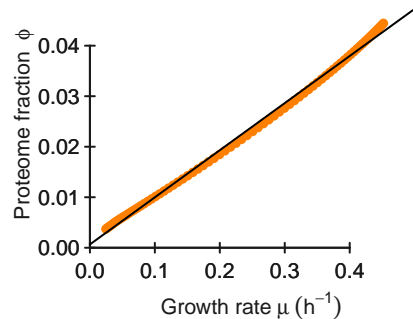
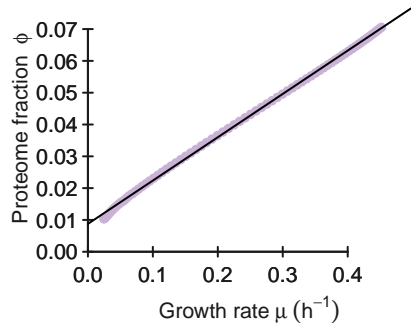
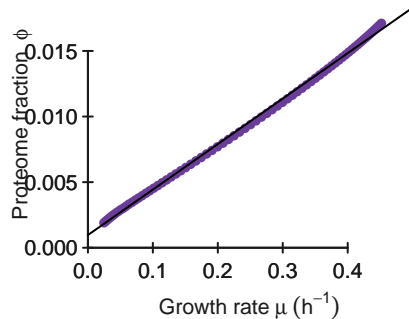
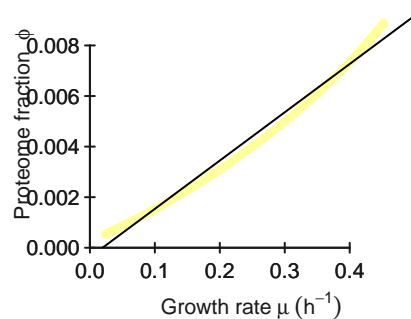
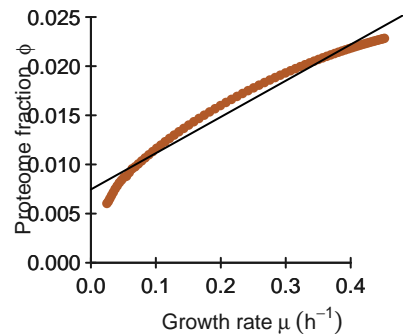
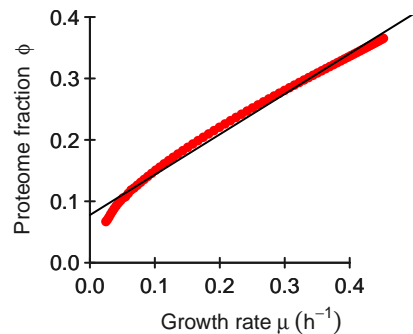
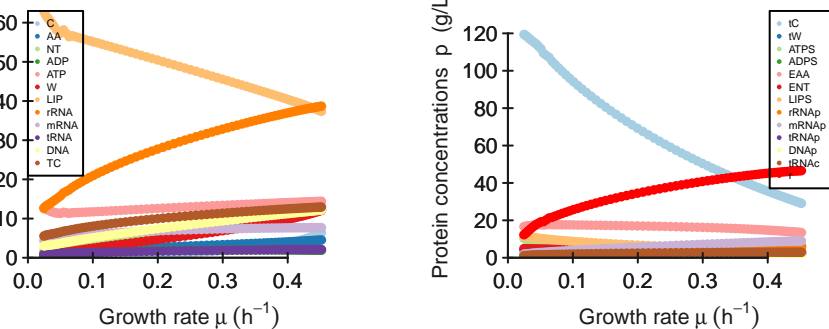
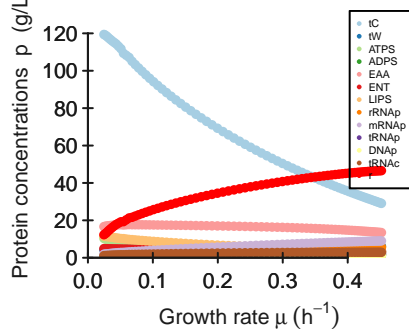
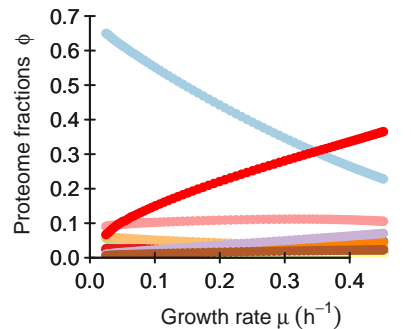
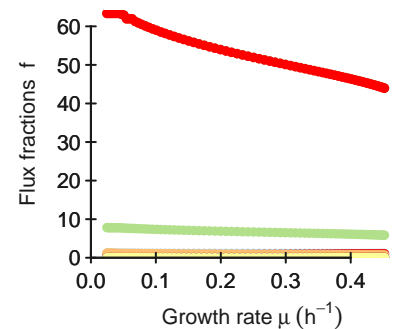
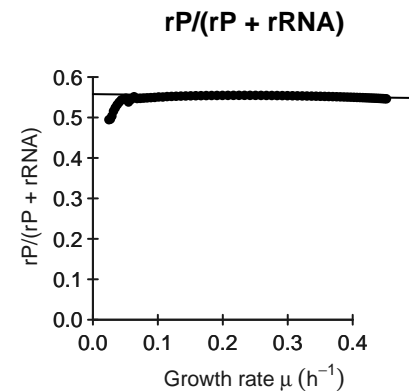
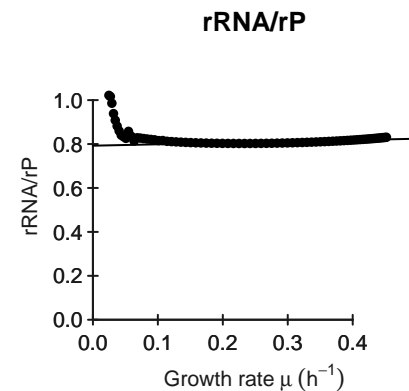
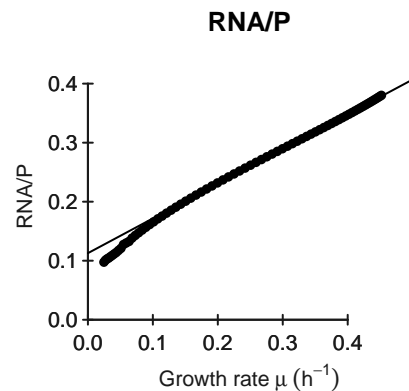
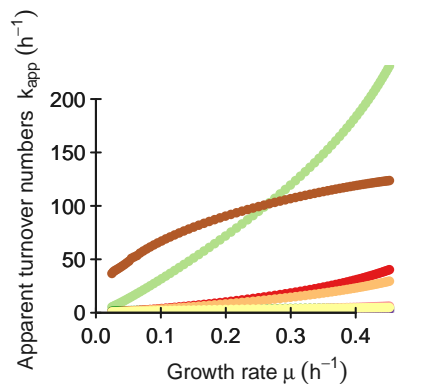
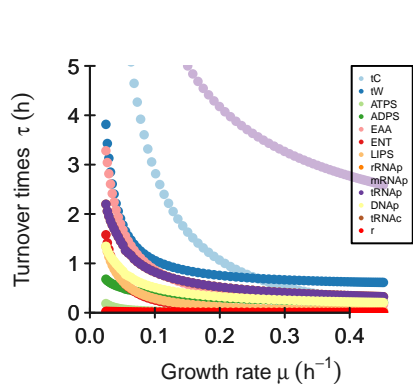
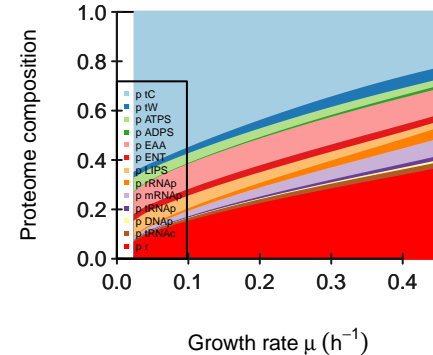
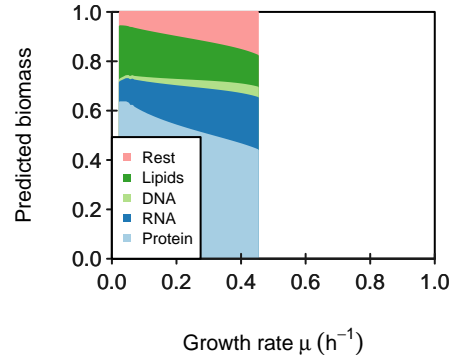
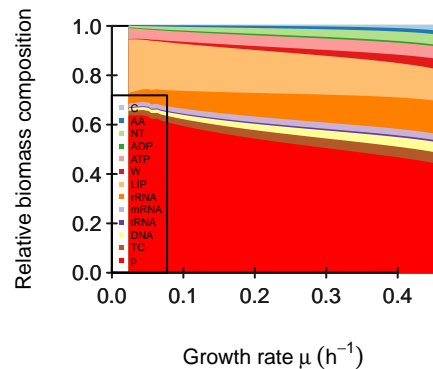
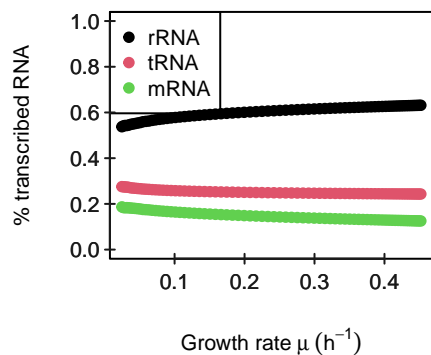
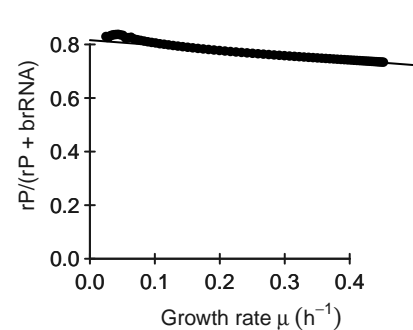


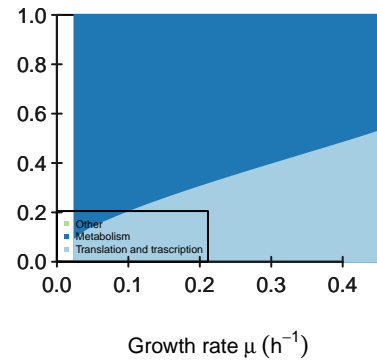
rRNAp**mRNAp****tRNAp****DNAp****tRNAc****r**Metabolite concentrations c^m (g/L)Protein concentrations p (g/L)Proteome fractions ϕ Flux fractions f 



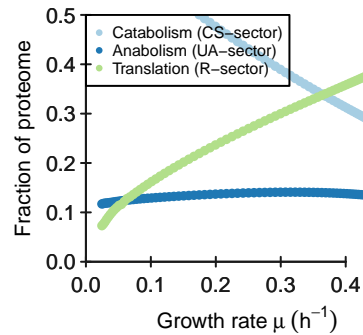
Protein mass fraction in ribosome



Proteome sectors



Proteome sectors



M

[illegible]

K

[illegible]

KA[illegible]

kcat

	tC	tW	ATPS	ADPS	EAA	ENT	LIPS	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
kcatf	17	6	747	10	9	161	54	8	1	8	12	10877	587
kcatb	2	1	75	1	1	16	5	0	0	0	0	0	0

Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]
	255	3.6	298.8	3.33333333333333	49.5	6.14930555555556	104.4	Inf	Inf	Inf	Inf	Inf	Inf

phi input

0.0364372469635628	0.0067476383265857	0.222672064777328	0.0310391363022942	0.0418353576248313	0.0574898785425101	0.0287449392712551	0.00958164642375169	0.002699055
[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	

average saturation input

2

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

minimal f constraint

[illegible]