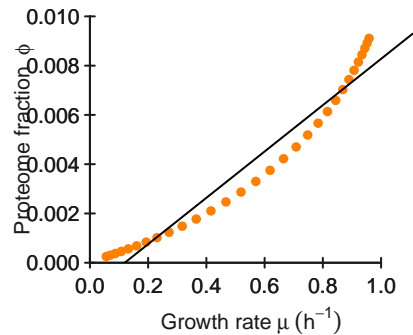
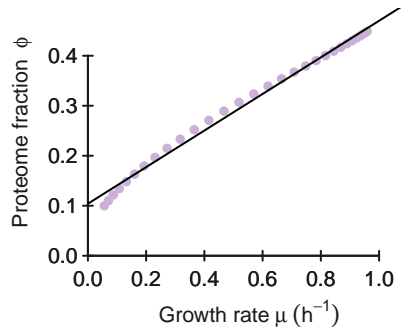
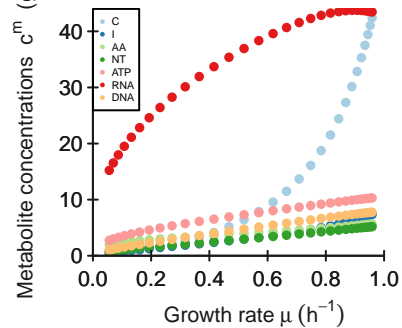
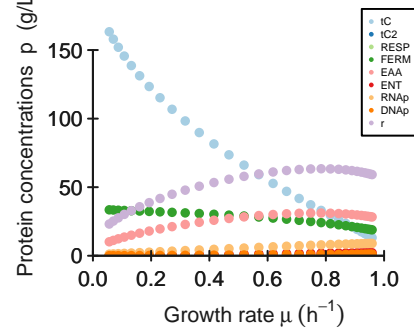
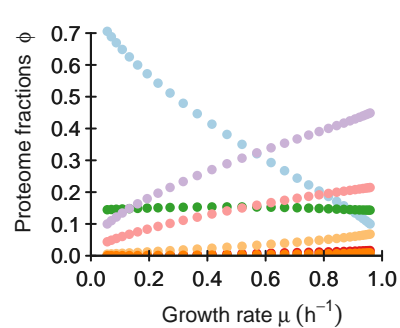
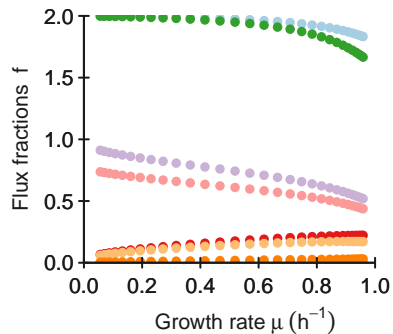
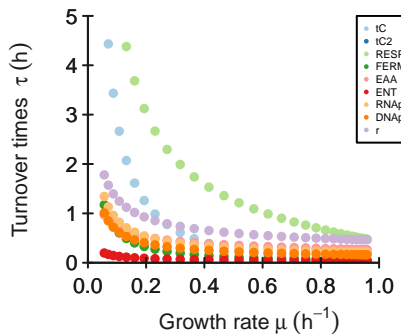
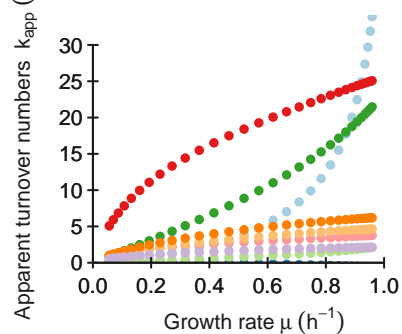
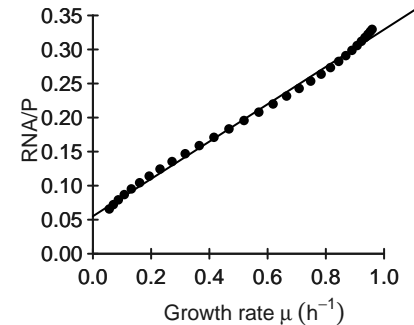
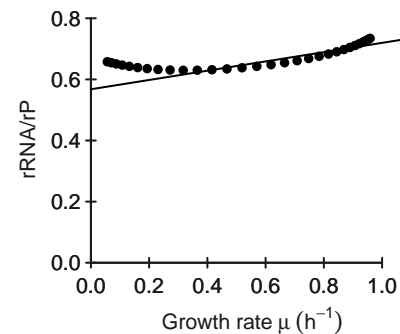
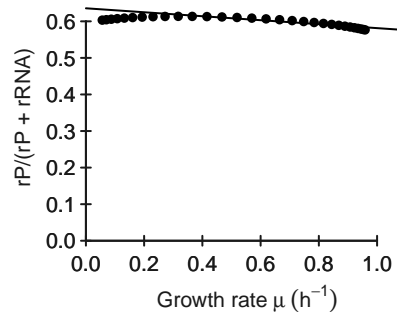
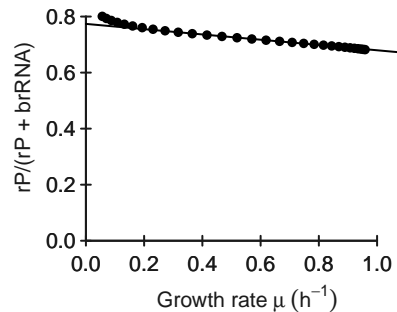


DNAp**r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})**RNA/P****rRNA/rP**

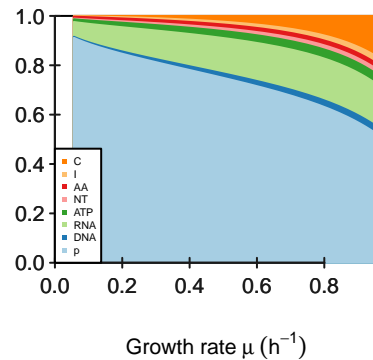
$rP/(rP + rRNA)$



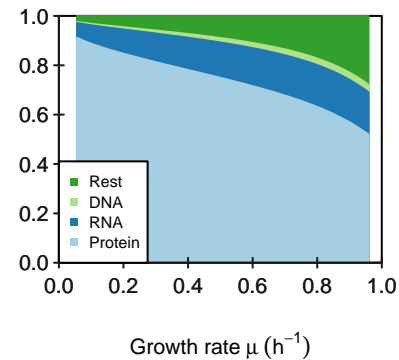
Protein mass fraction in ribosome



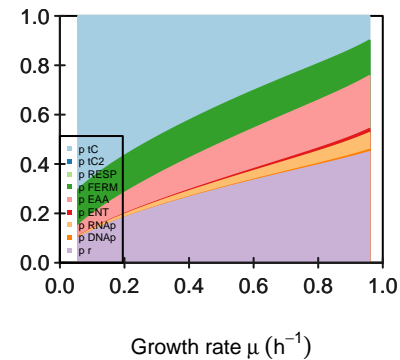
Relative biomass composition



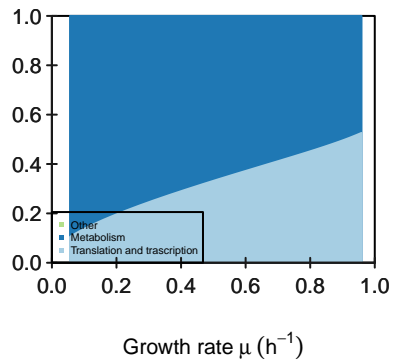
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

KA[illegible]

kcat

	tC	tC2	RESP	FERM	EAA	ENT	RNAp	DNAp	r
kcatf	43.7	14.1	10.6	52.9	5.5	42.2	8.4	11.2	5.5
kcatb	4	1	1	5	1	4	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	2731.25	3525	8.48	42.32	16.5	7.9125	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]

