A

Enviormental conditions

Glucose

Long-term Starvation

Uniform Growth Conditions

Multiplexed Data aquistion

RNA

Protein

Lipids

Metabolic Flux

Multi-system comparisons and mathematical modeling

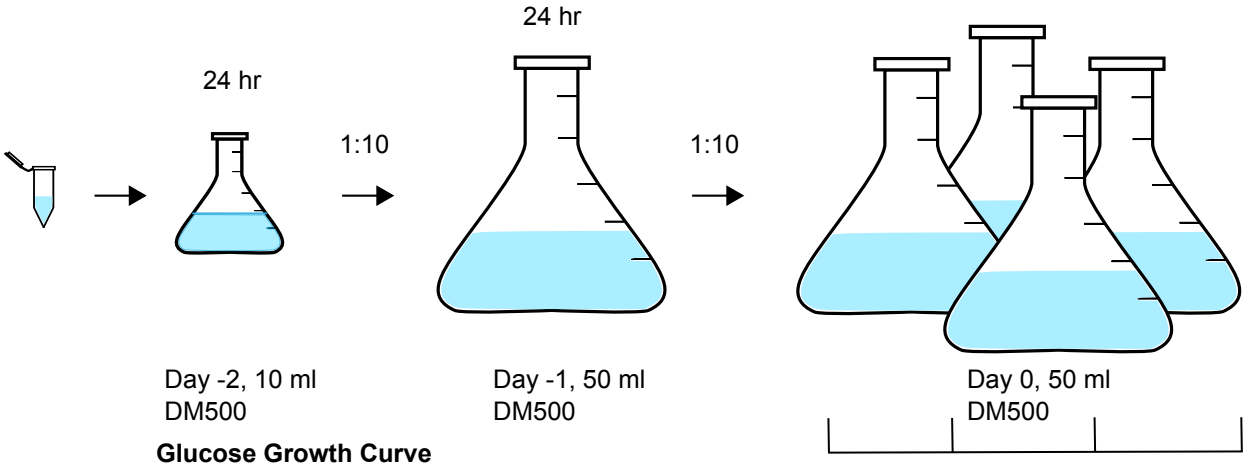
Gene regulation

Metabolic flux constraints

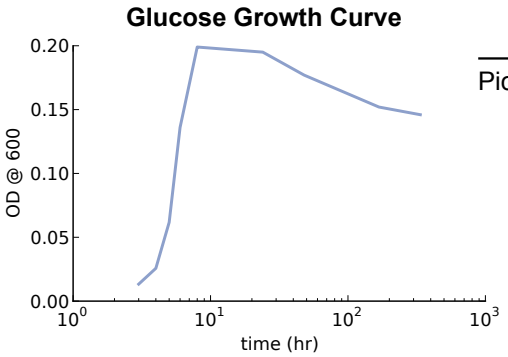
Lipid metabolism

B

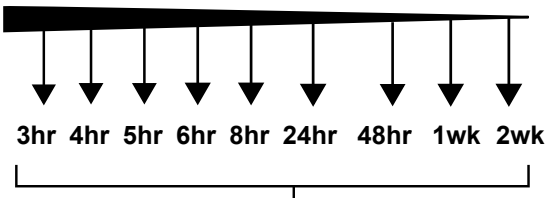
Glucose growth and long-term starvation



C



Pick time points



D

Transcriptomics

Total RNA isolation

rRNA depletion

RNA fragmentation

Library preparation

Sequencing

Proteomics

TFA lysis

Tripsin digest

LC/MS detection of peptides

Lipids

Isolation of 32P labeled Lipid A

Maldi-TOF MS

Isolation of Phospholipids

ESI MS

Metabolic Fluxes

Growth in 20% U-13C labeled glucose

Hydrolysis and Derivatization

GC-MS detection of labeled amino acids

A

RNA Cluster Centroids

Cluster Number

log10(t/t0)

B

Protein Cluster Centroids

Cluster Number

log10(t/t0)

C

Protein vs. $\int$ RNA(t)dt

P(ρ)

Correlation Coefficient

D

Protein vs. RNA

P(ρ)

Correlation Coefficient

E

ρ (Protein vs. $\int$ RNA(t)dt)

ρ (Protein vs. RNA)

F

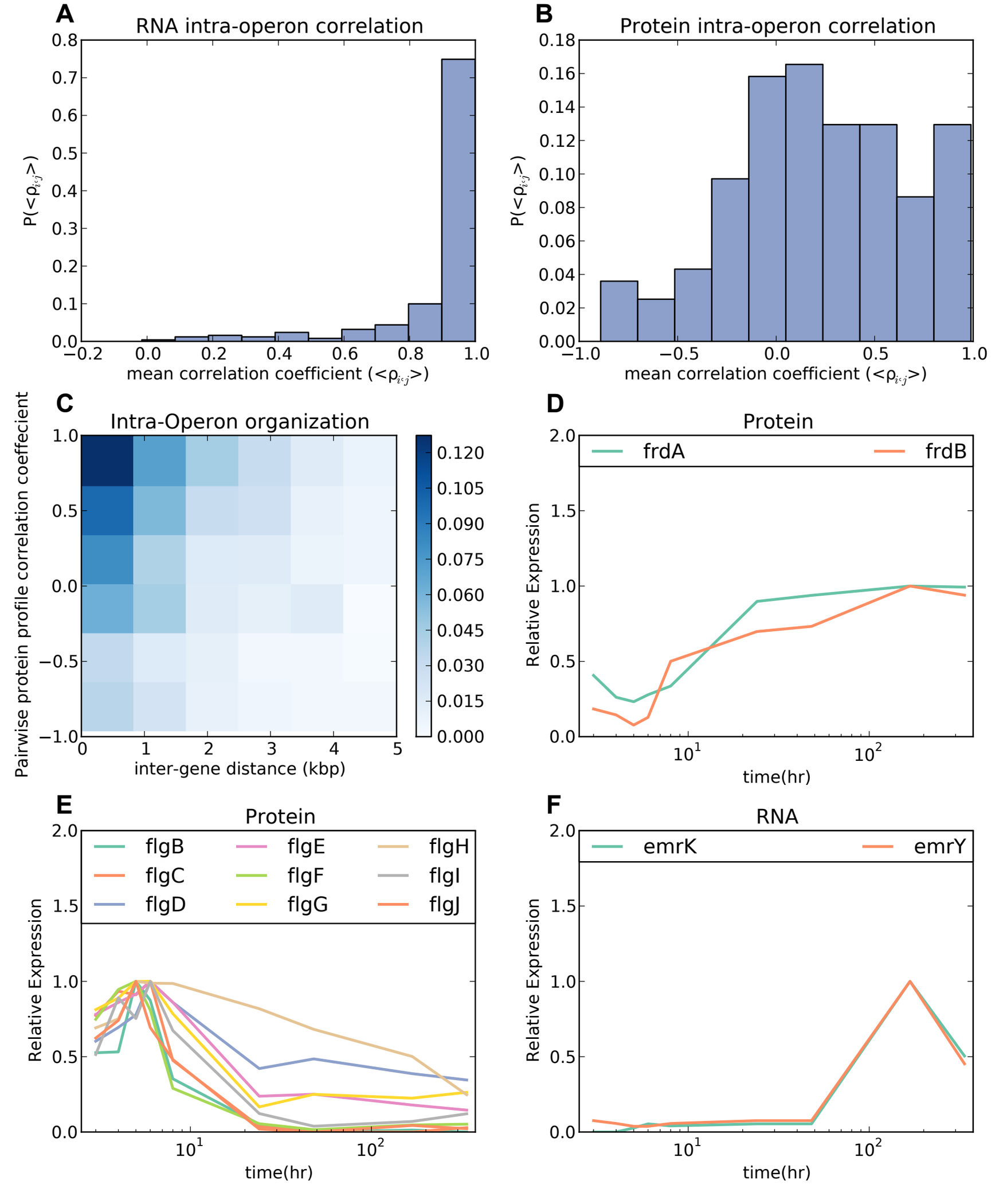
Absolute abundance at T=3hr

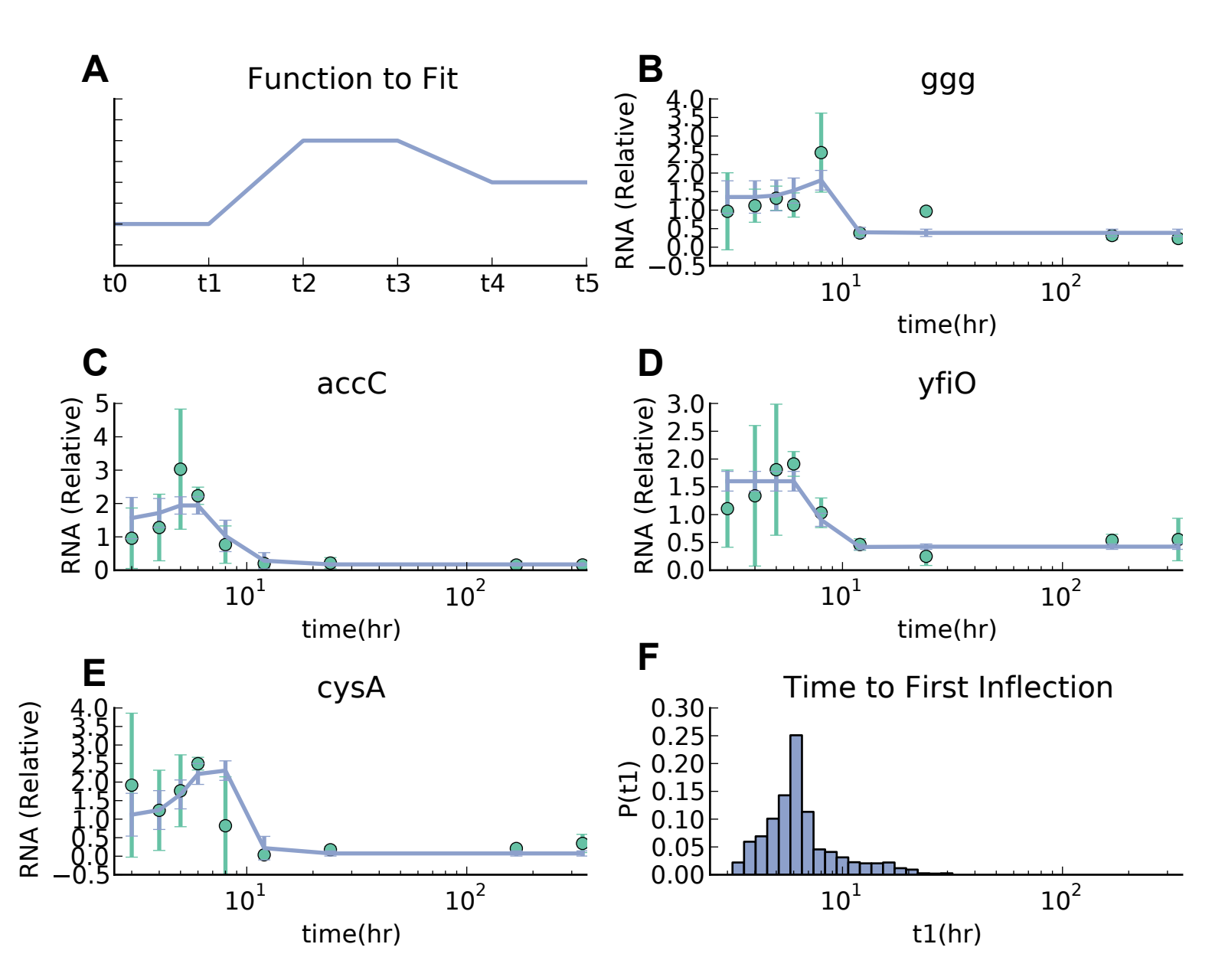
ρ=0.59

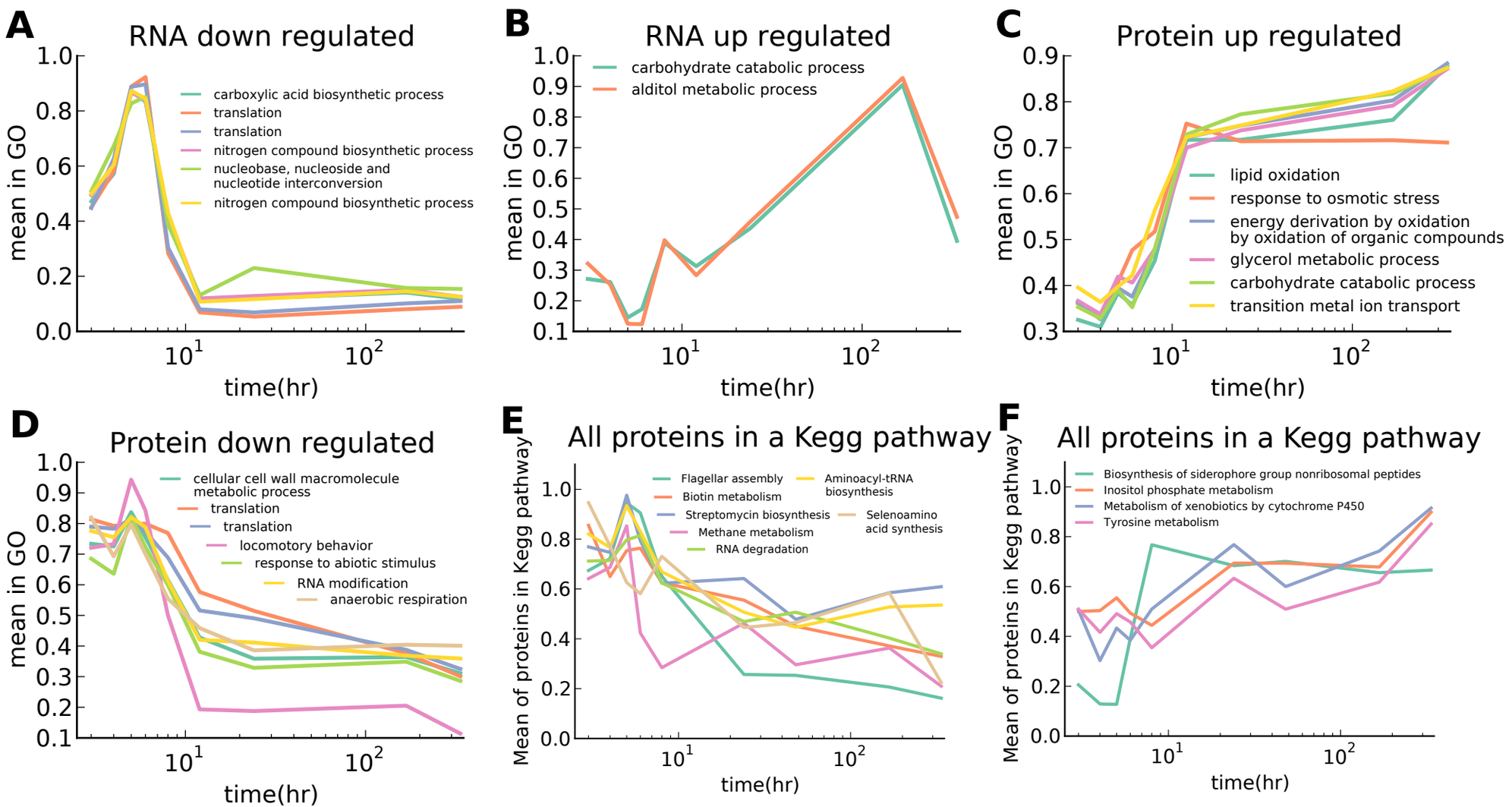
data

log10(protein/<protein>)

log10(RNA/<RNA>)


A
RNA intra-operon correlation
P(<ρi<j>)
mean correlation coefficient (<ρi<j>)
B
Protein intra-operon correlation
P(<ρi<j>)
mean correlation coefficient (<ρi<j>)
C
Intra-Operon organization
Pairwise protein profile correlation coeffecient
inter-gene distance (kbp)
D
Protein
frdA
frdB
Relative Expression
time(hr)
E
Protein
flgB
flgC
flgD
flgE
flgF
flgG
flgH
flgI
flgJ
Relative Expression
time(hr)
F
RNA
emrK
emrY
Relative Expression
time(hr)


A
Function to Fit
t0
t1
t2
t3
t4
t5
B
ggg
RNA (Relative)
time(hr)
C
accC
RNA (Relative)
time(hr)
D
yfiO
RNA (Relative)
time(hr)
E
cysA
RNA (Relative)
time(hr)
F
Time to First Inflection
P(t1)
t1(hr)


A
RNA down regulated
mean in GO
time(hr)
carboxylic acid biosynthetic process
translation
translation
nitrogen compound biosynthetic process
nucleobase, nucleoside and nucleotide interconversion
nitrogen compound biosynthetic process
B
RNA up regulated
mean in GO
time(hr)
carbohydrate catabolic process
alditol metabolic process
C
Protein up regulated
mean in GO
time(hr)
lipid oxidation
response to osmotic stress
energy derivation by oxidation by oxidation of organic compounds
glycerol metabolic process
carbohydrate catabolic process
transition metal ion transport
D
Protein down regulated
mean in GO
time(hr)
cellular cell wall macromolecule metabolic process
translation
translation
locomotory behavior
response to abiotic stimulus
RNA modification
anaerobic respiration
E
All proteins in a Kegg pathway
Mean of proteins in Kegg pathway
time(hr)
Flagellar assembly
Biotin metabolism
Streptomycin biosynthesis
Methane metabolism
RNA degradation
Aminoacyl-tRNA biosynthesis
Selenoamino acid synthesis
F
All proteins in a Kegg pathway
Mean of proteins in Kegg pathway
time(hr)
Biosynthesis of siderophore group nonribosomal peptides
Inositol phosphate metabolism
Metabolism of xenobiotics by cytochrome P450
Tyrosine metabolism

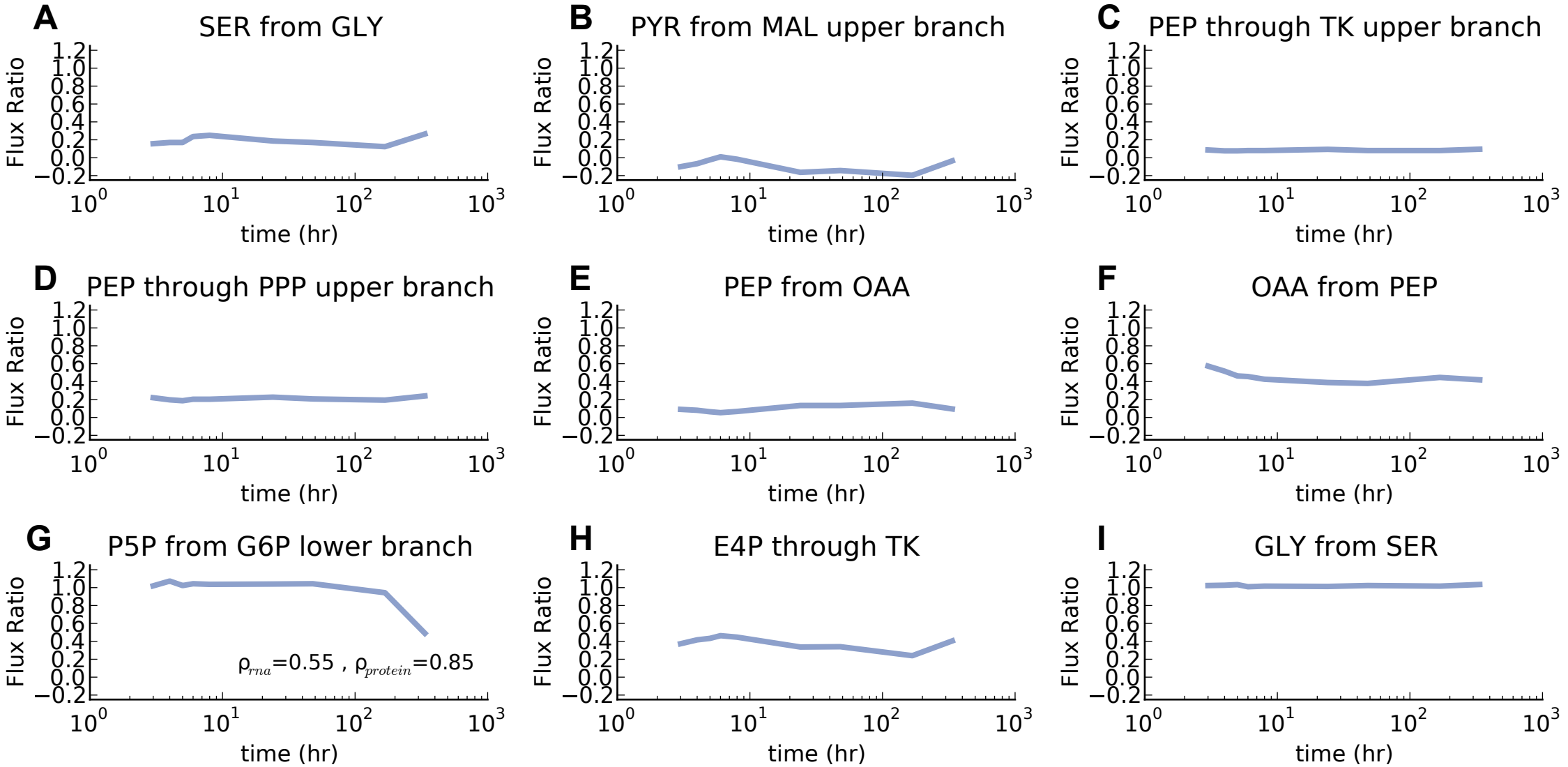
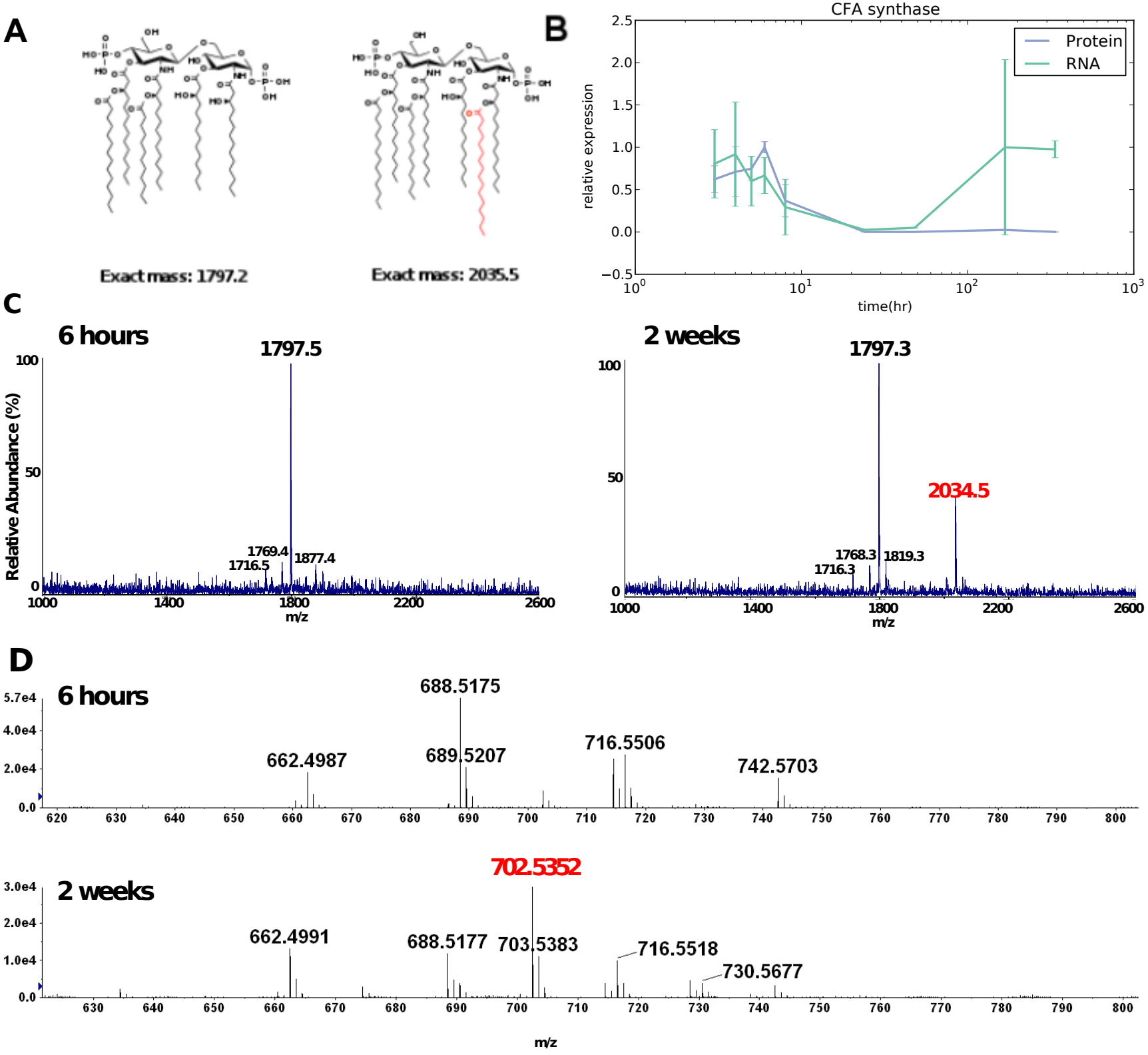

A
SER from GLY
B
PYR from MAL upper branch
C
PEP through TK upper branch
D
PEP through PPP upper branch
E
PEP from OAA
F
OAA from PEP
G
P5P from G6P lower branch
ρrna=0.55 , ρprotein=0.85
H
E4P through TK
I
GLY from SER
Flux Ratio
time (hr)

Fig 5


A
Exact mass: 1797.2
Exact mass: 2035.5
B
CFA synthase
Protein
RNA
relative expression
time(hr)
C
6 hours
1797.5
1769.4
1716.5
1877.4
Relative Abundance (%)
m/z
2 weeks
1797.3
2034.5
1768.3
1819.3
1716.3
m/z
D
6 hours
688.5175
662.4987
689.5207
716.5506
742.5703
Intensity
2 weeks
702.5352
662.4991
688.5177
703.5383
716.5518
730.5677
Intensity
m/z