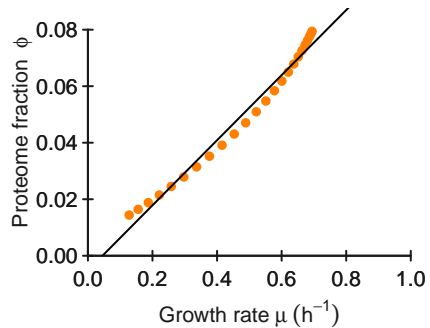
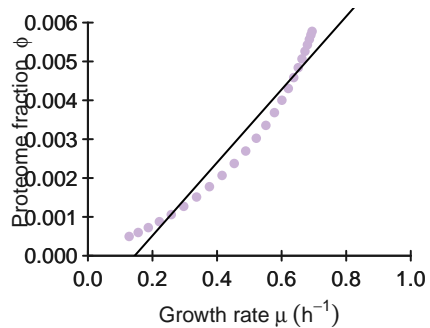


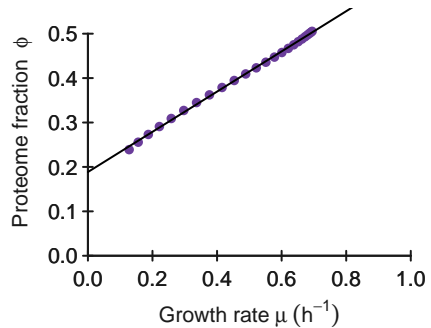
RNAP



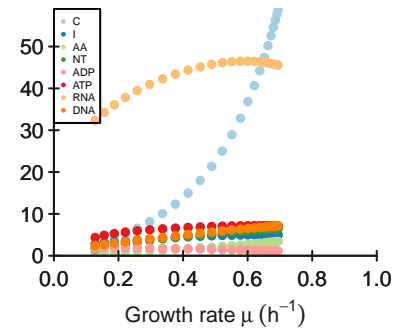
DNAP



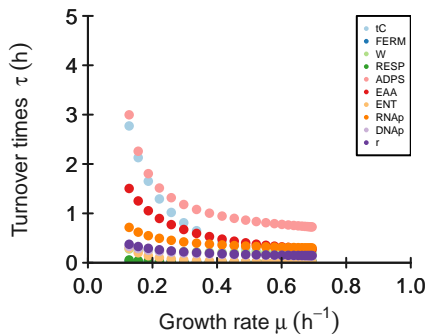
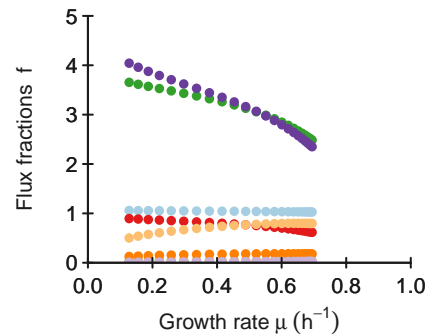
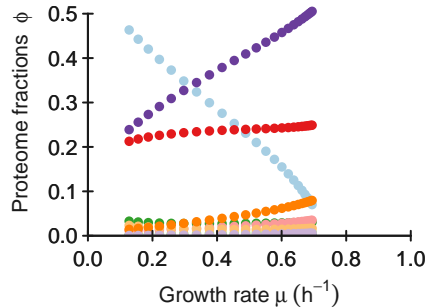
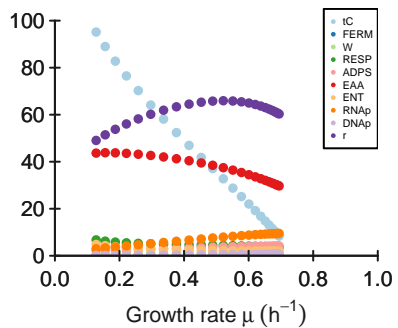
r



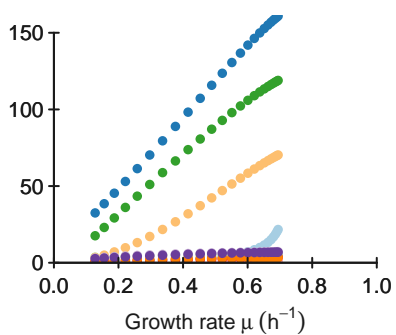
Metabolite concentrations c^m (g/L)



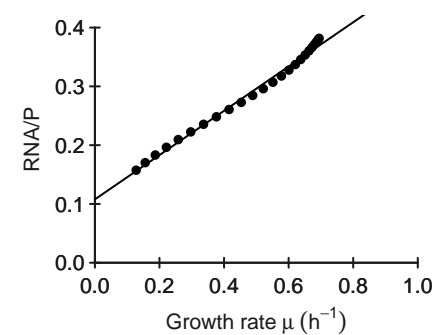
Protein concentrations p (g/L)



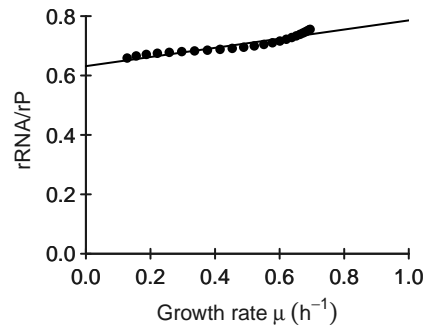
Apparent turnover numbers k_{app} (h^{-1})



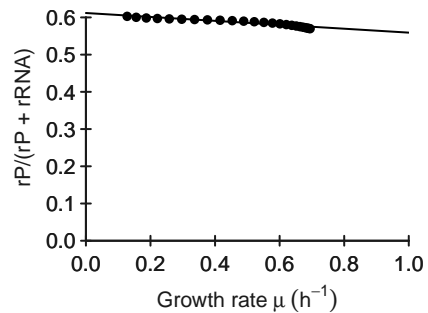
RNA/P



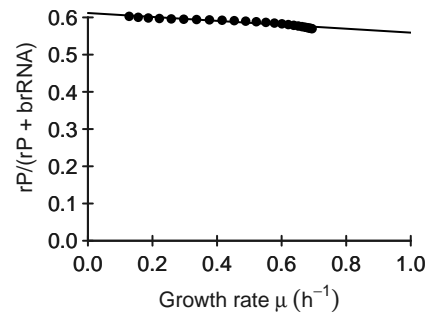
rRNA/rP



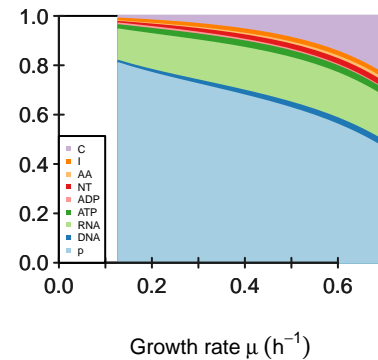
rP/(rP + rRNA)



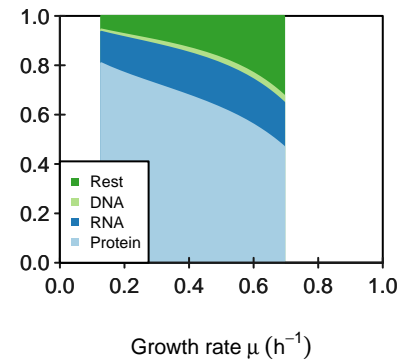
Protein mass fraction in ribosome



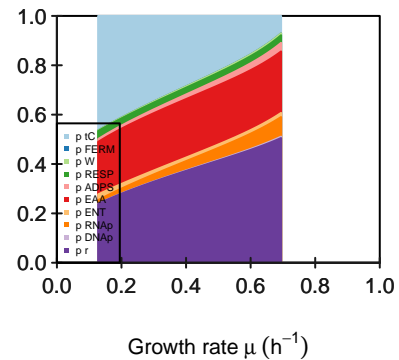
Relative biomass composition



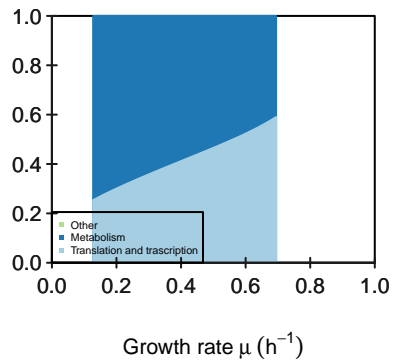
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	FERM	W	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	29	534	10	267	2	7	129	6	13	19
kcatb	3	53	1	27	1	1	13	0	0	0

Keq

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]	[10]
	2706.66666666667	10.0754716981132	20	1.97777777777778	2	0.7	0.992307692307692	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]