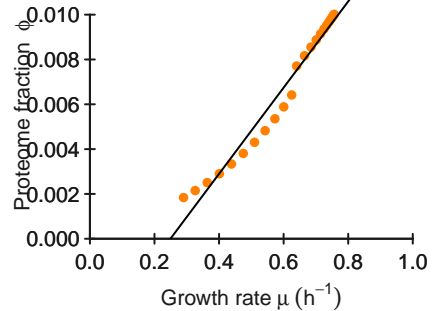
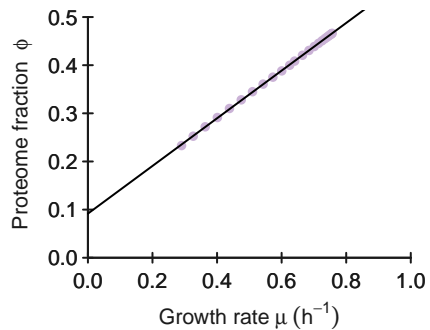


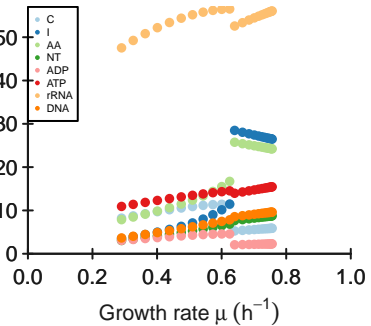
DNAp



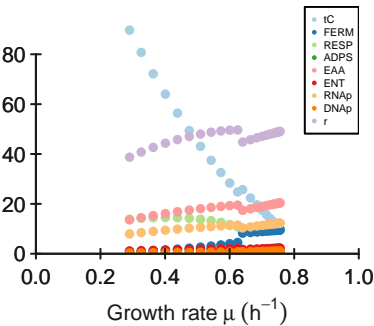
r



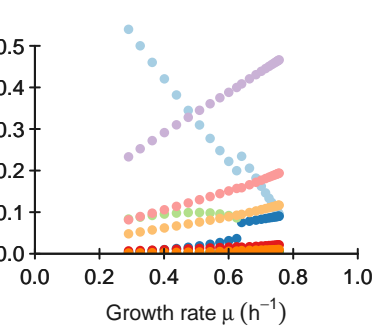
Metabolite concentrations c^m (g/L)



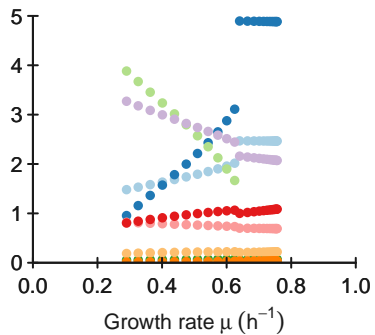
Protein concentrations p (g/L)



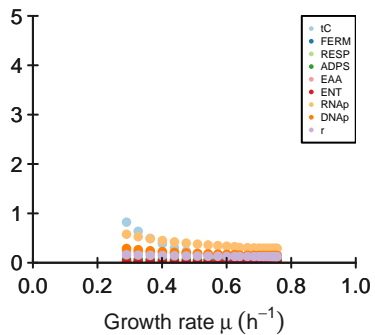
Proteome fractions ϕ



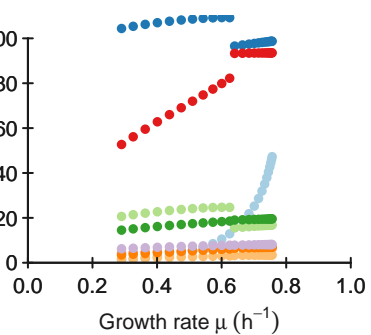
Flux fractions f



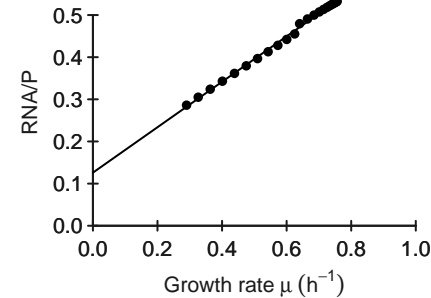
Turnover times τ (h)



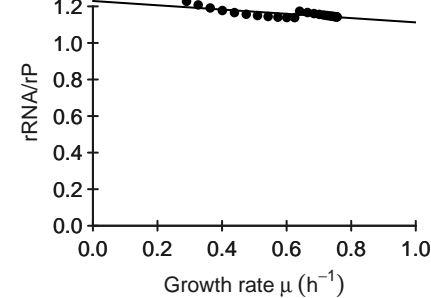
Apparent turnover numbers k_{app} (h^{-1})



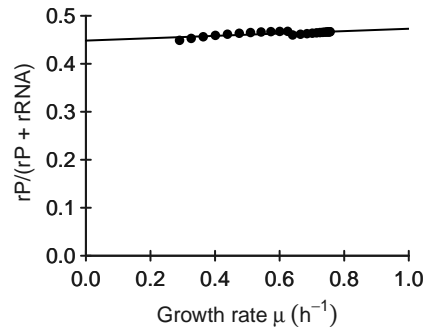
RNA/P



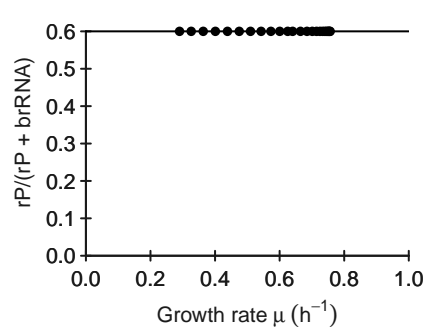
rRNA/rP



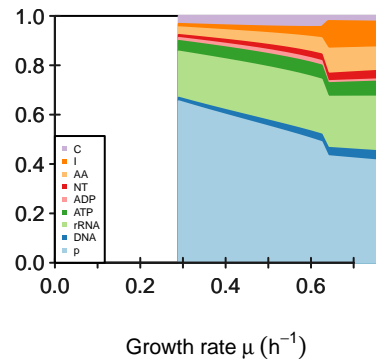
$rP/(rP + rRNA)$



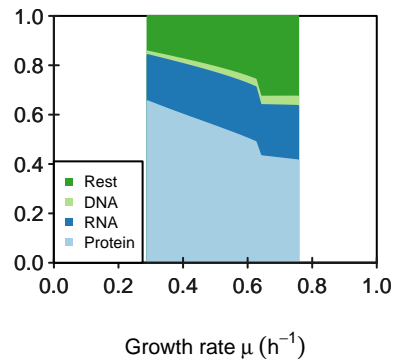
Protein mass fraction in ribosome



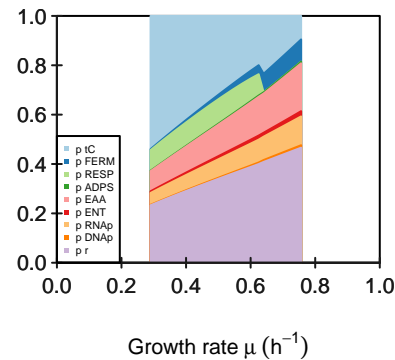
Relative biomass composition



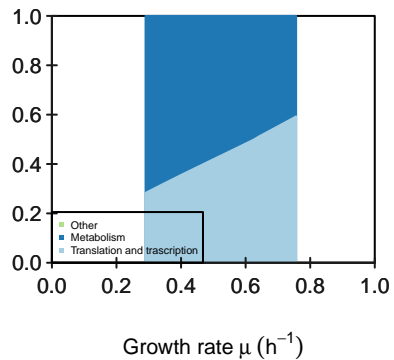
Predicted biomass



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	52	122	40.66666666666667	7	24	7	123	6	12	17
kcatb	0	0		0	0	0	0	0	0	0

Keq

[1,]	[,1] Inf	[,2] Inf	[,3] Inf	[,4] Inf	[,5] Inf	[,6] Inf	[,7] Inf	[,8] Inf	[,9] Inf
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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 phi constraint

[illegible]

minimal f constraint

[illegible]