

Supplementary file with: 7 ca dUfUHj Y[ Ybca ]Vg'cZW ntf]X'Z b[ ]'fY] YU']bg][ \ lg']bhc'k Y'cV'] UHY' V]cfc d\ ]WUbX'dUH c[ Yb]W]Z'ghmY'cZGnbW ntf]i a 'YbXcV]c]W a

Bart T.L.H. van de Vossenberg & Sven Warris, Hai D.T. Nguyen, Marga P.E. van Gent-Pelzer, David L. Joly, Henri C. van de Geest, Peter J.M. Bonants, Donna S. Smith, C. André Lévesque, Theo A.J. van der Lee

Supplementary file 3: KEGG pathway analysis

# *Chytridiomycota versus Ascomycota and Basidiomycota*

The following color codes are used:



Present in  $\geq 1$  in all groups: Obligate biotrophic chytrid (Obl\_Chyt), Culturable chytrid (Cult\_Chyt), Culturable control species (Cult\_CTRL), and Obligate or facultative biotrophic Control species (Obl\_CTRL)



Absent in both Obl\_Chyt and all Obl\_CTRL, but present both in  $\geq 1$  Cult\_Chyt and  $\geq 1$  Cult\_CTRL



Present in  $\geq 1$  Obl\_Chyt and  $\geq 1$  Obl\_CTRL, but absent in all Cult\_Chyt and Cult\_CTRL



Present in  $\geq 1$  in all groups except Obl\_Chyt



Present in  $\geq 1$  Obl\_Chyt, but absent in all other groups (Cult\_Chyt, Cult\_CTRL, Obl\_CTRL)



Present in  $\geq 1$  in any specimen included, but not following the grouping as described above

Numerical values in colored boxed {a, b, c, d} represent the number of Obl\_Chyt strains (a, max = 2), Cult\_Chyt strains (b, max = 9), Cult\_CTRL strains (c, max = 3) and Obl\_CTRL strains (d, max = 3) for which a element was predicted by Interproscan.

## Species and strains included

**Obl\_Chyt:** *Synchytrium endobioticum* LEV6574  
*Synchytrium endobioticum* MB42

**Cult\_Chyt:** *Batrachochytrium dendrobatidis* JAM81  
*Batrachochytrium dendrobatidis* JEL423  
*Chytridium confervae* CBS 675.73  
*Gonapodya prolifera* JEL478  
*Homolaphlyctis polyrhiza* JEL142  
*Powellomyces hirtus* CBS 809.83  
*Spizellomyces palustris*(= *Phlyctochytrium palustre*) CBS 455.65  
*Spizellomyces punctatus* DAOM BR117  
*Synchytrium microbalum* JEL517

**Cult\_CTRL:** *Saccharomyces cerevisiae* (SCE)  
*Cryptococcus neoformans* (CNE)  
*Neurospora crassa* (NCR)

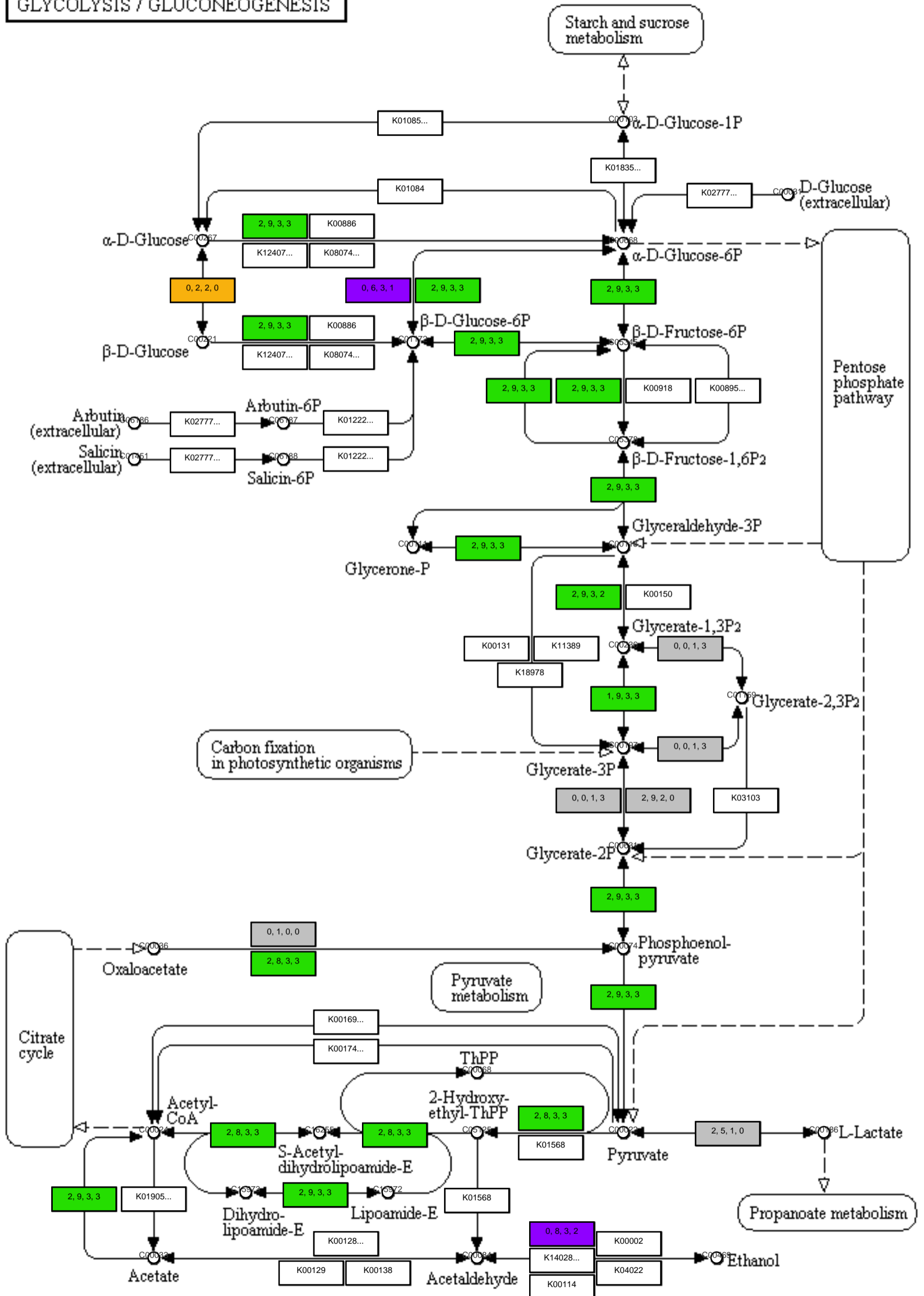
**Obl\_CTRL:** *Ustilago maydis* (UMA)  
*Melampsora larici-populina* (MLR)  
*Puccinia graminis* f.sp. *tritici* (PGR)



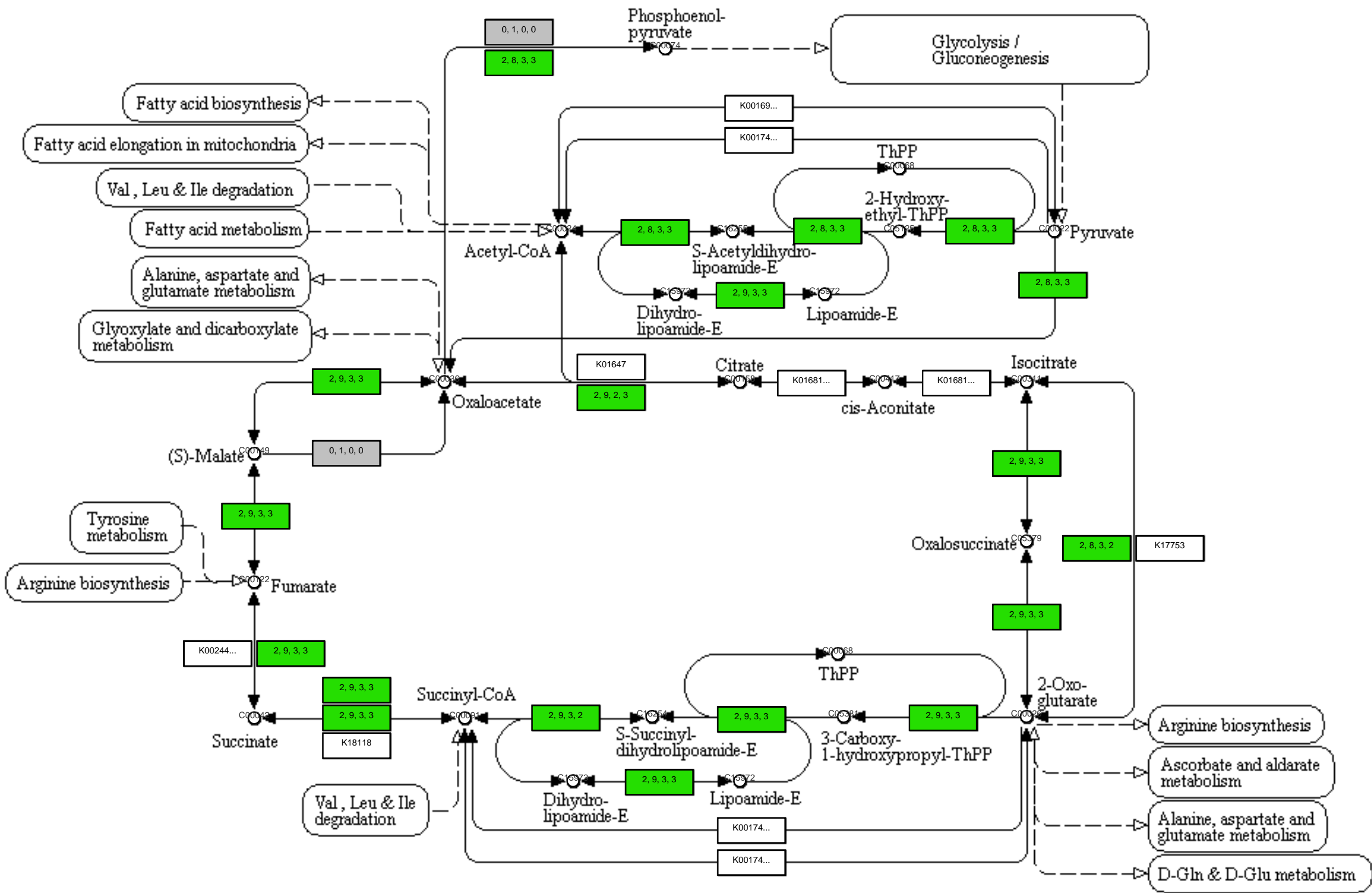
# 1. Carbohydrate metabolism

MAP	PATHWAY
10	Glycolysis / Gluconeogenesis
20	Citrate cycle (TCA cycle)
30	Pentose phosphate pathway
40	Pentose and glucuronate interconversions
51	Fructose and mannose metabolism
52	Galactose metabolism
53	Ascorbate and aldarate metabolism
500	Starch and sucrose metabolism
520	Amino sugar and nucleotide sugar metabolism
562	Inositol phosphate metabolism
620	Pyruvate metabolism
630	Glyoxylate and dicarboxylate metabolism
640	Propanoate metabolism
650	Butanoate metabolism
660	C5-Branched dibasic acid metabolism

# GLYCOLYSIS / GLUCONEOGENESIS



# CITRATE CYCLE (TCA CYCLE)









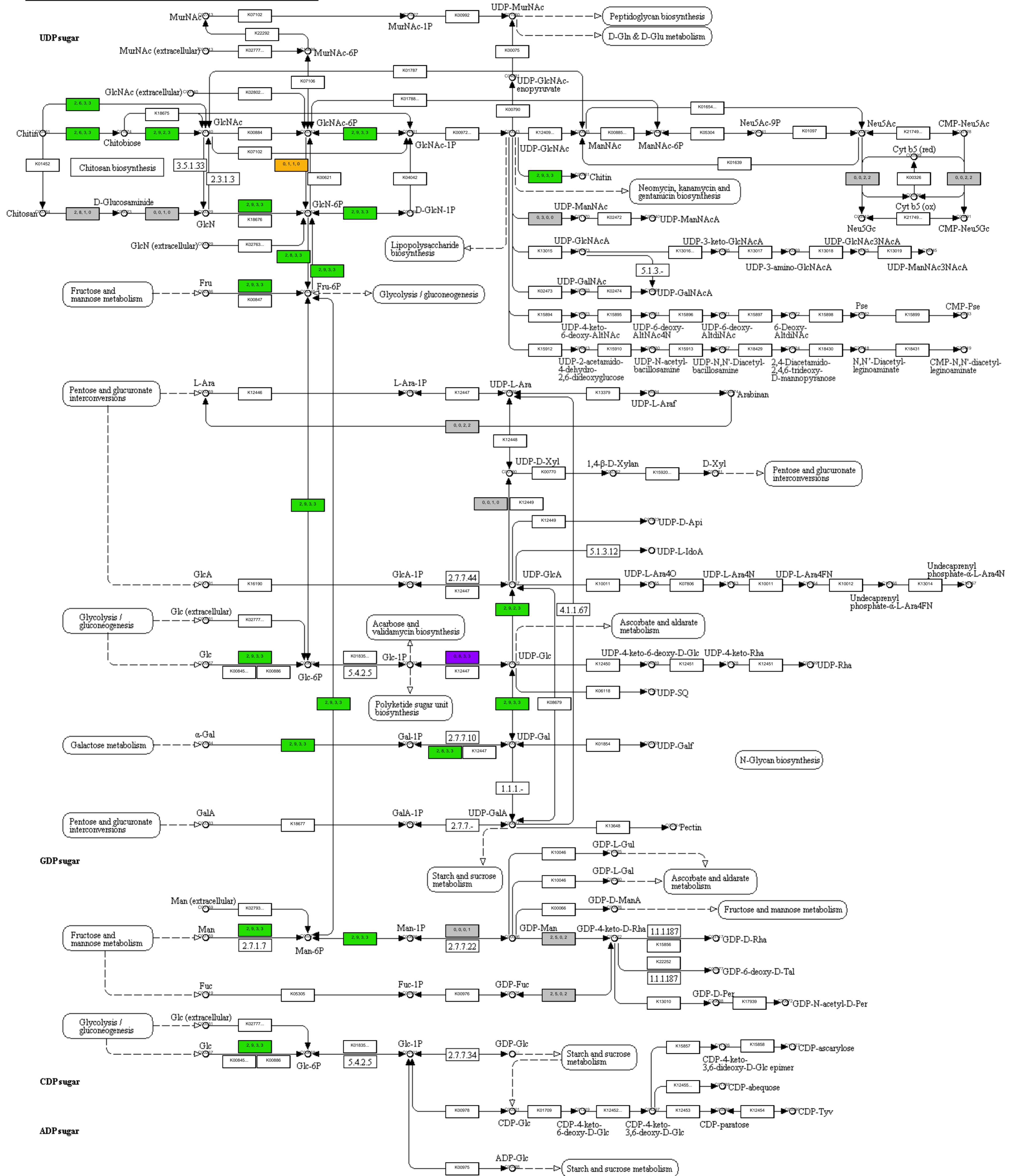






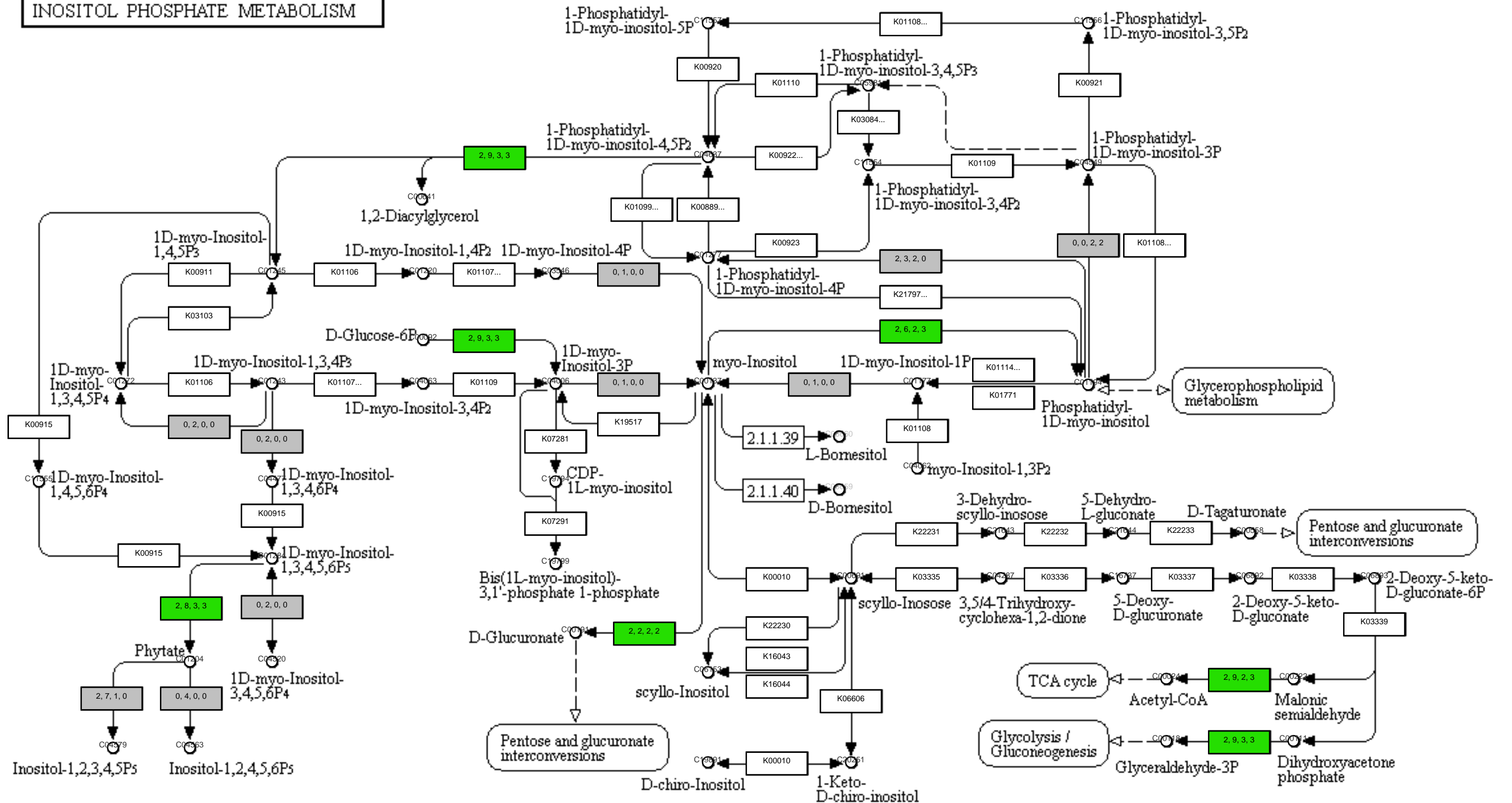


AMINO SUGAR AND NUCLEOTIDE SUGAR METABOLISM



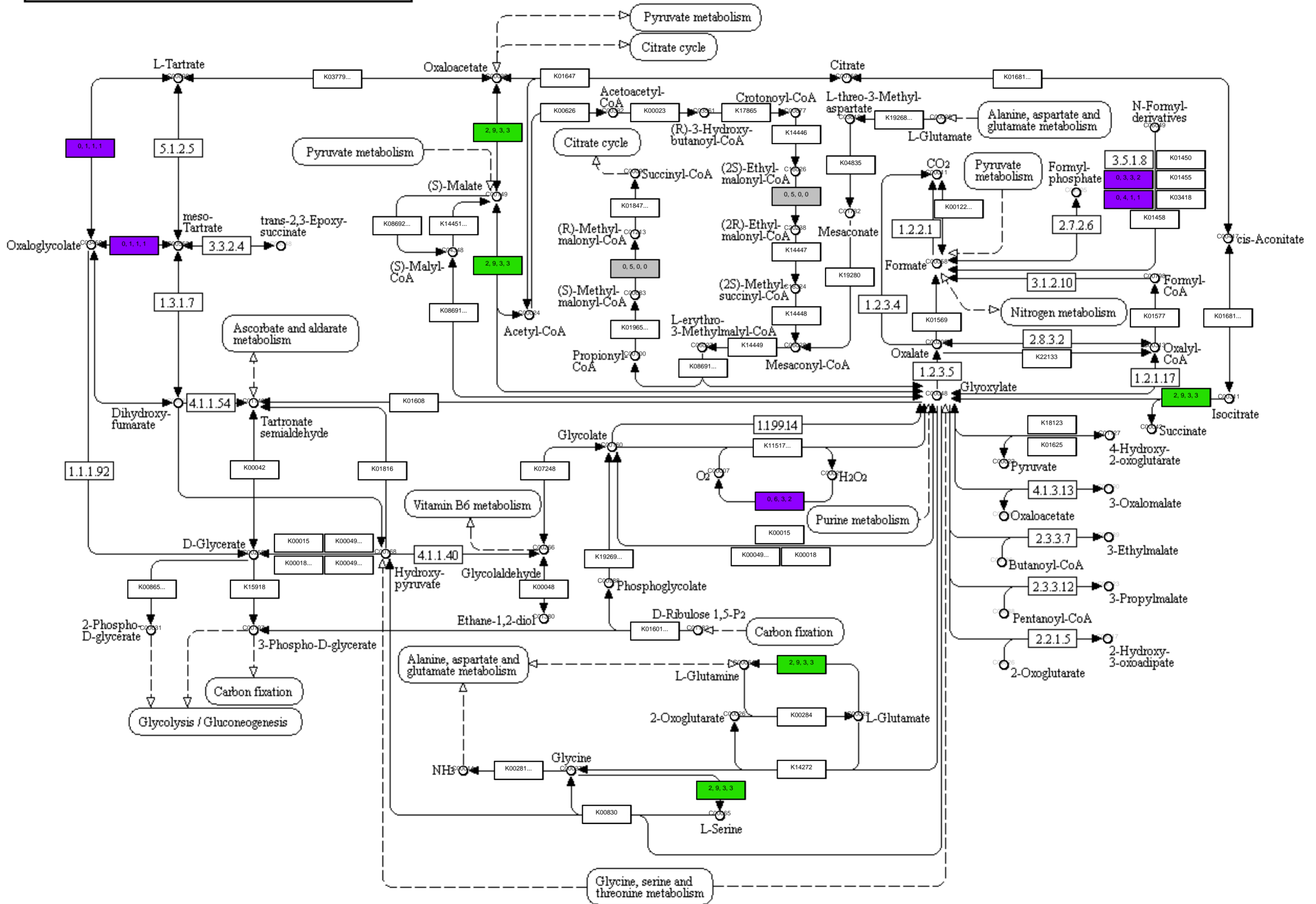


# INOSITOL PHOSPHATE METABOLISM





GLYOXYLATE AND DICARBOXYLATE METABOLISM

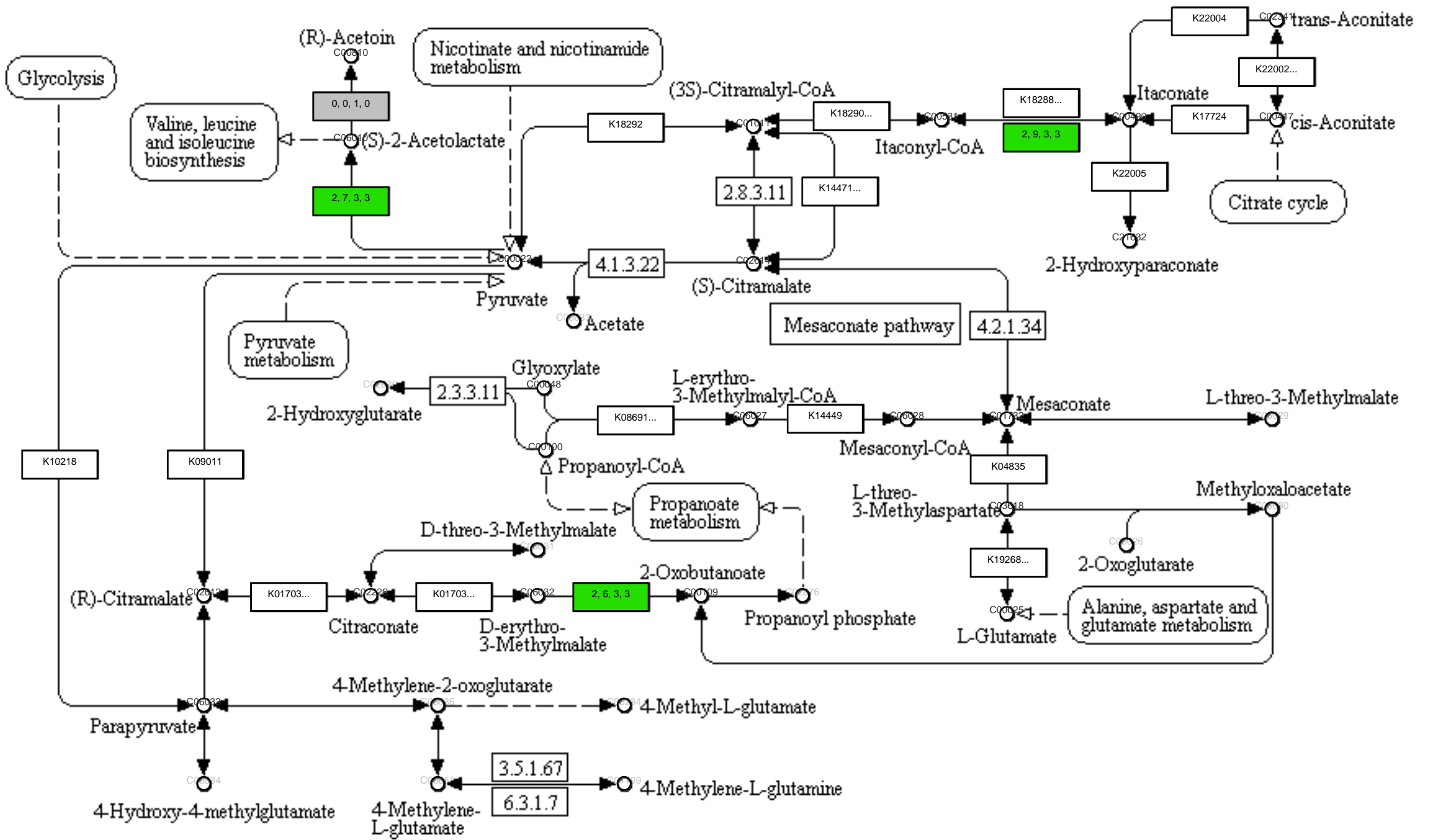








# C<sub>5</sub>-BRANCHED DIBASIC ACID METABOLISM

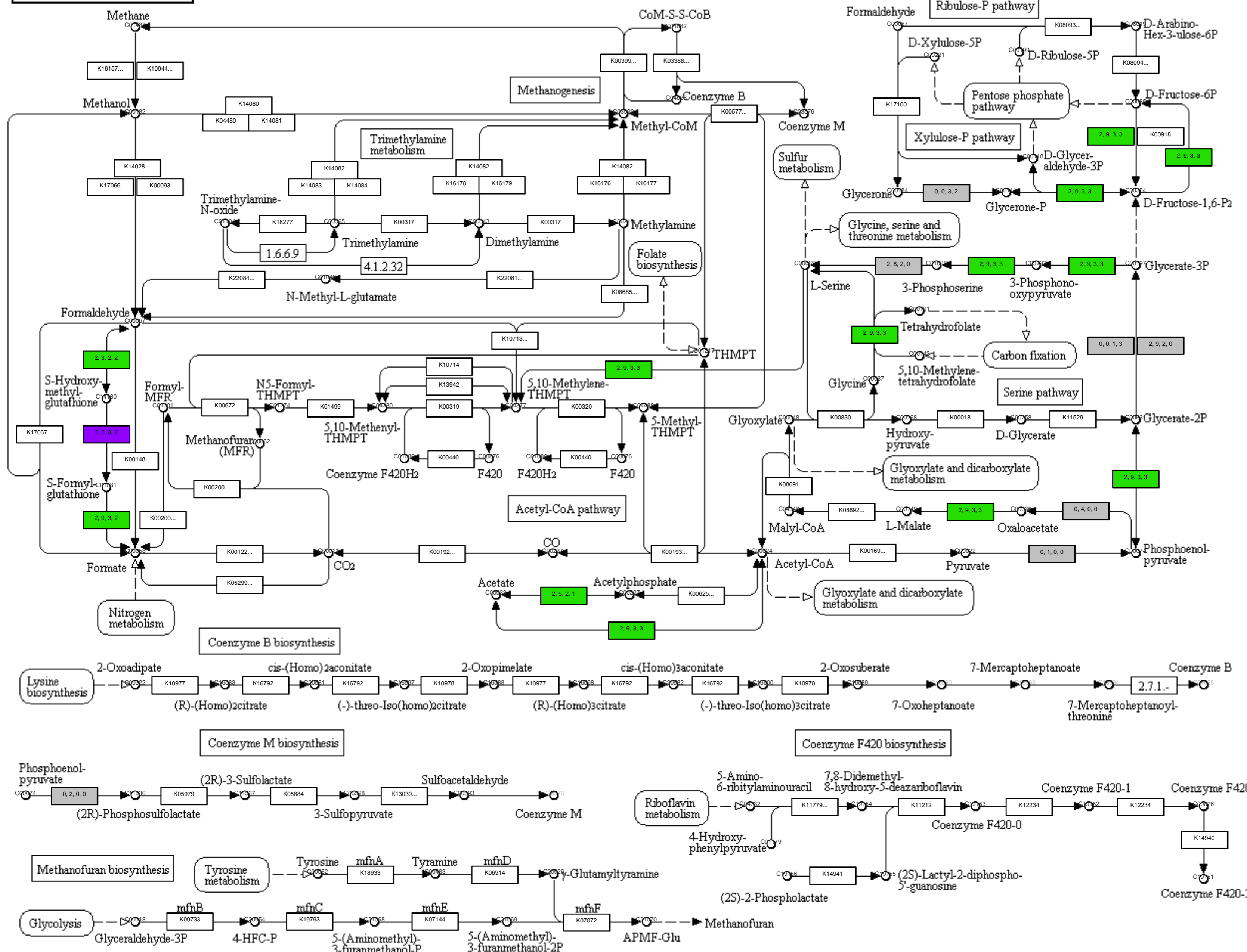


## 2. Energy metabolism

MAP	PATHWAY
<b>190</b>	Oxidative phosphorylation
<b>680</b>	Methane metabolism
<b>910</b>	Nitrogen metabolism
<b>920</b>	Sulfur metabolism

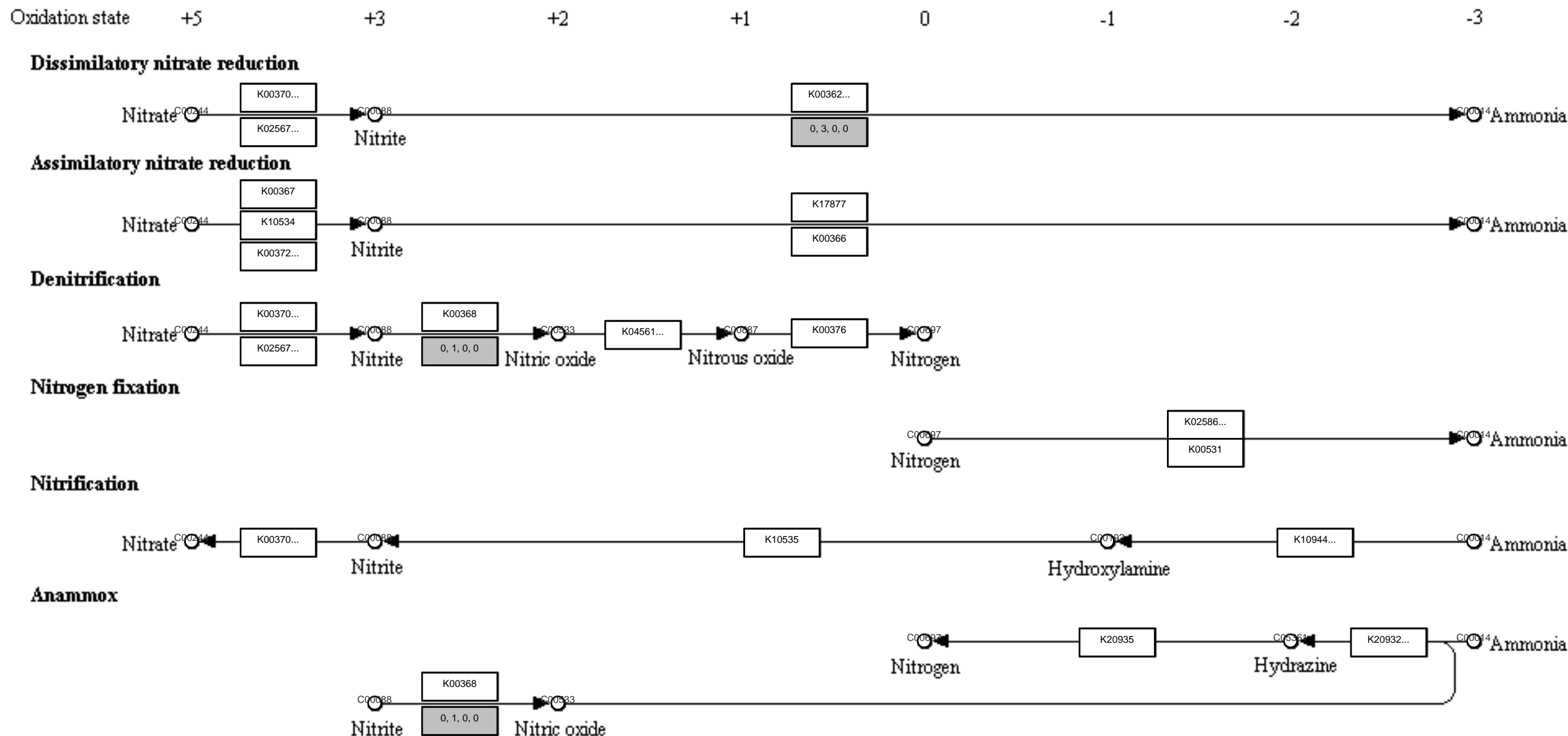
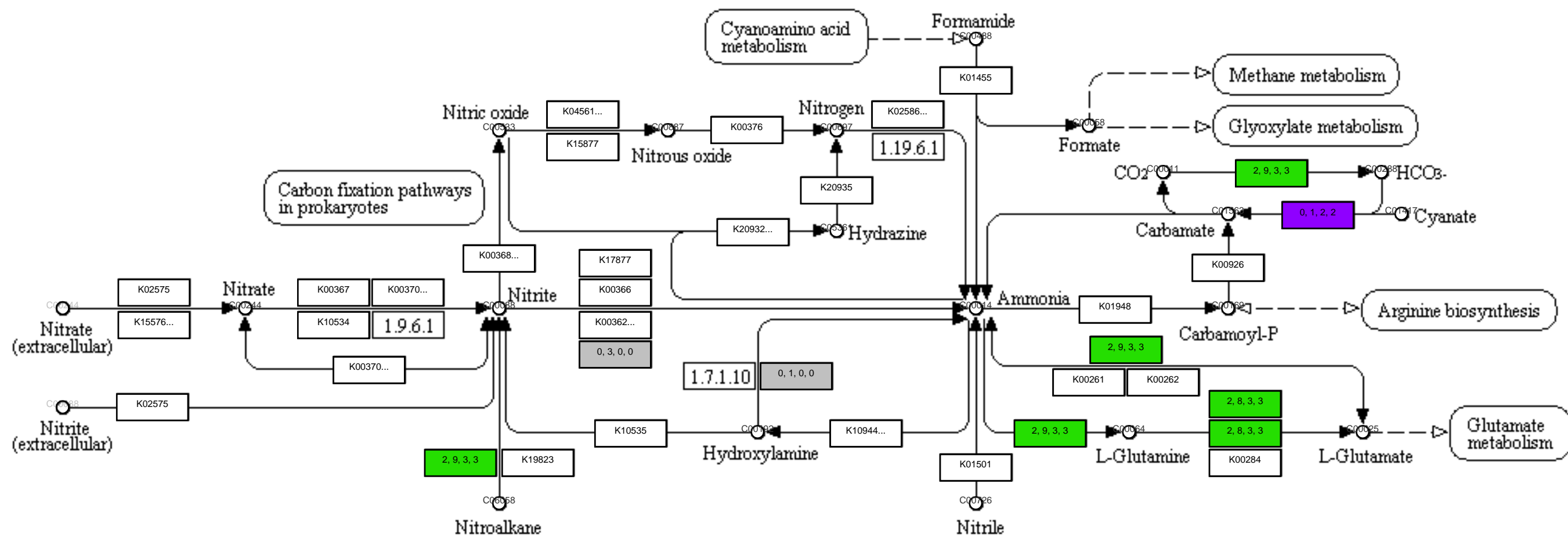


# METHANE METABOLISM

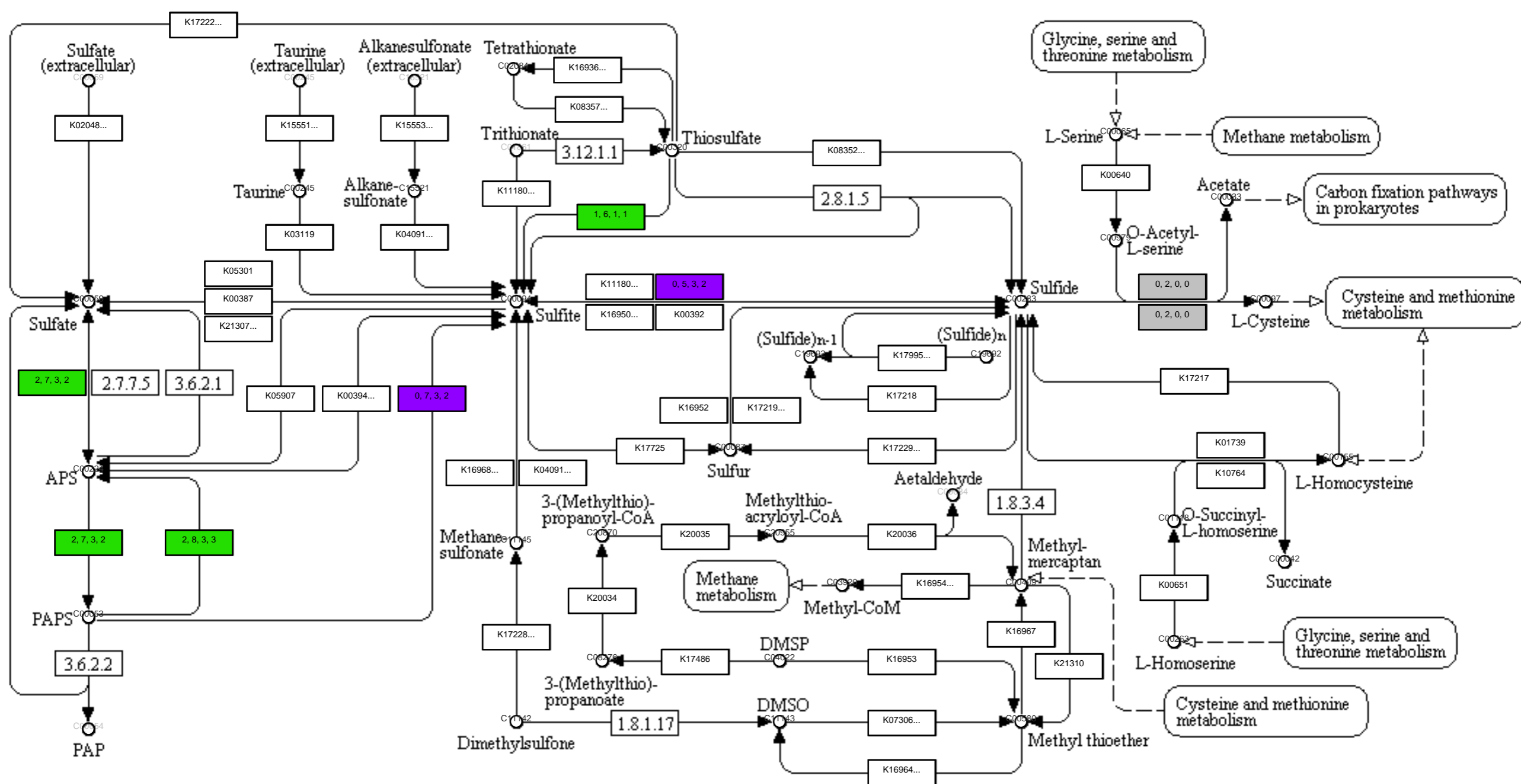




# NITROGEN METABOLISM

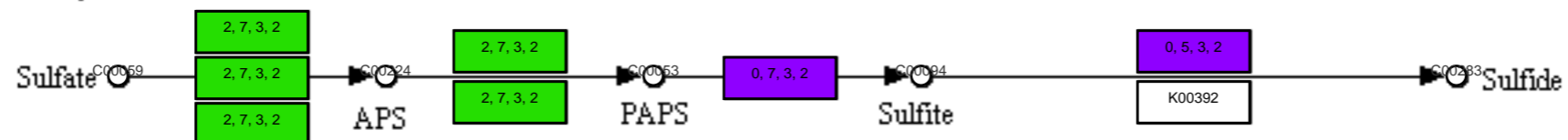


# SULFUR METABOLISM

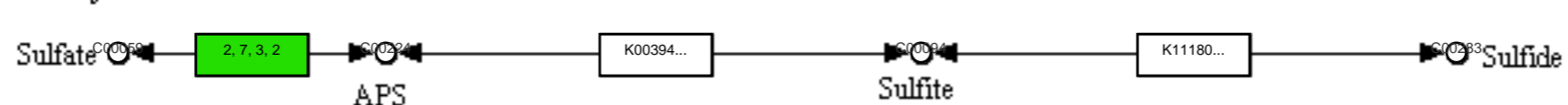


Oxidation state +6

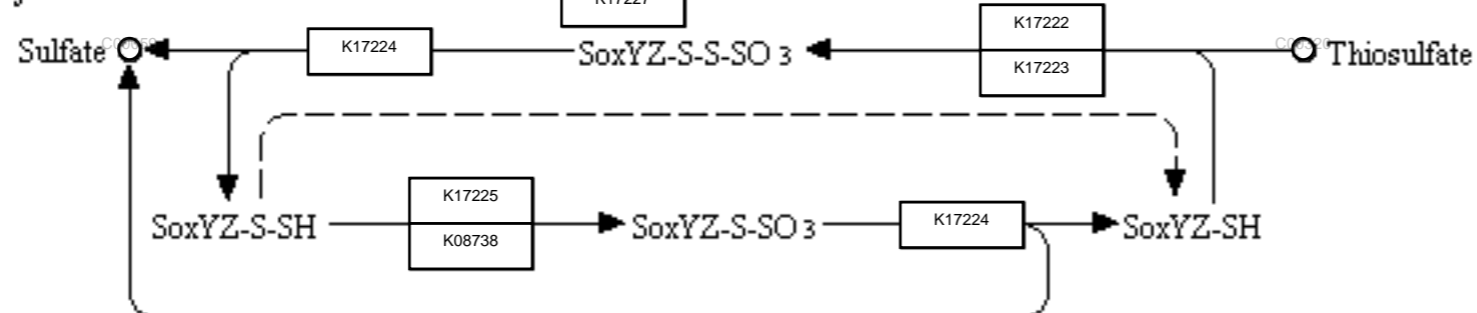
## Assimilatory sulfate reduction



## Dissimilatory sulfate reduction and oxidation



## SOX system

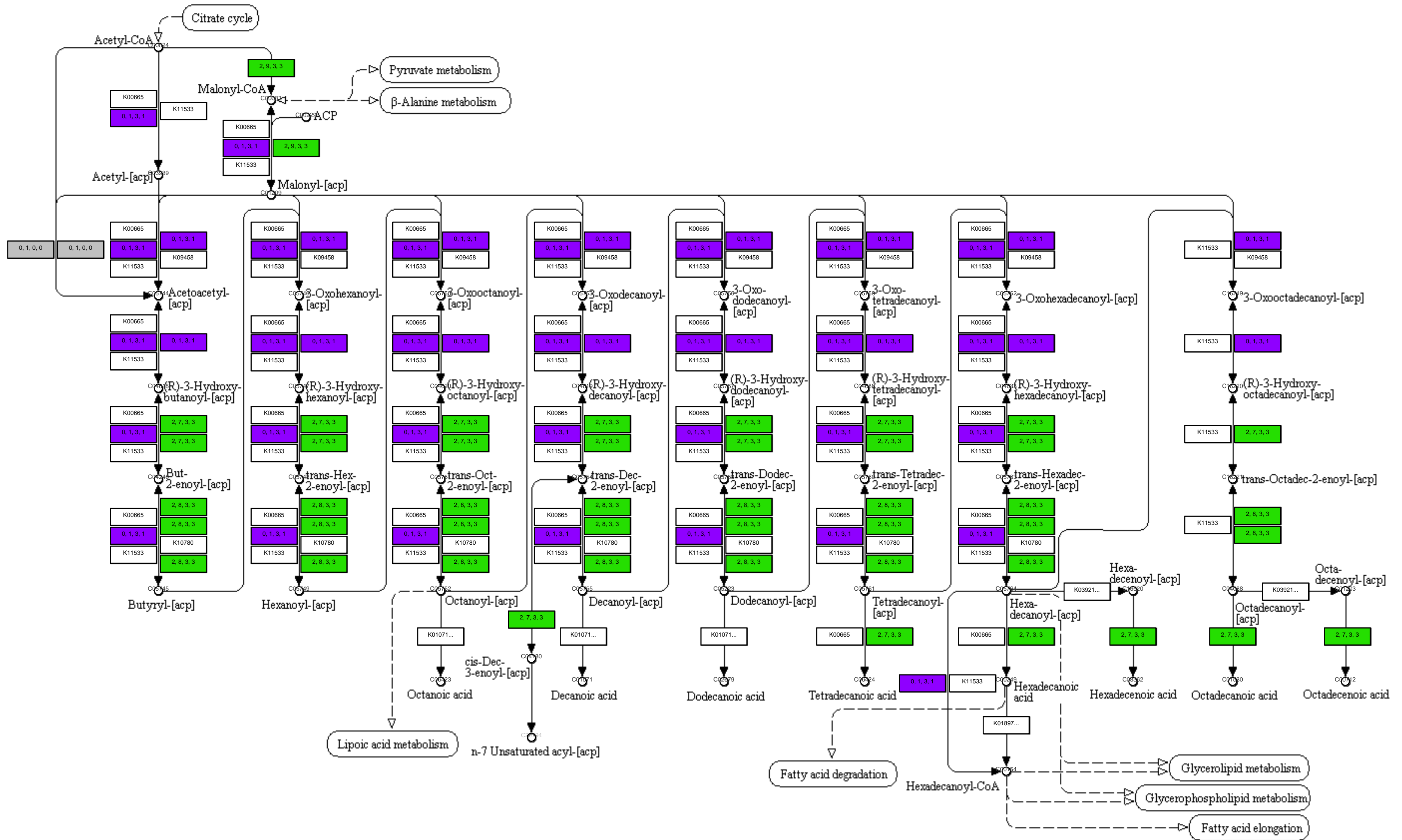


### 3. Lipid metabolism

MAP	PATHWAY
61	Fatty acid biosynthesis
62	Fatty acid elongation
71	Fatty acid degradation
72	Synthesis and degradation of ketone bodies
100	Steroid biosynthesis
561	Glycerolipid metabolism
564	Glycerophospholipid metabolism
565	Ether lipid metabolism
590	Arachidonic acid metabolism
592	alpha-Linolenic acid metabolism
600	Sphingolipid metabolism

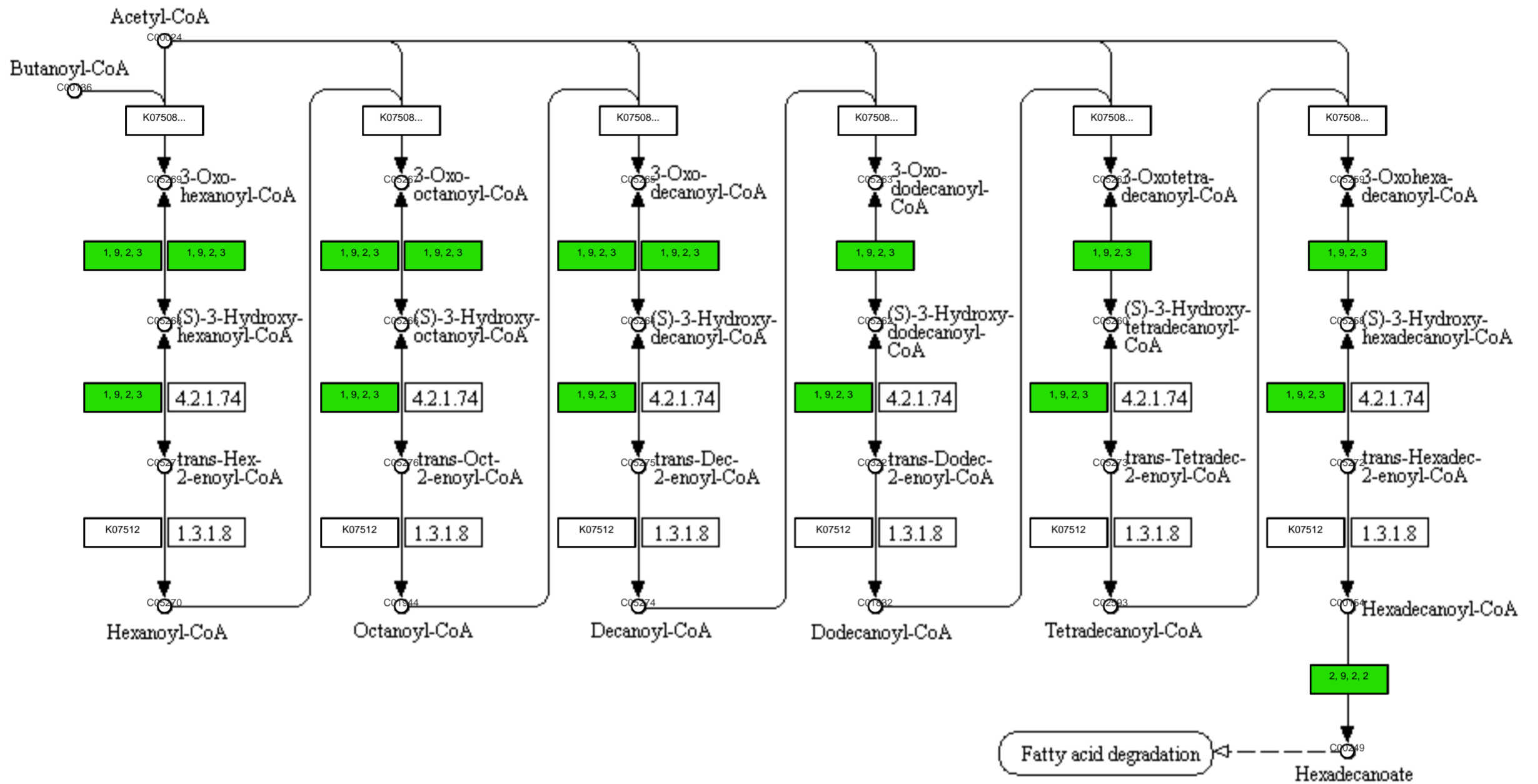


# FATTY ACID BIOSYNTHESIS

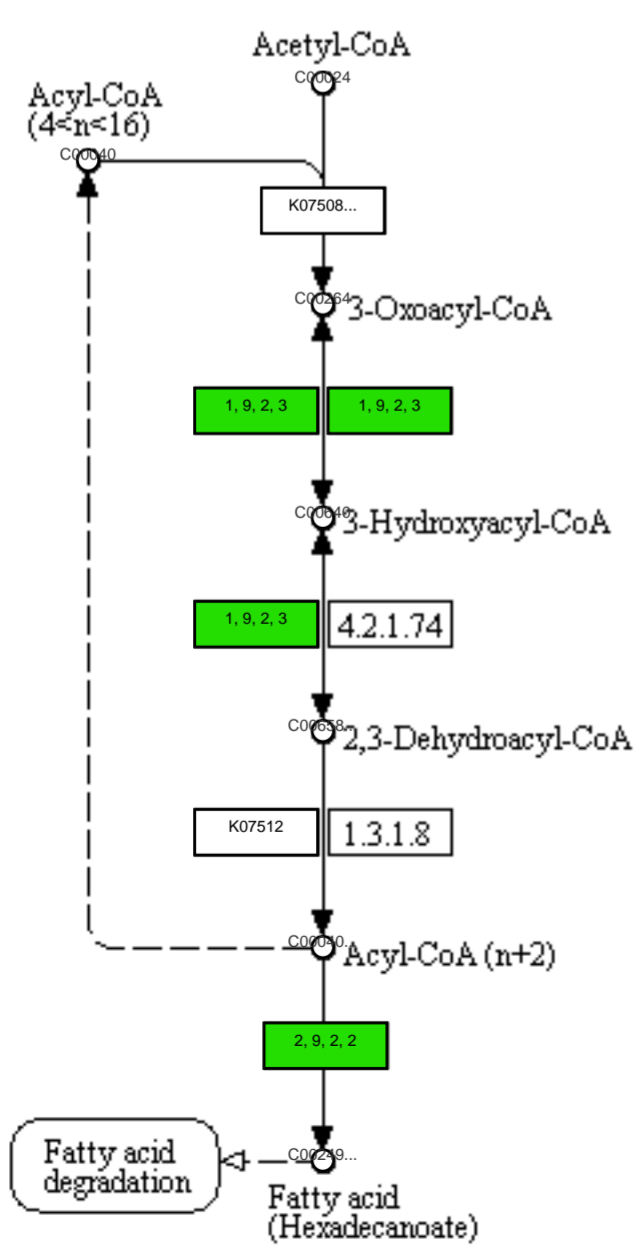


# FATTY ACID ELONGATION

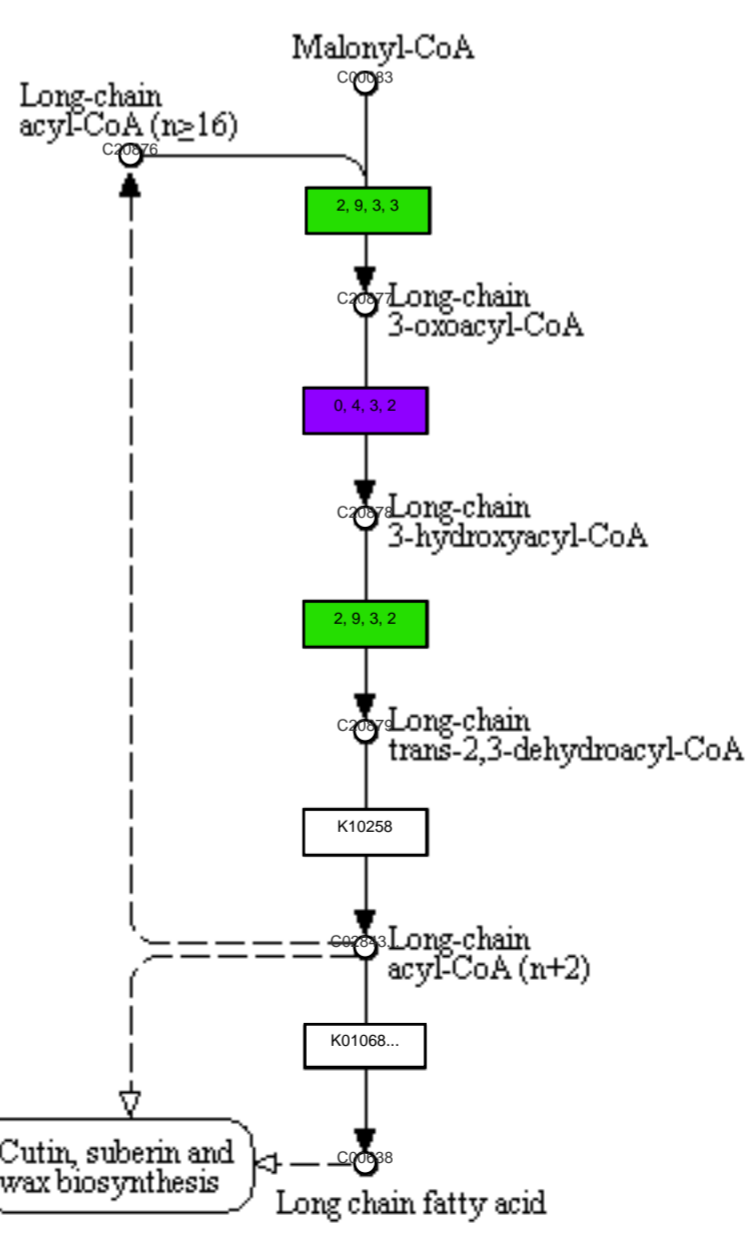
In mitochondria ( $4 < n < 16$ )



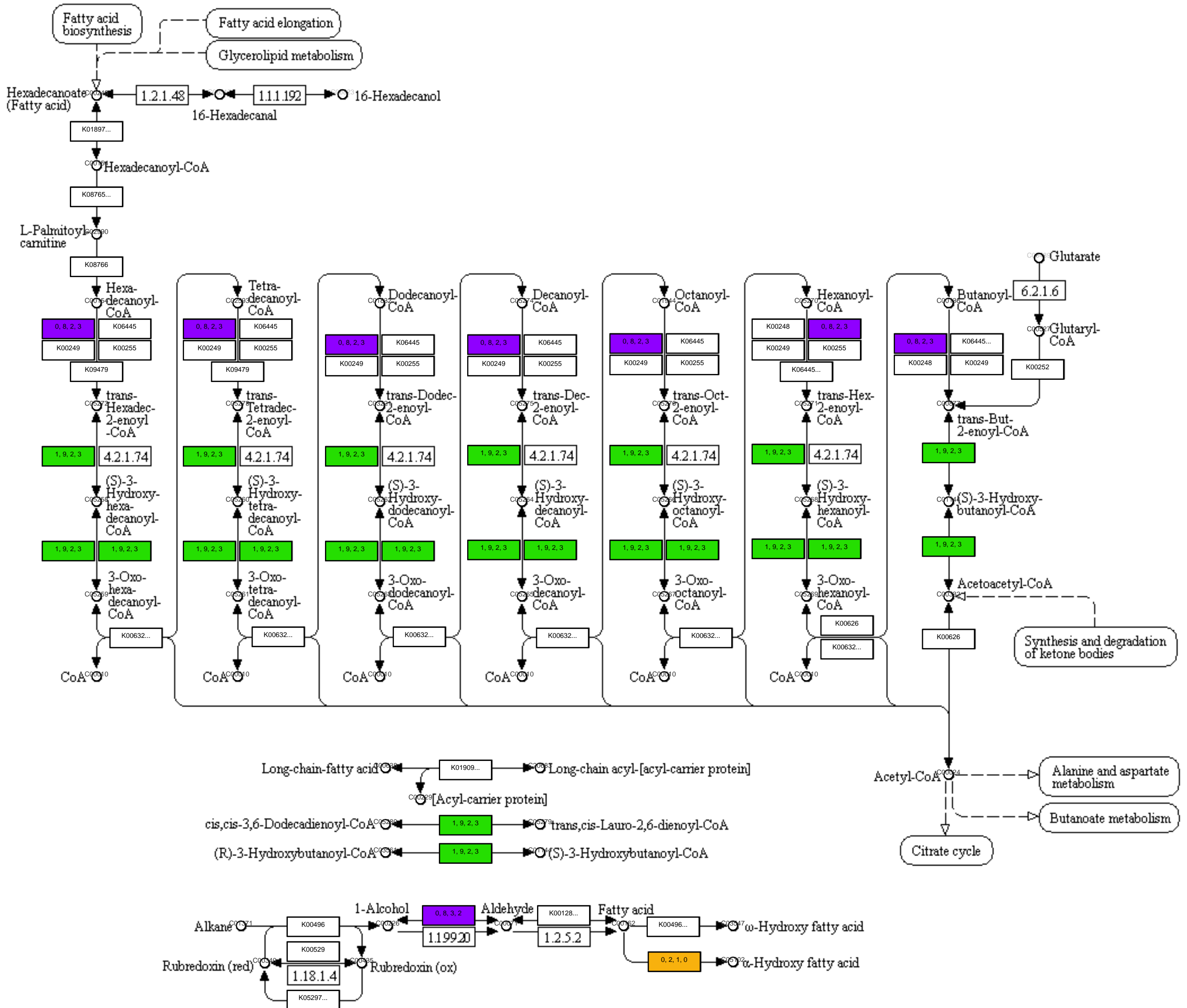
General forms  
In mitochondria ( $4 < n < 16$ )



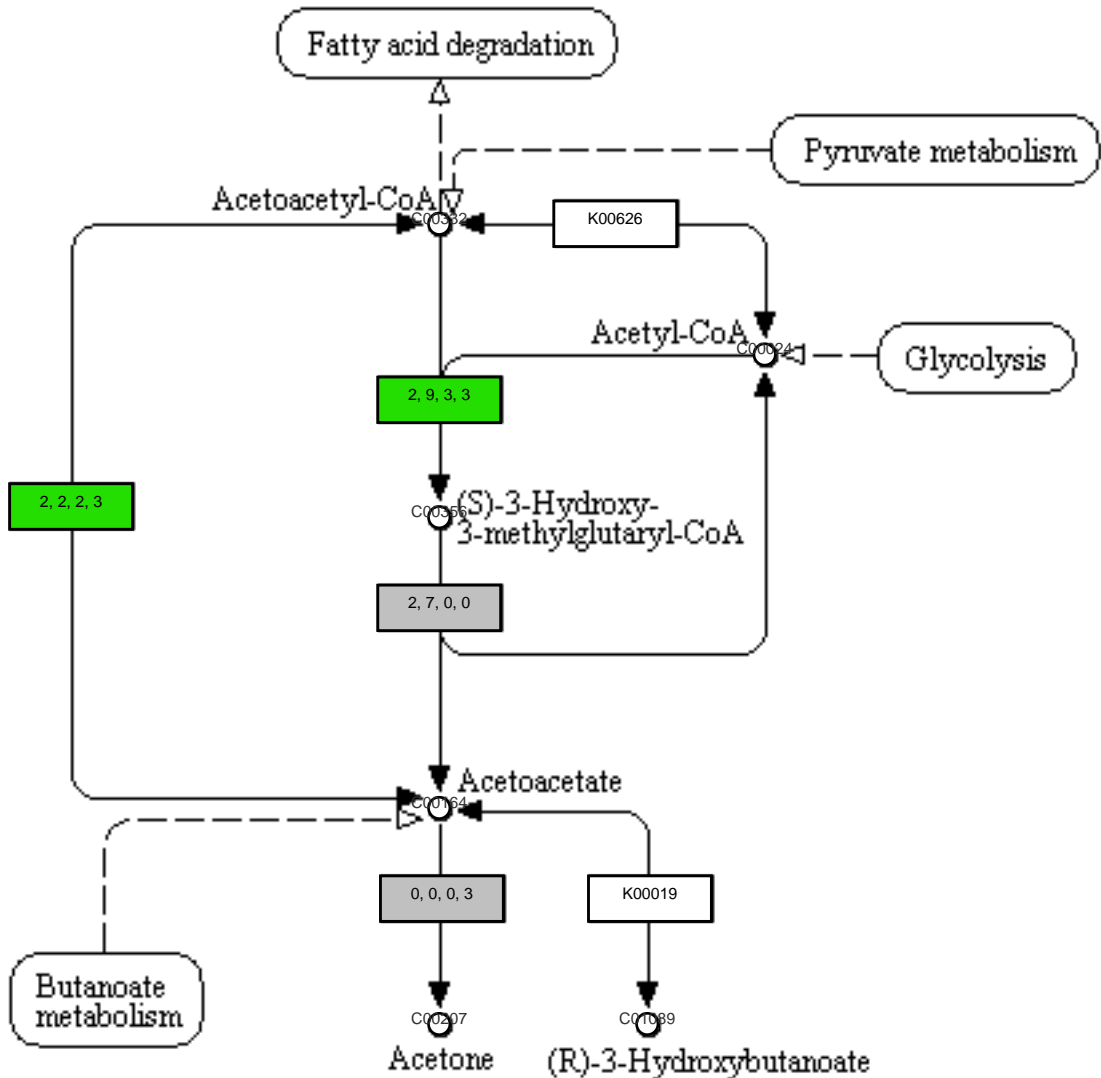
In endoplasmic reticulum ( $n \geq 16$ )



# FATTY ACID DEGRADATION

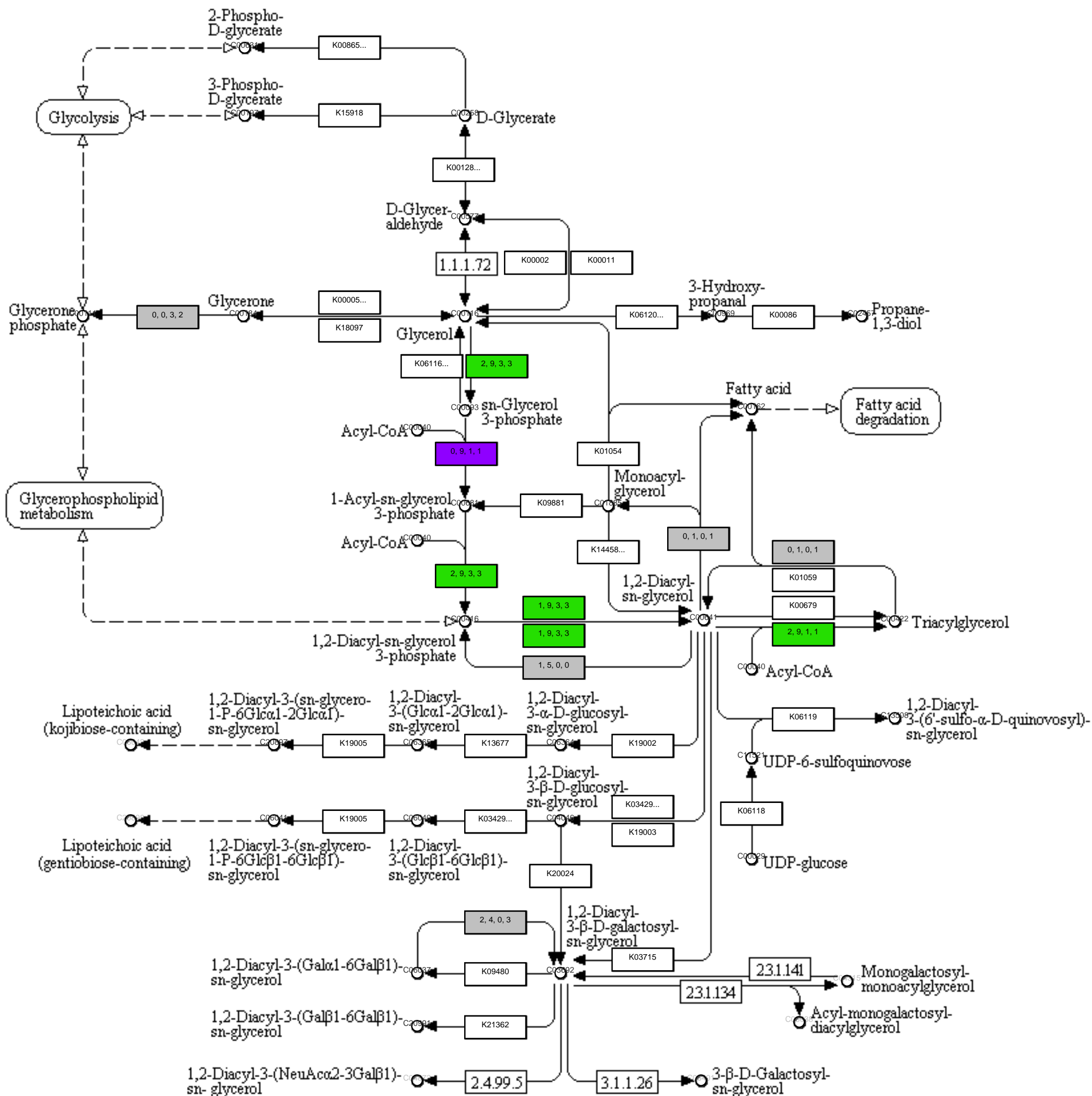


# SYNTHESIS AND DEGRADATION OF KETONE BODIES





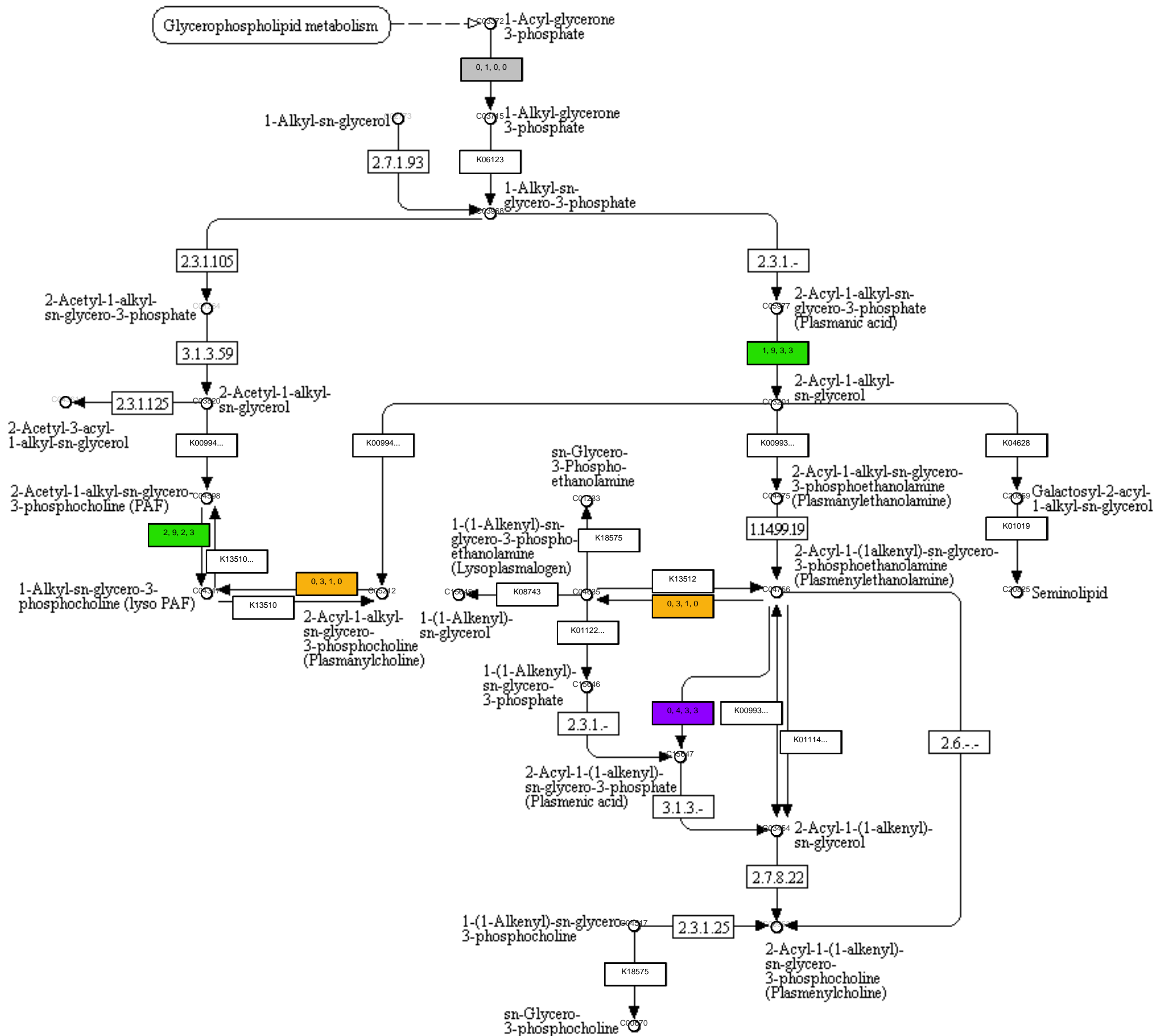
# GLYCEROLIPID METABOLISM







# ETHER LIPID METABOLISM







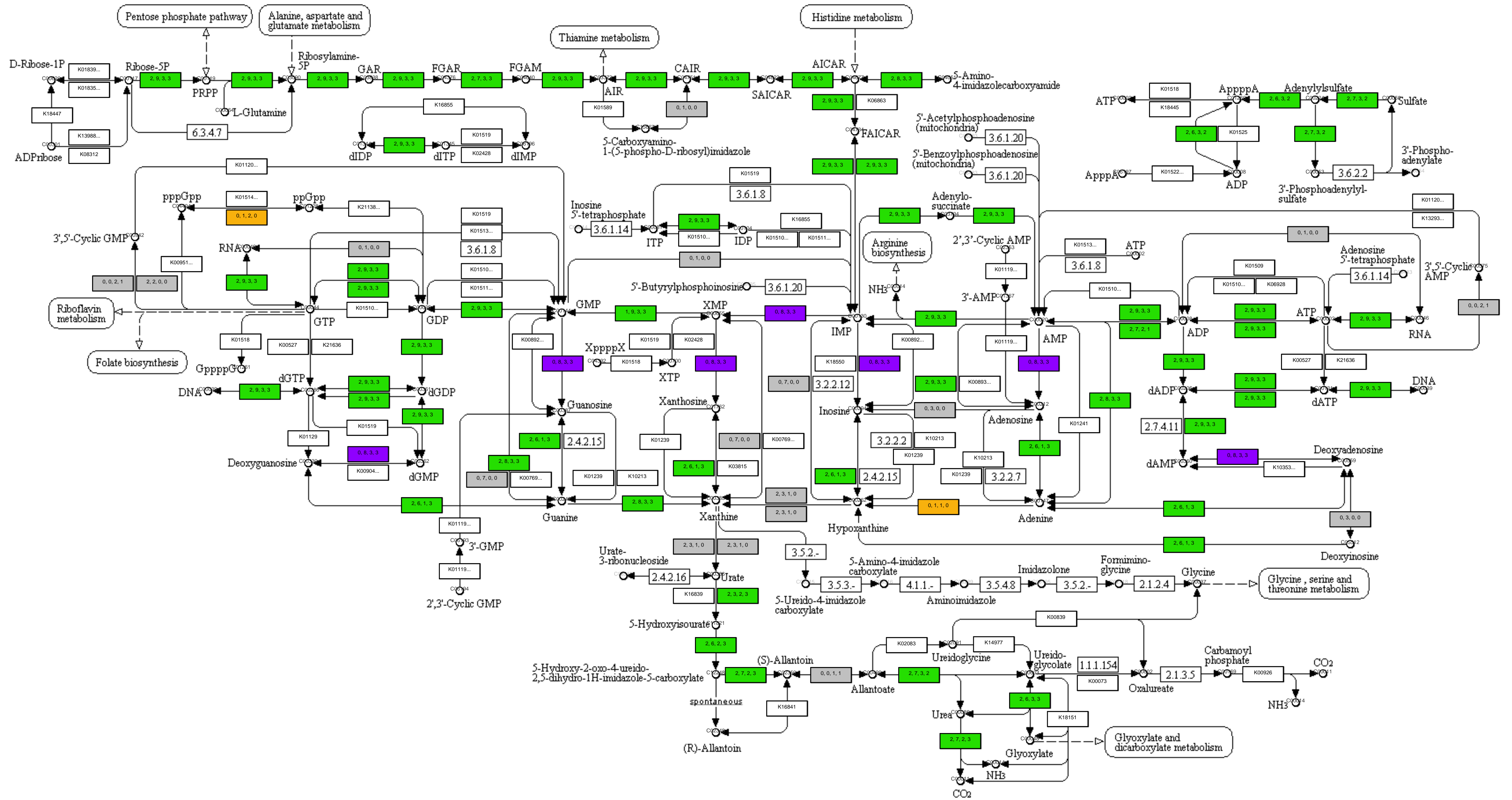




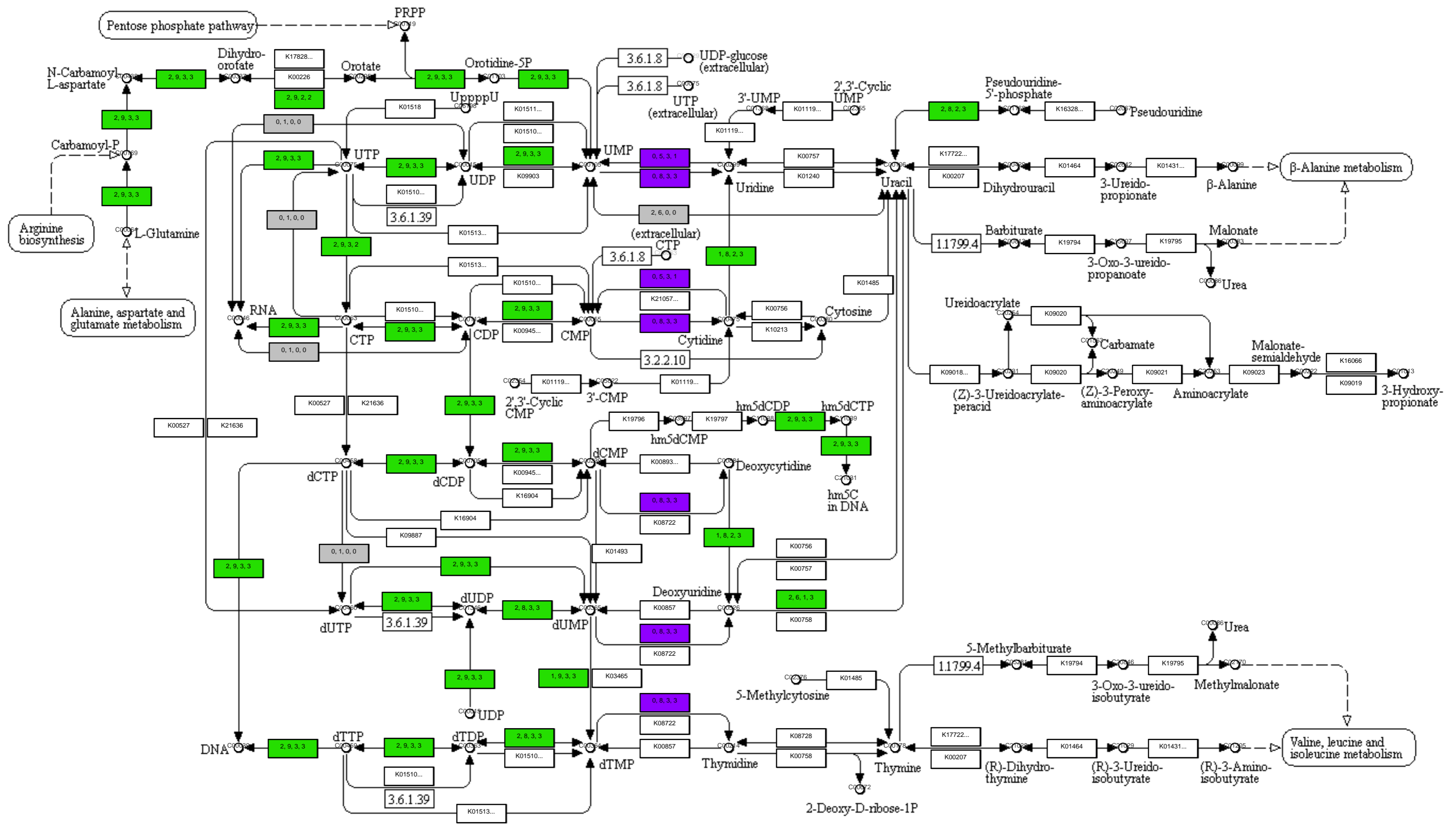
## 4. Nucleotide metabolism

MAP	PATHWAY
<b>230</b>	Purine metabolism
<b>240</b>	Pyrimidine metabolism

PURINE METABOLISM



# PYRIMIDINE METABOLISM

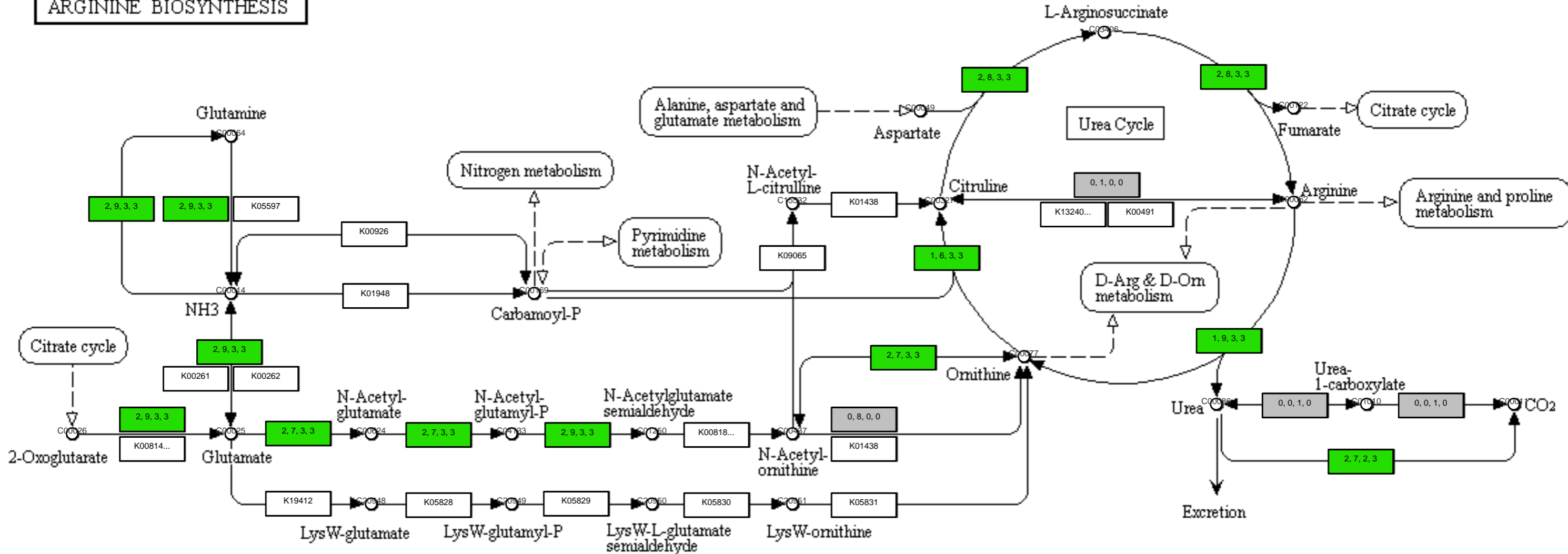


# 5. Amino Acid metabolism

MAP	PATHWAY
220	Arginine biosynthesis
250	Alanine, aspartate and glutamate metabolism
260	Glycine, serine and threonine metabolism
270	Cysteine and methionine metabolism
280	Valine, leucine and isoleucine degradation
290	Valine, leucine and isoleucine biosynthesis
300	Lysine biosynthesis
310	Lysine degradation
330	Arginine and proline metabolism
340	Histidine metabolism
350	Tyrosine metabolism
360	Phenylalanine metabolism
380	Tryptophan metabolism
400	Phenylalanine, tyrosine and tryptophan biosynthesis



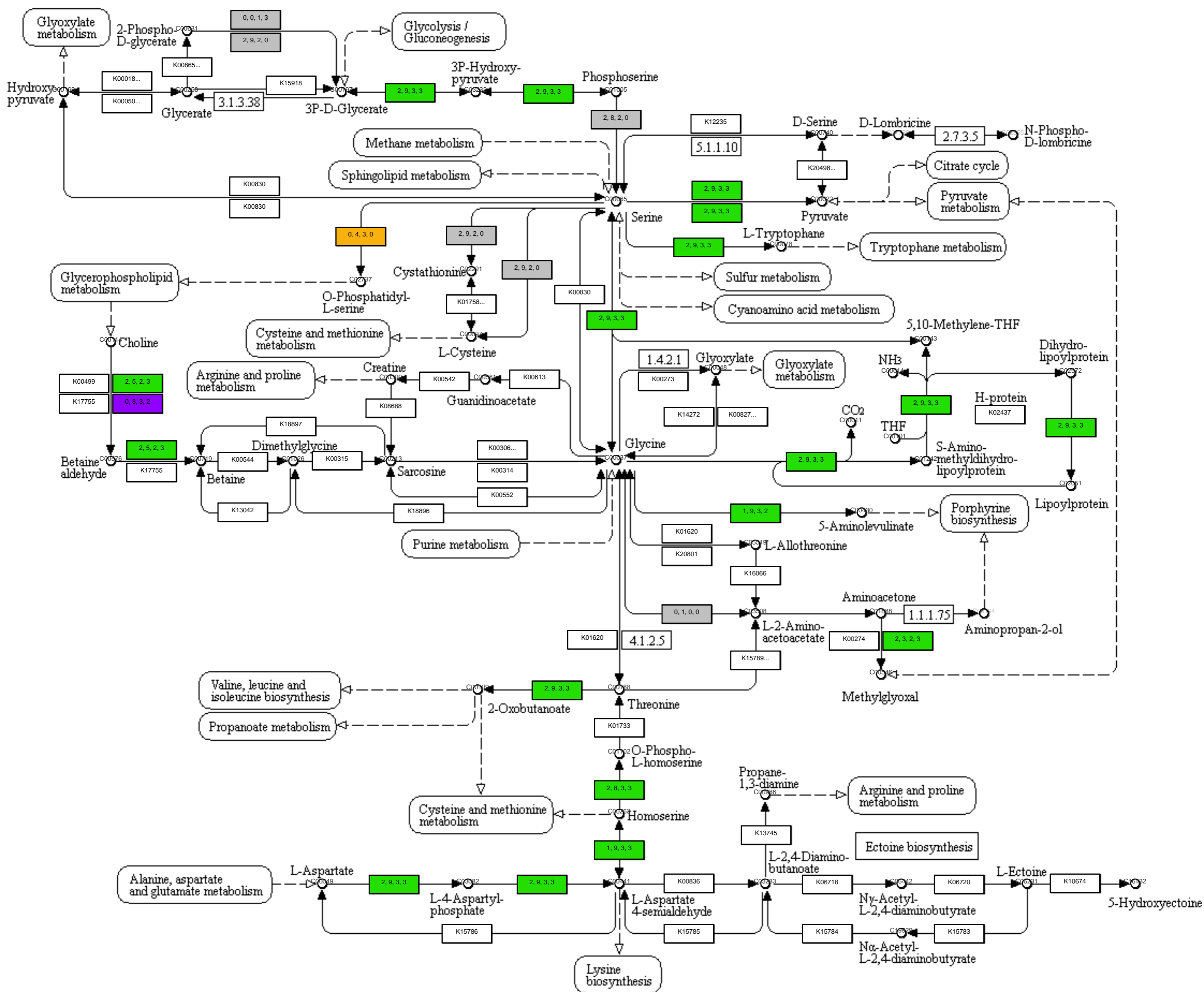
# ARGININE BIOSYNTHESIS





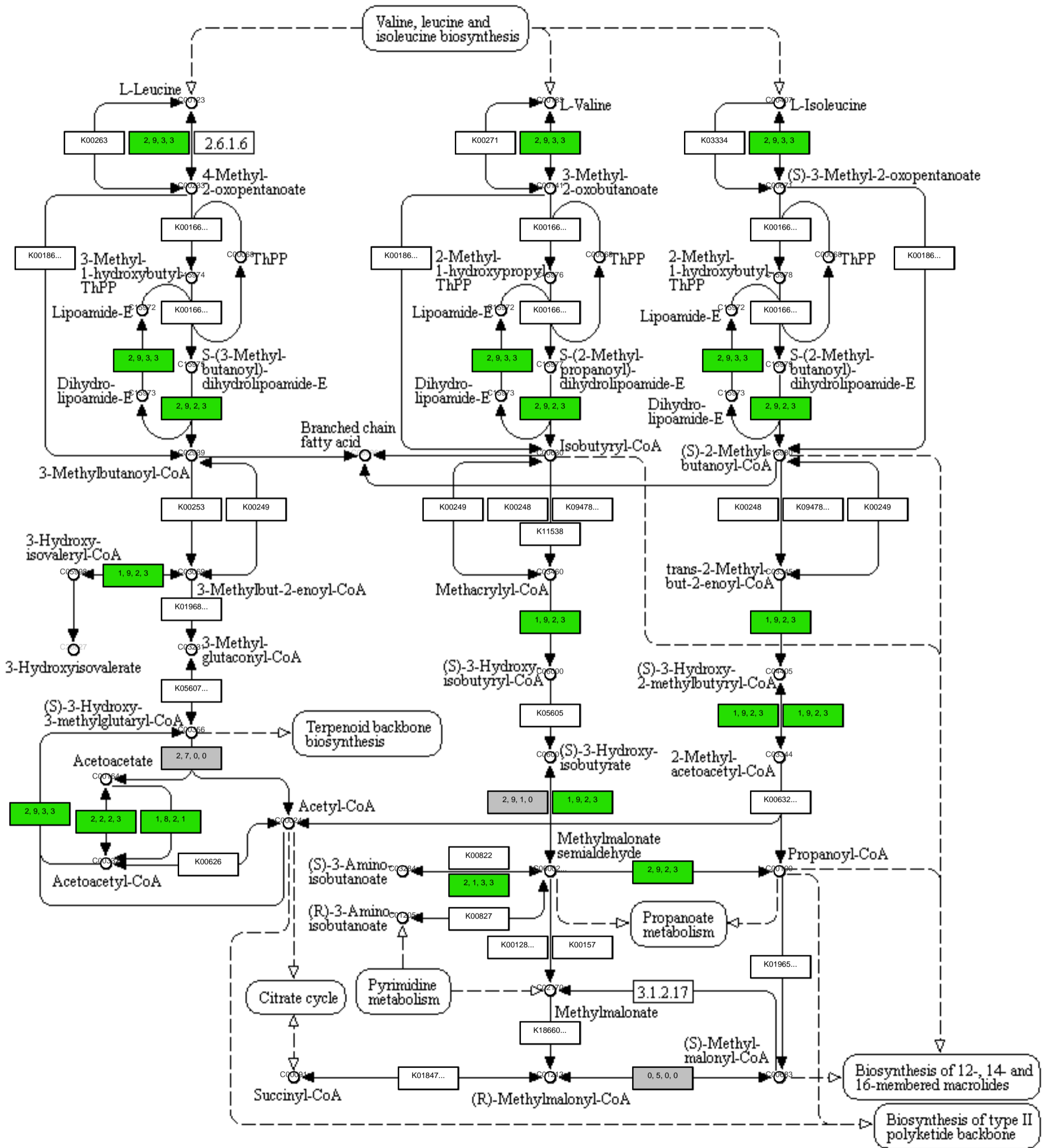


GLYCINE, SERINE AND THREONINE METABOLISM





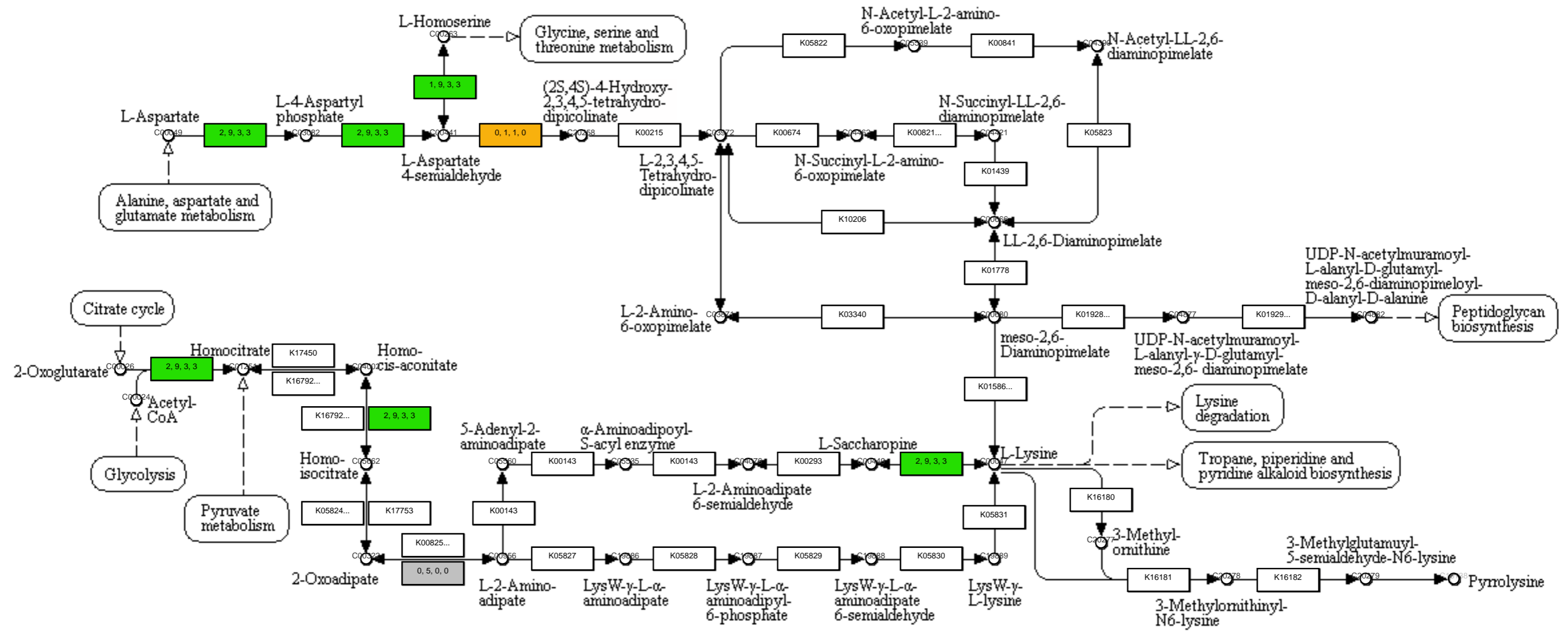
# VALINE, LEUCINE AND ISOLEUCINE DEGRADATION





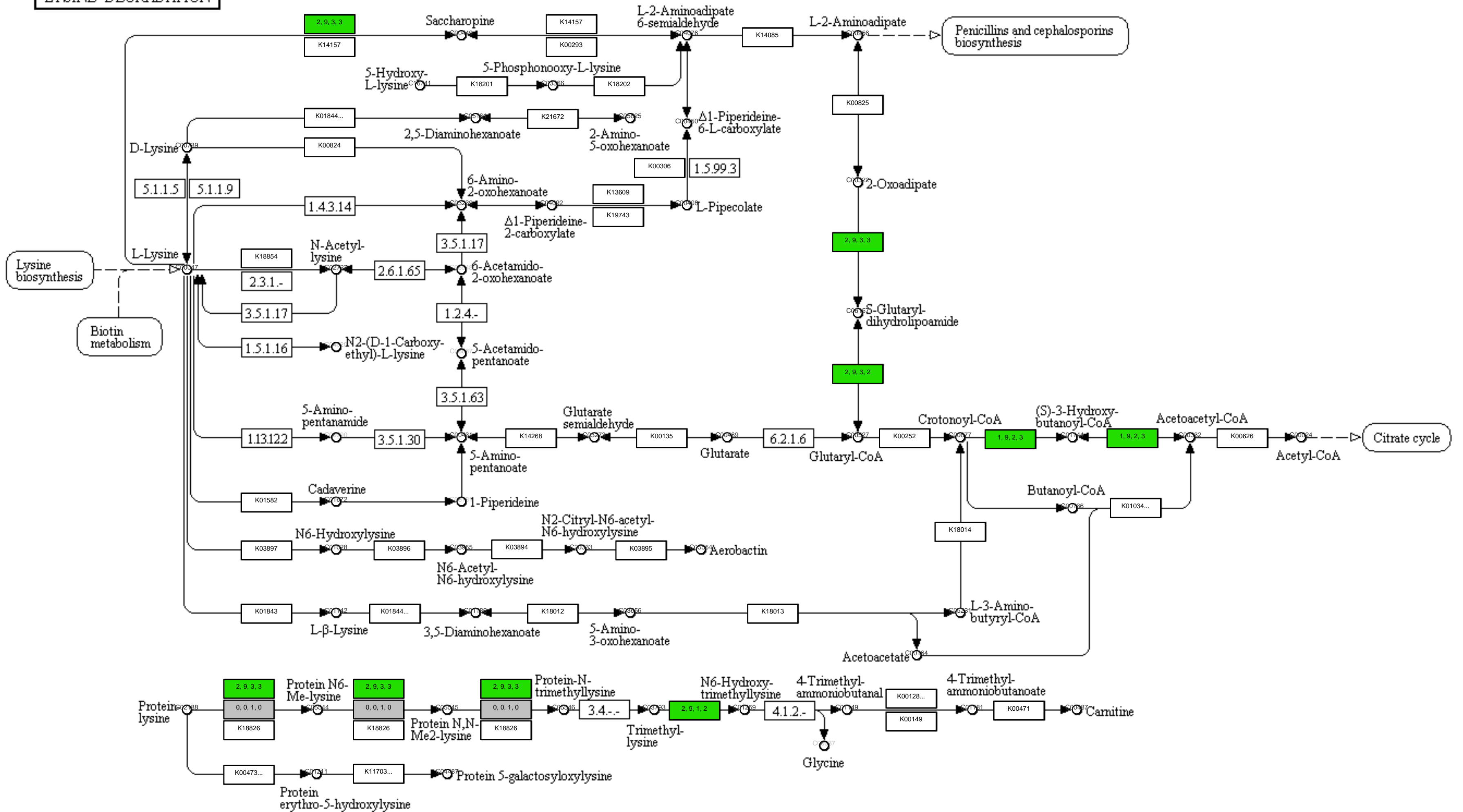


# LYSINE BIOSYNTHESIS

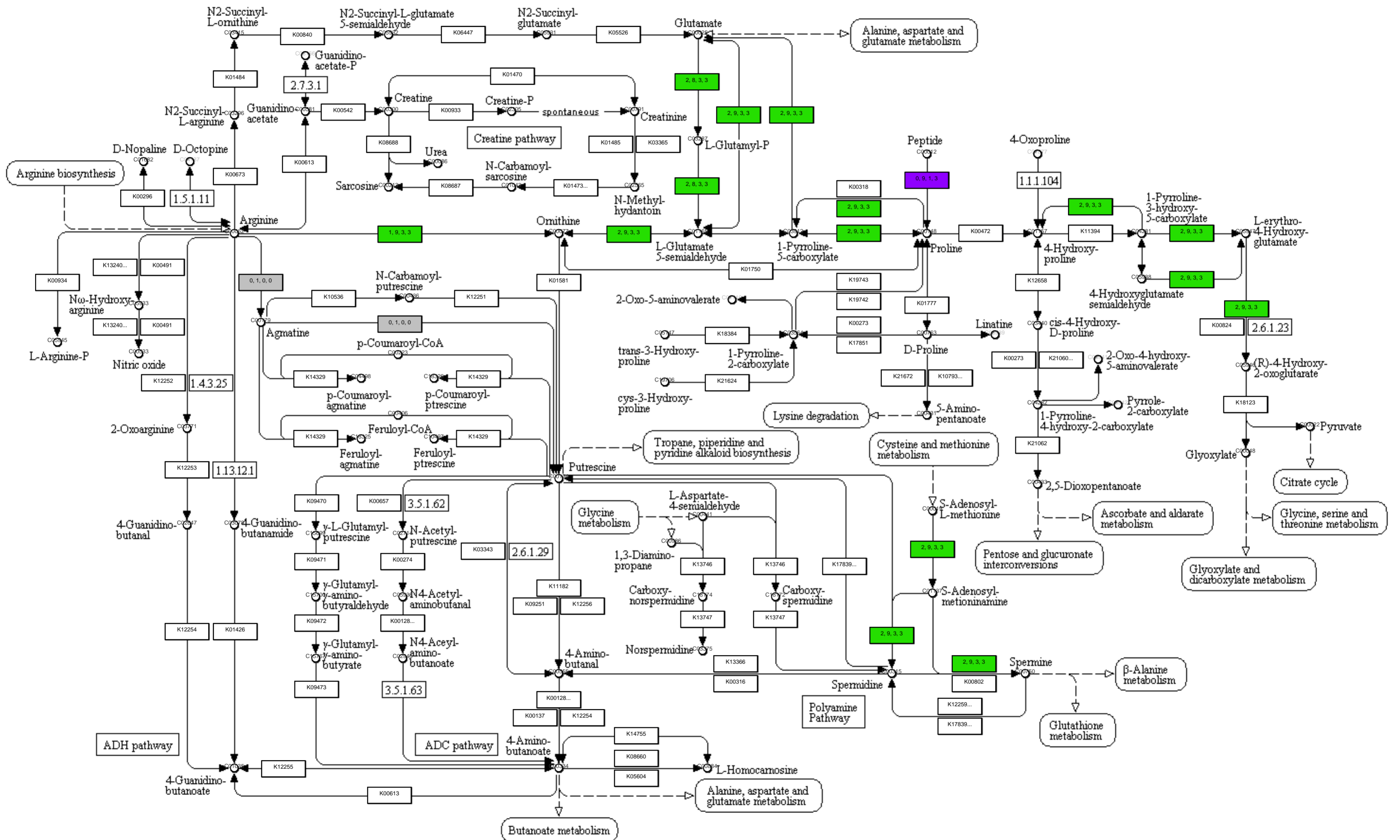




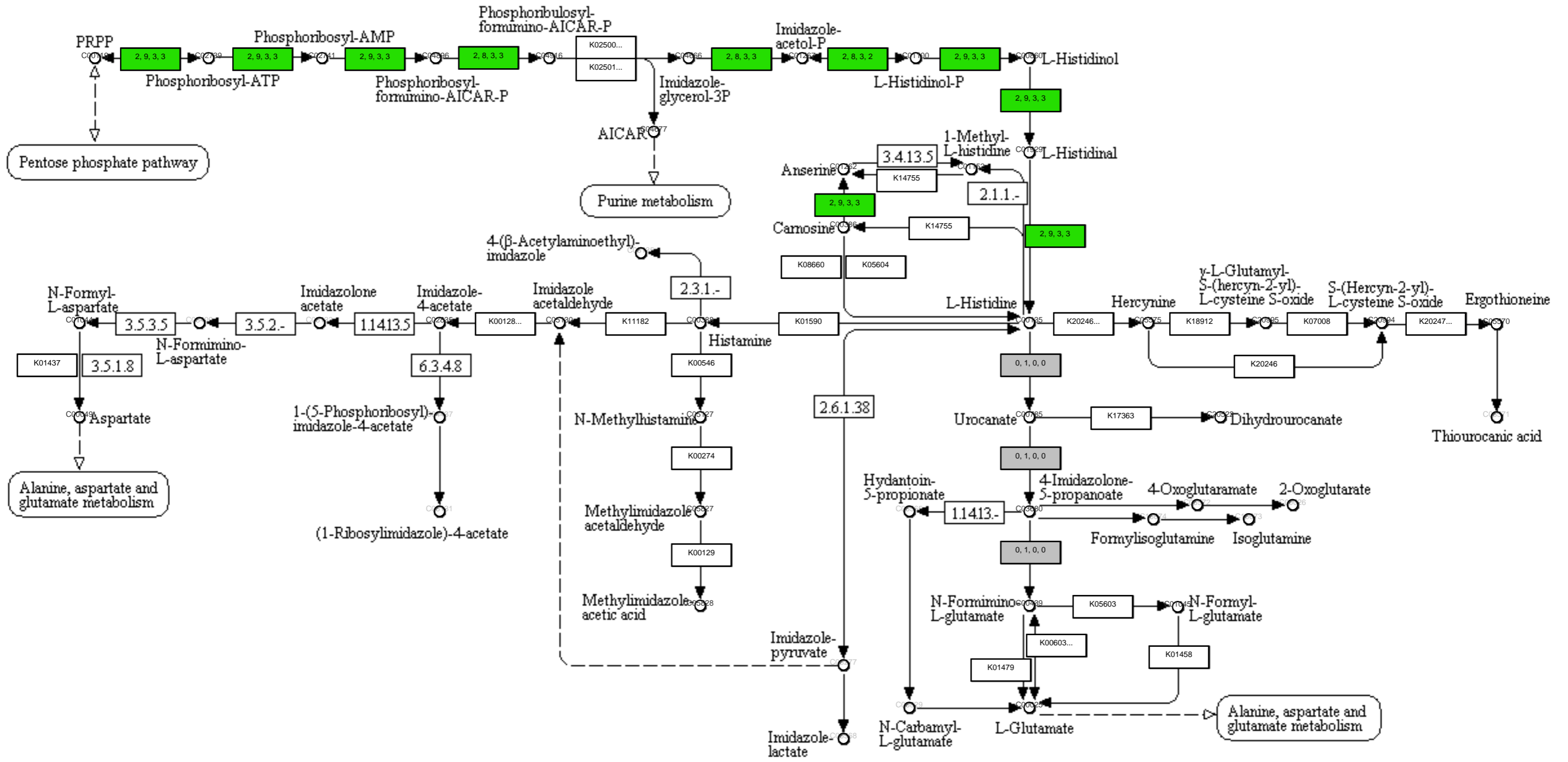
LYSINE DEGRADATION



ARGININE AND PROLINE METABOLISM



# HISTIDINE METABOLISM











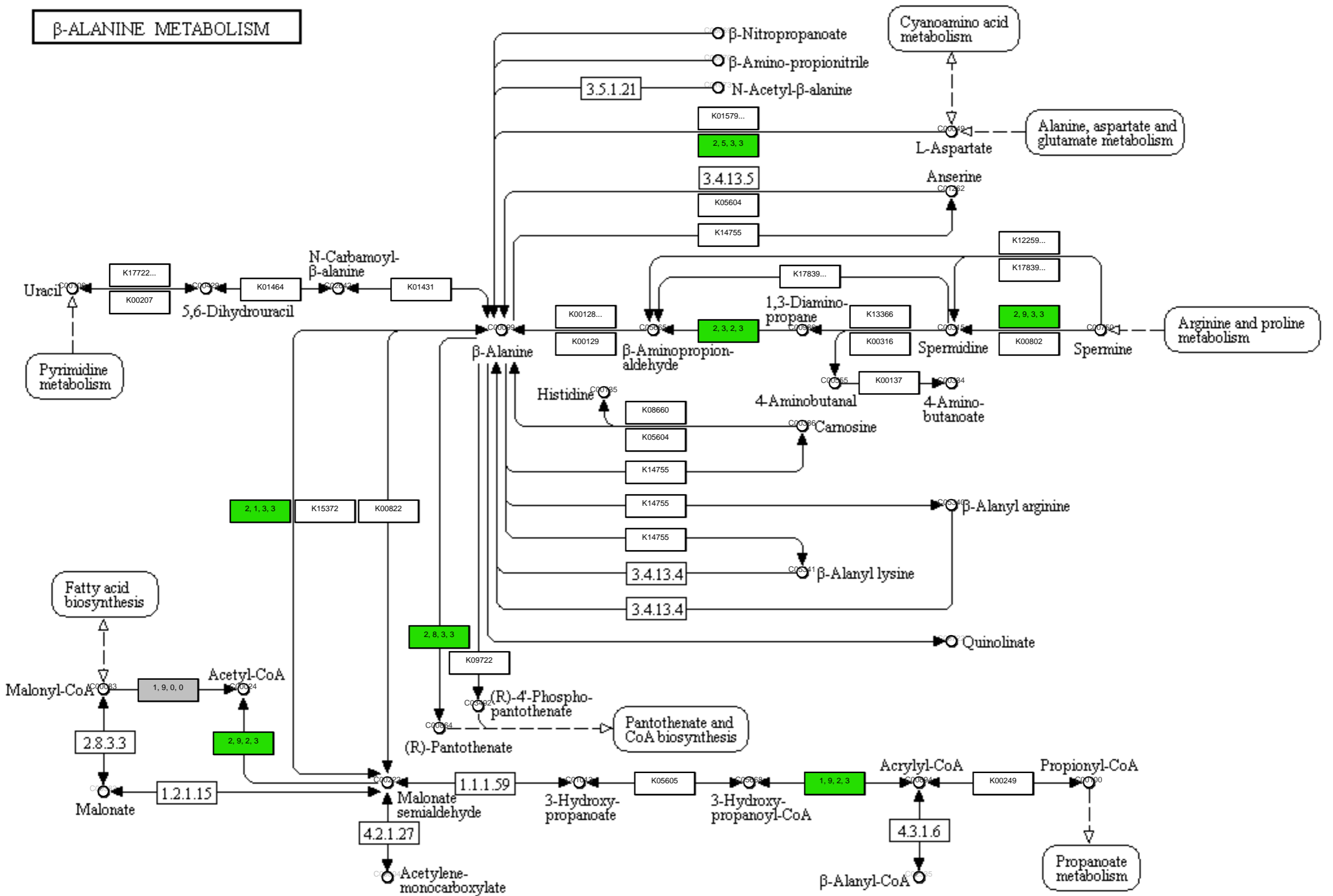




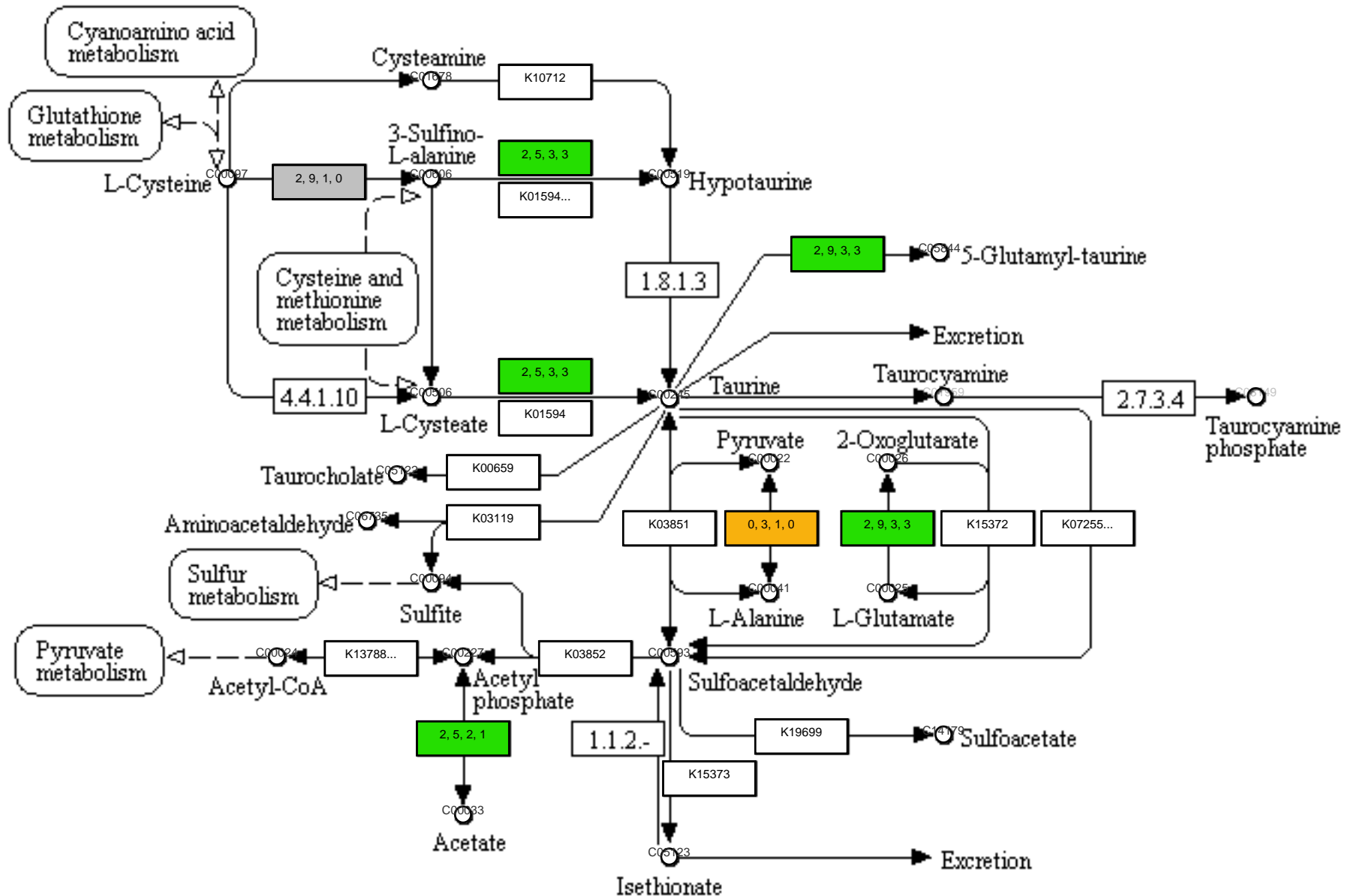
## 6. Metabolism of other amino acids

MAP	PATHWAY
410	beta-Alanine metabolism
430	Taurine and hypotaurine metabolism
440	Phosphonate and phosphinate metabolism
450	Selenocompound metabolism
460	Cyanoamino acid metabolism
480	Glutathione metabolism

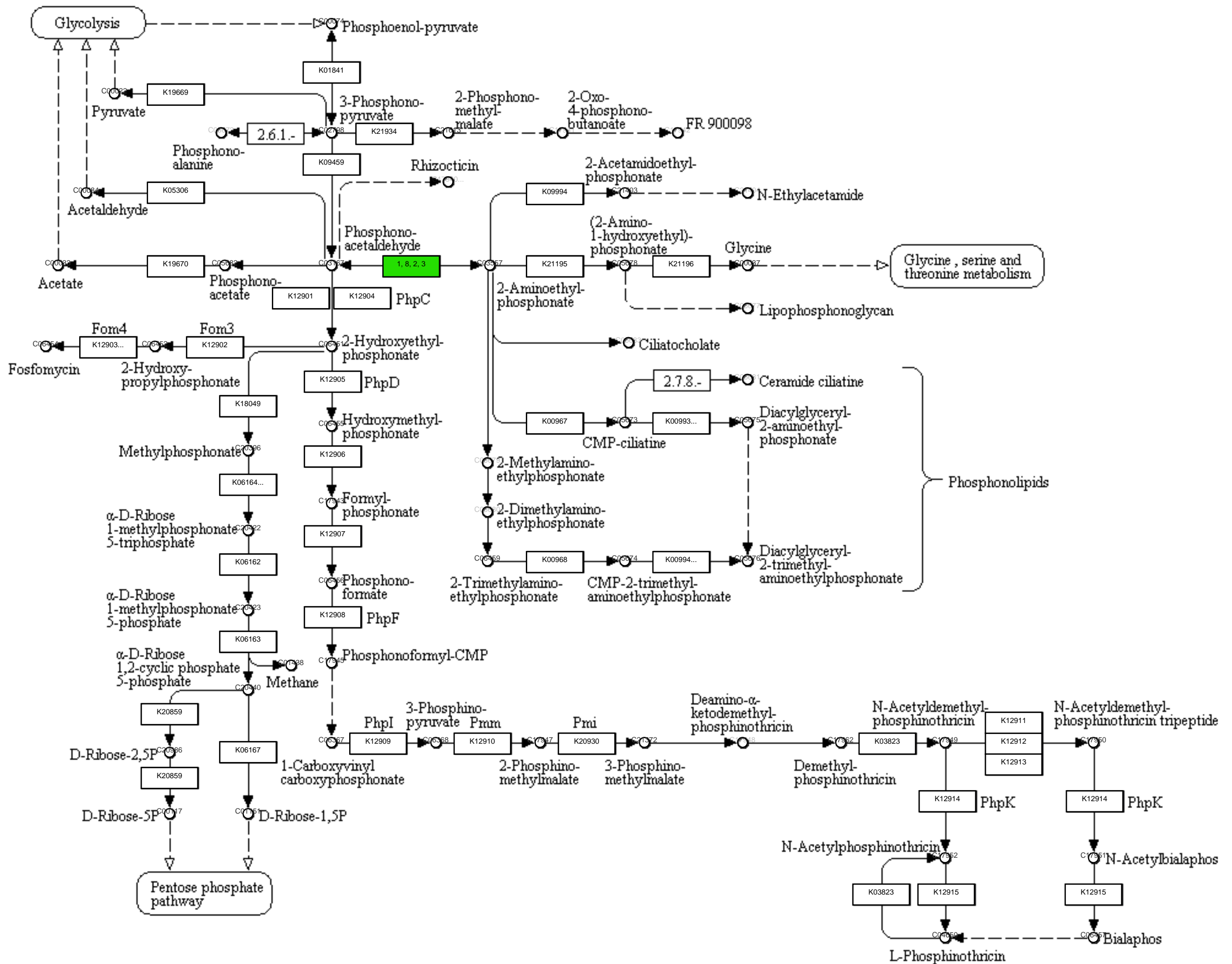
# β-ALANINE METABOLISM



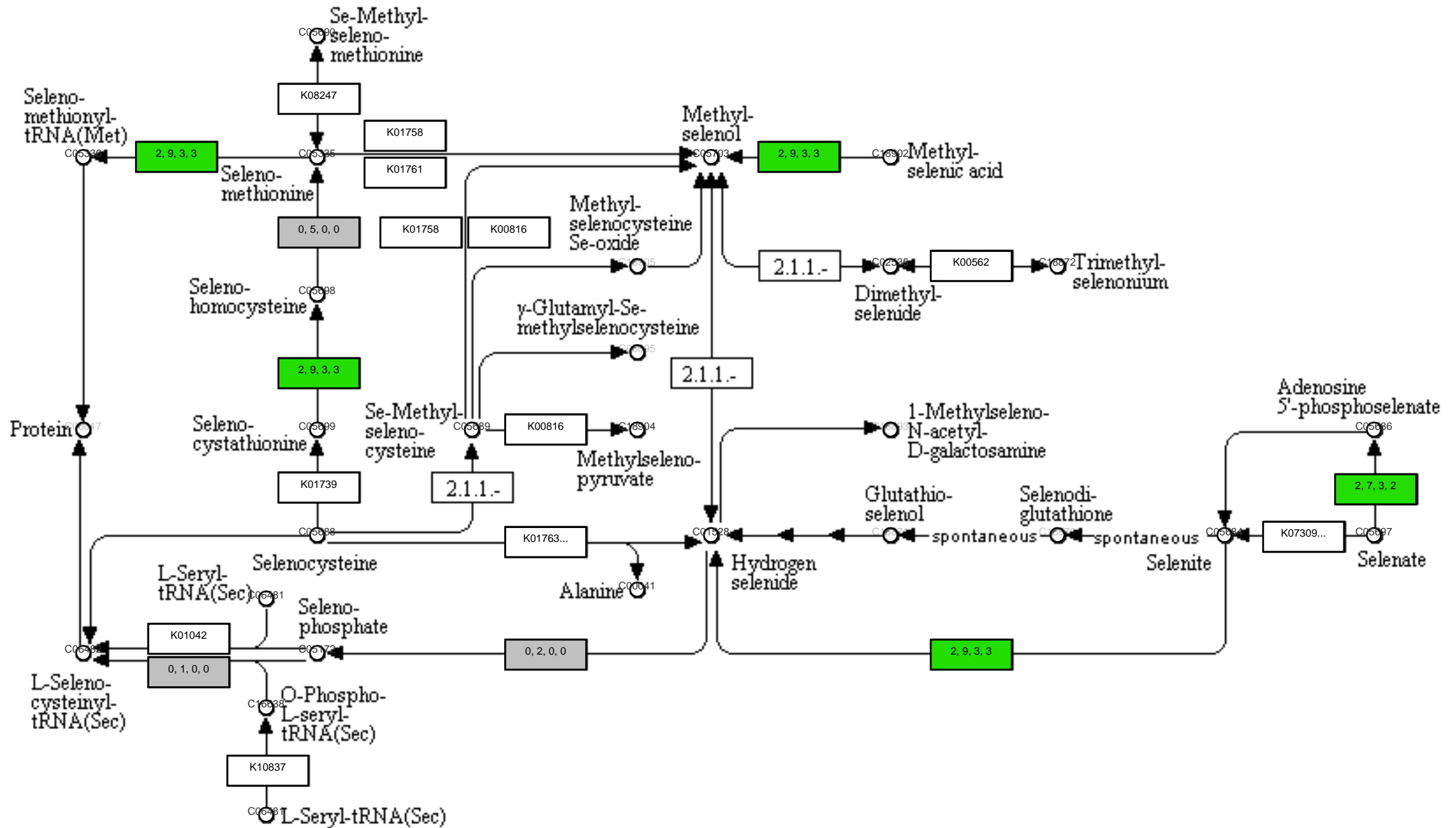
# TAURINE AND HYPOTAURINE METABOLISM



# PHOSPHONATE AND PHOSPHINATE METABOLISM

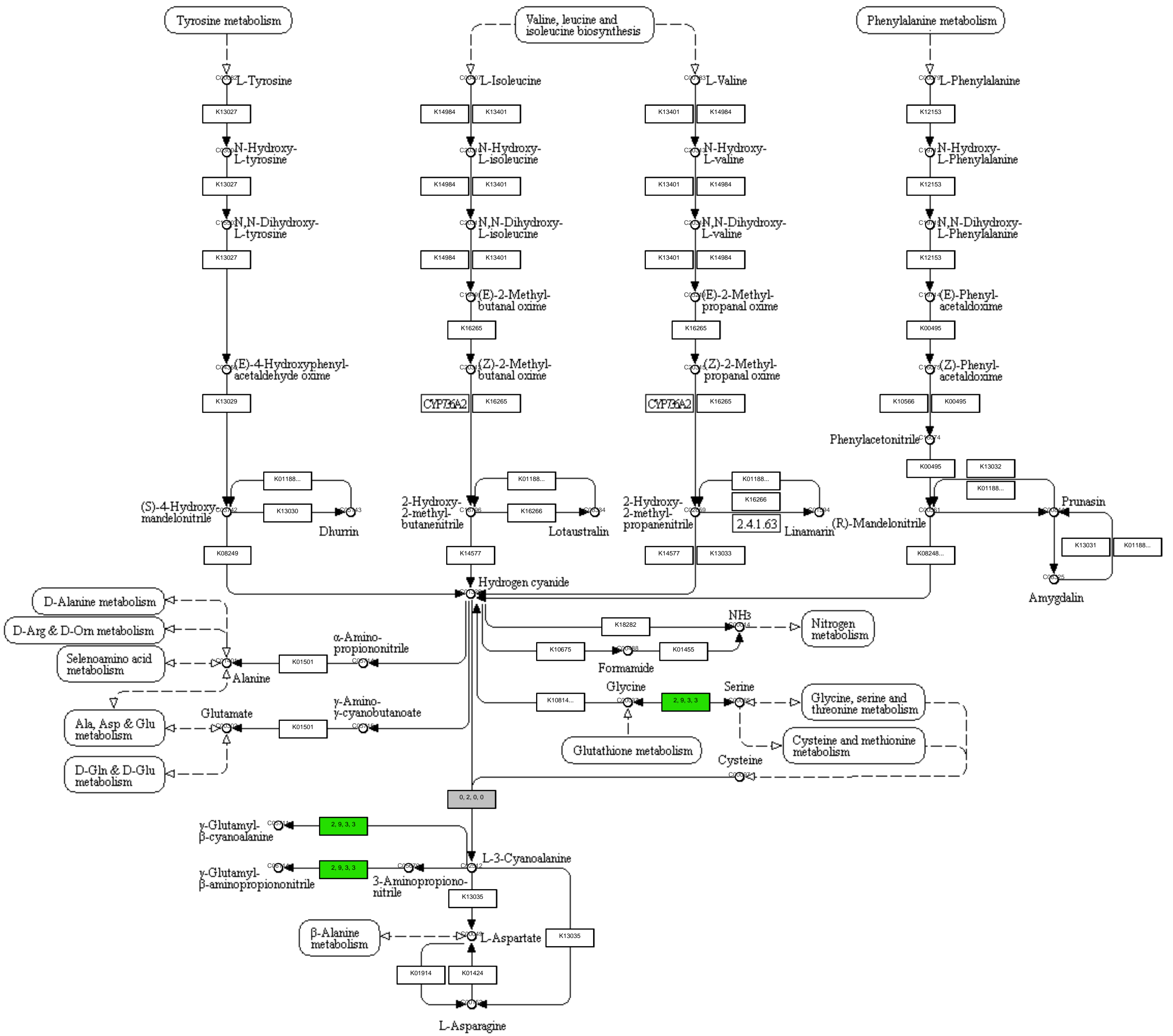


# SELENOCOMPOUND METABOLISM





CYANOAMINO ACID METABOLISM

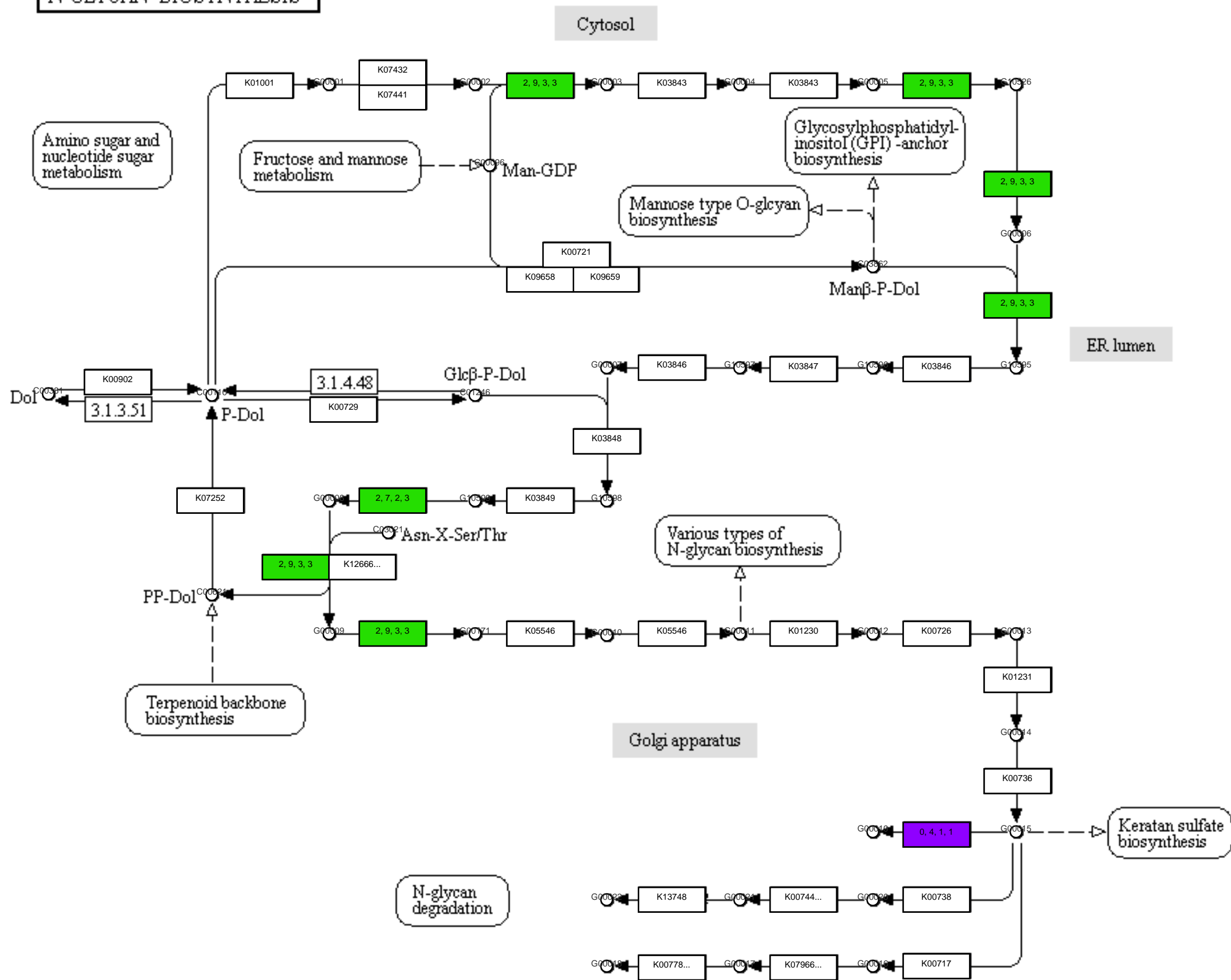




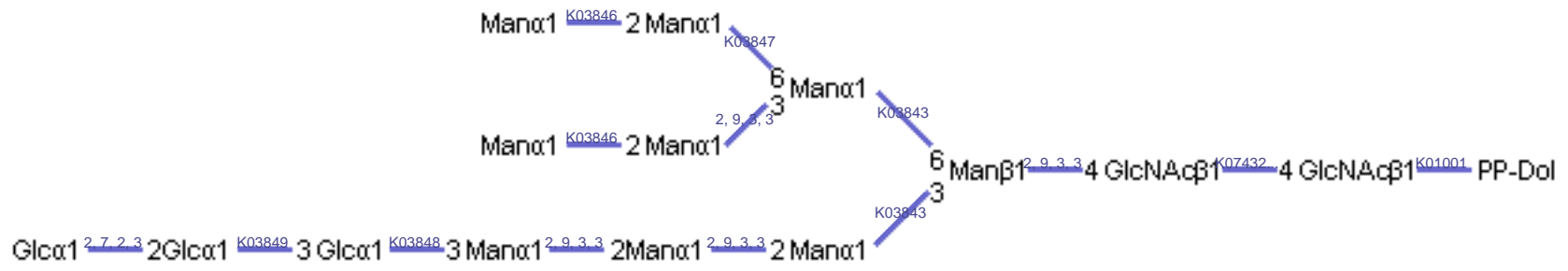
# 7. Glycan biosynthesis and metabolism

MAP	PATHWAY
<b>510</b>	N-Glycan biosynthesis
<b>513</b>	Various types of N-glycan biosynthesis
<b>531</b>	Glycosaminoglycan degradation
<b>563</b>	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis

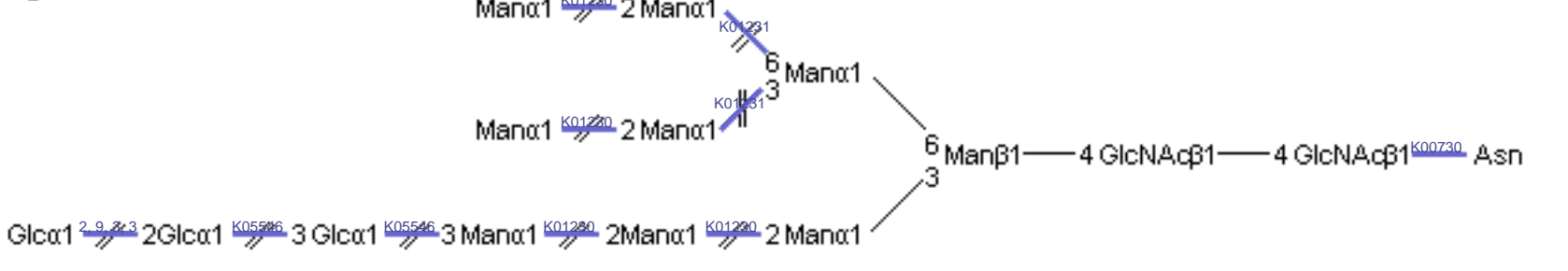
# N-GLYCAN BIOSYNTHESIS



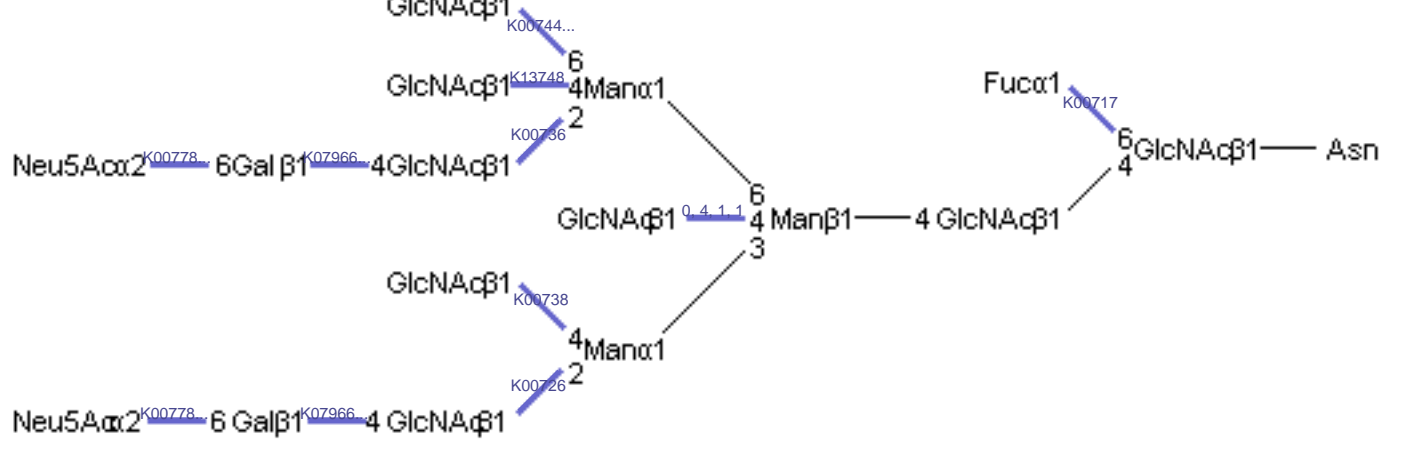
## N-glycan precursor biosynthesis



## Trimming to form core structure

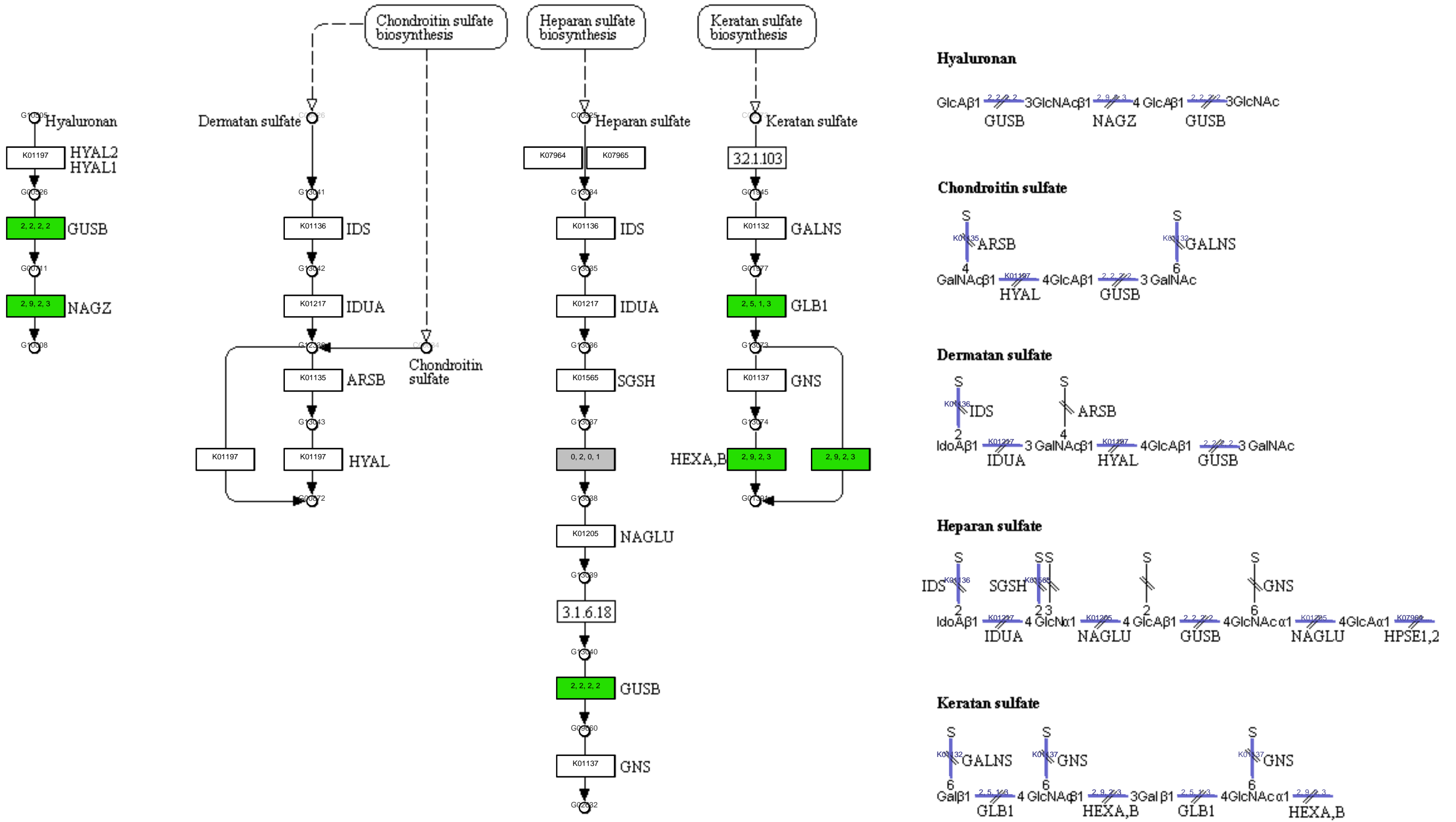


## Glycan extension from core structure



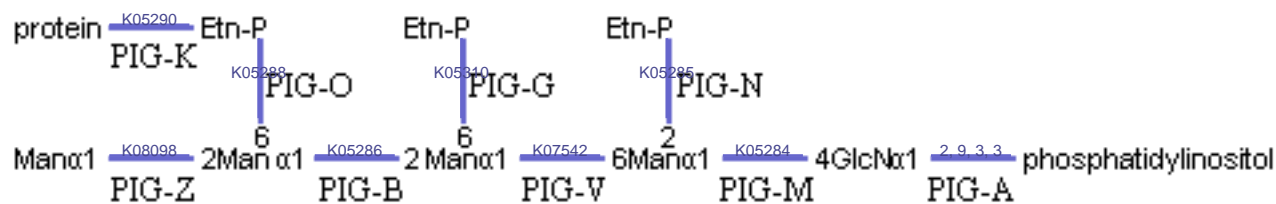
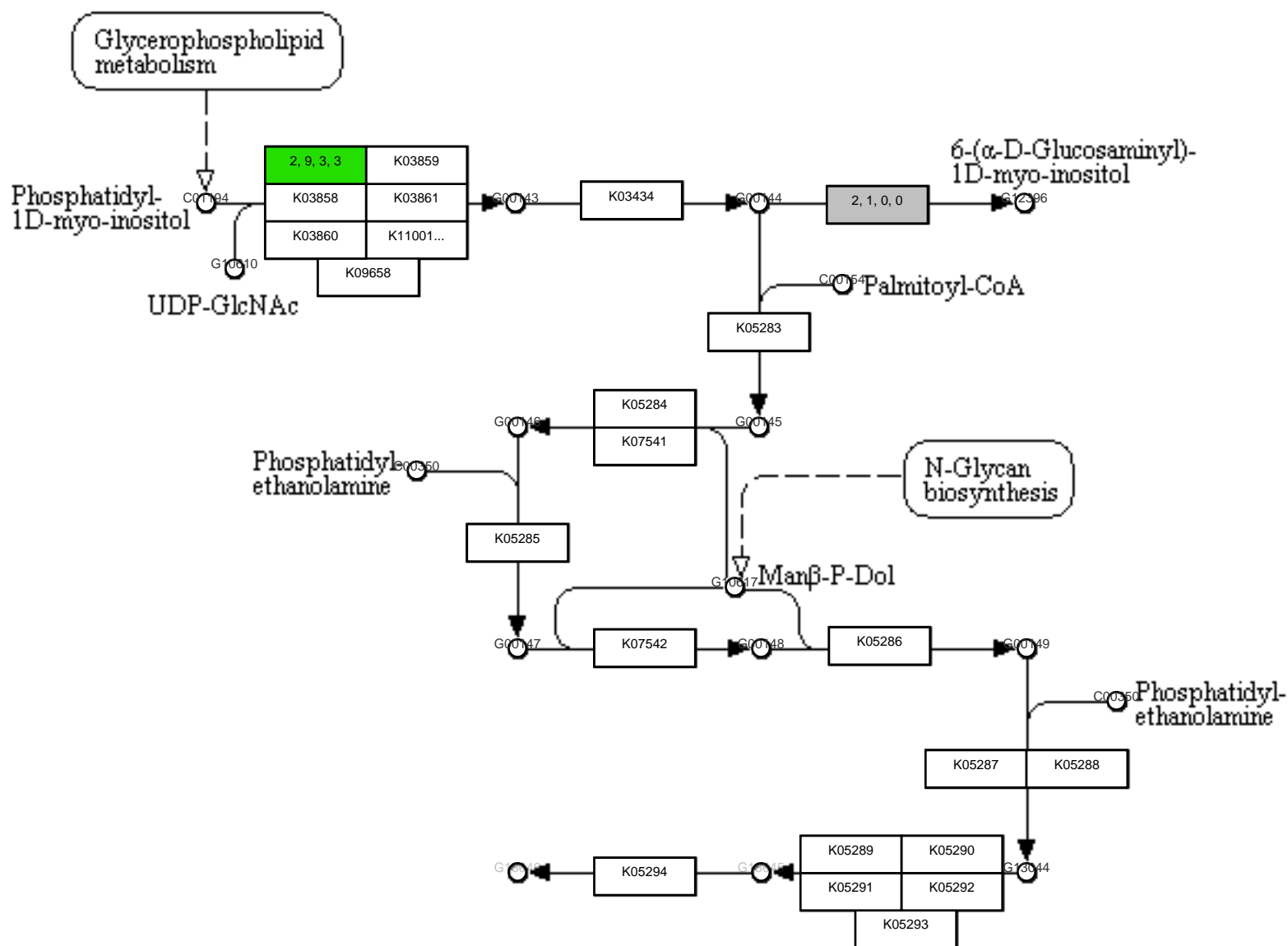


# GLYCOSAMINOGLYCAN DEGRADATION





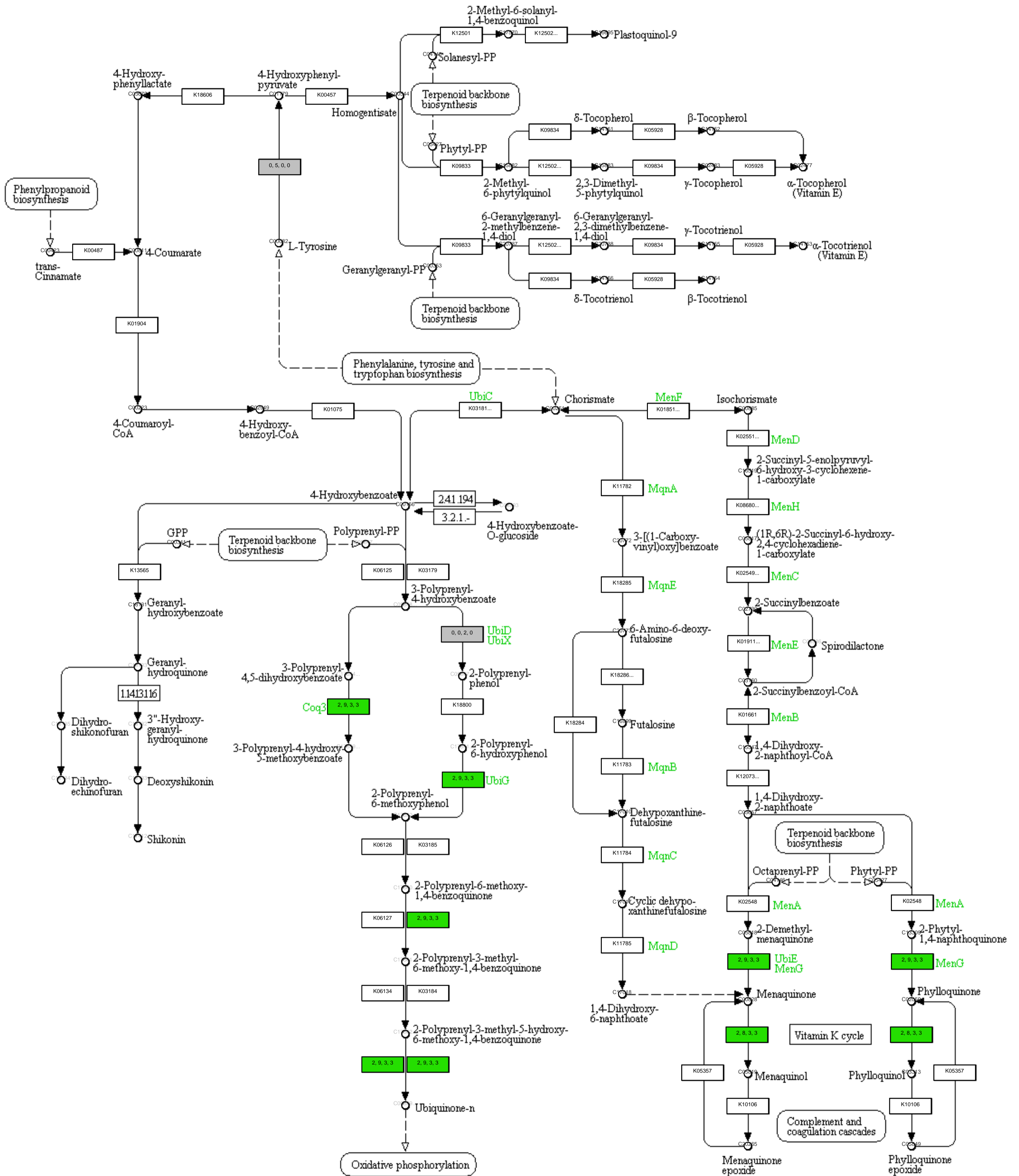
# GLYCOSYLPHOSPHATIDYLINOSITOL (GPI) - ANCHOR BIOSYNTHESIS



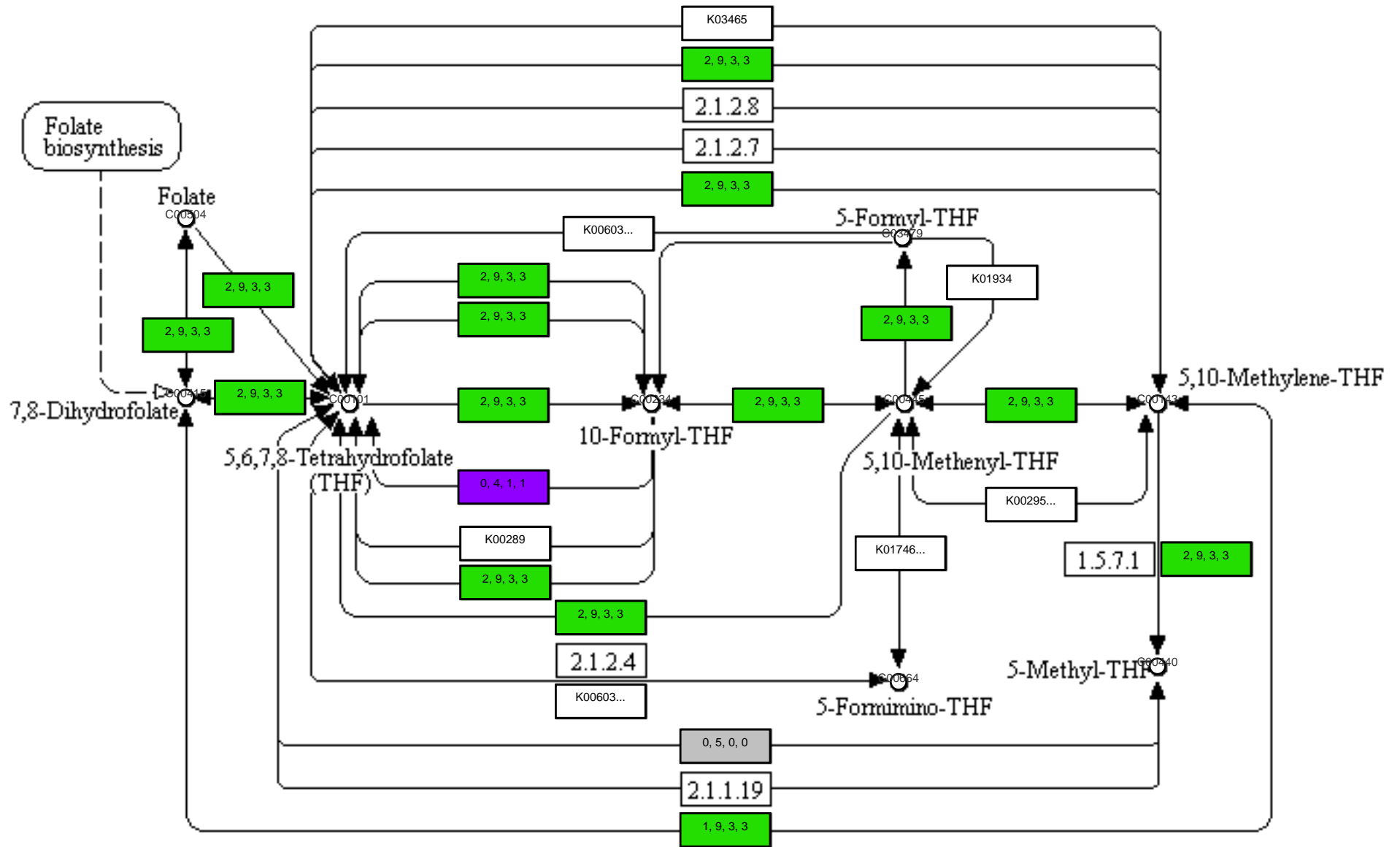
## 8. Metabolism of cofactors and vitamins

MAP	PATHWAY
130	Ubiquinone and other terpenoid-quinone biosynthesis
670	One carbon pool by folate
730	Thiamine metabolism
740	Riboflavin metabolism
750	Vitamin B6 metabolism
760	Nicotinate and nicotinamide metabolism
770	Pantothenate and CoA biosynthesis
780	Biotin metabolism
785	Lipoic acid metabolism
790	Folate biosynthesis
860	Porphyrin and chlorophyll metabolism

UBIQUINONE AND OTHER TERPENOID-QUINONE BIOSYNTHESIS



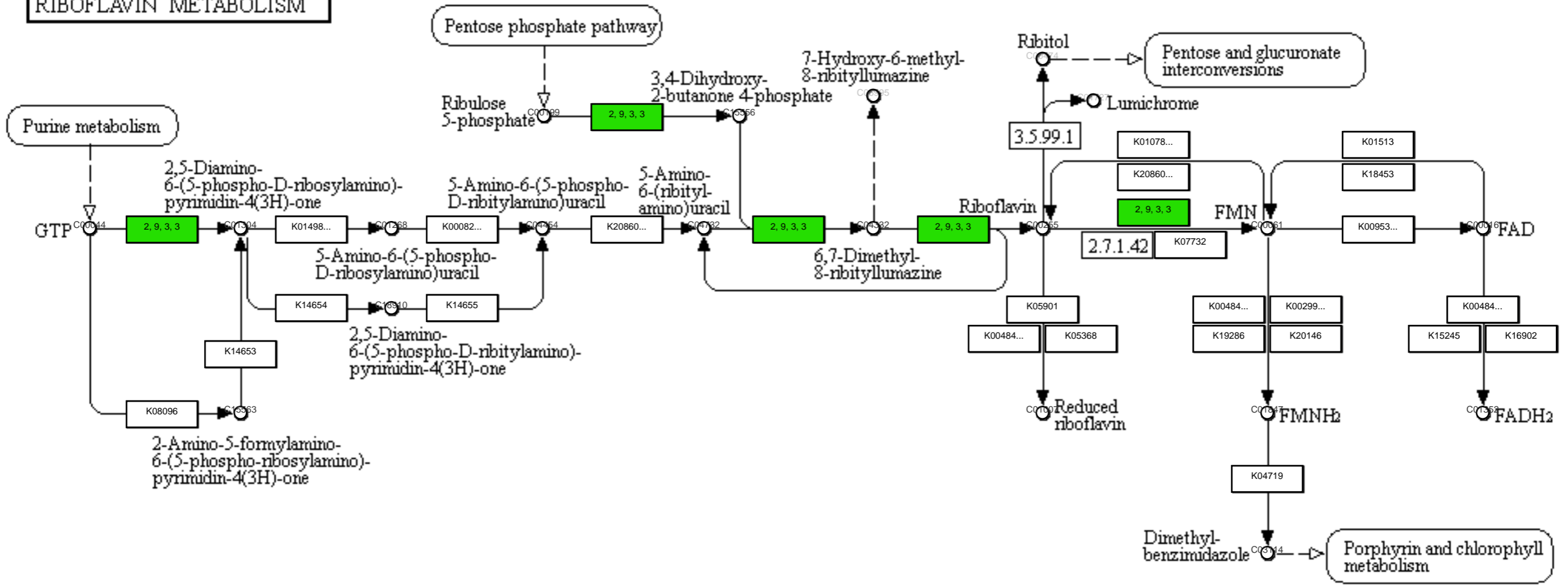
# ONE CARBON POOL BY FOLATE



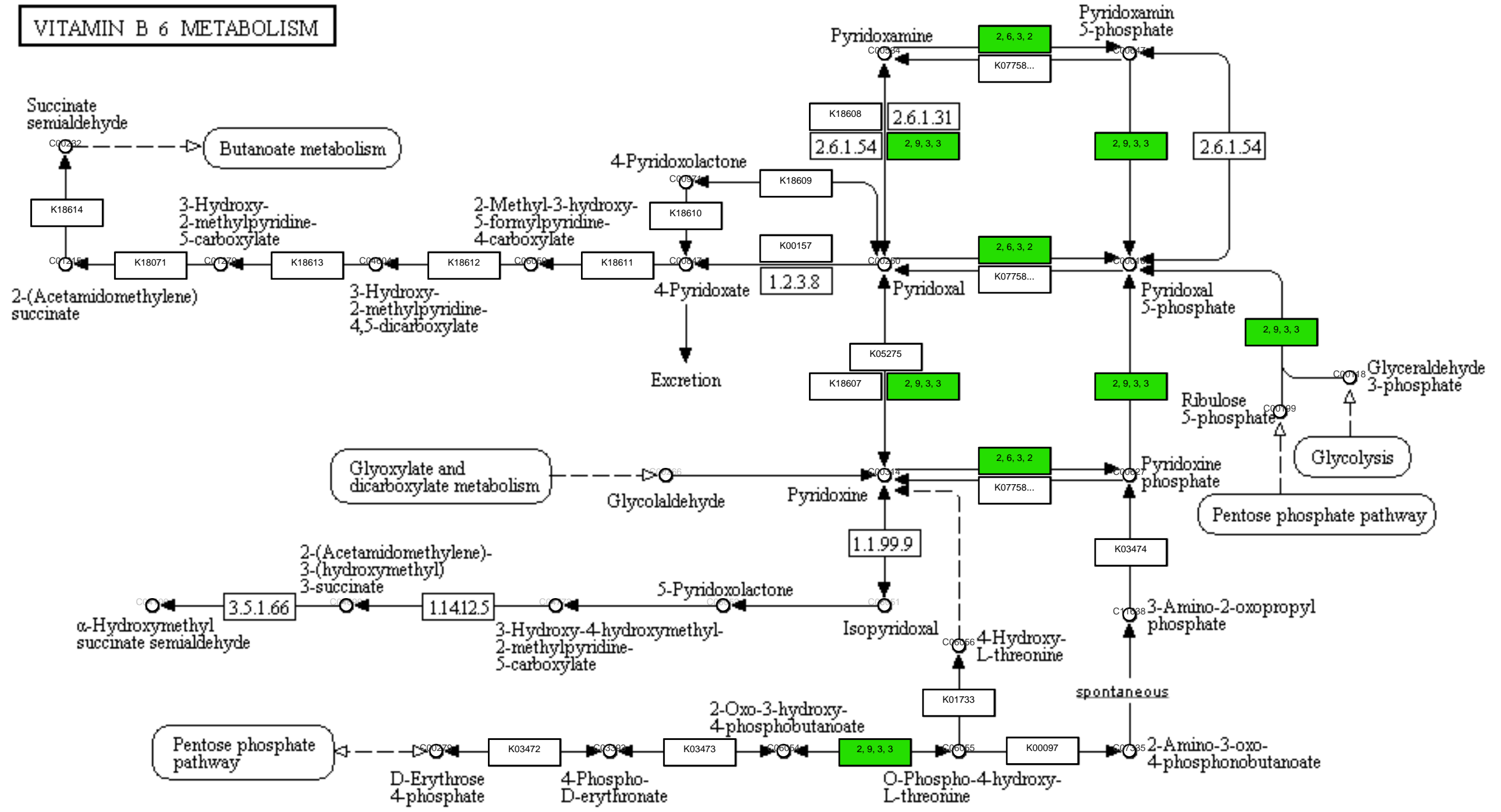




# RIBOFLAVIN METABOLISM



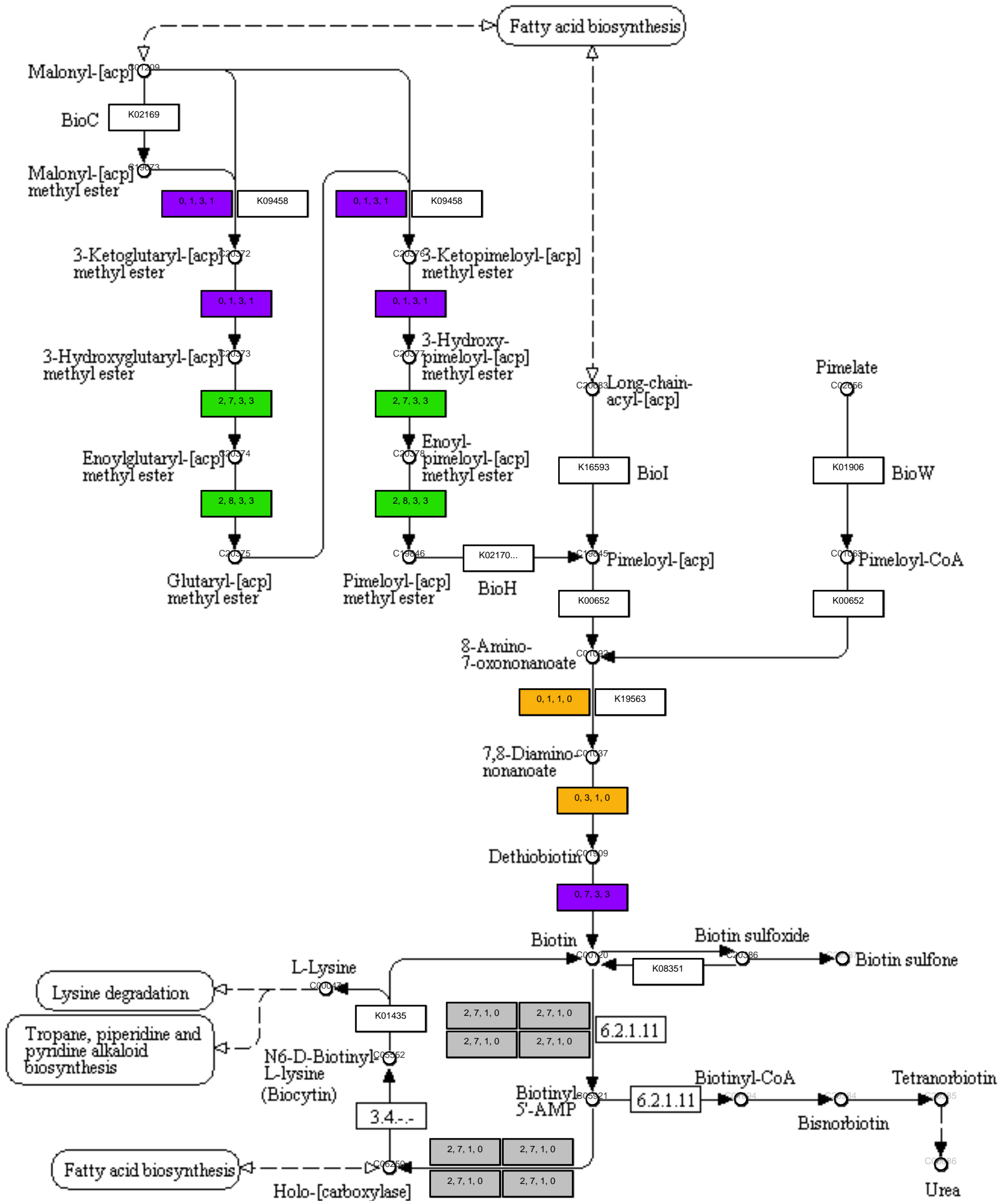
# VITAMIN B 6 METABOLISM





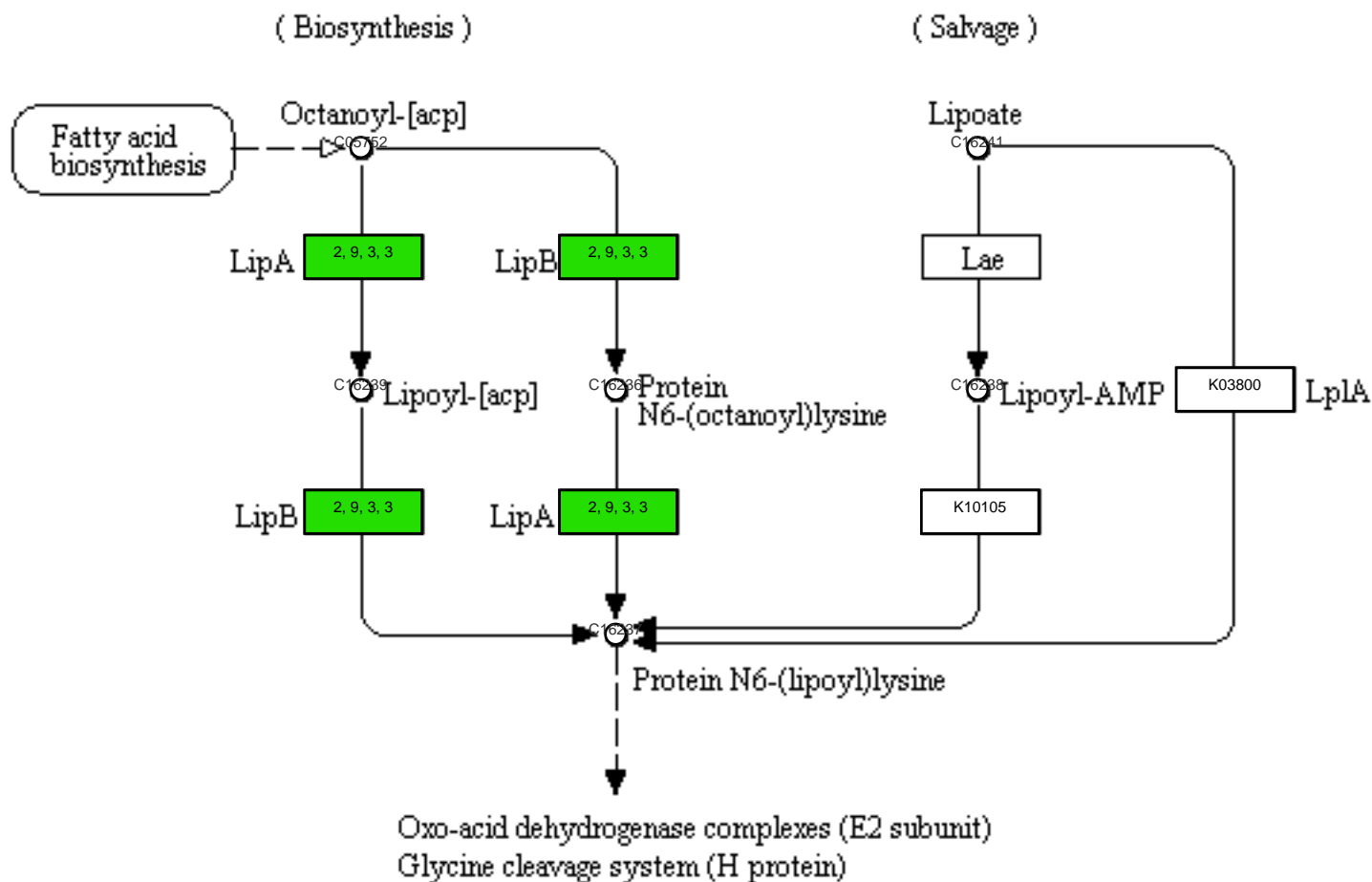


# BIOTIN METABOLISM



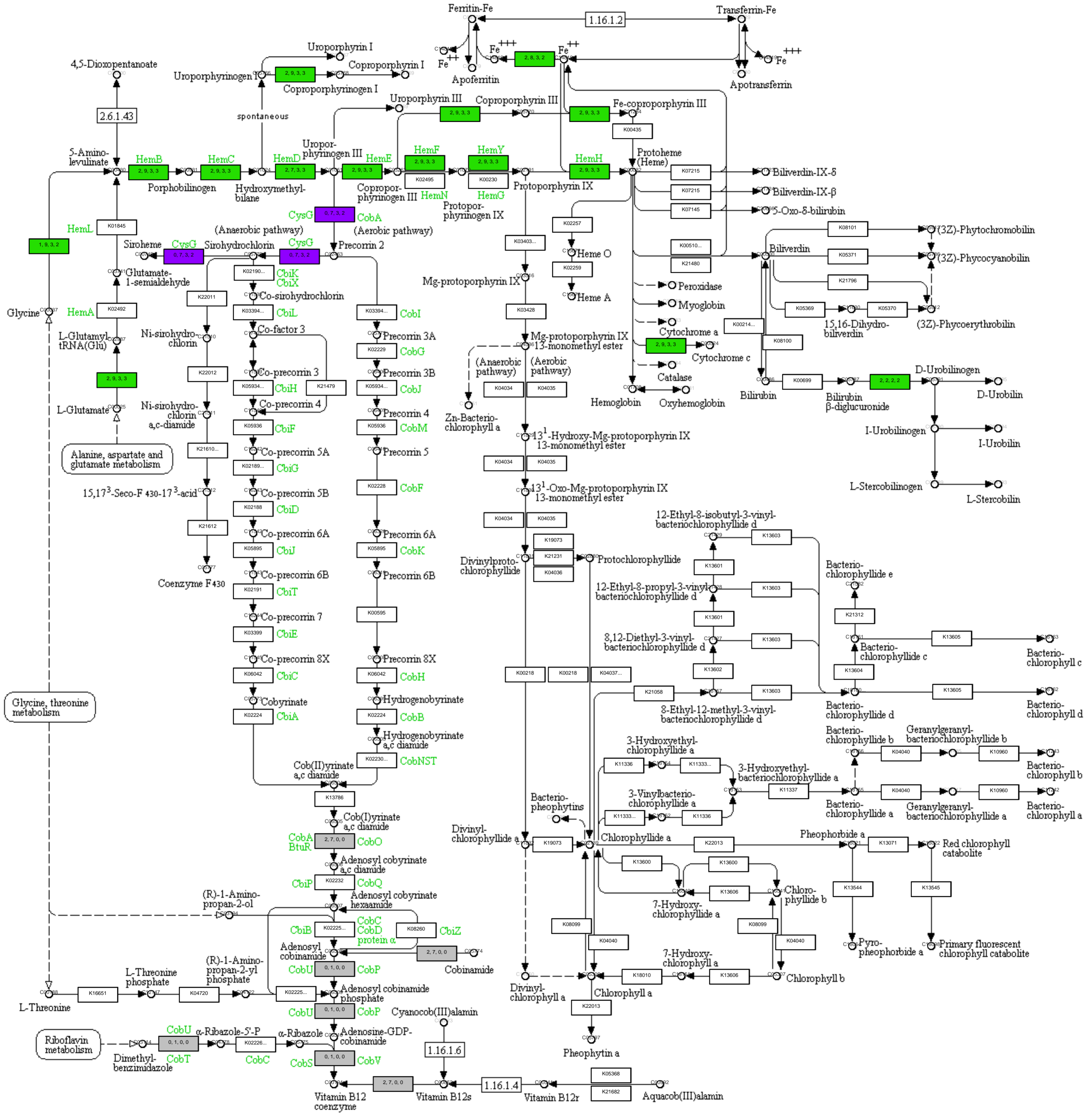


# LIPOIC ACID METABOLISM





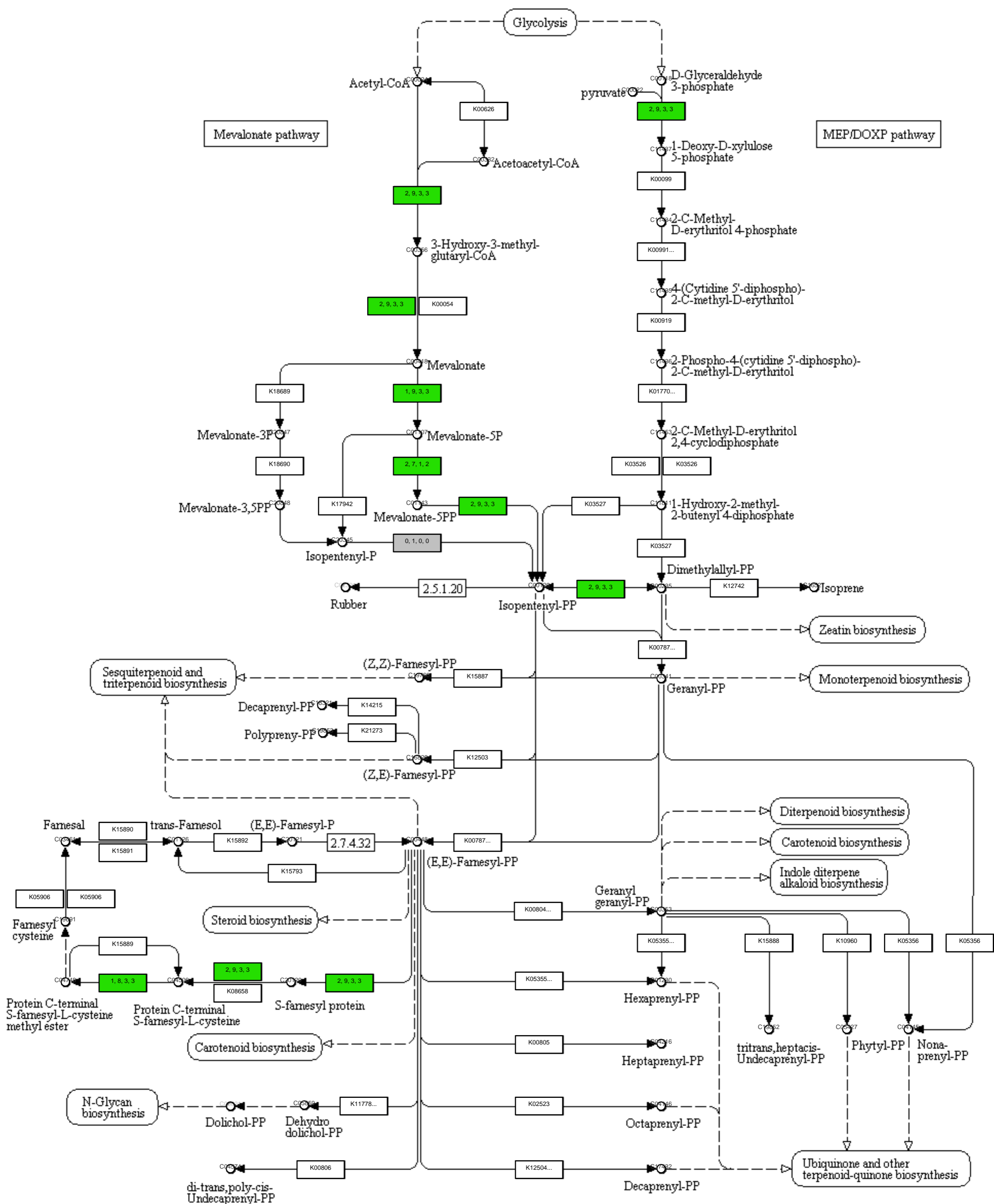
PORPHYRIN AND CHLOROPHYLL METABOLISM



# 9. Metabolism of terpenoids and polyketides

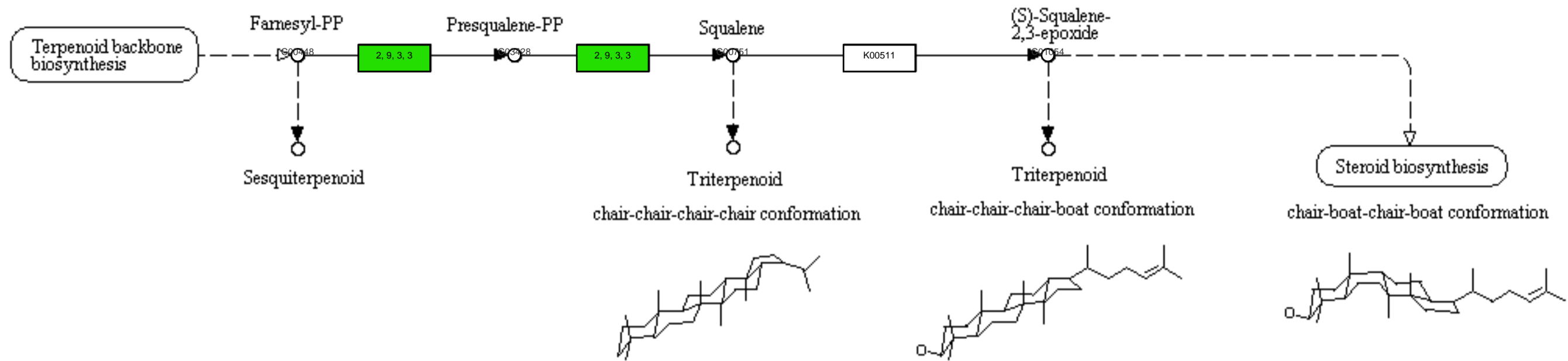
MAP	PATHWAY
<b>900</b>	Terpenoid backbone biosynthesis
<b>909</b>	Sesquiterpenoid and triterpenoid biosynthesis

TERPENOID BACKBONE BIOSYNTHESIS



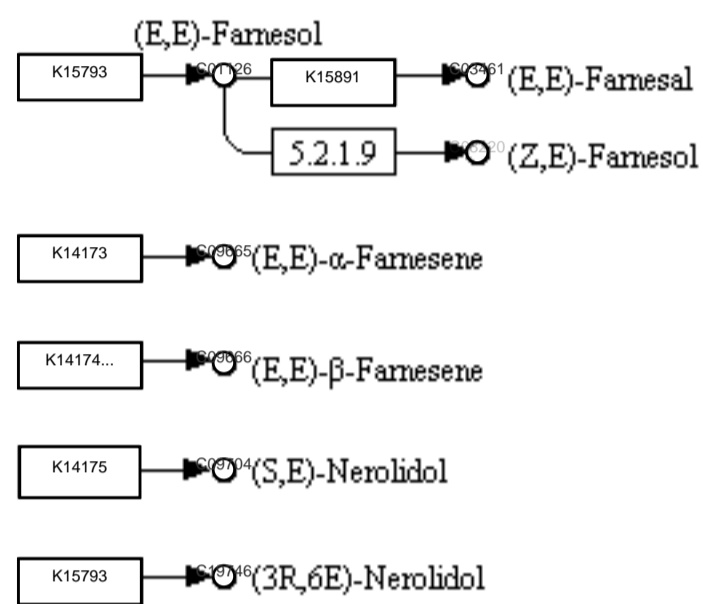


SESQUITERPENOID AND TRITERPENOID BIOSYNTHESIS

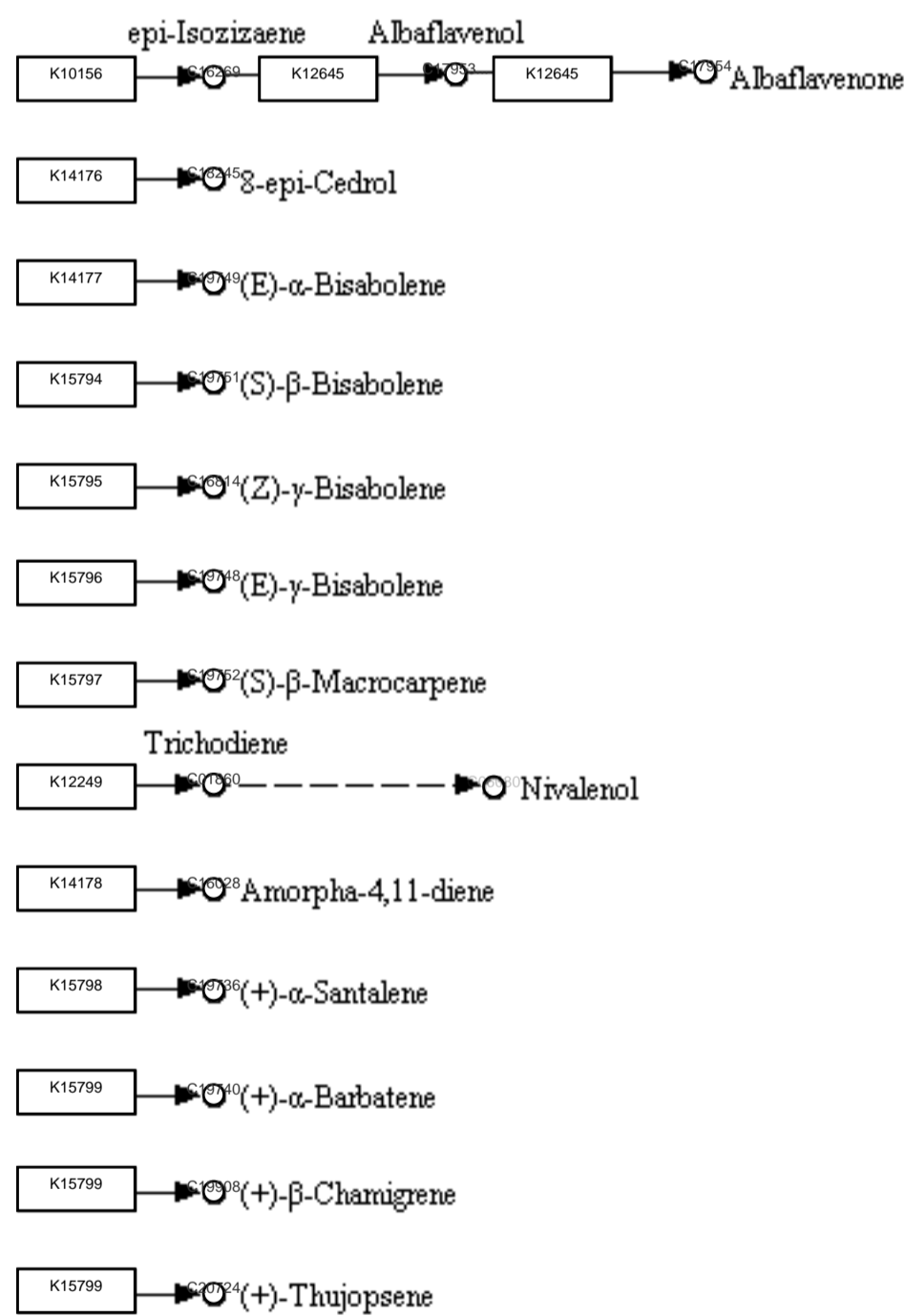


Sesquiterpenoid

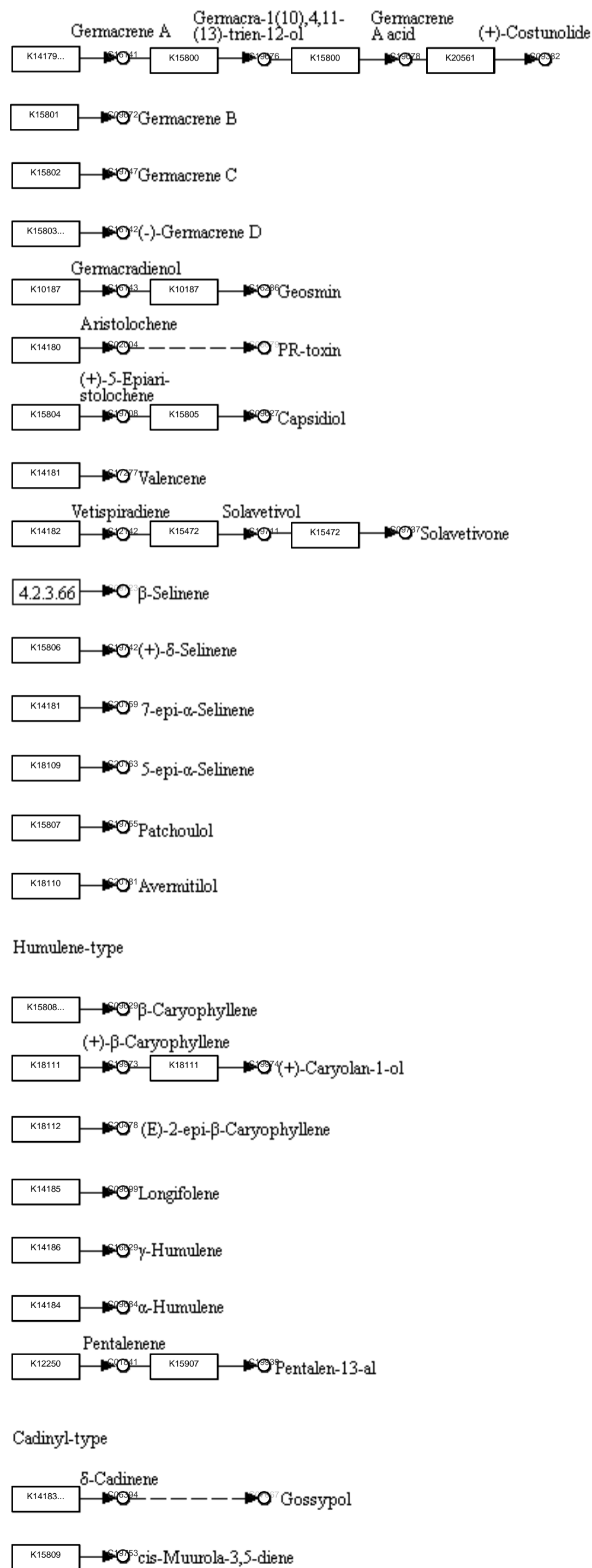
Acyclic sesquiterpenoid



Bisabolene-type

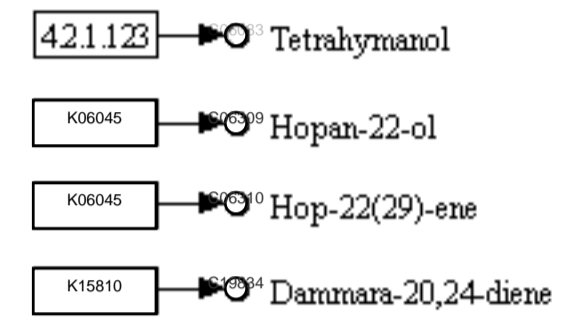


Germacren-type



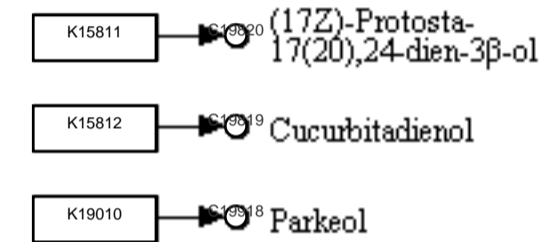
Triterpenoid chair-chair-chair-chair conformation

Hopene and Tetrahymanol

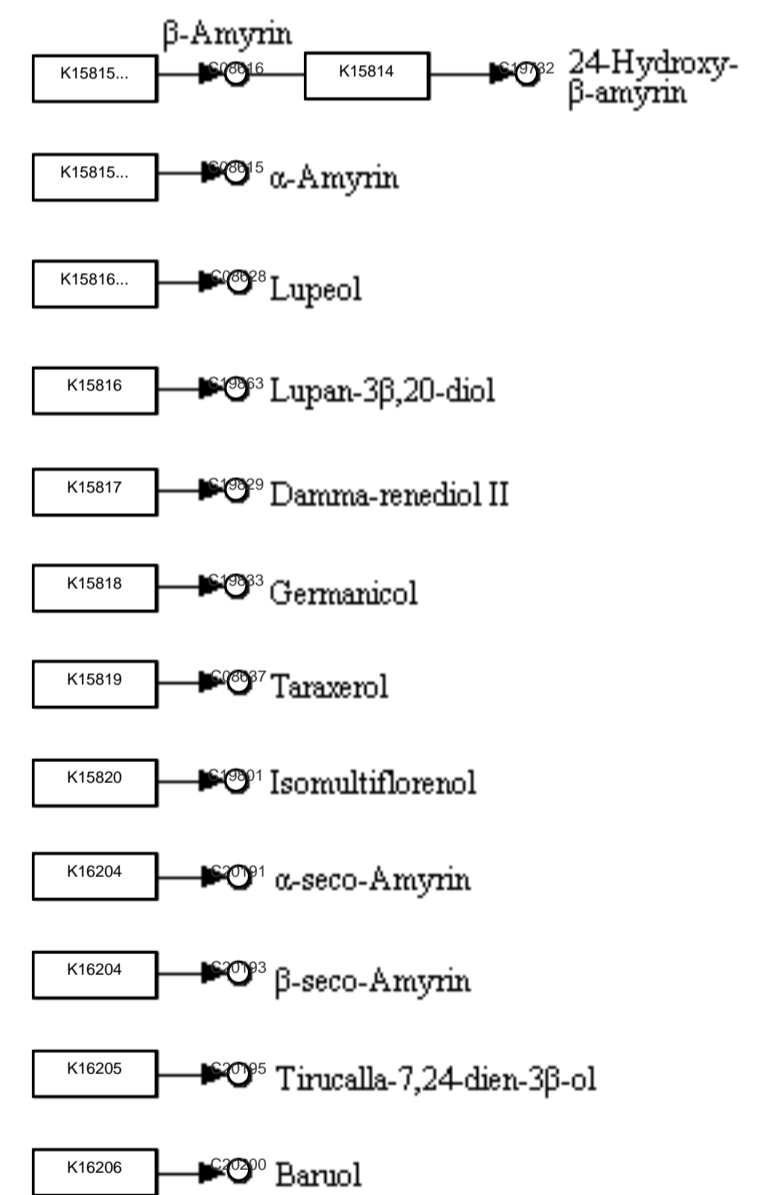


Triterpenoid chair-chair-chair-boat conformation

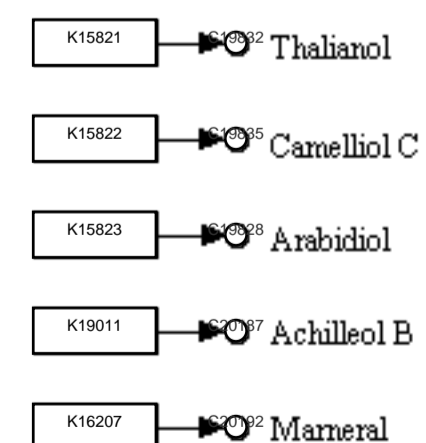
Protosteryl-type



Dammarenyl-type



Other-type





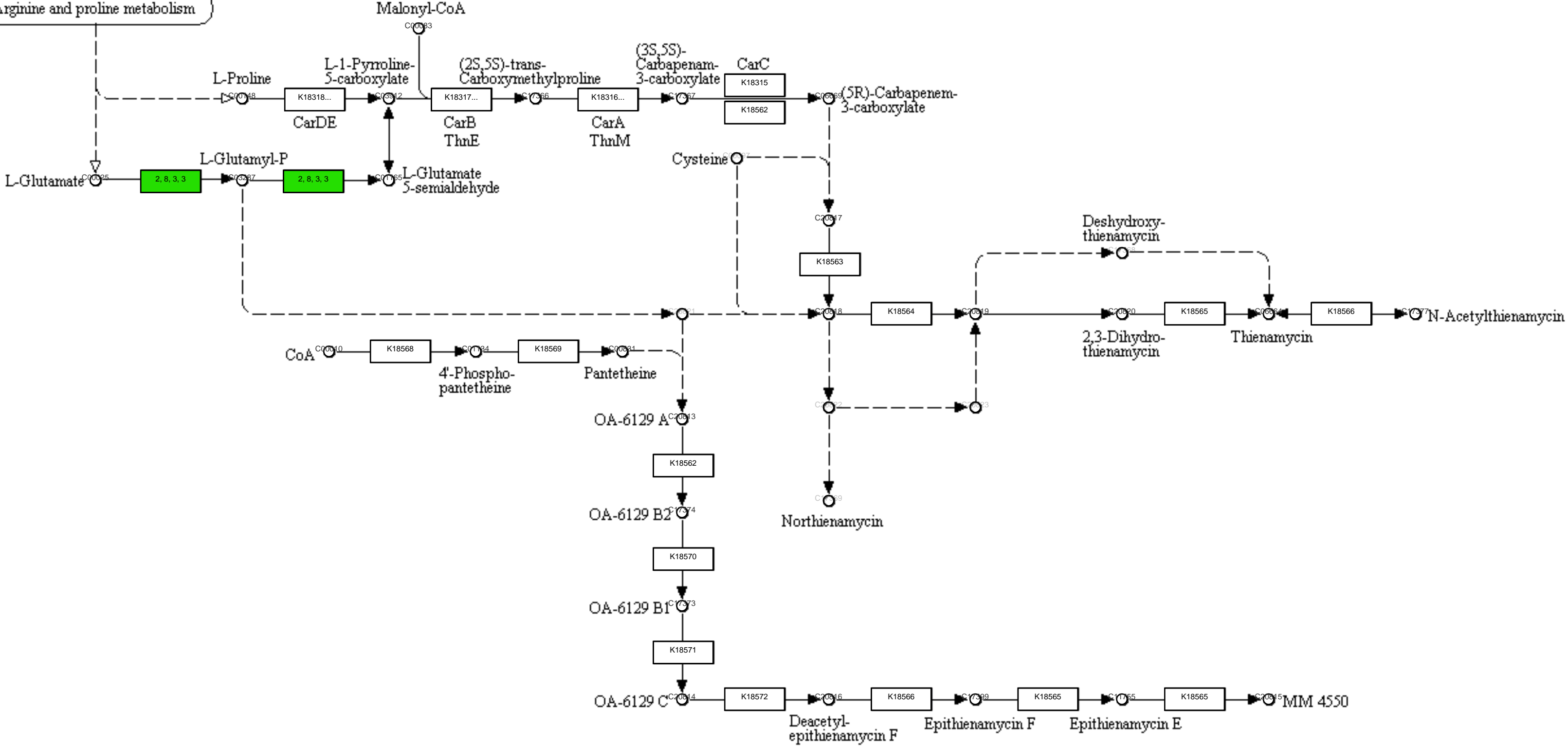
# 10. Biosynthesis of other secondary metabolites

MAP	PATHWAY
261	Monobactam biosynthesis
332	Carbapenem biosynthesis



# CARBAPENEM BIOSYNTHESIS

Arginine and proline metabolism



# 11. Xenobiotics biodegradation and metabolism

MAP	PATHWAY
<b>791</b>	Atrazine degradation

# ATRAZINE DEGRADATION

