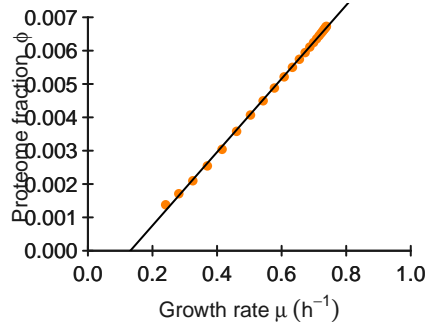
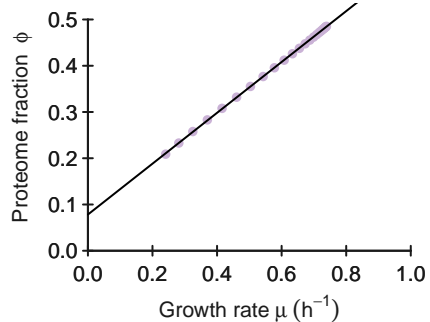


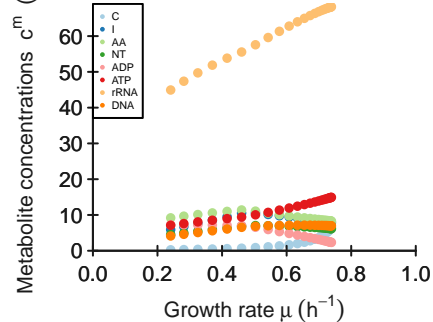
DNAp



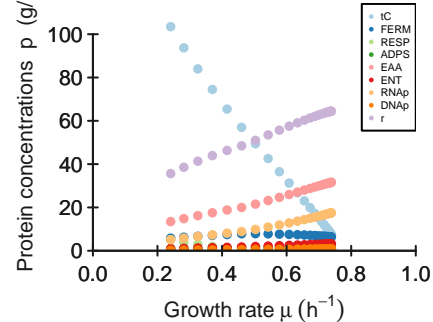
r



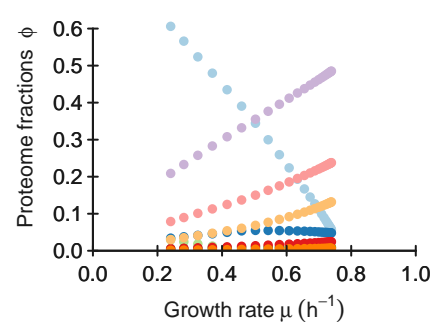
Metabolite concentrations c^m (g/L)



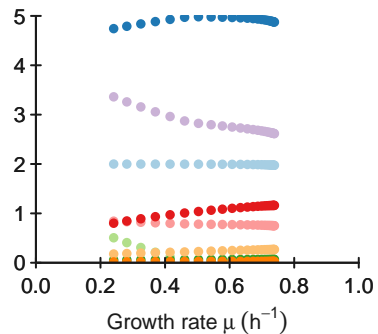
Protein concentrations p (g/L)



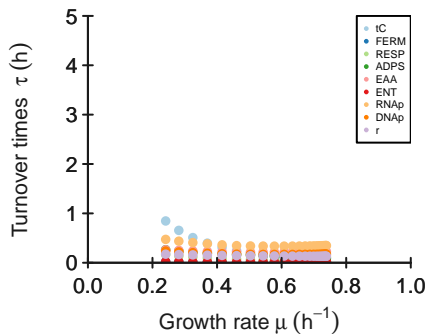
Proteome fractions ϕ



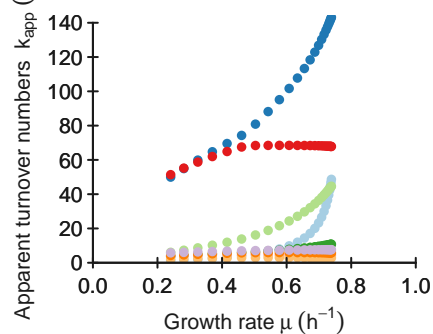
Flux fractions f



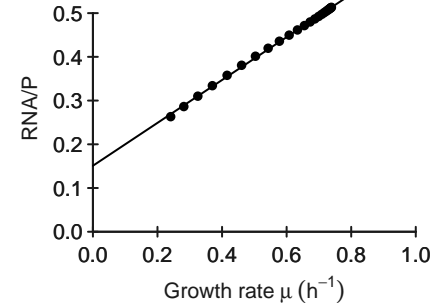
Turnover times τ (h)



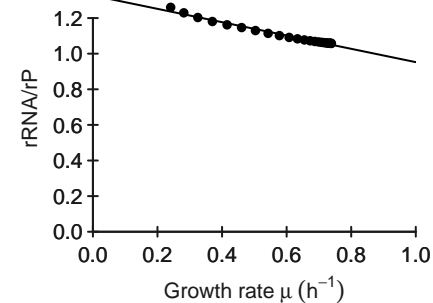
Apparent turnover numbers k_{app} (h^{-1})

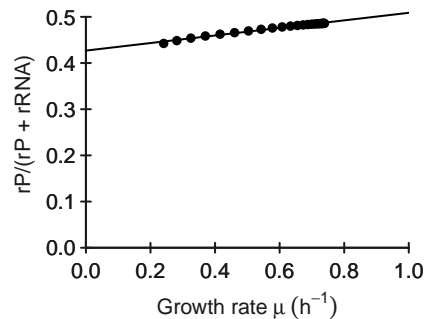
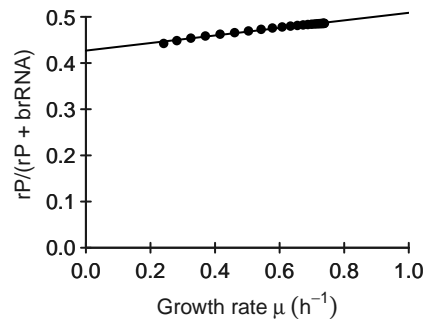
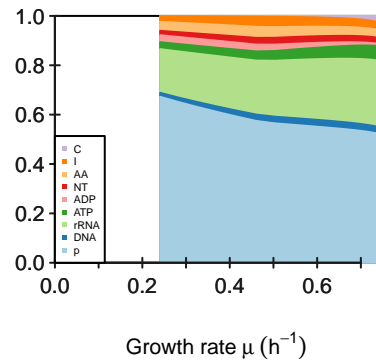
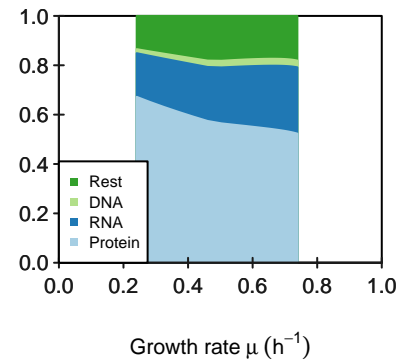
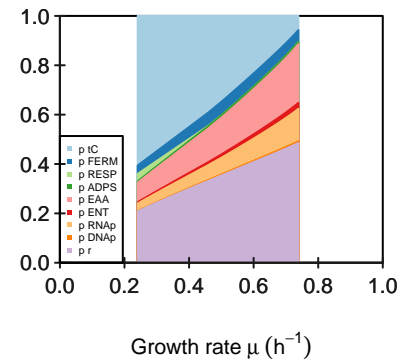
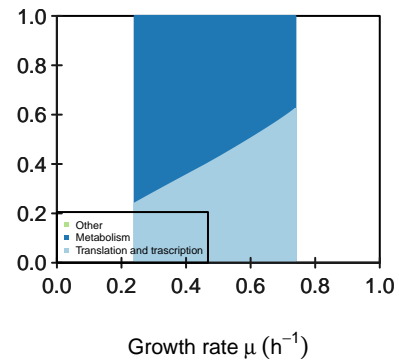


RNA/P



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]

K

[illegible]

kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAP	r
kcatf	56	254	169.33333333333333	24	7	123	6	12	17
kcatb	6	25	17	2	1	12	0	0	0

Keq

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]
	1306.666666666667	162.56	159.372549019608	6	28	7.6875	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

4

minimal f constraint

[illegible]