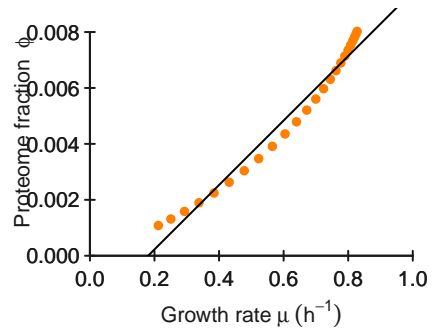
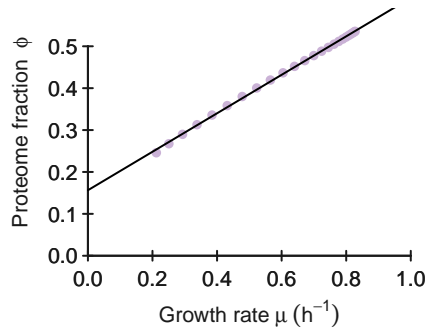


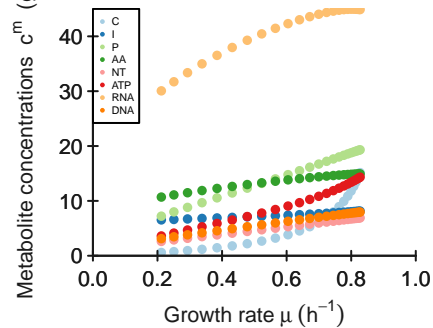
DNAP



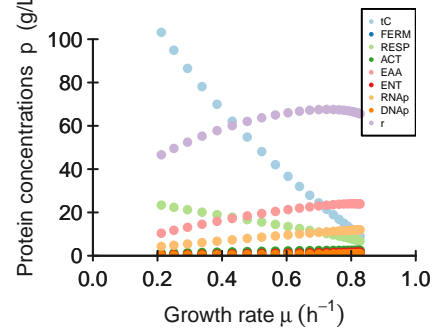
r



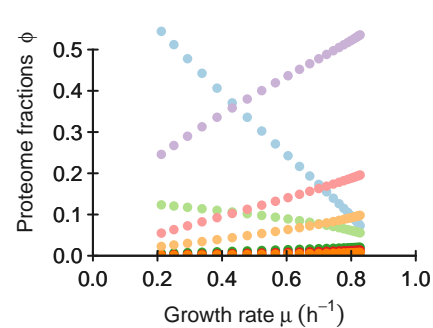
Metabolite concentrations c^m (g/L)



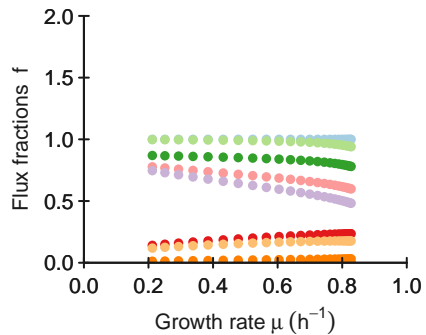
Protein concentrations p (g/L)



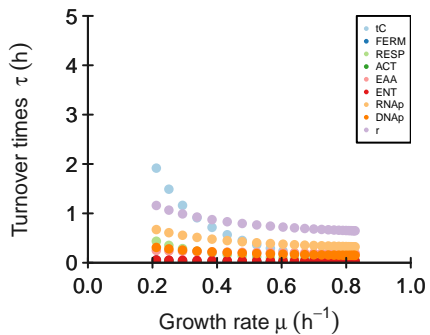
Proteome fractions ϕ



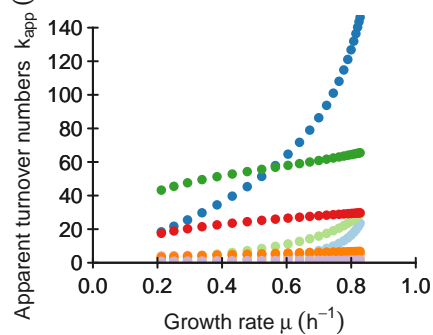
Flux fractions f



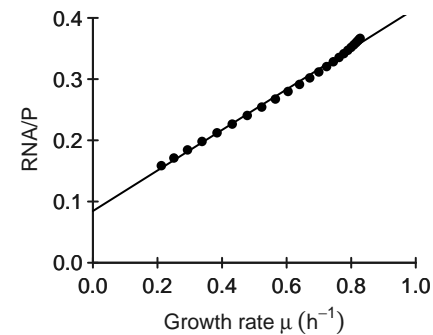
Turnover times τ (h)



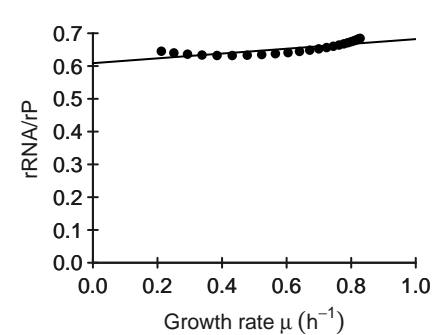
Apparent turnover numbers k_{app} (h^{-1})



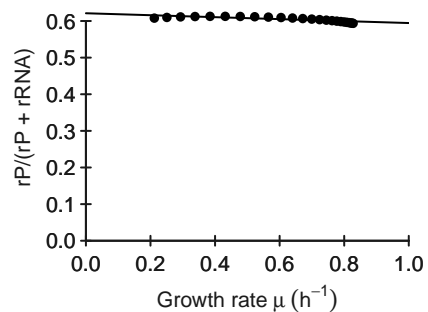
RNA/P



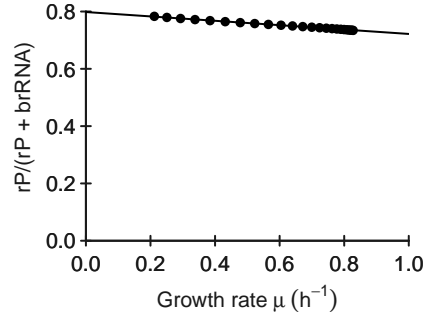
rRNA/rP



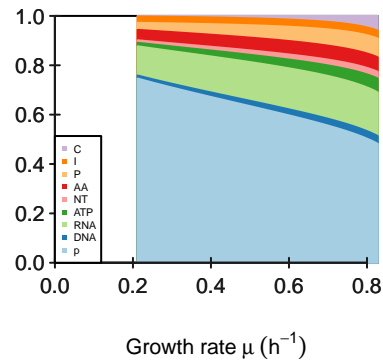
$rP/(rP + rRNA)$



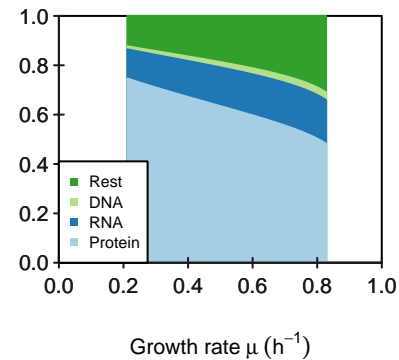
Protein mass fraction in ribosome



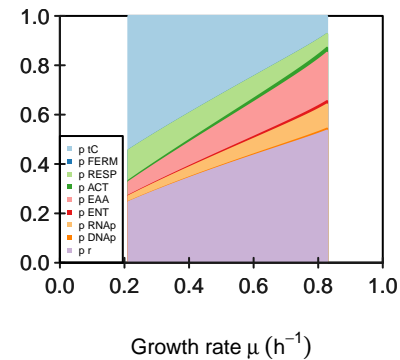
Relative biomass composition



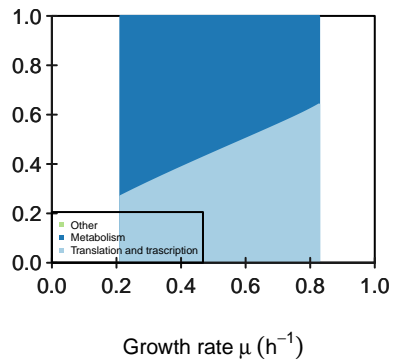
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

KA[illegible]

kcat

	tC	FERM	RESP	ACT	EAA	ENT	RNAp	DNAp	r
kcatf	29	500	100	115	7	45	6	13	4
kcatb	3	50	10	12	1	4	0	0	0

Keq

[1,]	1256.666666666667	[,1]	[,2]	[,3]	9.583333333333333	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
		840	168		28	5.625	Inf	Inf	Inf		

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.065	0.024	0.024	0.024	0.248	0.032	0.12	0.003	0.46

average saturation input

3

minimal phi constraint

[illegible]

minimal f constraint

[illegible]