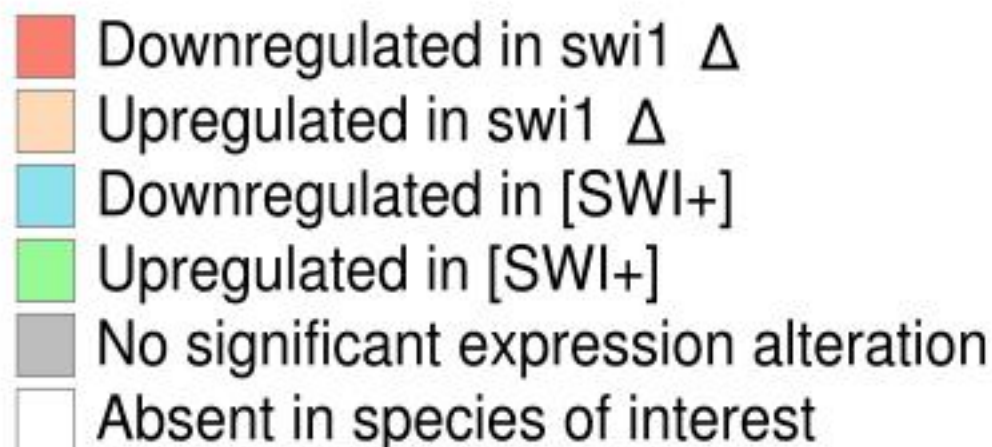


Figure S4. KEGG Pathway mapping of DEGs from [SWI+] and swi1Δ



A: Glycolysis and gluconeogenesis

B: Pentose phosphate pathway

C: Galactose metabolism

D: Purine metabolism

E: Pyrimidine metabolism

F: Alanine, aspartate and glutamate metabolism

G: Arginine biosynthesis

H: Tryptophan metabolism

I: Ribosome

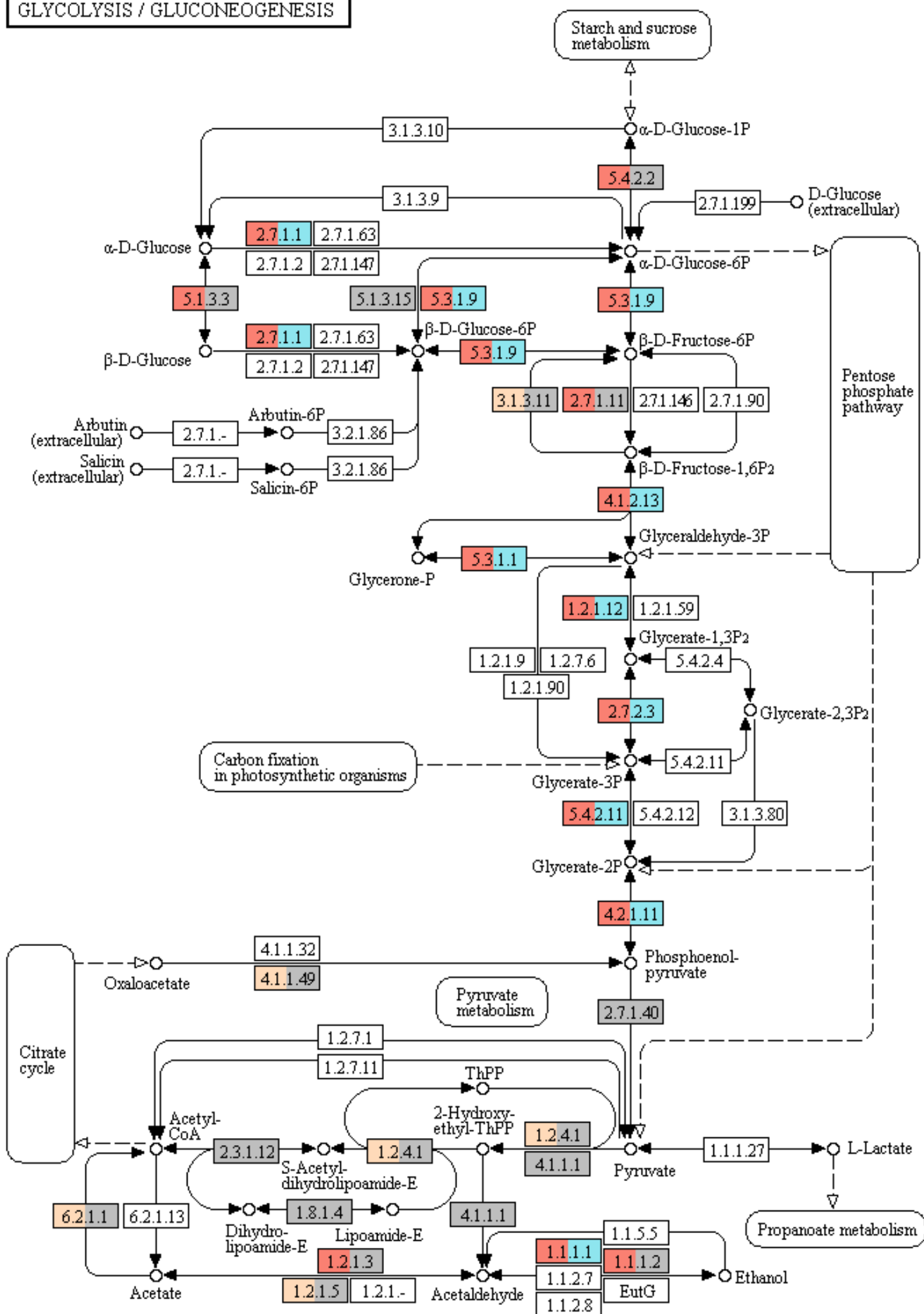
J: Ribosome biogenesis in eukaryotes

K: mRNA surveillance pathway

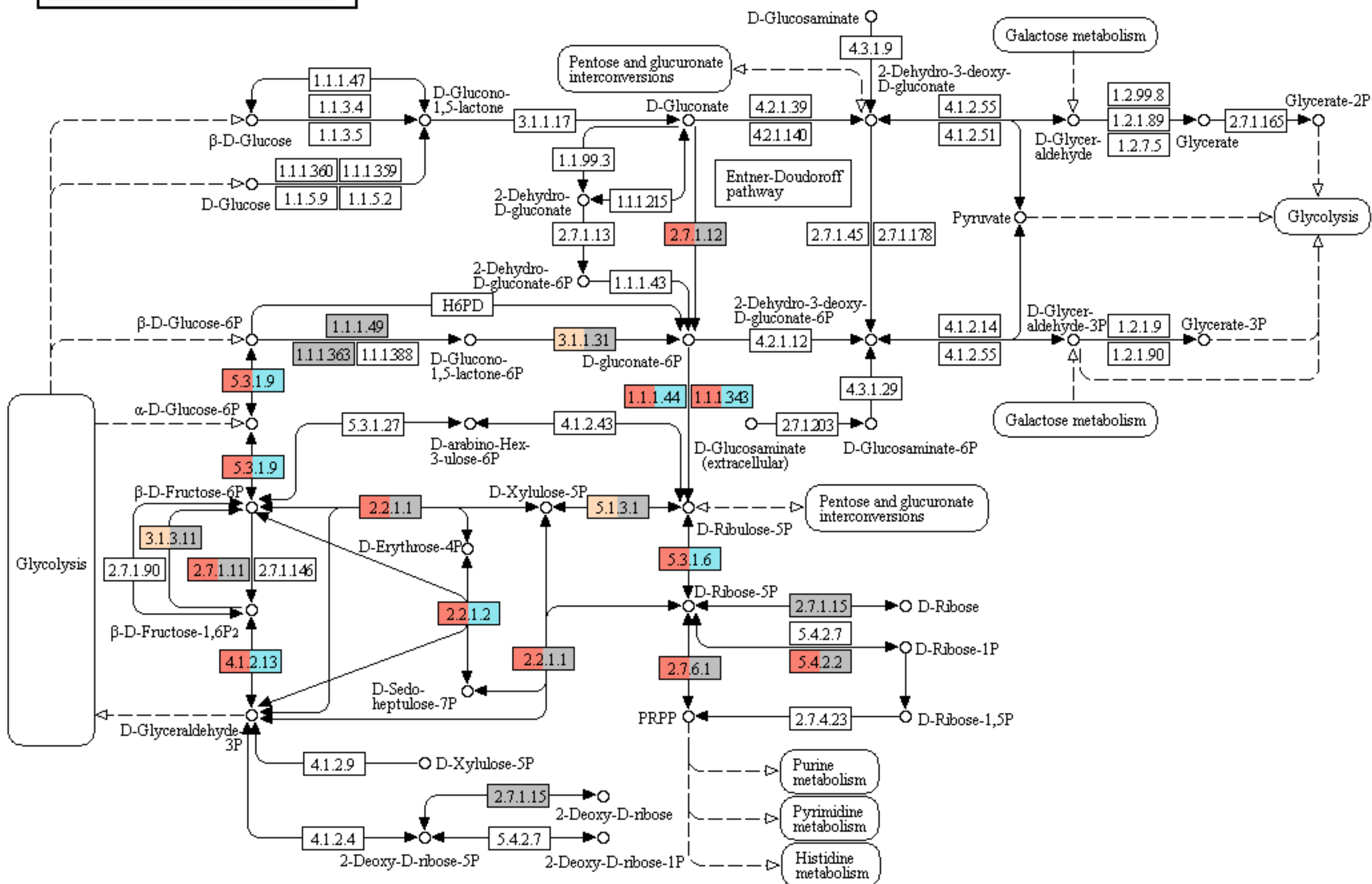
L: RNA transport

M: Aminoacyl-tRNA biosynthesis

## GLYCOLYSIS / GLUCONEOGENESIS

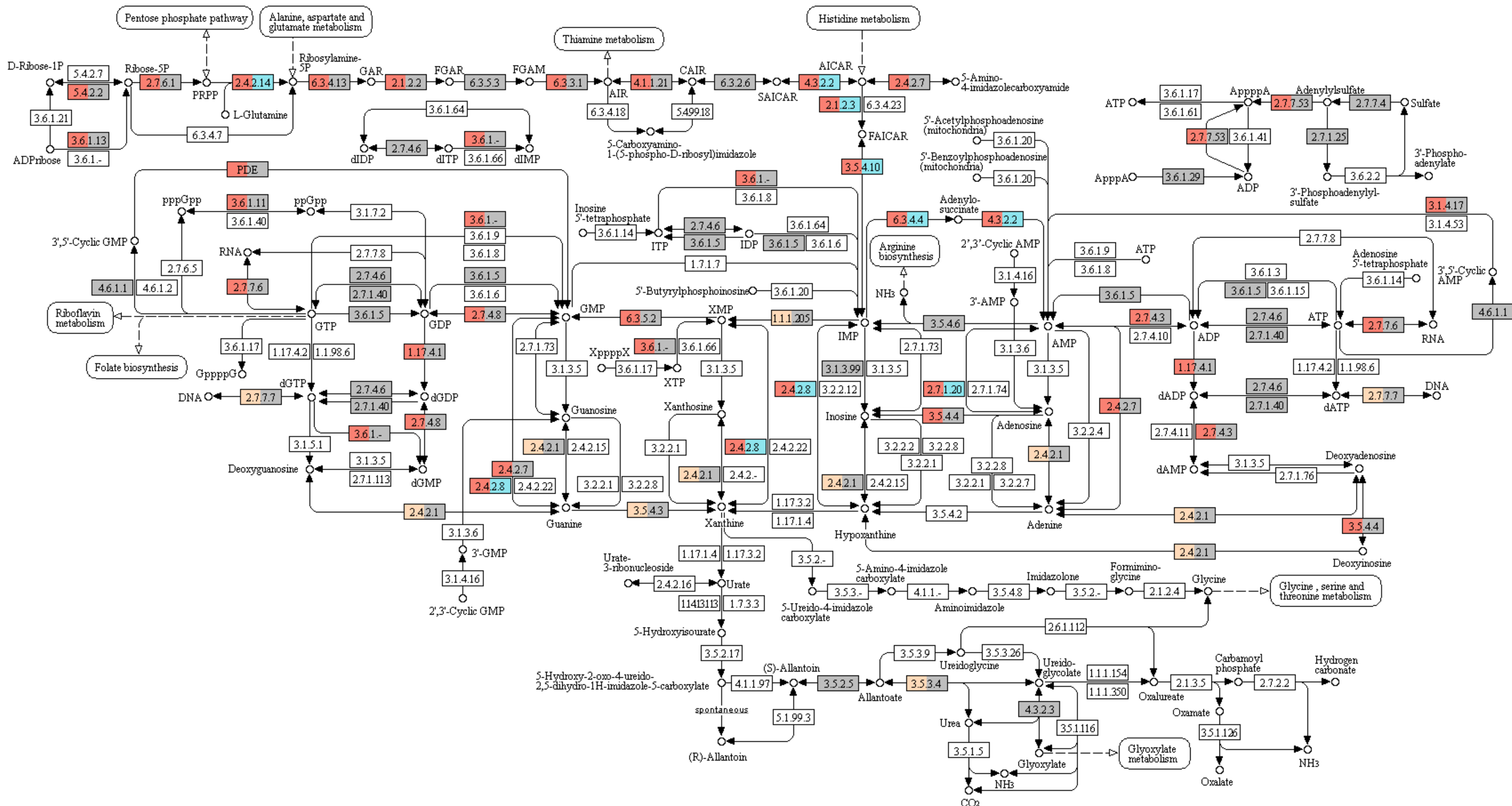


## PENTOSE PHOSPHATE PATHWAY



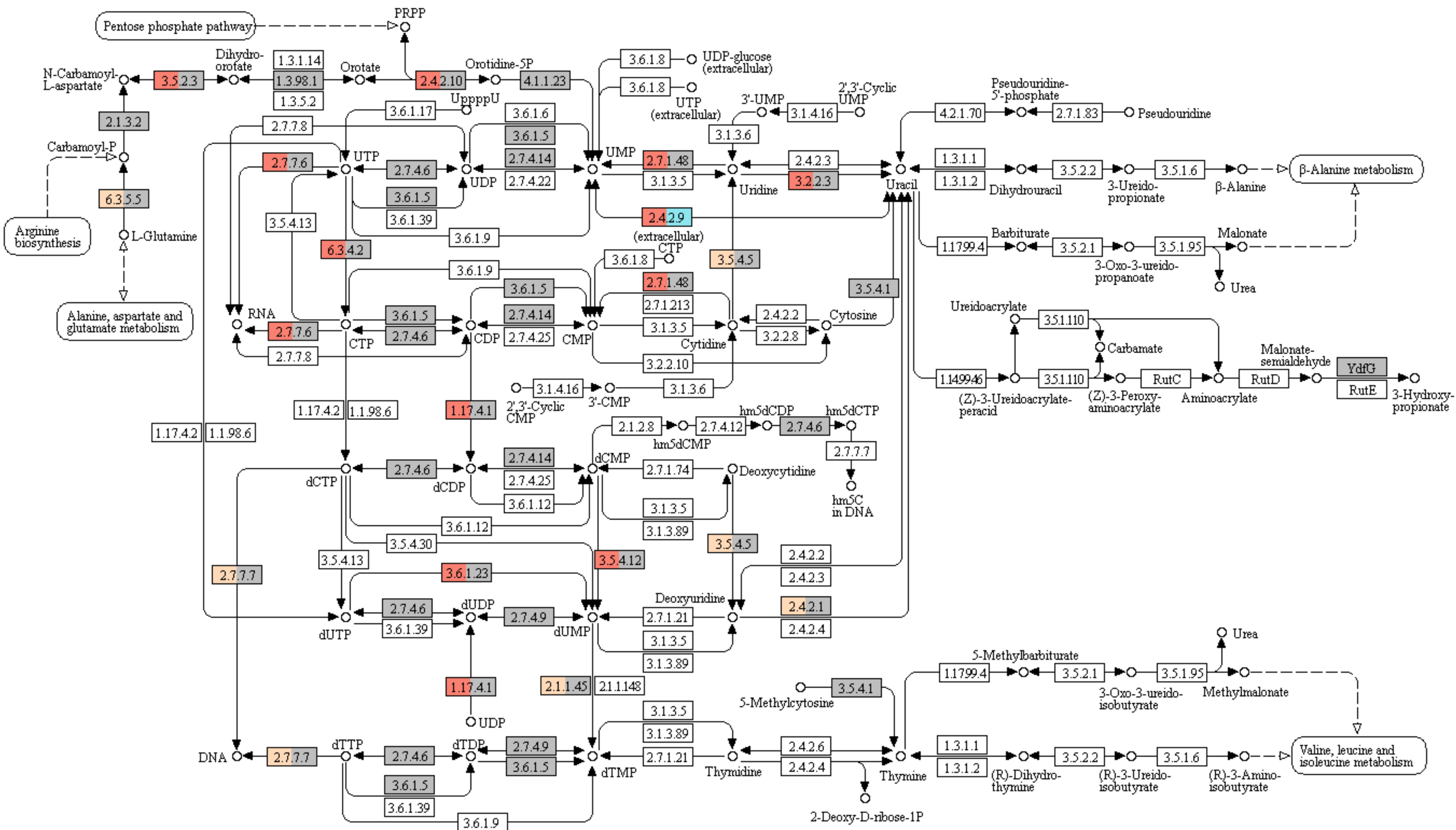


## PURINE METABOLISM

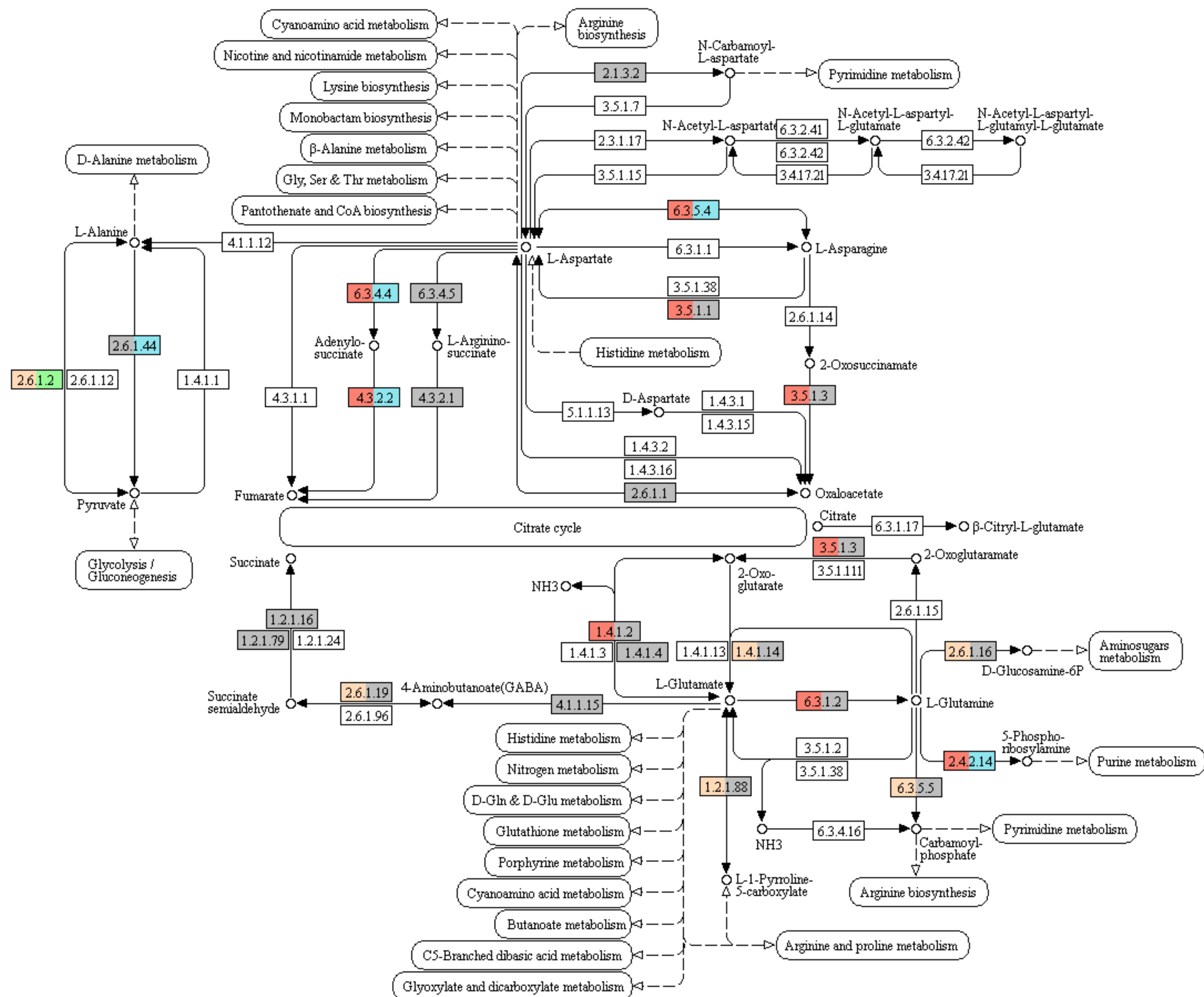




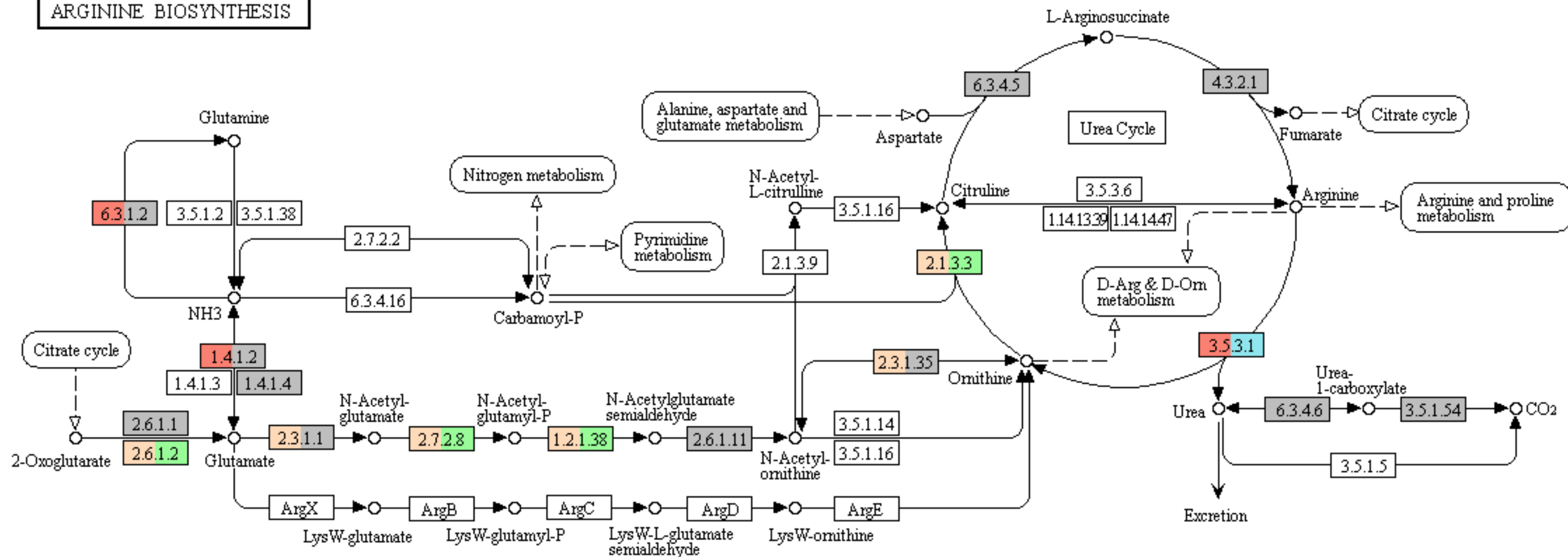
# PYRIMIDINE METABOLISM



## ALANINE, ASPARTATE AND GLUTAMATE METABOLISM

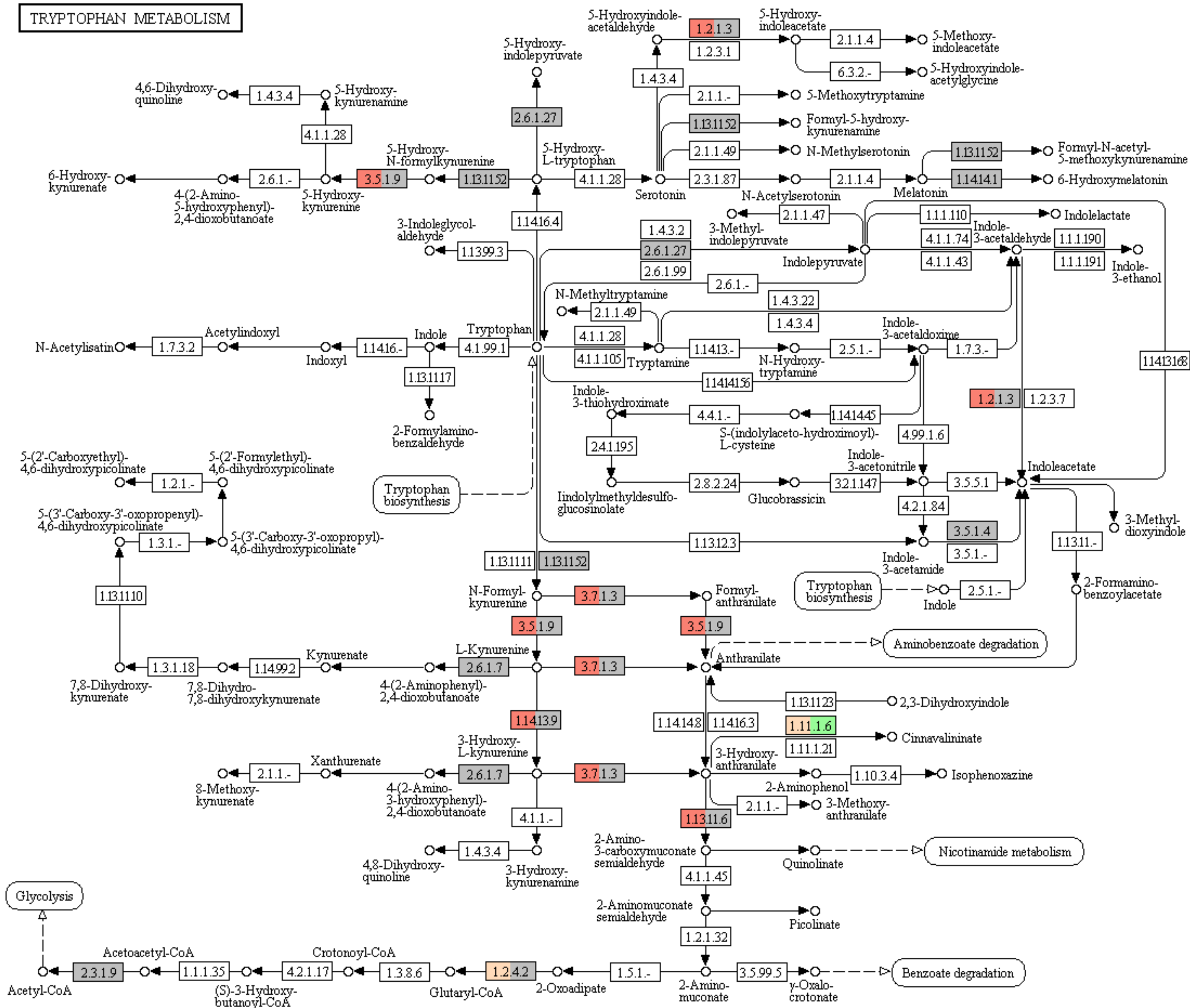


# ARGININE BIOSYNTHESIS

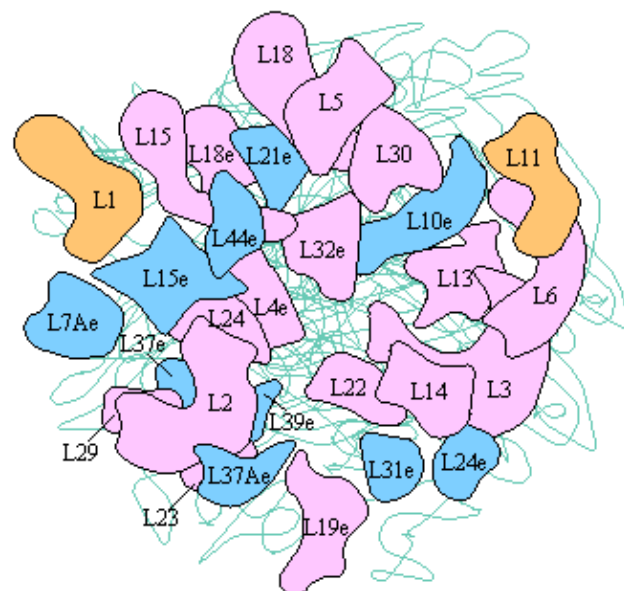




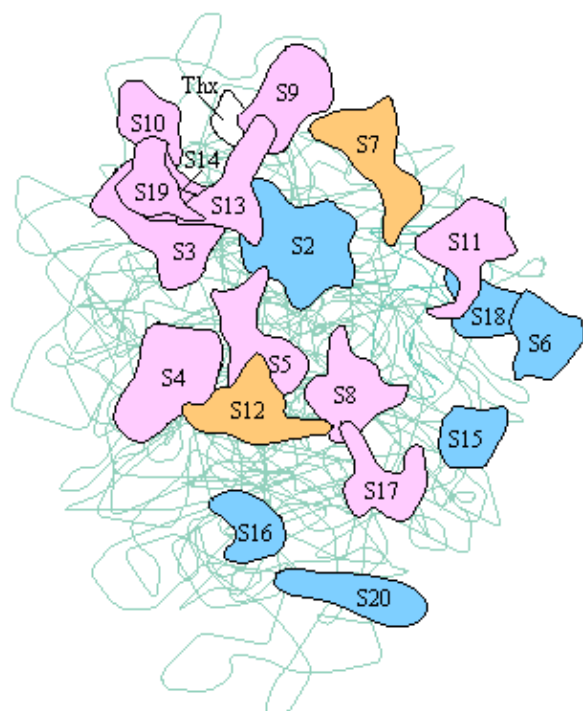
## TRYPTOPHAN METABOLISM



# RIBOSOME



Large subunit (*Haloarcula marismortui*)



Small subunit (*Thermus aquaticus*)

## Ribosomal RNAs

|                                  |     |    |      |     |
|----------------------------------|-----|----|------|-----|
| Bacteria / Archaea<br>Eukaryotes | 23S | 5S |      | 16S |
|                                  | 25S | 5S | 5.8S | 18S |

## Ribosomal proteins

|       |      |     |     |       |     |      |      |     |        |      |
|-------|------|-----|-----|-------|-----|------|------|-----|--------|------|
| EF-Tu | S10  | L3  | L4  | L23   | L2  | S19  | L22  | S3  | RP-L16 | L29  |
|       | S20e | L3e | L4e | L23Ae | L8e | S15e | L17e | S3e |        | L35e |

L7/L12  
stalk

|      |      |      |     |      |      |       |     |      |      |     |     |     |       |
|------|------|------|-----|------|------|-------|-----|------|------|-----|-----|-----|-------|
| S17  | L14  | L24  |     | L5   | S14  | S8    | L6  |      | L18  | S5  | L30 | L15 | SecY  |
| S11e | L23e | L26e | S4e | L11e | S29e | S15Ae | L9e | L32e | L19e | L5e | S2e | L7e | L27Ae |

|      |      |     |      |      |      |      |       |      |
|------|------|-----|------|------|------|------|-------|------|
| IF1  | L36  | S13 | S11  | S4   | RpoA | L17  | L13   | S9   |
|      |      |     |      |      |      |      |       |      |
| L34e | L14e |     | S18e | S14e | S9e  | L18e | L13Ae | S16e |

|                    |     |      |      |      |        |         |     |       |      |     |
|--------------------|-----|------|------|------|--------|---------|-----|-------|------|-----|
| EF-Tu <sub>G</sub> | S7  | S12  |      | L7A  | RpoC,B | L7/L12  | L12 | L10   | L1   | L11 |
|                    | S5e | S23e | L30e | L7Ae |        | LP1,LP2 | LP0 | L10Ae | L12e |     |

|      |       |     |      |     |     |     |     |     |     |     |    |     |    |
|------|-------|-----|------|-----|-----|-----|-----|-----|-----|-----|----|-----|----|
| S2   | EF-Ts | IF2 | S15  | IF3 | L35 | L20 | L34 | RF1 | L31 | L32 | L9 | S18 | S6 |
|      |       |     |      |     |     |     |     |     |     |     |    |     |    |
| S Ae |       |     | S13e |     |     |     |     |     |     |     |    |     |    |

|     |     |     |     |          |     |     |    |     |     |     |
|-----|-----|-----|-----|----------|-----|-----|----|-----|-----|-----|
| L28 | L33 | L21 | L27 | FtsY,Ffh | S16 | L19 | S1 | S20 | S21 | L25 |
|-----|-----|-----|-----|----------|-----|-----|----|-----|-----|-----|

|      |      |      |      |      |      |       |      |       |      |      |      |      |
|------|------|------|------|------|------|-------|------|-------|------|------|------|------|
| L10e | L13e | L15e | L21e | L24e | L31e | L35Ae | L37e | L37Ae | L39e | L40e | L41e | L44e |
|------|------|------|------|------|------|-------|------|-------|------|------|------|------|

|      |     |     |      |      |      |      |      |      |       |      |      |    |
|------|-----|-----|------|------|------|------|------|------|-------|------|------|----|
| S3Ae | S6e | S8e | S17e | S19e | S24e | S25e | S26e | S27e | S27Ae | S28e | S30e | LX |
|------|-----|-----|------|------|------|------|------|------|-------|------|------|----|

|     |       |      |      |      |      |      |      |
|-----|-------|------|------|------|------|------|------|
| L6e | L18Ae | L22e | L27e | L28e | L29e | L36e | L38e |
|-----|-------|------|------|------|------|------|------|

|     |      |      |      |
|-----|------|------|------|
| S7e | S10e | S12e | S21e |
|-----|------|------|------|

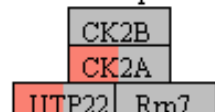
# RIBOSOME BIOGENESIS IN EUKARYOTES

## Ribosomal RNAs

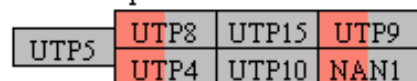


## 90S pre-ribosome components

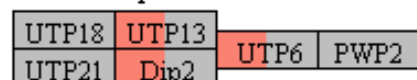
### UTP-C complex



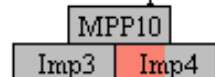
### t-UTP complex



### UTP-B complex

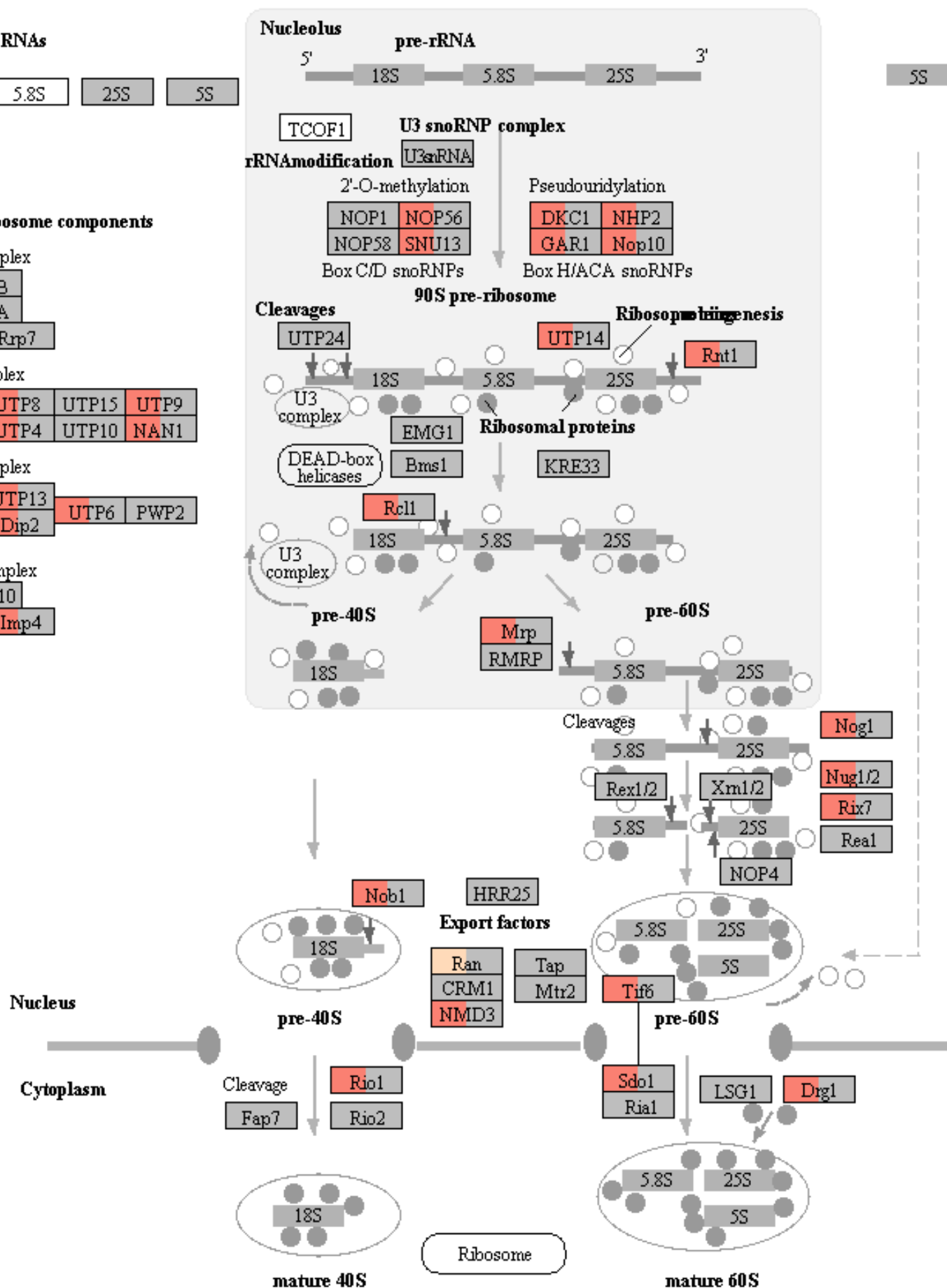


### MPP10 complex



Pol I

Pol III



# mRNA SURVEILLANCE PATHWAY

pre-mRNA

RNA polymerase II

5'-end capping

RNMT  
RNGTT

m7G

Splicing

Spliceosome

CBC  
m7G

CFIm  
CPSF  
CFIIm  
CstF

3'-end processing

Cleavage  
Poly(A) addition

EJC complex

CBC  
m7G

Upf3

Aberrant RNAs

Polyadenylation by  
TRAMP complex

Nuclear exosome  
RNA degradation

PABP2  
AAAAAAA

Export

SRm160  
Pirin

Tap

Nuclear Pore complex  
(NPC)

RNA transport

Nucleus

Cytoplasm

Ribosome binding

CBC  
m7G

Tap

60S

40S

Ribosome

EJC

AAAAAAA

Recognition of PTC  
(premature termination codon)

mammals  
EJC complex

Musashi

CBC  
m7G

PTC

EJC

Upf3

Stop codon

PABP1

AAAAAAA

eRF3

eRF1

Upf1

Upf2

eRF1

eRF3

Upf1

Upf2

Upf3

Stop codon

AAAAAAA

Assembly of  
the surveillance complex

CBC  
m7G

Upf1

eRF3

eRF1

EJC

Upf1

Upf2

Upf3

Stop codon

AAAAAAA

Decapping

Deadenylation

Cytoplasmic exosome

Ski complex

Nonsense-mediated decay  
(NMD)

RNA degradation

Translational stalling

Stem-loop

m7G

Stop codon

PABP1

AAAAAAA

Hbs1

Dom34

Hbs1

Dom34

m7G

Stop codon

PABP1

AAAAAAA

Hbs1

Dom34

Hbs1

Dom34

No-go decay  
(NGD)

Ski7

Cap binding complex  
(CBC)

CBP80  
CBP20

Exon-junction complex  
(EJC)

|      |        |       |         |       |
|------|--------|-------|---------|-------|
| Upf3 | Y14    | MLN51 | SAP18   | ACIN1 |
| MAGO | EIF4A3 | Pirin | Ref/Aly |       |

Transiently interacting factors

|     |       |        |
|-----|-------|--------|
| Tap | UAP56 | SRm160 |
| p15 | PYM   |        |

pre-mRNA 3'-end processing  
machinery

Cleavage factor Im (CFIm) complex

CPSF5 CPSF6/7 PAP

Cleavage factor IIm (CFIIm) complex

Clp1 Pcf11

Cleavage and polyadenylation  
specificity factor (CPSF) complex

(Saccharomyces cerevisiae)

|       |       |       |      |       |
|-------|-------|-------|------|-------|
| CPSF1 | CPSF2 | CPSF3 | MPE1 | PFS2  |
| Fip1  | CPSF4 |       | SWD2 | REF2  |
|       |       |       | GLC7 | SSU72 |

Cleavage stimulation factor (CSTF) complex

CSTF1 CSTF2 CSTF3  
SYMPK

m7G Lacking a stop codon AAAAAA

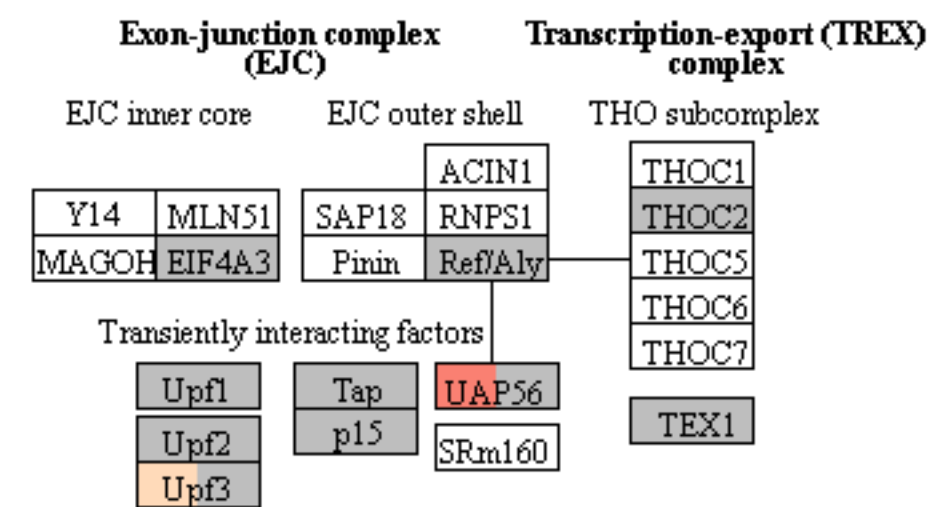
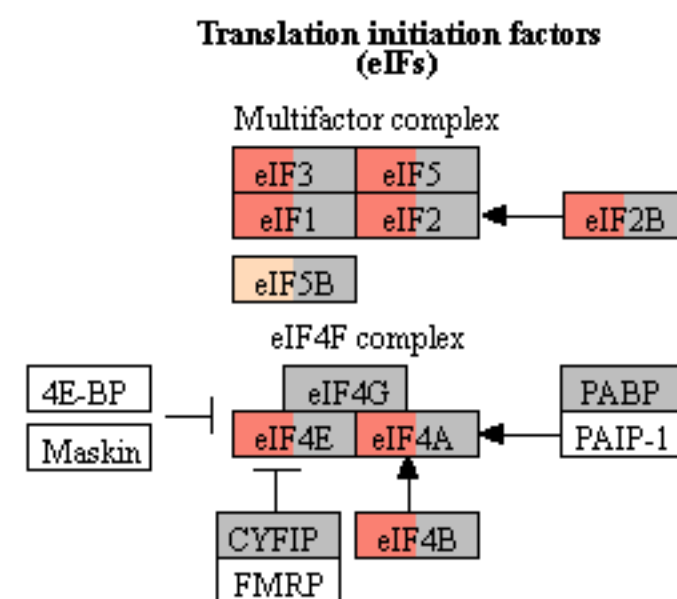
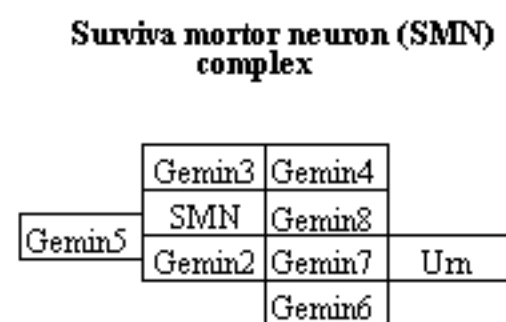
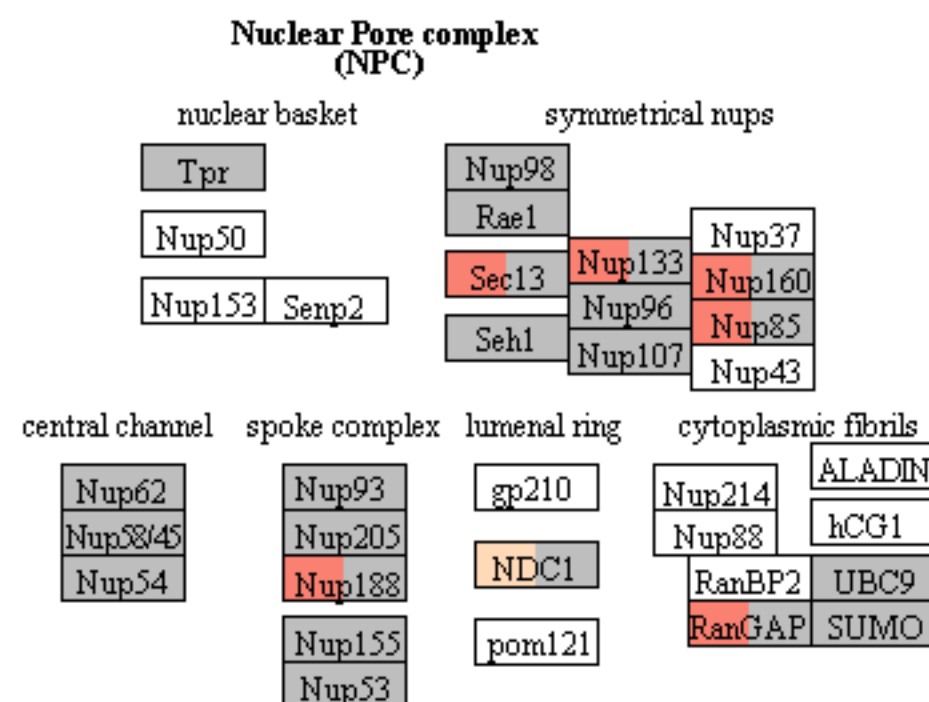
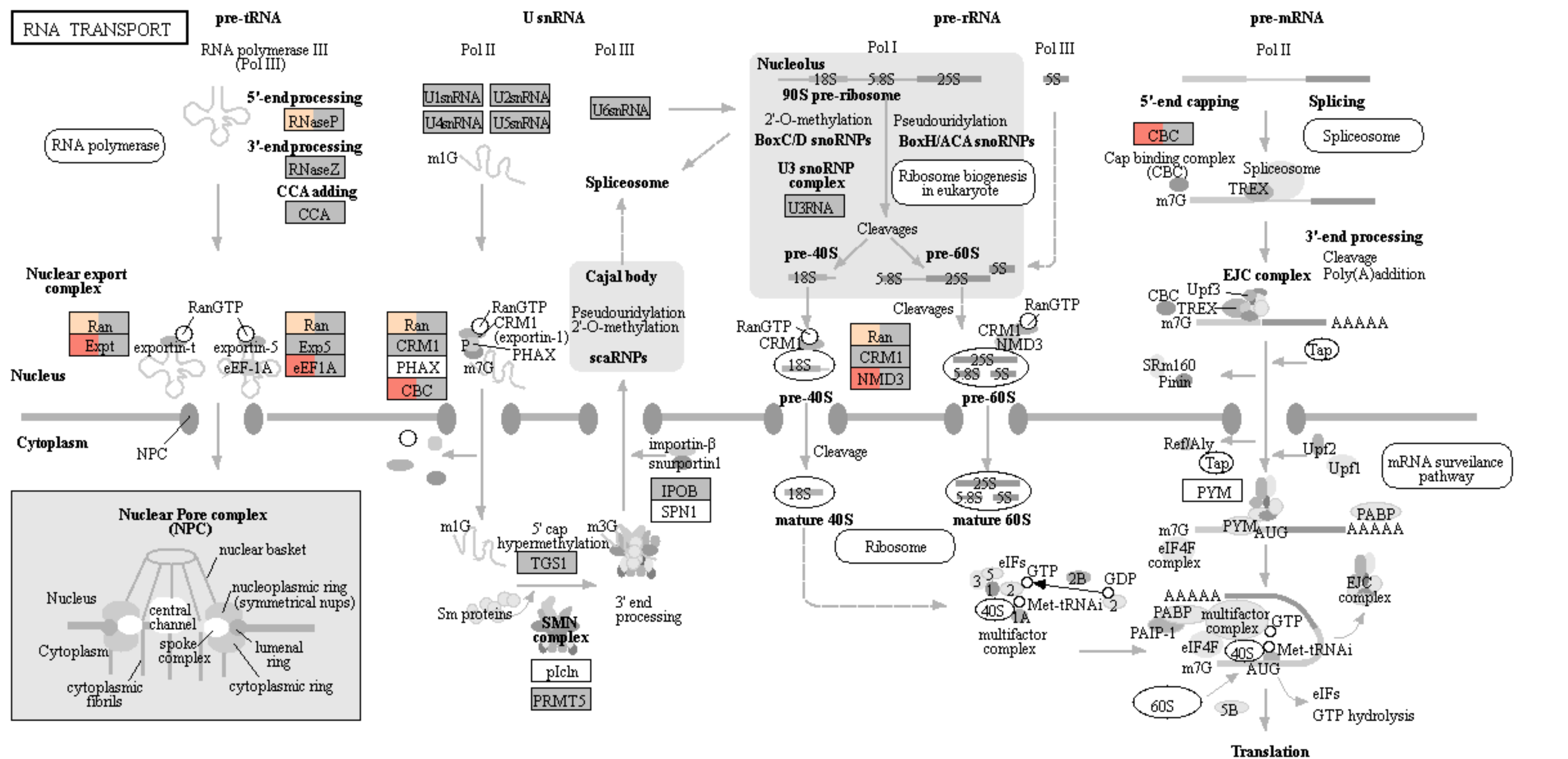
Recognition of  
empty A site

Ski7

m7G AAAAAA

Cytoplasmic exosome

Nonstop decay  
(NSD)





# AMINOACYL-tRNA BIOSYNTHESIS

