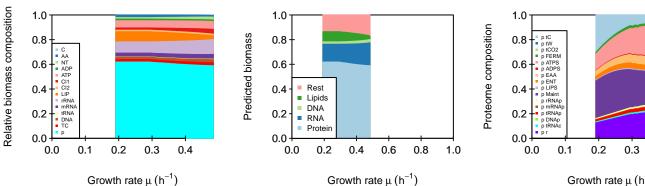
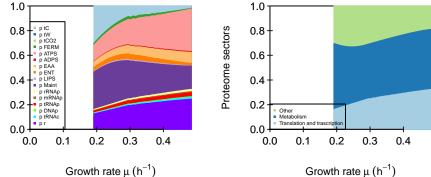
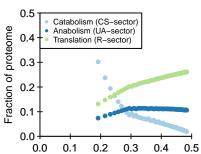


# Froteome sectors







Growth rate  $\mu$  (h<sup>-1</sup>)

	tC	tW	tCO2	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
С	1	0	0	-0.2	0	0	0	-0.167	0	0	0	0	Ö	Ö	0	0
AA	0	0	0	0	0	0	1	-0.167	0	0	0	0	0	0	-0.01	0
NT	0	0	0	0	0	-1	0	0.334	0	0	-1	-1	-1	-1	0	0
ADP	0	0	0	-0.8	-0.98	1	0	0.666	0.82	1	0	0	0	0	0.05	0.05
ATP	0	0	0	0.8	0.98	0	0	-0.666	-0.82	-1	0	0	0	0	-0.05	-0.05
CI1	0	-1	0	0.2	-0.02	0	-0.5	0	-0.18	0	0	0	0	0	0	0
CI2	0	0	-1	0	0.02	0	-0.5	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	0	0.18	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	1	0	-0.94	0.94
DNA	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.95	-0.95
р	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.01

	tC	tW	tCO2	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0.05	0	0	0	0	0	0	0	0	0	0	Ö	Ö	Ö	0	0
x_W	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_CO2	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0
С	0.5	0	0	0.5	0	0	0	1	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	5	5	0	0	0	0	0	0	6	0
NT	0	0	0	0	0	1	0	10	0	0	4	4	4	6	0	0
ADP	0	0	0	1	0.2	1	0	1	1	0	0	0	0	0	0	0
ATP	0	0	0	5	5	0	0	3	3	3	0	0	0	0	4	4
CI1	0	1	0	5	0.2	0	2	0	3	0	0	0	0	0	0	0
CI2	0	0	2	0	5	0	2	0	0	0	0	0	0	0	0	0
LIP	0	0	0	0	0	0	0	0	15	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
DNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
р	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

	tC	tW	tCO2	FERM	ATPS	ADPS	EAA	ENT	LIPS	Maint	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
x_C	0	0	0	0	0	0	0	0	0	0.005	0	0	Ō	0	0	0
x_W	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
x_CO2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
С	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ADP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATP	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CI1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CI2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LIP	60	60	60	0	0	0	0	0	0	0	0	0	0	0	0	0
rRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50
mRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3
tRNA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DNA	0	0	0	0	0	0	0	0	0	0	8	8	8	8	0	0
TC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
р	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

### kcat

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]	[,12]	[,13]	[,14]	[,15]	[,16]
kcatf	800	500	500	2500	50	14	12	220	73	81	15	10	2	16	15000	800
kcatb	80	50	50	250	5	1	1	22	7	0	0	0	0	0	0	0

## Keq

[1.]	[, <b>1</b> ]	[ <b>,2]</b> 30	[,3] 15	<b>[,4]</b> 500	<b>[,5]</b> 6250	[, <b>6]</b> 14	[,7] 15	<b>[8,]</b> 6,666666666666667	<b>[,9]</b> 17 3809523809524	[,10] Inf	[,11] Inf	[,12] Inf	[,13] Inf	[,14] Inf	[,15] Inf	[,16] Inf	

#### minimal phi constraint

 	 	 	Г	 	_	 _	 	

21	

[1,]

[,2] [,3] [,4] [,5] 0 0 0

[,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16] 0 0 0 0 0 0 0 0

#### minimal f constraint

[,6] [,7] [,8] [,9] [,10] [,11] [,12] [,13] [,14] [,15] [,16] 0 0 0 0 0 0 0

[,1] [,2] [,3] [,4] [,5] 0 0 0 0 0

[1,]