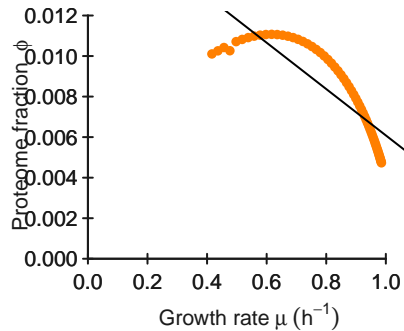
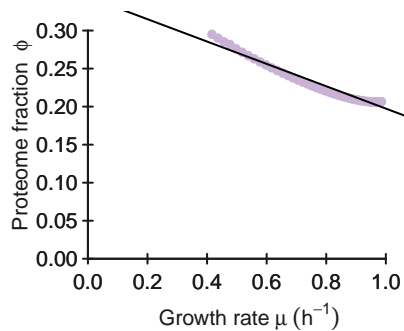


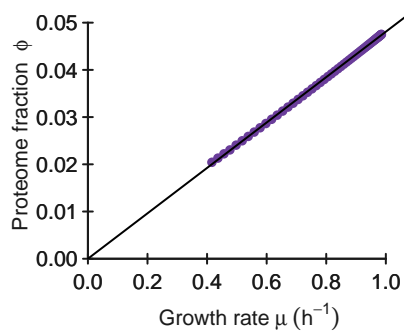
LIPS



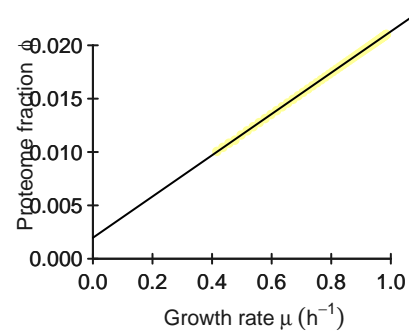
Maint



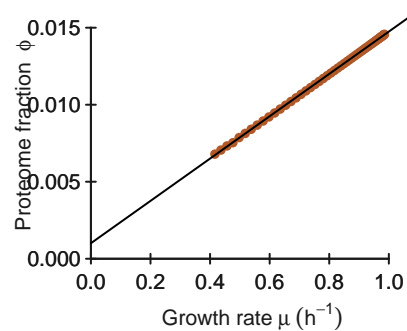
rRNAP



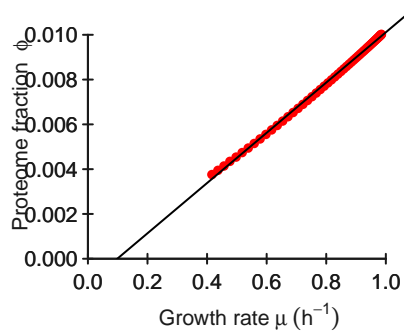
mRNAp



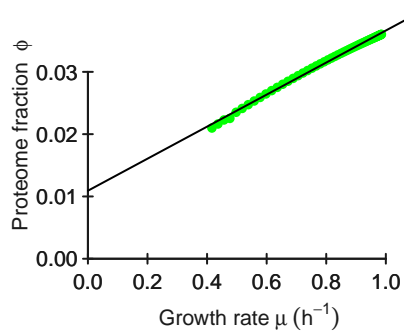
tRNA_p



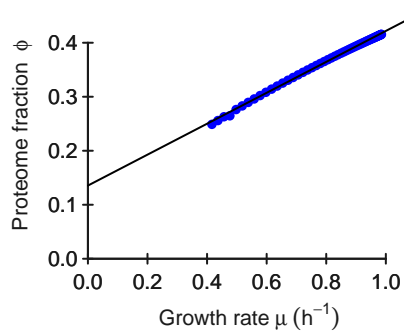
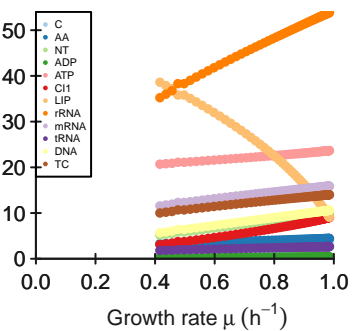
DNAp



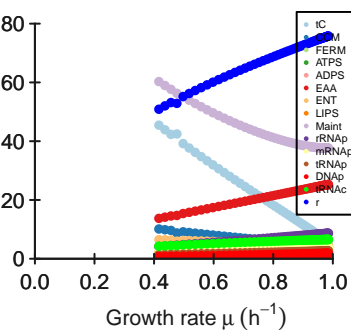
tRNA^{Ac}



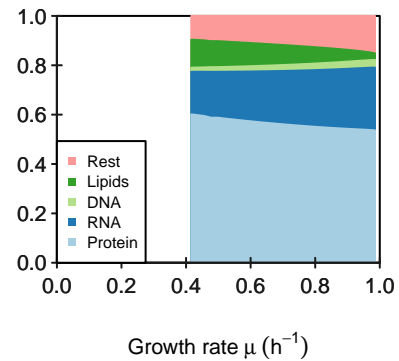
r

Metabolite concentrations c^m (g/L)

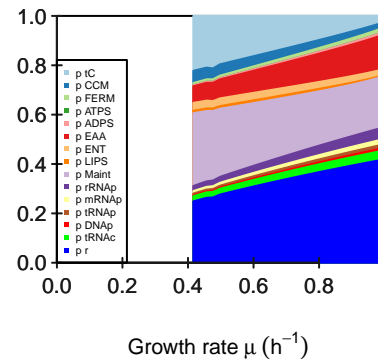
Protein concentrations p (g/L)



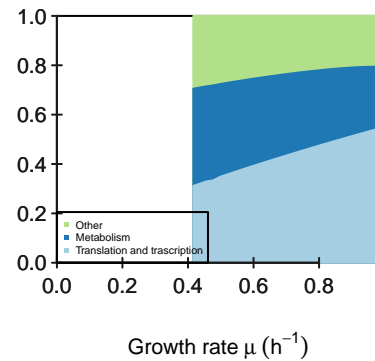
Predicted biomass



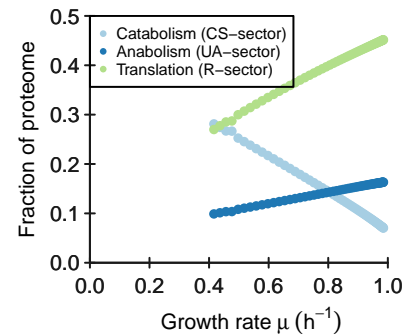
Proteome composition



Proteome sectors



Proteome sectors



M

[illegible]

K

[illegible]

KA[illegible]

kcat

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
kcatf	1000	100	1800	1800	14	12	150	73	81	15	10	15	16	10000	700
kcatb	100	10	180	180	1	1	15	7	0	0	0	0	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]
	2500	100	4e+05	4000	14	60	33.33333333333333	52.1428571428571	Inf	Inf	Inf	Inf	Inf	Inf	Inf

minimal phi constraint

[1,]	[1] 0	[2] 0	[3] 0	[4] 0	[5] 0	[6] 0	[7] 0	[8] 0	[9] 0	[10] 0	[11] 0	[12] 0	[13] 0	[14] 0	[15] 0
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minimal f constraint

[1,]	[,1] 0	[,2] 0	[,3] 0	[,4] 0	[,5] 0	[,6] 0	[,7] 0	[,8] 0	[,9] 8	[,10] 0	[,11] 0	[,12] 0	[,13] 0	[,14] 0	[,15] 0
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