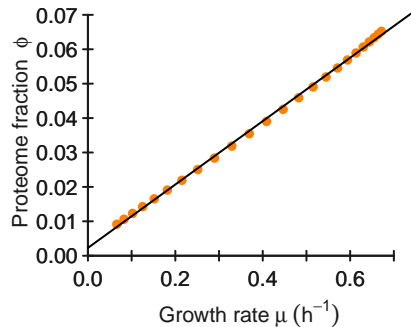
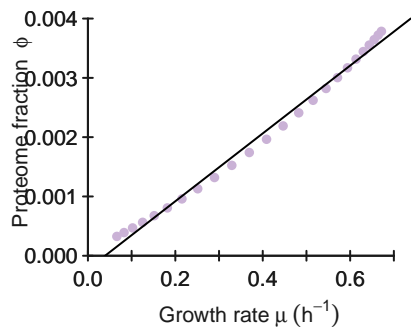


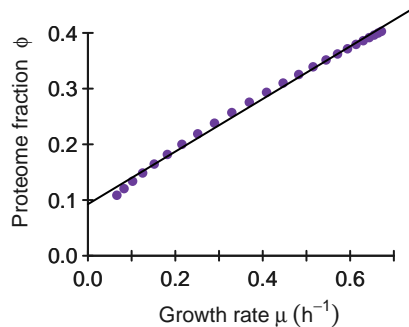
RNAP



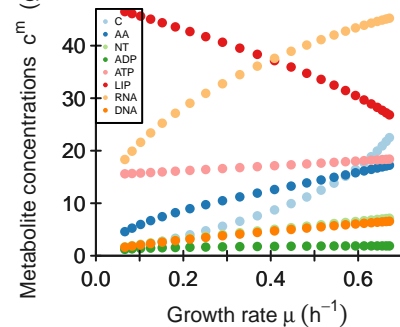
DNAP



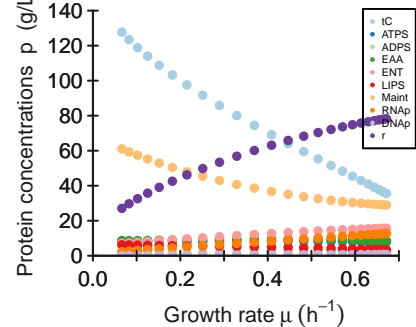
r



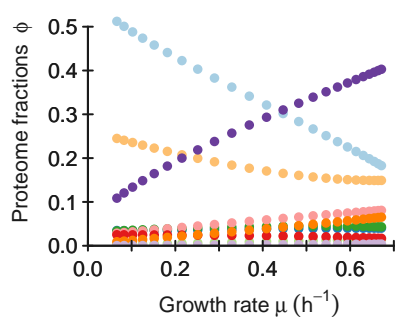
Metabolite concentrations c^m (g/L)



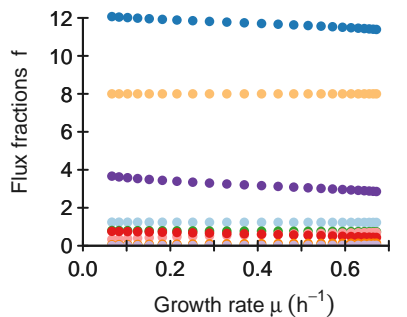
Protein concentrations p (g/L)



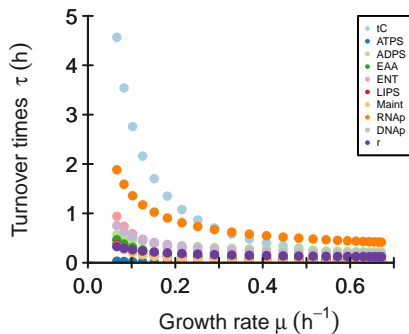
Proteome fractions ϕ



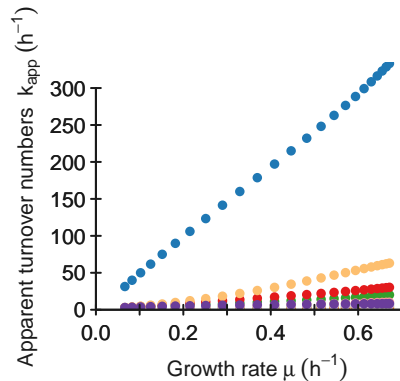
Flux fractions f



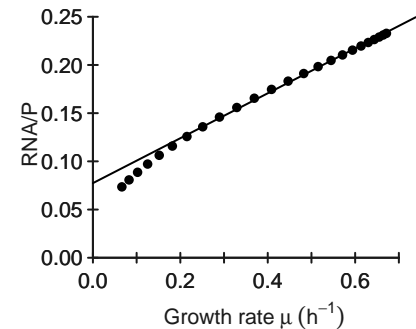
Turnover times τ (h)



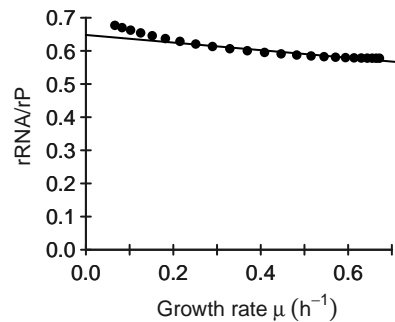
Apparent turnover numbers k_{app} (h^{-1})



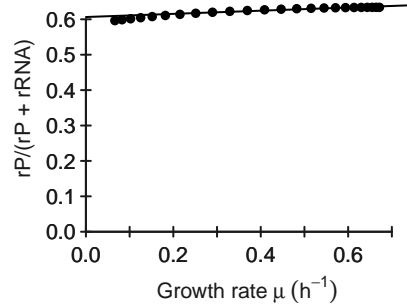
RNA/P



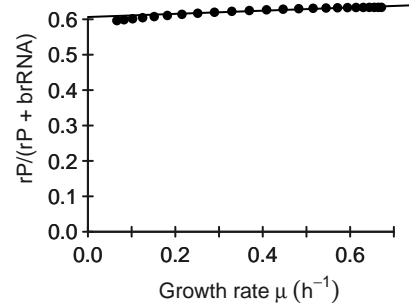
rRNA/rP



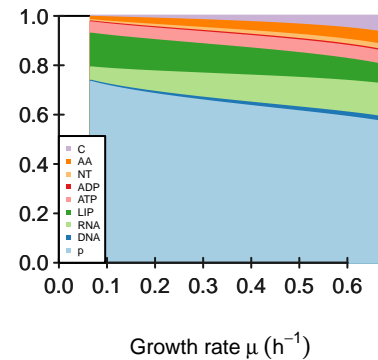
rP/(rP + rRNA)



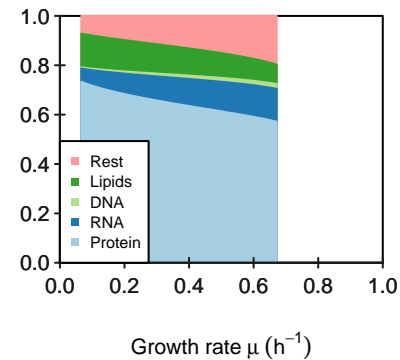
Protein mass fraction in ribosome



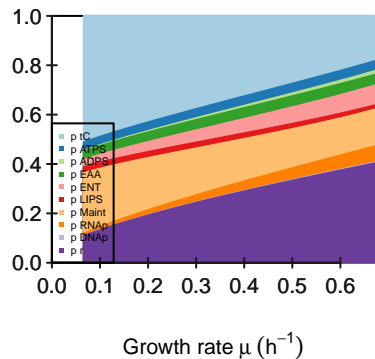
Relative biomass composition



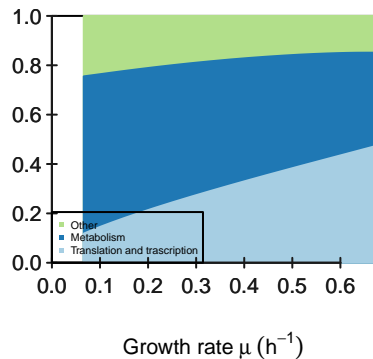
Predicted biomass



Proteome composition



Proteome sectors



M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	ATPS	ADPS	EAA	ENT	LIPS	Maint	RNAp	DNAp	r
kcatf	20	903	11	53	20	58	77	6	15	29
kcatb	2	90	1	5	2	6	0	0	0	0

Keq

[1,]	[,1] 2600	[,2] 156.074074074074	[,3] 3.66666666666667	[,4] 8.24444444444444	[,5] 0.864197530864197	[,6] 12.5308641975309	[,7] Inf	[,8] Inf	[,9] Inf	[,10] Inf
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phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
	0.11	0.023	0.005	0.032	0.16	0.031	0.2506	0.0794	0.002	0.307

average saturation input

3

minimal phi constraint

[illegible]

minimal f constraint

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
	0	0	0	0	0	0	8	0	0	0