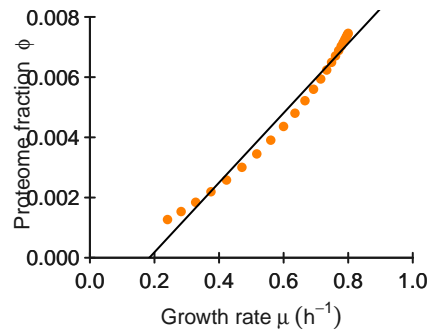
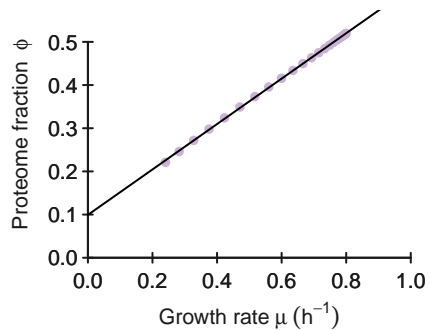
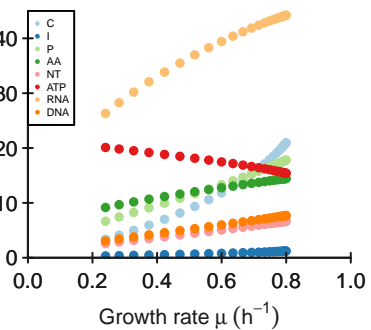
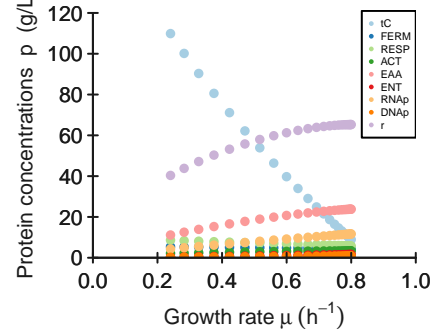
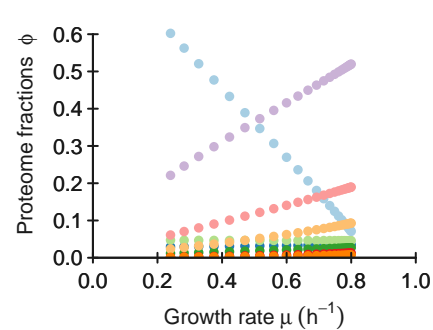
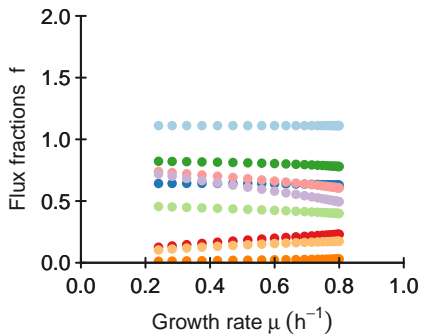
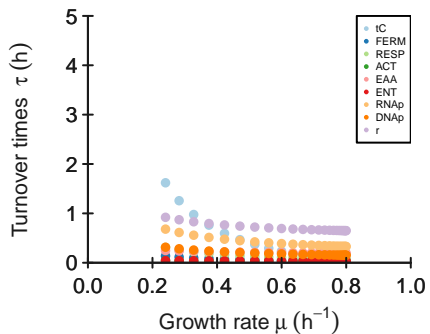
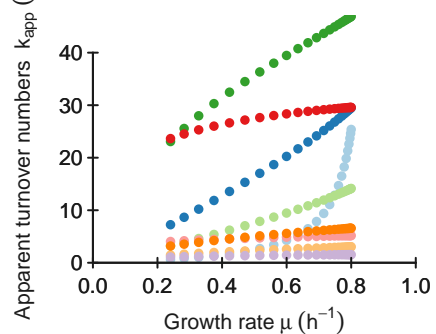
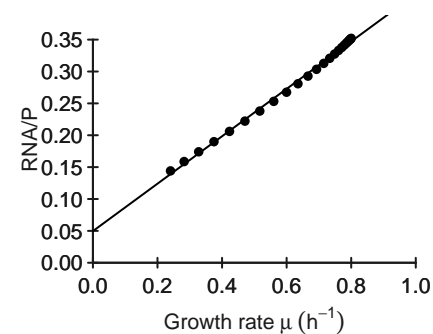
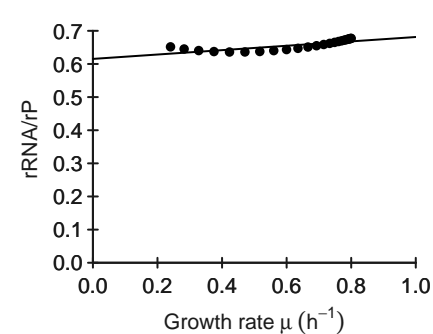
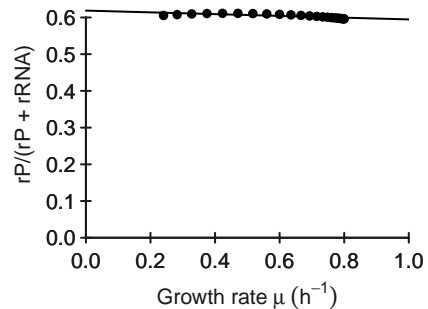
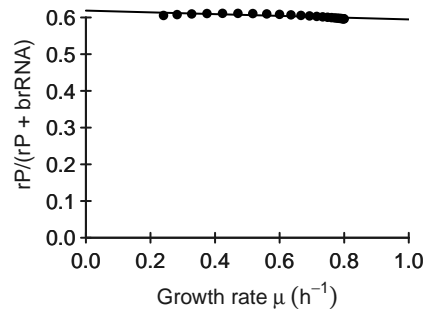


DNAp**r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f Turnover times τ (h)Apparent turnover numbers k_{app} (h^{-1})**RNA/P****rRNA/rP**

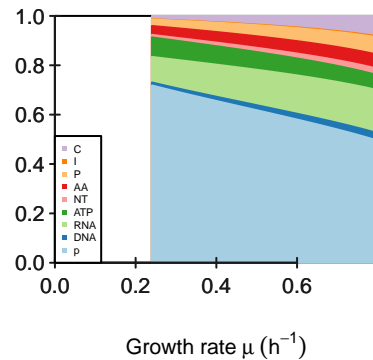
$rP/(rP + rRNA)$



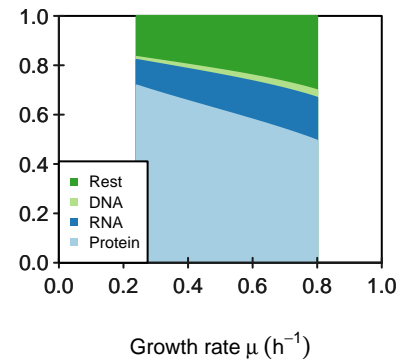
Protein mass fraction in ribosome



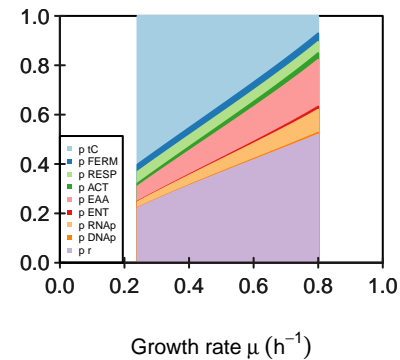
Relative biomass composition



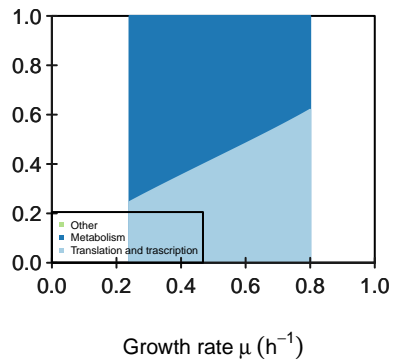
Predicted biomass



Proteome composition



Proteome sectors



keep_ribosome_kcat FALSE
keep_transport_kcat FALSE
maintenance_fun constant

M

[illegible]

kcat

	tC	FERM	RESP	ACT	EAA	ENT	RNAp	DNAp	r
kcatf	32	74	37	115	7	45	6	13	4
kcatb	3	7	4	12	1	4	0	0	0

Keq

[1,]	906.6666666666667	[,1]	31.7142857142857	[,2]	55.5	[,3]	28.75	[,4]	28	[,5]	5.625	[,6]	Inf	[,7]	Inf	[,8]	Inf	[,9]
------	-------------------	------	------------------	------	------	------	-------	------	----	------	-------	------	-----	------	-----	------	-----	------

phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.065	0.024	0.024	0.024	0.248	0.032	0.12	0.003	0.46

average saturation input

3

minimal f constraint

[illegible]