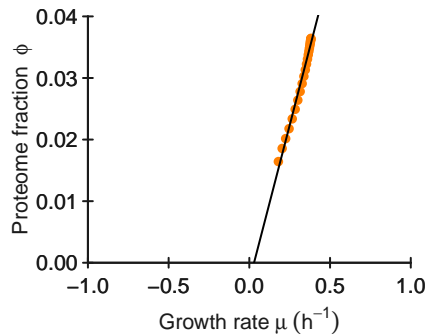
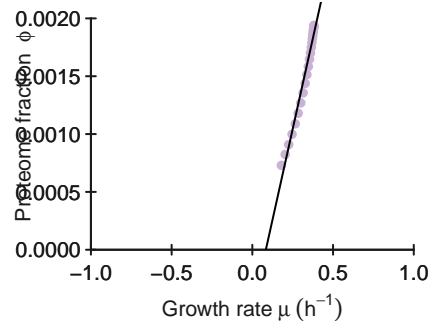


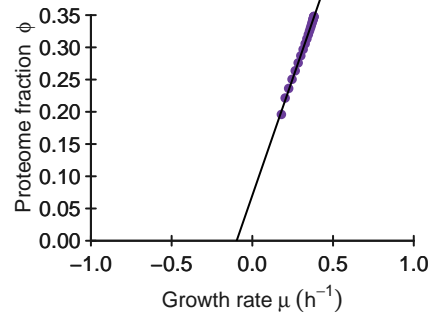
RNAp



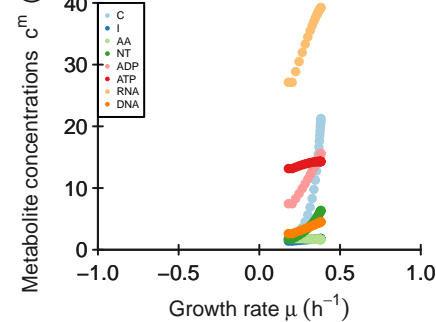
DNAp



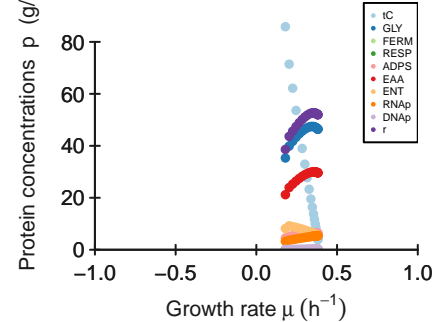
r



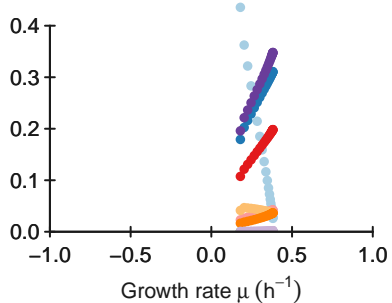
Metabolite concentrations c^m (g/L)



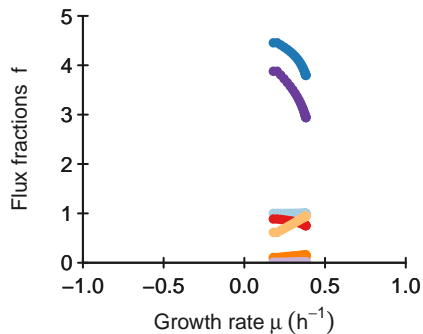
Protein concentrations p (g/L)



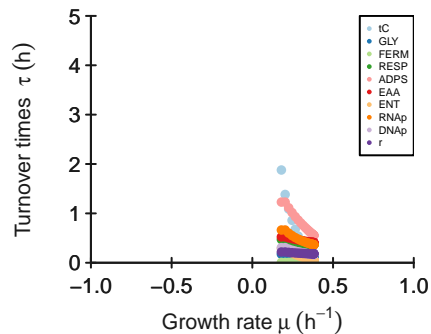
Proteome fractions ϕ



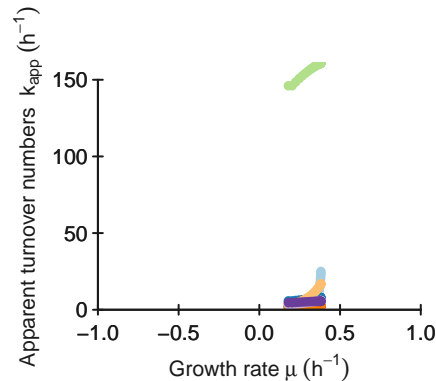
Flux fractions f



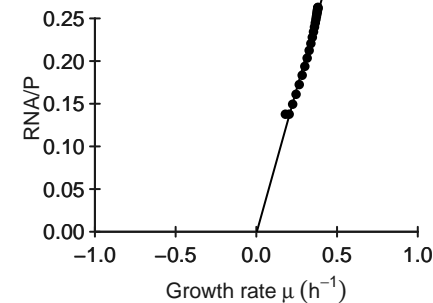
Turnover times τ (h)

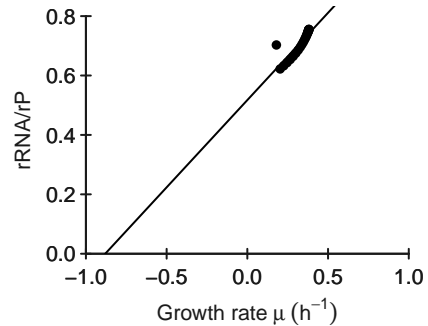
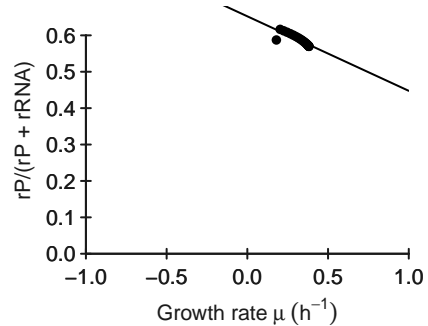
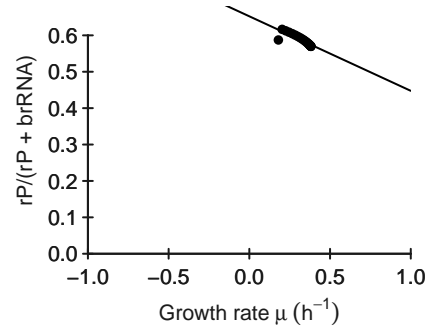
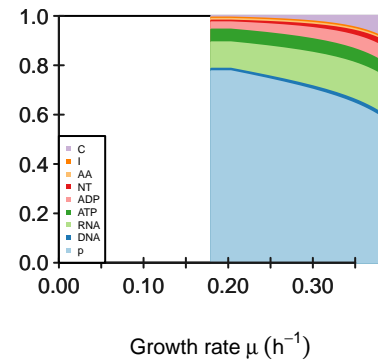
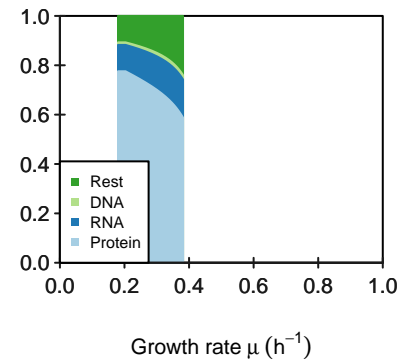
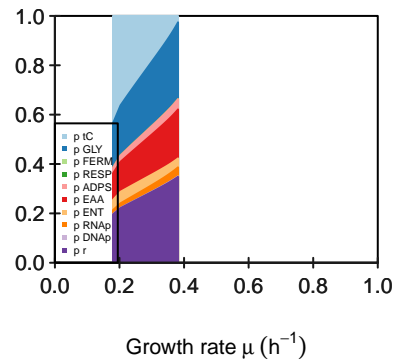
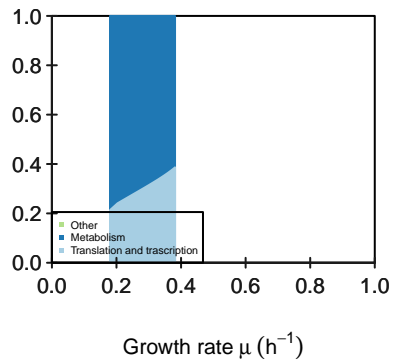


Apparent turnover numbers k_{app} (h^{-1})



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]

KA[illegible]

kcat

	tC	GLY	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	29	15	250	5	9	7	133	6	13	19
kcatb	3	2	25	1	1	1	13	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
	3770	45	100	300	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]