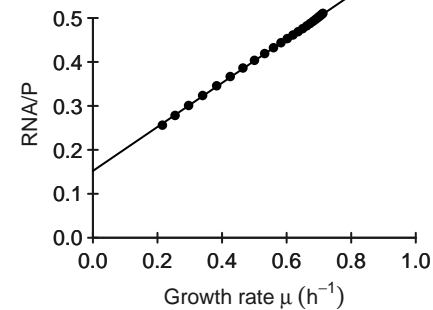
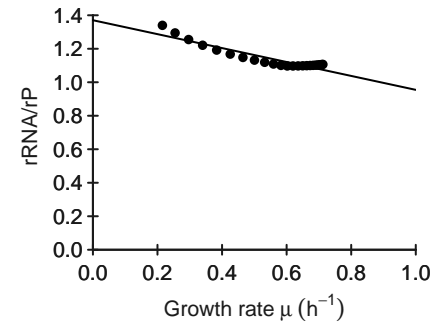
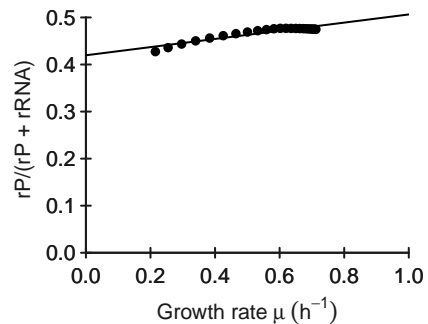
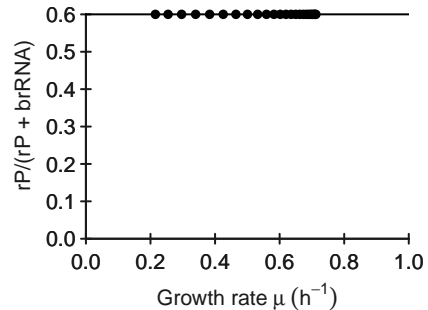


**DNAp****r**Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Flux fractions  $f$ Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )**RNA/P****rRNA/rP**

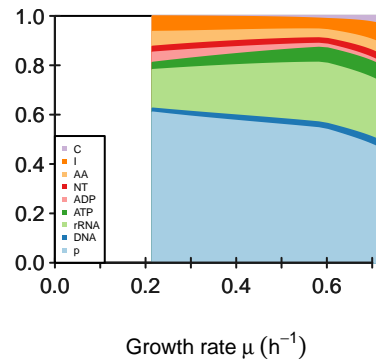
**$rP/(rP + rRNA)$**



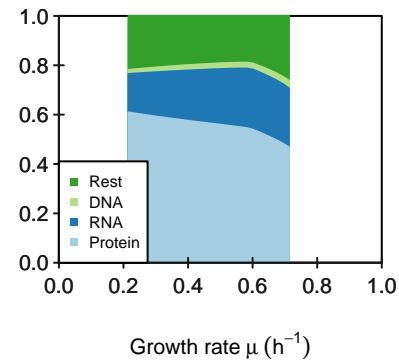
**Protein mass fraction in ribosome**



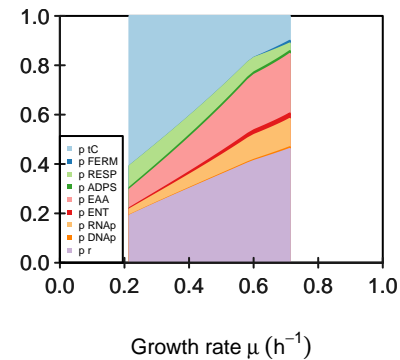
Relative biomass composition



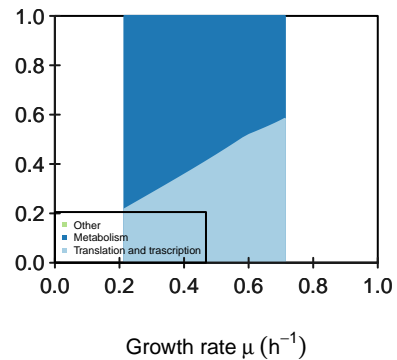
Predicted biomass



Proteome composition



Proteome sectors



keep\_ribosome\_kcat FALSE  
keep\_transport\_kcat FALSE  
maintenance\_fun constant

# M

[illegible]

**K**

[illegible]



## kcat

|       | tC | FERM | RESP | ADPS | EAA | ENT | RNAp | DNAp | r  |
|-------|----|------|------|------|-----|-----|------|------|----|
| kcatf | 29 | 730  | 365  | 26   | 7   | 149 | 6    | 13   | 19 |
| kcatb | 3  | 73   | 36   | 3    | 1   | 15  | 0    | 0    | 0  |



## Keq

| [1,] | [,1] | [,2] | [,3]             | [,4]             | [,5] | [,6]             | [,7] | [,8] | [,9] |
|------|------|------|------------------|------------------|------|------------------|------|------|------|
|      | 1160 | 200  | 202.777777777778 | 4.33333333333333 | 14   | 1.65555555555556 | Inf  | Inf  | 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]

