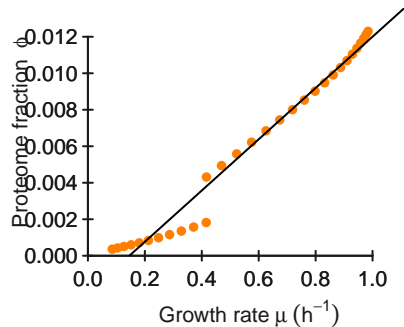
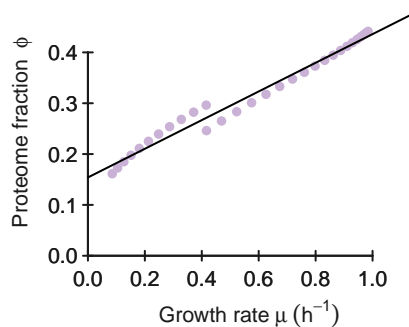


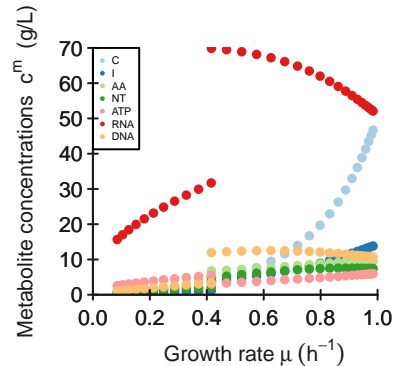
DNAp



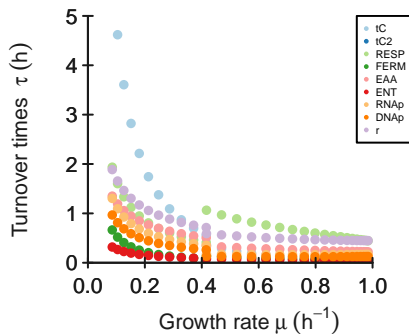
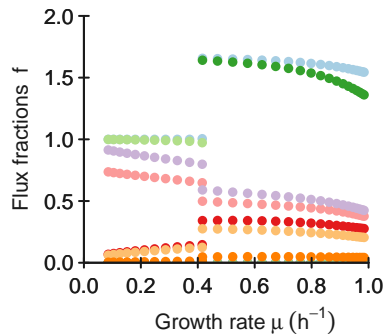
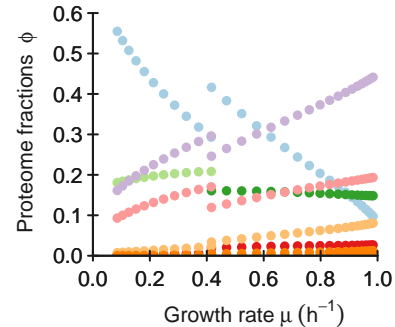
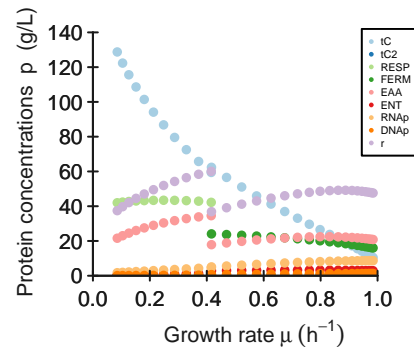
r



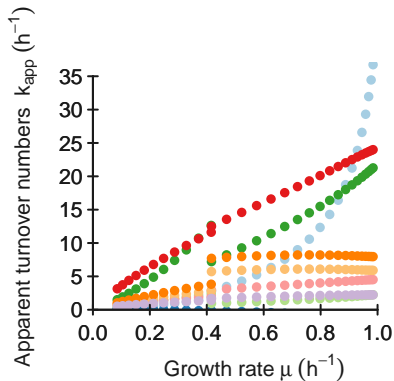
Metabolite concentrations c^m (g/L)



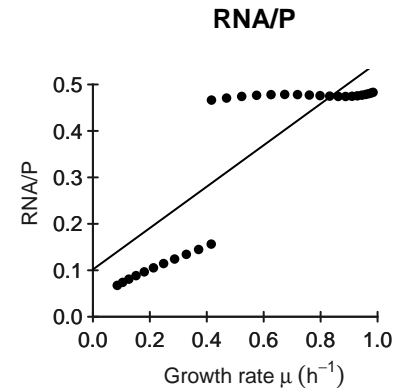
Protein concentrations p (g/L)



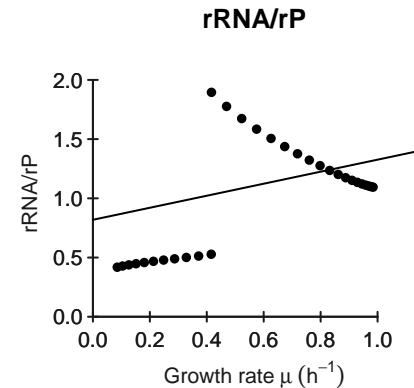
Apparent turnover numbers k_{app} (h^{-1})



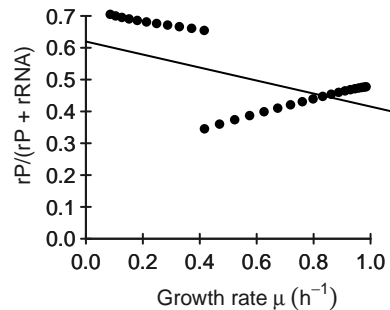
RNA/P



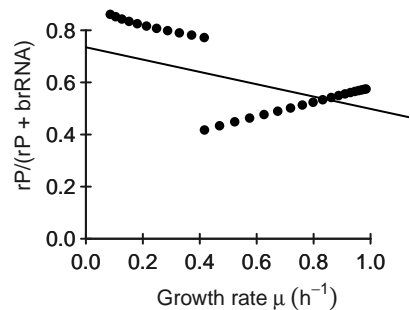
rRNA/rP



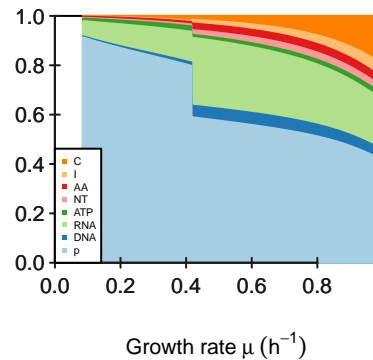
$rP/(rP + rRNA)$



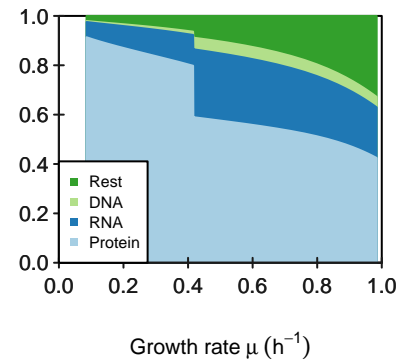
Protein mass fraction in ribosome



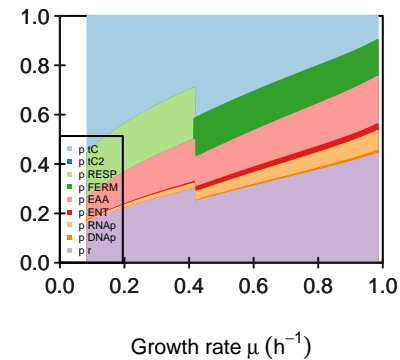
Relative biomass composition



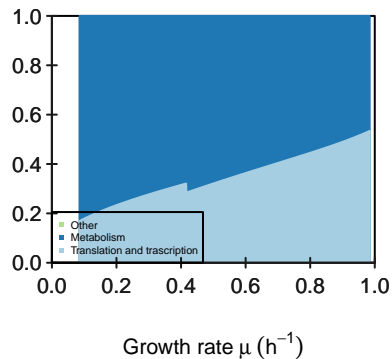
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
kcatf	48.2	15.5	11.7	58.3	6.1	46.5	9.2	12.4	6.1
kcatb	5	2	1	6	1	5	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
2410	1937.5	9.36	38.86666666666667	18.3	6.975	Inf	Inf	Inf	

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.06	0.005	0.065	0.004	0.248	0.035	0.119	0.003	0.461

average saturation input

3

minimal phi constraint

[illegible]

minimal f constraint

[illegible]