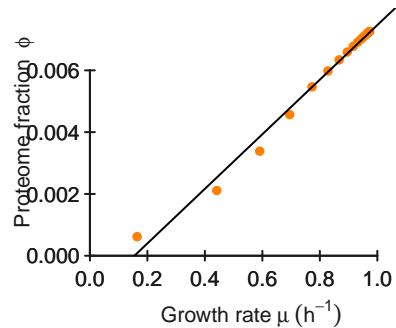
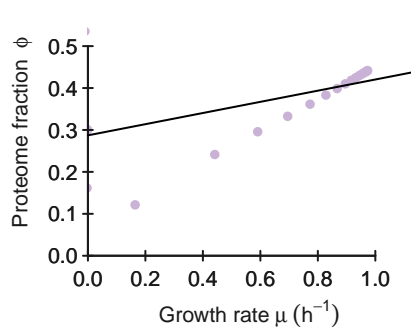
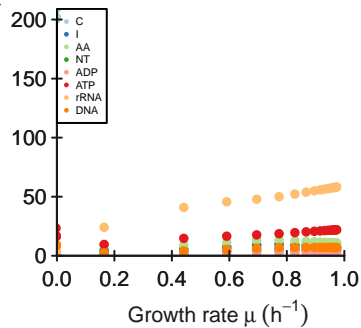
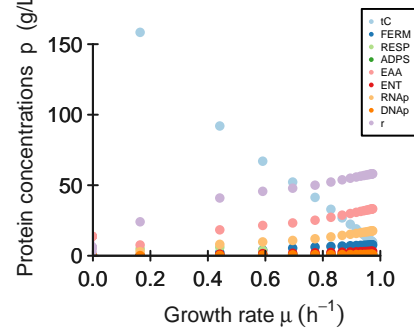
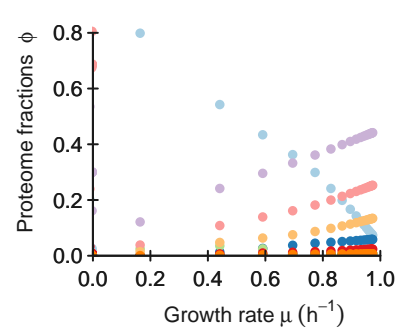
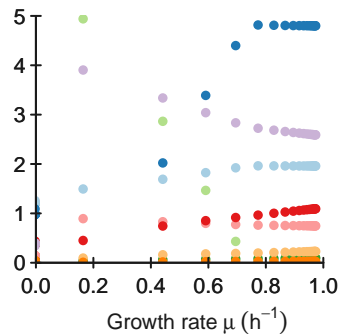
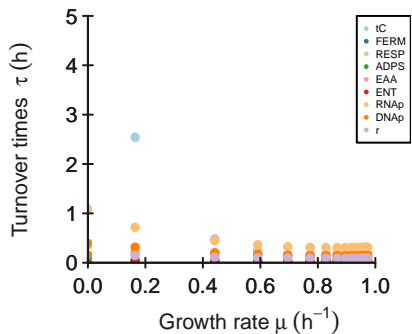
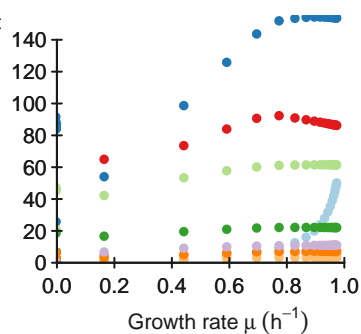
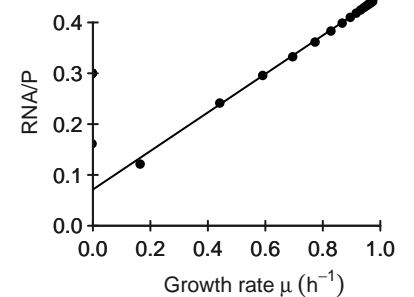
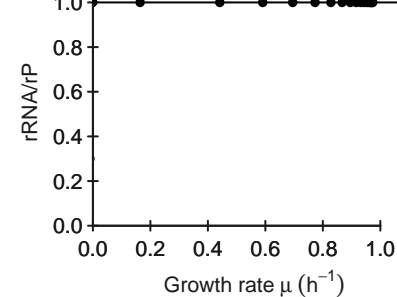
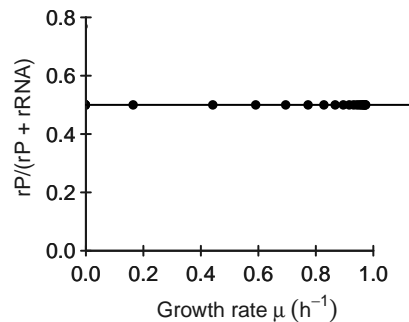
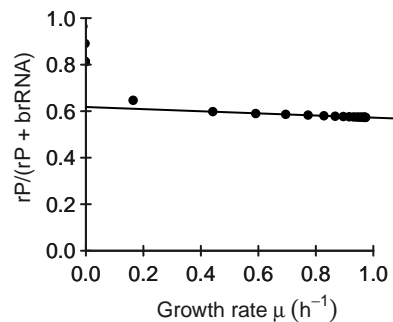


DNAp**r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})**RNA/P****rRNA/rP**

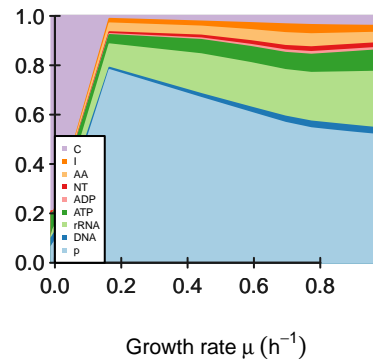
$rP/(rP + rRNA)$



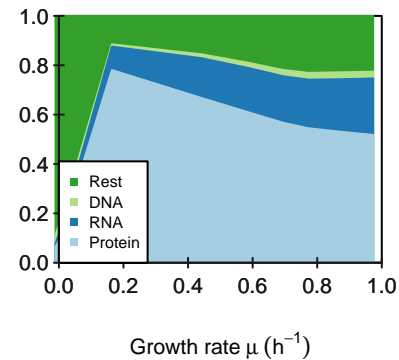
Protein mass fraction in ribosome



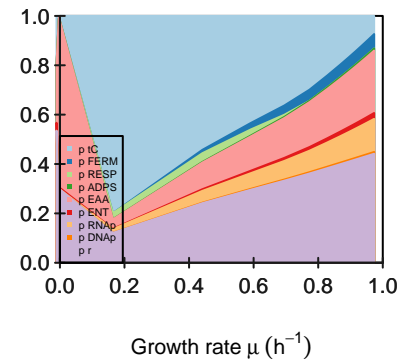
Relative biomass composition



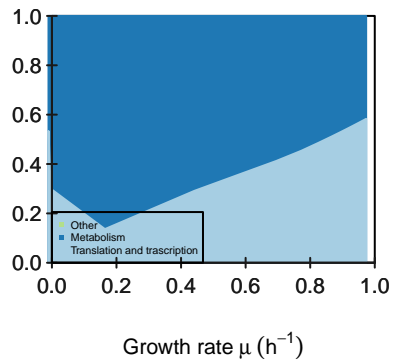
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	55.7	384.1	76.8	27.3	7.4	149.1	6.3	13.7	20
kcatb	6	38	8	3	1	15	1	1	2

Keq

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]
92.83333333333333	12.6348684210526	60	9.1	3.7	0.8283333333333333	6.3	13.7	1.66666666666667	

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]