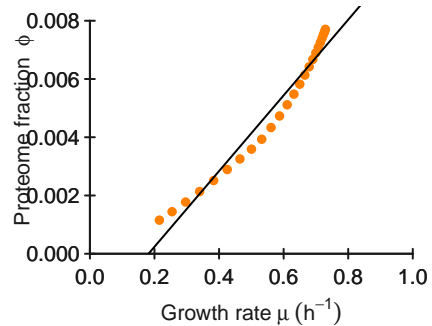
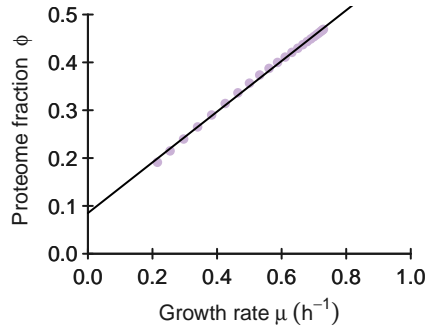
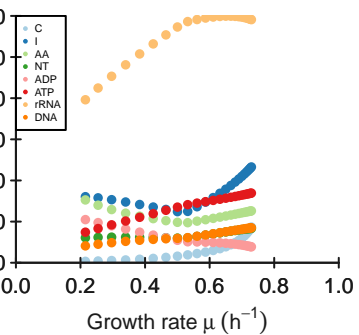
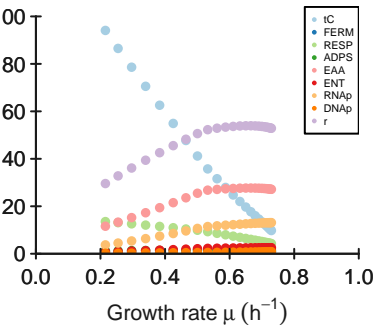
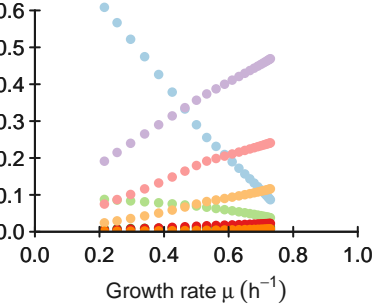
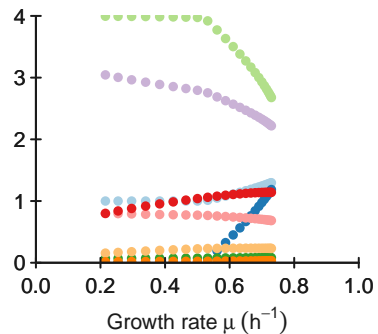
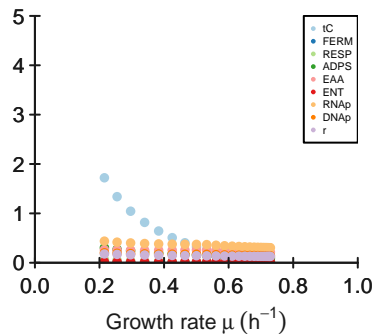
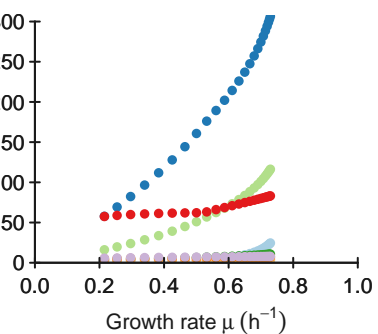
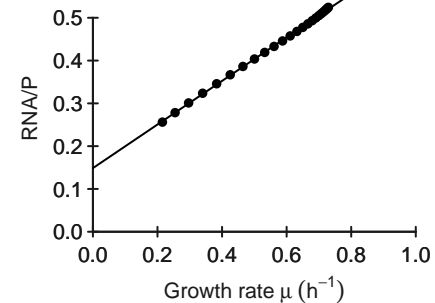
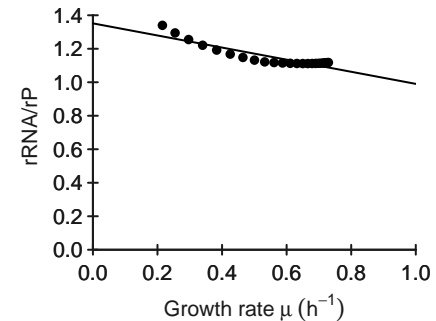
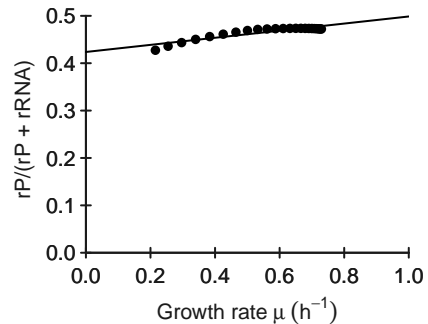
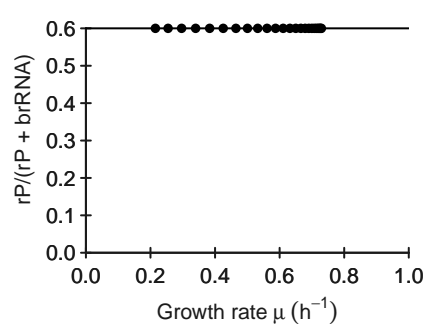


DNAp**r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})**RNA/P****rRNA/rP**

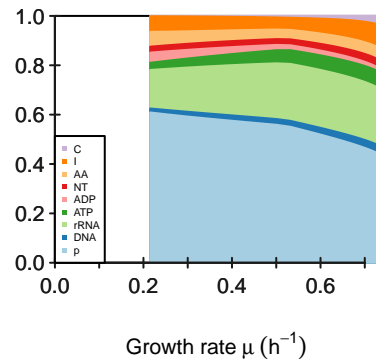
$rP/(rP + rRNA)$



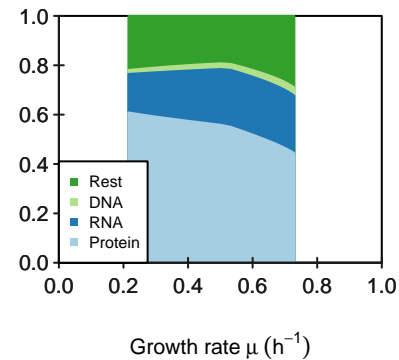
Protein mass fraction in ribosome



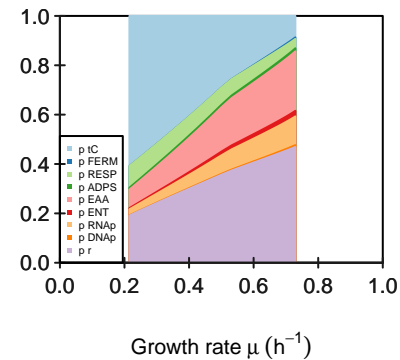
Relative biomass composition



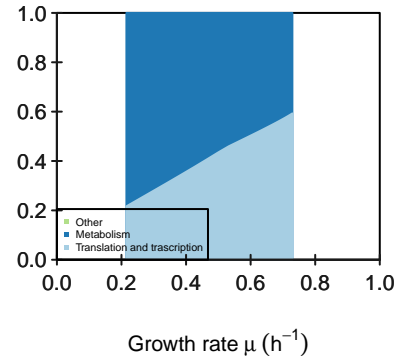
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	29	730	365	26	7	149	6	13	19
kcatb	3	73	36	3	1	15	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	1160	200	202.777777777778	4.33333333333333	14	1.65555555555556	Inf	Inf	Inf

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

3

minimal phi constraint

[illegible]

minimal f constraint

[illegible]