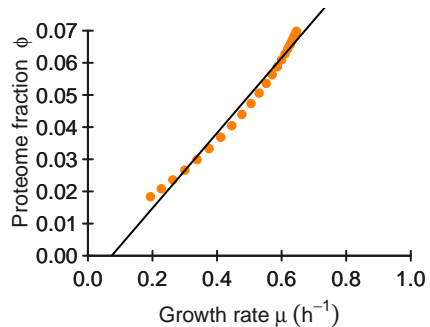
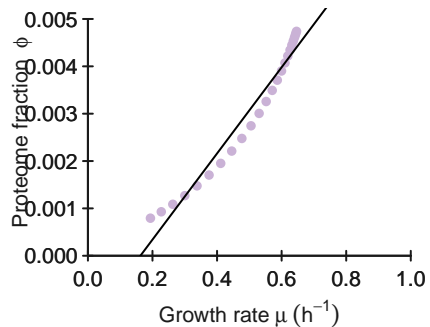


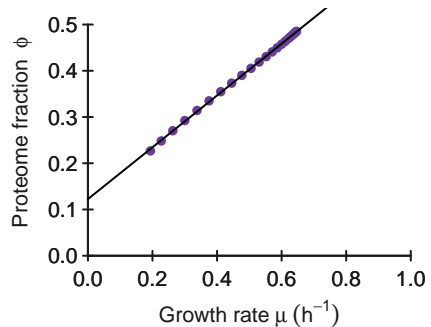
RNAP



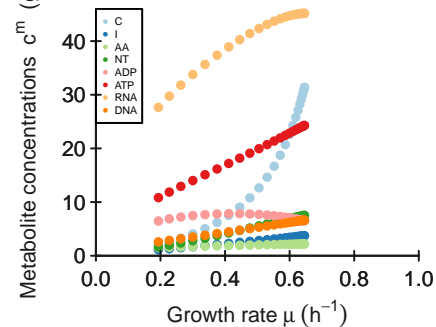
DNAp



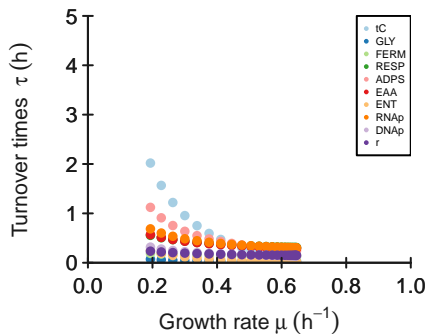
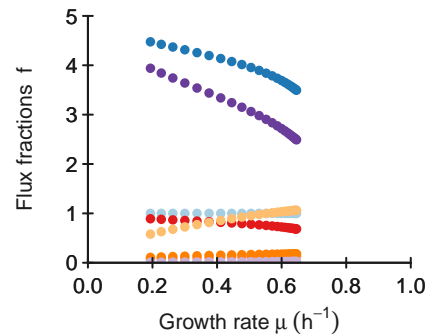
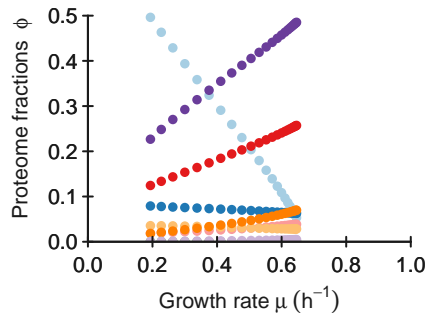
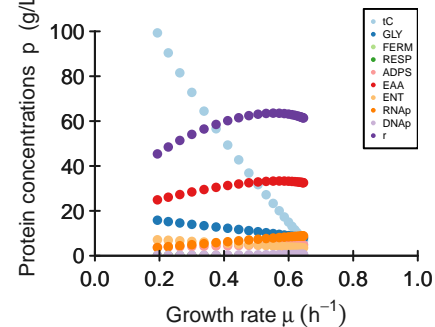
r



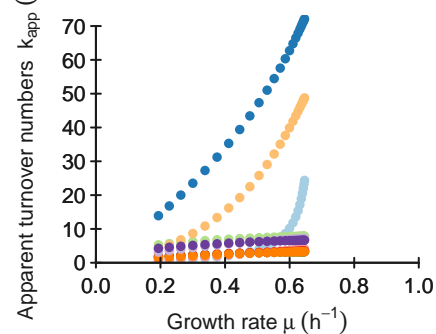
Metabolite concentrations c^m (g/L)



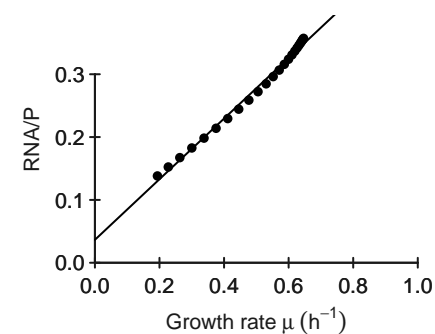
Protein concentrations p (g/L)



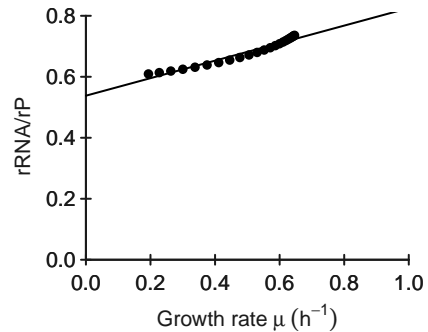
Apparent turnover numbers k_{app} (h^{-1})



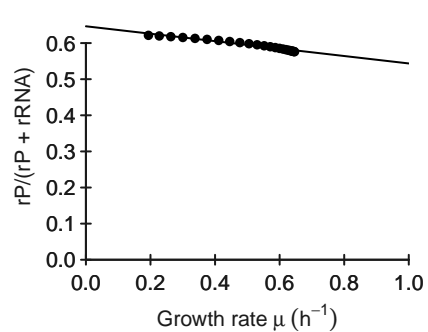
RNA/P



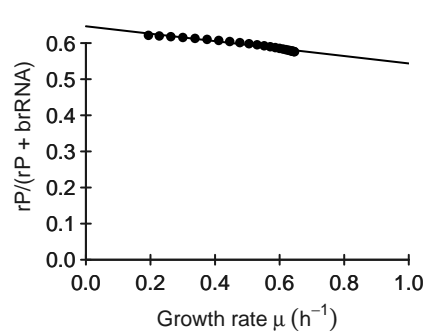
rRNA/rP



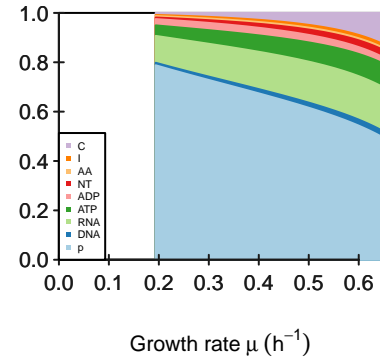
rP/(rP + rRNA)



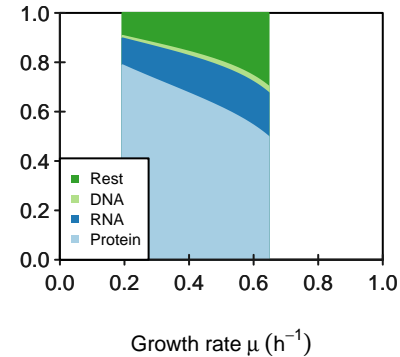
Protein mass fraction in ribosome



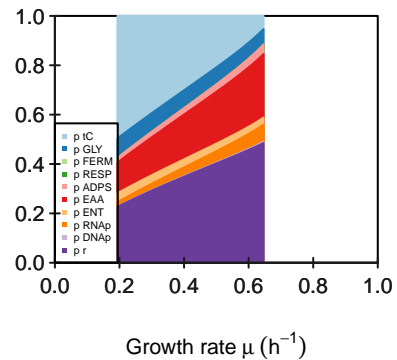
Relative biomass composition



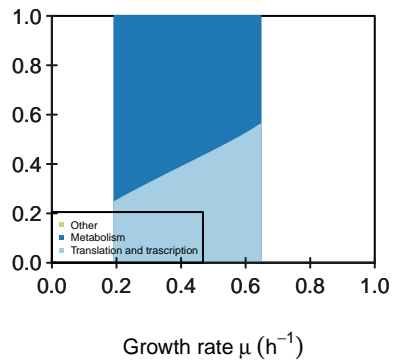
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	GLY	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	29	386	10	5	9	7	133	6	13	19
kcatb	3	39	1	1	1	1	13	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
3770	2.28402366863905	100	50	9	7	0.78698224852071	Inf	Inf	Inf	

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
	0.065	0.03	0.005	0.035	0.003	0.248	0.032	0.119	0.003	0.46

average saturation input

3

minimal phi constraint

[illegible]

minimal f constraint

[illegible]