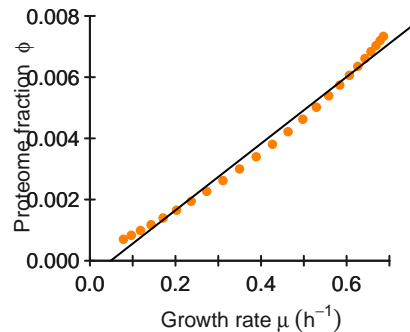
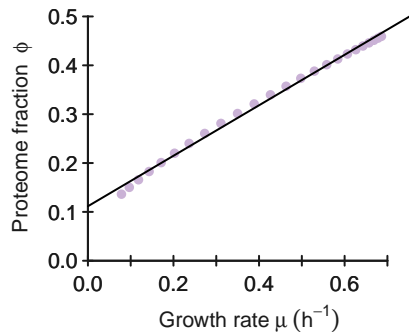
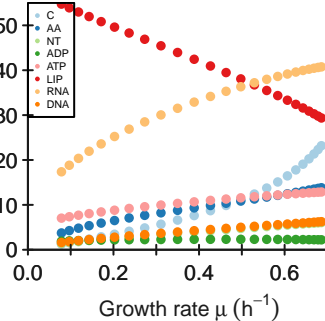
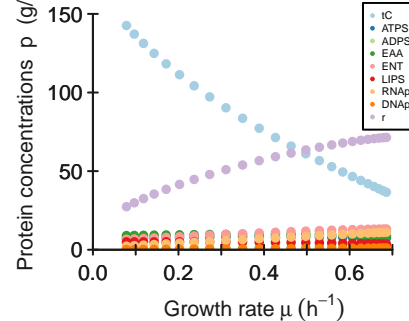
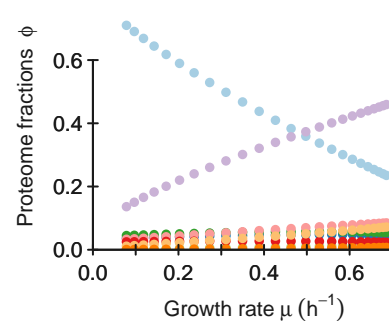
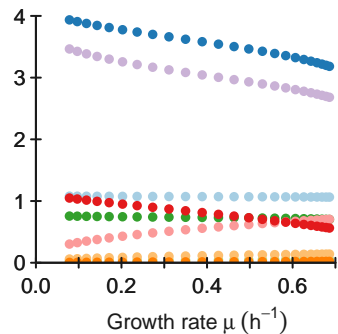
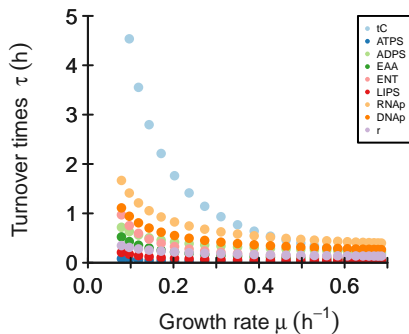
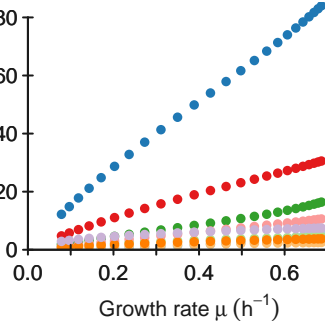
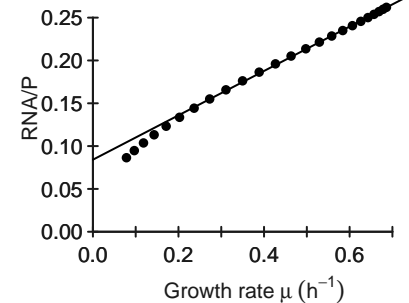
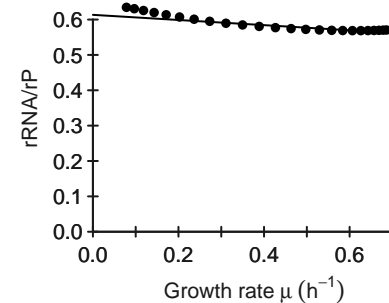
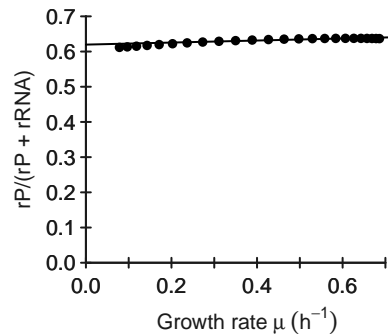
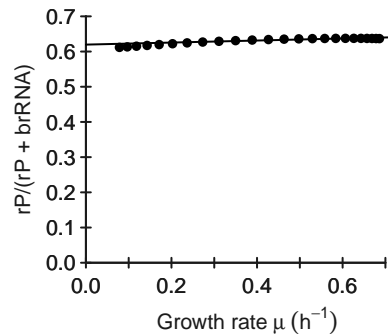


DNAp**r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})**RNA/P****rRNA/rP**

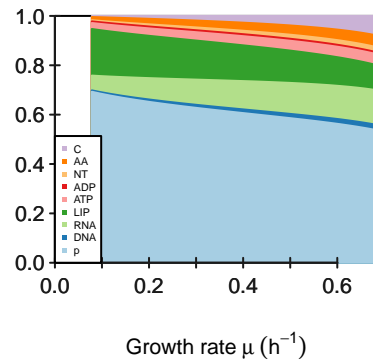
$rP/(rP + rRNA)$



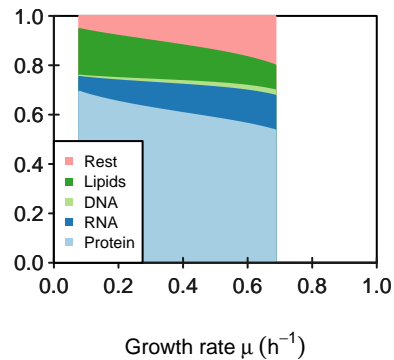
Protein mass fraction in ribosome



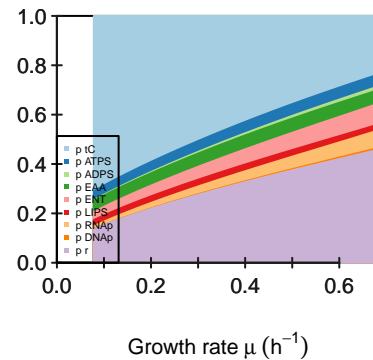
Relative biomass composition



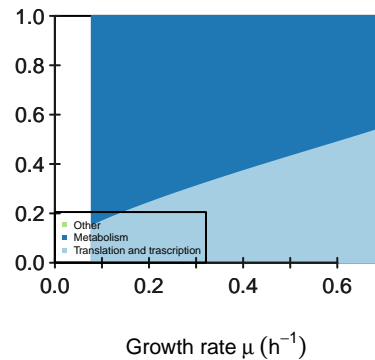
Predicted biomass



Proteome composition



Proteome sectors



M

[illegible]

kcat

	tC	ATPS	ADPS	EAA	ENT	LIPS	RNAp	DNAp	r
kcatf	14	201	10	41	20	49	6	9	22
kcatb	1	20	1	4	2	0	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
3640	134	5	6.833333333333333	1.666666666666667	Inf	Inf	Inf	Inf	

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.147	0.031	0.006	0.043	0.21	0.04	0.11	0.003	0.41

average saturation input

3

minimal phi constraint

[illegible]

