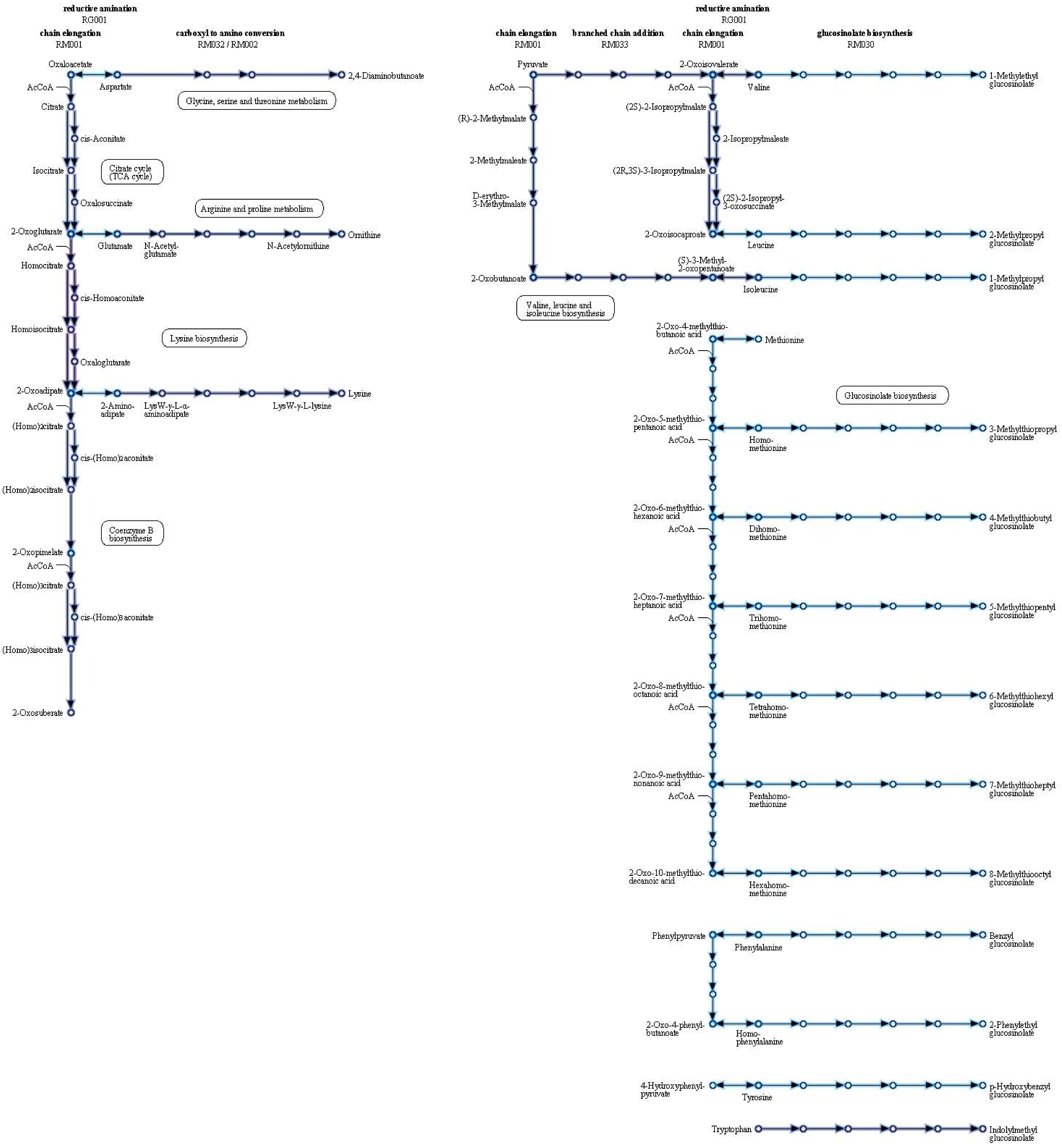
2-OXOCARBOXYLIC ACID METABOLISM



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ABC TRANSPORTERS

02010 3/12/14
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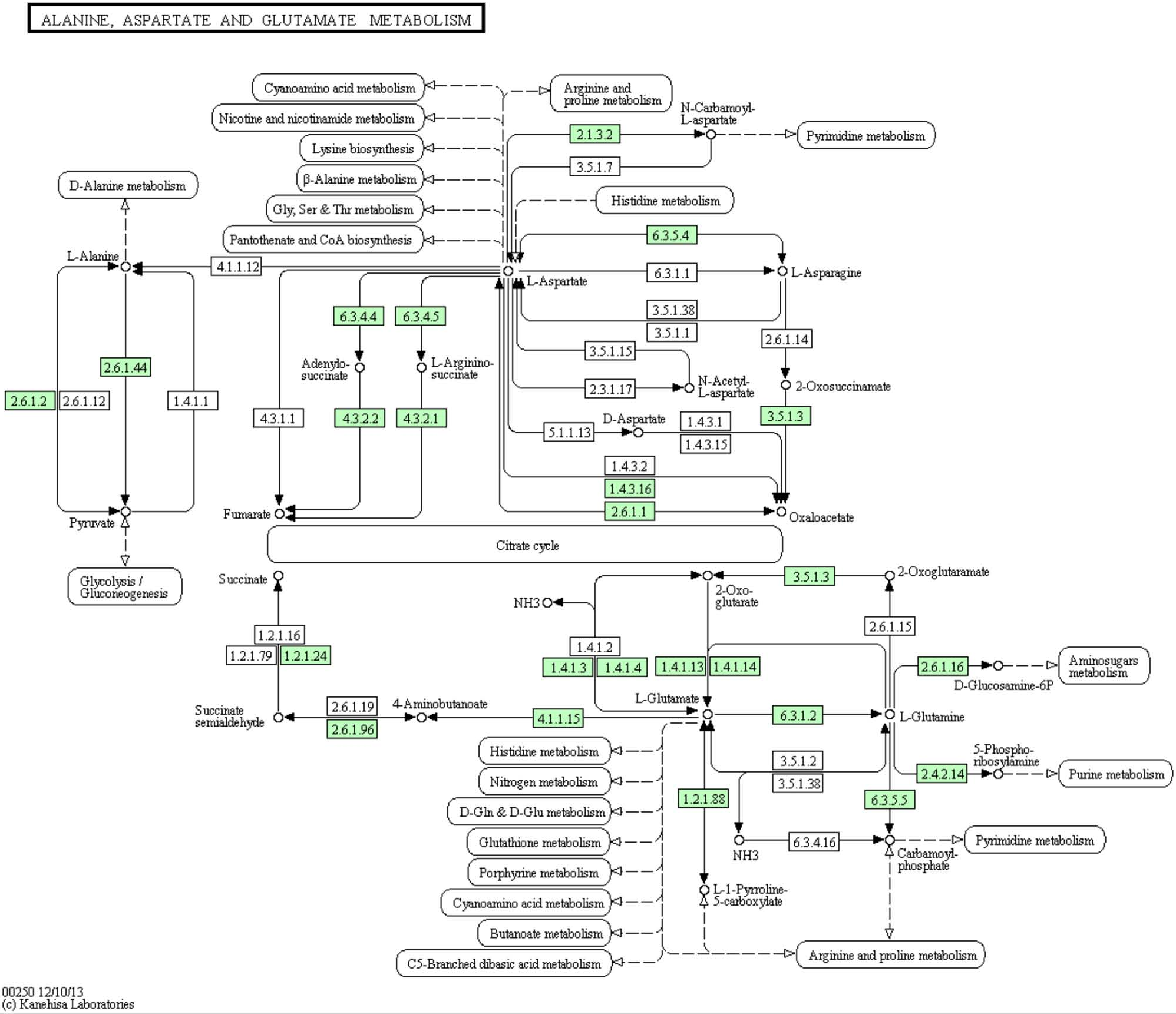
ALANINE, ASPARTATE AND GLUTAMATE METABOLISM
Cyanoamino acid metabolism
Arginine and proline metabolism
Nicotine and nicotinamide metabolism
Lysine biosynthesis
β-Alanine metabolism
Gly, Ser & Thr metabolism
Pantothenate and CoA biosynthesis
D-Alanine metabolism
N-Carbamoyl-L-aspartate
Pyrimidine metabolism
2.1.3.2
3.5.1.7
Histidine metabolism
6.3.5.4
L-Alanine
4.1.1.12
L-Aspartate
6.3.1.1
L-Asparagine
3.5.1.38
3.5.1.1
6.3.4.4
6.3.4.5
2.6.1.14
2.6.1.44
3.5.1.15
Adenylo-succinate
L-Arginino-succinate
N-Acetyl-L-aspartate
2.3.1.17
2-Oxosuccinamate
2.6.1.2
2.6.1.12
1.4.1.1
4.3.1.1
4.3.2.2
4.3.2.1
3.5.1.3
D-Aspartate
1.4.3.1
5.1.1.13
1.4.3.15
1.4.3.2
1.4.3.16
2.6.1.1
Fumarate
Pyruvate
Oxaloacetate
Citrate cycle
Glycolysis / Gluconeogenesis
Succinate
3.5.1.3
2-Oxoglutaramate
2-Oxo-glutarate
NH3
2.6.1.15
1.2.1.16
1.4.1.2
1.2.1.79
1.2.1.24
1.4.1.3
1.4.1.4
1.4.1.13
1.4.1.14
2.6.1.16
Aminosugars metabolism
D-Glucosamine-6P
L-Glutamate
Succinate semialdehyde
2.6.1.19
4-Aminobutanoate
4.1.1.15
6.3.1.2
L-Glutamine
2.6.1.96
Histidine metabolism
5-Phospho-ribosylamine
3.5.1.2
Nitrogen metabolism
2.4.2.14
Purine metabolism
3.5.1.38
D-Gln & D-Glu metabolism
1.2.1.88
6.3.5.5
Glutathione metabolism
NH3
6.3.4.16
Pyrimidine metabolism
Carbamoyl-phosphate
Porphyrine metabolism
L-1-Pyrroline-5-carboxylate
Cyanoamino acid metabolism
Butanoate metabolism
Arginine and proline metabolism
C5-Branched dibasic acid metabolism
00250 12/10/13
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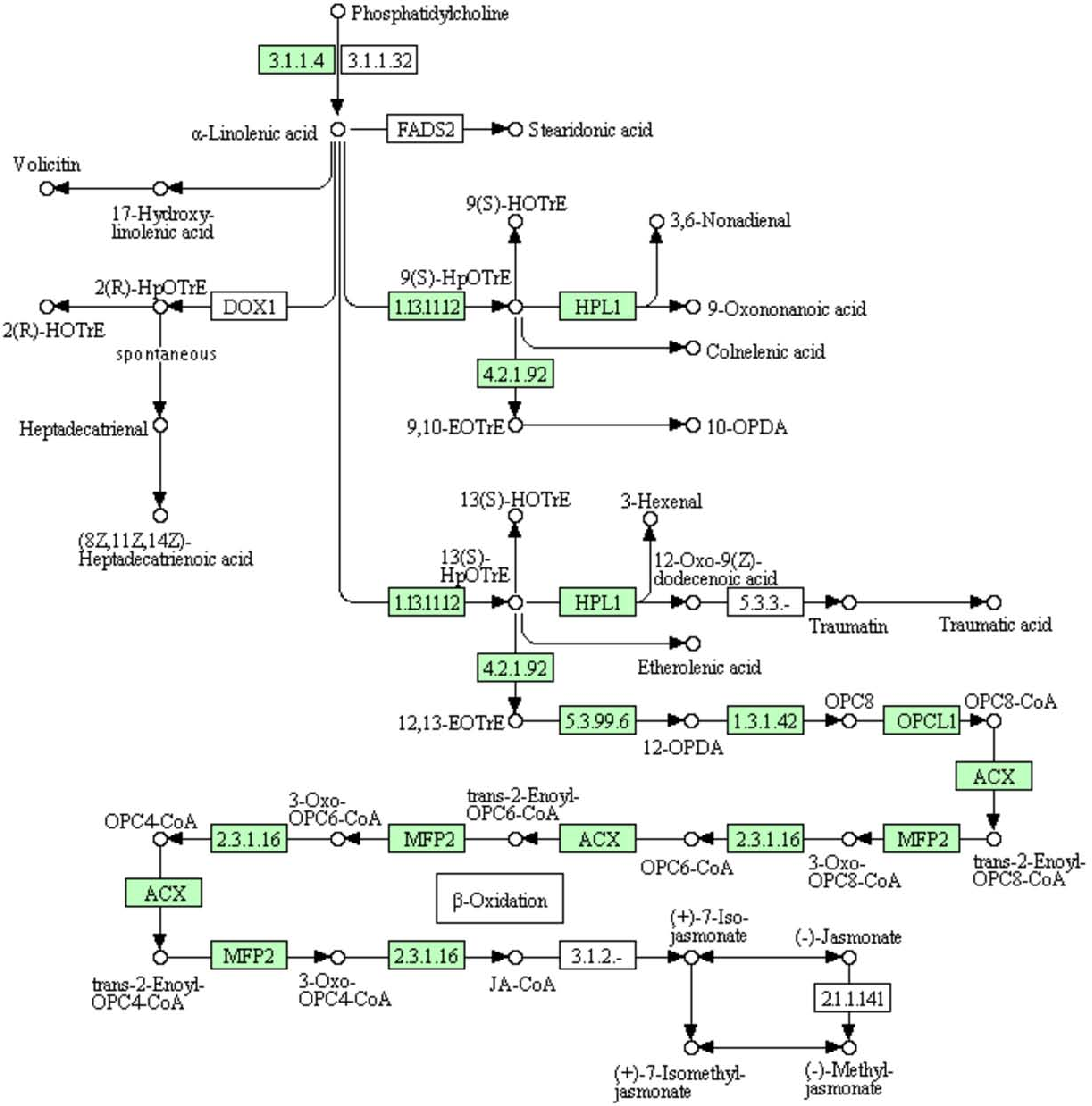
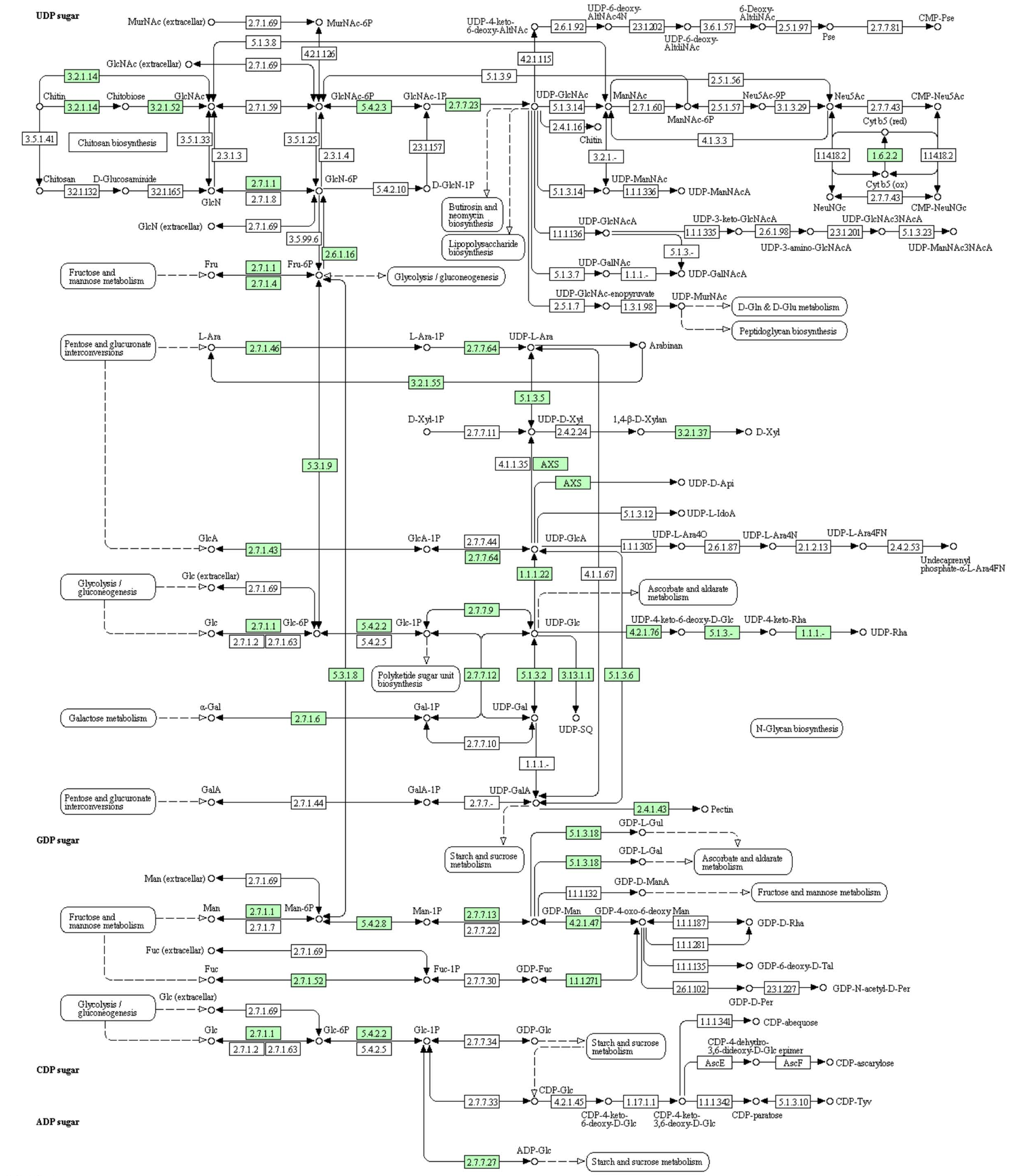
α-LINOLENIC ACID METABOLISM



00592 2/8/13

AMINO SUGAR AND NUCLEOTIDE SUGAR METABOLISM



00520 1/30/14
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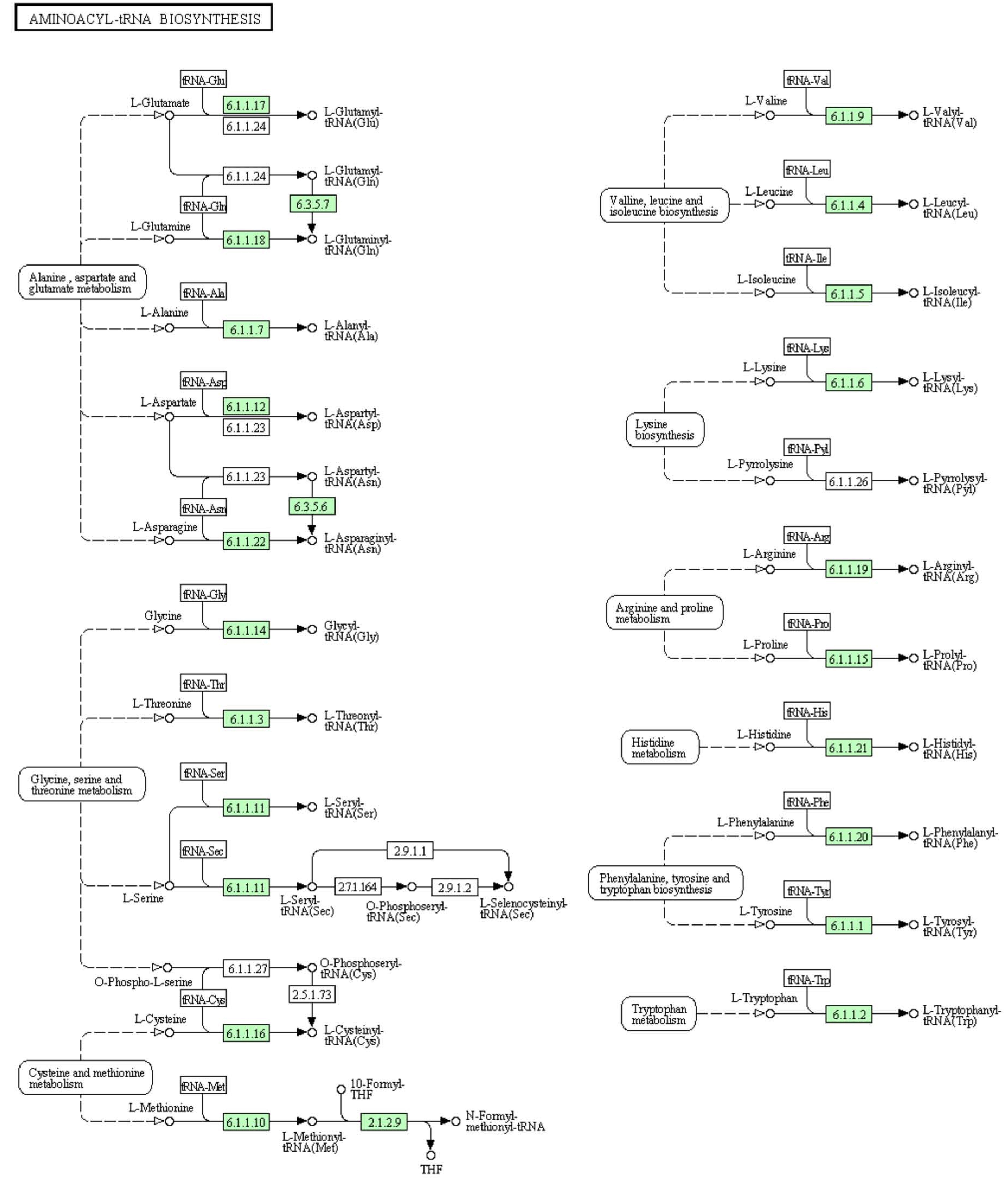

00970 4/17/13
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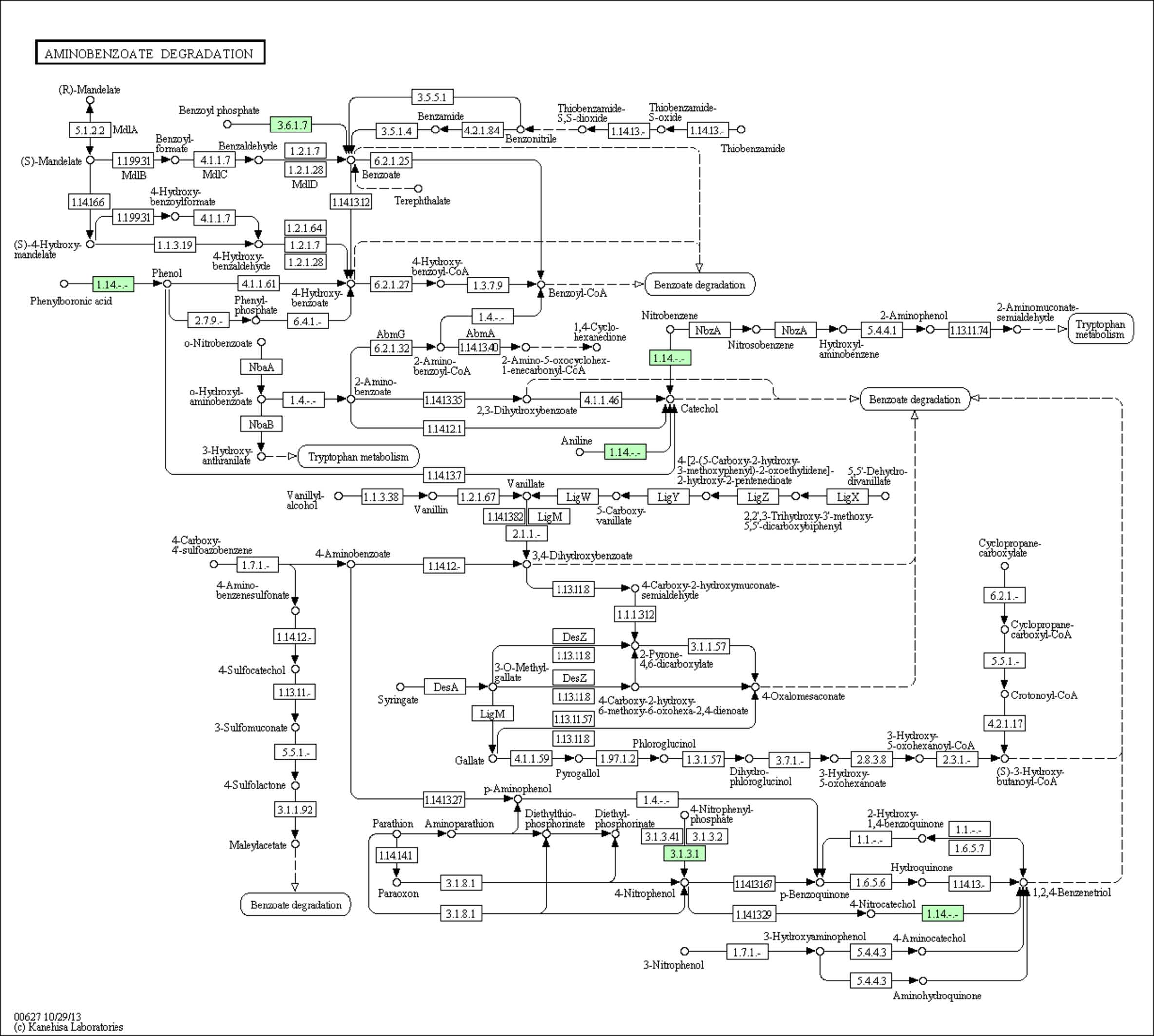
AMINOBENZOATE DEGRADATION
(R)-Mandelate
5.1.2.2 MdlA
(S)-Mandelate
1.1.99.31 MdlB
Benzoyl-formate
4.1.1.7 MdlC
Benzaldehyde
1.2.1.7
1.2.1.28 MdlD
Benzoyl phosphate
3.6.1.7
3.5.5.1
Benzamide
3.5.1.4
4.2.1.84
Benzonitrile
Thiobenzamide-S,S-dioxide
1.14.13.-
Thiobenzamide-S-oxide
1.14.13.-
Thiobenzamide
6.2.1.25
Benzoate
Terephthalate
1.14.13.12
1.14.16.6
4-Hydroxy-benzoylformate
1.1.99.31
4.1.1.7
(S)-4-Hydroxy-mandelate
1.1.3.19
4-Hydroxy-benzaldehyde
1.2.1.64
1.2.1.7
1.2.1.28
Phenylboronic acid
1.14.-.-
Phenol
4.1.1.61
4-Hydroxy-benzoate
6.2.1.27
4-Hydroxy-benzoyl-CoA
1.3.7.9
Benzoyl-CoA
Benzoate degradation
2.7.9.-
Phenyl-phosphate
6.4.1.-
1.4.-.-
AbmG
6.2.1.32
2-Amino-benzoyl-CoA
AbmA
1.14.13.40
2-Amino-5-oxocyclohex-1-enecarbonyl-CoA
1,4-Cyclo-hexanedione
o-Nitrobenzoate
NbaA
o-Hydroxyl-aminobenzoate
1.4.-.-
2-Amino-benzoate
1.14.13.35
2,3-Dihydroxybenzoate
4.1.1.46
1.14.12.1
NbaB
3-Hydroxy-anthranilate
Tryptophan metabolism
Nitrobenzene
NbzA
Nitrosobenzene
NbzA
Hydroxyl-aminobenzene
5.4.4.1
2-Aminophenol
1.13.11.74
2-Aminomuconate-semialdehyde
Tryptophan metabolism
1.14.-.-
Catechol
Benzoate degradation
Aniline
1.14.-.-
1.14.13.7
4-[2-(5-Carboxy-2-hydroxy-3-methoxyphenyl)-2-oxoethylidene]-2-hydroxy-2-pentenedioate
5,5'-Dehydro-divanillate
Vanillyl-alcohol
1.1.3.38
Vanillin
1.2.1.67
Vanillate
LigW
5-Carboxy-vanillate
LigY
LigZ
LigX
2,2',3-Trihydroxy-3'-methoxy-5,5'-dicarboxybiphenyl
1.14.13.82
LigM
2.1.1.-
3,4-Dihydroxybenzoate
4-Carboxy-4'-sulfoazobenzene
1.7.1.-
4-Aminobenzoate
1.14.12.-
4-Amino-benzenesulfonate
1.13.11.8
4-Carboxy-2-hydroxymuconate-semialdehyde
1.1.1.312
1.14.12.-
4-Sulfocatechol
1.13.11.-
3-Sulfomuconate
5.5.1.-
4-Sulfolactone
3.1.1.92
Maleylacetate
Benzoate degradation
DesZ
1.13.11.8
2-Pyrone-4,6-dicarboxylate
3.1.1.57
3-O-Methyl-gallate
DesZ
1.13.11.8
Syringate
DesA
4-Carboxy-2-hydroxy-6-methoxy-6-oxohexa-2,4-dienoate
4-Oxalomesaconate
LigM
1.13.11.57
1.13.11.8
Cyclopropane-carboxylate
6.2.1.-
Cyclopropane-carboxyl-CoA
5.5.1.-
Crotonoyl-CoA
4.2.1.17
Gallate
4.1.1.59
Pyrogallol
1.97.1.2
Phloroglucinol
1.3.1.57
Dihydro-phloroglucinol
3.7.1.-
3-Hydroxy-5-oxohexanoate
2.8.3.8
3-Hydroxy-5-oxohexanoyl-CoA
2.3.1.-
(S)-3-Hydroxy-butanoyl-CoA
1.14.13.27
p-Aminophenol
1.4.-.-
4-Nitrophenyl-phosphate
Parathion
Aminoparathion
Diethylthio-phosphorinate
Diethyl-phosphorinate
3.1.3.41
3.1.3.2
3.1.3.1
1.14.14.1
Paraoxon
3.1.8.1
4-Nitrophenol
1.14.13.167
p-Benzoquinone
2-Hydroxy-1,4-benzoquinone
1.1.-.-
1.1.-.-
1.6.5.7
1.6.5.6
Hydroquinone
1.14.13.-
1,2,4-Benzenetriol
3.1.8.1
1.14.13.29
4-Nitrocatechol
1.14.-.-
3-Nitrophenol
1.7.1.-
3-Hydroxyaminophenol
5.4.4.3
4-Aminocatechol
5.4.4.3
Aminohydroquinone
00627 10/29/13
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APOPTOSIS
Extrinsic Pathway
Death Ligand
Adaptor
Fas-L
Fas
TRAIL
TRAIL-R
FADD
TNFα
TNF-R1
TRADD
FADD
TRADD
RIP1
TRAF2
IL-1
IL-1R
TRADD
FADD
MyD88
IRAK
FLIP
Cytokine-cytokine receptor interaction
NIK
IAP
CASP6
Cleavage of Caspase Substrate
CASP10
Type 1
CASP3
DFF45
DFF40
Degradation
DNA Fragmentation
Apoptosis
CASP8
CASP7
Type 2
Bid
tBid
IAP
Mitochondrion
Bcl-2/XL
CytC
Apaf-1
CASP9
AIF
ENDO-G
Mitochondrion
Stress Signals
Intrinsic Pathway
NF-κB signaling pathway
+p
IKK
+p
IκBα
Degradation
NF-κB
DNA
Survival Genes
IAP
Bcl-XL
Bcl-2
Survival
DNA
Death Genes
Survival Factors
NGF
TrkA
IL-3R
IL-3
PI3K-Akt signaling pathway
PI3K
+p
Akt/PKB
+p
Bad
cAMP
PKA
+p
IL-3R
Homodimer
Bax
p53 signaling pathway
p53
Bcl-2
+p
ATM
Ca²⁺-induced Cell Death Pathways
[Ca²⁺]ᵢ Rises
ER Stres
Cn
-p
Bad
Apoptosis
Calpain
CASP12
CASP3
DNA Damage
Cell cycle
04210 10/2/12
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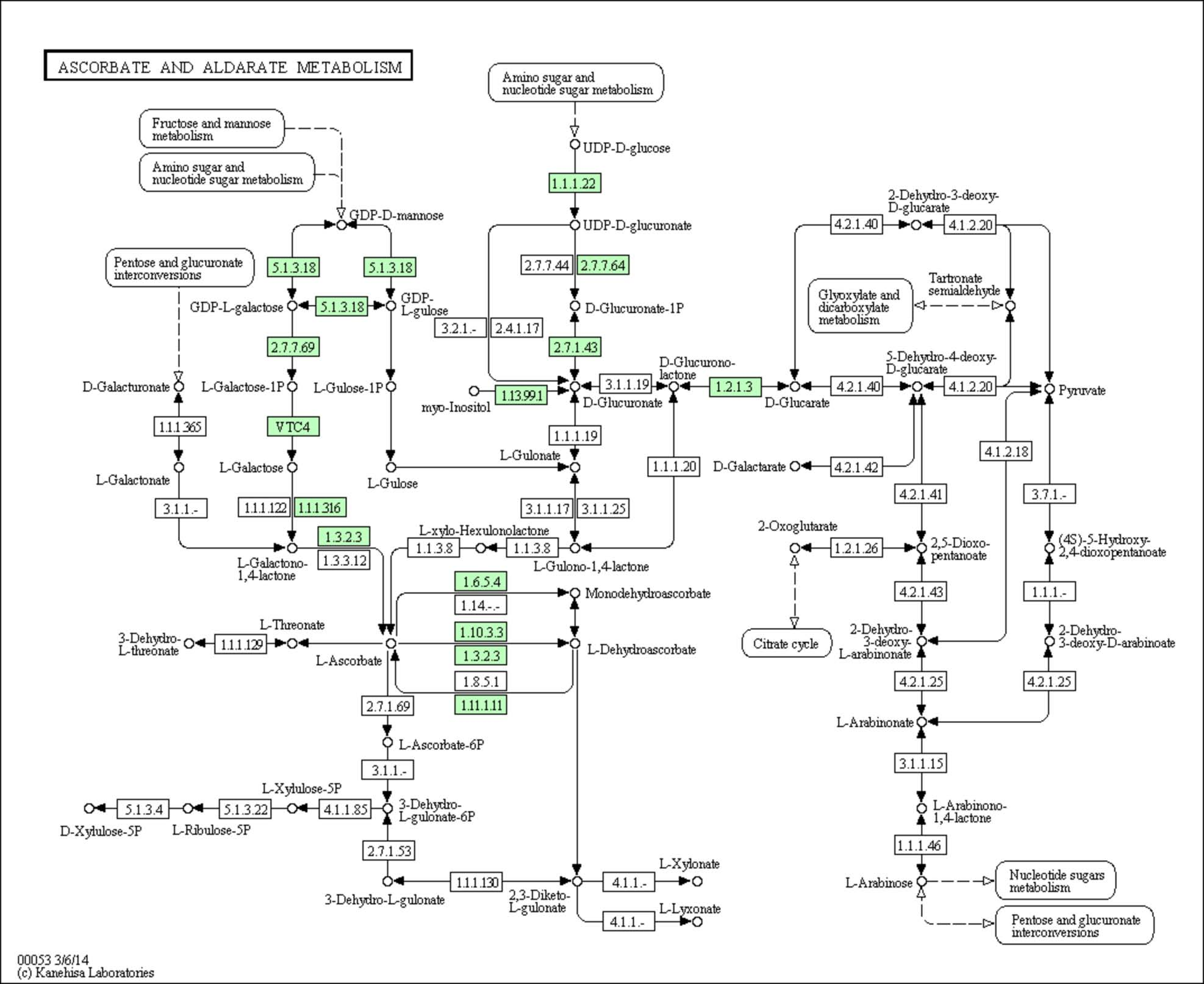
ARACHIDONIC ACID METABOLISM

00590 11/14/13

ARGININE AND PROLINE METABOLISM


ASCORBATE AND ALDARATE METABOLISM
Amino sugar and nucleotide sugar metabolism
Fructose and mannose metabolism
Amino sugar and nucleotide sugar metabolism
Pentose and glucuronate interconversions
UDP-D-glucose
1.1.1.22
UDP-D-glucuronate
GDP-D-mannose
5.1.3.18
5.1.3.18
5.1.3.18
GDP-L-galactose
GDP-L-gulose
2.7.7.44
2.7.7.64
D-Glucuronate-1P
3.2.1.-
2.4.1.17
2.7.7.69
2.7.1.43
D-Galacturonate
L-Galactose-1P
L-Gulose-1P
myo-Inositol
1.13.99.1
D-Glucuronate
3.1.1.19
D-Glucurono-lactone
1.2.1.3
D-Glucarate
1.1.1.365
VTC4
1.1.1.19
L-Gulonate
1.1.1.20
L-Galactonate
L-Galactose
L-Gulose
3.1.1.-
1.1.1.122
1.1.1.316
3.1.1.17
3.1.1.25
1.3.2.3
L-xylo-Hexulonolactone
1.1.3.8
1.1.3.8
L-Galactono-1,4-lactone
1.3.3.12
L-Gulono-1,4-lactone
1.6.5.4
1.14.-.-
Monodehydroascorbate
1.10.3.3
1.3.2.3
1.8.5.1
1.11.1.11
L-Threonate
3-Dehydro-L-threonate
1.1.1.129
L-Ascorbate
L-Dehydroascorbate
2.7.1.69
L-Ascorbate-6P
3.1.1.-
L-Xylulose-5P
D-Xylulose-5P
5.1.3.4
L-Ribulose-5P
5.1.3.22
4.1.1.85
3-Dehydro-L-gulonate-6P
2.7.1.53
3-Dehydro-L-gulonate
1.1.1.130
2,3-Diketo-L-gulonate
4.1.1.-
L-Xylonate
4.1.1.-
L-Lyxonate
2-Dehydro-3-deoxy-D-glucarate
4.2.1.40
4.1.2.20
Glyoxylate and dicarboxylate metabolism
Tartronate semialdehyde
5-Dehydro-4-deoxy-D-glucarate
4.2.1.40
4.1.2.20
Pyruvate
D-Galactarate
4.2.1.42
4.1.2.18
4.2.1.41
3.7.1.-
2-Oxoglutarate
1.2.1.26
2,5-Dioxo-pentanoate
(4S)-5-Hydroxy-2,4-dioxopentanoate
Citrate cycle
4.2.1.43
1.1.1.-
2-Dehydro-3-deoxy-L-arabinonate
2-Dehydro-3-deoxy-D-arabinoate
4.2.1.25
4.2.1.25
L-Arabinonate
3.1.1.15
L-Arabinono-1,4-lactone
1.1.1.46
L-Arabinose
Nucleotide sugars metabolism
Pentose and glucuronate interconversions
00053 3/6/14
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BACTERIAL SECRETION SYSTEM

Type I

Outer membrane protein (OMP)	TolC
Membrane fusion protein	HlyD
ABC transporter	HlyB

Type III

Needle	YscF		
	YscO	YscP	YscX
Secretin	YscC		
OMP	YscW		
Inner membrane protein (IMP)	YscJ	YscR	YscS
	YscT	YscU	YscV
ATPase	YscN		
ATPase-associated protein	YscQ	YscL	

Type II

Secretin	GspD		
OMP	GspS		
IMP	GspC	GspF	GspG
	GspH	GspI	GspJ
	GspK	GspL	GspM
ATPase	GspE		
Leaderpeptidase	GspO		

	Type Va	Vb	Vc
OMP	VacA	ShlB	YadA
		ShlA	YadB/C

Type IV

Periplasmic protein	VirB1		
Surface/pilus protein	VirB2	VirB3	VirB5
OMP	VirB7	VirB9	
IMP	VirB6	VirB8	VirB10
ATPase	VirB4	VirB11	VirD4

Type VI

Secreted substrate	VgrG		
	Hcp		
OMP	Lip		
IMP	IcmF	DotU	
ATPase	ClpV		
Regulatory protein	PpkA	Fha1	PppA

Sec-SRP

IMP	SecD/F	SecE	SecG
	SecY	YajC	YidC
ATPase	SecA		
Secretion monitor	SecM		
SRP receptor	FtsY		
Targeting protein	SecB	ffh	

Twin arginine targeting (Tat)

IMP	TatA	TatB	TatC	TatE

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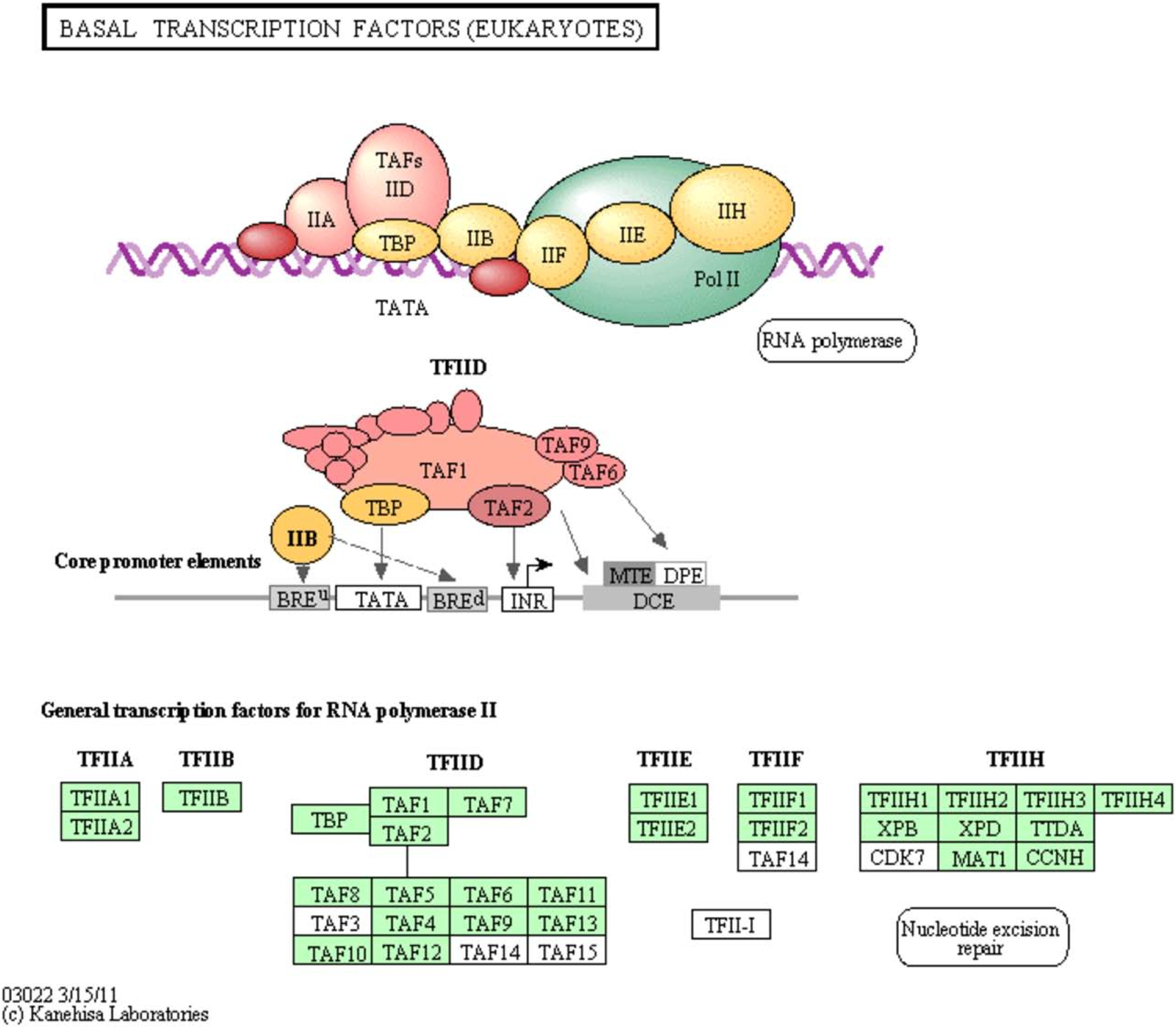
BASAL TRANSCRIPTION FACTORS (EUKARYOTES)
TAFs
IID
IIA
TBP
IIB
IIF
IIE
IIH
Pol II
TATA
RNA polymerase
TFIID
TAF9
TAF1
TAF6
TBP
TAF2
IIB
Core promoter elements
BREu
TATA
BREd
INR
MTE
DPE
DCE
General transcription factors for RNA polymerase II
TFIIA
TFIIA1
TFIIA2
TFIIB
TFIIB
TFIID
TBP
TAF1
TAF7
TAF2
TAF8
TAF5
TAF6
TAF11
TAF3
TAF4
TAF9
TAF13
TAF10
TAF12
TAF14
TAF15
TFIIE
TFIIE1
TFIIE2
TFIIF
TFIIF1
TFIIF2
TAF14
TFII-I
TFIIH
TFIIH1
TFIIH2
TFIIH3
TFIIH4
XPB
XPD
TTDA
CDK7
MAT1
CCNH
Nucleotide excision repair
03022 3/15/11
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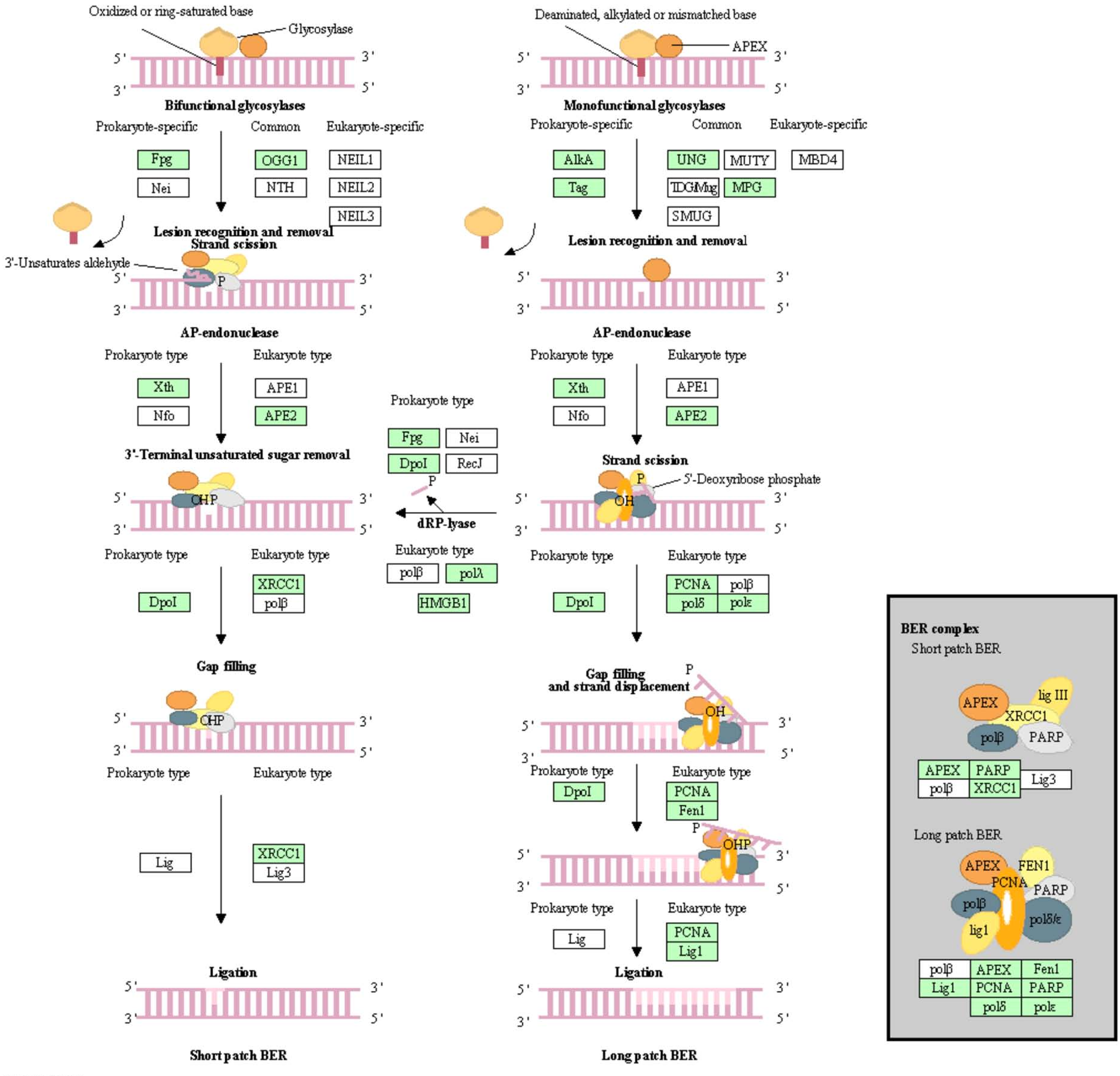
BASE EXCISION REPAIR



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β-ALANINE METABOLISM
β-Nitropropanoate
β-Amino-propionitrile
3.5.1.21
N-Acetyl-β-alanine
Cyanoamino acid metabolism
4.1.1.11
4.1.1.15
L-Aspartate
Alanine, aspartate and glutamate metabolism
3.4.13.5
3.4.13.20
6.3.2.11
Anserine
1.5.3.16
1.5.3.17
1.5.3.17
Uracil
1.3.1.1
1.3.1.2
5,6-Dihydrouracil
3.5.2.2
N-Carbamoyl-β-alanine
3.5.1.6
1.2.1.3
1.2.1.5
β-Alanine
β-Aminopropion-aldehyde
1.4.3.21
1,3-Diamino-propane
1.5.3.14
1.5.99.6
Spermidine
2.5.1.16
2.5.1.22
Spermine
Arginine and proline metabolism
Pyrimidine metabolism
4-Aminobutanal
1.2.1.19
4-Amino-butanoate
Histidine
3.4.13.18
3.4.13.20
Carnosine
6.3.2.11
6.3.2.11
β-Alanyl arginine
6.3.2.11
β-Alanyl lysine
3.4.13.4
3.4.13.4
2.6.1.19
2.6.1.55
2.6.1.18
6.3.2.1
Fatty acid biosynthesis
Malonyl-CoA
4.1.1.9
Acetyl-CoA
Quinolinate
2.8.3.3
1.2.1.18
(R)-Pantothenate
Pantothenate and CoA biosynthesis
Malonate
1.2.1.15
Malonate semialdehyde
1.1.1.59
3-Hydroxy-propanoate
3.1.2.4
3-Hydroxy-propanoyl-CoA
4.2.1.17
Acrylyl-CoA
1.3.8.7
Propionyl-CoA
4.3.1.6
β-Alanyl-CoA
Propanoate metabolism
4.2.1.27
Acetylene-monocarboxylate
00410 12/27/13
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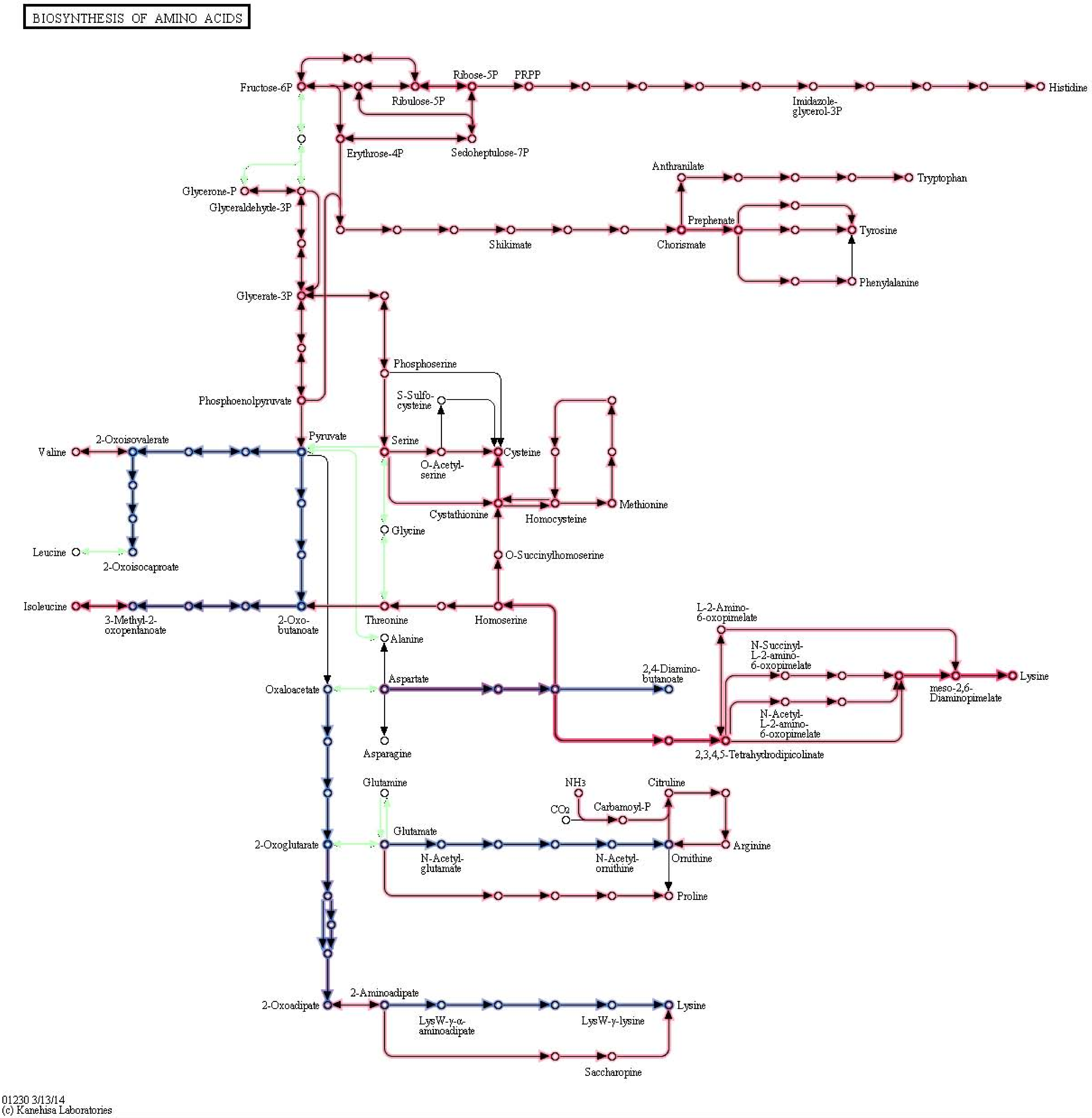
BIOSYNTHESIS OF AMINO ACIDS
Fructose-6P
Ribose-5P
PRPP
Ribulose-5P
Histidine
Imidazole-glycerol-3P
Erythrose-4P
Sedoheptulose-7P
Anthranilate
Tryptophan
Glycerone-P
Glyceraldehyde-3P
Prephenate
Tyrosine
Shikimate
Chorismate
Phenylalanine
Glycerate-3P
Phosphoserine
S-Sulfo-cysteine
Phosphoenolpyruvate
2-Oxoisovalerate
Valine
Pyruvate
Serine
Cysteine
O-Acetyl-serine
Methionine
Cystathionine
Homocysteine
Glycine
Leucine
2-Oxoisocaproate
O-Succinylhomoserine
Isoleucine
3-Methyl-2-oxopentanoate
2-Oxo-butanoate
Threonine
Homoserine
L-2-Amino-6-oxopimelate
Alanine
N-Succinyl-L-2-amino-6-oxopimelate
2,4-Diamino-butanoate
Aspartate
Oxaloacetate
Lysine
meso-2,6-Diaminopimelate
N-Acetyl-L-2-amino-6-oxopimelate
Asparagine
2,3,4,5-Tetrahydrodipicolinate
Glutamine
NH3
Citruline
CO2
Carbamoyl-P
Glutamate
2-Oxoglutarate
Arginine
N-Acetyl-glutamate
N-Acetyl-ornithine
Ornithine
Proline
2-Aminoadipate
2-Oxoadipate
Lysine
LysW-γ-α-aminoadipate
LysW-γ-lysine
Saccharopine
01230 3/13/14
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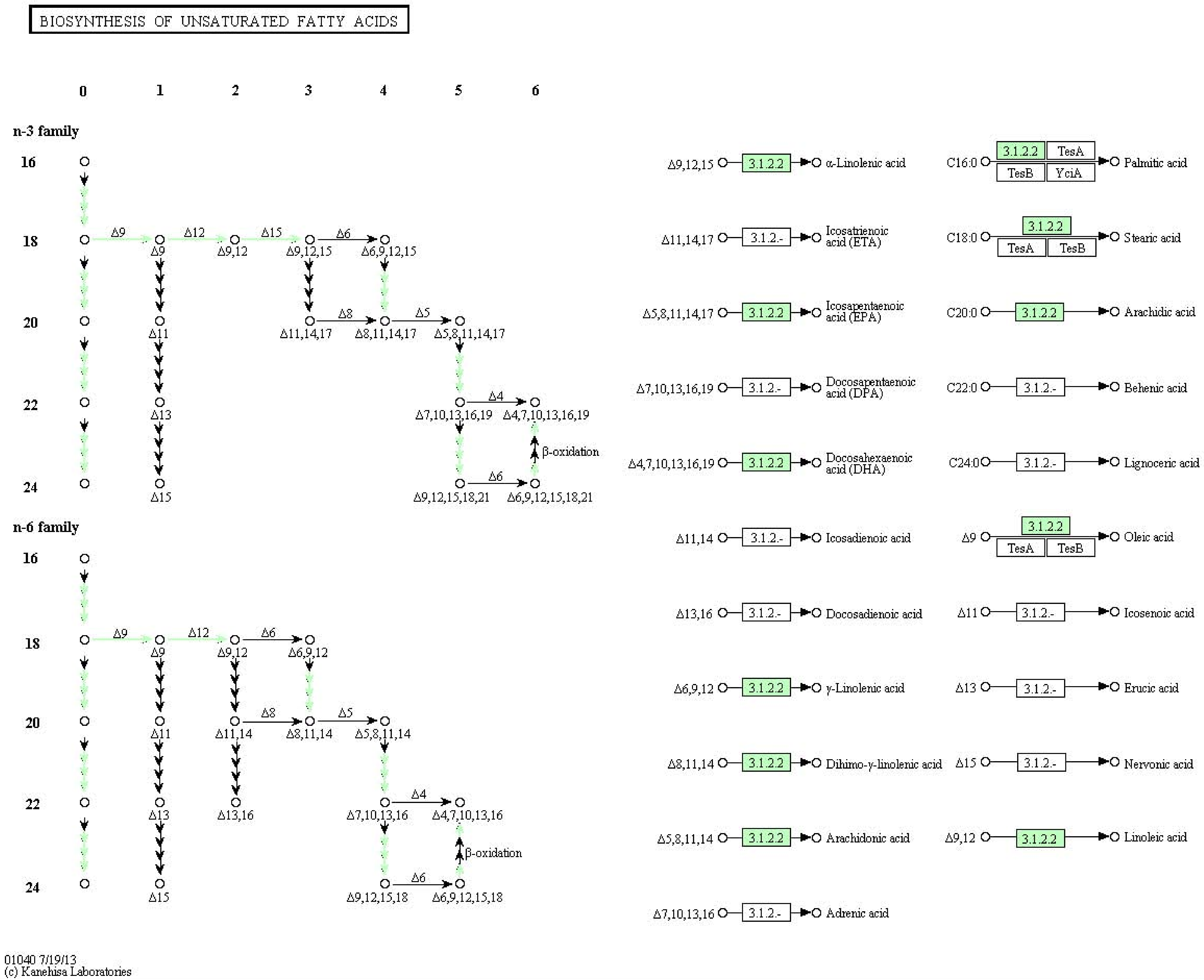
BIOSYNTHESIS OF UNSATURATED FATTY ACIDS
0
1
2
3
4
5
6
n-3 family
16
18
20
22
24
Δ9
Δ12
Δ15
Δ6
Δ8
Δ5
Δ4
Δ6
Δ9
Δ9,12
Δ9,12,15
Δ6,9,12,15
Δ11
Δ11,14,17
Δ8,11,14,17
Δ5,8,11,14,17
Δ13
Δ7,10,13,16,19
Δ4,7,10,13,16,19
β-oxidation
Δ15
Δ9,12,15,18,21
Δ6,9,12,15,18,21
n-6 family
16
18
20
22
24
Δ9
Δ12
Δ6
Δ8
Δ5
Δ4
Δ6
Δ9
Δ9,12
Δ6,9,12
Δ11
Δ11,14
Δ8,11,14
Δ5,8,11,14
Δ13
Δ13,16
Δ7,10,13,16
Δ4,7,10,13,16
β-oxidation
Δ15
Δ9,12,15,18
Δ6,9,12,15,18
Δ9,12,15
3.1.2.2
α-Linolenic acid
Δ11,14,17
3.1.2.-
Icosatrienoic acid (ETA)
Δ5,8,11,14,17
3.1.2.2
Icosapentaenoic acid (EPA)
Δ7,10,13,16,19
3.1.2.-
Docosapentaenoic acid (DPA)
Δ4,7,10,13,16,19
3.1.2.2
Docosahexaenoic acid (DHA)
Δ11,14
3.1.2.-
Icosadienoic acid
Δ13,16
3.1.2.-
Docosadienoic acid
Δ6,9,12
3.1.2.2
γ-Linolenic acid
Δ8,11,14
3.1.2.2
Dihimo-γ-linolenic acid
Δ5,8,11,14
3.1.2.2
Arachidonic acid
Δ7,10,13,16
3.1.2.-
Adrenic acid
C16:0
3.1.2.2
TesA
TesB
YciA
Palmitic acid
C18:0
3.1.2.2
TesA
TesB
Stearic acid
C20:0
3.1.2.2
Arachidic acid
C22:0
3.1.2.-
Behenic acid
C24:0
3.1.2.-
Lignoceric acid
Δ9
3.1.2.2
TesA
TesB
Oleic acid
Δ11
3.1.2.-
Icosenoic acid
Δ13
3.1.2.-
Erucic acid
Δ15
3.1.2.-
Nervonic acid
Δ9,12
3.1.2.2
Linoleic acid
01040 7/19/13
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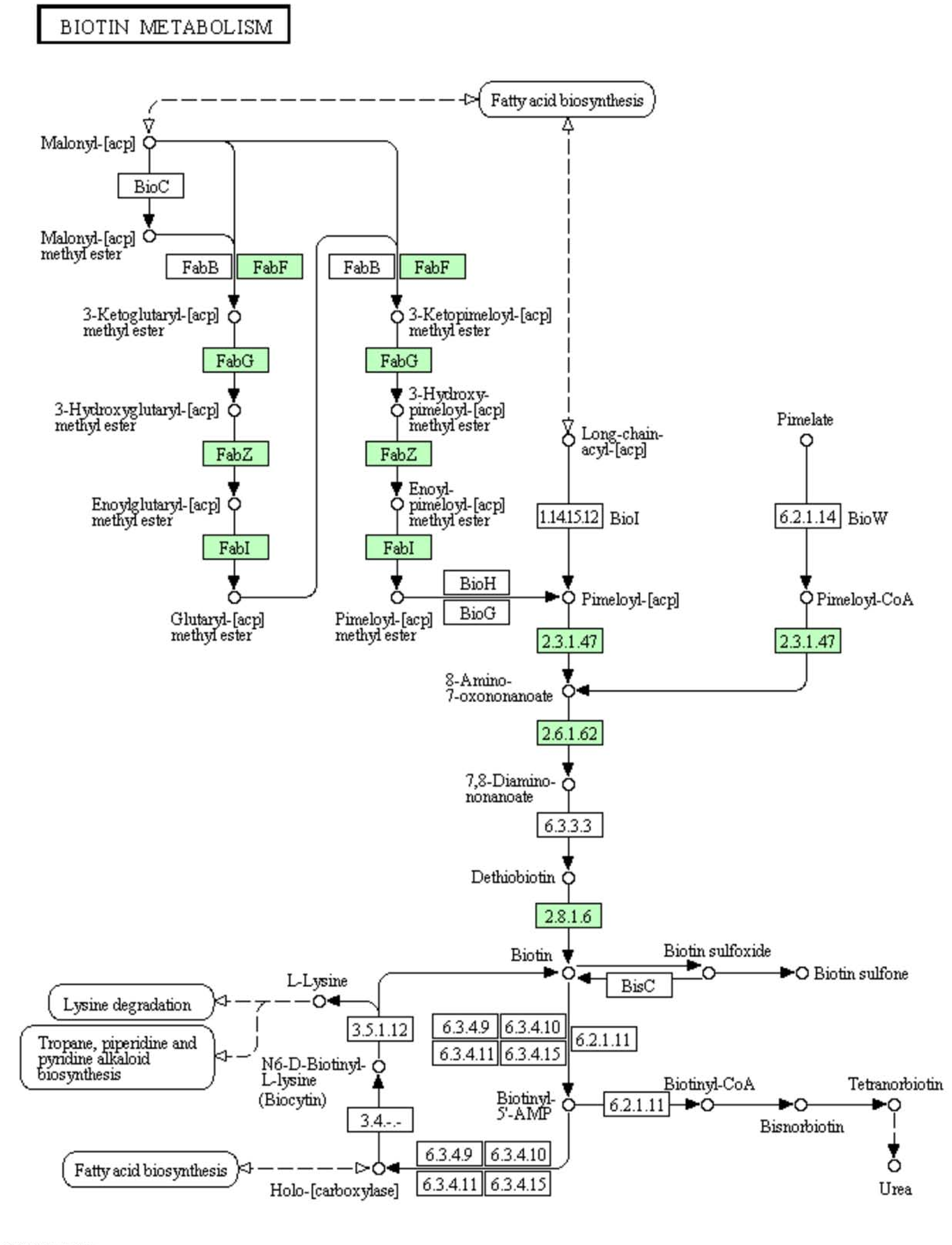

00780 1/8/14
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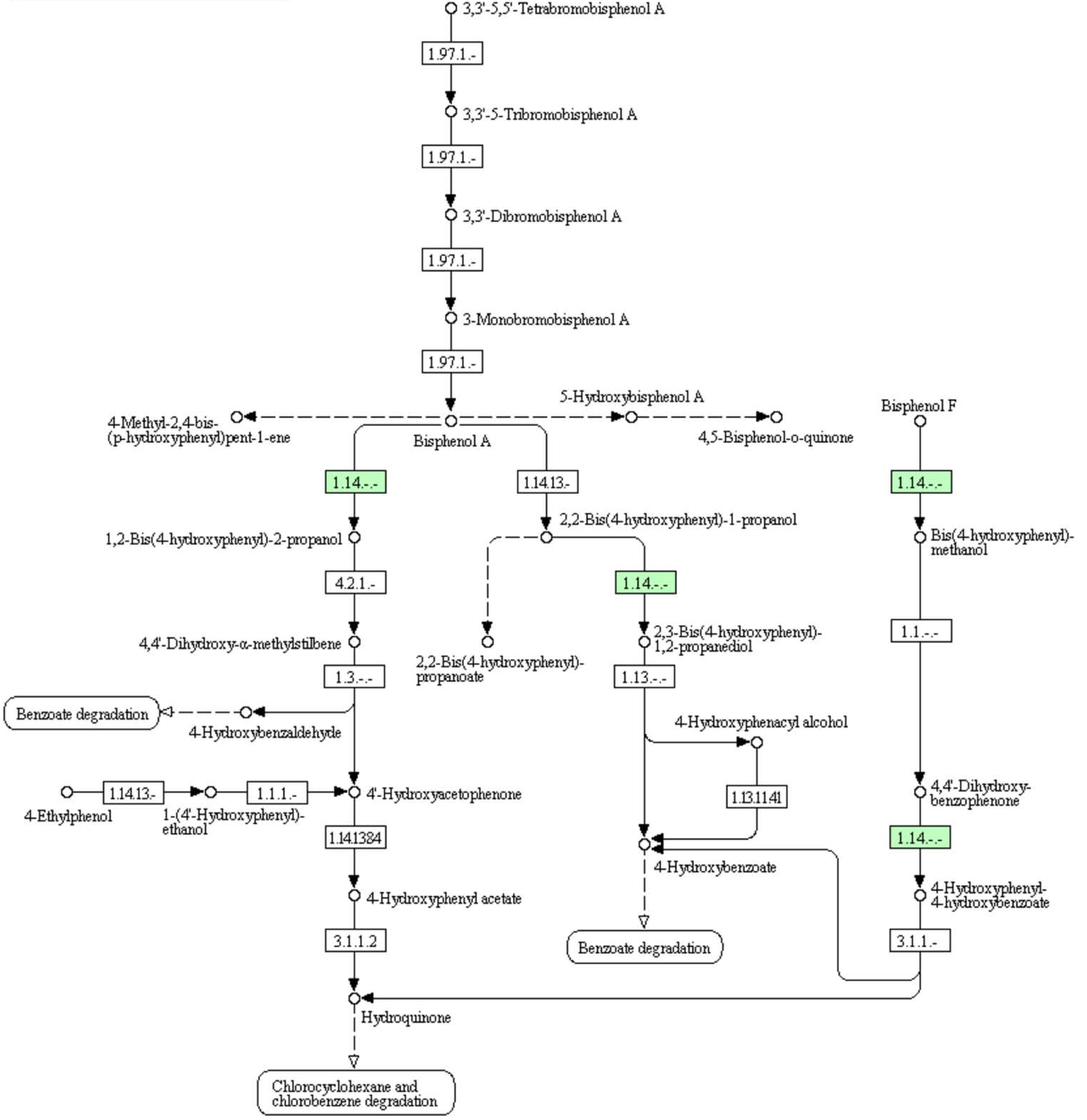
BISPHENOL DEGRADATION



00363 7/11/12
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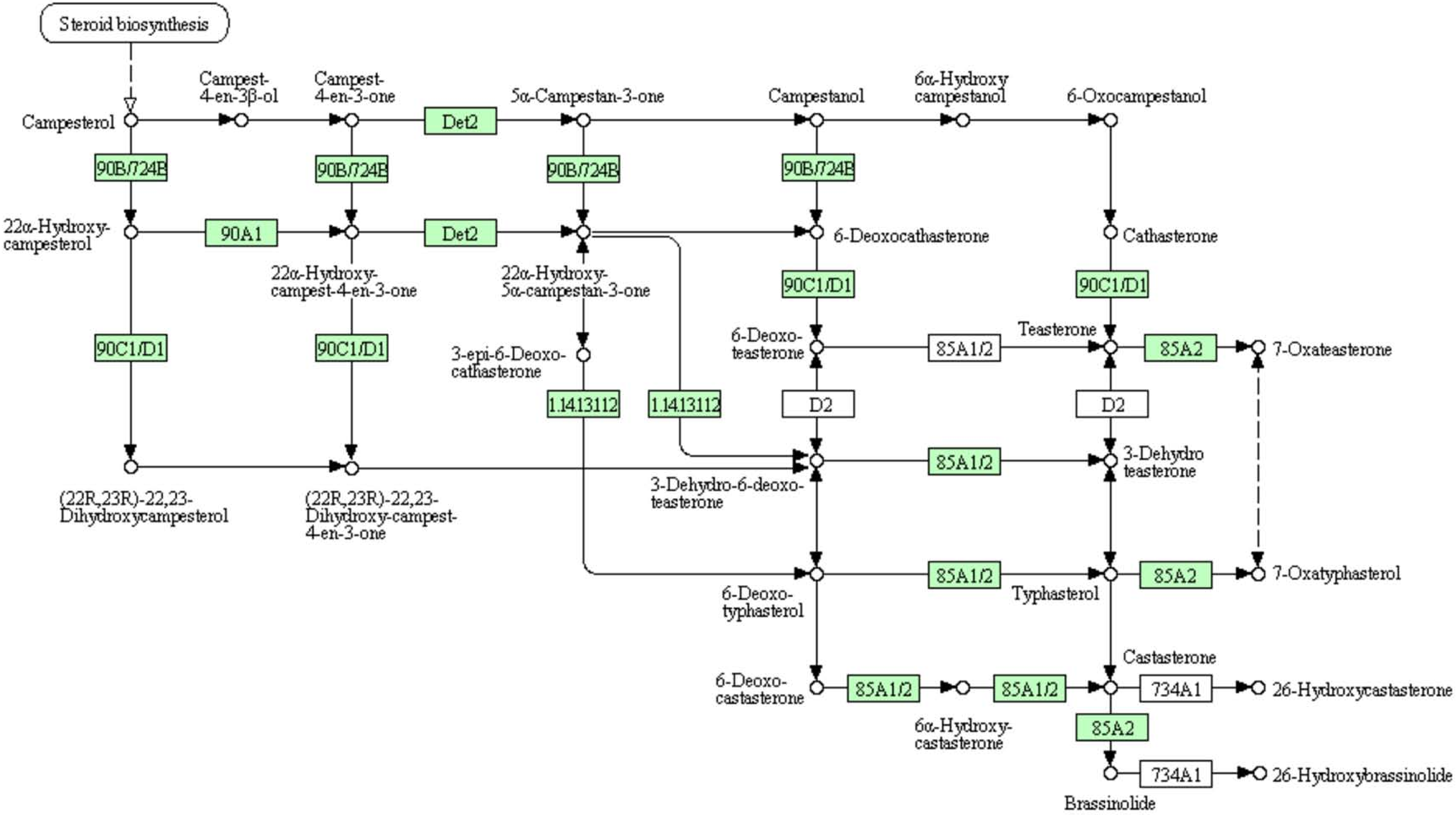
BRASSINOSTEROID BIOSYNTHESIS



00905 4/18/13
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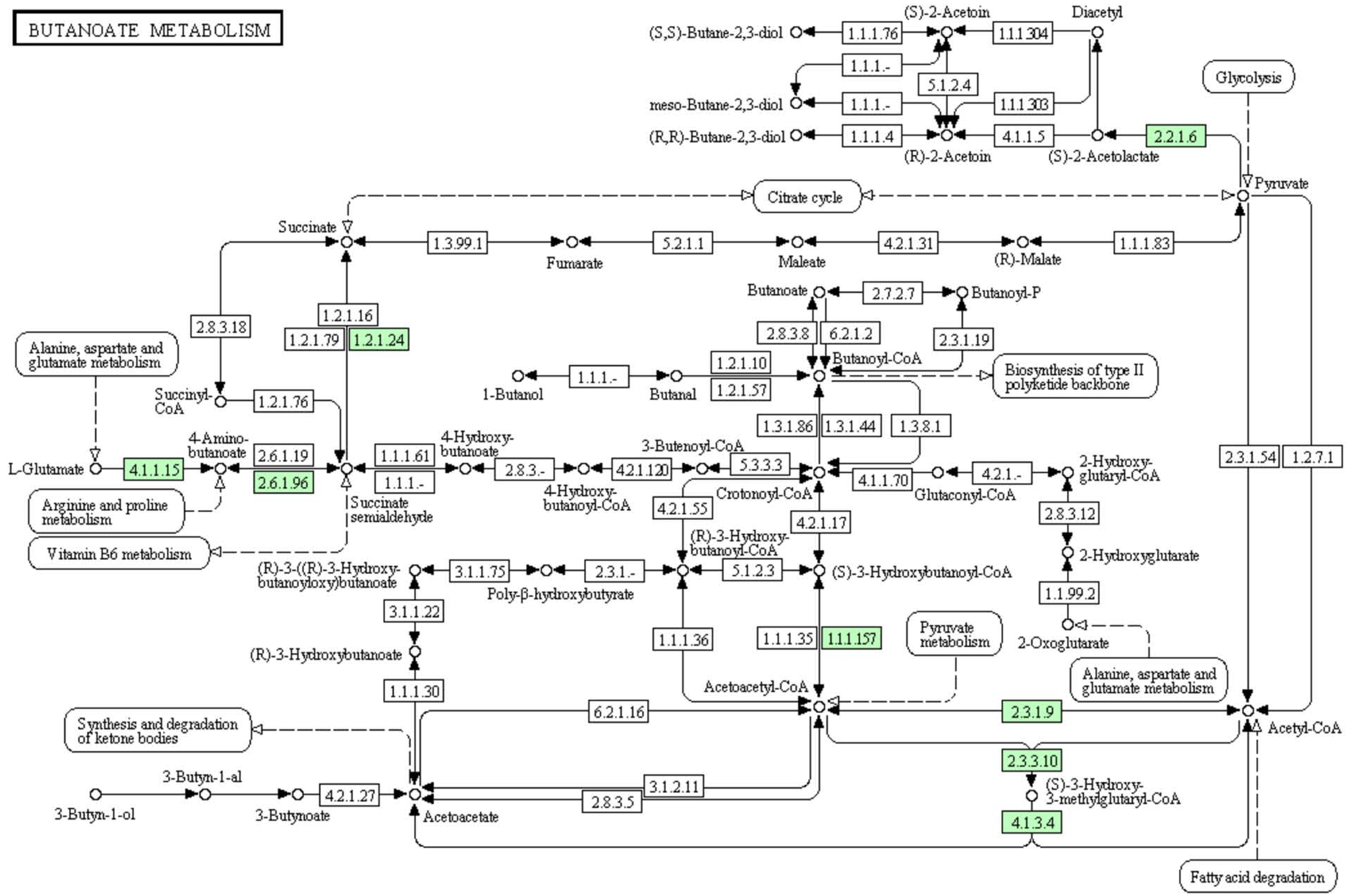

00650 12/26/13
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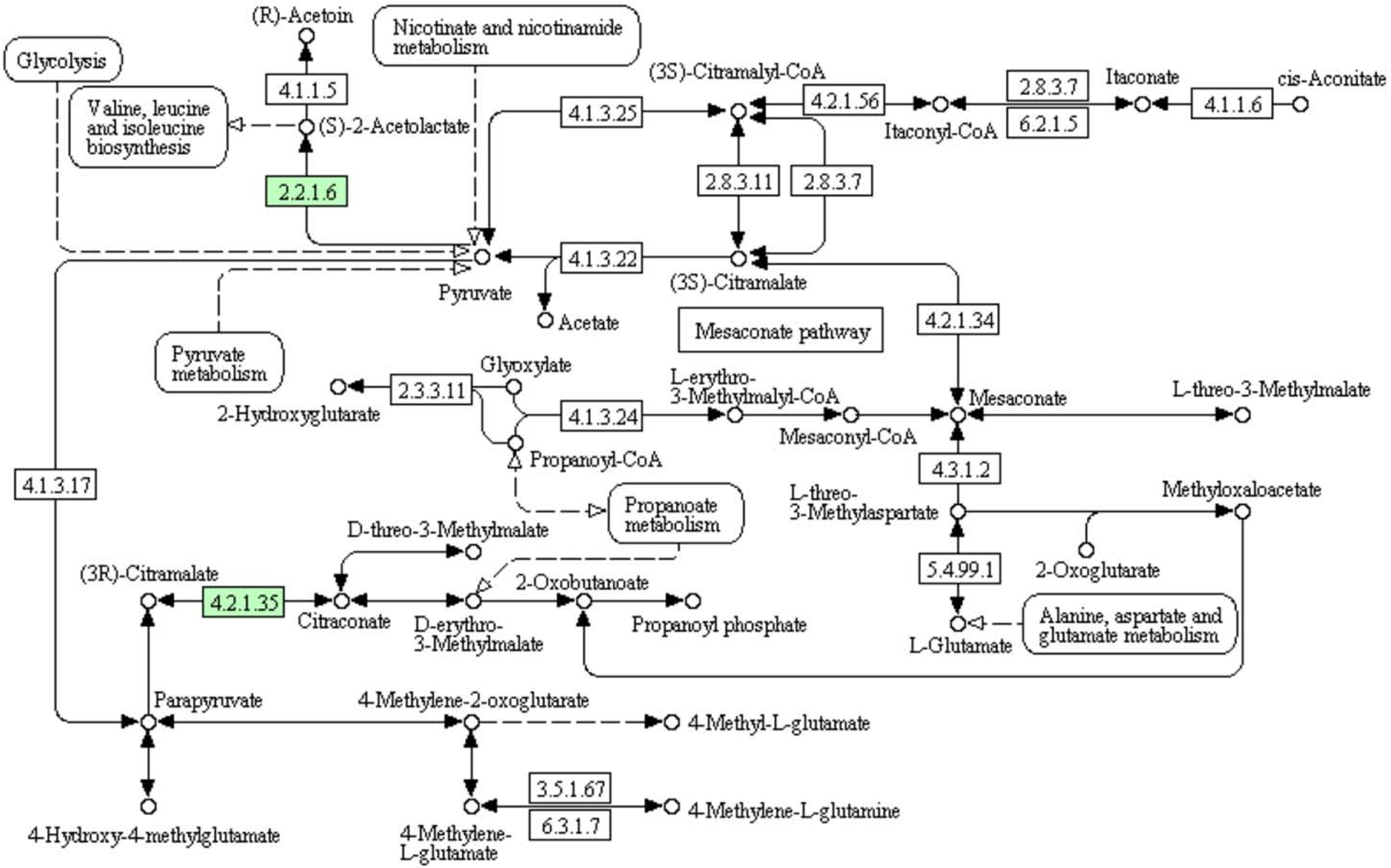
C$_5$-BRANCHED DIBASIC ACID METABOLISM



00660 11/12/13
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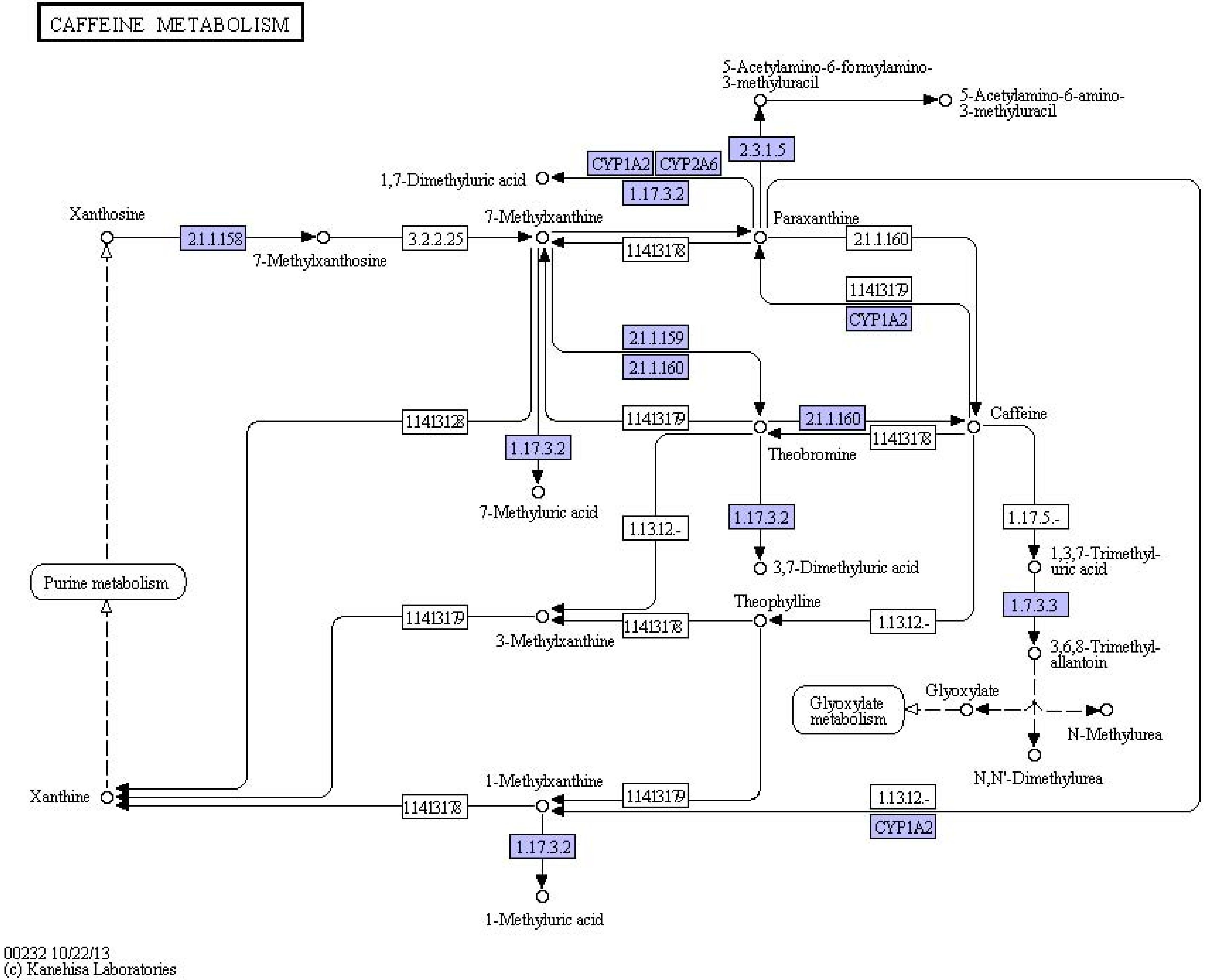
CAFFEINE METABOLISM
5-Acetylamino-6-formylamino-3-methyluracil
5-Acetylamino-6-amino-3-methyluracil
2.3.1.5
CYP1A2
CYP2A6
1.17.3.2
1,7-Dimethyluric acid
Xanthosine
2.1.1.158
7-Methylxanthosine
3.2.2.25
7-Methylxanthine
1.14.13.178
Paraxanthine
2.1.1.160
1.14.13.179
CYP1A2
2.1.1.159
2.1.1.160
1.14.13.128
1.14.13.179
2.1.1.160
Caffeine
1.14.13.178
Theobromine
1.17.3.2
7-Methyluric acid
1.13.12.-
1.17.3.2
3,7-Dimethyluric acid
1.17.5.-
1,3,7-Trimethyluric acid
Purine metabolism
1.7.3.3
Theophylline
1.14.13.179
3-Methylxanthine
1.14.13.178
1.13.12.-
3,6,8-Trimethylallantoin
Glyoxylate metabolism
Glyoxylate
N-Methylurea
N,N'-Dimethylurea
1-Methylxanthine
Xanthine
1.14.13.178
1.14.13.179
1.13.12.-
CYP1A2
1.17.3.2
1-Methyluric acid
00232 10/22/13
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CALCIUM SIGNALING PATHWAY
NCX
Na+
PMCA
Neurotransmitter, autacoid
GPCR
Gs
ADCY
cAMP
PKA
ER/SR
+p
PLN
ORAI
STIM
Depletion of Ca2+ stores
VOCs
CaV1
Membrane depolarization
CaV2
CaV3
SERCA
RYR
Neurotransmitter, autacoid
ROC
Neurotransmitter, hormone, autacoid
GPCR
Gq
PLCδ
Growth factor
PTK
PLCβ
IP3
IP3R
PLCγ
Antigen
TCR
BCR
cAMP
PLCε
Sperm
PLCζ
DAG
?
ATP
cADPR
CD38
NAADP
NAADPR
NADH
?
SPHK
S1P
?
MCU
Mitochondrion
VDAC
NCX
Na+
ANT
Cyp-D
Ca2+
TnC
MLCK
PHK
Contraction
Metabolism
MAPK signalng pathway
Apoptosis
CALM
CaN
CAMK
Proliferation
Fertilization
Learning and memory
Long term potentiation
Long term depression
NOS
ADCY
PDE1
Other signaling pathways
FAK2
IP3 3K
PKC
Phosphatidylinositol signaling pathway
Exocytosis
Secretion
04020 5/29/13
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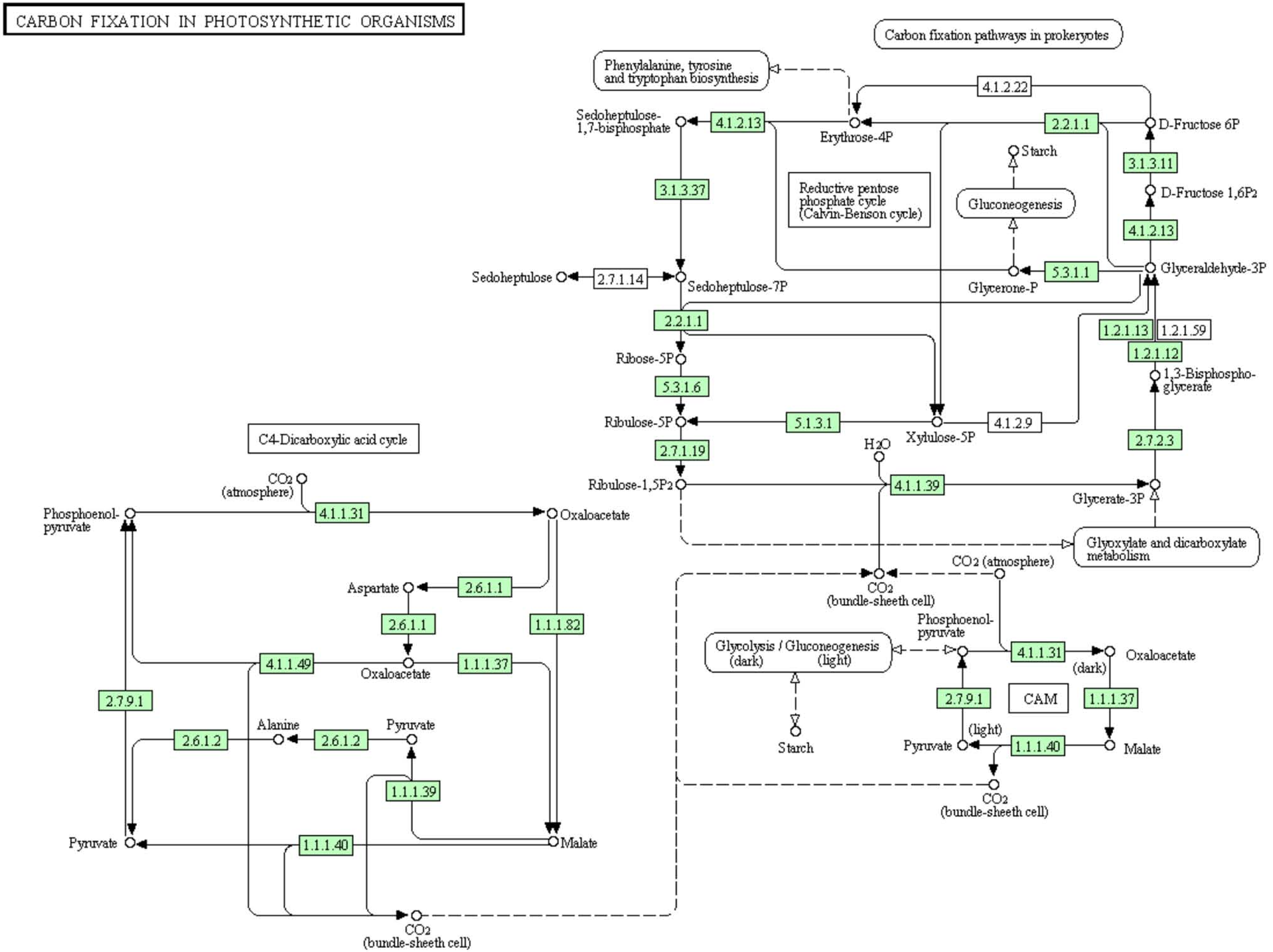
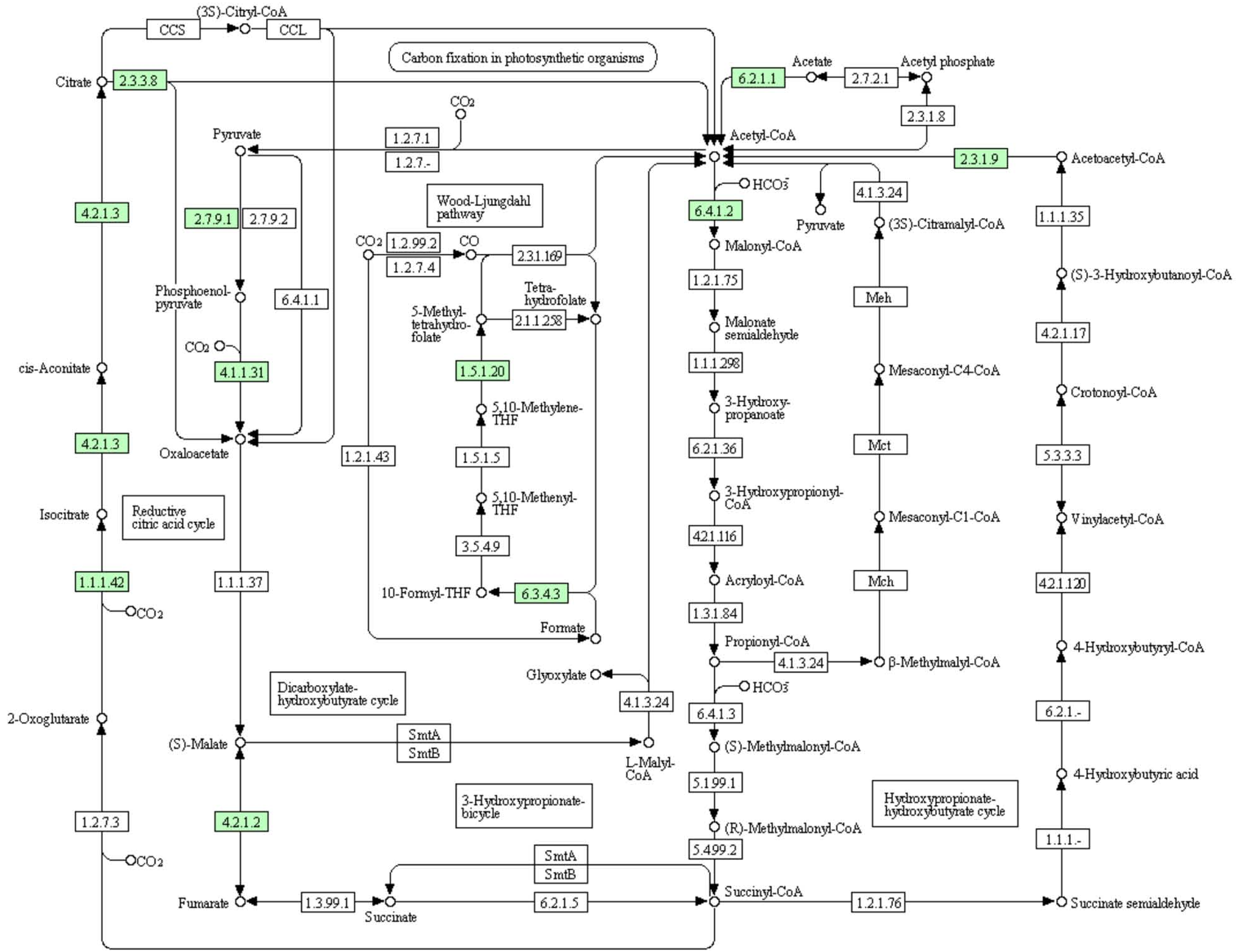

CARBON FIXATION IN PHOTOSYNTHETIC ORGANISMS
Carbon fixation pathways in prokeryotes
Phenylalanine, tyrosine and tryptophan biosynthesis
4.1.2.22
Sedoheptulose-1,7-bisphosphate
4.1.2.13
Erythrose-4P
2.2.1.1
D-Fructose 6P
Starch
3.1.3.11
3.1.3.37
Reductive pentose phosphate cycle (Calvin-Benson cycle)
Gluconeogenesis
D-Fructose 1,6P2
4.1.2.13
Sedoheptulose
2.7.1.14
Sedoheptulose-7P
5.3.1.1
Glycerone-P
Glyceraldehyde-3P
2.2.1.1
1.2.1.13
1.2.1.59
1.2.1.12
Ribose-5P
1,3-Bisphospho-glycerate
5.3.1.6
Ribulose-5P
5.1.3.1
Xylulose-5P
4.1.2.9
2.7.2.3
C4-Dicarboxylic acid cycle
2.7.1.19
H2O
Ribulose-1,5P2
4.1.1.39
Glycerate-3P
CO2 (atmosphere)
Phosphoenol-pyruvate
4.1.1.31
Oxaloacetate
Glyoxylate and dicarboxylate metabolism
CO2 (atmosphere)
CO2 (bundle-sheeth cell)
Aspartate
2.6.1.1
2.6.1.1
1.1.1.82
Phosphoenol-pyruvate
Glycolysis / Gluconeogenesis
(dark)
(light)
4.1.1.31
Oxaloacetate
(dark)
4.1.1.49
Oxaloacetate
1.1.1.37
2.7.9.1
CAM
1.1.1.37
2.7.9.1
Alanine
Pyruvate
2.6.1.2
2.6.1.2
Starch
(light)
Pyruvate
1.1.1.40
Malate
1.1.1.39
CO2 (bundle-sheeth cell)
Pyruvate
1.1.1.40
Malate
CO2 (bundle-sheeth cell)

00710 9/5/13

CARBON FIXATION PATHWAYS IN PROKARYOTES



00720 1/22/14
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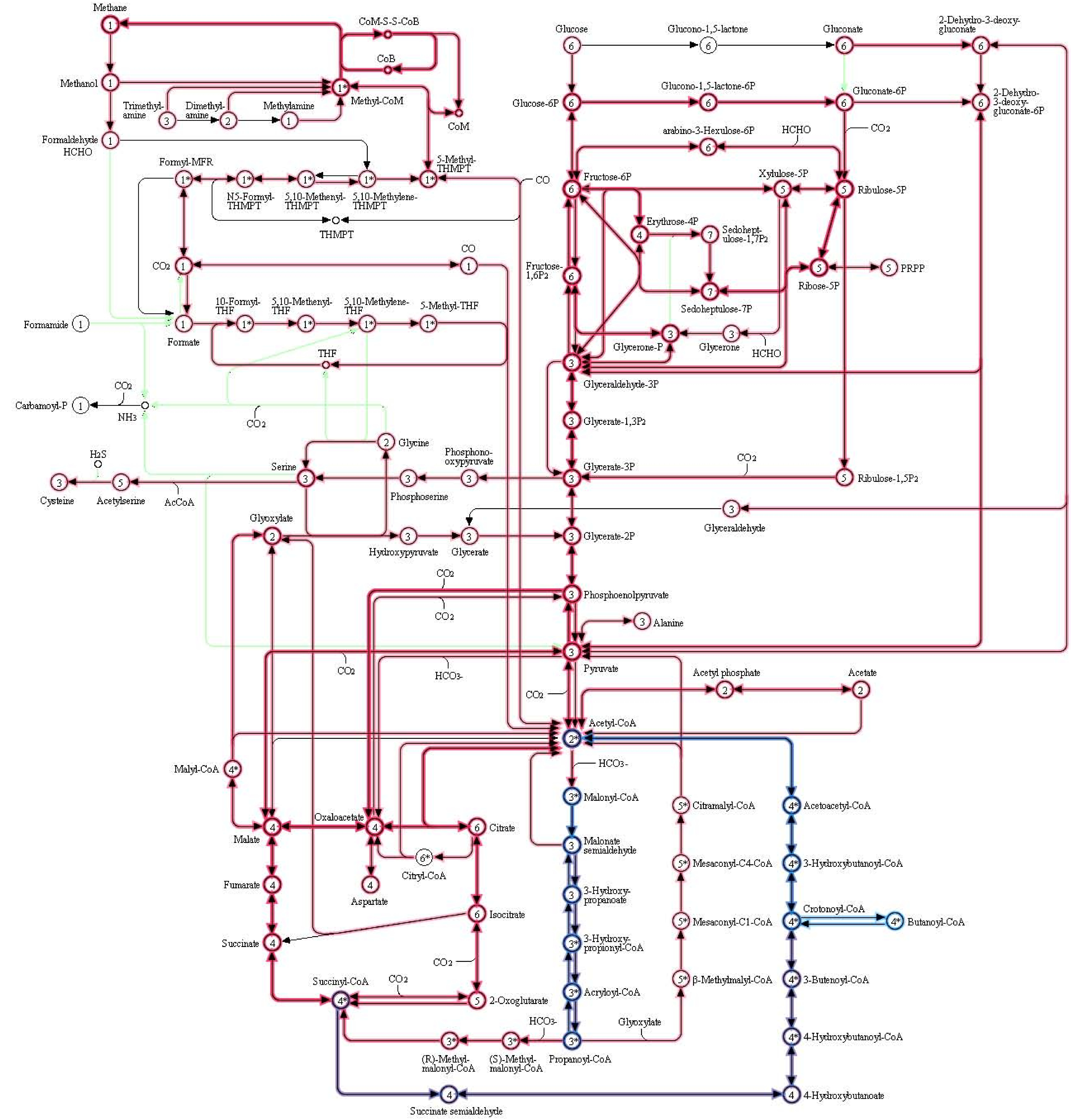
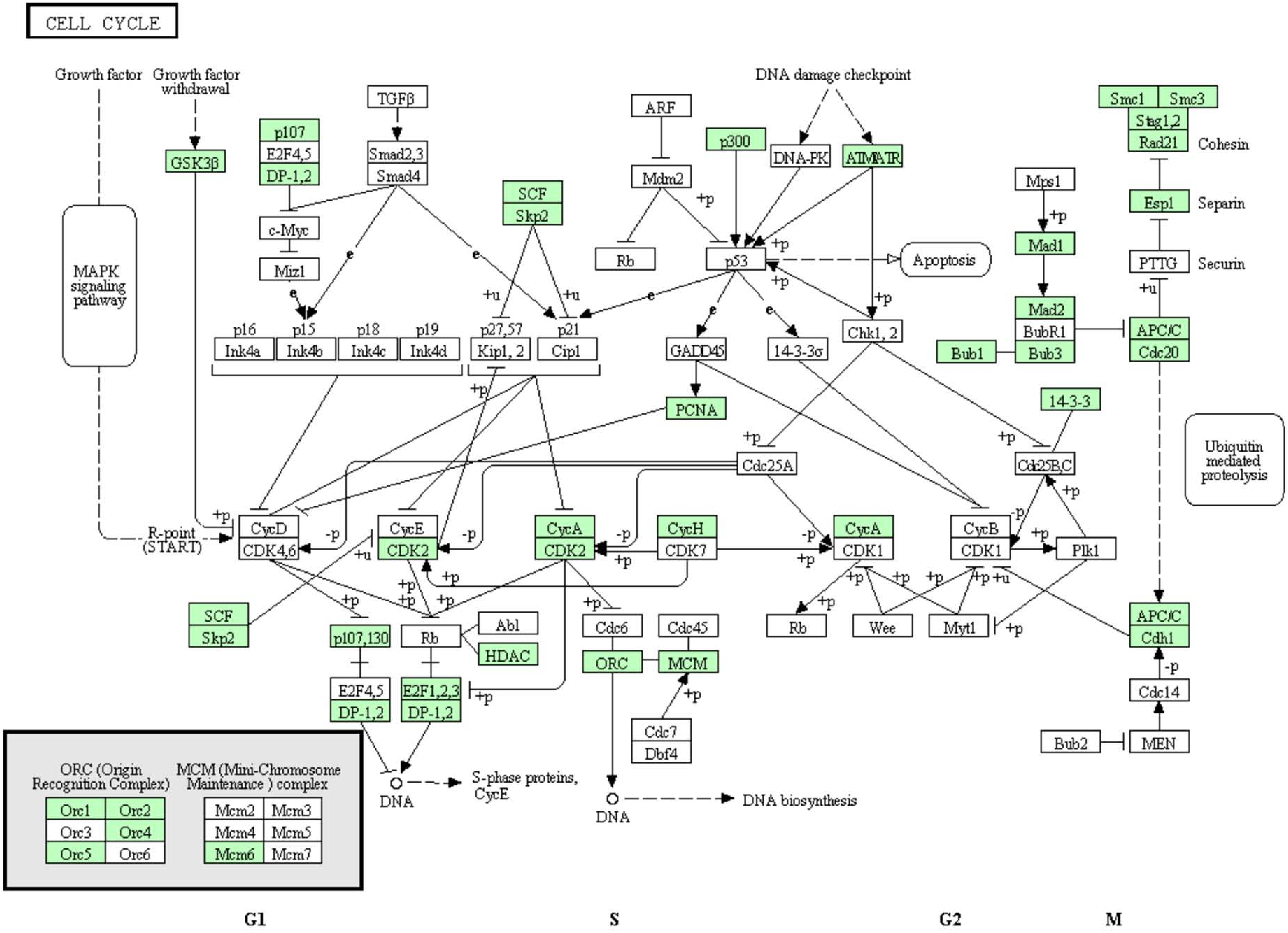
CARBON METABOLISM

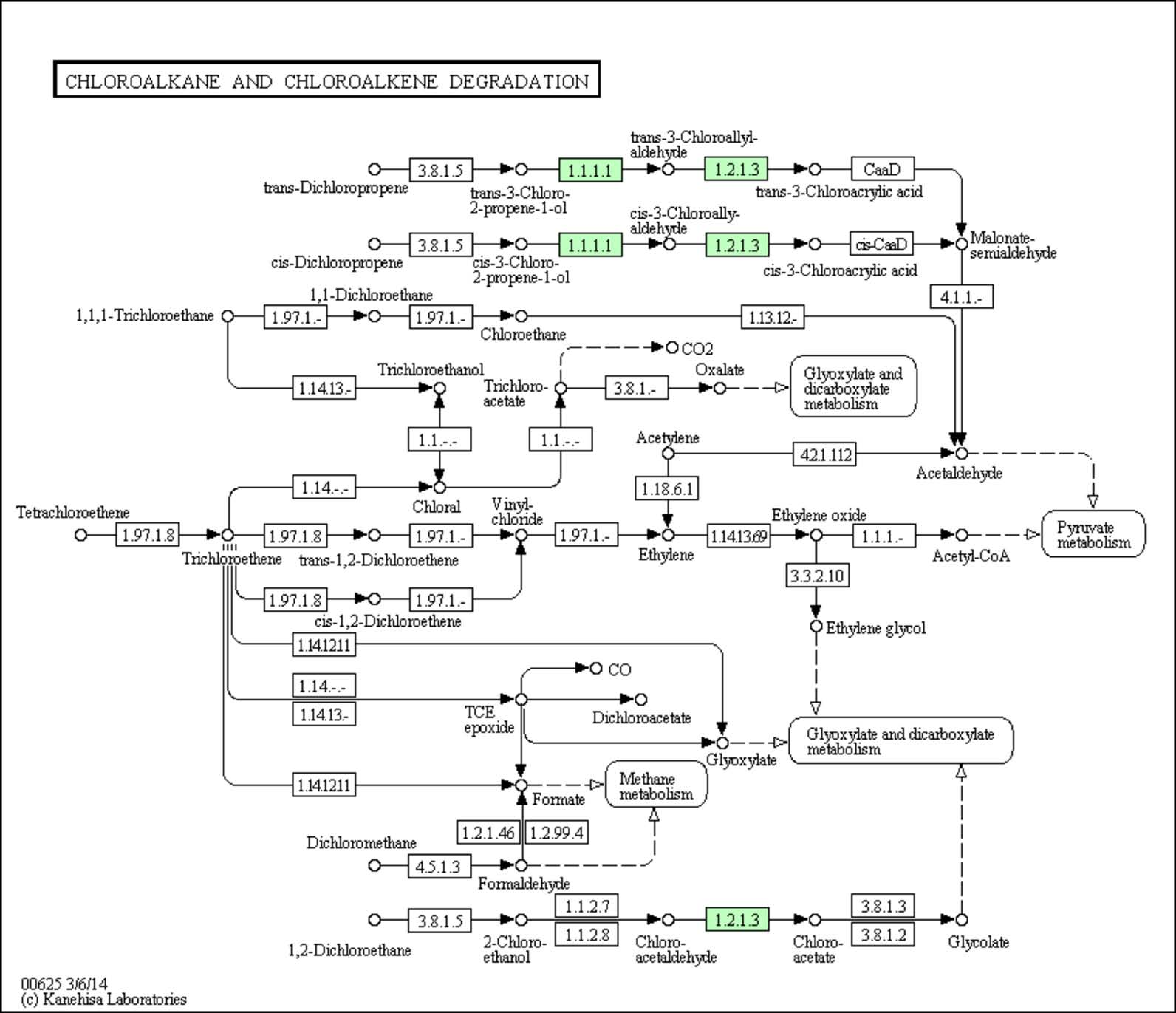


01200 3/13/14

CAROTENOID BIOSYNTHESIS


CELL CYCLE
Growth factor
Growth factor withdrawal
GSK3β
MAPK signaling pathway
R-point (START)
p107
E2F4,5
DP-1,2
TGFβ
Smad2,3
Smad4
c-Myc
Miz1
SCF
Skp2
ARF
Mdm2
Rb
p300
DNA damage checkpoint
DNA-PK
ATM/ATR
p53
Apoptosis
p16
Ink4a
p15
Ink4b
p18
Ink4c
p19
Ink4d
p27,57
Kip1, 2
p21
Cip1
GADD45
14-3-3σ
Chk1, 2
PCNA
Mps1
Mad1
Mad2
BubR1
Bub1
Bub3
Smc1
Smc3
Stag1,2
Rad21
Cohesin
Esp1
Separin
PTTG
Securin
APC/C
Cdc20
14-3-3
Ubiquitin mediated proteolysis
Cdc25A
Cdc25B,C
CycD
CDK4,6
CycE
CDK2
CycA
CDK2
CycH
CDK7
CycA
CDK1
CycB
CDK1
Plk1
SCF
Skp2
p107,130
Rb
Abl
HDAC
E2F4,5
DP-1,2
E2F1,2,3
DP-1,2
Cdc6
Cdc45
ORC
MCM
Cdc7
Dbf4
Rb
Wee
Myt1
APC/C
Cdh1
Cdc14
Bub2
MEN
DNA
S-phase proteins, CycE
DNA
DNA biosynthesis
ORC (Origin Recognition Complex)
Orc1
Orc2
Orc3
Orc4
Orc5
Orc6
MCM (Mini-Chromosome Maintenance) complex
Mcm2
Mcm3
Mcm4
Mcm5
Mcm6
Mcm7
+p
-p
+u
e
G1
S
G2
M

04110 8/7/13


CHLOROALKANE AND CHLOROALKENE DEGRADATION
trans-3-Chloroallyl-aldehyde
trans-Dichloropropene
3.8.1.5
1.1.1.1
1.2.1.3
CaaD
trans-3-Chloro-2-propene-1-ol
trans-3-Chloroacrylic acid
cis-3-Chloroally-aldehyde
cis-Dichloropropene
3.8.1.5
1.1.1.1
1.2.1.3
cis-CaaD
Malonate-semialdehyde
cis-3-Chloro-2-propene-1-ol
cis-3-Chloroacrylic acid
4.1.1.-
1,1-Dichloroethane
1,1,1-Trichloroethane
1.97.1.-
1.97.1.-
1.13.12.-
Chloroethane
CO2
Trichloroethanol
1.14.13.-
Trichloro-acetate
3.8.1.-
Oxalate
Glyoxylate and dicarboxylate metabolism
1.1.-.-
1.1.-.-
Acetylene
4.2.1.112
Acetaldehyde
1.14.-.-
1.18.6.1
Chloral
Vinyl-chloride
Ethylene oxide
Tetrachloroethene
1.97.1.8
1.97.1.8
1.97.1.-
1.97.1.-
1.14.13.69
1.1.1.-
Pyruvate metabolism
Trichloroethene
trans-1,2-Dichloroethene
Ethylene
Acetyl-CoA
3.3.2.10
1.97.1.8
1.97.1.-
cis-1,2-Dichloroethene
Ethylene glycol
1.14.12.11
CO
1.14.-.-
TCE epoxide
Dichloroacetate
1.14.13.-
Glyoxylate and dicarboxylate metabolism
Glyoxylate
Methane metabolism
1.14.12.11
Formate
1.2.1.46
1.2.99.4
Dichloromethane
4.5.1.3
Formaldehyde
1.1.2.7
3.8.1.3
3.8.1.5
1.2.1.3
1.1.2.8
3.8.1.2
2-Chloro-ethanol
Chloro-acetaldehyde
Chloro-acetate
Glycolate
1,2-Dichloroethane
00625 3/6/14
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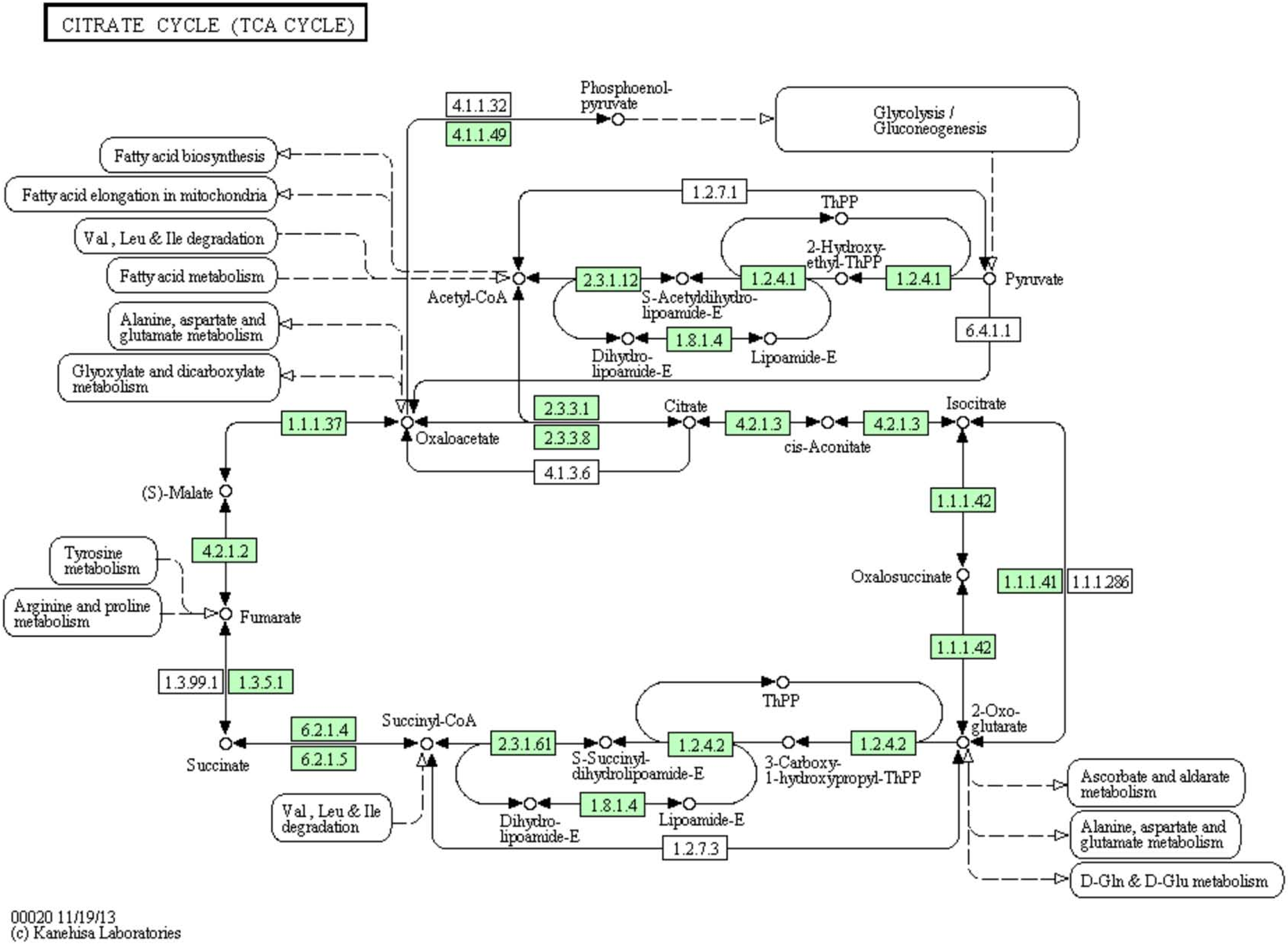
CHLOROCYCLOHEXANE AND CHLOROBENZENE DEGRADATION

00361 3/6/14


CITRATE CYCLE (TCA CYCLE)
4.1.1.32
4.1.1.49
Phosphoenol-pyruvate
Glycolysis / Gluconeogenesis
Fatty acid biosynthesis
Fatty acid elongation in mitochondria
Val , Leu & Ile degradation
Fatty acid metabolism
Alanine, aspartate and glutamate metabolism
Glyoxylate and dicarboxylate metabolism
1.2.7.1
ThPP
2-Hydroxy-ethyl-ThPP
2.3.1.12
1.2.4.1
1.2.4.1
Pyruvate
Acetyl-CoA
S-Acetyldihydro-lipoamide-E
1.8.1.4
Dihydro-lipoamide-E
Lipoamide-E
6.4.1.1
2.3.3.1
2.3.3.8
Citrate
4.2.1.3
4.2.1.3
cis-Aconitate
Isocitrate
1.1.1.37
Oxaloacetate
4.1.3.6
(S)-Malate
4.2.1.2
1.1.1.42
Oxalosuccinate
1.1.1.41
1.1.1.286
1.1.1.42
Tyrosine metabolism
Arginine and proline metabolism
Fumarate
1.3.99.1
1.3.5.1
ThPP
Succinyl-CoA
6.2.1.4
6.2.1.5
2.3.1.61
S-Succinyl-dihydrolipoamide-E
1.2.4.2
3-Carboxy-1-hydroxypropyl-ThPP
1.2.4.2
2-Oxo-glutarate
Succinate
Val , Leu & Ile degradation
Dihydro-lipoamide-E
1.8.1.4
Lipoamide-E
1.2.7.3
Ascorbate and aldarate metabolism
Alanine, aspartate and glutamate metabolism
D-Gln & D-Glu metabolism
00020 11/19/13
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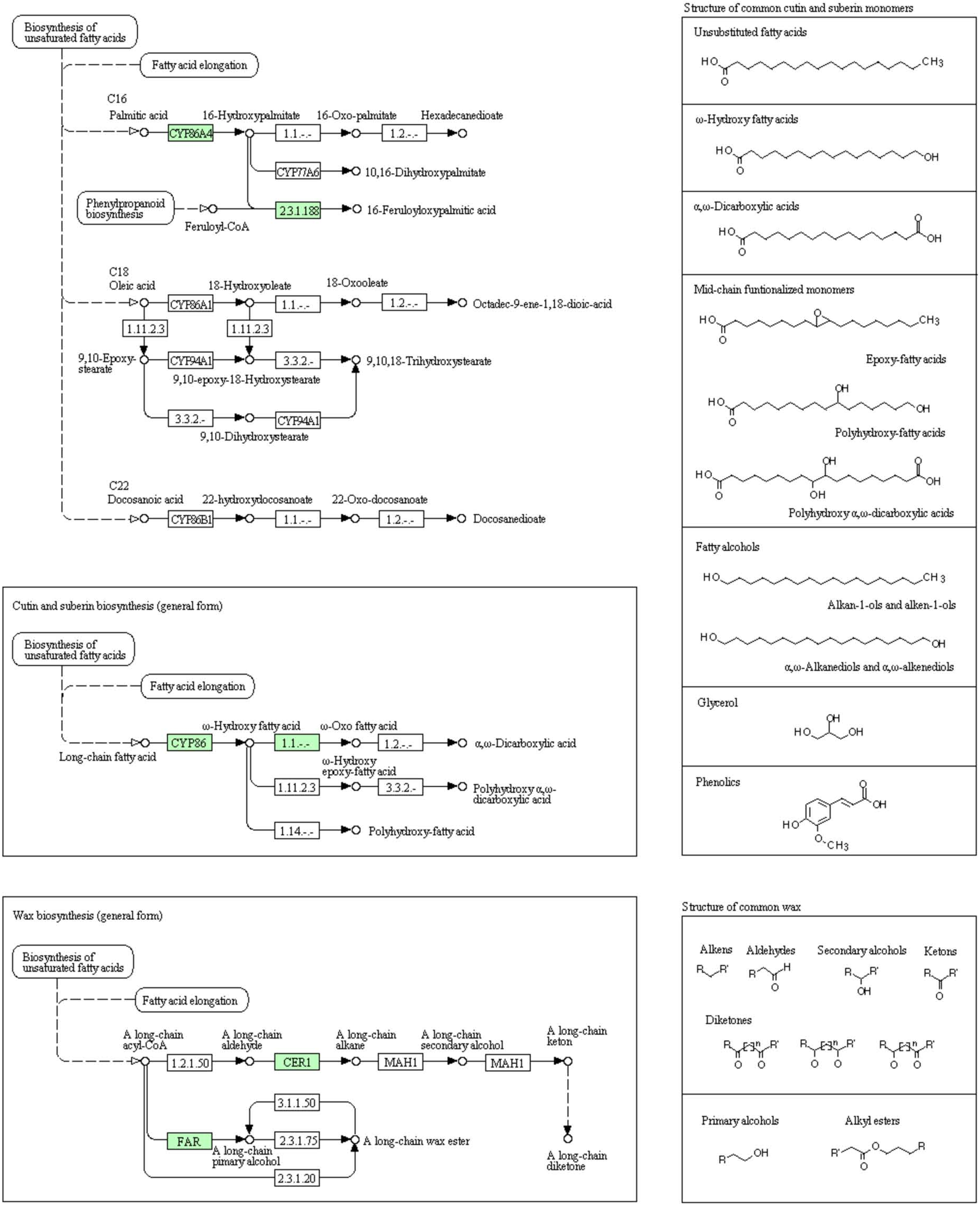
CUTIN, SUBERINE AND WAX BIOSYNTHESIS



00073 8/23/11
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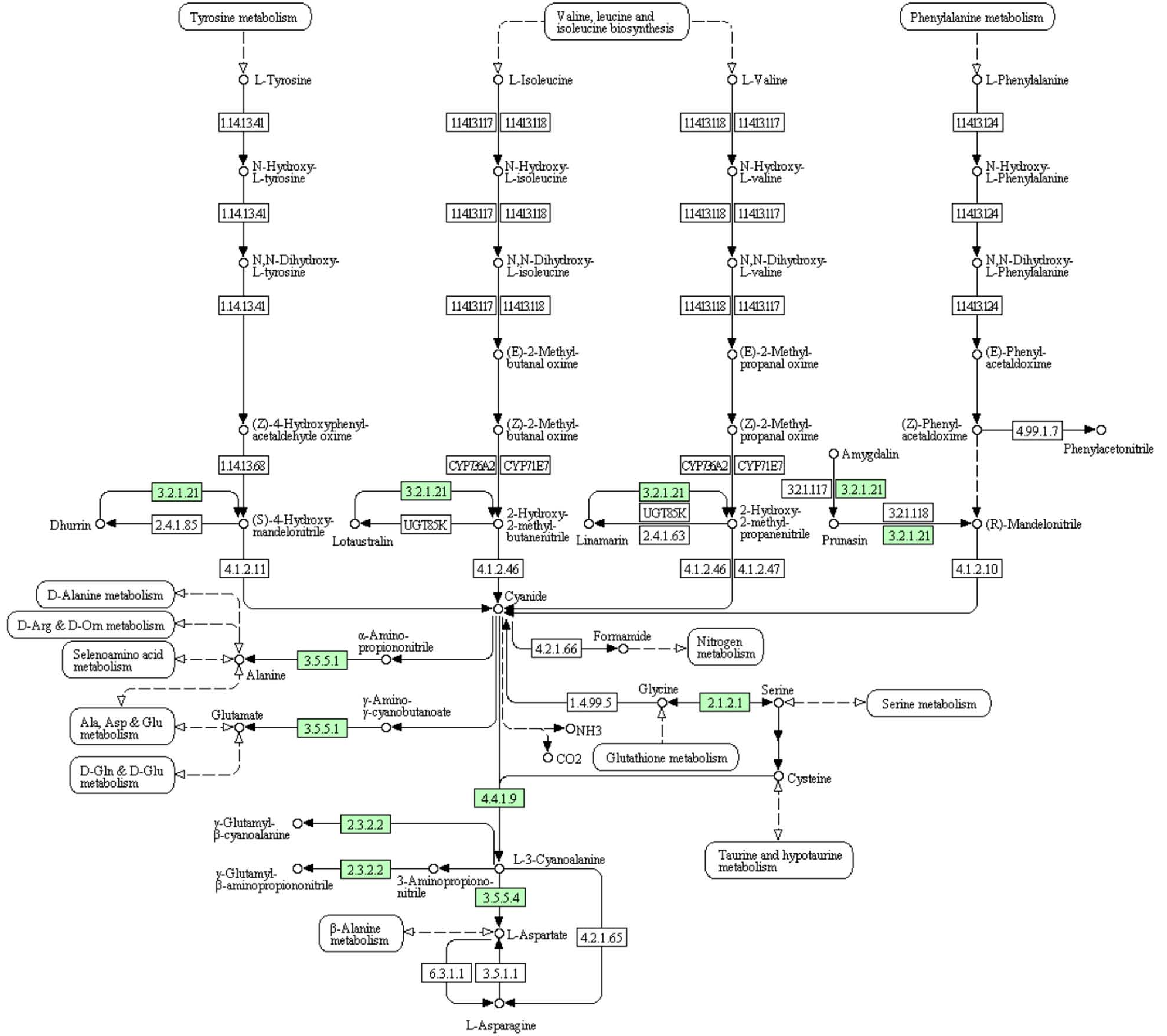
CYANOAMINO ACID METABOLISM



00460 8/29/12
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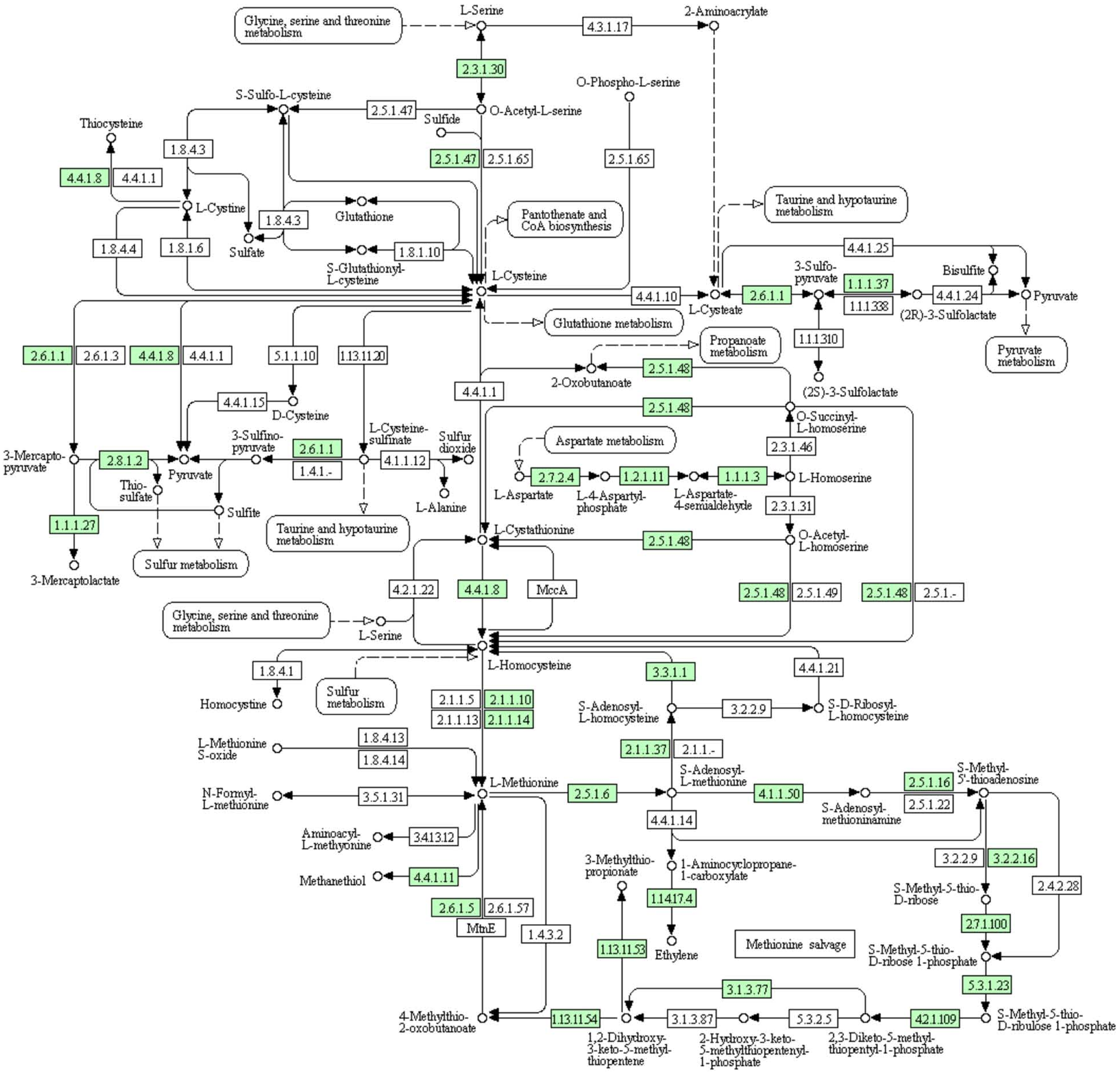
CYSTEINE AND METHIONINE METABOLISM



00270 2/4/14
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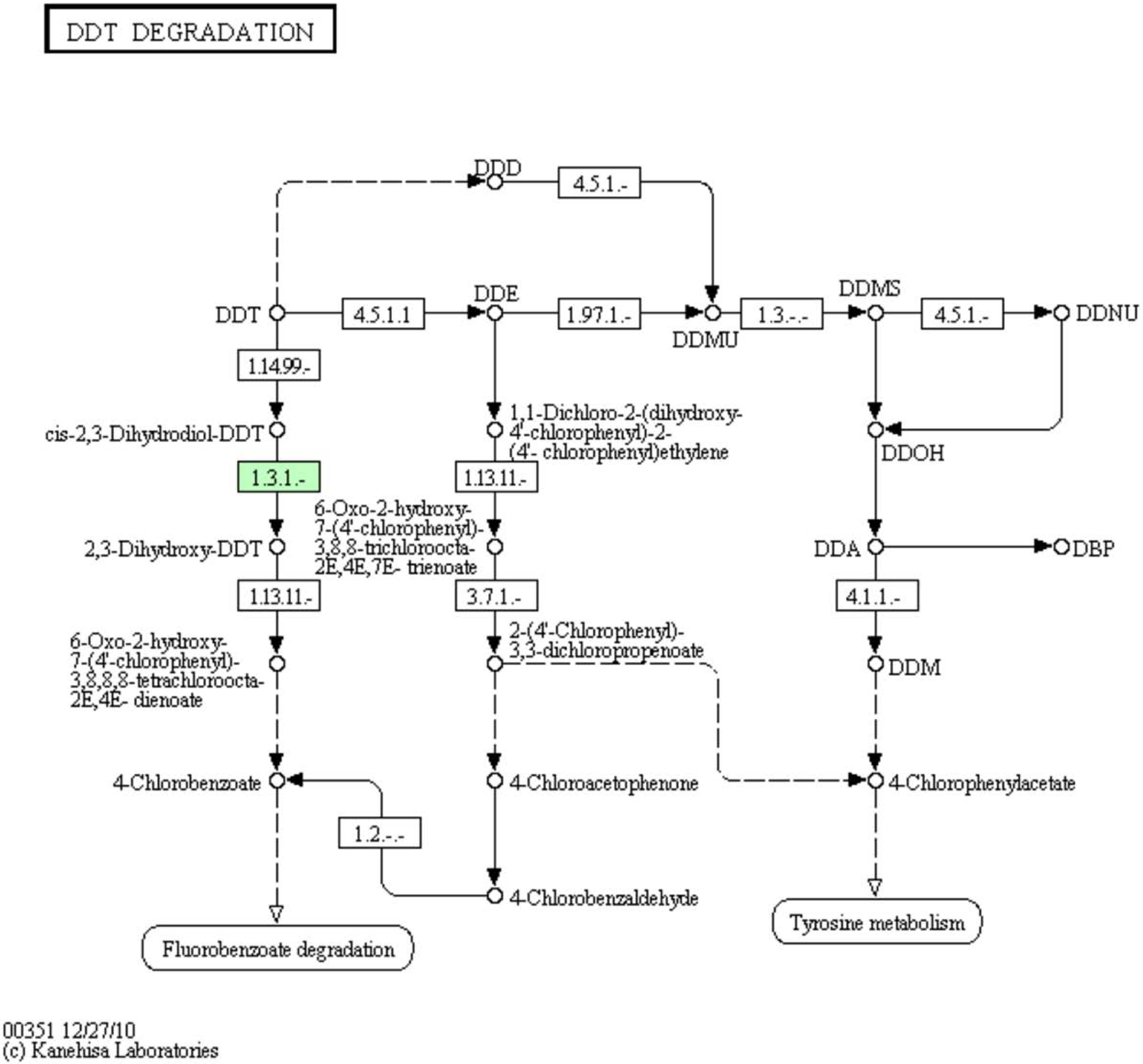
DDT DEGRADATION
DDD
4.5.1.-
DDT
4.5.1.1
DDE
1.97.1.-
DDMU
1.3.-.-
DDMS
4.5.1.-
DDNU
1.14.99.-
cis-2,3-Dihydrodiol-DDT
1.3.1.-
2,3-Dihydroxy-DDT
1.13.11.-
6-Oxo-2-hydroxy-7-(4'-chlorophenyl)-3,8,8,8-tetrachloroocta-2E,4E- dienoate
4-Chlorobenzoate
1.2.-.-
Fluorobenzoate degradation
1,1-Dichloro-2-(dihydroxy-4'-chlorophenyl)-2-(4'- chlorophenyl)ethylene
1.13.11.-
6-Oxo-2-hydroxy-7-(4'-chlorophenyl)-3,8,8-trichloroocta-2E,4E,7E- trienoate
3.7.1.-
2-(4'-Chlorophenyl)-3,3-dichloropropenoate
4-Chloroacetophenone
4-Chlorobenzaldehyde
DDOH
DDA
DBP
4.1.1.-
DDM
4-Chlorophenylacetate
Tyrosine metabolism
00351 12/27/10
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01220 3/19/14
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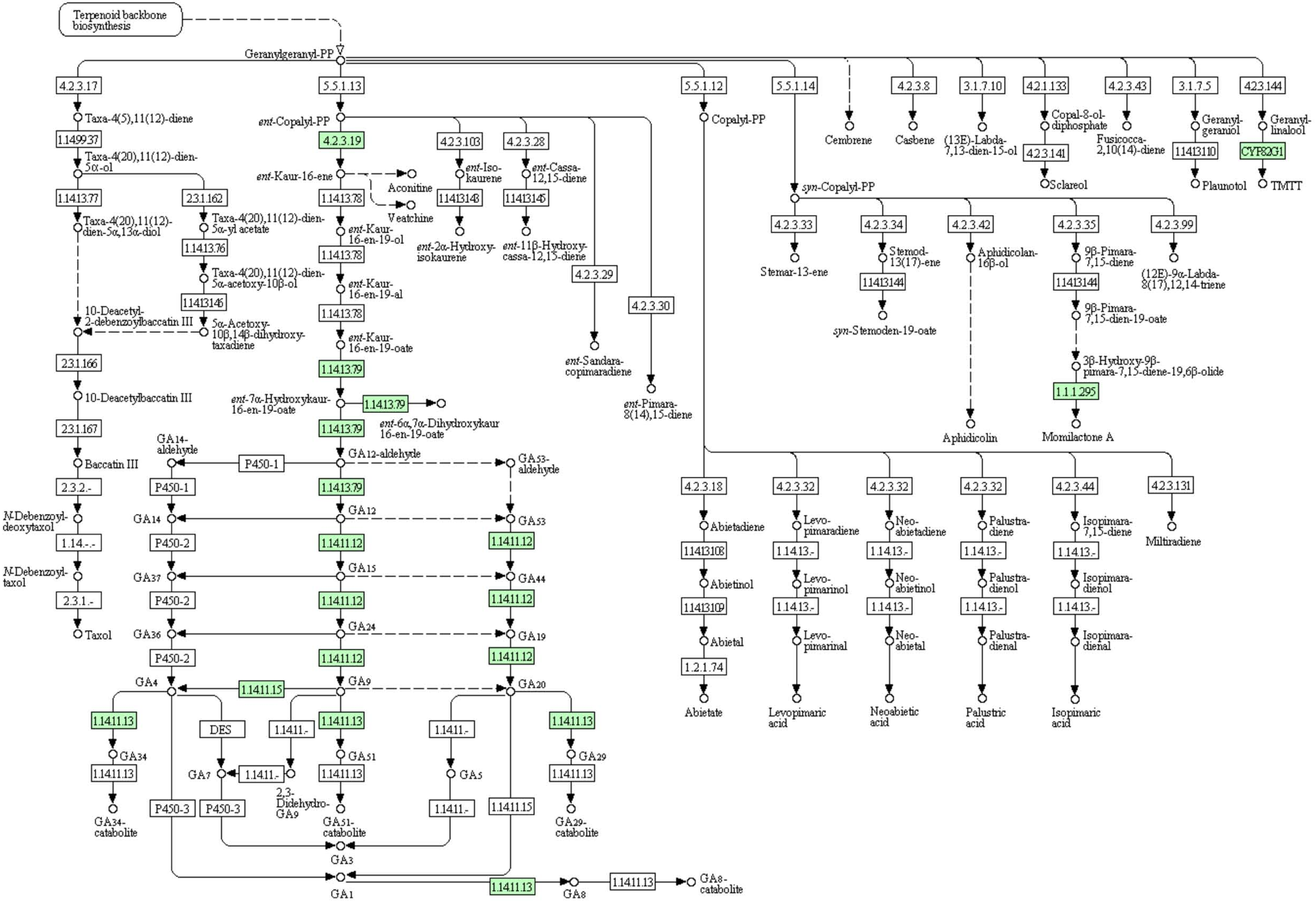
DITERPENOID BIOSYNTHESIS



00904 3/13/14
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DNA REPLICATION
Replication complex (Prokaryotes)
lagging strand
5'
3'
RNase H / pol I
Removal of RNA primer
Gap-filling
lig
DNA ligase
Joining of
Okazaki fragment
pol III core
clamp
β
τ
γδ complex
τ
primase
DnaG
primer
leading strand
5'
3'
β
pol III core
DnaB
3'
5'
DNA polymerase III holoenzyme
SSB
helicase
DNA polymerase III holoenzyme
θ
ε
α
pol III core
γ & τ
clamp
ψ
δ'
γδ complex
β
χ
δ
helicase
DnaB
primase
DnaG
SSB
DNA polymerase I
DNA ligase
RNaseH
DpoI
Lig
Replication complex (Eukaryotes)
lagging strand
5'
3'
RNase HI or Dna2
Removal of RNA primer
Gap-filling
lig I
FEN1
DNA ligase I
Joining of
Okazaki fragment
DNA polymerase δ
complex
δ
clamp
PCNA
clamp loader
RFC
DNA polymerase α-primase
complex
α-prim
primer
leading strand
5'
3'
RFC
PCNA
ε
MCM
2-7
3'
5'
DNA polymerase ε
complex
RPA
helicase
DNA polymerase α-primase complex
α1
α2
Pri1
Pri2
DNA polymerase δ complex
δ1
δ2
δ3
δ4
DNA polymerase ε complex
ε1
ε2
ε3
ε4
MCM complex (helicase)
Mcm2
Mcm3
Mcm4
Mcm5
Mcm6
Mcm7
RPA
RFA1
RFA2/4
RPA3
clamp
PCNA
clamp loader
RFC1
RFC2/4
RFC3/5
helicase
Dna2
RNaseH1
RNaseH2A
RNaseH2B
RNaseH2C
Fen1
DNA ligase
Lig1
03030 10/20/10
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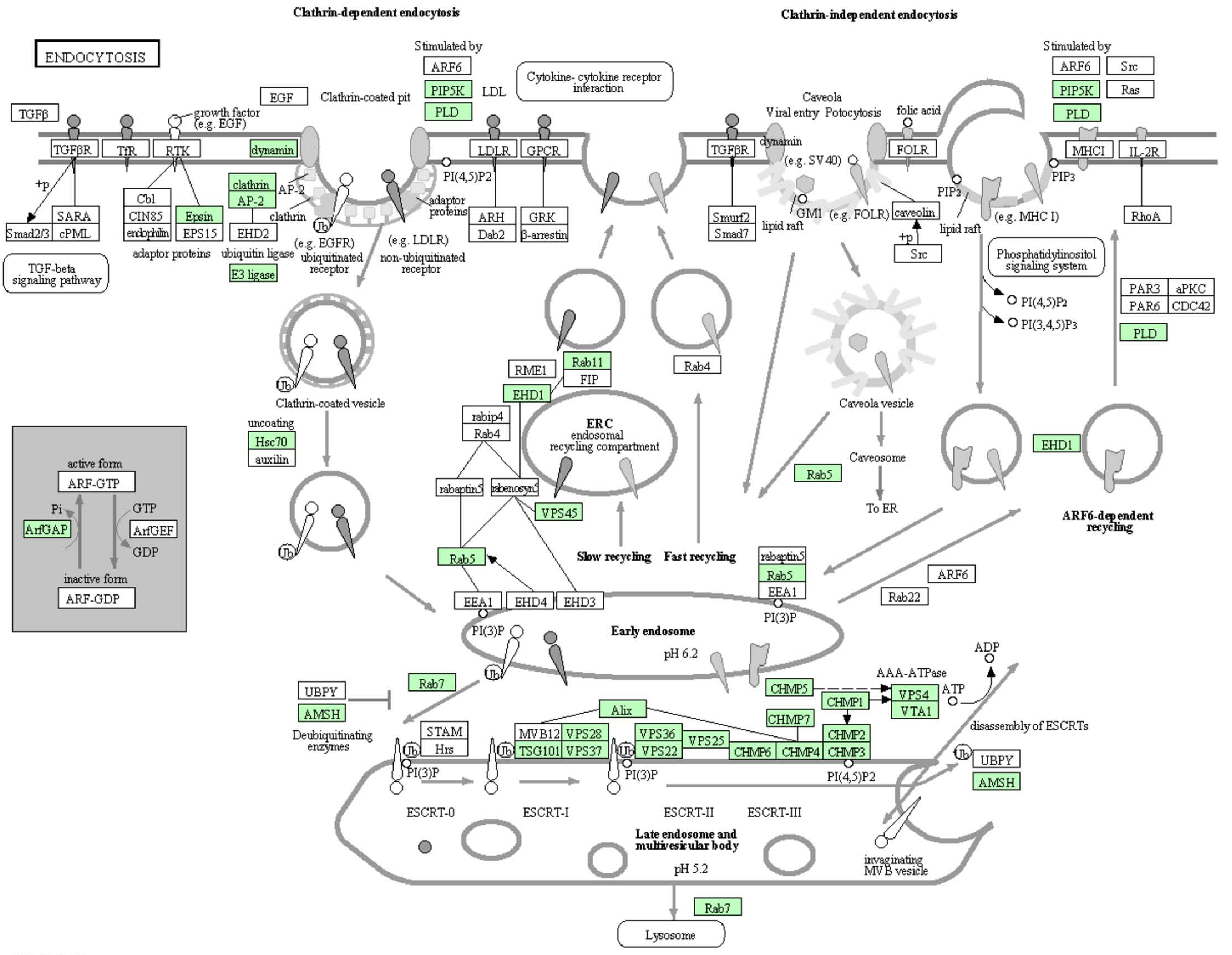
DRUG METABOLISM - OTHER ENZYMES

00983 10/28/13



04144 12/18/13
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ERBB SIGNALING PATHWAY
EGF
TGFα
AR
BTC
HB-EGF
EPR
NRG1
NRG2
NRG3
NRG4
(EGFR)
ErbB-1
ErbB-1
ErbB-1
ErbB-2
(HER2/Neu)
ErbB-2
ErbB-2
ErbB-3
ErbB-3
ErbB-2
ErbB-3
ErbB-4
ErbB-4
ErbB-2
ErbB-4
Calcium signaling pathway
PLCγ
+p
IP3
DG
ER
Ca2+
CAMK
Cellular targets
PKC
Cellular targets
Cbl
+p
Receptor ubiquitylation
Degradation
STAT5
+p
DNA
Src
FAK
+p
Adhesion Migration
Crk
+p
Abl
Nck
PAK
JNKK
JNK
+p
Jun
Elk
+p
DNA
Activation by ErbB2 overexpression (cancers)
MAPK signaling pathway
No signaling
Shc
+p
Grb2
Sos
Ras
Raf
+p
MEK
+p
ERK
+p
Myc
Elk
DNA
Grb2
STAT5
+p
DNA
GAB1
mTOR
+p
p70S6K
+p
eIF-4EBP
+p
Protein synthesis
mTOR signaling pathway
PI3K
PIP3
PKB/Akt
+p
Bad
Cell survival
+p
GSK-3
Metabolism
+p
p27
+p
p21
Cell cycle progression
PI3K-Akt signaling pathway
Cell cycle
Pancreatic cancer
Non-small cell lung cancer
Proliferation
Survival
Angiogenesis
Adhesion
Migration / Invasion
Differentiation
Glioma
Endometrial cancer
04012 8/2/13
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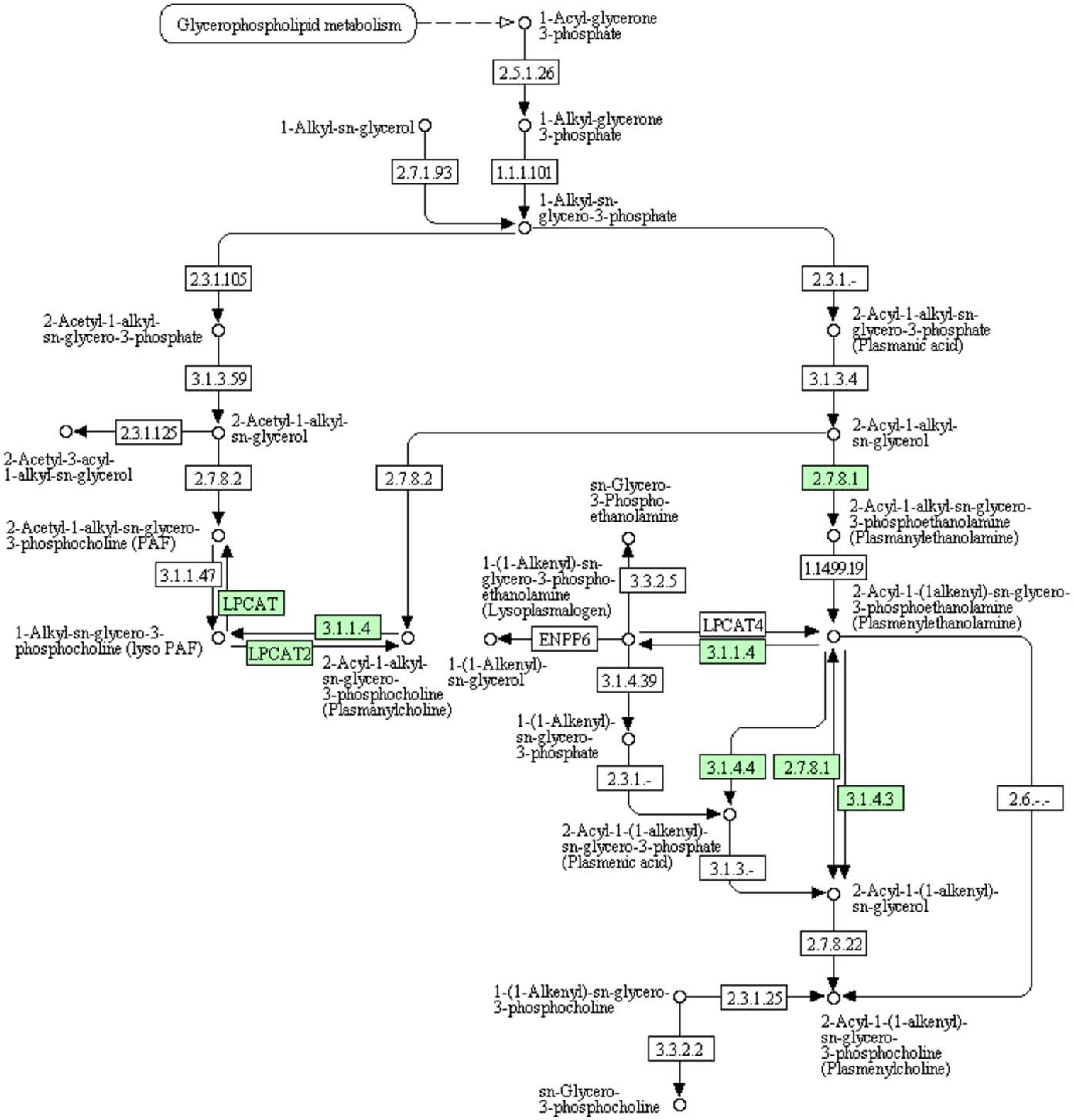
ETHER LIPID METABOLISM



00565 4/17/13
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FATTY ACID BIOSYNTHESIS

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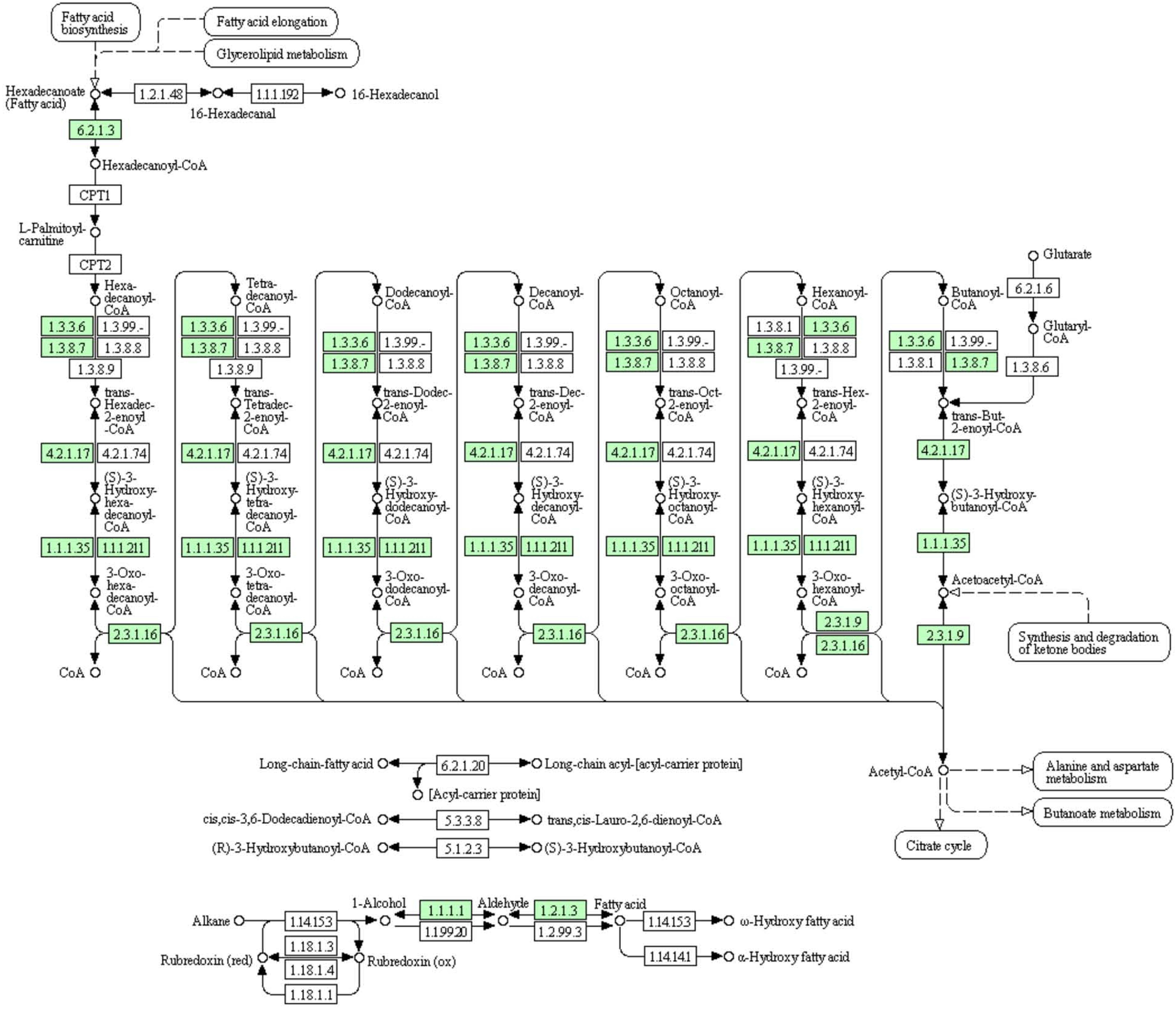
FATTY ACID DEGRADATION



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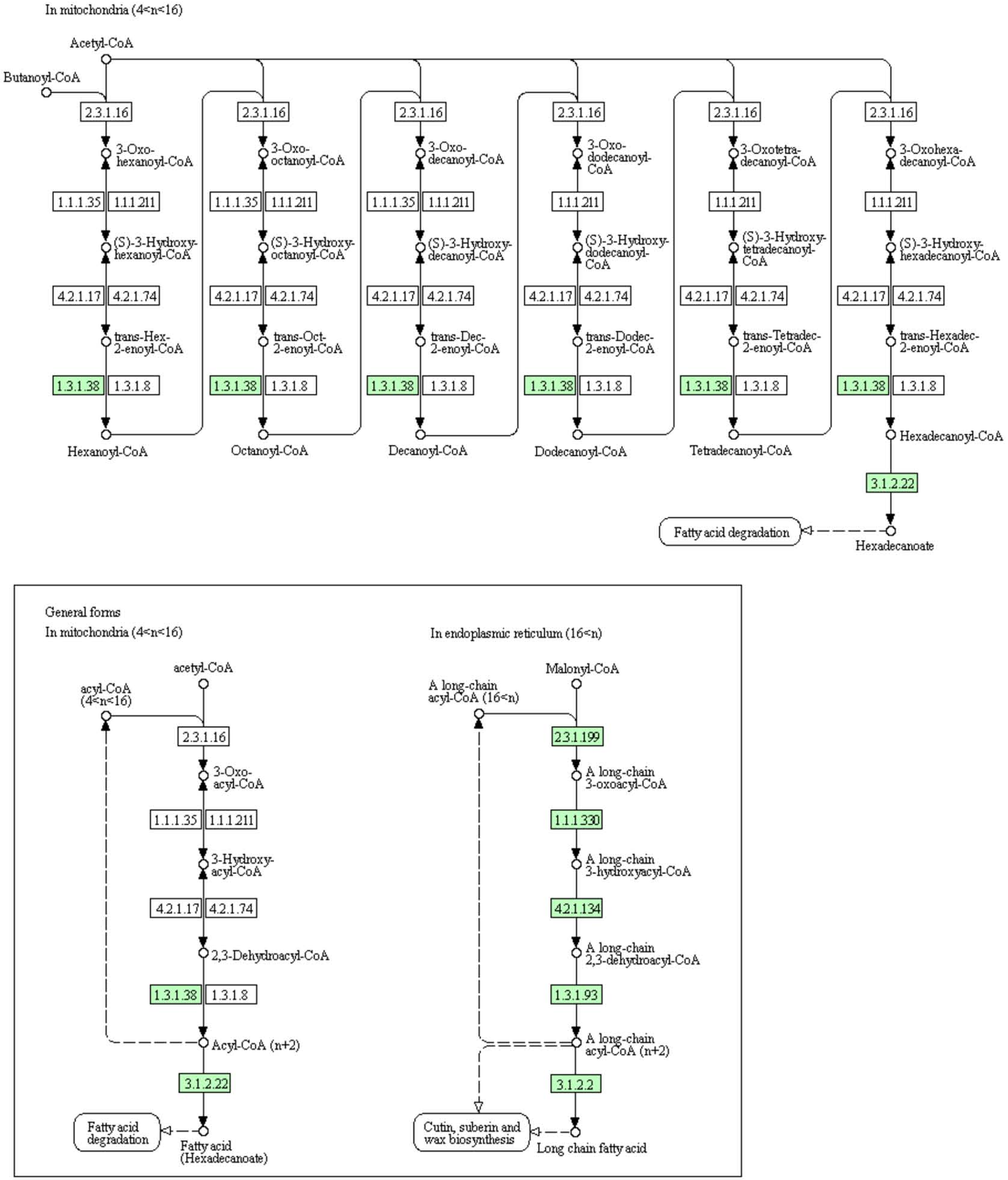
FATTY ACID ELONGATION



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FATTY ACID METABOLISM
in mitochondria
RM018 / RM020
in cytoplasm / plastid
RM021
Citrate cycle
Acetyl-CoA
Malonyl-CoA (MalCoA)
ACP
Acetyl-[acp] (AcACP)
Malonyl-[acp] (MalACP)
Acetyl-CoA
Acetyl-CoA (AcCoA)
2*
Butanoyl-CoA
4*
AcCoA
Butanoyl-[acp]
MalACP
Hexanoyl-CoA
6*
Hexanoyl-[acp]
Octanoyl-CoA
8*
Octanoyl-[acp]
Decanoyl-CoA
10*
Decanoyl-[acp]
Dodecanoyl-CoA
12*
Dodecanoyl-[acp]
Tetradecanoyl-CoA
14*
Tetradecanoyl-[acp]
Hexadecanoyl-CoA
16*
Palmitoylcarnitine
Hexadecanoyl-CoA (Palmitoyl-CoA)
Palmitic acid
16
Hexadecanoyl-[acp]
MalCoA
in endoplasmic reticulum
18*
Stearoyl-CoA/ACP
Icosanoyl-CoA
20*
Docosanoyl-CoA
22*
Tetracosanoyl-CoA
24*
Δ9
Δ11
Δ13
Δ15
Δ9,12
Δ6,9,12
Δ11,14
Δ8,11,14
Δ13,16
Δ9,12,15
Δ6,9,12,15
Δ11,14,17
Δ8,11,14,17
Δ5,8,11,14
Δ5,8,11,14,17
Δ7,10,13,16
Δ4,7,10,13,16
Δ7,10,13,16,19
Δ4,7,10,13,16,19
Δ9,12,15,18
Δ6,9,12,15,18
Δ9,12,15,18,21
Δ6,9,12,15,18,21
01212 10/8/13
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FLAVONE AND FLAVONOL BIOSYNTHESIS

00944 5/13/13

FLAVONOID BIOSYNTHESIS

00941 5/13/13


FOCAL ADHESION
ECM
ITGA
ITGB
ECM-receptor interaction
PKC
Caveolin
Fyn
Cytokine-cytokine receptor interaction
GF
RTK
Src
RhoGAP
RhoGEF
+p
Calpain
Paxillin
Talin
Filamin
Actinin
Zyxin
VASP
Vinculin
Parvin
ILK
PTEN
-p
FAK
PI3K
PIP3
Phosphatidyl inositol signaling system
p130Cas
Crk
DOCK1
GRF2
C3G
Shc
Grb2
Sos
Ha-Ras
Raf-1
RhoA
PIP5K
PIP2
ROCK
MLCP
MLC
MLCK
mDia1
PDK1
Akt/PKB
GSK-3β
β-Catenin
Cdc42
Vav
Rac
PAK
Rap1
B-Raf
JNK
c-Jun
MEK1
ERK1/2
Elk1
Bad
Bcl-2
DNA
CycD
cIAPs
Actin
Actin polymerization
Regulation of actin cytoskeleton
Wnt signaling pathway
PI3K-Akt signaling pathway
MAPK signaling pathway
Cell cycle
Cell motility
Stress fiber / FA formation
Filopodia Lamellipodia formation
FA turnover
Cell proliferation
Cell survival
04510 8/8/13
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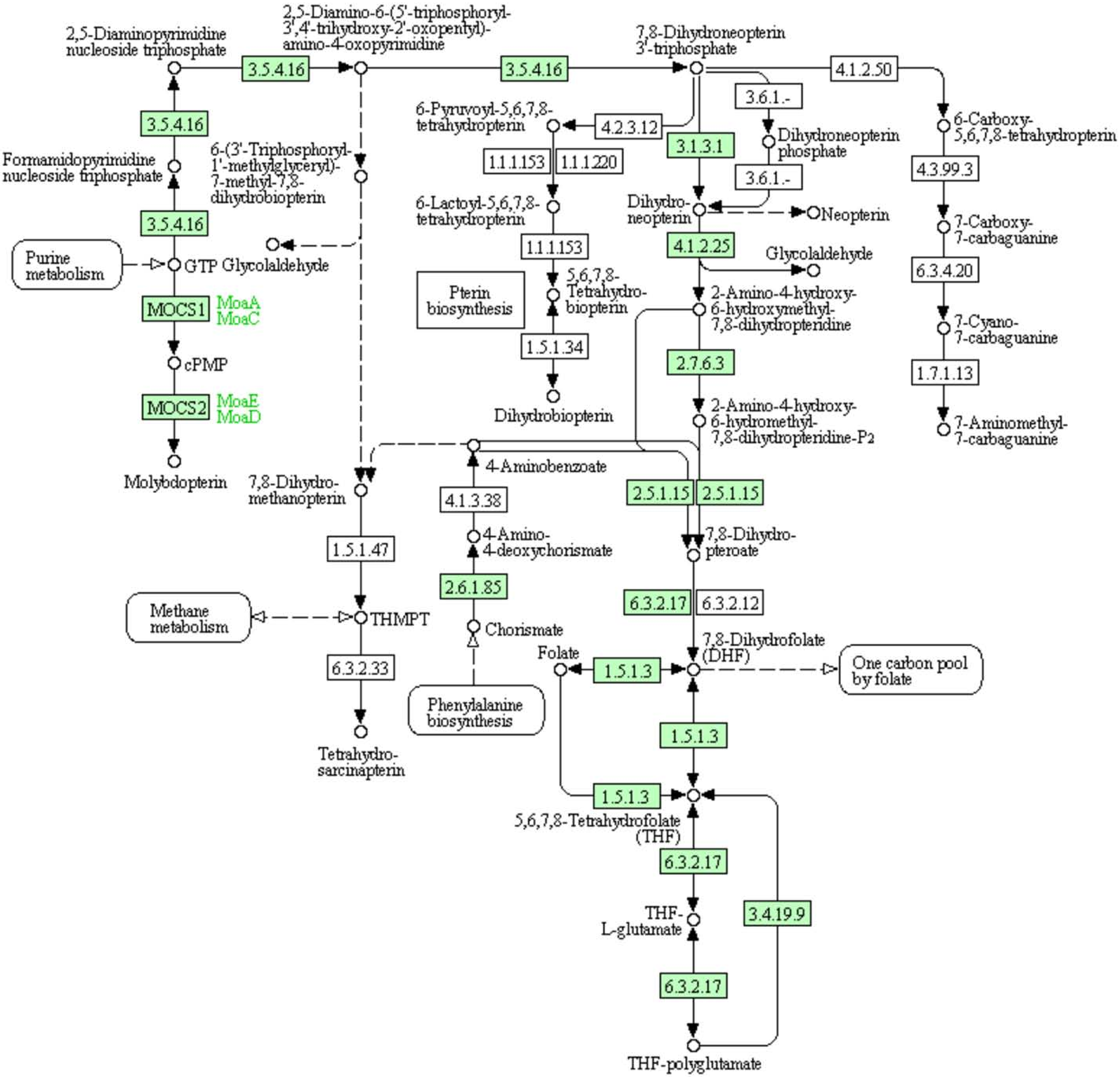
FOLATE BIOSYNTHESIS



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FOXO SIGNALING PATHWAY
TGF-β
TGFβR
TGF-β signaling pathway
Smad4
Smad3
Smad4
Smad3
Low nutrients (glucose, O2)
ADP
AMP
LKB1
AMPK
Energy metabolism
Glycolysis/ Glucogenesis
Citrate cycle/ TCA cycle
Oxidative phosphorylation
Glucose
GLUT4
ROS
JNK
MST1
Ubiquitin-mediated proteolysis
Ubiquitination
NLK
SKP2
MDM2
SET9
+m
+p
+p
+p
+p
+p
IGF1
IGF1R
INS
INSR
IRS
PI3K
Insulin signaling pathway
-p
PTEN
IKKα/β
PIP3
PDK1/2
Akt
SGK
+p
+p
+p
+p
PI3K-Akt signaling pathway
FOXO
+p
+p
+p
+m
Homer
PIKE-L
Glutamate
mGluR
CK1
IL-6
IL-10
STAT3
Jak-STAT signaling pathway
PRMT1
CDK2
DNA damage
p38
EGF
EGFR
Grb2
SOS
Ras
Raf
+p
MEK1/2
+p
ERK1/2
MAPK signaling pathway
Neuro-Developmental Signal
Acetylated
FOXO
CBP
SIRT1
FOXO
Deacetylated
-u
USP7
FoxG1
DNA
CyclinB
CyclinD
CyclinG2
p15
p19
p21
p27
Cell cycle regulation
Cell cycle
p130
Plk
Gadd45
FasL
Bim
TRAIL
Bcl-6
Apoptosis
Apoptosis
BNIP3
Atg12
ATG8
Autophagy
Regulation of autophagy
Catalase
MnSOD
Gadd45
ATM
Oxidative stress resistance & DNA repair
PEPCK
G6PC
Metabolism
Glycolysis / Gluconeogenesis
Bcl-6
IL-7R
KLF2
EDG1/6
Immuno-regulation
RAG-1/2
atrogin-1
Muscle atrophy
04068 12/24/13
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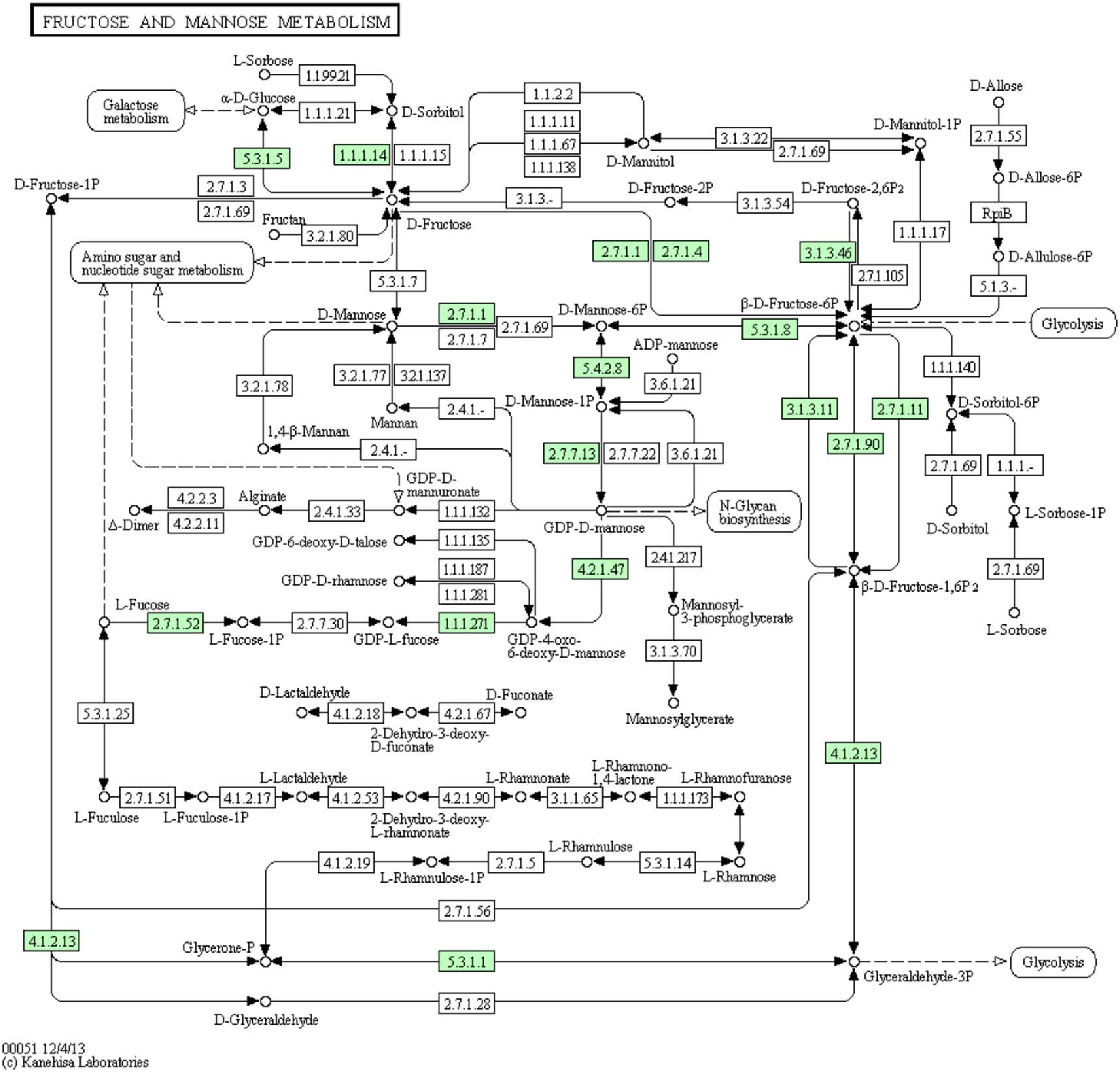
FRUCTOSE AND MANNOSE METABOLISM
L-Sorbose
1.1.99.21
Galactose metabolism
α-D-Glucose
1.1.1.21
D-Sorbitol
1.1.2.2
1.1.1.11
1.1.1.67
1.1.1.138
D-Mannitol
3.1.3.22
2.7.1.69
D-Mannitol-1P
D-Allose
2.7.1.55
D-Allose-6P
RpiB
D-Allulose-6P
5.1.3.-
5.3.1.5
1.1.1.14
1.1.1.15
D-Fructose-1P
2.7.1.3
2.7.1.69
Fructan
3.2.1.80
D-Fructose
3.1.3.-
D-Fructose-2P
3.1.3.54
D-Fructose-2,6P2
1.1.1.17
Amino sugar and nucleotide sugar metabolism
5.3.1.7
2.7.1.1
2.7.1.4
3.1.3.46
2.7.1.105
β-D-Fructose-6P
Glycolysis
D-Mannose
2.7.1.1
2.7.1.69
2.7.1.7
D-Mannose-6P
5.3.1.8
ADP-mannose
5.4.2.8
3.6.1.21
3.2.1.78
3.2.1.77
3.2.1.137
Mannan
2.4.1.-
D-Mannose-1P
1.1.1.140
D-Sorbitol-6P
3.1.3.11
2.7.1.11
2.7.1.90
1,4-β-Mannan
2.4.1.-
2.7.7.13
2.7.7.22
3.6.1.21
2.7.1.69
1.1.1.-
GDP-D-mannuronate
4.2.2.3
4.2.2.11
Alginate
2.4.1.33
1.1.1.132
Δ-Dimer
GDP-D-mannose
N-Glycan biosynthesis
D-Sorbitol
L-Sorbose-1P
GDP-6-deoxy-D-talose
1.1.1.135
1.1.1.187
1.1.1.281
GDP-D-rhamnose
4.2.1.47
2.4.1.217
2.7.1.69
β-D-Fructose-1,6P2
L-Fucose
2.7.1.52
L-Fucose-1P
2.7.7.30
GDP-L-fucose
1.1.1.271
GDP-4-oxo-6-deoxy-D-mannose
Mannosyl-3-phosphoglycerate
3.1.3.70
L-Sorbose
Mannosylglycerate
D-Lactaldehyde
4.1.2.18
4.2.1.67
D-Fuconate
2-Dehydro-3-deoxy-D-fuconate
5.3.1.25
4.1.2.13
L-Lactaldehyde
L-Rhamnonate
L-Rhamnono-1,4-lactone
L-Rhamnofuranose
2.7.1.51
4.1.2.17
4.1.2.53
4.2.1.90
3.1.1.65
1.1.1.173
L-Fuculose
L-Fuculose-1P
2-Dehydro-3-deoxy-L-rhamnonate
L-Rhamnulose
4.1.2.19
2.7.1.5
5.3.1.14
L-Rhamnulose-1P
L-Rhamnose
2.7.1.56
4.1.2.13
Glycerone-P
5.3.1.1
Glyceraldehyde-3P
Glycolysis
2.7.1.28
D-Glyceraldehyde
00051 12/4/13
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GALACTOSE METABOLISM
1.1.3.9
1.1.1.48
1.1.1.120
3.1.1.25
D-Galactono-1,4-lactone
D-Galactonate
4.2.1.6
2-Dehydro-3-deoxy-D-galactonate
2.7.1.58
2-Dehydro-3-deoxy-D-galactonate-6P
4.1.2.21
D-Glyceraldehyde-3P
Glycolysis
Amino sugar and nucleotide sugar metabolism
UDP-glucose
Pentose and glucuronate interconversions
2.7.7.9
D-Galactose
2.7.1.6
α-D-Galactose-1P
2.7.7.12
α-D-Glucose-1P
5.1.3.2
Glycerone-P
2.7.7.10
UDP-galactose
4.1.2.40
3.2.1.23
Galactan
2.4.1.123
Galactinol
2.4.1.22
3.2.1.23
3.2.1.108
Lactose
5.4.2.2
2.4.1.82
Raffinose
3.2.1.22
Sucrose
2.7.1.69
3.1.3.9
2.7.1.1
2.7.1.2
α-D-Glucose
α-D-Glucose-6P
N-Acetyl-D-galactosamine
D-Tagatose-1,6P2
2.4.1.67
3.2.1.22
Stachyose
3.2.1.26
3.2.1.22
Galactinol
D-myo-Inositol
Lactose-6'P
Glycolysis
3.2.1.26
2.7.1.69
3.2.1.20
3.2.1.10
Manninotriose
D-Galactosamine
N-Acetyl-D-galactosamine-6P
3.2.1.22
Melibiitol
D-Sorbitol
Fructose and mannose metabolism
3.2.1.22
Melibiose
2.7.1.11
2.7.1.144
3.2.1.85
3.2.1.22
2.7.1.69
3.5.1.25
3.2.1.22
Epimelibiose
D-Mannose
5.3.1.-
D-Galactosamine-6P
D-Galactose
D-Glucose
D-Fructose
3.2.1.22
Galactosyl-glycerol
Glycerol
D-Galactose-6P
5.3.1.26
Galactitol
D-Tagatose
1.1.1.21
1.1.1.16
2.7.1.101
D-Tagatose-6P
2.7.1.69
1.1.1.251
Galactitol-1P
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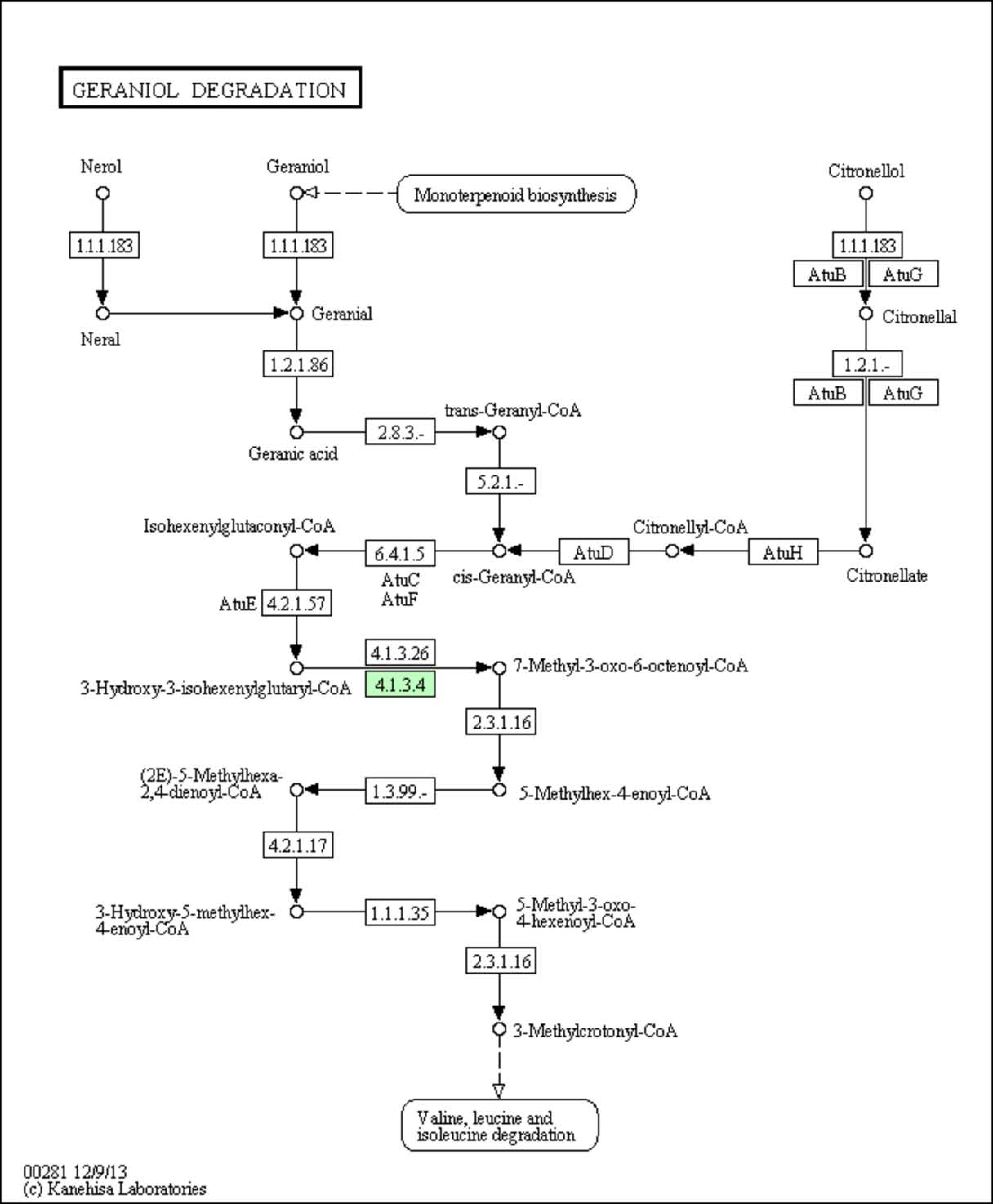
GERANIOL DEGRADATION
Nerol
Geraniol
Monoterpenoid biosynthesis
Citronellol
1.1.1.183
1.1.1.183
1.1.1.183
AtuB
AtuG
Neral
Geranial
Citronellal
1.2.1.86
1.2.1.-
AtuB
AtuG
Geranic acid
2.8.3.-
trans-Geranyl-CoA
5.2.1.-
Isohexenylglutaconyl-CoA
6.4.1.5
AtuC
AtuF
cis-Geranyl-CoA
AtuD
Citronellyl-CoA
AtuH
Citronellate
AtuE
4.2.1.57
3-Hydroxy-3-isohexenylglutaryl-CoA
4.1.3.26
4.1.3.4
7-Methyl-3-oxo-6-octenoyl-CoA
2.3.1.16
(2E)-5-Methylhexa-2,4-dienoyl-CoA
1.3.99.-
5-Methylhex-4-enoyl-CoA
4.2.1.17
3-Hydroxy-5-methylhex-4-enoyl-CoA
1.1.1.35
5-Methyl-3-oxo-4-hexenoyl-CoA
2.3.1.16
3-Methylcrotonyl-CoA
Valine, leucine and isoleucine degradation
00281 12/9/13
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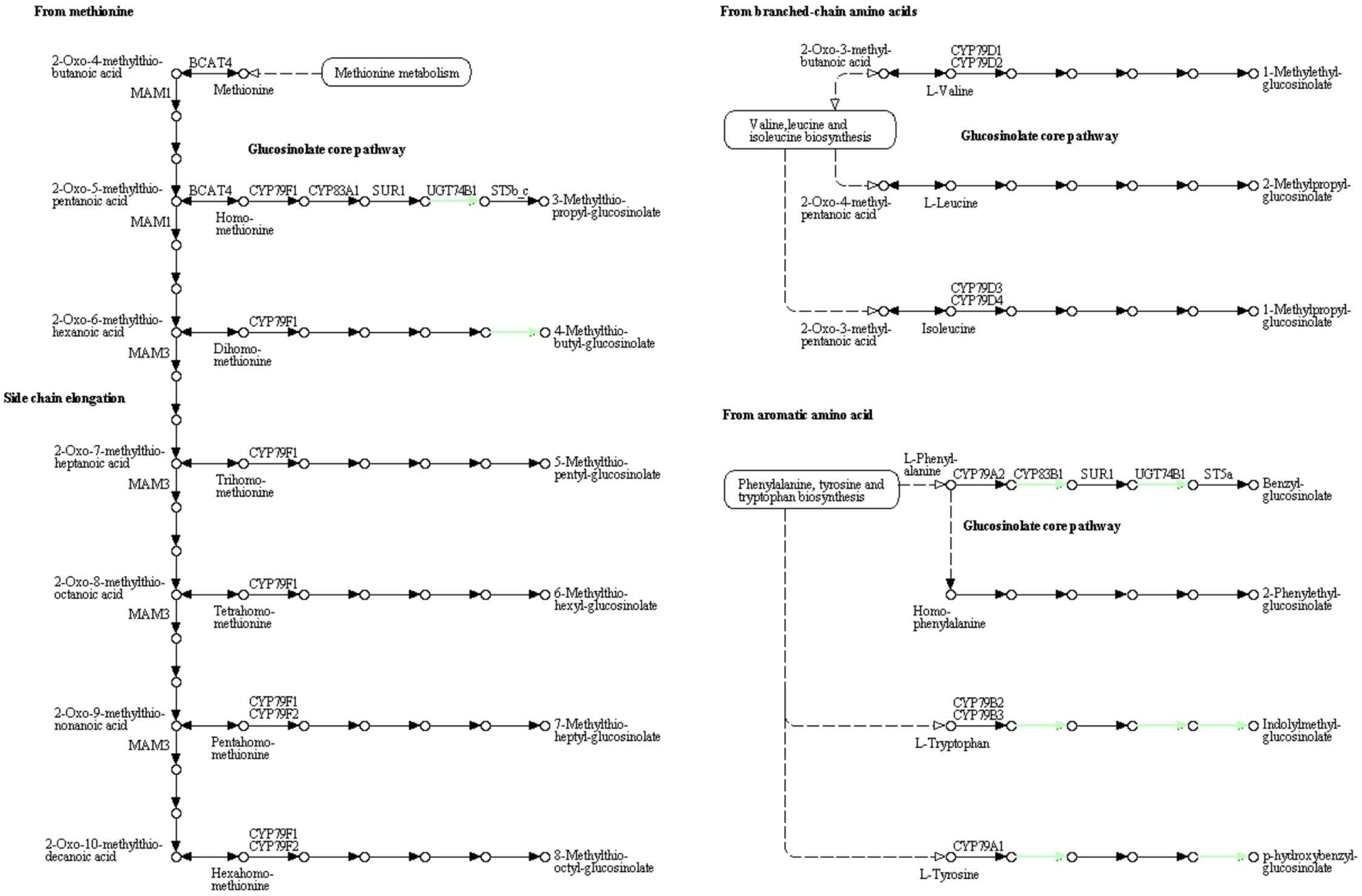
GLUCOSINOLATE BIOSYNTHESIS



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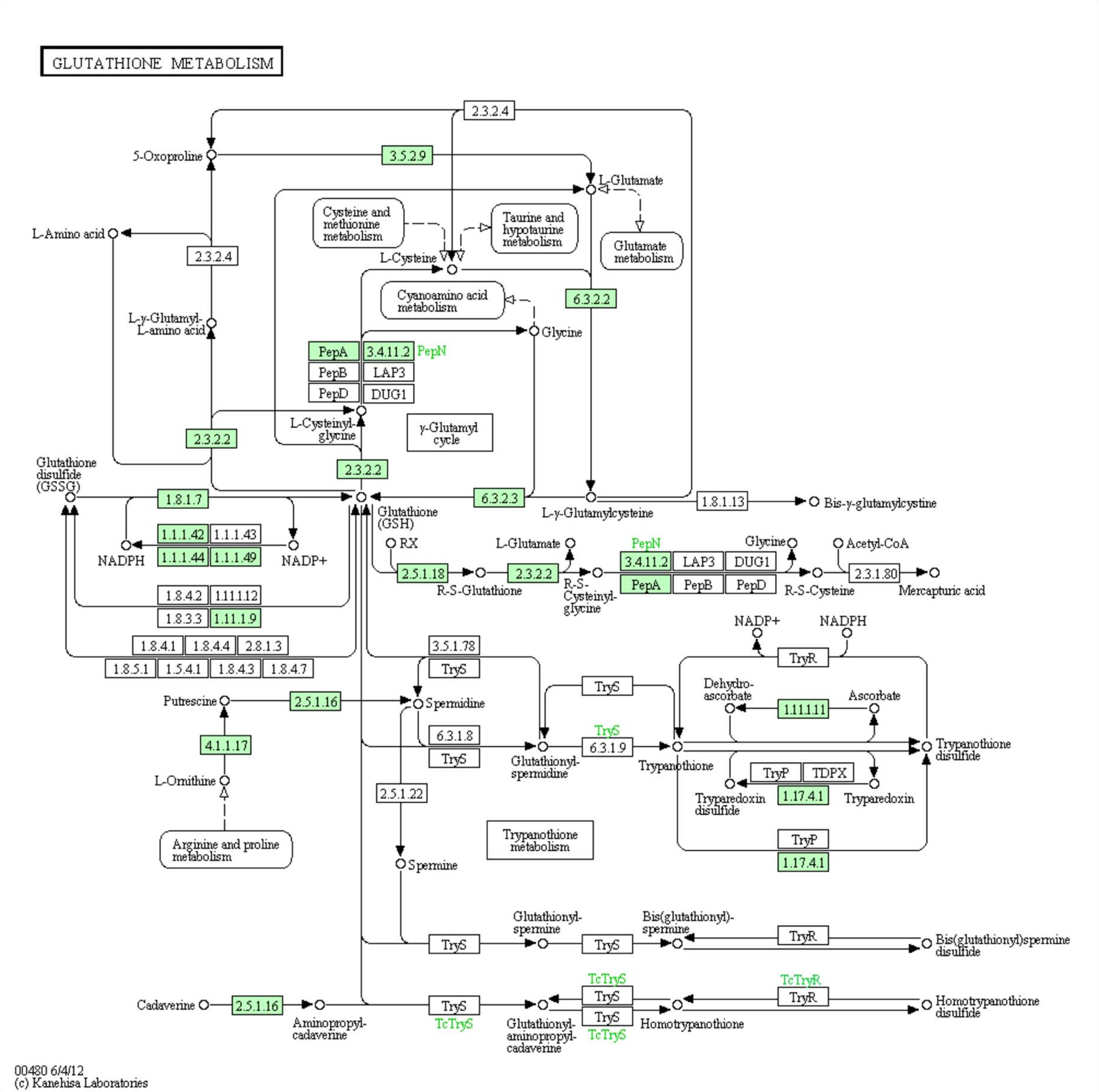
GLUTATHIONE METABOLISM
2.3.2.4
5-Oxoproline
3.5.2.9
L-Glutamate
Cysteine and methionine metabolism
Taurine and hypotaurine metabolism
Glutamate metabolism
L-Amino acid
2.3.2.4
L-Cysteine
Cyanoamino acid metabolism
6.3.2.2
L-γ-Glutamyl-L-amino acid
Glycine
PepA
3.4.11.2
PepN
PepB
LAP3
PepD
DUG1
L-Cysteinyl-glycine
γ-Glutamyl cycle
2.3.2.2
2.3.2.2
Glutathione disulfide (GSSG)
1.8.1.7
6.3.2.3
Glutathione (GSH)
L-γ-Glutamylcysteine
1.8.1.13
Bis-γ-glutamylcystine
1.1.1.42
1.1.1.43
1.1.1.44
1.1.1.49
NADPH
NADP+
RX
L-Glutamate
PepN
Glycine
Acetyl-CoA
2.5.1.18
2.3.2.2
3.4.11.2
LAP3
DUG1
2.3.1.80
PepA
PepB
PepD
R-S-Glutathione
R-S-Cysteinyl-glycine
R-S-Cysteine
Mercapturic acid
1.8.4.2
1.11.1.12
1.8.3.3
1.11.1.9
NADP+
NADPH
1.8.4.1
1.8.4.4
2.8.1.3
3.5.1.78
TryR
1.8.5.1
1.5.4.1
1.8.4.3
1.8.4.7
TryS
TryS
Dehydro-ascorbate
Ascorbate
Putrescine
2.5.1.16
Spermidine
1.11.1.11
TryS
4.1.1.17
6.3.1.8
6.3.1.9
Trypanothione disulfide
TryS
Glutathionyl-spermidine
Trypanothione
L-Ornithine
TryP
TDPX
2.5.1.22
Tryparedoxin disulfide
1.17.4.1
Tryparedoxin
Arginine and proline metabolism
Trypanothione metabolism
TryP
1.17.4.1
Spermine
Glutathionyl-spermine
Bis(glutathionyl)-spermine
TryS
TryS
TryR
Bis(glutathionyl)spermine disulfide
TcTryS
TcTryR
Cadaverine
2.5.1.16
TryS
TryS
TryR
Homotrypanothione disulfide
TryS
Aminopropyl-cadaverine
TcTryS
Glutathionyl-aminopropyl-cadaverine
TcTryS
Homotrypanothione
00480 6/4/12
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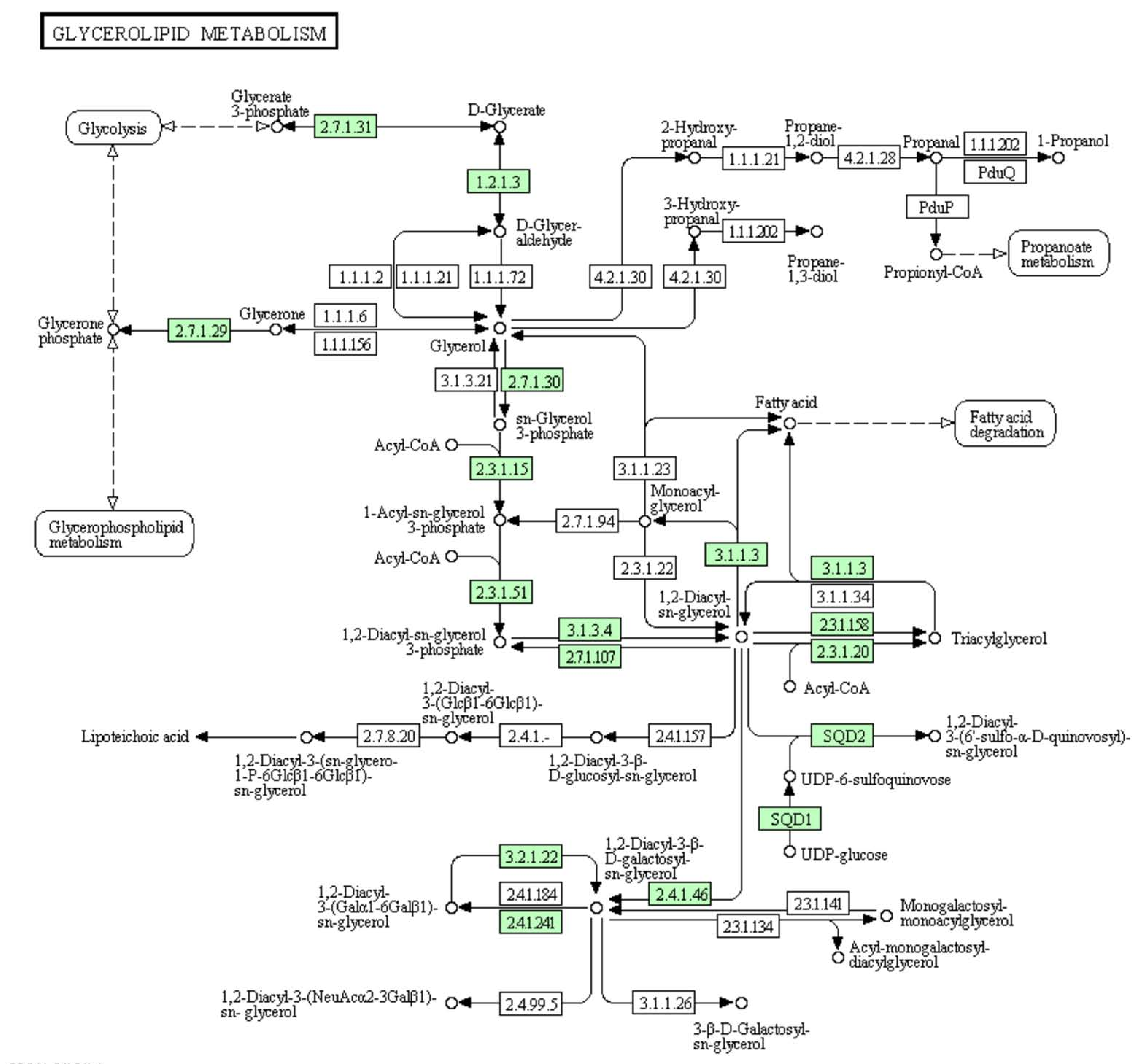
GLYCEROLIPID METABOLISM
Glycolysis
Glycerate 3-phosphate
2.7.1.31
D-Glycerate
1.2.1.3
D-Glyceraldehyde
2-Hydroxypropanal
1.1.1.21
Propane-1,2-diol
4.2.1.28
Propanal
1.1.1.202
1-Propanol
PduQ
PduP
Propionyl-CoA
Propanoate metabolism
3-Hydroxypropanal
1.1.1.202
Propane-1,3-diol
4.2.1.30
4.2.1.30
1.1.1.2
1.1.1.21
1.1.1.72
Glycerone phosphate
2.7.1.29
Glycerone
1.1.1.6
1.1.1.156
Glycerol
3.1.3.21
2.7.1.30
sn-Glycerol 3-phosphate
Acyl-CoA
2.3.1.15
Glycerophospholipid metabolism
Fatty acid
Fatty acid degradation
3.1.1.23
Monoacylglycerol
1-Acyl-sn-glycerol 3-phosphate
2.7.1.94
Acyl-CoA
2.3.1.51
2.3.1.22
3.1.1.3
3.1.1.3
3.1.1.34
1,2-Diacyl-sn-glycerol
1,2-Diacyl-sn-glycerol 3-phosphate
3.1.3.4
2.7.1.107
2.3.1.158
2.3.1.20
Triacylglycerol
Acyl-CoA
1,2-Diacyl-3-(Glcβ1-6Glcβ1)-sn-glycerol
Lipoteichoic acid
2.7.8.20
2.4.1.-
2.4.1.157
1,2-Diacyl-3-(sn-glycero-1-P-6Glcβ1-6Glcβ1)-sn-glycerol
1,2-Diacyl-3-β-D-glucosyl-sn-glycerol
SQD2
1,2-Diacyl-3-(6'-sulfo-α-D-quinovosyl)-sn-glycerol
UDP-6-sulfoquinovose
SQD1
UDP-glucose
3.2.1.22
1,2-Diacyl-3-β-D-galactosyl-sn-glycerol
1,2-Diacyl-3-(Galα1-6Galβ1)-sn-glycerol
2.4.1.184
2.4.1.241
2.4.1.46
2.3.1.141
Monogalactosylmonoacylglycerol
2.3.1.134
Acyl-monogalactosyldiacylglycerol
1,2-Diacyl-3-(NeuAcα2-3Galβ1)-sn- glycerol
2.4.99.5
3.1.1.26
3-β-D-Galactosyl-sn-glycerol
00561 3/10/14
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GLYCEROPHOSPHOLIPID METABOLISM
Glycerolipid metabolism
1.1.1.261
sn-Glycerol-1P
2.5.1.41
2.5.1.42
2,3-Bis-(O-geranylgeranyl)-sn-glycerol-1P
2.7.7.67
2.7.8.38
2,3-Bis-O-(geranylgeranyl)-sn-glycero-1-phospho-L-serine
3-(O-Geranylgeranyl)-sn-glycerol-1P
1.3.1.101
1.3.99.34
CDP-2,3-bis-O-(geranylgeranyl)-sn-glycerol
2,3-Bis-(O-phytanyl)-sn-glycerol-1P
1.1.1.8
1.1.1.94
1.1.3.21
1.1.5.3
Glycerone-P
3.6.1.16
sn-Glycerol-3P
2.7.7.39
CDP-glycerol
Acyl-CoA
Acyl-CoA
2.3.1.15
2.3.1.-
2.3.1.42
1-Acyl-glycerone-3P
1.1.1.101
1-Acyl-sn-glycerol-3P
2-Acyl-sn-glycerol-3P
Acyl-CoA
Acyl-CoA
Ether lipid metaboilsm
2.3.1.51
2.3.1.52
3.1.4.4
1,2-Diacyl-sn-glycerol-3P
3.1.3.4
2.7.1.107
2.7.1.174
3.1.4.4
GPI-anchor biosynthesis
3.6.1.26
2.7.7.41
2.7.8.24
LPIAT
3.1.1.52
2.7.8.11
1-Acyl-sn-glycero-3-phosphoinositol
Phosphatidyl-1D-myo-inositol
CDP-diacyl-glycerol
2.7.8.8
Inositol phosphate metabolism
2.7.8.5
Phosphatidyl-glycerophosphate
3.1.3.27
Phosphatidyl-glycerol
LCLAT
CLD1
Cls
Cardiolipin
Monolyso-cardiolipin
Aminoacyl-phosphatidylglycerol
3.1.4.3
1,2-Diacyl-sn-glycerol
LPGAT
Lysophosphatidylglycerol
Phosphatidylcholine (Lecithin)
2.3.1.43
3.1.1.4
1-Acyl-sn-glycero-3-phosphocholine
LPCAT
3.1.1.32
2.3.1.62
3.1.1.5
3.1.1.5
3.1.4.2
3.1.4.46
sn-Glycerol-3P
sn-glycero-3-Phosphocholine
2-Acyl-sn-glycero-3-phosphocholine
2.1.1.71
2.1.1.16
PEMT
Dimethyl-phosphatidyl-ethanolamine
2.7.8.2
3.1.4.3
CDP-choline
2.7.7.15
Phospho-choline
2.7.1.32
3.1.3.75
Choline
2.3.1.6
3.1.1.7
O-Acetylcholine
2.1.1.71
2.1.1.16
PEMT
Ptdss1
Monomethyl-phosphatidyl-ethanolamine
2.1.1.17
BTA1
BtaA
DGHS
BTA1
BtaB
DGTS
2.1.1.103
Phosphodimethyl-ethanolamine
2.1.1.103
N-Methylethanol-amine phosphate
2.1.1.103
Pyruvate metabolism
Glycolysis
L-Serine-phospho-ethanolamine
3.1.4.13
1,2-Diacyl-sn-glycerol
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4.3.1.7
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2.7.1.82
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2.7.7.14
Phospho-ethanolamine
Ethanolamine
4.3.3.-
Diethanolamine
4.3.3.-
Triethanolamine
3.1.4.3
2.7.8.1
1-Acyl-sn-glycero-3-phosphoserine
LPSAT
1-Acyl-sn-glycero-3-phosphoethanolamine
3.1.1.4
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sn-glycero-3-Phospho-ethanolamine
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3.1.1.5
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3.1.4.46
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4.1.1.65
2.7.8.29
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3.1.1.32
3.1.1.32
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2.3.1.40
2-Acyl-sn-glycero-3-phosphoethanolamine
Glycine, serine, and threonine metabolism
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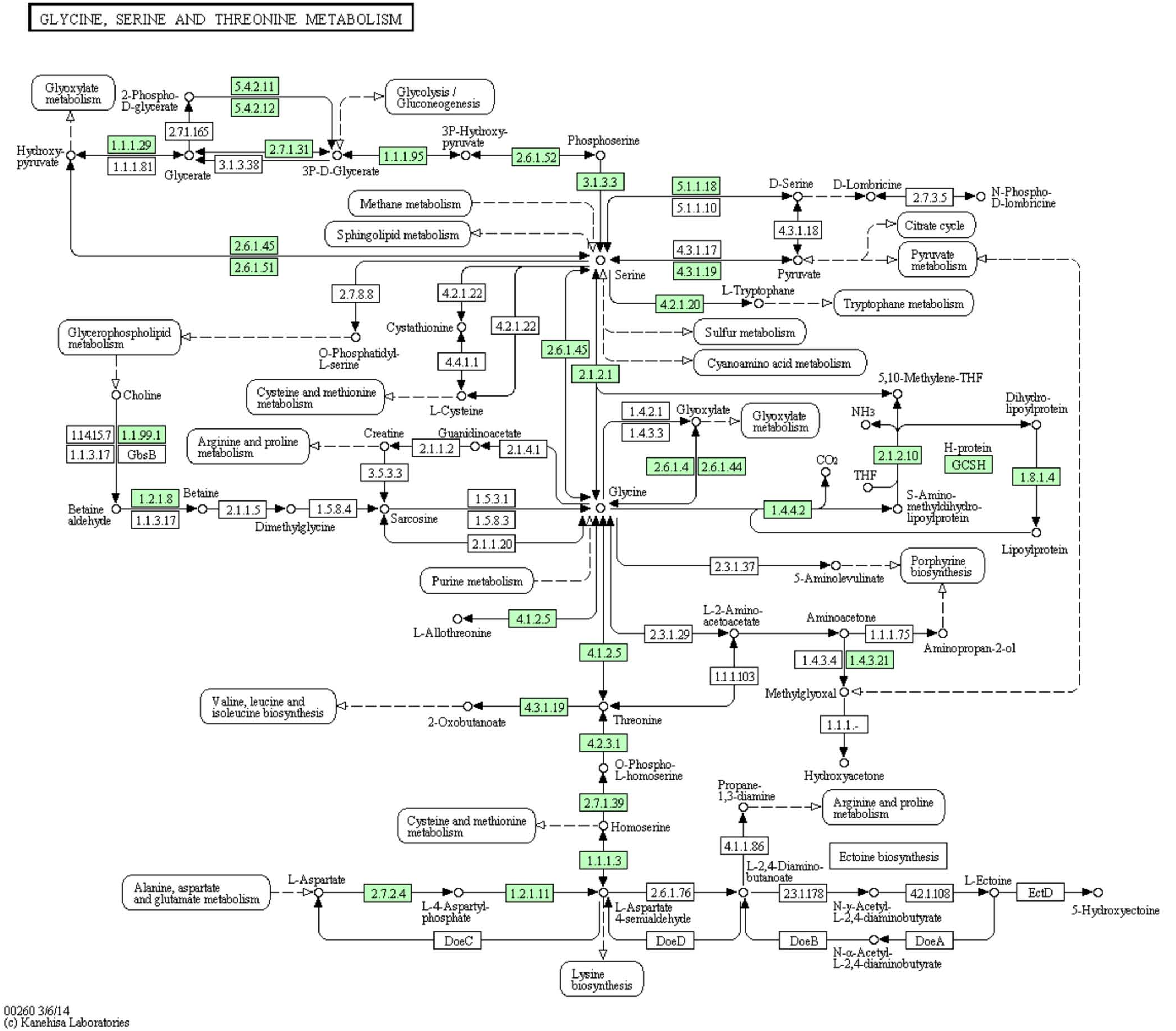
GLYCINE, SERINE AND THREONINE METABOLISM
Glyoxylate metabolism
2-Phospho-D-glycerate
5.4.2.11
5.4.2.12
Glycolysis / Gluconeogenesis
2.7.1.165
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1.1.1.29
1.1.1.81
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2.7.1.31
3.1.3.38
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1.1.1.95
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2.6.1.52
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4.2.1.20
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2.6.1.44
2.1.2.10
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CO2
THF
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1.2.1.8
1.1.3.17
Betaine
2.1.1.5
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1.5.8.4
Sarcosine
1.5.3.1
1.5.8.3
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2.1.1.20
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1.4.3.21
1.1.1.103
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2.3.1.178
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4.2.1.108
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EctD
5-Hydroxyectoine
DoeC
DoeD
DoeB
N-α-Acetyl-L-2,4-diaminobutyrate
DoeA
Lysine biosynthesis
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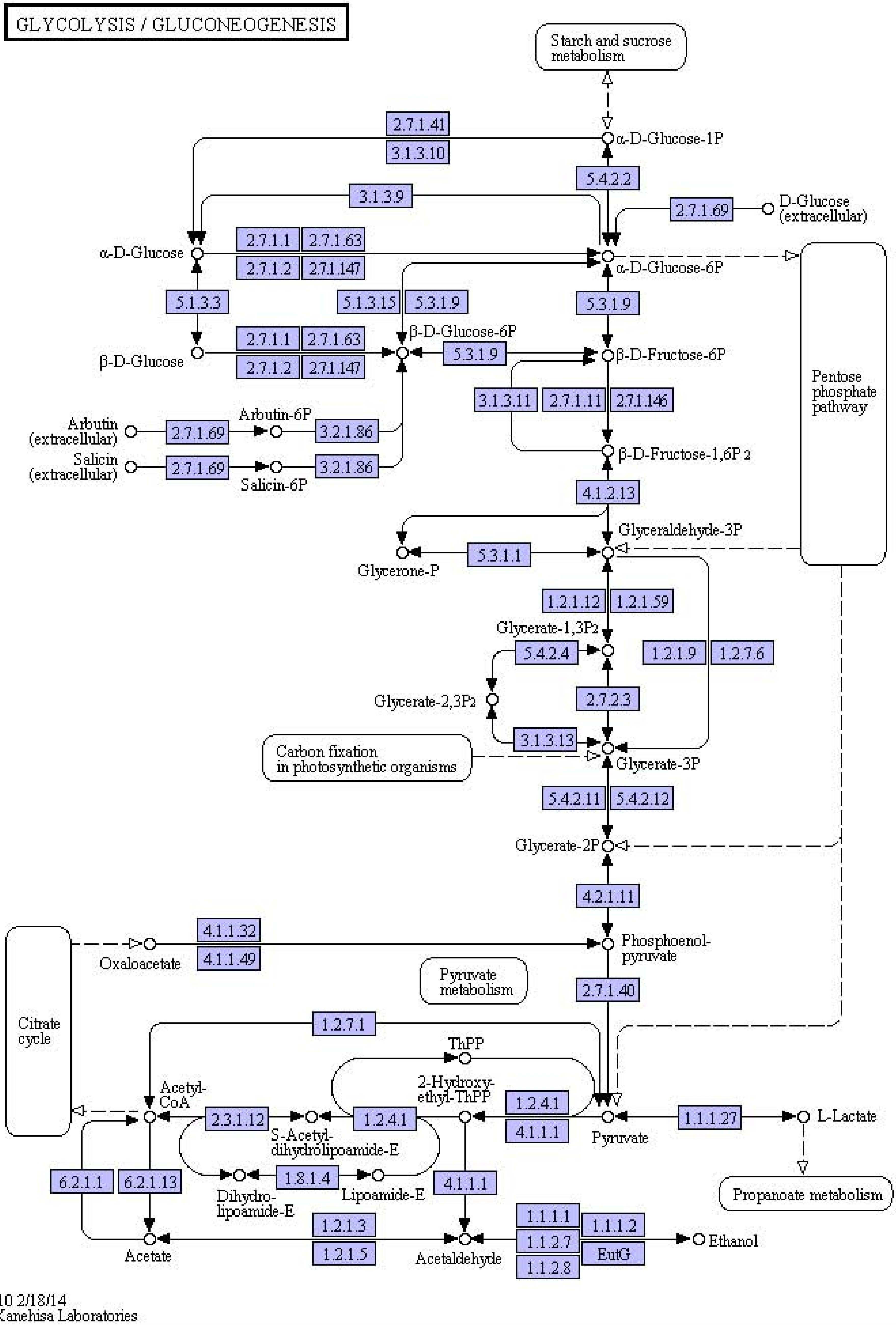
GLYCOLYSIS / GLUCONEOGENESIS
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2.7.1.41
3.1.3.10
α-D-Glucose-1P
5.4.2.2
3.1.3.9
2.7.1.69
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α-D-Glucose
2.7.1.1
2.7.1.63
2.7.1.2
2.7.1.147
α-D-Glucose-6P
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5.1.3.15
5.3.1.9
5.3.1.9
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β-D-Glucose
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2.7.1.2
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5.3.1.9
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2.7.1.146
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3.2.1.86
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3.2.1.86
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5.3.1.1
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2.7.1.40
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2.3.1.12
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1.2.4.1
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1.2.1.3
1.2.1.5
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1.1.1.1
1.1.2.7
1.1.2.8
1.1.1.2
EutG
Ethanol
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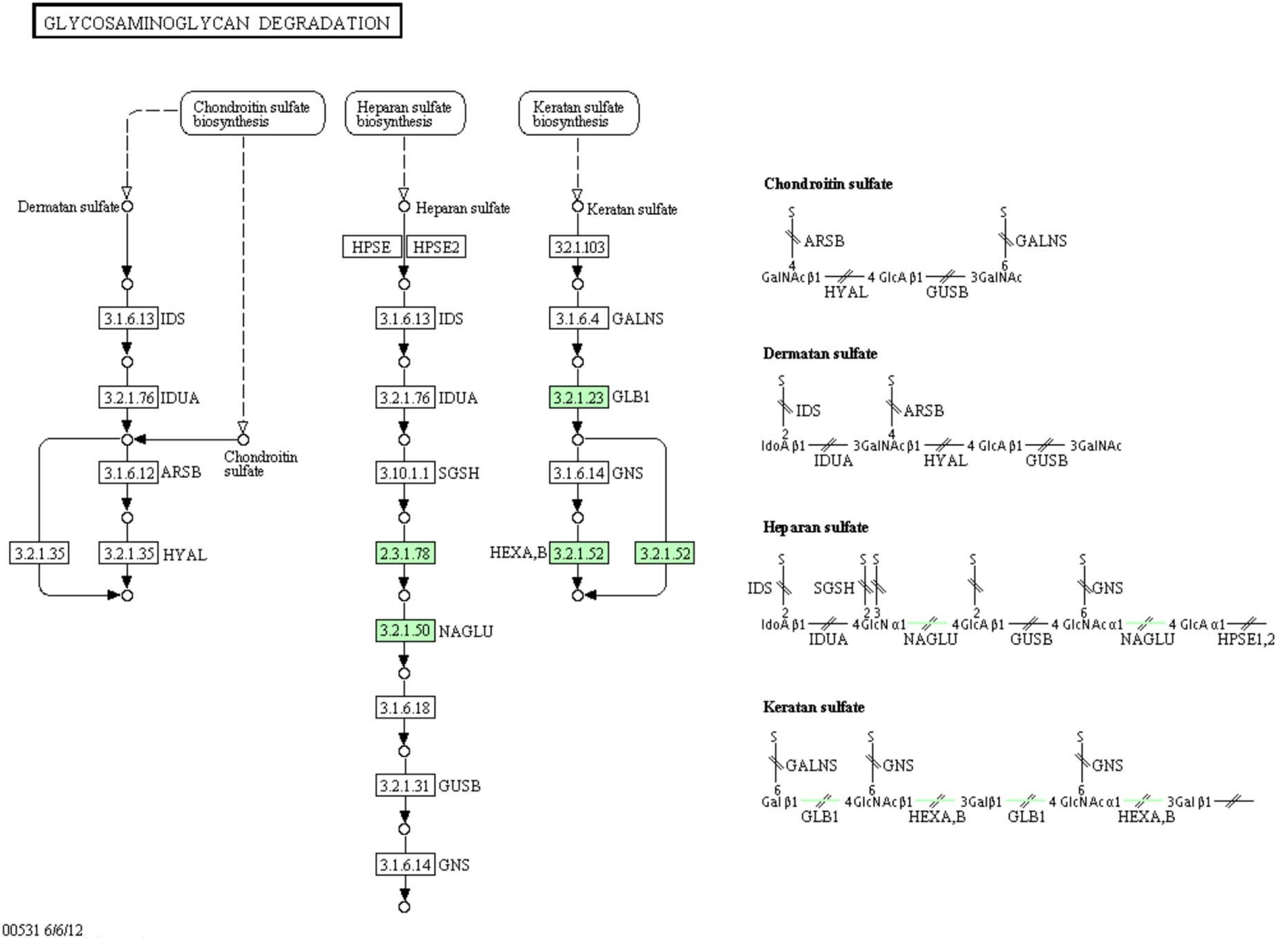

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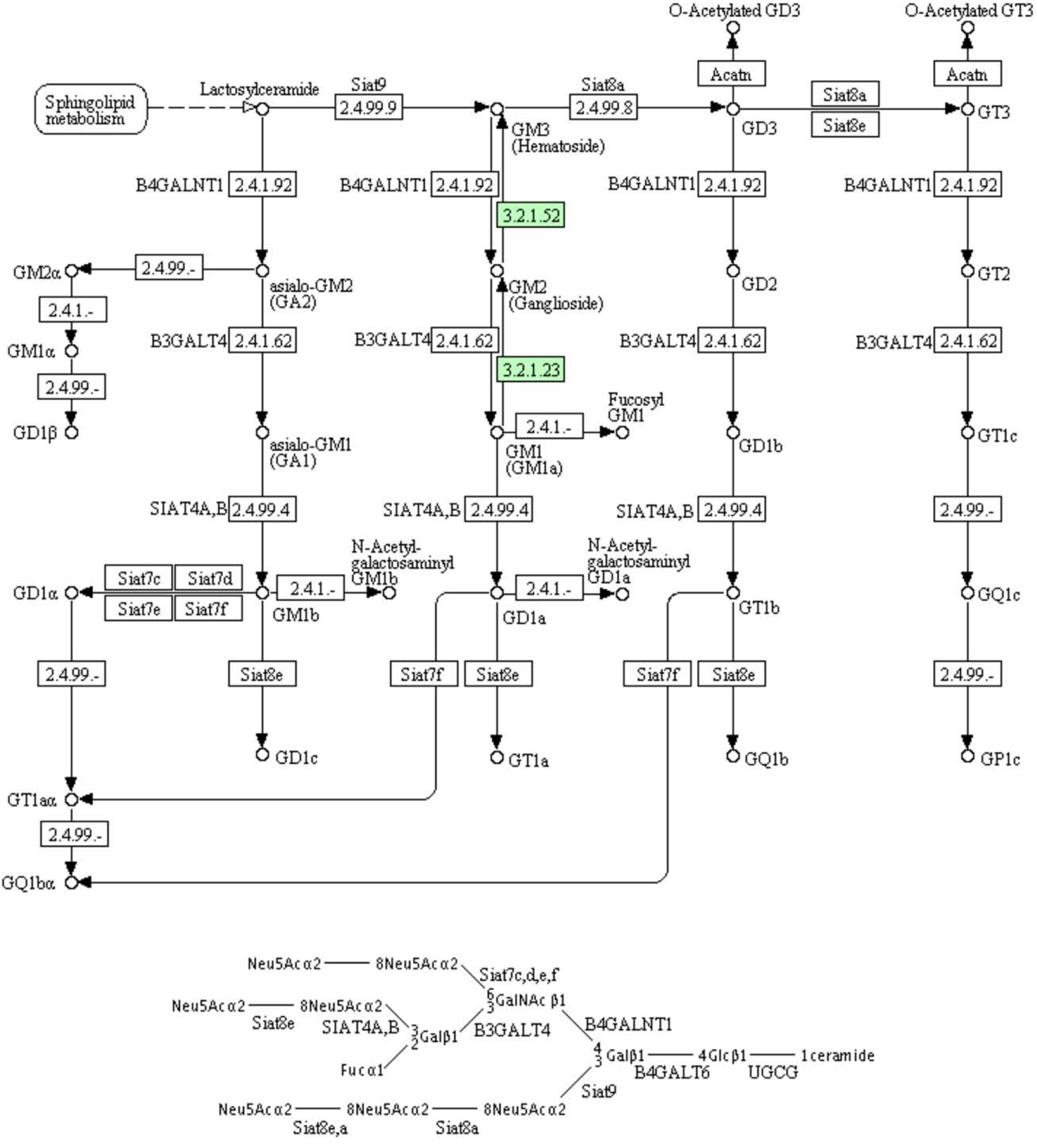
GLYCOSPHINGOLIPID BIOSYNTHESIS - GANGLIO SERIES



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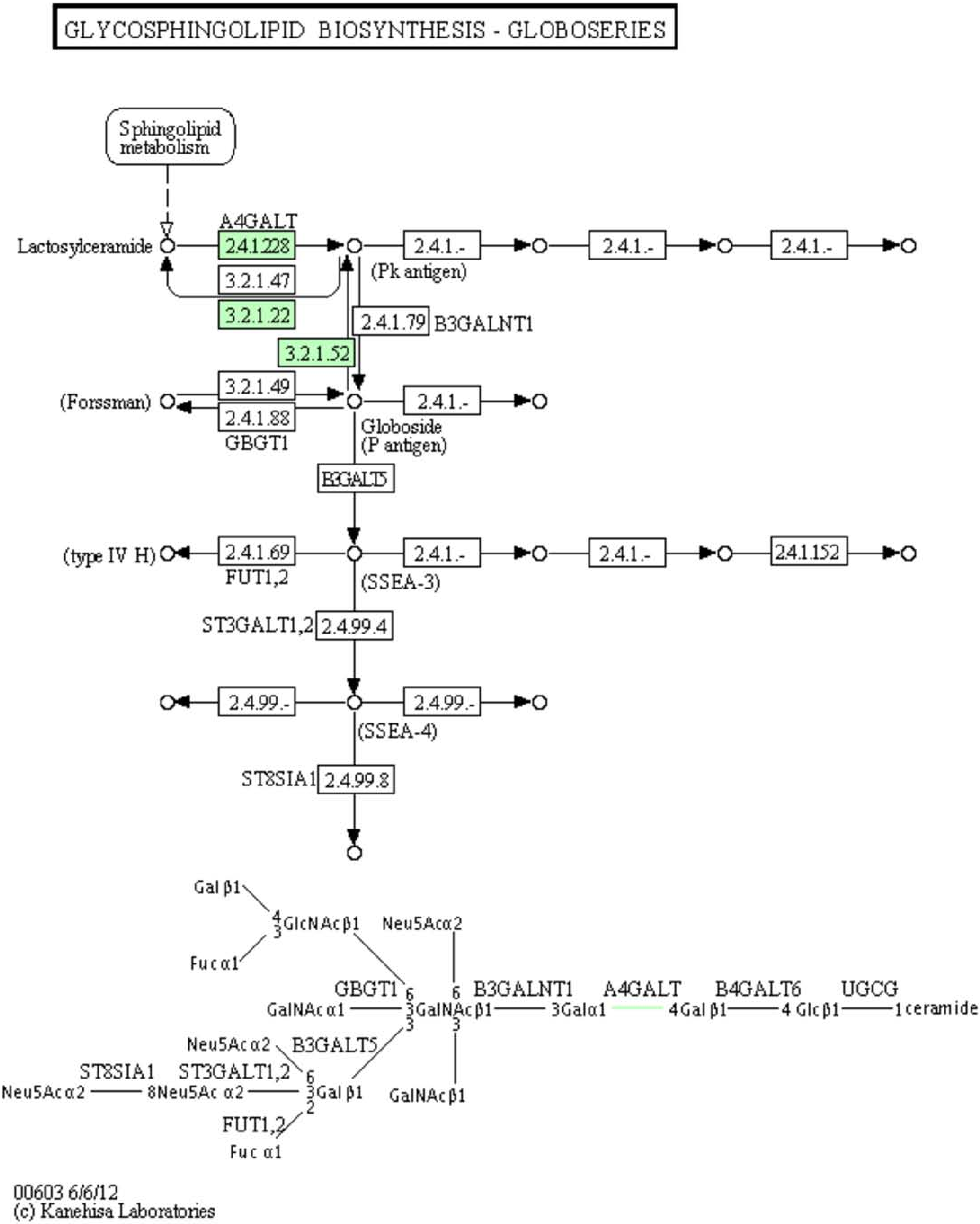
GLYCOSPHINGOLIPID BIOSYNTHESIS - GLOBOSERIES
Sphingolipid metabolism
Lactosylceramide
A4GALT
2.4.1.228
3.2.1.47
3.2.1.22
3.2.1.52
(Pk antigen)
2.4.1.-
2.4.1.-
2.4.1.-
2.4.1.79
B3GALNT1
(Forssman)
3.2.1.49
2.4.1.88
GBGT1
Globoside
(P antigen)
2.4.1.-
B3GALT5
(type IV H)
2.4.1.69
FUT1,2
(SSEA-3)
2.4.1.-
2.4.1.-
2.4.1.152
ST3GALT1,2
2.4.99.4
2.4.99.-
2.4.99.-
(SSEA-4)
ST8SIA1
2.4.99.8
Gal β1
4
3
GlcNAc β1
Fuc α1
Neu5Ac α2
GBGT1
6
6
B3GALNT1
A4GALT
B4GALT6
UGCG
GalNAc α1
3
GalNAc β1
3Gal α1
4Gal β1
4 Glc β1
1ceramide
3
3
Neu5Ac α2
B3GALT5
ST8SIA1
ST3GALT1,2
6
Neu5Ac α2
8Neu5Ac α2
3Gal β1
2
GalNAc β1
FUT1,2
Fuc α1
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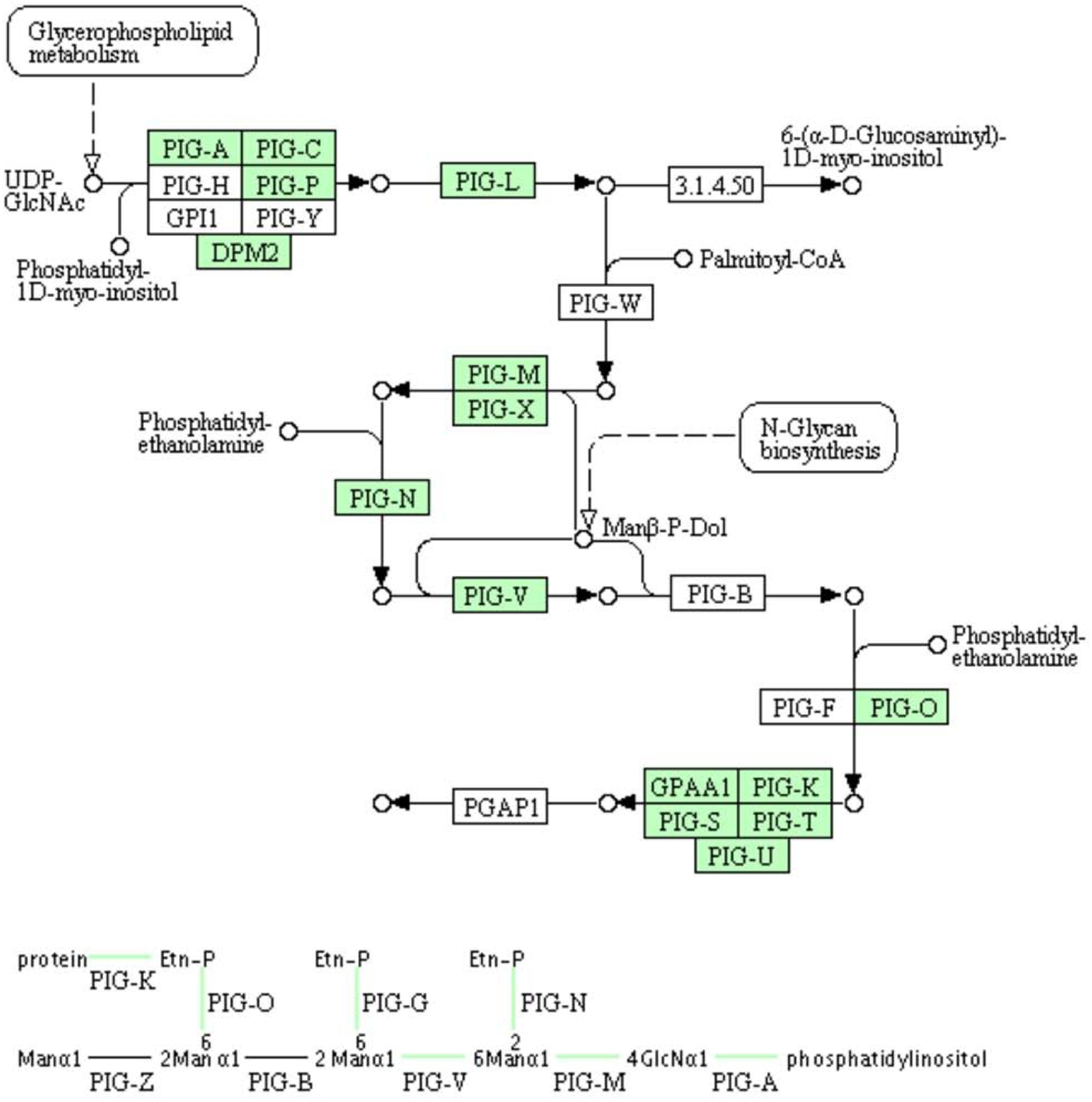
GLYCOSYLPHOSPHATIDYLINOSITOL (GPI) - ANCHOR BIOSYNTHESIS



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GLYOXYLATE AND DICARBOXYLATE METABOLISM

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04066 5/30/13
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HISTIDINE METABOLISM
PRPP
2.4.2.17
Phosphoribosyl-ATP
3.6.1.31
Phosphoribosyl-AMP
3.5.4.19
Phosphoribosyl-formimino-AICAR-P
5.3.1.16
Phosphoribulosyl-formimino-AICAR-P
HisF
HisH
Imidazole-glycerol-3P
AICAR
Purine metabolism
4.2.1.19
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2.6.1.9
L-Histidinol-P
3.1.3.15
L-Histidinol
1.1.1.23
L-Histidinal
Pentose phosphate pathway
1-Methyl-L-histidine
3.4.13.5
6.3.2.11
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2.1.1.-
2.1.1.22
Carnosine
6.3.2.11
1.1.1.23
3.4.13.18
3.4.13.20
4-(β-Acetylaminoethyl)-imidazole
2.3.1.-
N-Formyl-L-aspartate
3.5.3.5
N-Formimino-L-aspartate
3.5.2.-
Imidazolone acetate
1.14.13.5
Imidazole-4-acetate
1.2.1.3
Imidazole acetaldehyde
1.4.3.22
Histamine
4.1.1.22
4.1.1.28
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Ergothioneine
Thiourocanic acid
3.5.1.15
3.5.1.8
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Alanine, aspartate and glutamate metabolism
6.3.4.8
1-(5-Phosphoribosyl)-imidazole-4-acetate
(1-Ribosylimidazole)-4-acetate
2.1.1.8
N-Methylhistamine
1.4.3.4
Methylimidazole acetaldehyde
1.2.1.5
Methylimidazole-acetic acid
2.6.1.38
Imidazole-pyruvate
Imidazole-lactate
4.3.1.3
Urocanate
1.3.99.33
Dihydrourocanate
4.2.1.49
4-Imidazolone-5-propanoate
4-Oxoglutaramate
2-Oxoglutarate
Formylisoglutamine
Isoglutamine
Hydantoin-5-propionate
1.14.13.-
3.5.2.7
N-Formimino-L-glutamate
3.5.3.13
N-Formyl-L-glutamate
2.1.2.5
3.5.3.8
3.5.1.68
N-Carbamyl-L-glutamate
L-Glutamate
Alanine, aspartate and glutamate metabolism
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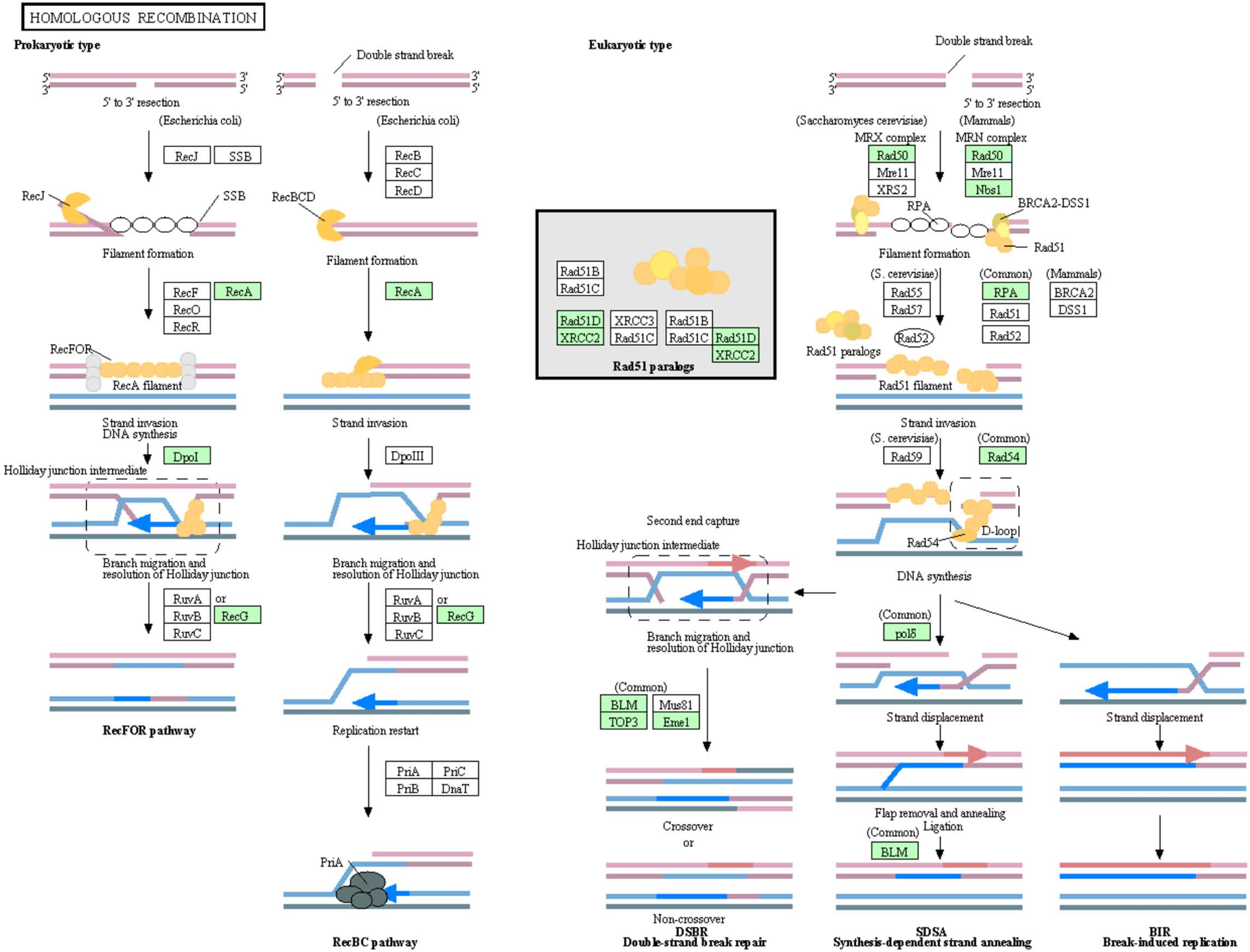

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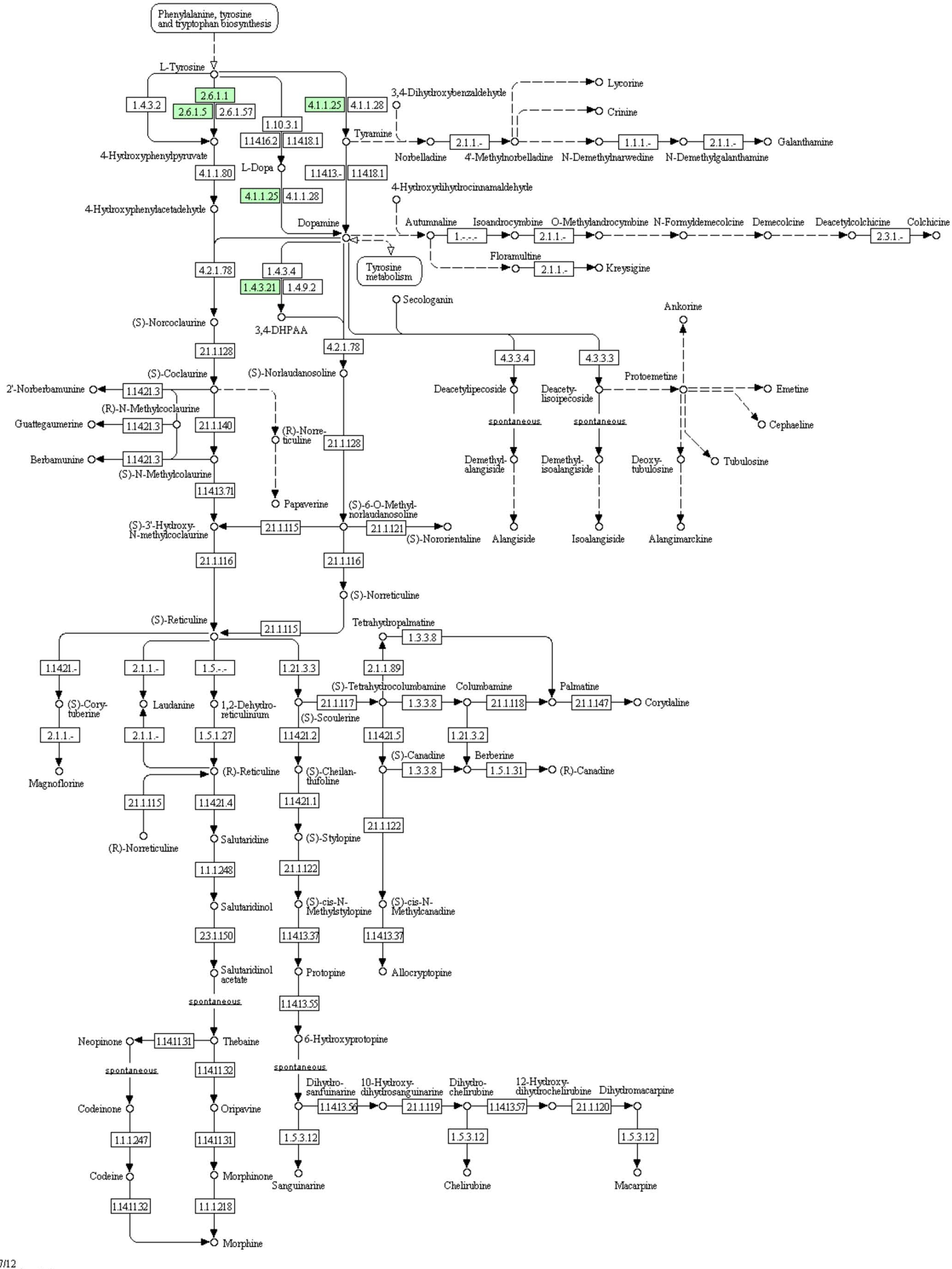
ISOQUINOLINE ALKALOID BIOSYNTHESIS



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LIMONENE AND PINENE DEGRADATION

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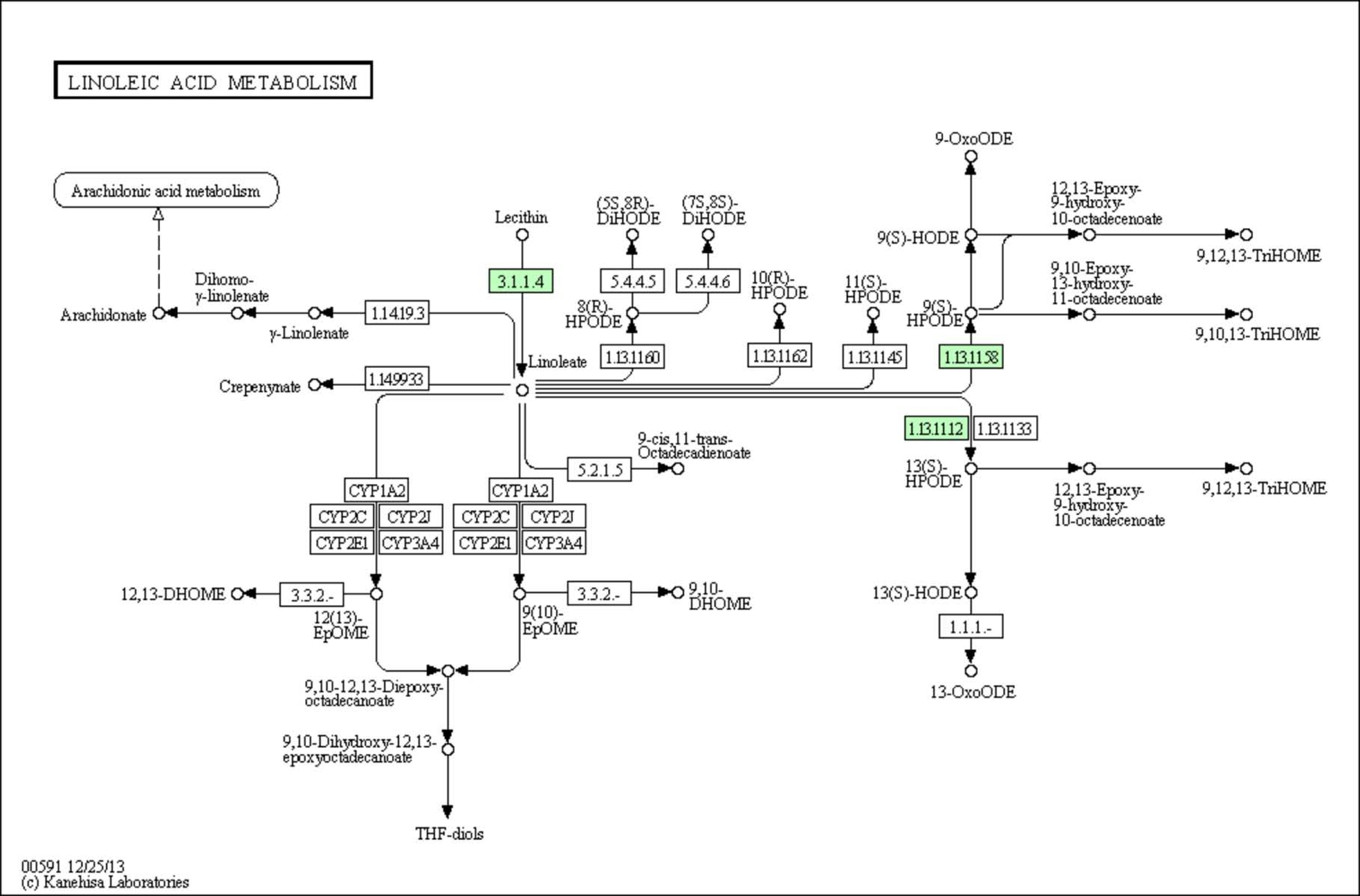
LINOLEIC ACID METABOLISM
Arachidonic acid metabolism
Lecithin
3.1.1.4
Linoleate
Arachidonate
Dihomo-γ-linolenate
γ-Linolenate
1.14.19.3
Crepenynate
1.14.99.33
(5S,8R)-DiHODE
(7S,8S)-DiHODE
5.4.4.5
5.4.4.6
8(R)-HPODE
1.13.11.60
10(R)-HPODE
1.13.11.62
11(S)-HPODE
1.13.11.45
9-OxoODE
9(S)-HODE
9(S)-HPODE
1.13.11.58
12,13-Epoxy-9-hydroxy-10-octadecenoate
9,12,13-TriHOME
9,10-Epoxy-13-hydroxy-11-octadecenoate
9,10,13-TriHOME
1.13.11.12
1.13.11.33
13(S)-HPODE
12,13-Epoxy-9-hydroxy-10-octadecenoate
9,12,13-TriHOME
13(S)-HODE
1.1.1.-
13-OxoODE
5.2.1.5
9-cis,11-trans-Octadecadienoate
CYP1A2
CYP2C
CYP2J
CYP2E1
CYP3A4
CYP1A2
CYP2C
CYP2J
CYP2E1
CYP3A4
12,13-DHOME
3.3.2.-
12(13)-EpOME
9(10)-EpOME
3.3.2.-
9,10-DHOME
9,10-12,13-Diepoxy-octadecanoate
9,10-Dihydroxy-12,13-epoxyoctadecanoate
THF-diols
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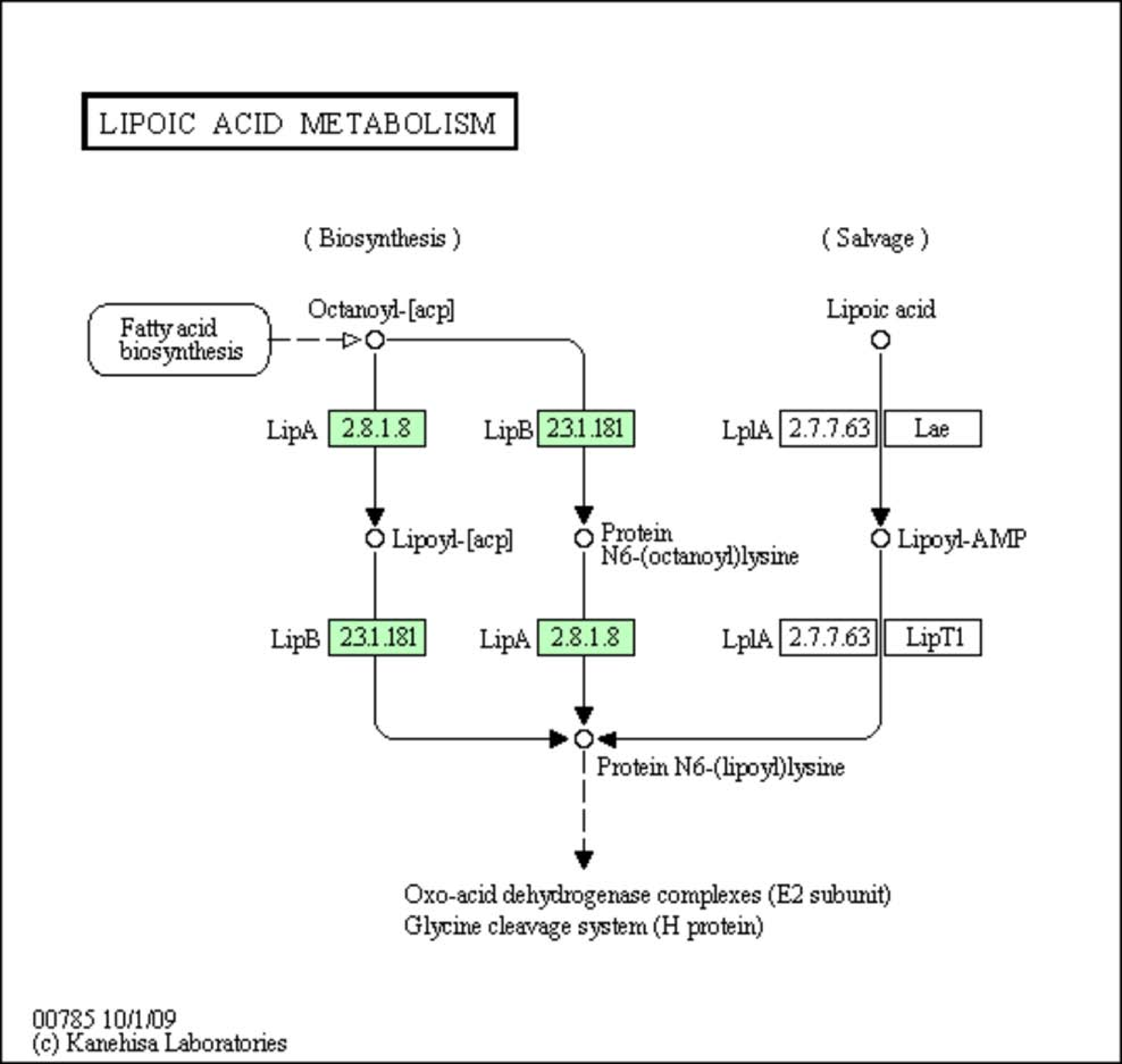
LIPOIC ACID METABOLISM
(Biosynthesis)
(Salvage)
Fatty acid biosynthesis
Octanoyl-[acp]
Lipoic acid
LipA
2.8.1.8
LipB
2.3.1.181
LplA
2.7.7.63
Lae
Lipoyl-[acp]
Protein N6-(octanoyl)lysine
Lipoyl-AMP
LipB
2.3.1.181
LipA
2.8.1.8
LplA
2.7.7.63
LipT1
Protein N6-(lipoyl)lysine
Oxo-acid dehydrogenase complexes (E2 subunit)
Glycine cleavage system (H protein)
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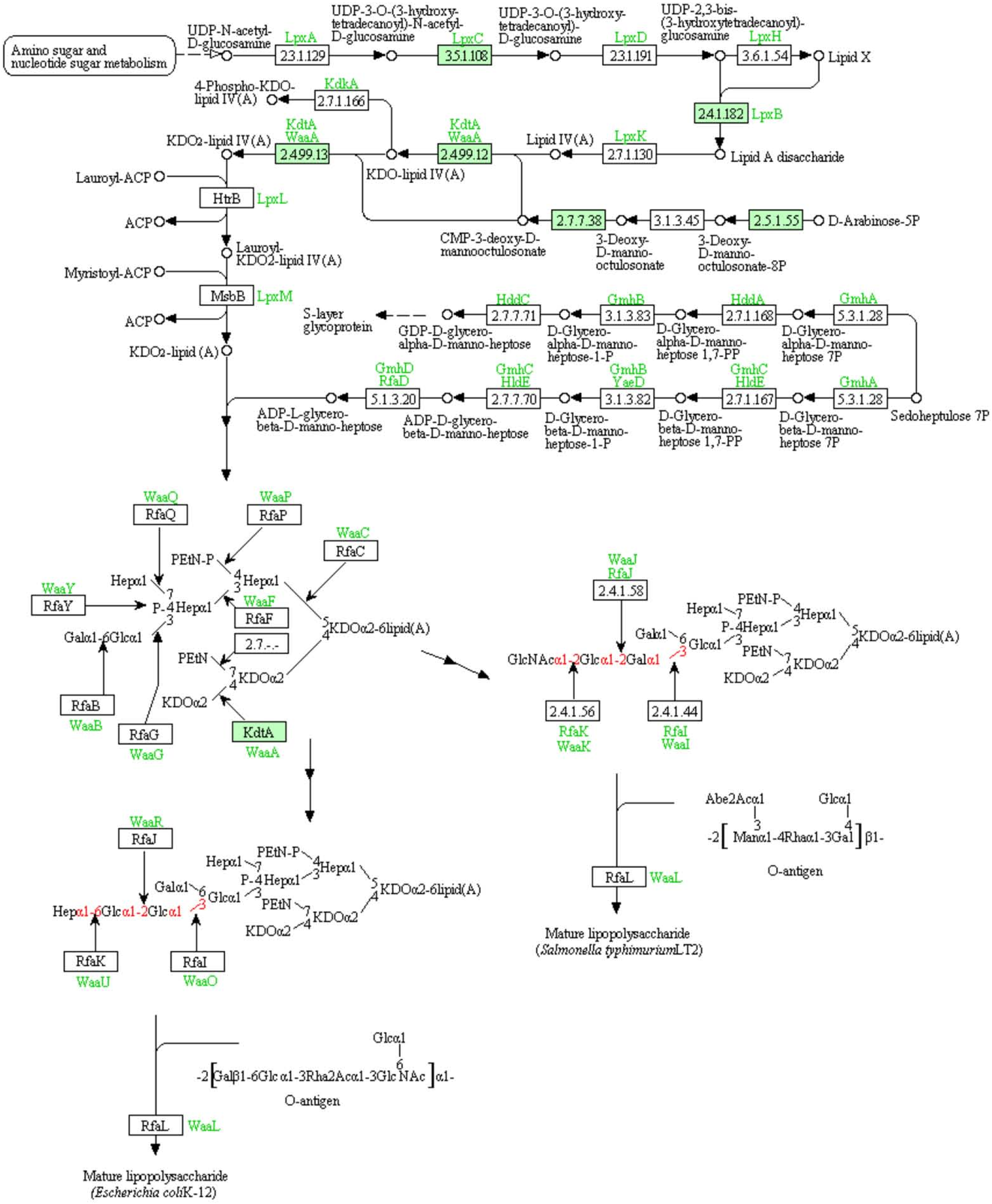
LIPOPOLYSACCHARIDE BIOSYNTHESIS



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LYSINE BIOSYNTHESIS
L-Homoserine
Glycine, serine and threonine metabolism
1.1.1.3
L-4-Aspartyl phosphate
(2S,4S)-4-Hydroxy-2,3,4,5-tetrahydro-dipicolinate
L-Aspartate
2.7.2.4
1.2.1.11
4.3.3.7
1.17.1.8
L-Aspartate 4-semialdehyde
L-2,3,4,5-Tetrahydro-dipicolinate
Alanine, aspartate and glutamate metabolism
2.3.1.89
N-Acetyl-L-2-amino-6-oxopimelate
2.6.1.-
N-Acetyl-LL-2,6-diaminopimelate
N-Succinyl-LL-2,6-diaminopimelate
2.3.1.117
2.6.1.17
3.5.1.47
N-Succinyl-L-2-amino-6-oxopimelate
3.5.1.18
2.6.1.83
LL-2,6-Diaminopimelate
5.1.1.7
UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-meso-2,6-diaminopimeloyl-D-alanyl-D-alanine
Peptidoglycan biosynthesis
L-2-Amino-6-oxopimelate
1.4.1.16
6.3.2.13
6.3.2.10
meso-2,6-Diaminopimelate
UDP-N-acetylmuramoyl-L-alanyl-D-γ-glutamyl-meso-2,6- diaminopimelate
Citrate cycle
Homocitrate
4.2.1.-
Homo-cis-aconitate
2-Oxoglutarate
2.3.3.14
4.2.1.114
Acetyl-CoA
4.2.1.114
4.2.1.36
4.1.1.20
Lysine degradation
5-Adenyl-2-aminoadipate
α-Aminoadipoyl-S-acyl enzyme
L-Saccharopine
Homo-isocitrate
1.2.1.31
1.2.1.31
1.5.1.10
1.5.1.7
L-Lysine
Tropane, piperidine and pyridine alkaloid biosynthesis
Glycolysis
L-2-Aminoadipate 6-semialdehyde
PylB
Pyruvate metabolism
1.1.1.87
1.1.1.286
1.2.1.31
LysK
3-Methyl-ornithine
2.6.1.39
3-Methylglutamuyl-5-semialdehyde-N6-lysine
LysX
LysZ
LysY
LysJ
2.6.1.57
PylC
PylD
Pyrrolysine
2-Oxoadipate
L-2-Amino-adipate
LysW-γ-L-α-aminoadipate
LysW-γ-L-α-aminoadipyl-6-phosphate
LysW-γ-L-α-aminoadipate 6-semialdehyde
LysW-γ-L-lysine
3-Methylornithinyl-N6-lysine
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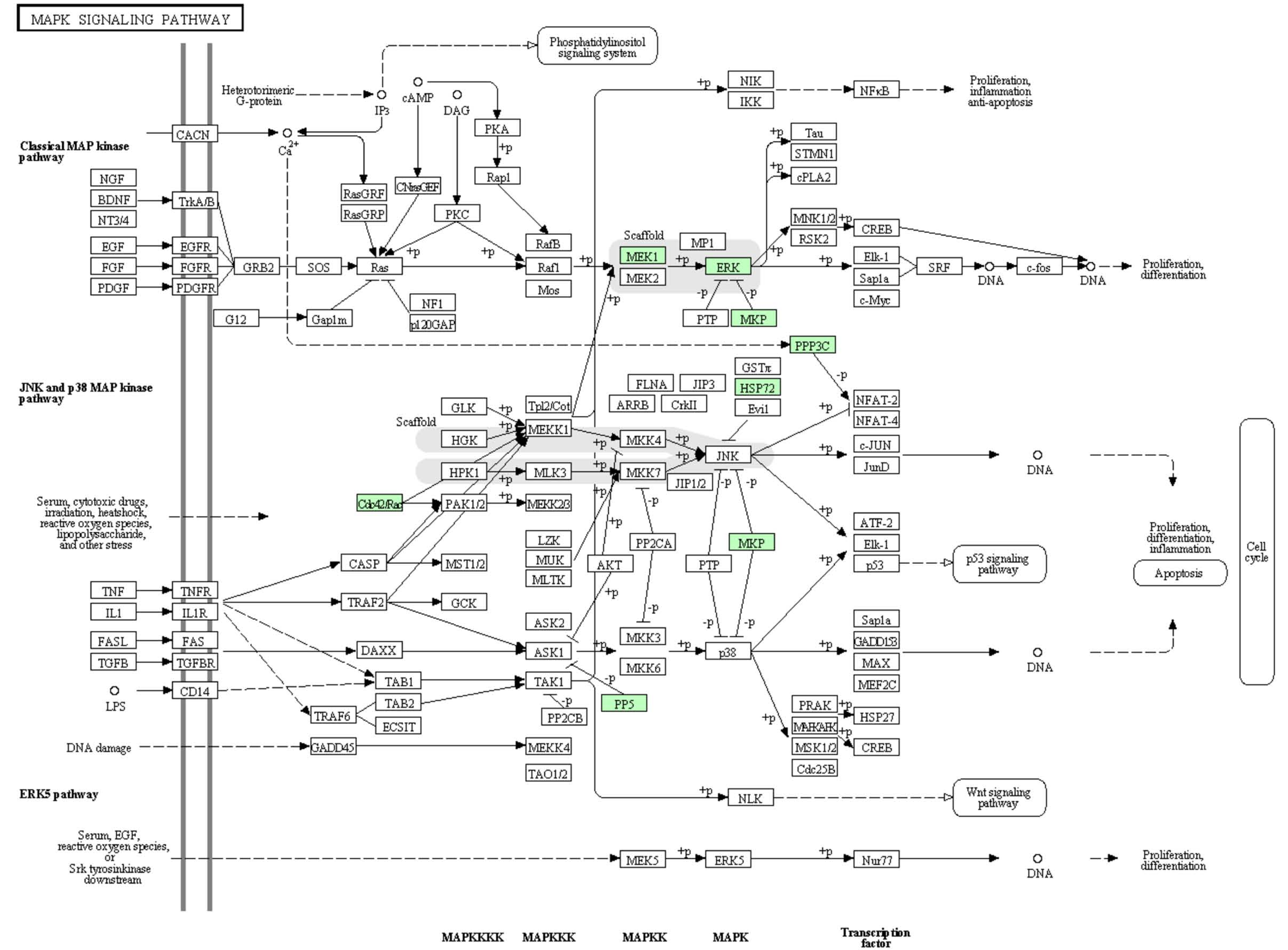
MAPK SIGNALING PATHWAY
Phosphatidylinositol signaling system
Heterotorimeric G-protein
IP3
cAMP
DAG
Ca2+
CACN
PKA
+p
Rap1
RasGRF
CNrasGEF
RasGRP
PKC
RafB
Classical MAP kinase pathway
NGF
BDNF
NT3/4
TrkA/B
EGF
EGFR
FGF
FGFR
PDGF
PDGFR
GRB2
SOS
Ras
Raf1
Mos
NF1
p120GAP
G12
Gap1m
NIK
IKK
NFκB
Proliferation, inflammation anti-apoptosis
Tau
STMN1
cPLA2
MNK1/2
RSK2
CREB
Scaffold
MP1
MEK1
MEK2
ERK
-p
PTP
MKP
Elk-1
Sap1a
c-Myc
SRF
DNA
c-fos
DNA
Proliferation, differentiation
PPP3C
JNK and p38 MAP kinase pathway
GSTπ
HSP72
Evi1
FLNA
JIP3
ARRB
CrkII
NFAT-2
NFAT-4
GLK
Tpl2/Cot
Scaffold
HGK
MEKK1
MKK4
JNK
c-JUN
JunD
DNA
HPK1
MLK3
MKK7
JIP1/2
Serum, cytotoxic drugs, irradiation, heatshock, reactive oxygen species, lipopolysaccharide, and other stress
Cdc42/Rac
PAK1/2
MEKK2/3
PP2CA
LZK
MUK
MLTK
AKT
PTP
MKP
ATF-2
Elk-1
p53
p53 signaling pathway
Proliferation, differentiation, inflammation
Apoptosis
Cell cycle
CASP
MST1/2
TNF
TNFR
IL1
IL1R
TRAF2
GCK
FASL
FAS
DAXX
ASK2
ASK1
MKK3
MKK6
p38
Sap1a
GADD153
MAX
MEF2C
DNA
TGFB
TGFBR
LPS
CD14
TAB1
TAB2
TRAF6
ECSIT
TAK1
PP2CB
PP5
PRAK
MAPKAPK
MSK1/2
Cdc25B
HSP27
CREB
DNA damage
GADD45
MEKK4
TAO1/2
NLK
Wnt signaling pathway
ERK5 pathway
Serum, EGF, reactive oxygen species, or Srk tyrosinkinase downstream
MEK5
ERK5
Nur77
DNA
Proliferation, differentiation
MAPKKK
MAPKKK
MAPKK
MAPK
Transcription factor

04010 2/14/14

MEIOSIS - yeast

04113 5/29/13
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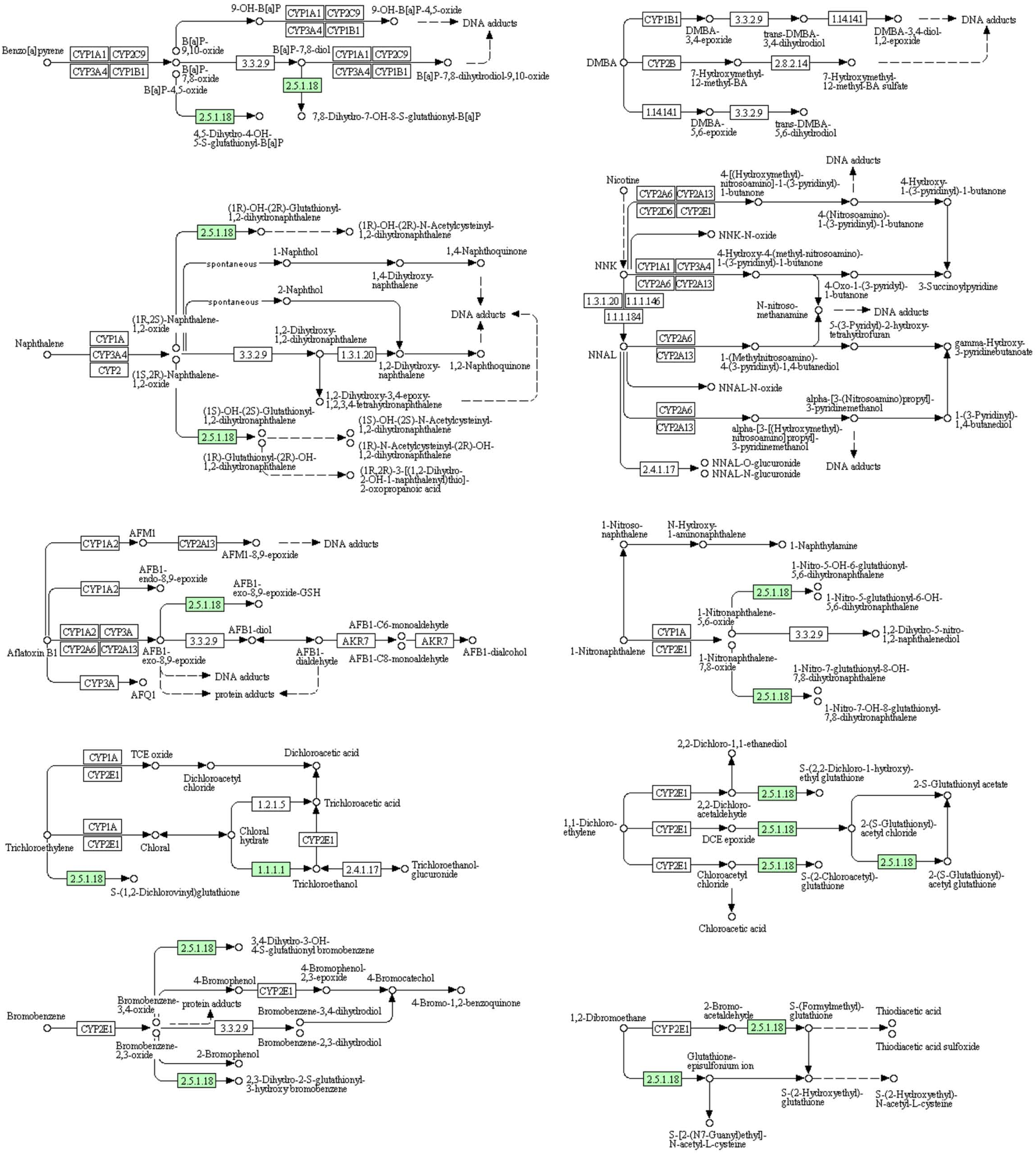
METABOLISM OF XENOBIOTICS BY CYTOCHROME P450



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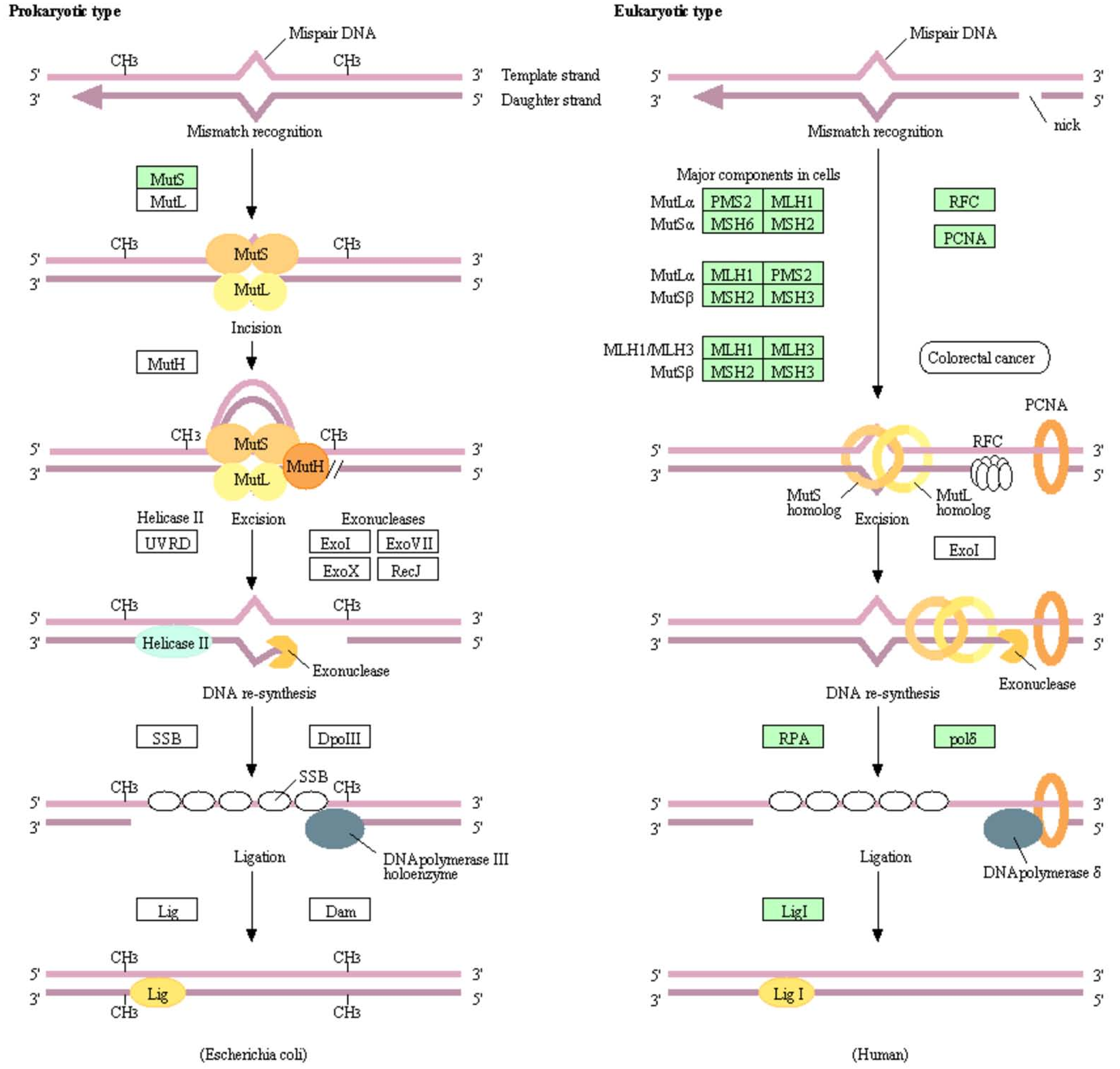
MISMATCH REPAIR



03430 10/20/10
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MONOTERPENOID BIOSYNTHESIS
Terpenoid backbone biosynthesis
Geranyl-PP
(+)-Bornyl-diphosphate
Camphene
5.5.1.8
4.2.3.-
3.1.7.3
4.2.3.25
4.2.3.15
4.2.3.26
4.2.3.16
4.2.3.20
4.2.3.119
4.2.3.120
4.2.3.10
4.2.3.11
4.2.3.108
4.2.3.111
Geraniol degradation
Geraniol
5.4.4.4
(+)-Linalool
4.2.1.127
Myrcene
(-)-Linalool
1.14.13.152
10-Hydroxy-geraniol
1.1.1.324
10-Oxogeranial
Iridodial
Iridotrial
1.14.13.151
1.14.13.151
8-Hydroxylinalool
1.14.13.151
8-Oxolinalool
(-)-(S)-Limonene
(+)-(R)-Limonene
1.14.13.47
1.14.13.48
1.14.13.49
1.14.13.80
(-)-trans-Isopiperitenol
(-)-trans-Carveol
Perillyl alcohol
(+)-trans-Carveol
1.1.1.223
1.1.1.243
1.1.1.275
(-)-Isopiperitenone
(-)-Carvone
(+)-(S)-Carvone
1.3.1.82
(+)-cis-Isopulegone
(+)-Pulegone
1.3.1.81
1.14.13.104
1.3.1.81
(+)-Menthofuran
(+)-Isomenthone
(-)-Menthone
1.1.1.207
1.1.1.208
1.14.13.105
(-)-Menthol
(+)-Neomenthol
(4R,7S)-7-Isopropyl-4-methyloxepan-2-one
(-)-α-Pinene
(-)-β-Pinene
(-)-endo-Fenchol
Sabinene hydrate
α-Terpineol
4.2.3.108
1,8-Cineole
1.14.13.156
6-endo-Hydroxycineole
1.1.1.241
6-Oxocineole
1.14.13.51
1,6,6-Trimethyl-2,7-dioxabicyclo-[3.2.2]nonan-3-one
spontaneous
4,5-Dihydro-5,5-dimethyl-4-(3-oxobutyl)furan-2(3H)-onehexanoate
Limonene and pinene degradation
7-Deoxy-loganin
7-Deoxy-loganate
1.14.13.74
1.14.13.74
Loganin
2.1.1.50
Loganate
10-Deoxy-geniposidic acid
1.3.3.9
1.3.3.9
Secologanin
2.1.1.50
Secologanate
Geniposidic acid
Asperuloside
Indole alkaloid biosynthesis
00902 3/13/14
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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
Upf3
CBC
m7G
PABP2
AAAAAAA
Aberrant RNAs
Polyadenylation by TRAMP complex
Nuclear exosome
RNA degradation
Export
SRm160
Pinin
Tap
RNA transport
Nuclear Pore complex (NPC)
Nucleus
Cytoplasm
Ref/Aly
Tap
Ribosome binding
CBC
60S
EJC
m7G
40S
AAAAAAA
Ribosome
Cap binding complex (CBC)
CBP80
CBP20
Exon-junction complex (EJC)
Upf3
ACIN1
Y14
MLN51
SAP18
RNPS1
MAGOH
EIF4A3
Pinin
Ref/Aly
Transiently interacting factors
Tap
p15
UAP56
SRm160
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
mammals
EJC complex
Musashi
PABP1
Recognition of PTC (premature termination codon)
CBC
PTC
EJC
Upf3
Stop codon
m7G
AAAAAAA
Lacking a stop codon
m7G
AAAA
Recognition of empty A site
Ski7
Ski7
m7G
AAAAAA
eRF3
eRF1
Upf1
Upf2
Assembly of the surveillance complex
eRF1
eRF3
Upf1
Upf2
Upf3
+p
SMG1
SMG7
PP2A
SMG5
SMG6
Upf1
eRF3
Upf2
Upf3
CBC
eRF1
EJC
Stop codon
m7G
AAAAAAA
Translational stalling
Stem-loop
Stop codon
PABP1
m7G
AAAAAAA
Hbs1
Dom34
Hbs1
Dom34
Hbs1
Dom34
Stop codon
m7G
AAAAAAA
Cytoplasmic exosome
Decapping
Deadenylation
Cytoplasmic exosome
Ski complex
RNA degradation
Cytoplasmic exosome
Ski7
Nonstop decay (NSD)
Nonsense-mediated decay (NMD)
No-go decay (NGD)
03015 9/30/11
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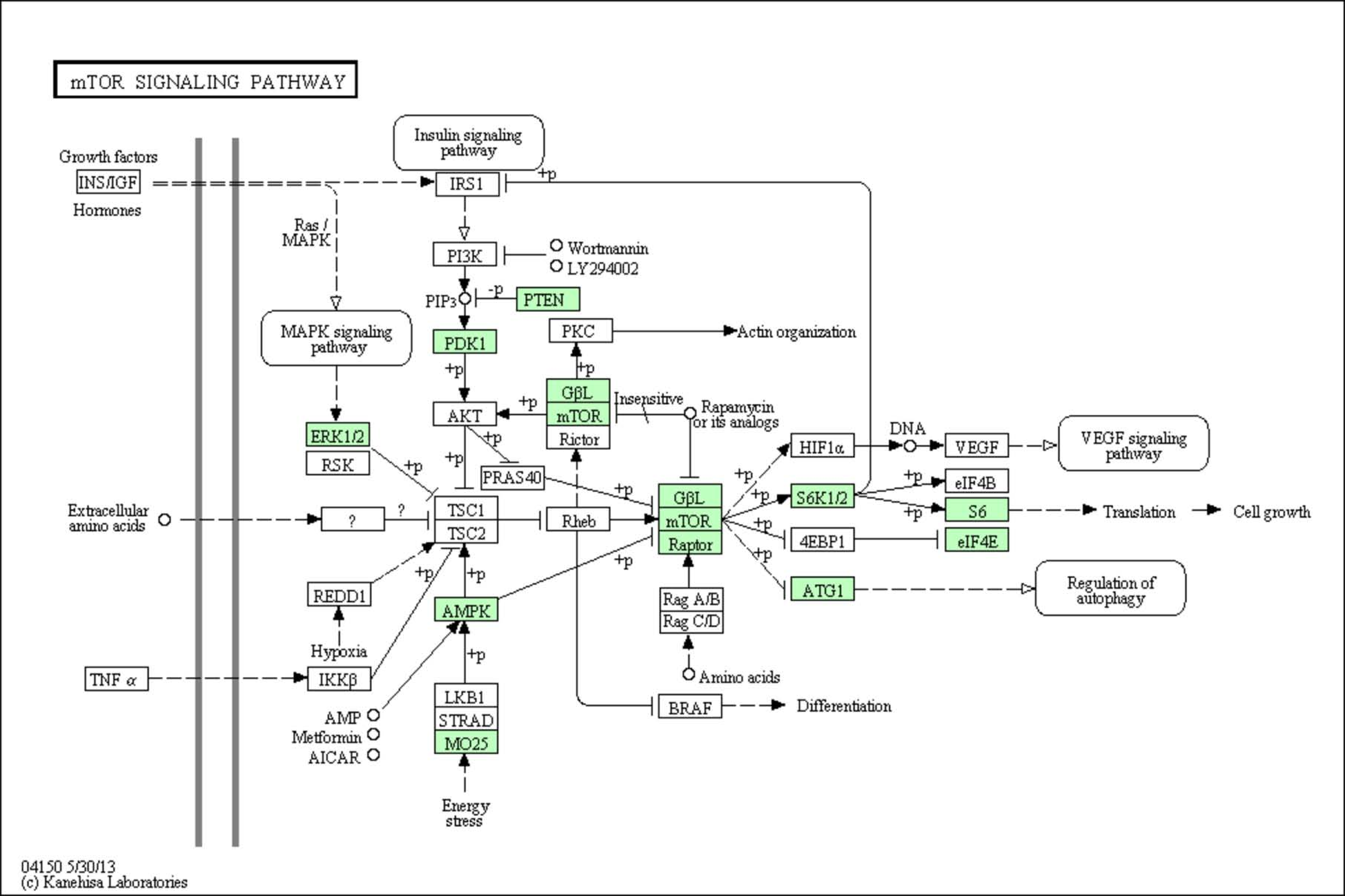
mTOR SIGNALING PATHWAY
Growth factors
INS/IGF
Hormones
Insulin signaling pathway
IRS1
+p
Ras / MAPK
PI3K
Wortmannin
LY294002
PIP3
-p
PTEN
MAPK signaling pathway
PDK1
PKC
Actin organization
+p
+p
GβL
mTOR
Rictor
Insensitive
Rapamycin or its analogs
AKT
+p
ERK1/2
RSK
+p
+p
+p
PRAS40
+p
DNA
HIF1α
VEGF
VEGF signaling pathway
+p
+p
eIF4B
S6K1/2
+p
S6
Translation
Cell growth
Extracellular amino acids
?
?
TSC1
TSC2
Rheb
GβL
mTOR
Raptor
+p
4EBP1
eIF4E
+p
ATG1
Regulation of autophagy
REDD1
+p
+p
+p
AMPK
Rag A/B
Rag C/D
Hypoxia
TNF α
IKKβ
+p
Amino acids
LKB1
STRAD
MO25
BRAF
Differentiation
AMP
Metformin
AICAR
Energy stress
04150 5/30/13
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NAPHTHALENE DEGRADATION
Naphthalene-1,6-disulfonate
Naphthalene-2,6-disulfonate
1.14.99.-
1,2-Dihydroxy-naphthalene-6-sulfonate
1.13.11.-
(Z)-4-(2-Hydroxy-5-sulfonatophenyl)-2-oxo-3-butenoate
5-Sulfosalicylate
Gentisate
Tyrosine metabolism
Naphthalene-1-sulfonate
Naphthalene-2-sulfonate
1.14.99.-
1.14.13.172
Naphthalene
1.14.12.12
cis-1,2-Dihydroxy-1,2-dihydronaphthalene
1.3.1.29
1,2-Dihydroxy-naphthalene
1.13.11.56
2-Hydroxychromene-2-carboxylate
5.99.1.4
trans-o-Hydroxy-benzylidenepyruvate
4.1.2.45
Salicylaldehyde
1.2.1.65
Salicylate
1.14.13.1
Catechol
Benzoate degradation
1-Methylnaphthalene
1.14.12.12
cis-1,2-Dihydroxy-1,2-dihydro-8-methylnaphthalene
1.3.1.29
1,2-Dihydroxy-8-methylnaphthalene
1.13.-.-
2-Hydroxy-8-methyl-chromene-2-carboxylate
5.3.99.-
2-Hydroxy-3-methyl-benzalpyruvate
4.2.1.-
3-Methylsalicylaldehyde
1.2.1.-
3-Methylsalicylate
1.14.13.1
3-Methyl-catechol
Xylene degradation
1.14.13.-
1-Hydroxymethyl-naphthalene
1.1.1.1
1-Naphthaldehyde
1.2.1.-
1-Naphthoate
1.14.12.-
cis-1,2-Dihydroxy-1,2-dihydro-8-carboxynaphthalene
1.1.-.-
1,2-Dihydroxy-8-carboxynaphthalene
1.13.-.-
2-Carboxy-2-hydroxy-8-carboxychromene
5.3.99.-
2-Hydroxy-3-carboxy-benzalpyruvate
4.2.1.-
3-Formyl-salicylate
1.2.3.-
2-Hydroxy-isophthalic acid
4.1.1.-
cis-1,2-Dihydroxy-1,2-dihydro-7-methylnaphthalene
1.14.12.12
4-Methylsalicylate
1.14.13.1
4-Methyl-catechol
Xylene degradation
1-Hydroxy-2-naphthoate
Succinyl-CoA
2-Methylnaphthalene
NmsABC
4.1.99.-
Naphthyl-2-methyl-succinic acid
BnsEF
2.8.3.-
Naphthyl-2-methyl-succinyl-CoA
1.3.99.-
BnsG
BnsH
4.2.1.-
Naphthyl-2-methylene-succinyl-CoA
Naphthyl-2-hydroxymethyl-succinyl CoA
1.1.-.-
BnsCD
BnsAB
2.3.1.-
Naphthyl-2-oxomethyl-succinyl-CoA
2-Naphthoyl-CoA
2.8.3.-
NmoAB
2-Naphthoate
5,6,7,8-Tetrahydro-2-naphthoic acid
cis-2-Carboxycyclohexyl-acetate
Decahydro-2-naphthoic acid
Tetralin
1.14.13.-
1.1.1.1
2-Naphthaldehyde
1.2.1.-
4-Formylsalicylic acid
2-Hydroxymethyl-naphthalene
1.14.12.12
cis-1,2-Dihydroxy-1,2-dihydro-7-hydroxy-methylnaphthalene
1,2-Dihydroxy-7-hydroxymethylnaphthalene
1.3.1.29
1.13.-.-
2-Hydroxy-7-hydroxymethyl-chromene-2-carboxylate
5.3.99.-
2-Hydroxy-4-hydroxymethyl-benzalpyruvate
4.2.1.-
4-Hydroxy-methylsalicylaldehyde
1.2.1.-
4-Hydroxy-methylsalicylate
1.14.13.1
4-Hydroxy-methylcatechol
00626 7/29/13
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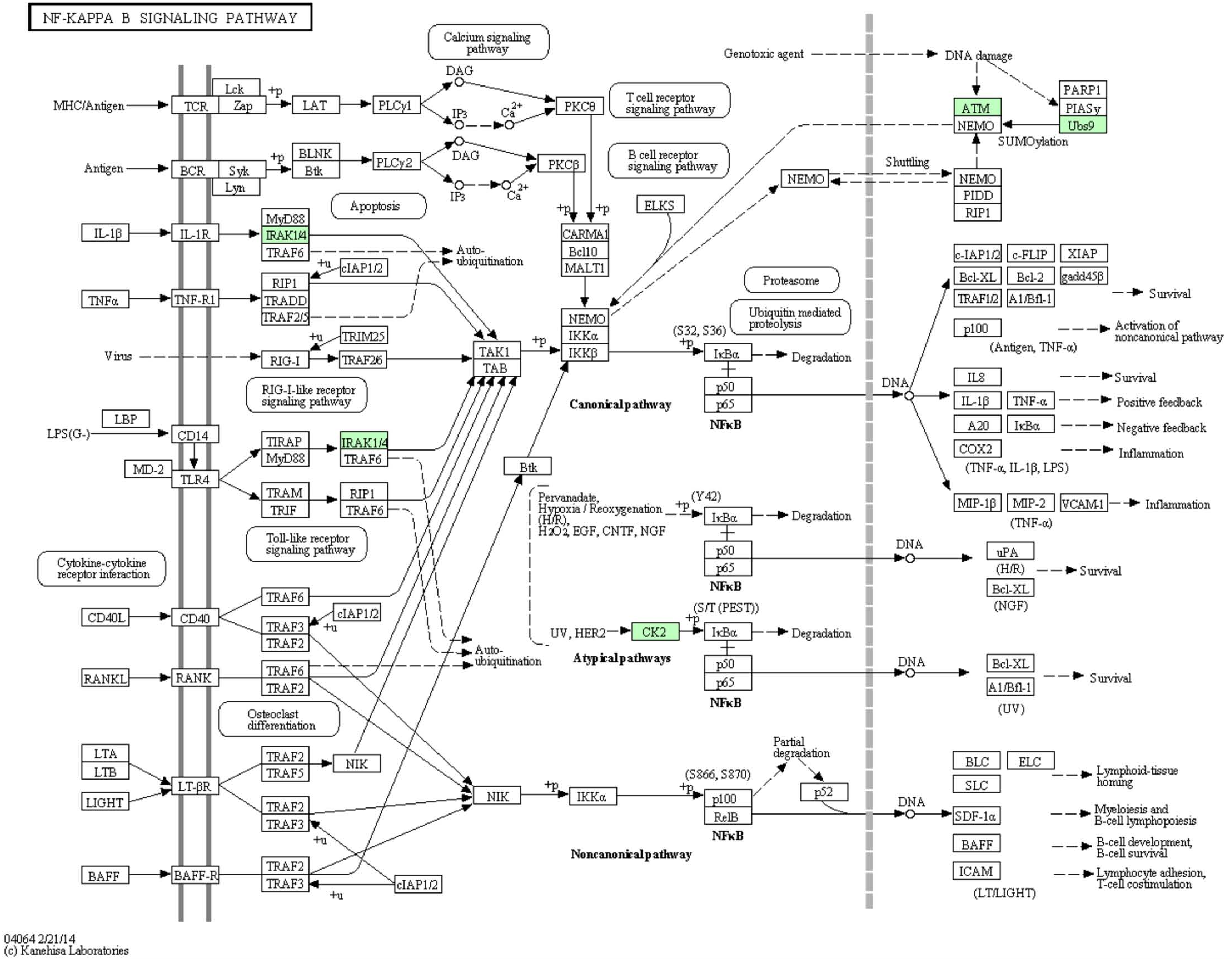
NF-KAPPA B SIGNALING PATHWAY
Calcium signaling pathway
MHC/Antigen
TCR
Lck
Zap
+p
LAT
PLCγ1
DAG
IP3
Ca2+
PKCθ
T cell receptor signaling pathway
Antigen
BCR
Syk
Lyn
+p
BLNK
Btk
PLCγ2
DAG
IP3
Ca2+
PKCβ
B cell receptor signaling pathway
Apoptosis
IL-1β
IL-1R
MyD88
IRAK1/4
TRAF6
Auto-ubiquitination
+u
cIAP1/2
TNFα
TNF-R1
RIP1
TRADD
TRAF2/5
+p
+p
CARMA1
Bcl10
MALT1
ELKS
NEMO
IKKα
IKKβ
Virus
RIG-I
+u
TRIM25
TRAF2/6
TAK1
TAB
+p
RIG-I-like receptor signaling pathway
LBP
LPS(G-)
CD14
MD-2
TLR4
TIRAP
MyD88
IRAK1/4
TRAF6
TRAM
TRIF
RIP1
TRAF6
Btk
Toll-like receptor signaling pathway
Cytokine-cytokine receptor interaction
CD40L
CD40
TRAF6
TRAF3
TRAF2
cIAP1/2
+u
Auto-ubiquitination
RANKL
RANK
TRAF6
TRAF2
Osteoclast differentiation
LTA
LTB
LIGHT
LT-βR
TRAF2
TRAF5
NIK
TRAF2
TRAF3
+u
BAFF
BAFF-R
TRAF2
TRAF3
+u
cIAP1/2
NIK
+p
IKKα
Canonical pathway
(S32, S36)
+p
IκBα
Degradation
p50
p65
NFκB
Proteasome
Ubiquitin mediated proteolysis
Genotoxic agent
DNA damage
ATM
NEMO
PARP1
PIASy
Ubc9
SUMOylation
NEMO
Shuttling
NEMO
PIDD
RIP1
Pervanadate, Hypoxia / Reoxygenation (H/R), H2O2, EGF, CNTF, NGF
+p
(Y42)
IκBα
Degradation
p50
p65
NFκB
UV, HER2
CK2
+p
(S/T (PEST))
IκBα
Degradation
p50
p65
NFκB
Atypical pathways
Partial degradation
(S866, S870)
+p
p100
RelB
NFκB
p52
Noncanonical pathway
DNA
c-IAP1/2
c-FLIP
XIAP
Bcl-XL
Bcl-2
gadd45β
TRAF1/2
A1/Bfl-1
Survival
p100
(Antigen, TNF-α)
Activation of noncanonical pathway
IL8
Survival
IL-1β
TNF-α
Positive feedback
A20
IκBα
Negative feedback
COX2
Inflammation
(TNF-α, IL-1β, LPS)
MIP-1β
MIP-2
VCAM-1
Inflammation
(TNF-α)
DNA
uPA
(H/R)
Survival
Bcl-XL
(NGF)
DNA
Bcl-XL
A1/Bfl-1
Survival
(UV)
DNA
BLC
ELC
SLC
Lymphoid-tissue homing
SDF-1α
Myeloiesis and B-cell lymphopoiesis
BAFF
B-cell development, B-cell survival
ICAM
Lymphocyte adhesion, T-cell costimulation
(LT/LIGHT)
04064 2/21/14
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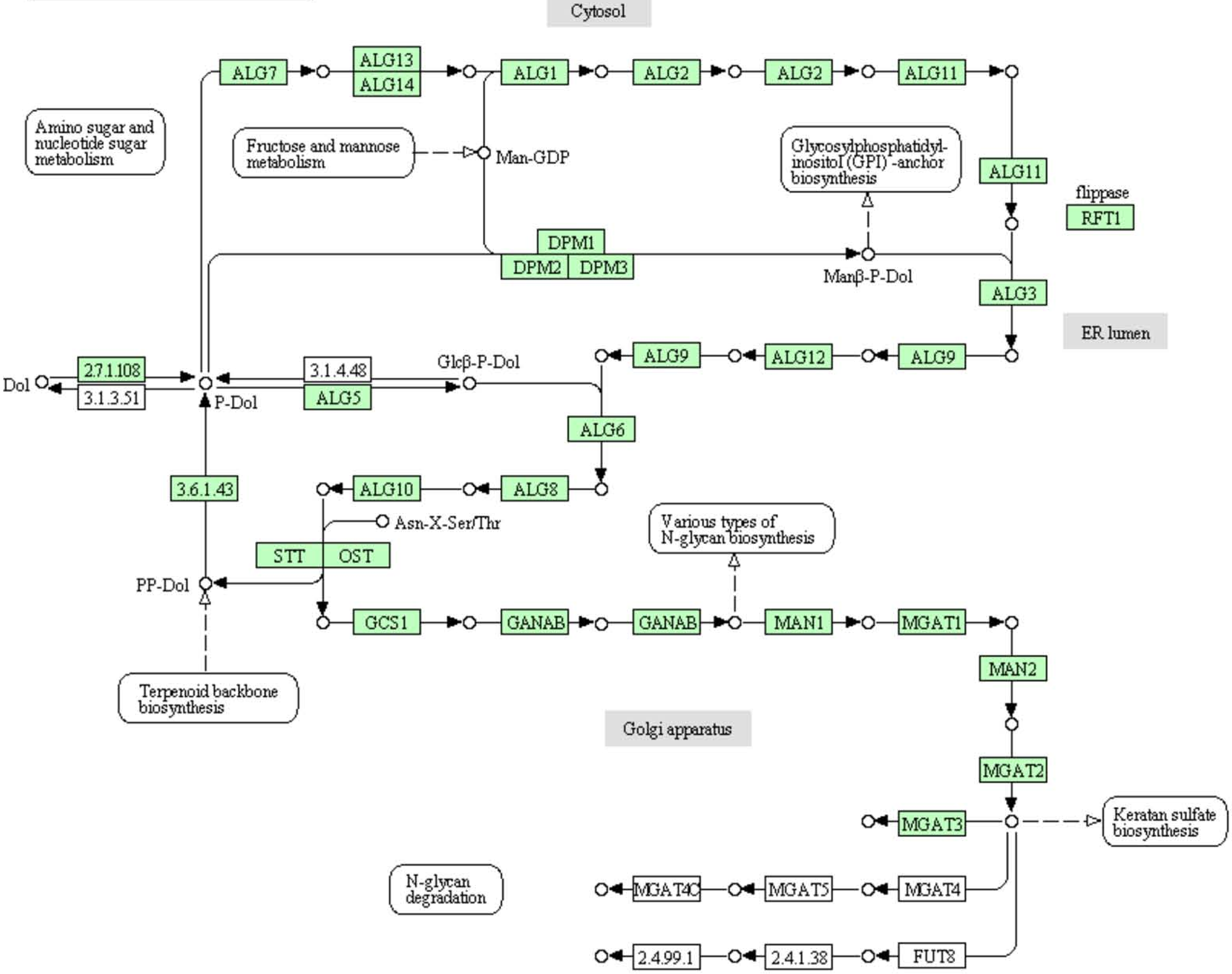
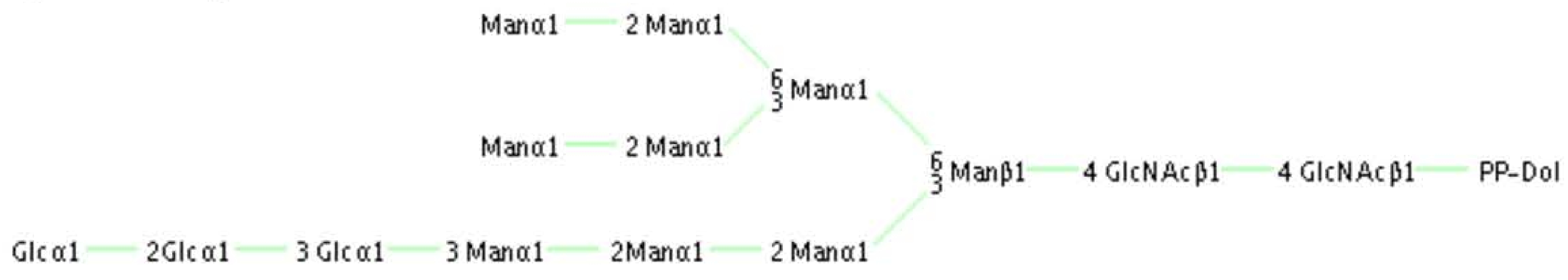
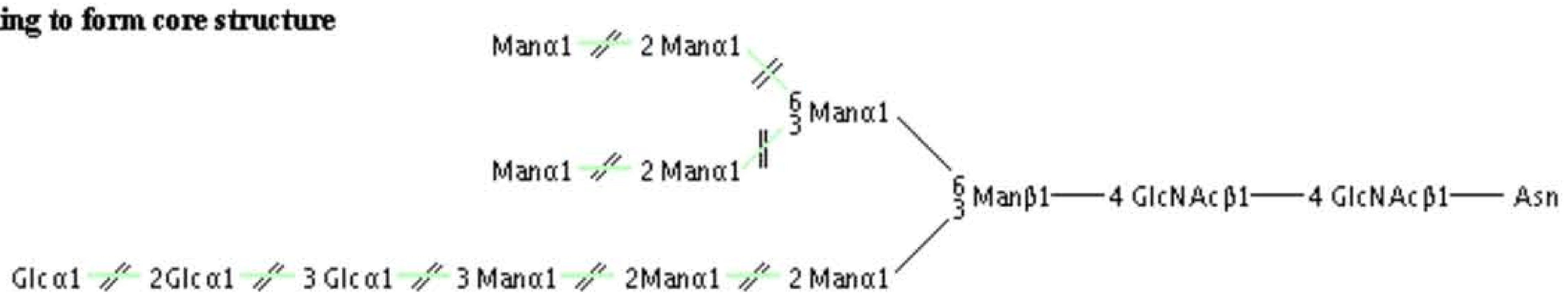
N-GLYCAN BIOSYNTHESIS



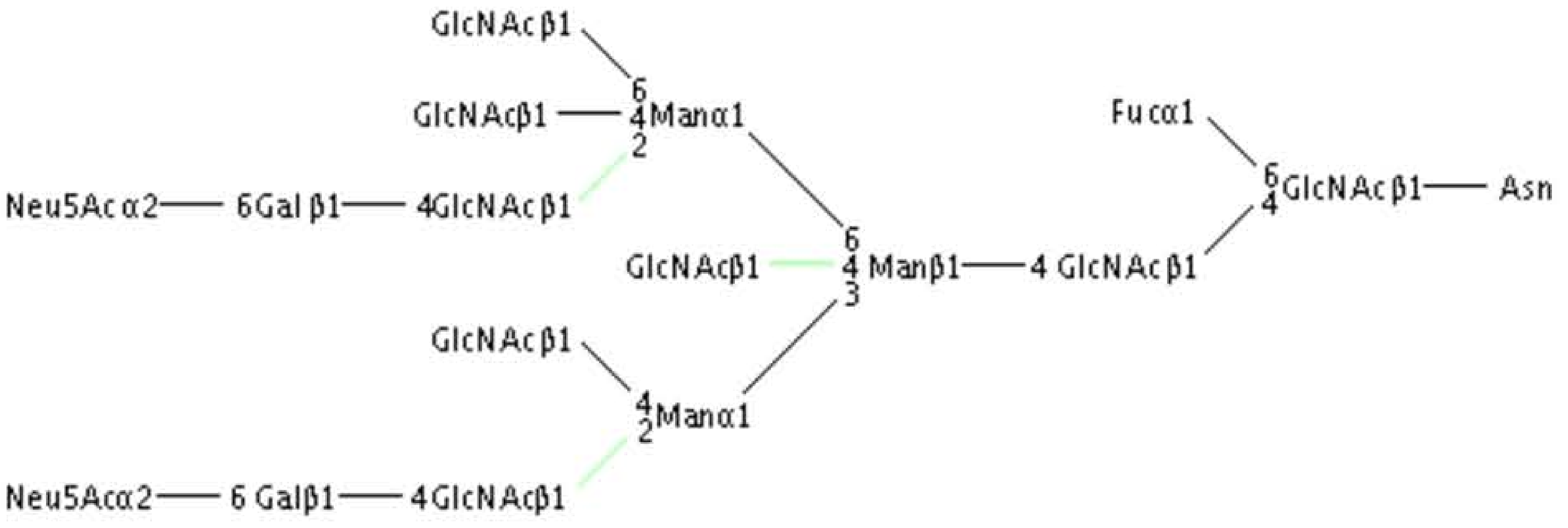
N-glycan precursor biosynthesis



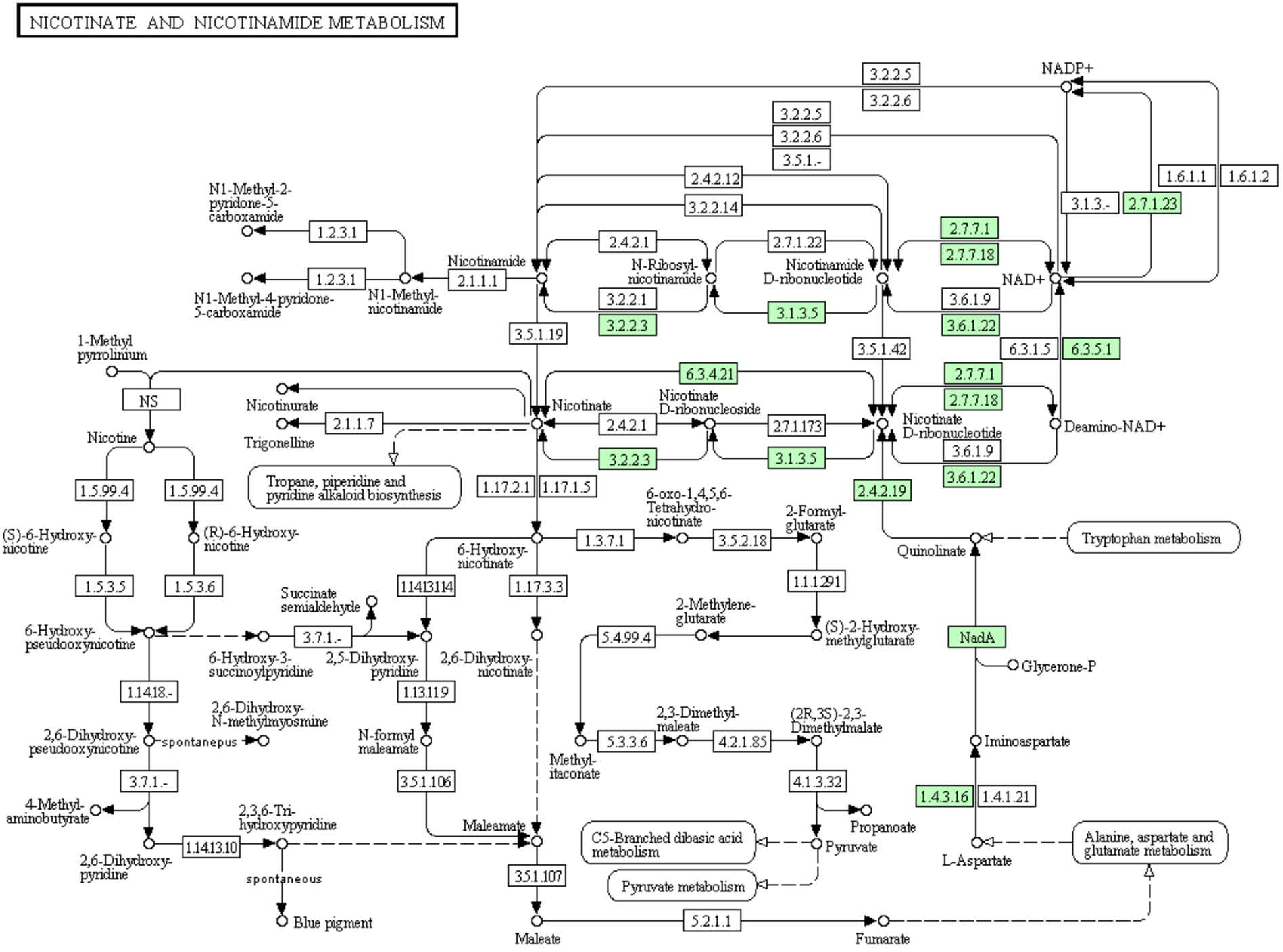
Trimming to form core structure



Glycan extension from core structure



00510 6/26/12



00760 2/20/14
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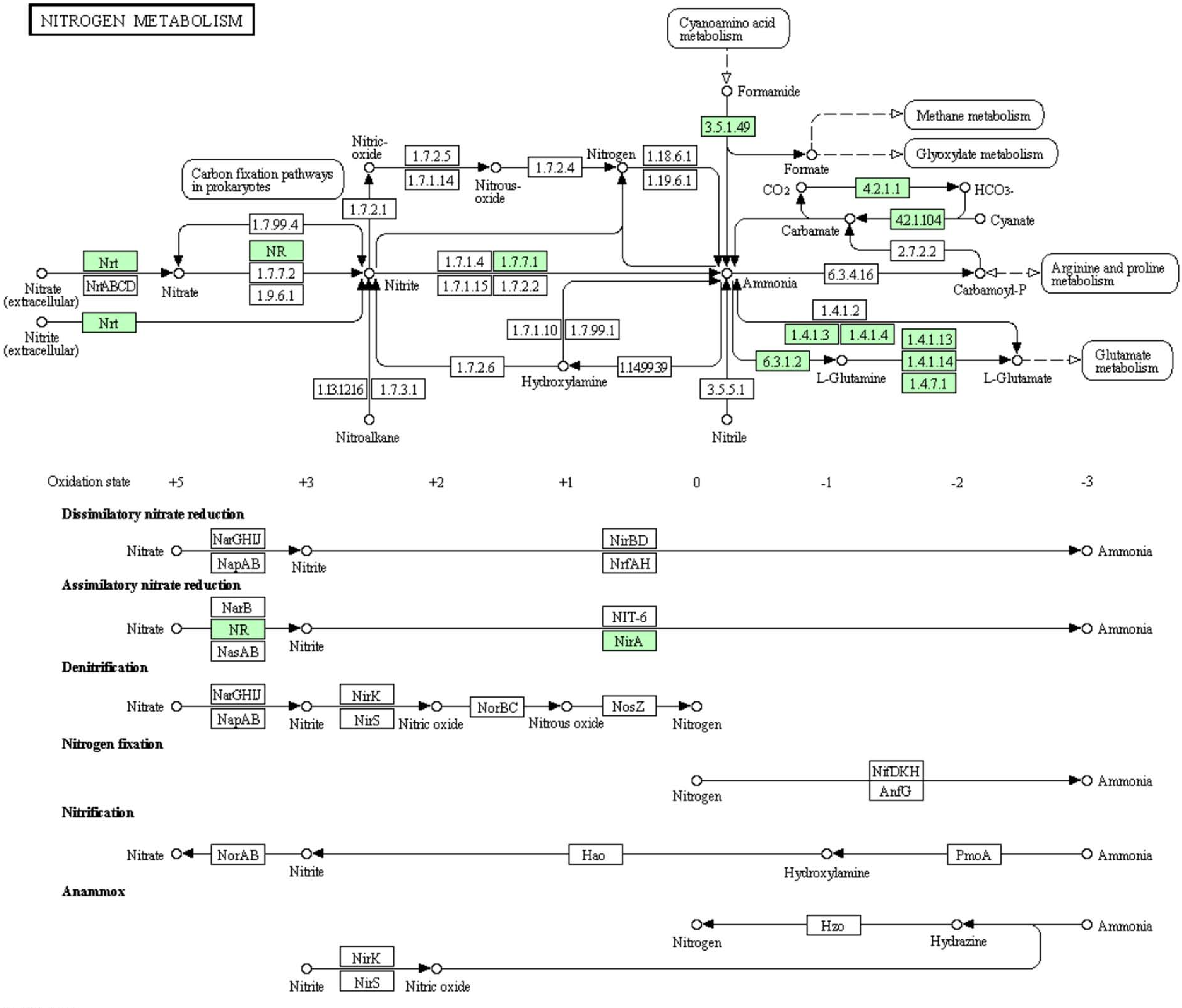
NITROGEN METABOLISM
Cyanoamino acid metabolism
Formamide
3.5.1.49
Methane metabolism
Glyoxylate metabolism
Formate
CO2
4.2.1.1
HCO3-
Carbamate
4.2.1.104
Cyanate
2.7.2.2
Carbon fixation pathways in prokaryotes
Nitric-oxide
1.7.2.5
1.7.1.14
Nitrous-oxide
1.7.2.4
Nitrogen
1.18.6.1
1.19.6.1
1.7.2.1
1.7.99.4
Nrt
NrtABCD
Nitrate (extracellular)
Nitrate
NR
1.7.7.2
1.9.6.1
Nitrite
1.7.1.4
1.7.7.1
1.7.1.15
1.7.2.2
Ammonia
6.3.4.16
Carbamoyl-P
Arginine and proline metabolism
Nrt
Nitrite (extracellular)
1.4.1.2
1.4.1.3
1.4.1.4
1.4.1.13
1.4.1.14
1.4.7.1
1.7.1.10
1.7.99.1
6.3.1.2
L-Glutamine
L-Glutamate
Glutamate metabolism
1.7.2.6
Hydroxylamine
1.14.99.39
1.13.12.16
1.7.3.1
3.5.5.1
Nitroalkane
Nitrile
Oxidation state
+5
+3
+2
+1
0
-1
-2
-3
Dissimilatory nitrate reduction
Nitrate
NarGHIJ
NapAB
Nitrite
NirBD
NrfAH
Ammonia
Assimilatory nitrate reduction
Nitrate
NarB
NR
NasAB
Nitrite
NIT-6
NirA
Ammonia
Denitrification
Nitrate
NarGHIJ
NapAB
Nitrite
NirK
NirS
Nitric oxide
NorBC
Nitrous oxide
NosZ
Nitrogen
Nitrogen fixation
Nitrogen
NifDKH
AnfG
Ammonia
Nitrification
Nitrate
NorAB
Nitrite
Hao
Hydroxylamine
PmoA
Ammonia
Anammox
Nitrogen
Hzo
Hydrazine
Ammonia
Nitrite
NirK
NirS
Nitric oxide
00910 1/9/14
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04621 10/2/12
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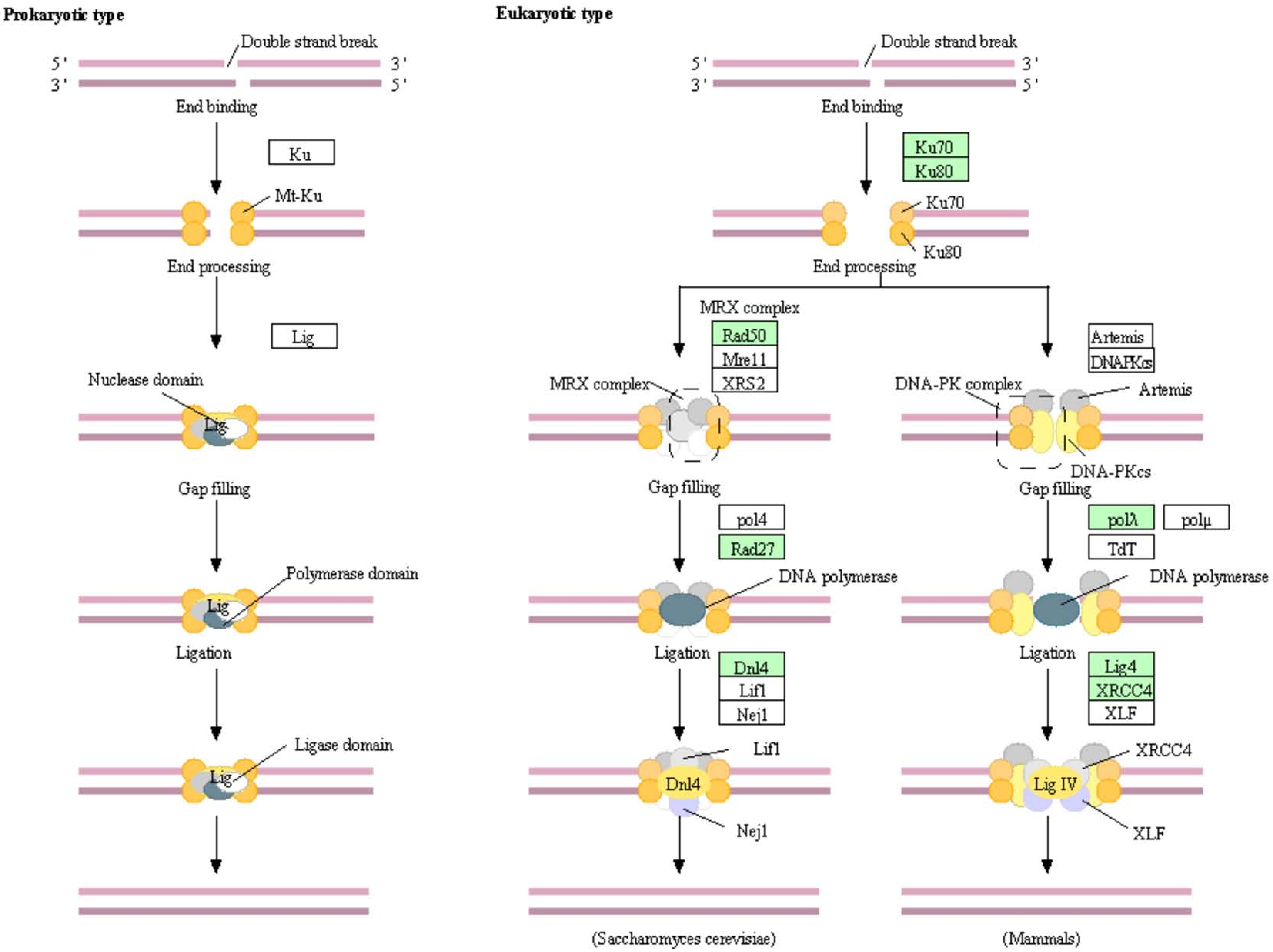
NON-HOMOLOGOUS END-JOINING



03450 8/1/11
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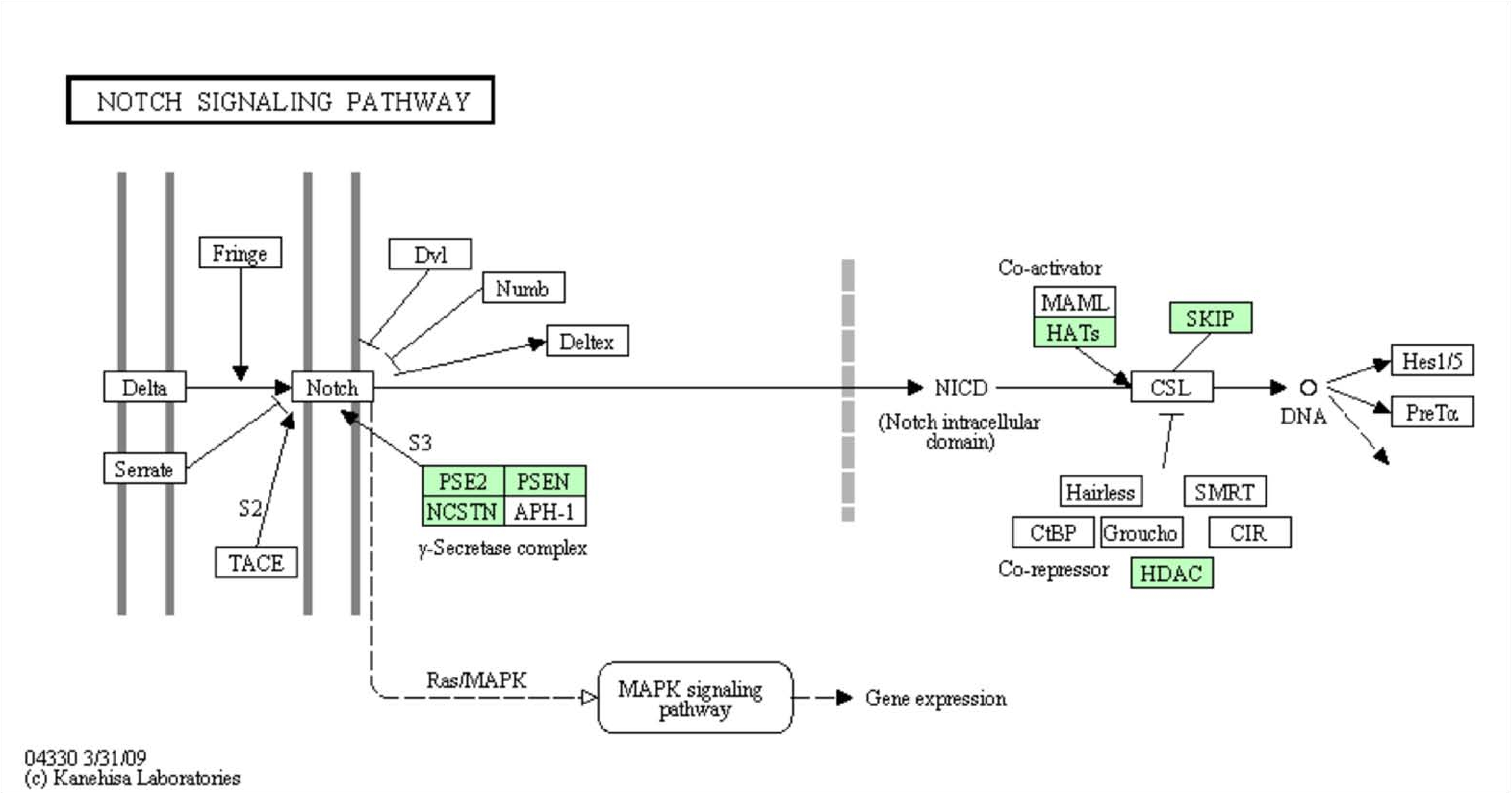
NOTCH SIGNALING PATHWAY
Fringe
Dvl
Numb
Deltex
Delta
Notch
Serrate
S2
TACE
S3
PSE2
PSEN
NCSTN
APH-1
γ-Secretase complex
NICD
(Notch intracellular domain)
Co-activator
MAML
HATs
SKIP
CSL
DNA
Hes1/5
PreTα
Hairless
SMRT
CtBP
Groucho
CIR
Co-repressor
HDAC
Ras/MAPK
MAPK signaling pathway
Gene expression
04330 3/31/09
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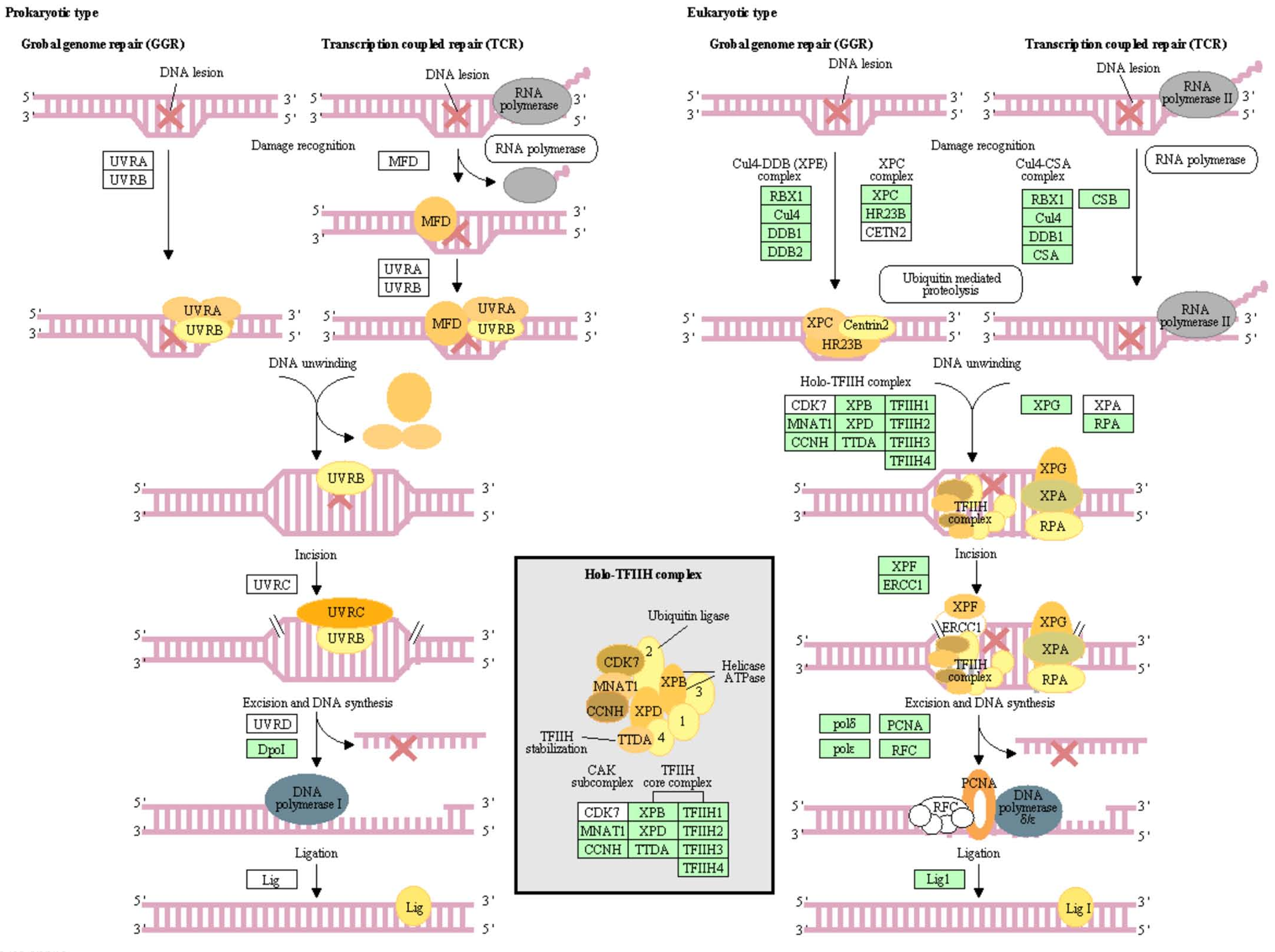
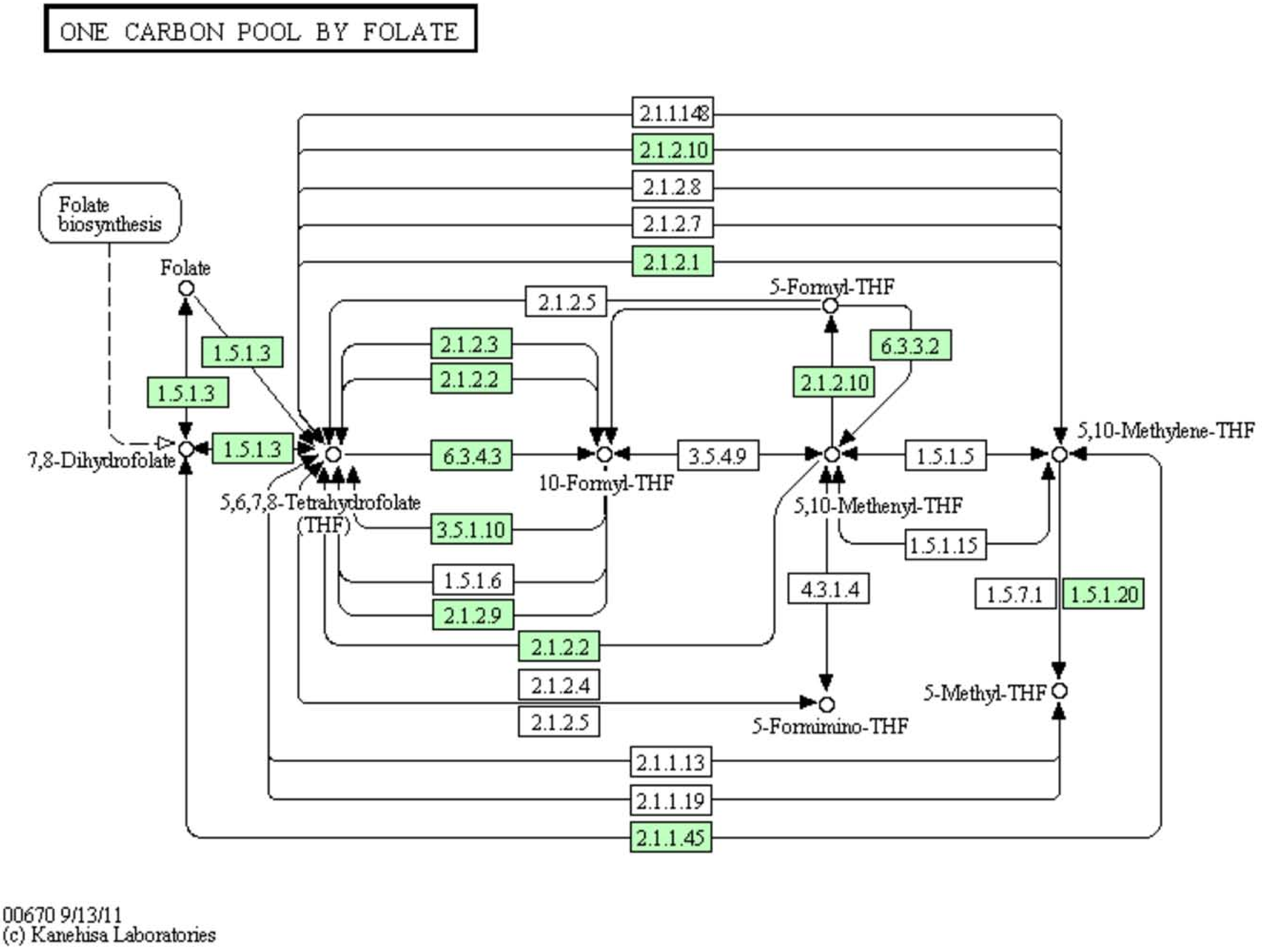
NUCLEOTIDE EXCISION REPAIR




ONE CARBON POOL BY FOLATE
Folate biosynthesis
Folate
7,8-Dihydrofolate
5,6,7,8-Tetrahydrofolate (THF)
10-Formyl-THF
5-Formyl-THF
5,10-Methenyl-THF
5,10-Methylene-THF
5-Methyl-THF
5-Formimino-THF
2.1.1.148
2.1.2.10
2.1.2.8
2.1.2.7
2.1.2.1
2.1.2.5
6.3.3.2
2.1.2.3
2.1.2.2
1.5.1.3
1.5.1.3
1.5.1.3
2.1.2.10
6.3.4.3
3.5.4.9
1.5.1.5
3.5.1.10
1.5.1.15
1.5.1.6
4.3.1.4
1.5.7.1
1.5.1.20
2.1.2.9
2.1.2.2
2.1.2.4
2.1.2.5
2.1.1.13
2.1.1.19
2.1.1.45
00670 9/13/11
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OOCYTE MEIOSIS
INS
IGF1
Progesterone
Progesterone-mediated oocyte maturation
IGF1R
?
PGR
AR
AC
Aurora-A
Xenopus oocyte
cAMP
+p
CPEB
PKA
MAPK signaling pathway
Early translation of maternal mRNAs
Mos
MEK1
p42MAPK
Rsk1/2
C3H-4
Ringo
Cdc2
Cdk2
Xp38γ
PP1
Plk1
SCF
β-TrCP
Emi1
Myt1
14-3-3
Cdc25C
Plkk1
APC/C
Cdc20
Ubiquitin mediated proteolysis
+u
-p
MPF
CycB2/B5
Cdc2
Prevent DNA replication
Bipolar spindle formation
Meiosis I progression
Dgradation of CycB
Meiosis I exit
SCF
β-TrCP
Emi2
APC/C
Cdc20
Securin
Separase
Arm cohesin
Rec8
STAG3
SMC1
SMC3
Plk1
CPEB
Late translation of maternal mRNAs
Late-late translation of maternal mRNAs
Bub1
Mad1/2
CycE
Cdk2
APC/C
Cdc20
MPF
CycB1/B4
Cdc2
Meiosis II arrest
Dgradation of CycB
Meiosis II resumption
Sgo
B56
PP2A
Securin
Separase
Pericentromeric cohesin
Rec8
STAG3
SMC1
SMC3
Meiosis II exit
Fertilization
Plc-ζ
IP_3
IP_3R
Ca^{2+}
Calm
CaN
CamKII
Plk1
PP2A
SCF
β-TrCP
Emi2
Cdc25C
Delay to reentry into Meiosis
Prophase I
GVBD
Meiosis I
Interkinesis
Meiosis II
04114 5/29/13
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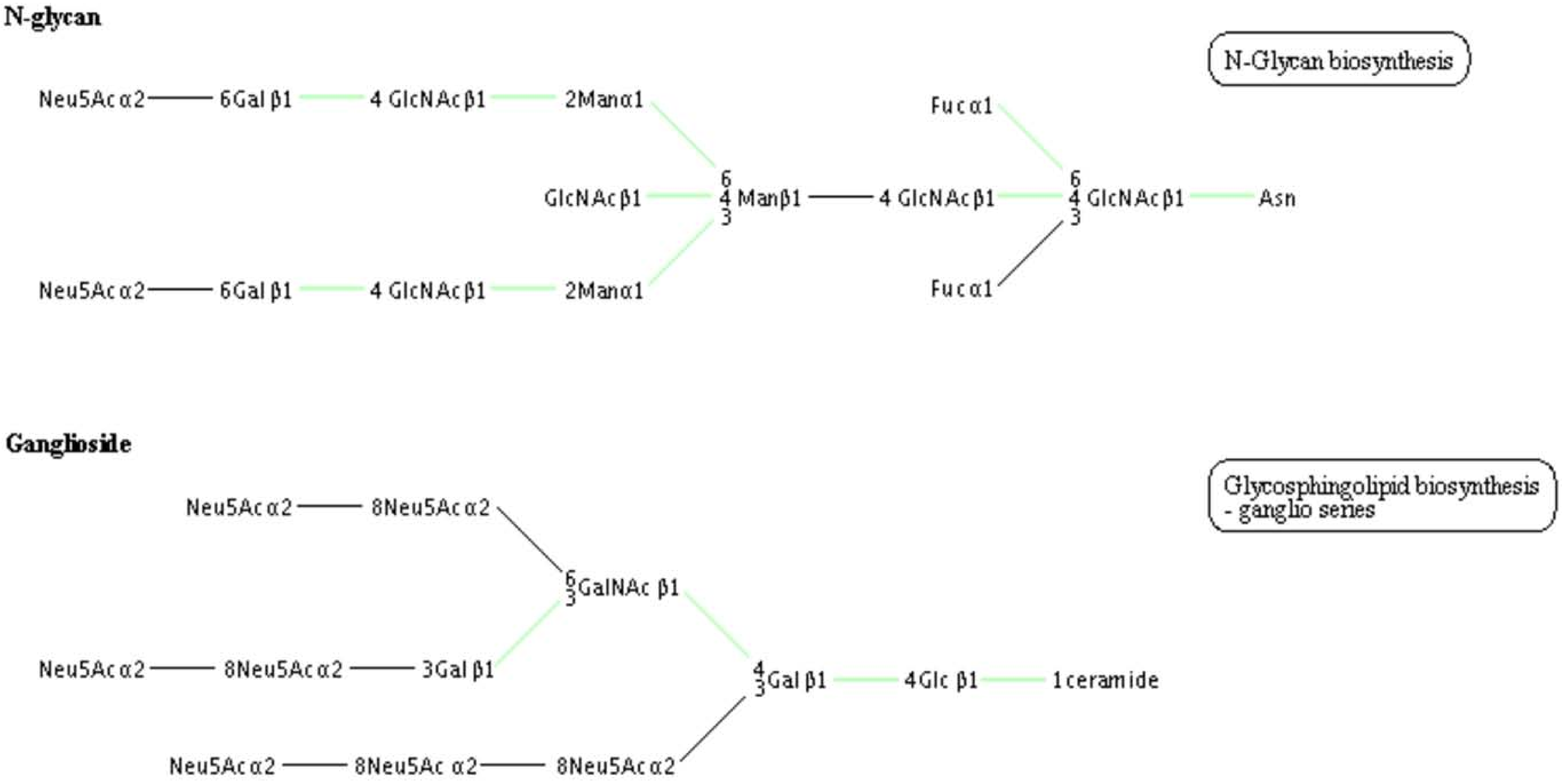
OTHER GLYCAN DEGRADATION



00511 6/3/13

OXIDATIVE PHOSPHORYLATION

NADH dehydrogenase

E	ND1	ND2	ND3	ND4	ND4L	ND5	ND6										
E	Ndufs1	Ndufs2	Ndufs3	Ndufs4	Ndufs5	Ndufs6	Ndufs7	Ndufs8	Ndufv1	Ndufv2	Ndufv3						
B/A	NuoA	NuoB	NuoC	NuoD	NuoE	NuoF	NuoG	NuoH	NuoI	NuoJ	NuoK	NuoL	NuoM	NuoN			
B/A	NdhC	NdhK	NdhJ	NdhH	NdhA	NdhI	NdhG	NdhE	NdhF	NdhD	NdhB	NdhL	NdhM	NdhN	HoxE	HoxF	HoxU
E	Ndufa1	Ndufa2	Ndufa3	Ndufa4	Ndufa5	Ndufa6	Ndufa7	Ndufa8	Ndufa9	Ndufa10	Ndufab1	Ndufa11	Ndufa12	Ndufa13			
E	Ndufb1	Ndufb2	Ndufb3	Ndufb4	Ndufb5	Ndufb6	Ndufb7	Ndufb8	Ndufb9	Ndufb10	Ndufb11	Ndufc1	Ndufc2				

Succinate dehydrogenase / Fumarate reductase

E	SDHC	SDHD	SDHA	SDHB
B/A	SdhC	SdhD	SdhA	SdhB
		FrdA	FrdB	FrdC	FrdD

Cytochrome c reductase

E/B/A	ISP	Cytb	Cyt1						
E				COR1	QCR2	QCR6	QCR7	QCR8	QCR9	QCR10

Cytochrome c oxidase

														E/B/A		
E	COX10	COX3	COX1	COX2	COX4	COX5A	COX5B	COX6A	COX6B	COX6C	COX7A	COX7B	COX7C	COX8	COX11	COX15	COX17
B/A	CyoE	CyoD	CyoC	CyoB	CyoA											
		CoxD	CoxC	CoxA	CoxB											
		QoxD	QoxC	QoxB	QoxA											

Cytochrome c oxidase , cbb3-type

B	I	II	IV	III

Cytochrome bd complex

B/A	CydA	CydB

F-type ATPase (Bacteria)

beta	alpha	gamma	delta	epsilon	c	a	b

F-type ATPase (Eukaryotes)

beta	alpha	gamma	OSCP	delta	epsilon	c	a
b	e	f6	f	8			
d	f	h	j	k	g		

V-type ATPase (Prokaryotes)

A	B	C	D	E	F	I	K

V-type ATPase (Eukaryotes)

A	B	C	D	E	F	G	H
I	AC39	54kD	S1	lipid			

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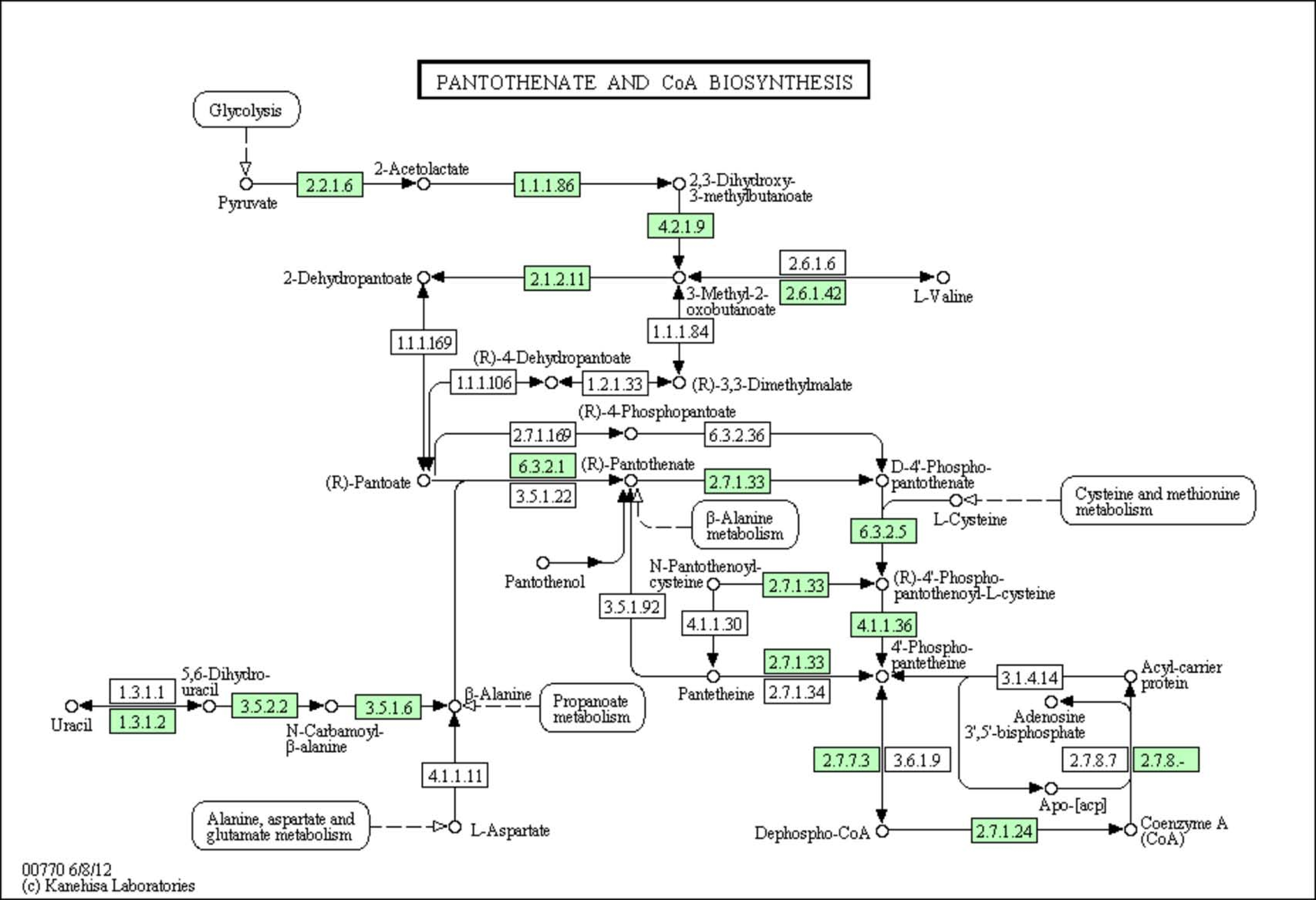
PANTOTHENATE AND CoA BIOSYNTHESIS
Glycolysis
Pyruvate
2.2.1.6
2-Acetolactate
1.1.1.86
2,3-Dihydroxy-3-methylbutanoate
4.2.1.9
2-Dehydropantoate
2.1.2.11
2.6.1.6
2.6.1.42
L-Valine
3-Methyl-2-oxobutanoate
1.1.1.84
1.1.1.169
(R)-4-Dehydropantoate
1.1.1.106
1.2.1.33
(R)-3,3-Dimethylmalate
(R)-4-Phosphopantoate
2.7.1.169
6.3.2.36
6.3.2.1
(R)-Pantothenate
(R)-Pantoate
3.5.1.22
2.7.1.33
D-4'-Phosphopantothenate
Cysteine and methionine metabolism
L-Cysteine
β-Alanine metabolism
6.3.2.5
Pantothenol
N-Pantothenoyl-cysteine
2.7.1.33
(R)-4'-Phosphopantothenoyl-L-cysteine
3.5.1.92
4.1.1.30
4.1.1.36
4'-Phosphopantetheine
2.7.1.33
3.1.4.14
Acyl-carrier protein
Pantetheine
2.7.1.34
5,6-Dihydrouracil
1.3.1.1
1.3.1.2
Uracil
3.5.2.2
3.5.1.6
β-Alanine
Propanoate metabolism
N-Carbamoyl-β-alanine
Adenosine 3',5'-bisphosphate
2.7.7.3
3.6.1.9
2.7.8.7
2.7.8.-
4.1.1.11
Apo-[acp]
Alanine, aspartate and glutamate metabolism
L-Aspartate
Dephospho-CoA
2.7.1.24
Coenzyme A (CoA)
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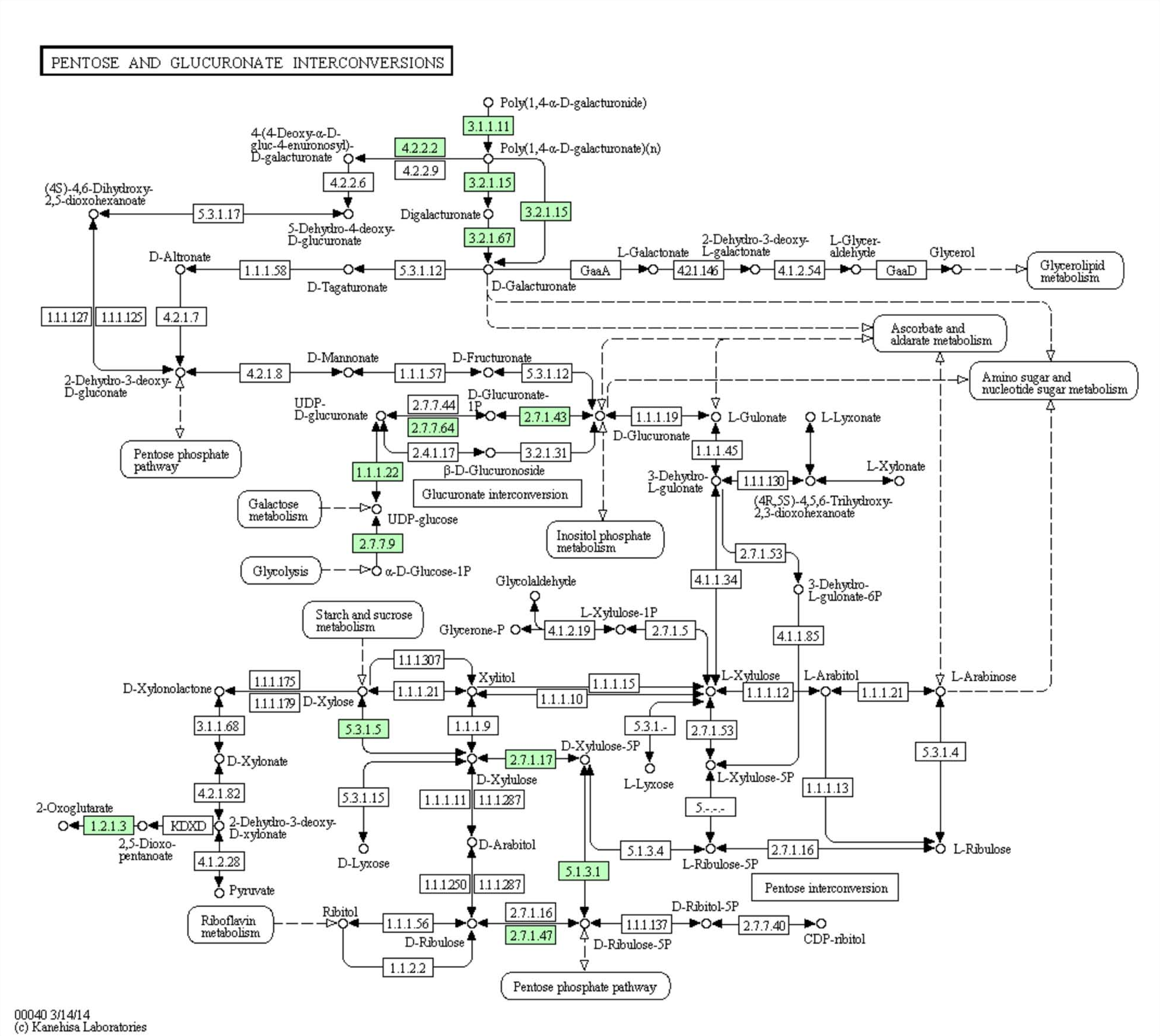
PENTOSE AND GLUCURONATE INTERCONVERSIONS
Poly(1,4-α-D-galacturonide)
3.1.1.11
Poly(1,4-α-D-galacturonate)(n)
4-(4-Deoxy-α-D-gluc-4-enuronosyl)-D-galacturonate
4.2.2.2
4.2.2.9
4.2.2.6
3.2.1.15
3.2.1.15
(4S)-4,6-Dihydroxy-2,5-dioxohexanoate
5.3.1.17
5-Dehydro-4-deoxy-D-glucuronate
Digalacturonate
3.2.1.67
D-Altronate
1.1.1.58
D-Tagaturonate
5.3.1.12
D-Galacturonate
GaaA
L-Galactonate
4.2.1.146
2-Dehydro-3-deoxy-L-galactonate
4.1.2.54
L-Glycer-aldehyde
GaaD
Glycerol
Glycerolipid metabolism
1.1.1.127
1.1.1.125
4.2.1.7
Ascorbate and aldarate metabolism
D-Mannonate
D-Fructuronate
2-Dehydro-3-deoxy-D-gluconate
4.2.1.8
1.1.1.57
5.3.1.12
Amino sugar and nucleotide sugar metabolism
UDP-D-glucuronate
2.7.7.44
D-Glucuronate-1P
2.7.1.43
1.1.1.19
L-Gulonate
L-Lyxonate
2.7.7.64
D-Glucuronate
Pentose phosphate pathway
2.4.1.17
3.2.1.31
1.1.1.45
β-D-Glucuronoside
L-Xylonate
1.1.1.22
3-Dehydro-L-gulonate
1.1.1.130
Glucuronate interconversion
(4R,5S)-4,5,6-Trihydroxy-2,3-dioxohexanoate
Galactose metabolism
UDP-glucose
Inositol phosphate metabolism
2.7.7.9
2.7.1.53
Glycolysis
α-D-Glucose-1P
4.1.1.34
3-Dehydro-L-gulonate-6P
Glycolaldehyde
L-Xylulose-1P
Starch and sucrose metabolism
Glycerone-P
4.1.2.19
2.7.1.5
4.1.1.85
1.1.1.307
Xylitol
1.1.1.15
L-Xylulose
L-Arabitol
L-Arabinose
D-Xylonolactone
1.1.1.175
1.1.1.179
D-Xylose
1.1.1.21
1.1.1.10
1.1.1.12
1.1.1.21
3.1.1.68
5.3.1.5
1.1.1.9
5.3.1.-
2.7.1.53
5.3.1.4
D-Xylonate
2.7.1.17
D-Xylulose-5P
D-Xylulose
L-Lyxose
L-Xylulose-5P
4.2.1.82
5.3.1.15
1.1.1.11
1.1.1.287
1.1.1.13
2-Oxoglutarate
1.2.1.3
KDXD
2-Dehydro-3-deoxy-D-xylonate
5.-.-.-
2,5-Dioxo-pentanoate
D-Arabitol
4.1.2.28
D-Lyxose
5.1.3.4
L-Ribulose-5P
2.7.1.16
L-Ribulose
5.1.3.1
Pyruvate
1.1.1.250
1.1.1.287
Pentose interconversion
Riboflavin metabolism
Ribitol
1.1.1.56
2.7.1.16
D-Ribitol-5P
1.1.1.137
2.7.7.40
CDP-ribitol
D-Ribulose
2.7.1.47
D-Ribulose-5P
1.1.2.2
Pentose phosphate pathway
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PENTOSE PHOSPHATE PATHWAY

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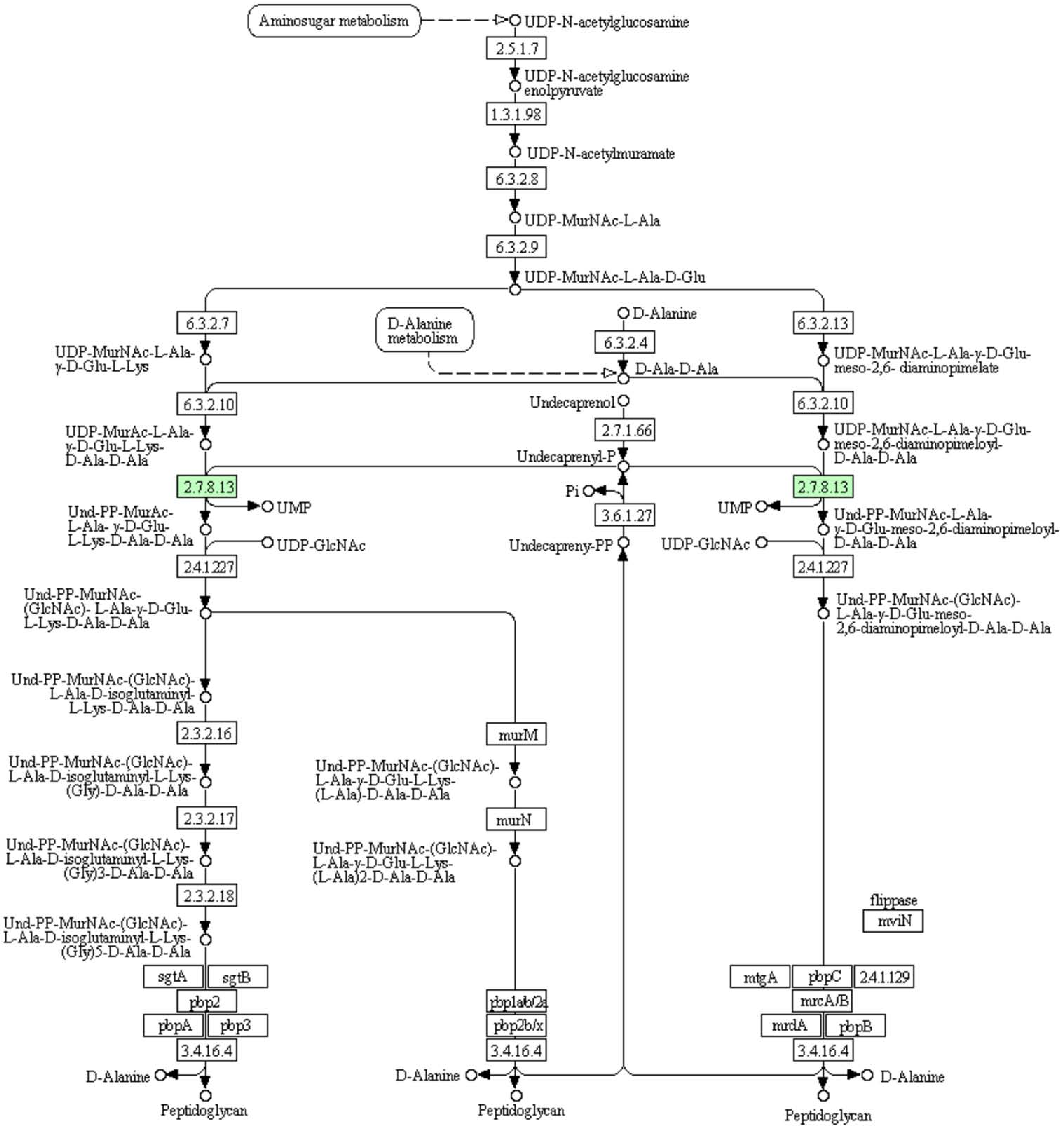
PEPTIDOGLYCAN BIOSYNTHESIS



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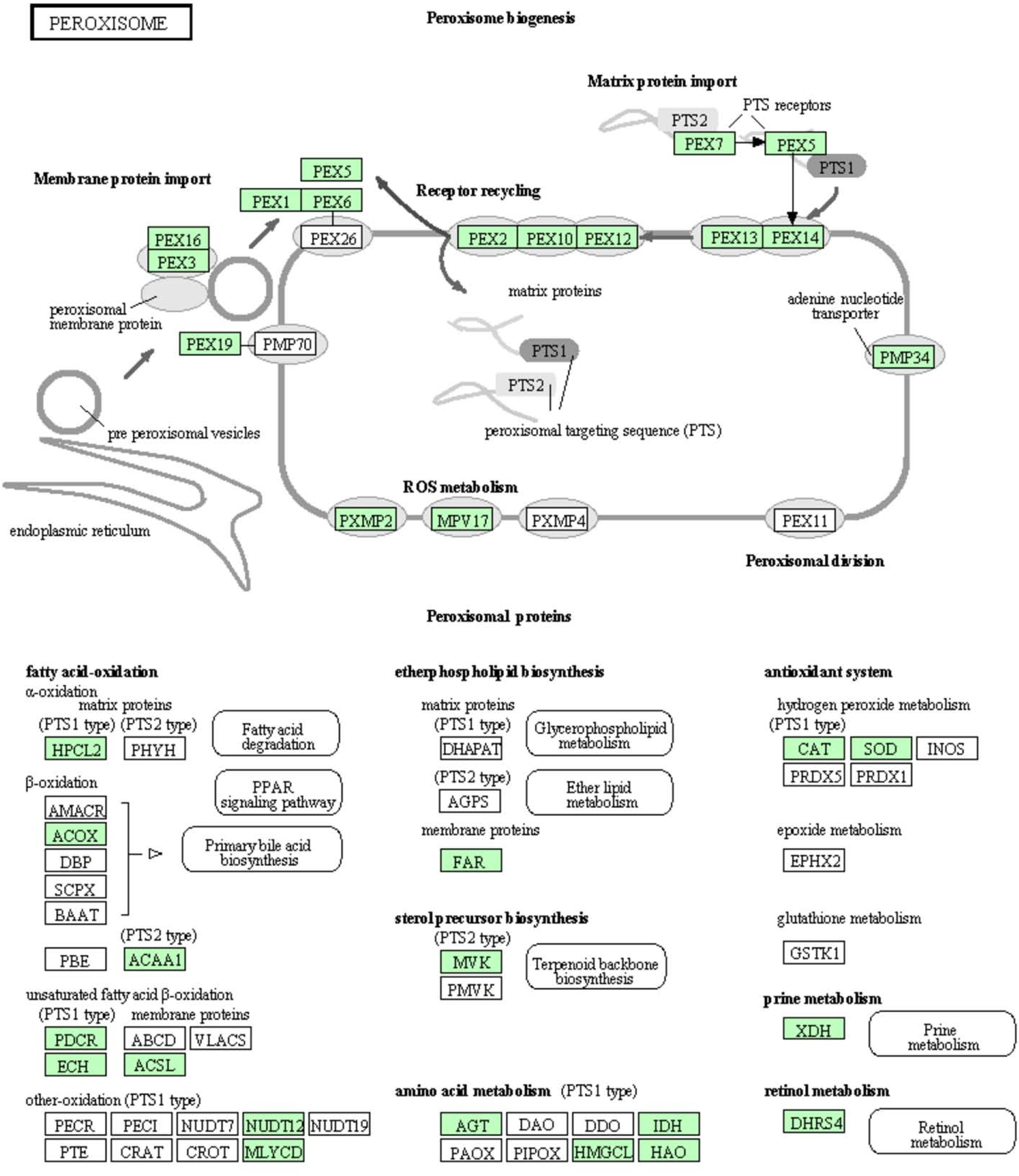
PEROXISOME
Peroxisome biogenesis
Matrix protein import
PTS2
PTS receptors
PEX7
PEX5
PTS1
Membrane protein import
PEX5
PEX1
PEX6
Receptor recycling
PEX16
PEX3
PEX26
PEX2
PEX10
PEX12
PEX13
PEX14
peroxisomal membrane protein
matrix proteins
adenine nucleotide transporter
PEX19
PMP70
PTS1
PMP34
PTS2
pre peroxisomal vesicles
peroxisomal targeting sequence (PTS)
ROS metabolism
endoplasmic reticulum
PXMP2
MPV17
PXMP4
PEX11
Peroxisomal division
Peroxisomal proteins
fatty acid-oxidation
α-oxidation
matrix proteins
(PTS1 type)
(PTS2 type)
HPCL2
PHYH
Fatty acid degradation
β-oxidation
PPAR signaling pathway
AMACR
ACOX
DBP
SCPX
BAAT
Primary bile acid biosynthesis
(PTS2 type)
PBE
ACAA1
unsaturated fatty acid β-oxidation
(PTS1 type)
membrane proteins
PDCR
ECH
ABCD
VLACS
ACSL
other-oxidation (PTS1 type)
PECR
PECI
NUDT7
NUDT12
NUDT19
PTE
CRAT
CROT
MLYCD
etherphospholipid biosynthesis
matrix proteins
(PTS1 type)
DHAPAT
Glycerophospholipid metabolism
(PTS2 type)
AGPS
Ether lipid metabolism
membrane proteins
FAR
sterol precursor biosynthesis
(PTS2 type)
MVK
PMVK
Terpenoid backbone biosynthesis
amino acid metabolism (PTS1 type)
AGT
DAO
DDO
IDH
PAOX
PIPOX
HMGCL
HAO
antioxidant system
hydrogen peroxide metabolism
(PTS1 type)
CAT
SOD
INOS
PRDX5
PRDX1
epoxide metabolism
EPHX2
glutathione metabolism
GSTK1
prine metabolism
XDH
Prine metabolism
retinol metabolism
DHRS4
Retinol metabolism

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PHENYLALANINE METABOLISM
Phenylalanine, tyrosine and tryptophan biosynthesis
Tropane, piperidine and pyridine alkaloid biosynthesis
Tyrosine
1.14.16.1
Tyrosine metabolism
Phenylalanine
5.1.1.11
D-Phenylalanine
2.3.1.36
N-Acetyl-D-phenylalanine
4.3.1.24
4.3.1.25
2.3.1.53
N-Acetyl-L-phenylalanine
1.4.1.20
2.6.1.1
2.6.1.5
2.6.1.9
2.6.1.57
2.6.1.58
1.4.3.2
1.4.99.1
2.6.1.21
4.1.1.28
4.1.1.53
Phenylethylamine
1.4.3.4
1.4.3.21
1.4.9.2
4.1.1.43
4.1.1.-
Phenylpyruvate
5.3.2.1
2-Hydroxy-3-phenylpropanoate
1.1.1.222
1.1.1.237
Phenyllactate
1.13.12.9
1.11.1.7
1.11.1.21
1.13.11.27
Phenylacetaldehyde
1.1.1.90
Phenylethylalcohol
1.2.1.5
1.2.1.39
2-Phenylacetamide
3.5.1.4
Phenylacetate
1.14.13.-
2-Hydroxyphenylacetate
Styrene degradation
2,6-Dihydroxyphenylacetate
4-Hydroxyphenylacetate
3-Hydroxyphenylacetate
3.1.2.-
6.2.1.30
Phenylacetyl-CoA
1.17.5.1
Phenylglyoxylyl-CoA
3.1.2.25
Phenylglyoxylate
1.2.1.58
Benzoyl-CoA
Benzoate degradation
2-Oxepin-2(3H)-ylideneacetyl-CoA
3-Oxo-5,6-dehydrosuberyl-CoA
1.14.13.149
5.3.3.18
3.3.2.12
1.17.1.7
2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA
3-Oxo-5,6-dehydrosuberyl-CoA semialdehyde
PaaJ/G
Acetyl-CoA
2.3.1.192
2.3.1.13
2.3.1.14
Phenylacetylglycine
Phenylacetylglutamine
3-Oxoadipyl-CoA
1.1.1.157
PaaF
(3S)-3-Hydroxyadipyl-CoA
2,3-Dehydroadipyl-CoA
PaaJ
Succinyl-CoA
Citrate cycle
1-Phenylpropane-1,2-dione
2.6.1.-
Cathinone
Norpseudoephedrine
2.1.1.-
Pseudoephedrine
Norephedrine
2.1.1.-
Ephedrine
1.5.1.18
(R)-2-Methylimino-1-phenylpropan-1-ol
Salicylate
1.14.13.-
Benzoate
3.5.1.32
Hippurate
2.3.1.71
Benzoyl-CoA
Benzoate degradation
1.14.13.11
trans-Cinnamate
1.14.13.14
trans-2-Hydroxycinnamate
trans-4-Hydroxycinnamate
1.3.1.31
1.3.1.11
Phenylpropanoate
3-Hydroxyphenylpropanoate
2-Hydroxyphenylpropanoate
6.2.1.12
4-Coumaroyl-CoA
4-Hydroxybenzoate
trans-3-Hydroxycinnamate
1.14.12.19
1.14.12.19
1.14.13.-
CI-dihydrodiol
PP-dihydrodiol
1.14.13.127
1.14.13.127
1.14.13.4
Caffeoyl-CoA
2.1.1.104
Benzoate degradation
1.3.1.87
1.3.1.87
trans-2,3-Dihydroxycinnamate
2,3-Dihydroxyphenylpropanoate
Feruloyl-CoA
1.13.11.16
1.13.11.16
4.2.1.101
Valine, leucine, isoleucine degradation
2-Hydroxy-6-oxononatrienedioate
2-Hydroxy-6-oxonona-2,4-diene-1,9-dioate
4-Hydroxy-3-methoxyphenyl-beta-hydroxypropionyl-CoA
3.7.1.-
3.7.1.-
Succinate
Citrate cycle
4.1.2.41
Isobutyryl-CoA
cis-2-Hydroxypenta-2,4-dienoate
Vanillin
Malonyl-CoA
Fumarate
4.2.1.80
4-Hydroxy-2-oxovalerate
Vanillylamine
8-Methyl-6-nonenoic acid
4.1.3.39
Acetaldehyde
Pyruvate metabolism
Pyruvate
Capsaicin
Glycolysis
00360 6/17/13
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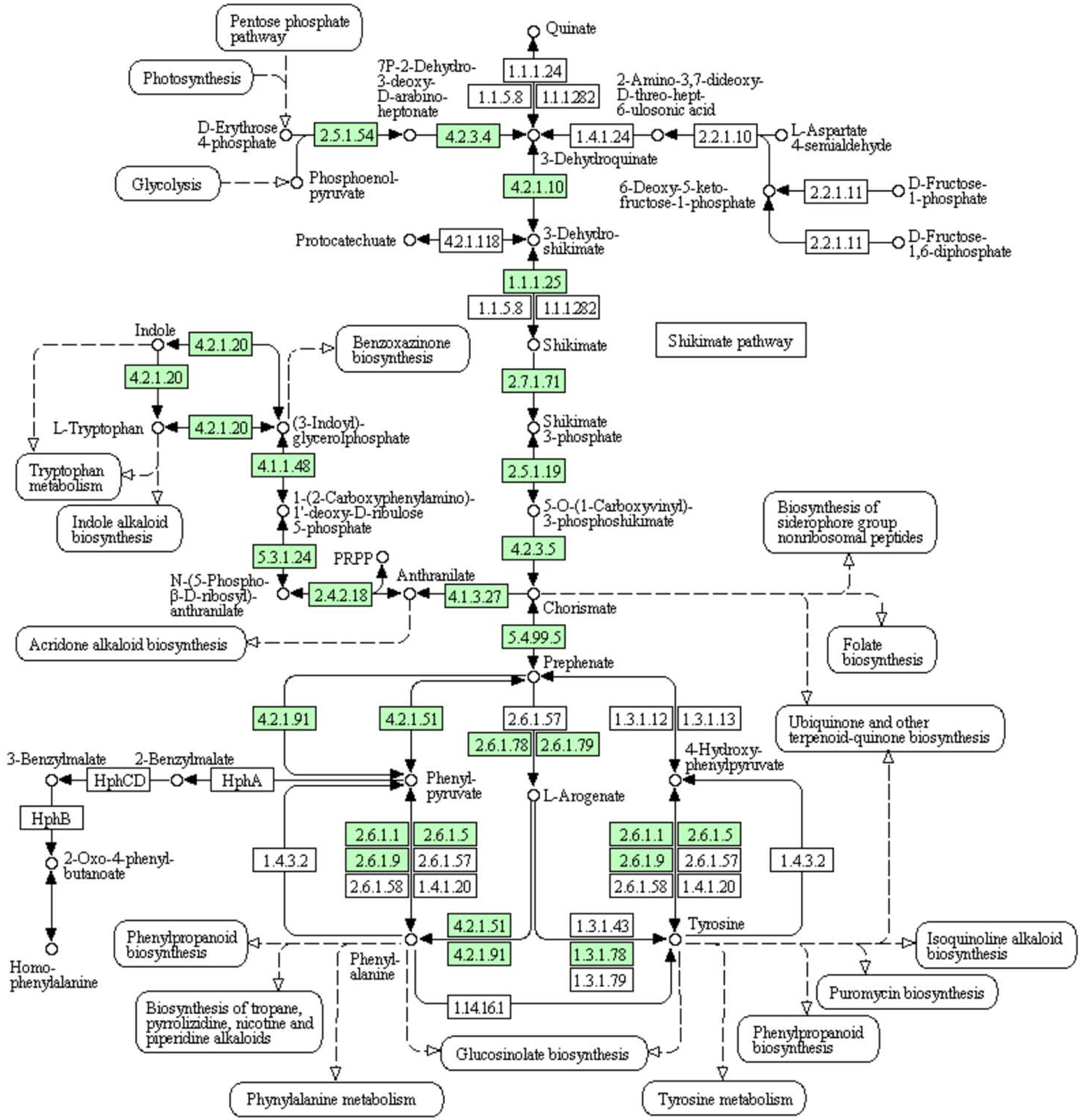
PHENYLALANINE, TYROSINE AND TRYPTOPHAN BIOSYNTHESIS



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PHENYLPROPANOID BIOSYNTHESIS
Spermidine
Phenylalanine,tyrosine and tryptophan biosynthesis
N1,N5,N10-Tricoumaroyl-spermidine
1.14.13.-
N1,N5,N10-Tricaffeoyl-spermidine
2.1.1.-
N1,N5,N10-Triferuloyl-spermidine
1.14.13.-
N1,N5,N10-Tri-(hydroxyferuloyl)-spermidine
2.1.1.-
N1,N5-Di(hydroxyferuloyl)-N10-sinapoyl-spermidine
Phenylalanine
Tyrosine
4.3.1.24
4.3.1.25
4.3.1.23
4.3.1.25
3-(2-Carboxyethenyl)-cis,cis-muconate
1.13.11.22
Scopoletin
2.4.1.128
Scopolin
Cinnamic acid
1.14.13.11
p-Coumaric acid
1.14.13.-
Caffeic-acid
2.1.1.68
Ferulic acid
F5H
5-Hydroxyferulic acid
2.1.1.68
Sinapic acid
2.4.1.120
1-O-Sinapoyl-β-D-glucose
2.3.1.92
Sinapoyl-malate
2.3.1.91
3.1.1.49
Sinapoyl-choline
1.14.13.14
4.1.1.-
4-Hydroxystyrene
4.1.1.-
3,4-Dihydroxy-styrene
6.2.1.12
6.2.1.12
6.2.1.12
6.2.1.12
6.2.1.12
6.2.1.12
2.3.1.133
1.14.13.36
2.3.1.133
p-Coumaroyl shikimic acid
Caffeoyl shikimic acid
trans-2-Hydroxy-cinnamate
Cinnamoyl-CoA
1.14.13.11
p-Coumaroyl-CoA
1.14.13.-
Caffeoyl-CoA
2.1.1.104
Feruloyl-CoA
5-Hydroxy-feruloyl-CoA
2.1.1.104
Sinapoyl-CoA
2.4.1.114
2.3.1.99
1.2.1.68
1.2.1.68
p-Coumaroyl quinic acid
2.3.1.133
1.14.13.36
2.3.1.133
Caffeoyl quinic acid
β-D-Glucosyl-2-coumarate
1.2.1.44
1.2.1.44
1.2.1.44
1.2.1.44
1.2.1.44
1.2.1.44
5.2.1.-
Coniferyl-aldehyde
5-Hydroxy-coniferaldehyde
Caffeyl-aldehyde
p-Coumaraldehyde
1.14.13.-
2.1.1.68
F5H
2.1.1.68
Sinapaldehyde
Cinnamaldehyde
β-D-Glucosyl-2-coumarinate
Flavonoid biosynthesis
1.1.1.195
1.1.1.195
1.1.1.195
1.1.1.195
1.1.1.195
3.2.1.21
Stilbenoid,diarylheptanoid and gingerol biosynthesis
p-Coumaryl alcohol
Caffeyl-alcohol
2.1.1.68
Coniferyl-alcohol
F5H
5-Hydroxy-coniferyl alcohol
2.1.1.68
Sinapyl alcohol
p-Coumaryl acetate
CFAT
Coniferyl acetate
CFAT
Coumarinate
3.2.1.126
3.2.1.126
3.2.1.126
1.1.1.318
1.1.1.319
1.11.1.7
1.11.1.21
1.1.1.318
1.1.1.319
1.11.1.7
1.11.1.21
1.11.1.7
1.11.1.21
1.11.1.7
1.11.1.21
2.4.1.111
2.4.1.111
2.4.1.111
Chavicol
Isochavicol
Eugenol
Isoeugenol
Coumarine
2.1.1.146
2.1.1.279
2.1.1.146
2.1.1.146
2.1.1.279
p-Hydroxy-phenyl lignin
4-Hydroxycinnamyl-alcohol 4-D-glucoside
Guaiacyl lignin
Coniferin
5-Hydroxy-guaiacyl lignin
Syringyl lignin
Syringin
Methylchavicol
Anethole
Methyleugenol
Isomethyleugenol
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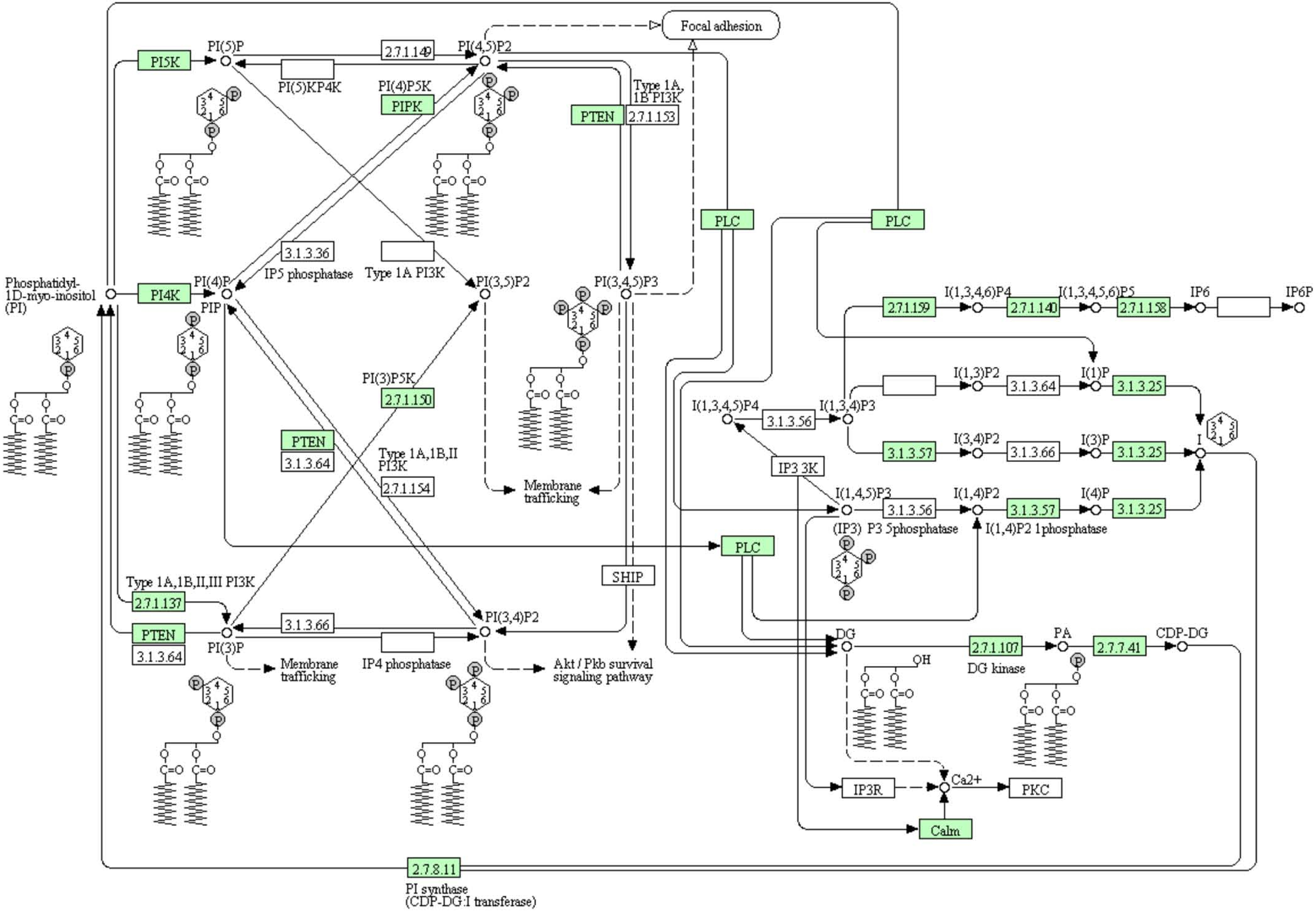
PHOSPHATIDYLINOSITOL SIGNALING SYSTEM



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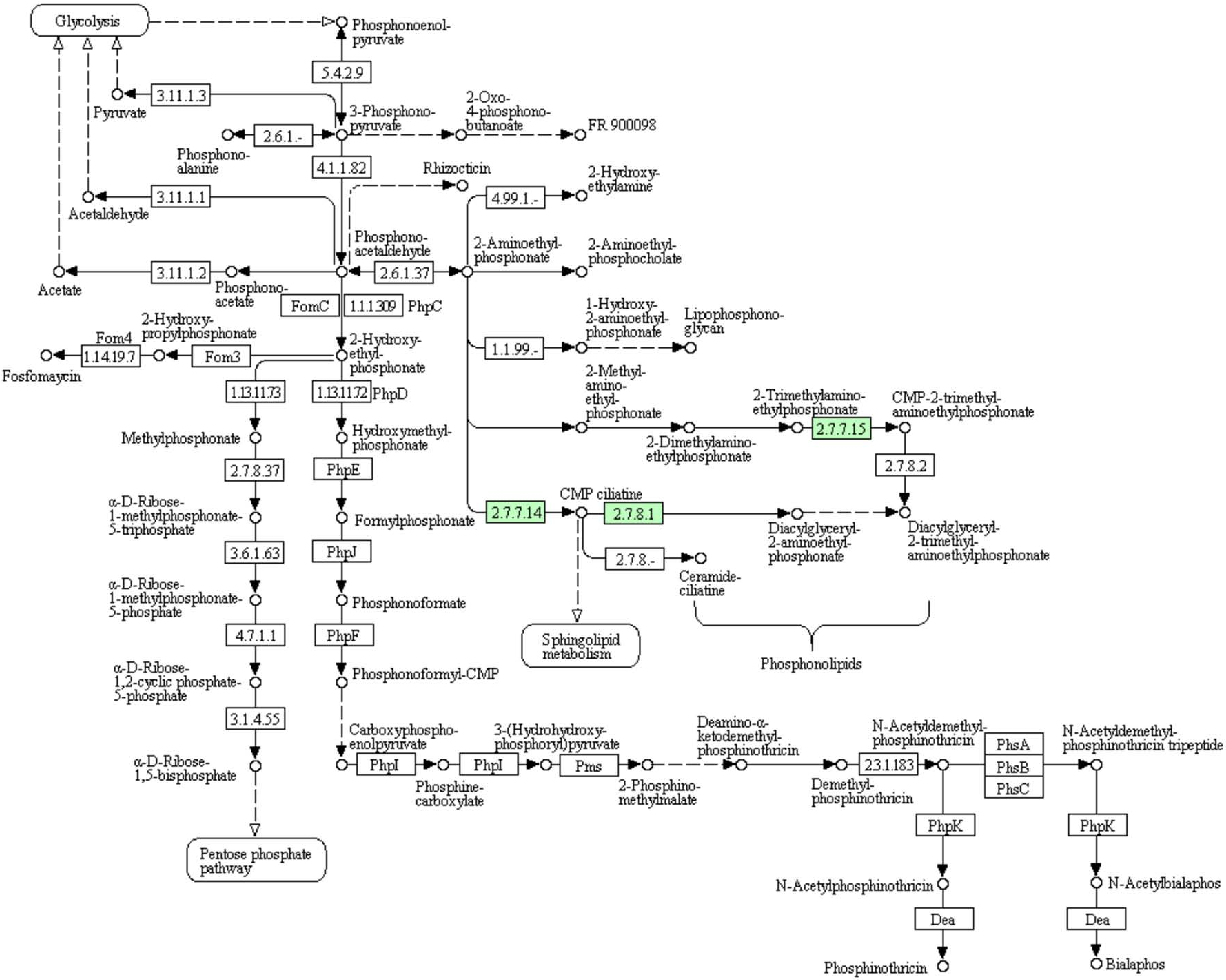
PHOSPHONATE AND PHOSPHINATE METABOLISM



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PHOTOSYNTHESIS - ANTENNA PROTEINS

Allophycocyanin(AP)

ApcA	ApcB	ApcC	ApcD	ApcE	ApcF

Phycocyanin(PC) / Phycoerythrocyanin(PEC)

CpcA	CpcB	CpcC	CpcD	CpcE	CpcF	CpcG

Phycoerythrin(PE)

CpeA	CpeB	CpeC	CpeD	CpeE	CpeR	CpeS	CpeT	CpeU	CpeY	CpeZ

Light-harvesting chlorophyll protein complex(LHC)

Lhca1	Lhca2	Lhca3	Lhca4	Lhca5

Lhcb1	Lhcb2	Lhcb3	Lhcb4	Lhcb5	Lhcb6	Lhcb7

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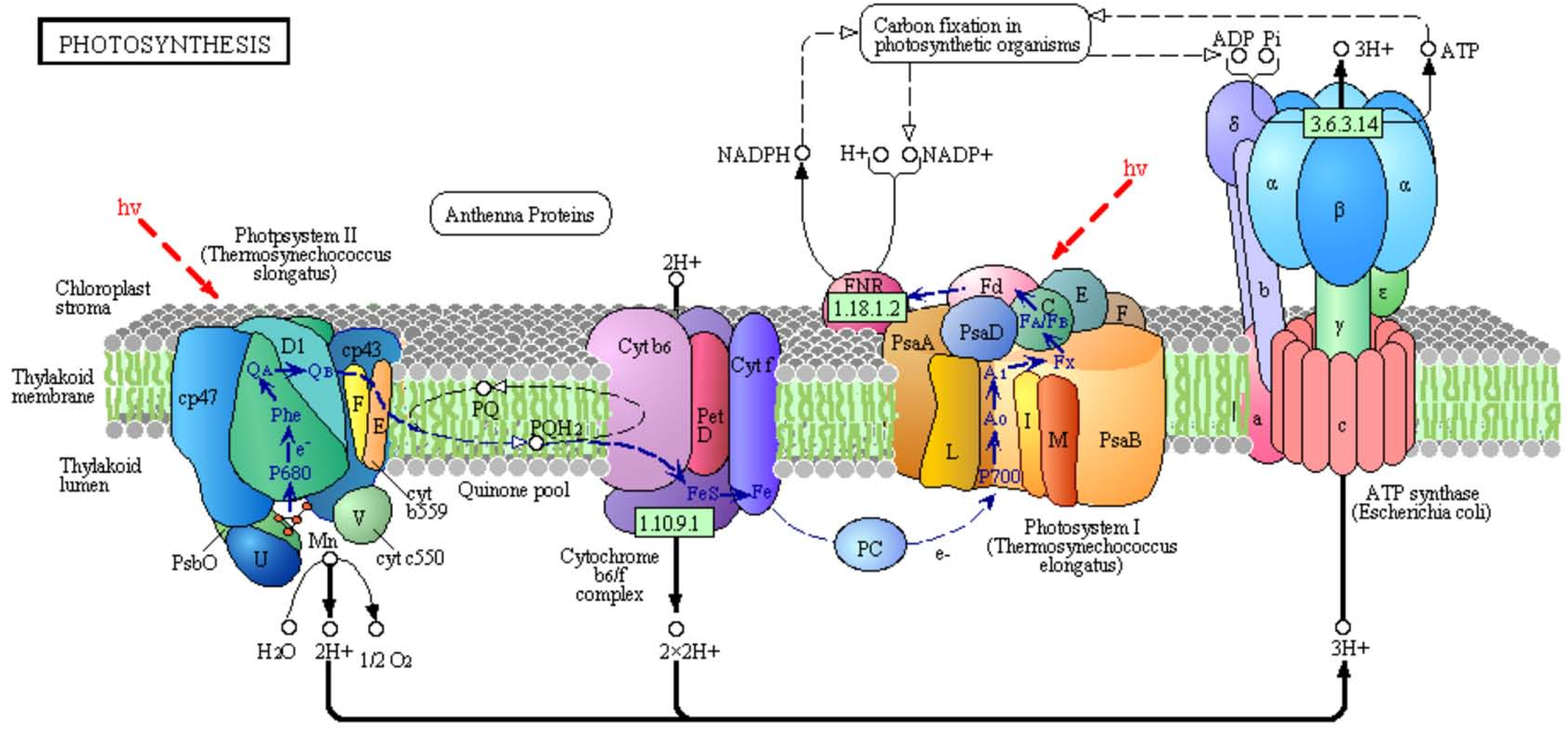
PHOTOSYNTHESIS



Photosystem II

D1	D2	cp43	cp47	cyt b559	
PsbA	PsbD	PsbC	PsbB	PsbE	PsbF

						MSP	OEC
Psb L	Psb J	Psb K	Psb M	Psb H	Psb I	Psb O	Psb P
Psb Q	Psb R	Psb S	Psb T	Psb U	Psb V	Psb W	Psb X
Psb Y	Psb Z	Psb 27	Psb 28	Psb28-2			

Photosystem I

PsaA	PsaB	PsaC	PsaD	PsaE	PsaF	PsaG	PsaH
PsaI	PsaJ	PsaK	PsaL	PsaM	PsaN	PsaO	PsaX

Cytochrome b6/f complex

PetB	PetD	PetA	PetC	PetL	PetM	PetN	PetG

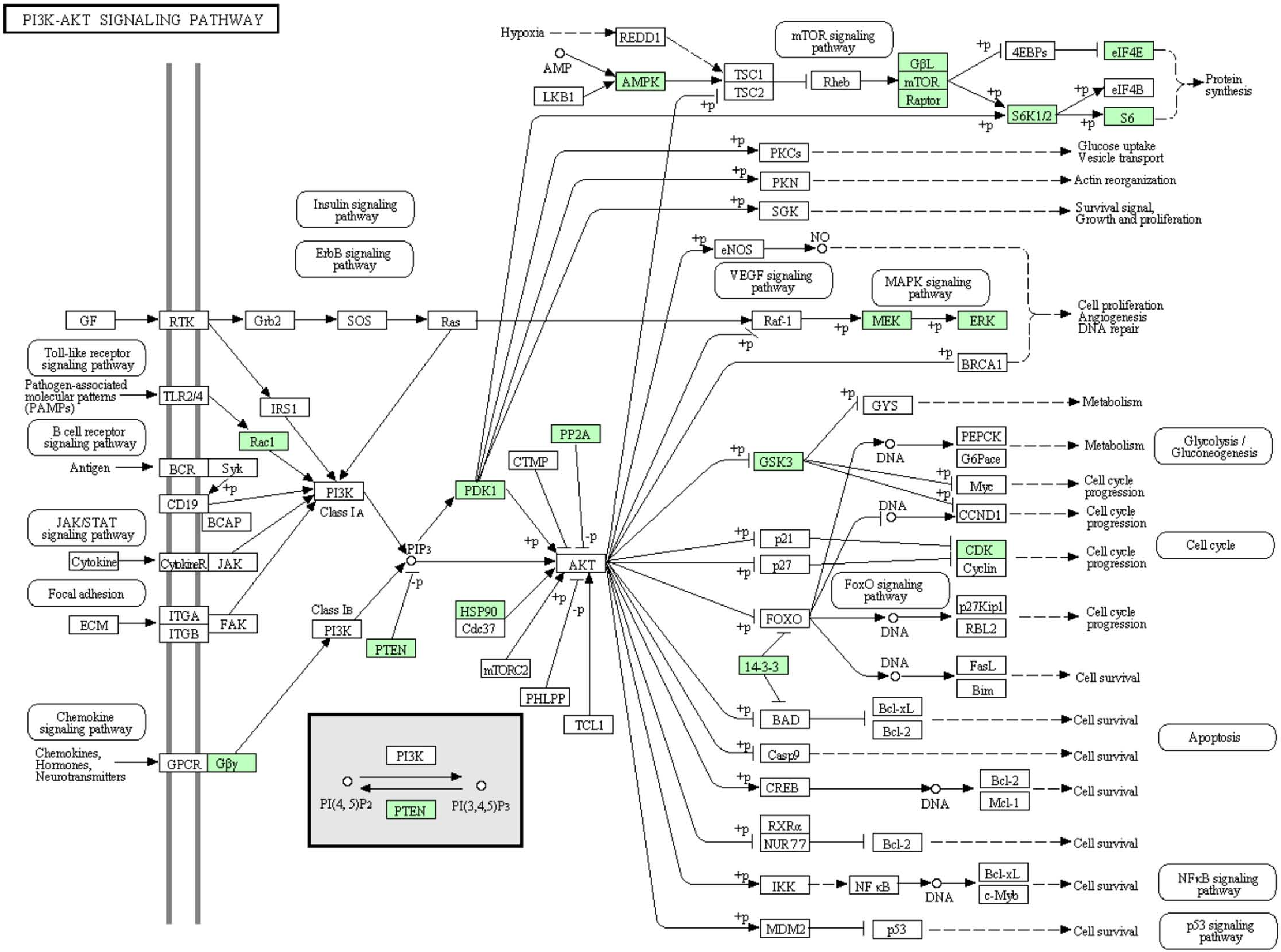
Photosynthethic electron transport

PC	Fd	FNR	cyt c6
PetE	PetF	PetH	PetJ

F-type ATPase

beta	alpha	gamma	delta	epsilon	c	a	b

00195 1/15/14



04151 12/26/13
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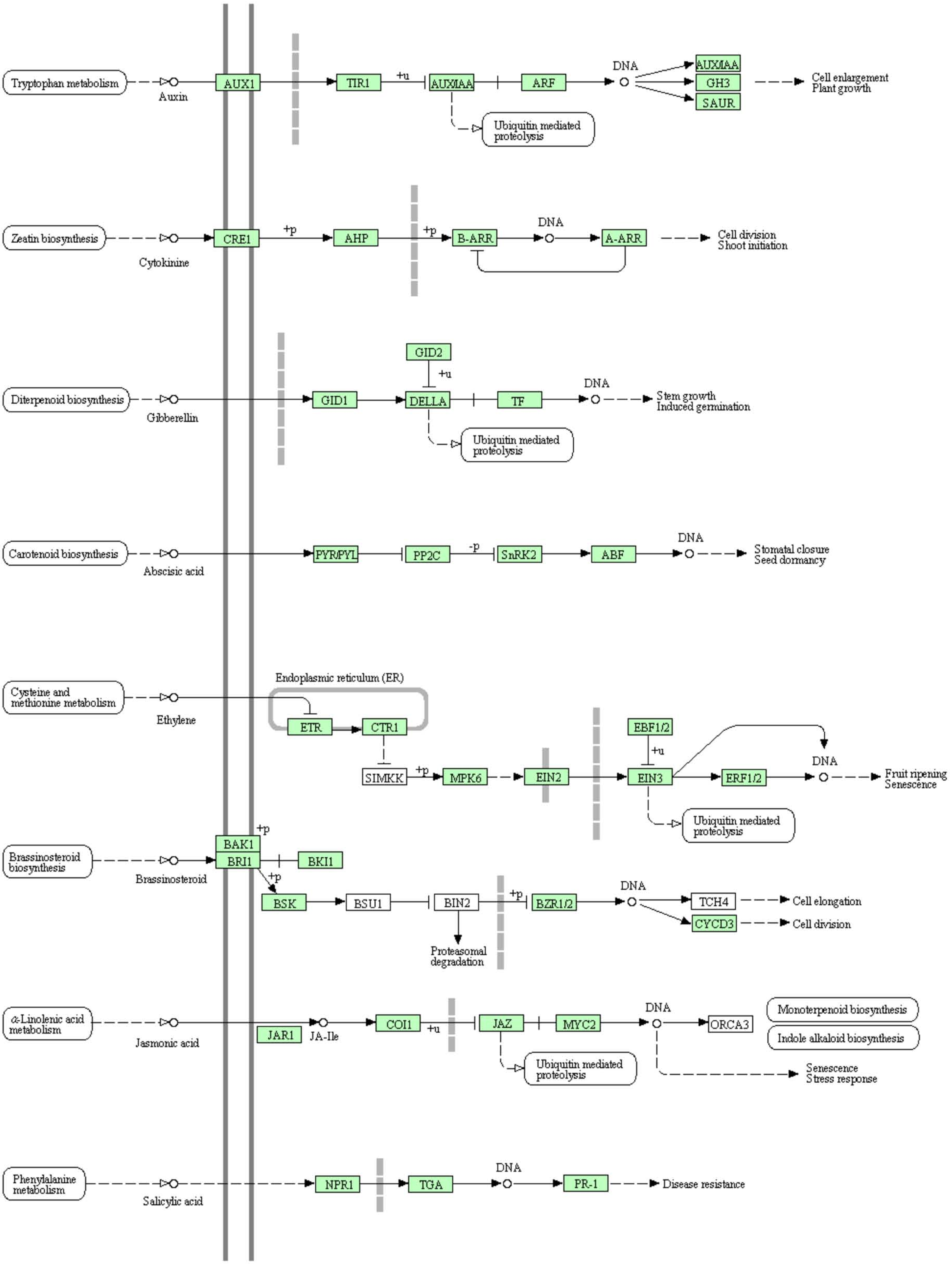
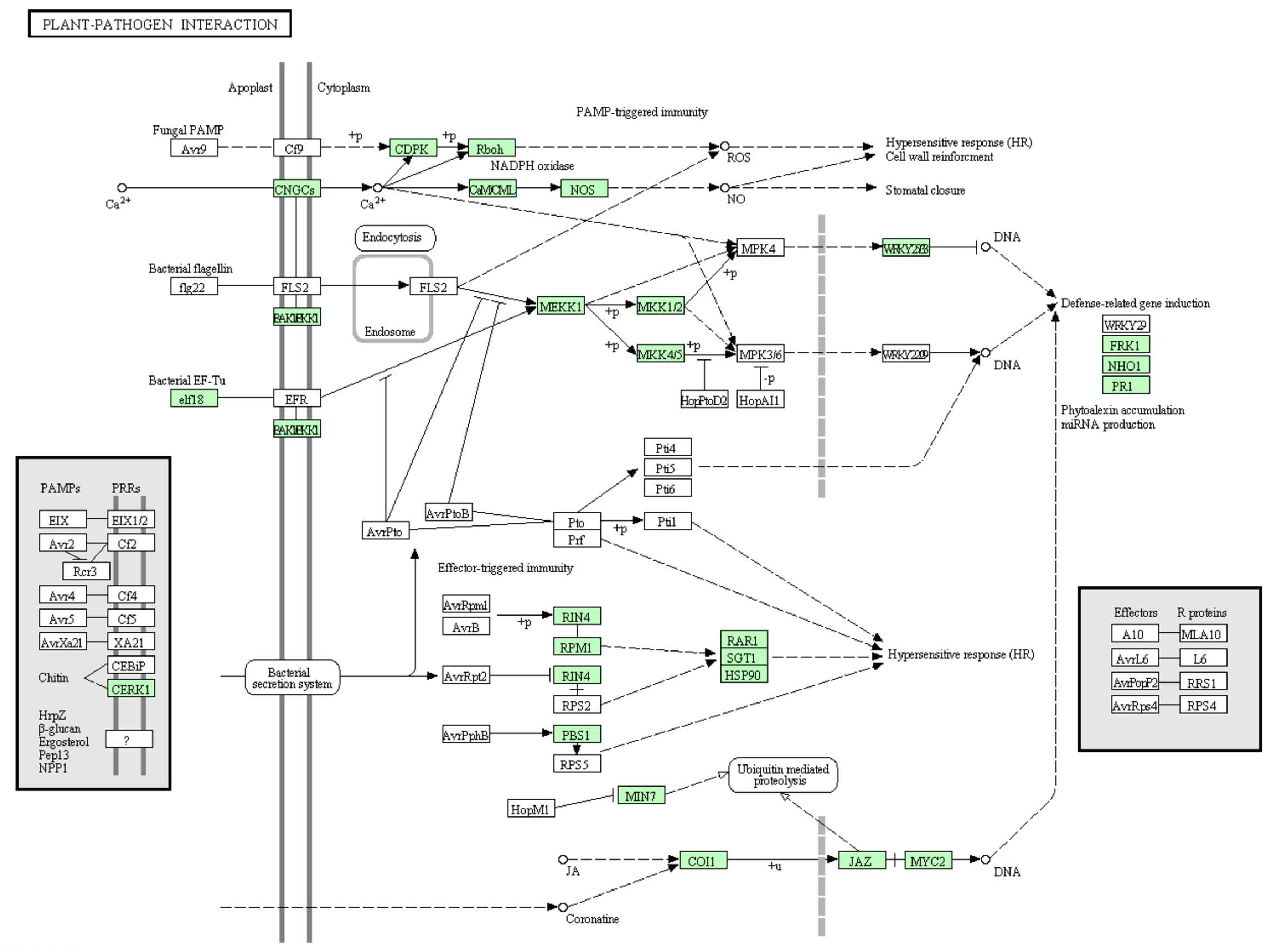
PLANT HORMONE SIGNAL TRANSDUCTION



04075 10/30/12


PLANT-PATHOGEN INTERACTION
Apoplast
Cytoplasm
PAMP-triggered immunity
Fungal PAMP
Avr9
Cf9
+p
CDPK
+p
Rboh
NADPH oxidase
ROS
Hypersensitive response (HR)
Cell wall reinforcment
Ca2+
CNGCs
Ca2+
CaM/CML
NOS
NO
Stomatal closure
Endocytosis
Endosome
MPK4
WRKY25/33
DNA
+p
Bacterial flagellin
flg22
FLS2
FLS2
BAK1/BKK1
MEKK1
+p
MKK1/2
Defense-related gene induction
WRKY29
FRK1
NHO1
PR1
+p
MKK4/5
+p
MPK3/6
WRKY22/29
DNA
-p
HopPtoD2
HopAI1
Bacterial EF-Tu
elf18
EFR
BAK1/BKK1
Phytoalexin accumulation
miRNA production
Pti4
Pti5
Pti6
PAMPs
PRRs
EIX
EIX1/2
Avr2
Cf2
Rcr3
Avr4
Cf4
Avr5
Cf5
AvrXa21
XA21
Chitin
CEBiP
CERK1
HrpZ
β-glucan
Ergosterol
Pep13
NPP1
?
AvrPtoB
AvrPto
Pto
Prf
+p
Pti1
Effector-triggered immunity
AvrRpm1
AvrB
+p
RIN4
RPM1
RAR1
SGT1
HSP90
Hypersensitive response (HR)
Bacterial secretion system
AvrRpt2
RIN4
RPS2
AvrPphB
PBS1
RPS5
Effectors
R proteins
A10
MLA10
AvrL6
L6
AvrPopP2
RRS1
AvrRps4
RPS4
Ubiquitin mediated proteolysis
HopM1
MIN7
JA
COI1
+u
JAZ
MYC2
DNA
Coronatine
04626 5/18/12
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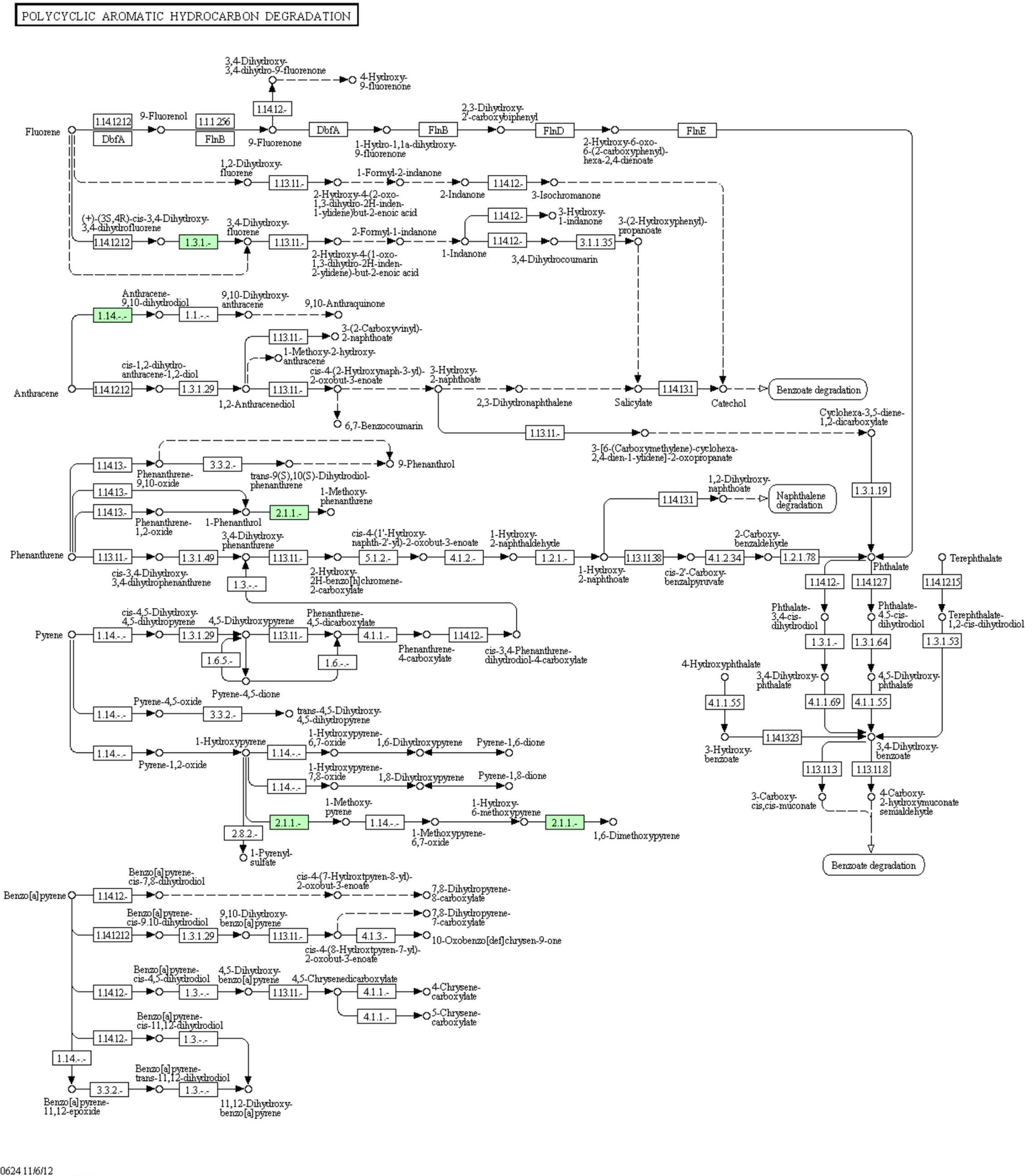
POLYCYCLIC AROMATIC HYDROCARBON DEGRADATION
3,4-Dihydroxy-3,4-dihydro-9-fluorenone
4-Hydroxy-9-fluorenone
1.14.12.-
Fluorene
1.14.12.12
DbfA
9-Fluorenol
1.1.1.256
FlnB
9-Fluorenone
DbfA
1-Hydro-1,1a-dihydroxy-9-fluorenone
FlnB
2,3-Dihydroxy-2'-carboxybiphenyl
FlnD
2-Hydroxy-6-oxo-6-(2-carboxyphenyl)-hexa-2,4-dienoate
FlnE
1,2-Dihydroxy-fluorene
1.13.11.-
1-Formyl-2-indanone
2-Hydroxy-4-(2-oxo-1,3-dihydro-2H-inden-1-ylidene)but-2-enoic acid
2-Indanone
1.14.12.-
3-Isochromanone
(+)-(3S,4R)-cis-3,4-Dihydroxy-3,4-dihydrofluorene
1.14.12.12
1.3.1.-
3,4-Dihydroxy-fluorene
1.13.11.-
2-Formyl-1-indanone
2-Hydroxy-4-(1-oxo-1,3-dihydro-2H-inden-2-ylidene)-but-2-enoic acid
1-Indanone
1.14.12.-
3-Hydroxy-1-indanone
1.14.12.-
3,4-Dihydrocoumarin
3.1.1.35
3-(2-Hydroxyphenyl)-propanoate
Anthracene-9,10-dihydrodiol
1.14.-.-
1.1.-.-
9,10-Dihydroxy-anthracene
9,10-Anthraquinone
1.13.11.-
3-(2-Carboxyvinyl)-2-naphthoate
1-Methoxy-2-hydroxy-anthracene
Anthracene
1.14.12.12
cis-1,2-dihydro-anthracene-1,2-diol
1.3.1.29
1,2-Anthracenediol
1.13.11.-
cis-4-(2-Hydroxynaph-3-yl)-2-oxobut-3-enoate
6,7-Benzocoumarin
3-Hydroxy-2-naphthoate
2,3-Dihydronaphthalene
Salicylate
1.14.13.1
Catechol
Benzoate degradation
1.13.11.-
3-[6-(Carboxymethylene)-cyclohexa-2,4-dien-1-ylidene]-2-oxopropanate
Cyclohexa-3,5-diene-1,2-dicarboxylate
1.3.1.19
1.14.13.-
Phenanthrene-9,10-oxide
3.3.2.-
trans-9(S),10(S)-Dihydrodiol-phenanthrene
9-Phenanthrol
1.14.13.-
1.14.13.-
Phenanthrene-1,2-oxide
1-Phenanthrol
2.1.1.-
1-Methoxy-phenanthrene
1.14.13.1
1,2-Dihydroxy-naphthoate
Naphthalene degradation
Phenanthrene
1.13.11.-
cis-3,4-Dihydroxy-3,4-dihydrophenanthrene
1.3.1.49
3,4-Dihydroxy-phenanthrene
1.3.-.-
1.13.11.-
2-Hydroxy-2H-benzo[h]chromene-2-carboxylate
5.1.2.-
cis-4-(1'-Hydroxy-naphth-2'-yl)-2-oxobut-3-enoate
4.1.2.-
1-Hydroxy-2-naphthaldehyde
1.2.1.-
1-Hydroxy-2-naphthoate
1.13.11.38
cis-2'-Carboxy-benzalpyruvate
4.1.2.34
2-Carboxy-benzaldehyde
1.2.1.78
Phthalate
Terephthalate
1.14.12.-
1.14.12.7
1.14.12.15
Phthalate-3,4-cis-dihydrodiol
Phthalate-4,5-cis-dihydrodiol
Terephthalate-1,2-cis-dihydrodiol
1.3.1.-
1.3.1.64
1.3.1.53
4-Hydroxyphthalate
3,4-Dihydroxy-phthalate
4,5-Dihydroxy-phthalate
4.1.1.55
4.1.1.69
4.1.1.55
3-Hydroxy-benzoate
1.14.13.23
3,4-Dihydroxy-benzoate
1.13.11.3
1.13.11.8
3-Carboxy-cis,cis-muconate
4-Carboxy-2-hydroxymuconate semialdehyde
Benzoate degradation
Pyrene
1.14.-.-
cis-4,5-Dihydroxy-4,5-dihydropyrene
1.3.1.29
4,5-Dihydroxypyrene
1.13.11.-
Phenanthrene-4,5-dicarboxylate
4.1.1.-
Phenanthrene-4-carboxylate
1.14.12.-
cis-3,4-Phenanthrene-dihydrodiol-4-carboxylate
1.6.5.-
1.6.-.-
Pyrene-4,5-dione
1.14.-.-
Pyrene-4,5-oxide
3.3.2.-
trans-4,5-Dihydroxy-4,5-dihydropyrene
1.14.-.-
Pyrene-1,2-oxide
1-Hydroxypyrene
1.14.-.-
1-Hydroxypyrene-6,7-oxide
1,6-Dihydroxypyrene
Pyrene-1,6-dione
1.14.-.-
1-Hydroxypyrene-7,8-oxide
1,8-Dihydroxypyrene
Pyrene-1,8-dione
2.1.1.-
1-Methoxy-pyrene
1.14.-.-
1-Methoxypyrene-6,7-oxide
1-Hydroxy-6-methoxypyrene
2.1.1.-
1,6-Dimethoxypyrene
2.8.2.-
1-Pyrenyl-sulfate
Benzo[a]pyrene
1.14.12.-
Benzo[a]pyrene-cis-7,8-dihydrodiol
cis-4-(7-Hydroxtpyren-8-yl)-2-oxobut-3-enoate
7,8-Dihydropyrene-8-carboxylate
Benzo[a]pyrene-cis-9,10-dihydrodiol
1.14.12.12
1.3.1.29
9,10-Dihydroxy-benzo[a]pyrene
1.13.11.-
7,8-Dihydropyrene-7-carboxylate
4.1.3.-
10-Oxobenzo[def]chrysen-9-one
cis-4-(8-Hydroxtpyren-7-yl)-2-oxobut-3-enoate
Benzo[a]pyrene-cis-4,5-dihydrodiol
1.14.12.-
1.3.-.-
4,5-Dihydroxy-benzo[a]pyrene
1.13.11.-
4,5-Chrysenedicarboxylate
4.1.1.-
4-Chrysene-carboxylate
4.1.1.-
5-Chrysene-carboxylate
1.14.12.-
Benzo[a]pyrene-cis-11,12-dihydrodiol
1.3.-.-
1.14.-.-
Benzo[a]pyrene-11,12-epoxide
3.3.2.-
Benzo[a]pyrene-trans-11,12-dihydrodiol
1.3.-.-
11,12-Dihydroxy-benzo[a]pyrene
00624 11/6/12
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POLYKETIDE SUGAR UNIT BIOSYNTHESIS

00523 2/4/14
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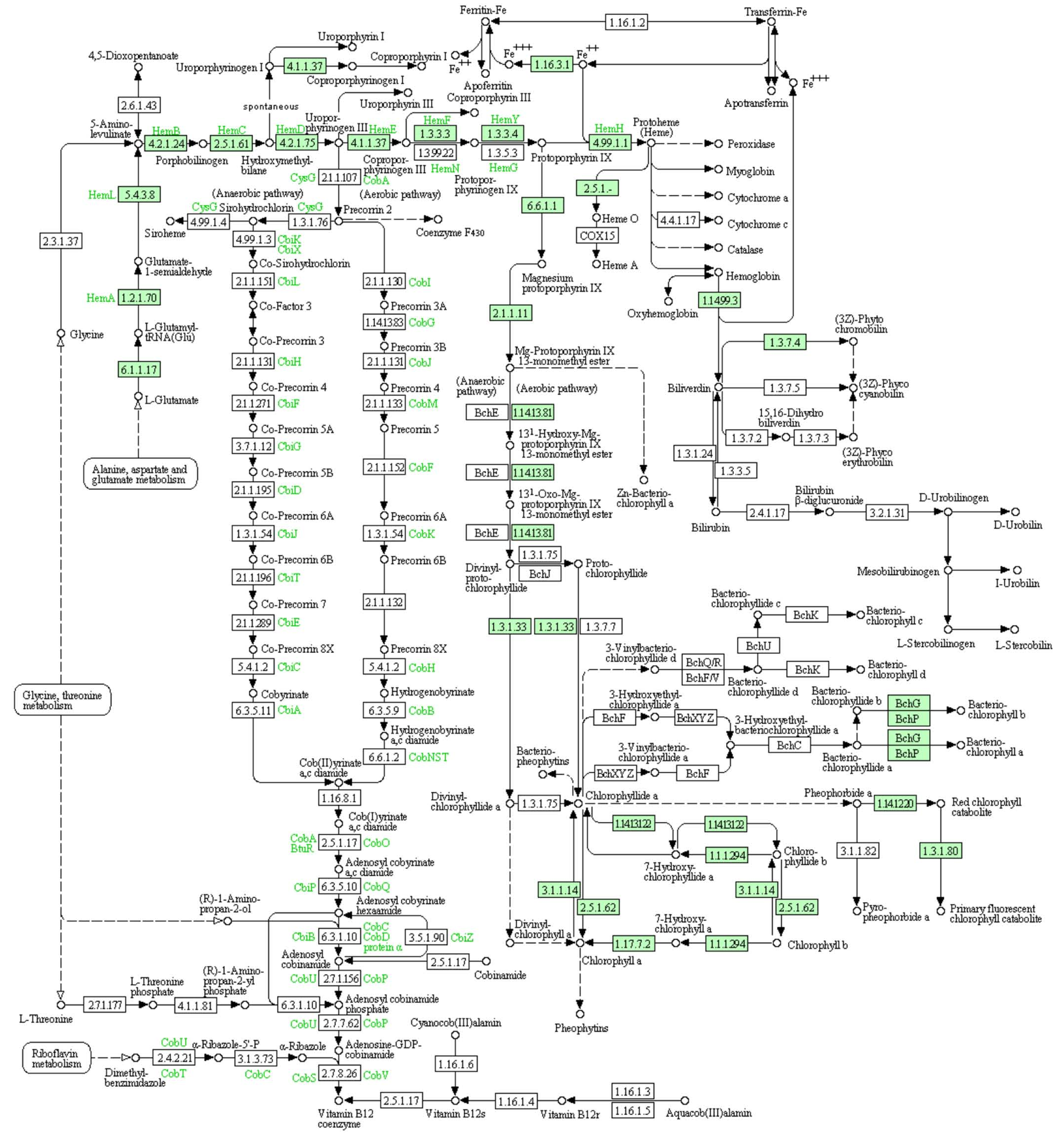
PORPHYRIN AND CHLOROPHYLL METABOLISM



00860 2/13/14
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PROPANOATE METABOLISM
Cysteine and methionine metabolism
1-Aminocyclopropane-1-carboxylate
3.5.99.7
2-Hydroxybutyrate
1.1.1.27
(S)-2-Methylmalate
2-Oxo-butanoate
Propanoyl phosphate
2.7.2.1
2.7.2.15
Propanoate
1.2.7.1
2.3.1.8
2.3.1.222
6.2.1.1
6.2.1.17
Propionyl-adenylate
2.8.3.1
6.2.1.13
2.3.1.54
6.2.1.1
6.2.1.17
β-Alanine metabolism
Valine, leucine and isoleucine degradation
C5-Branched dibasic acid metabolism
3-Chloroacrylic acid degradation
Pyruvate metabolism
Glycolysis
Lactate
2.8.3.1
Lactoyl-CoA
4.2.1.54
4.1.1.9
2.8.3.3
6.4.1.2
2.1.3.1
Acetyl-CoA
Malonyl-CoA
3-Oxo-propionyl-CoA
1.2.1.75
2.3.1.9
1.2.1.18
Acetoacetyl-CoA
Malonate semialdehyde
1.1.1.59
3-Hydroxy-propanoate
3.1.2.4
3-Hydroxy-propionyl-CoA
4.2.1.17
Acryloyl-CoA
1.3.8.7
Propanoyl-CoA
2.8.3.8
Acetoacetate
4.1.1.4
Acetone
1.1.1.80
2-Propanol
2.6.1.19
2.6.1.18
β-Alanine
β-Alanyl-CoA
4.3.1.6
4.2.1.27
Propynoate
1.2.99.3
1.2.1.3
2-Propyn-1-al
1.1.2.8
2-Propyn-1-ol
Pantothenate and CoA biosynthesis
2-Methyl-citrate
2.3.3.5
4.2.1.79
(2S,3R)-3-Hydroxybutane-1,2,3-tricarboxylate
4.2.1.99
2-Methyl-cis-aconitate
4.1.3.30
6.2.1.4
6.2.1.5
Succinate
Succinyl-CoA
Citrate cycle
5.4.99.2
6.4.1.3
2.1.3.1
4.1.1.41
(S)-2-Methyl-malonyl-CoA
5.1.99.1
(R)-Methyl-malonyl-CoA
3.1.2.17
Methyl-malonate
1.2.1.27
(S)-Methyl-malonate-semialdehyde
L-Valine
1.2.1.18
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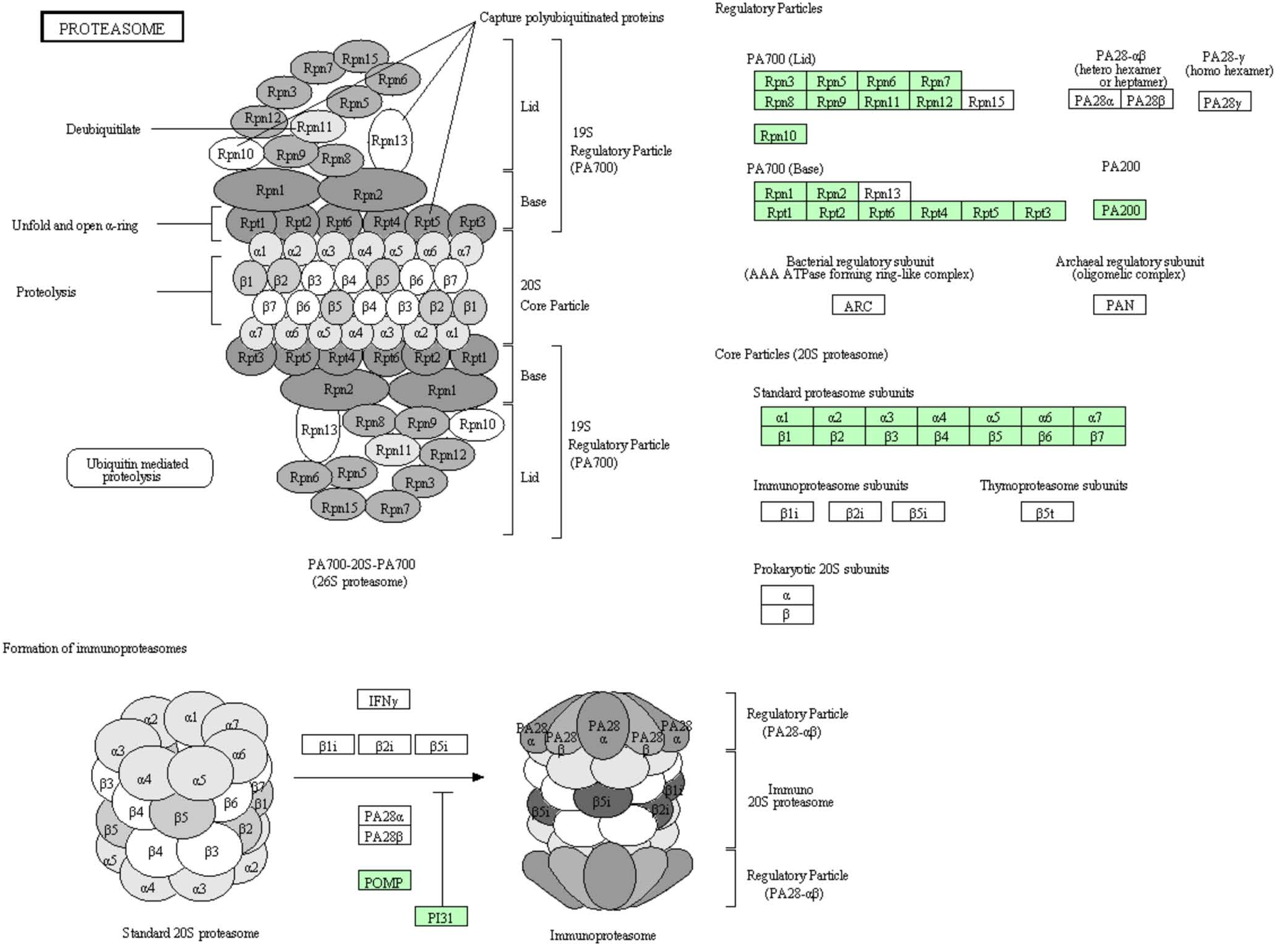

03050 12/1/10
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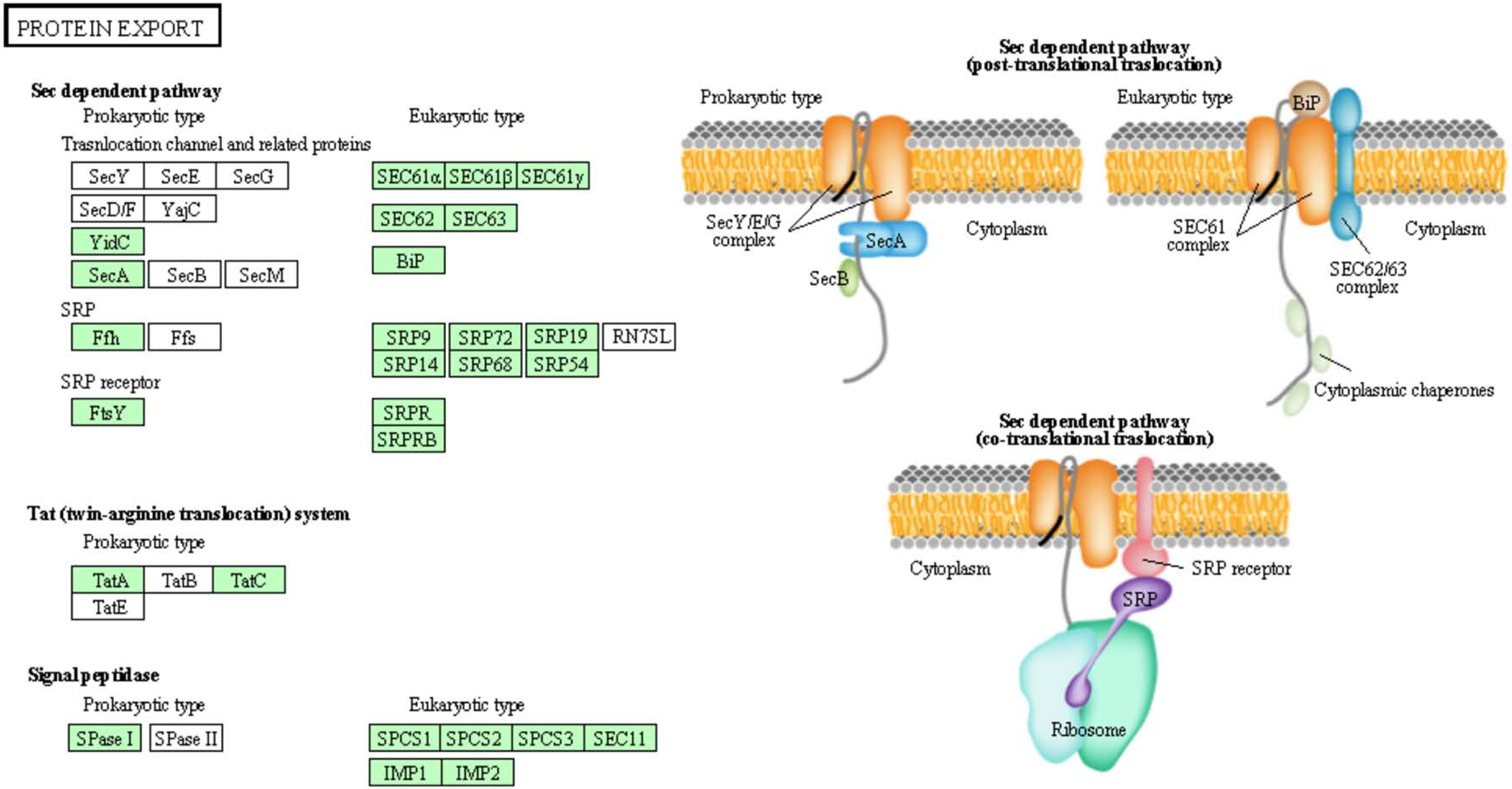

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PROTEIN PROCESSING IN ENDOPLASMIC RETICULUM

04141 12/27/10
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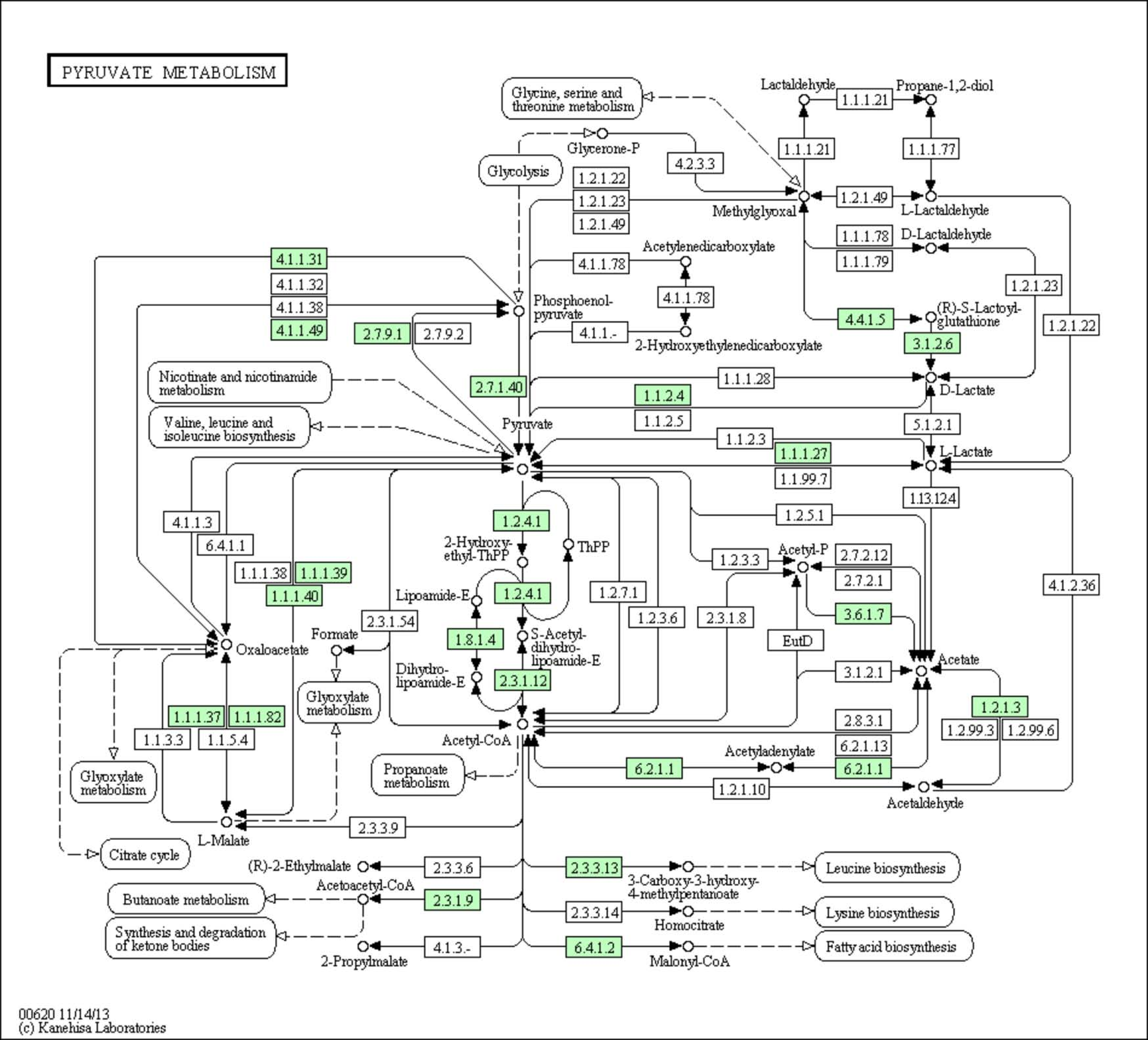
PYRIMIDINE METABOLISM


PYRUVATE METABOLISM
Glycine, serine and threonine metabolism
Lactaldehyde
1.1.1.21
Propane-1,2-diol
Glycerone-P
4.2.3.3
1.1.1.21
1.1.1.77
Glycolysis
1.2.1.22
1.2.1.23
1.2.1.49
1.2.1.49
Methylglyoxal
L-Lactaldehyde
1.1.1.78
D-Lactaldehyde
1.1.1.79
4.1.1.31
Acetylenedicarboxylate
4.1.1.32
4.1.1.78
1.2.1.23
4.1.1.38
Phosphoenol-pyruvate
4.1.1.78
4.4.1.5
(R)-S-Lactoyl-glutathione
1.2.1.22
4.1.1.49
2.7.9.1
2.7.9.2
4.1.1.-
2-Hydroxyethylenedicarboxylate
3.1.2.6
Nicotinate and nicotinamide metabolism
2.7.1.40
1.1.1.28
D-Lactate
1.1.2.4
Valine, leucine and isoleucine biosynthesis
1.1.2.5
5.1.2.1
Pyruvate
1.1.2.3
L-Lactate
1.1.1.27
1.1.99.7
1.13.12.4
4.1.1.3
1.2.4.1
1.2.5.1
6.4.1.1
2-Hydroxy-ethyl-ThPP
ThPP
Acetyl-P
2.7.2.12
1.2.3.3
1.1.1.38
1.1.1.39
2.7.2.1
4.1.2.36
1.1.1.40
Lipoamide-E
1.2.4.1
1.2.7.1
1.2.3.6
2.3.1.8
2.3.1.54
3.6.1.7
Formate
EutD
Oxaloacetate
1.8.1.4
S-Acetyl-dihydro-lipoamide-E
Acetate
Dihydro-lipoamide-E
3.1.2.1
Glyoxylate metabolism
2.3.1.12
1.2.1.3
1.1.1.37
1.1.1.82
2.8.3.1
1.2.99.3
1.2.99.6
1.1.3.3
1.1.5.4
Acetyl-CoA
6.2.1.13
Glyoxylate metabolism
Acetyladenylate
Propanoate metabolism
6.2.1.1
6.2.1.1
1.2.1.10
Acetaldehyde
2.3.3.9
L-Malate
Citrate cycle
(R)-2-Ethylmalate
2.3.3.6
2.3.3.13
Leucine biosynthesis
Acetoacetyl-CoA
3-Carboxy-3-hydroxy-4-methylpentanoate
Butanoate metabolism
2.3.1.9
2.3.3.14
Lysine biosynthesis
Homocitrate
Synthesis and degradation of ketone bodies
2-Propylmalate
4.1.3.-
6.4.1.2
Fatty acid biosynthesis
Malonyl-CoA
00620 11/14/13
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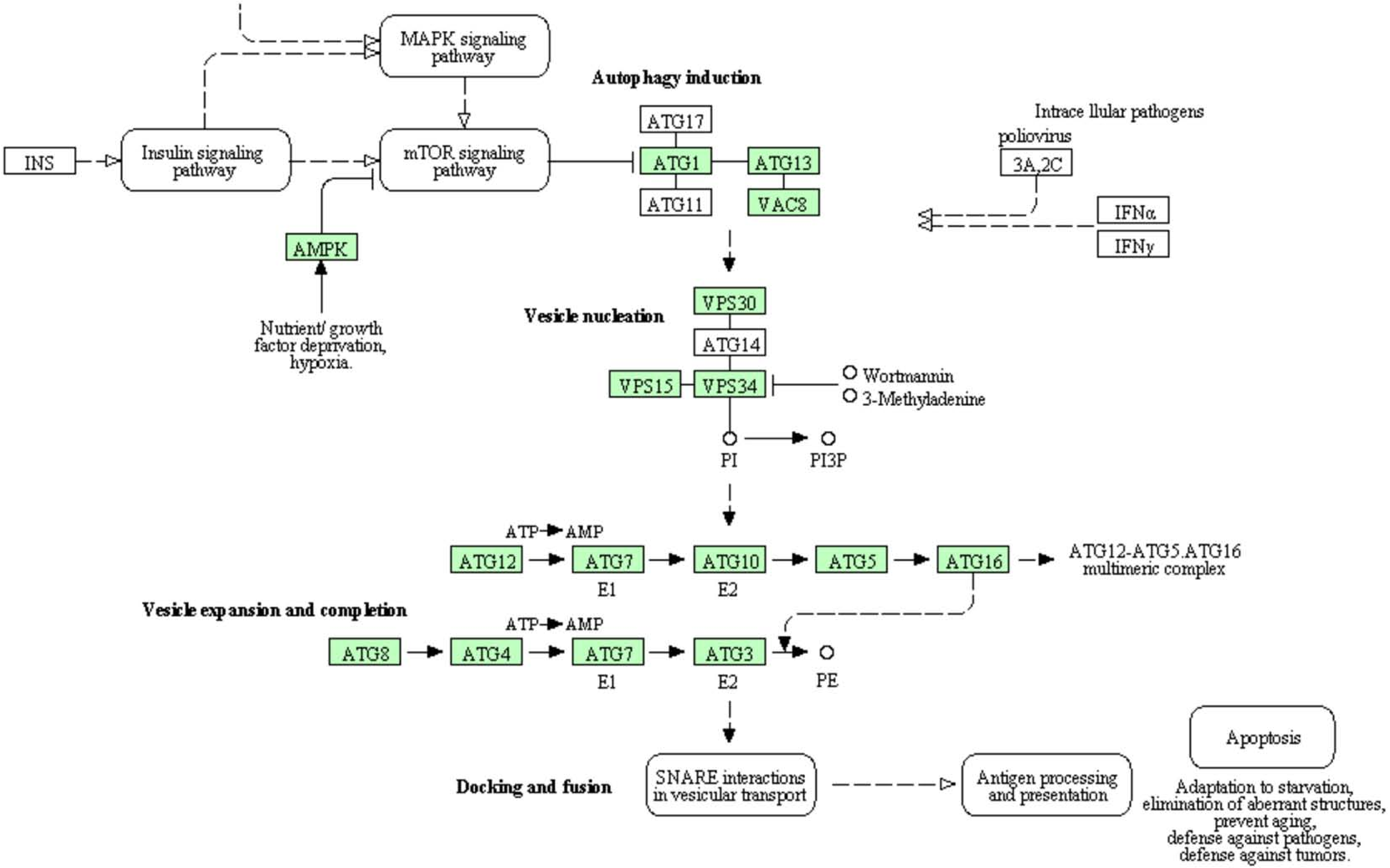
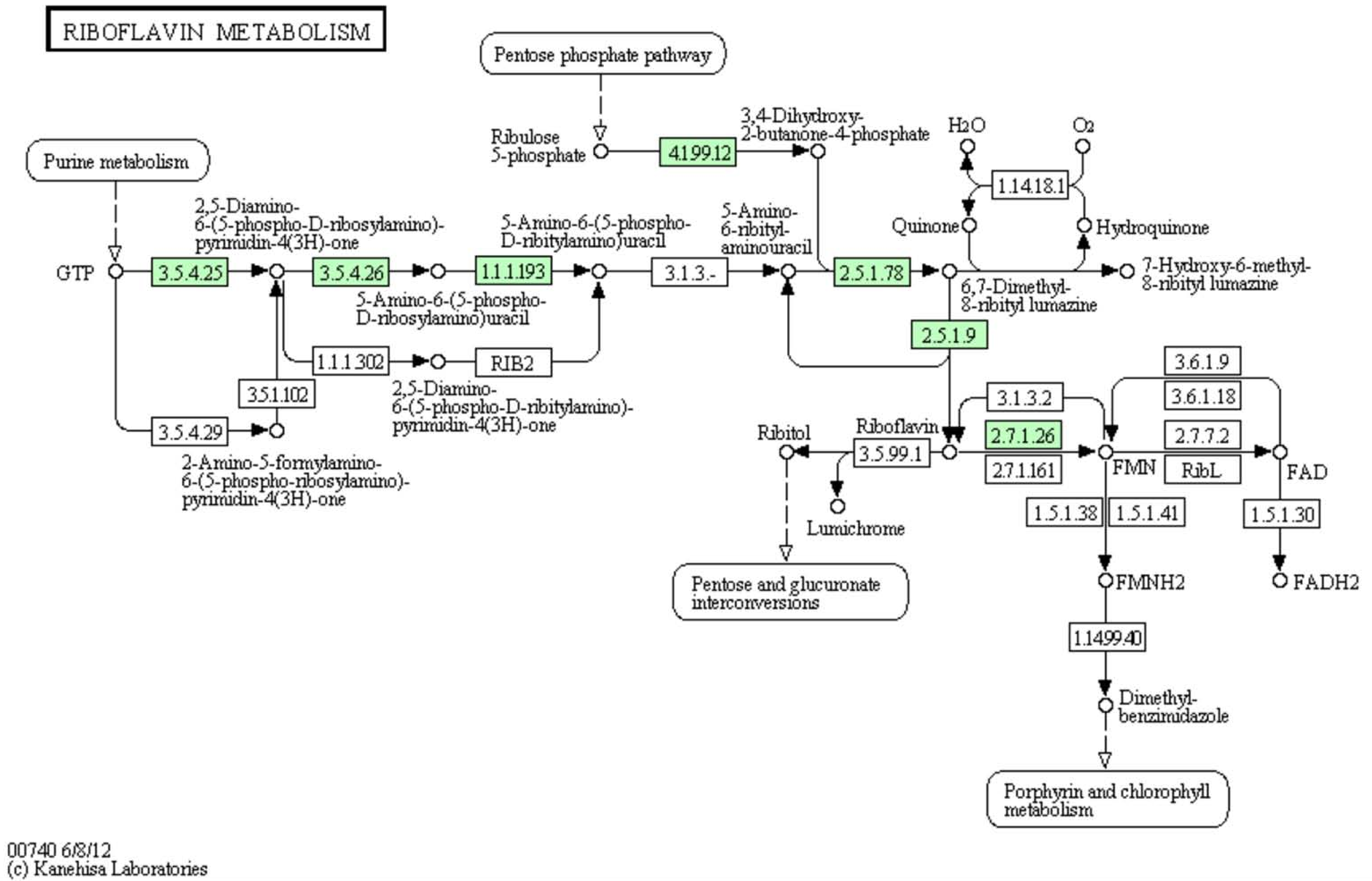
REGULATION OF AUTOPHAGY



04140 1/22/14


RIBOFLAVIN METABOLISM
Pentose phosphate pathway
Purine metabolism
Ribulose 5-phosphate
4.1.99.12
3,4-Dihydroxy-2-butanone-4-phosphate
H2O
O2
1.14.18.1
Quinone
Hydroquinone
GTP
3.5.4.25
2,5-Diamino-6-(5-phospho-D-ribosylamino)-pyrimidin-4(3H)-one
3.5.4.26
5-Amino-6-(5-phospho-D-ribosylamino)uracil
1.1.1.193
5-Amino-6-(5-phospho-D-ribitylamino)uracil
3.1.3.-
5-Amino-6-ribityl-aminouracil
2.5.1.78
6,7-Dimethyl-8-ribityl lumazine
7-Hydroxy-6-methyl-8-ribityl lumazine
2.5.1.9
1.1.1.302
RIB2
2,5-Diamino-6-(5-phospho-D-ribitylamino)-pyrimidin-4(3H)-one
3.5.1.102
3.5.4.29
2-Amino-5-formylamino-6-(5-phospho-ribosylamino)-pyrimidin-4(3H)-one
Ribitol
Riboflavin
3.5.99.1
Lumichrome
3.1.3.2
2.7.1.26
2.7.1.161
3.6.1.9
3.6.1.18
2.7.7.2
RibL
FMN
FAD
1.5.1.38
1.5.1.41
1.5.1.30
FMNH2
FADH2
1.14.99.40
Dimethyl-benzimidazole
Pentose and glucuronate interconversions
Porphyrin and chlorophyll metabolism
00740 6/8/12
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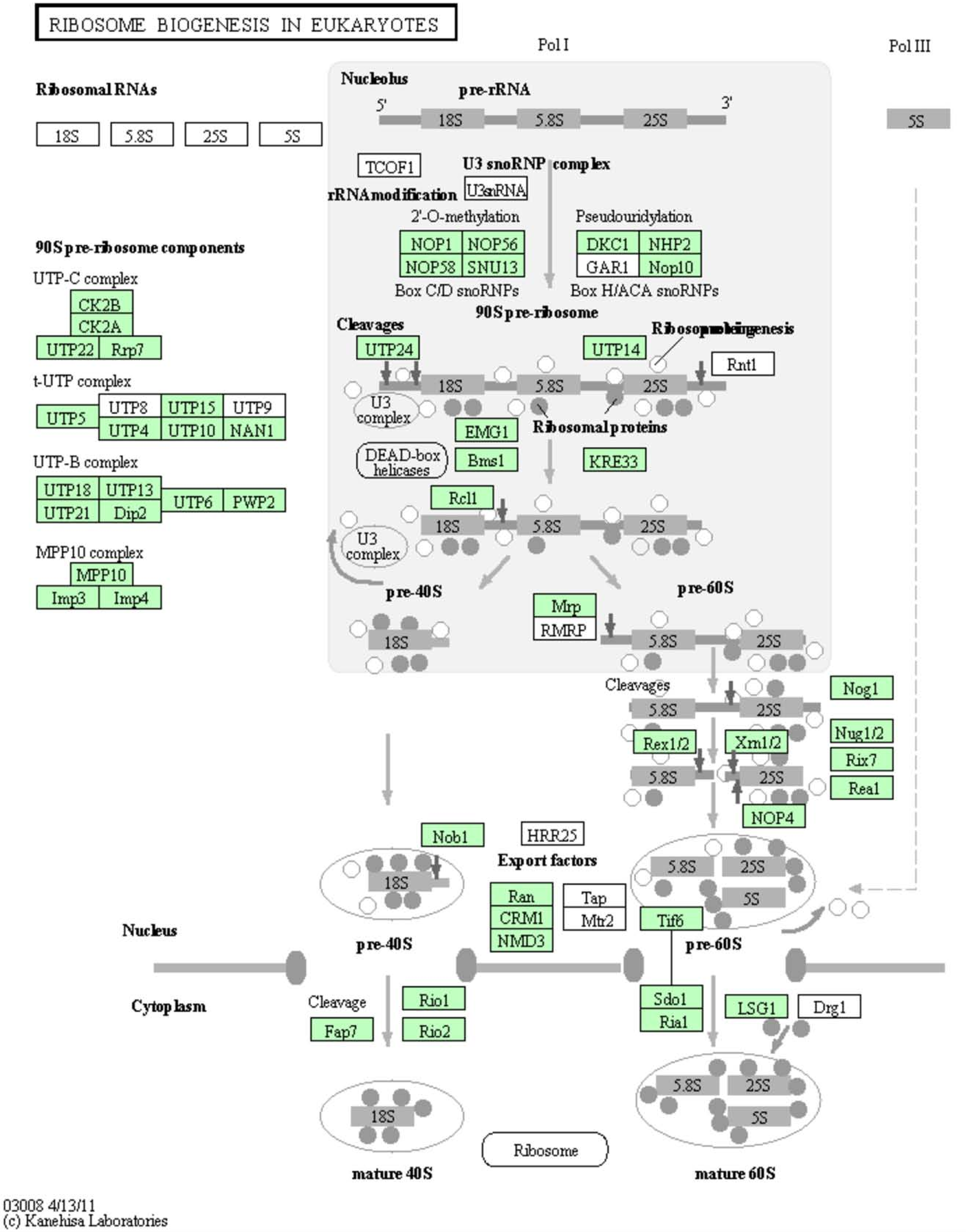
RIBOSOME BIOGENESIS IN EUKARYOTES
Pol I
Pol III
Ribosomal RNAs
18S
5.8S
25S
5S
Nucleolus
pre-rRNA
5'
3'
TCOF1
U3 snoRNP complex
U3snRNA
rRNA modification
2'-O-methylation
Pseudouridylation
NOP1
NOP56
NOP58
SNU13
DKC1
NHP2
GAR1
Nop10
Box C/D snoRNPs
Box H/ACA snoRNPs
90S pre-ribosome components
UTP-C complex
CK2B
CK2A
UTP22
Rrp7
t-UTP complex
UTP5
UTP8
UTP15
UTP9
UTP4
UTP10
NAN1
UTP-B complex
UTP18
UTP13
UTP21
Dip2
UTP6
PWP2
MPP10 complex
MPP10
Imp3
Imp4
90S pre-ribosome
Cleavages
UTP24
UTP14
Rnt1
U3 complex
EMG1
Ribosomal proteins
DEAD-box helicases
Bms1
KRE33
Rcl1
pre-40S
pre-60S
Mrp
RMRP
Cleavages
Nog1
Rex1/2
Xrn1/2
Nug1/2
Rix7
Rea1
NOP4
Nob1
HRR25
Export factors
Ran
CRM1
NMD3
Tap
Mtr2
Tif6
pre-40S
pre-60S
Nucleus
Cytoplasm
Cleavage
Rio1
Fap7
Rio2
Sdo1
Ria1
LSG1
Drg1
Ribosome
mature 40S
mature 60S
03008 4/13/11
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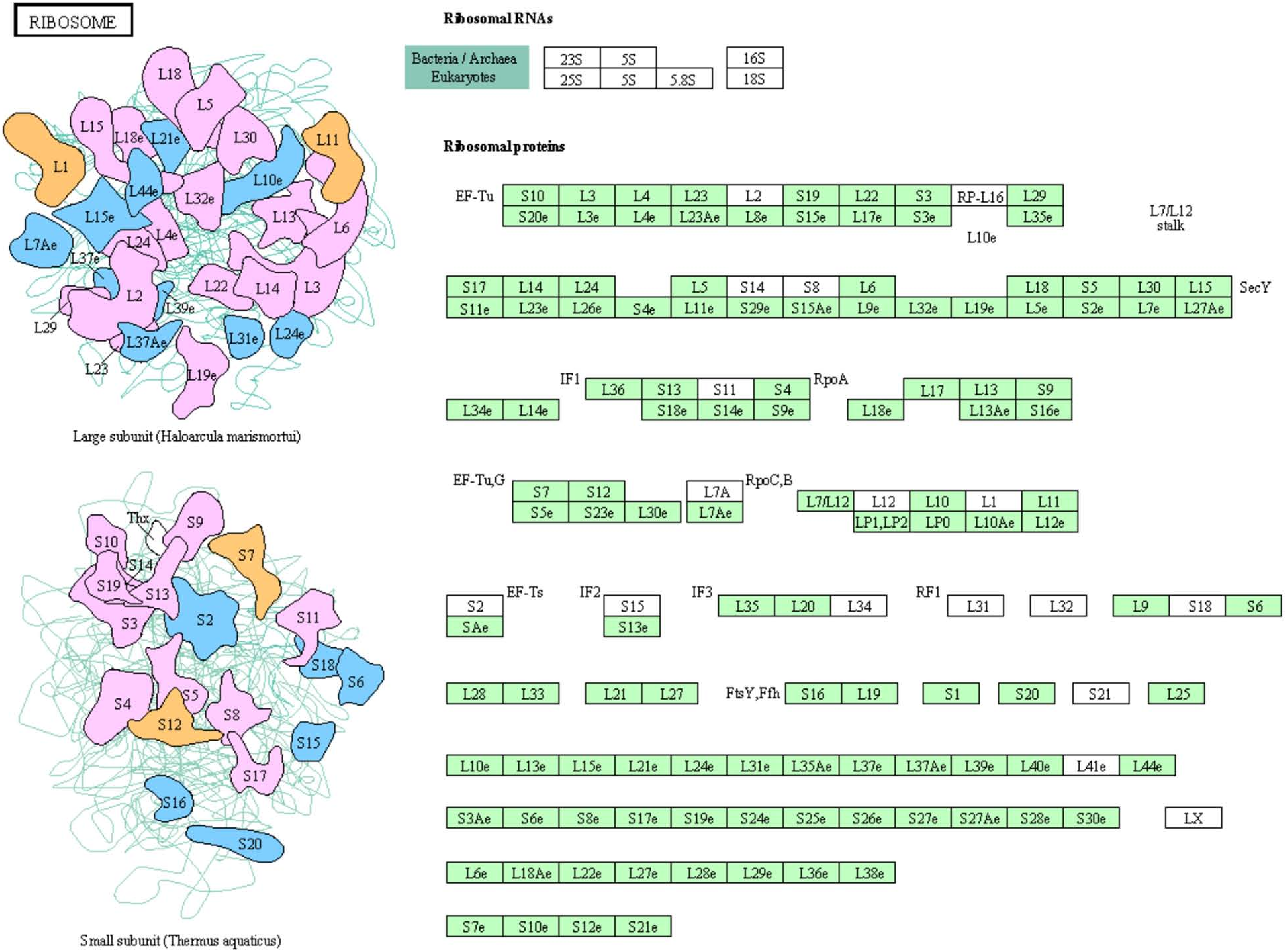

03010 7/29/13
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RIG-I-LIKE RECEPTOR SIGNALING PATHWAY

04622 5/25/12
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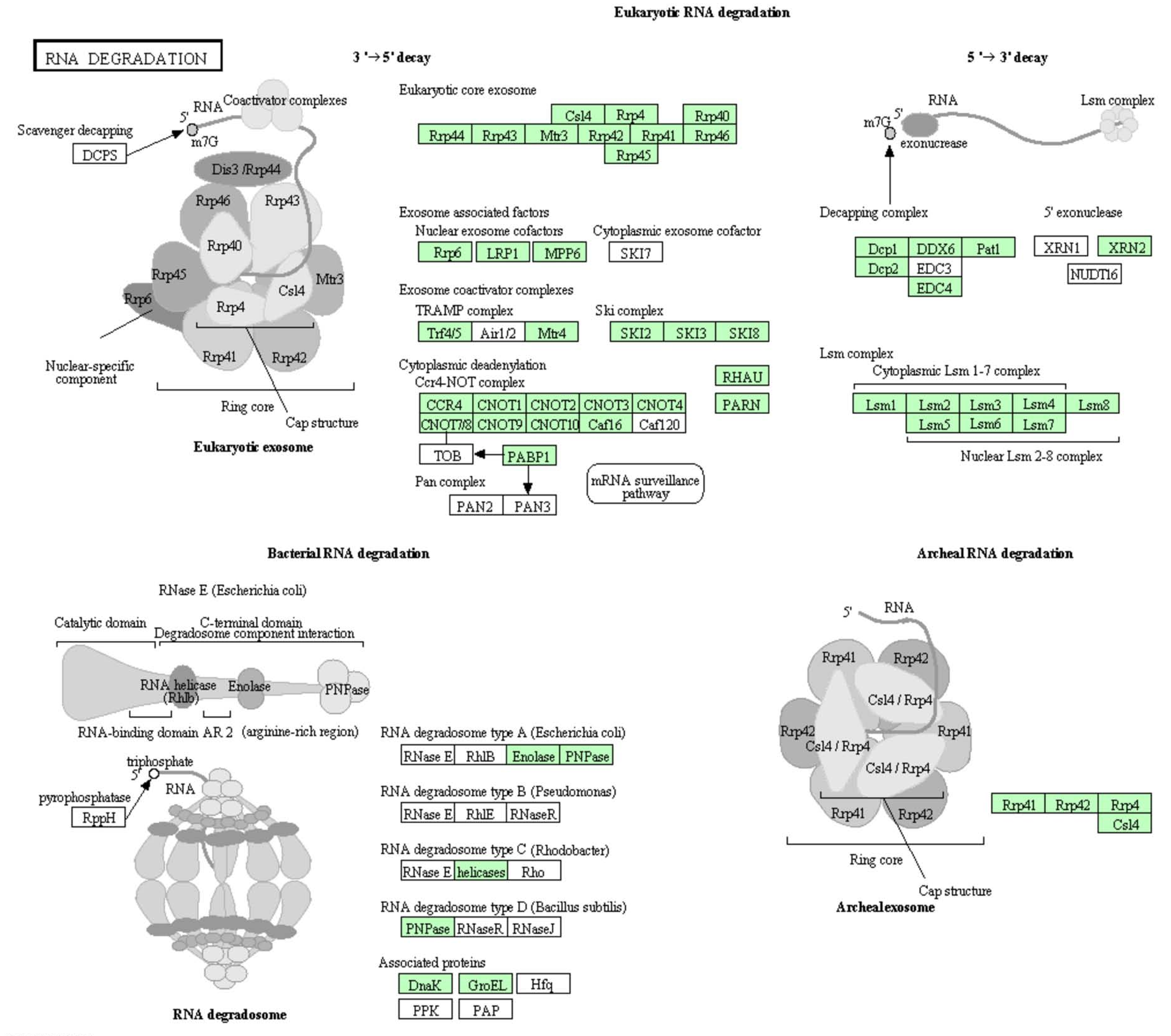
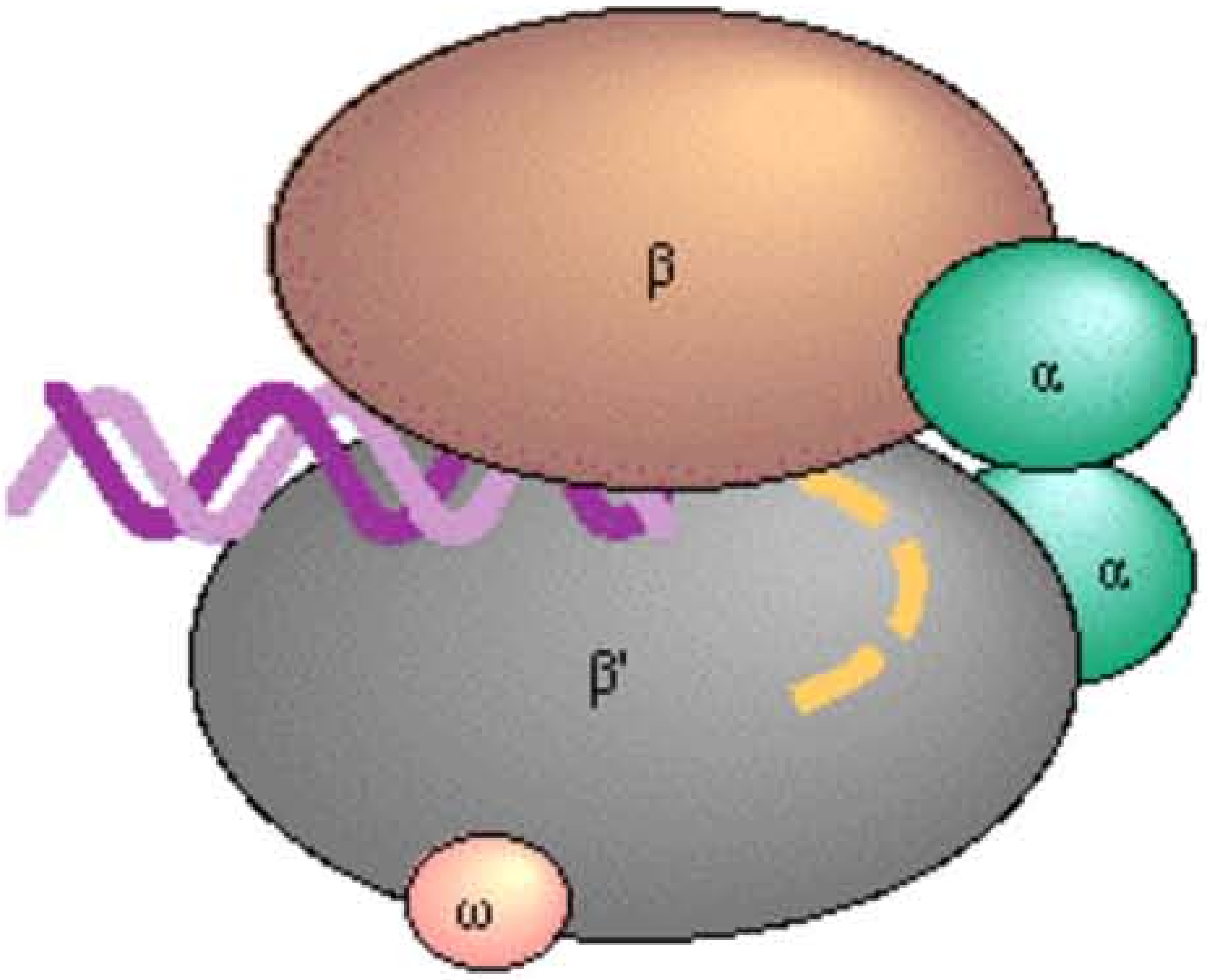
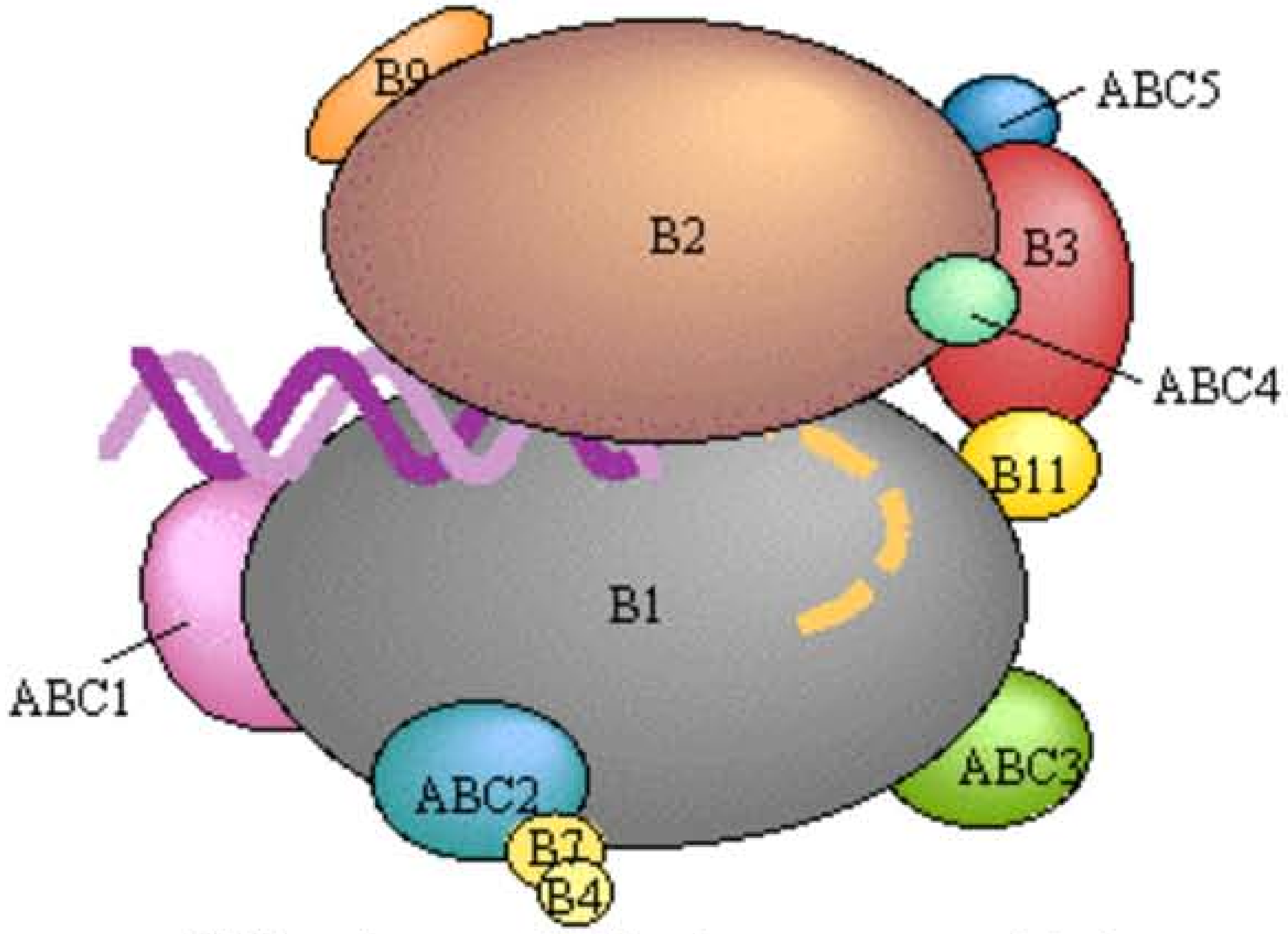


03018 12/27/13

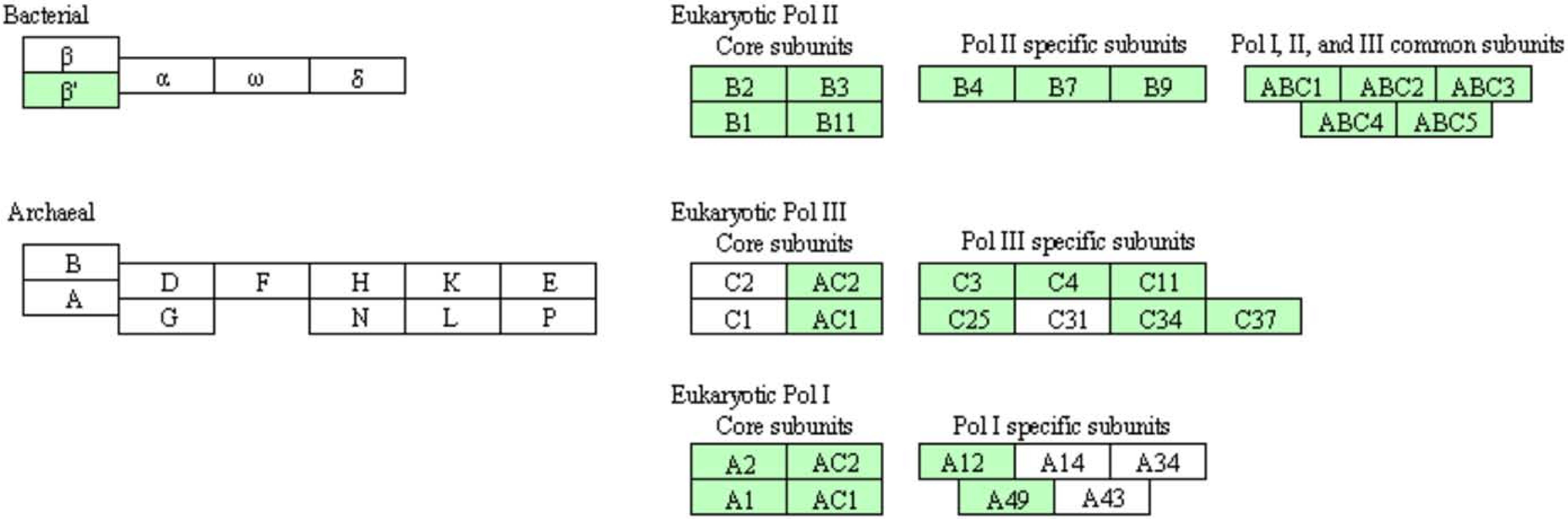
RNA POLYMERASE



RNA polymerase (Thermus aquaticus)



RNA polymerase II (Saccharomyces cerevisiae)



03020 3/25/11

03013 9/21/11
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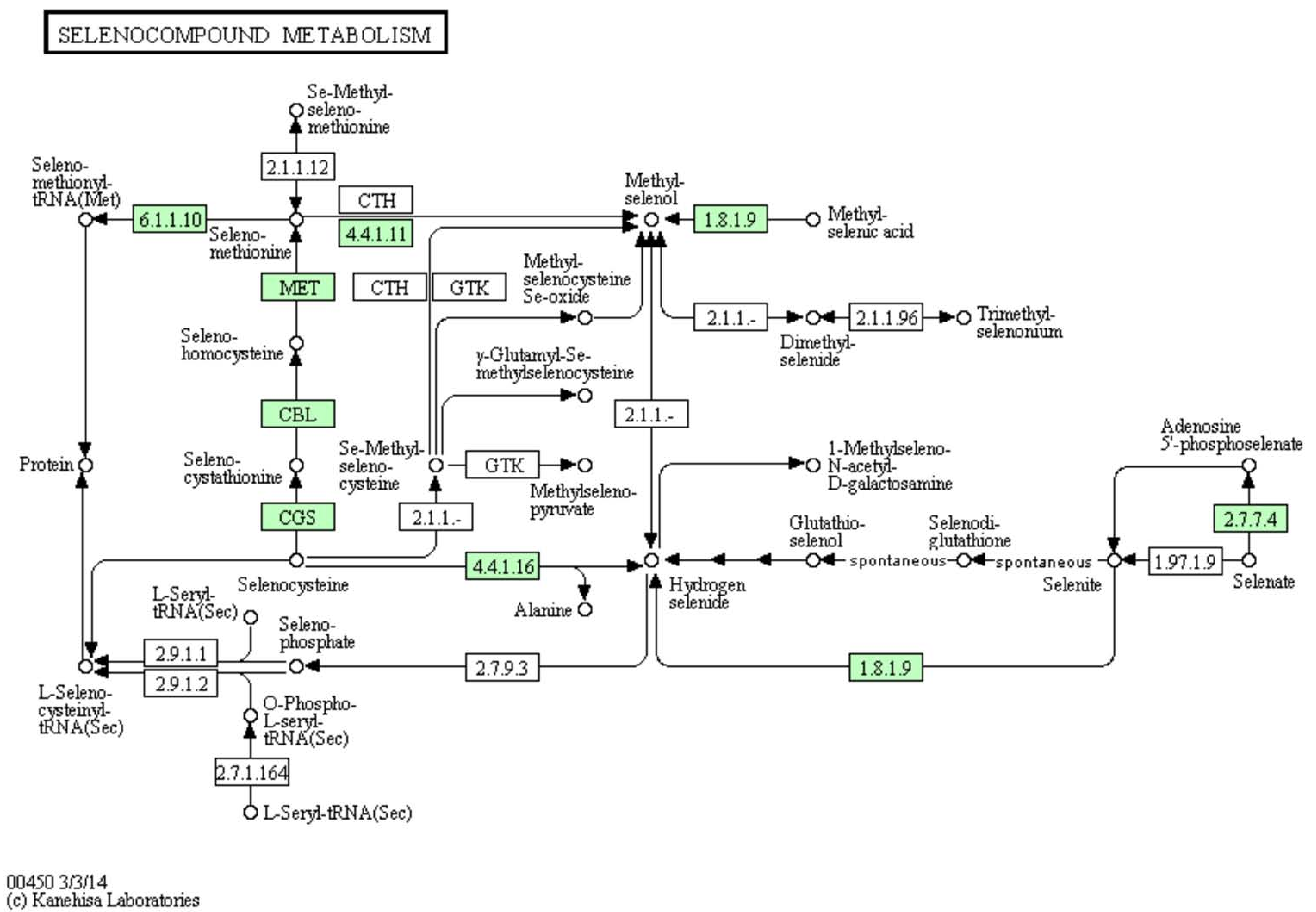
SELENOCOMPOUND METABOLISM
Se-Methyl-selenomethionine
2.1.1.12
Seleno-methionyl-tRNA(Met)
6.1.1.10
CTH
4.4.1.11
Methyl-selenol
1.8.1.9
Methyl-selenic acid
Seleno-methionine
MET
CTH
GTK
Methyl-selenocysteine Se-oxide
2.1.1.-
Dimethyl-selenide
2.1.1.96
Trimethyl-selenonium
Seleno-homocysteine
γ-Glutamyl-Se-methylselenocysteine
CBL
2.1.1.-
Adenosine 5'-phosphoselenate
Protein
Seleno-cystathionine
Se-Methyl-seleno-cysteine
GTK
1-Methylseleno-N-acetyl-D-galactosamine
Methylseleno-pyruvate
CGS
2.1.1.-
2.7.7.4
Glutathio-selenol
Selenodi-glutathione
spontaneous
spontaneous
1.97.1.9
Selenocysteine
4.4.1.16
Selenite
Selenate
Alanine
Hydrogen selenide
L-Seryl-tRNA(Sec)
Seleno-phosphate
2.9.1.1
2.9.1.2
2.7.9.3
1.8.1.9
L-Seleno-cysteinyl-tRNA(Sec)
O-Phospho-L-seryl-tRNA(Sec)
2.7.1.164
L-Seryl-tRNA(Sec)
00450 3/3/14
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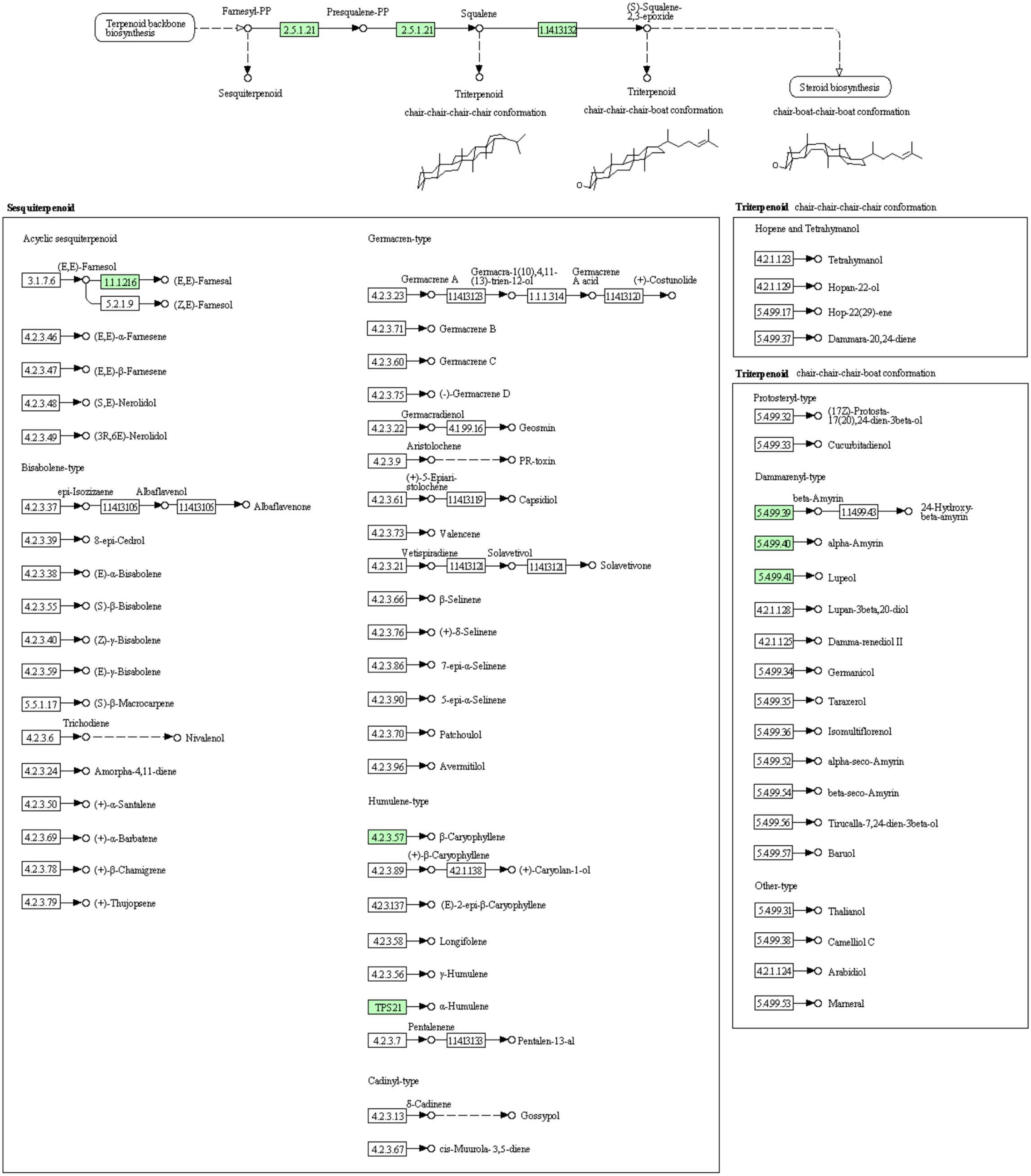
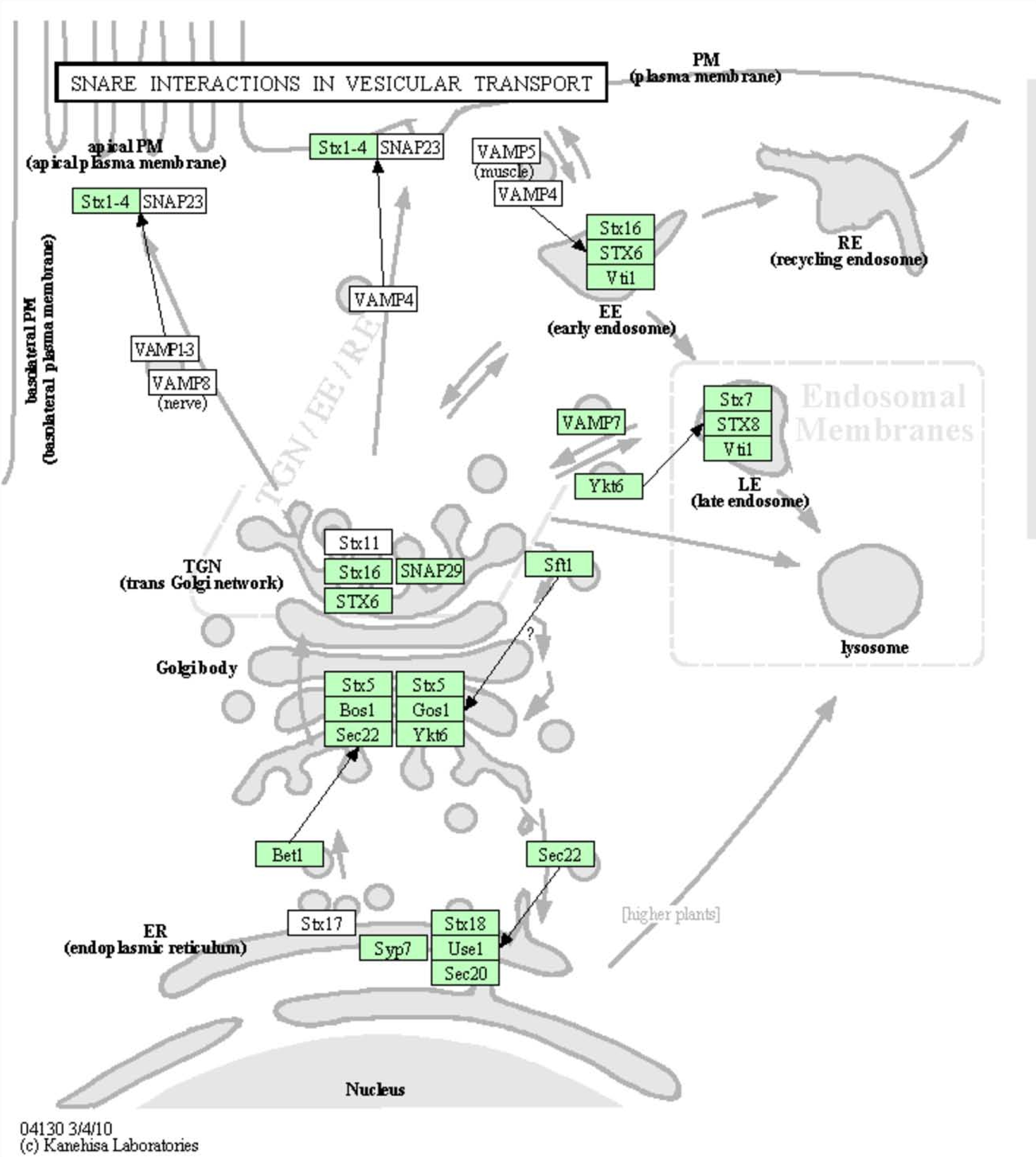
SESQUITERPENOID AND TRITERPENOID BIOSYNTHESIS



00909 3/13/14


SNARE INTERACTIONS IN VESICULAR TRANSPORT
PM
(plasma membrane)
apical PM
(apical plasma membrane)
basolateral PM
(basolateral plasma membrane)
Stx1-4
SNAP23
Stx1-4
SNAP23
VAMP5
(muscle)
VAMP4
Stx16
STX6
Vti1
EE
(early endosome)
RE
(recycling endosome)
VAMP4
VAMP13
VAMP8
(nerve)
TGN / EE / RE
Endosomal Membranes
VAMP7
Stx7
STX8
Vti1
Ykt6
LE
(late endosome)
Stx11
Stx16
SNAP29
STX6
Sft1
TGN
(trans Golgi network)
?
lysosome
Golgi body
Stx5
Bos1
Sec22
Stx5
Gos1
Ykt6
Bet1
Sec22
[higher plants]
ER
(endoplasmic reticulum)
Stx17
Syp7
Stx18
Use1
Sec20
Nucleus
04130 3/4/10
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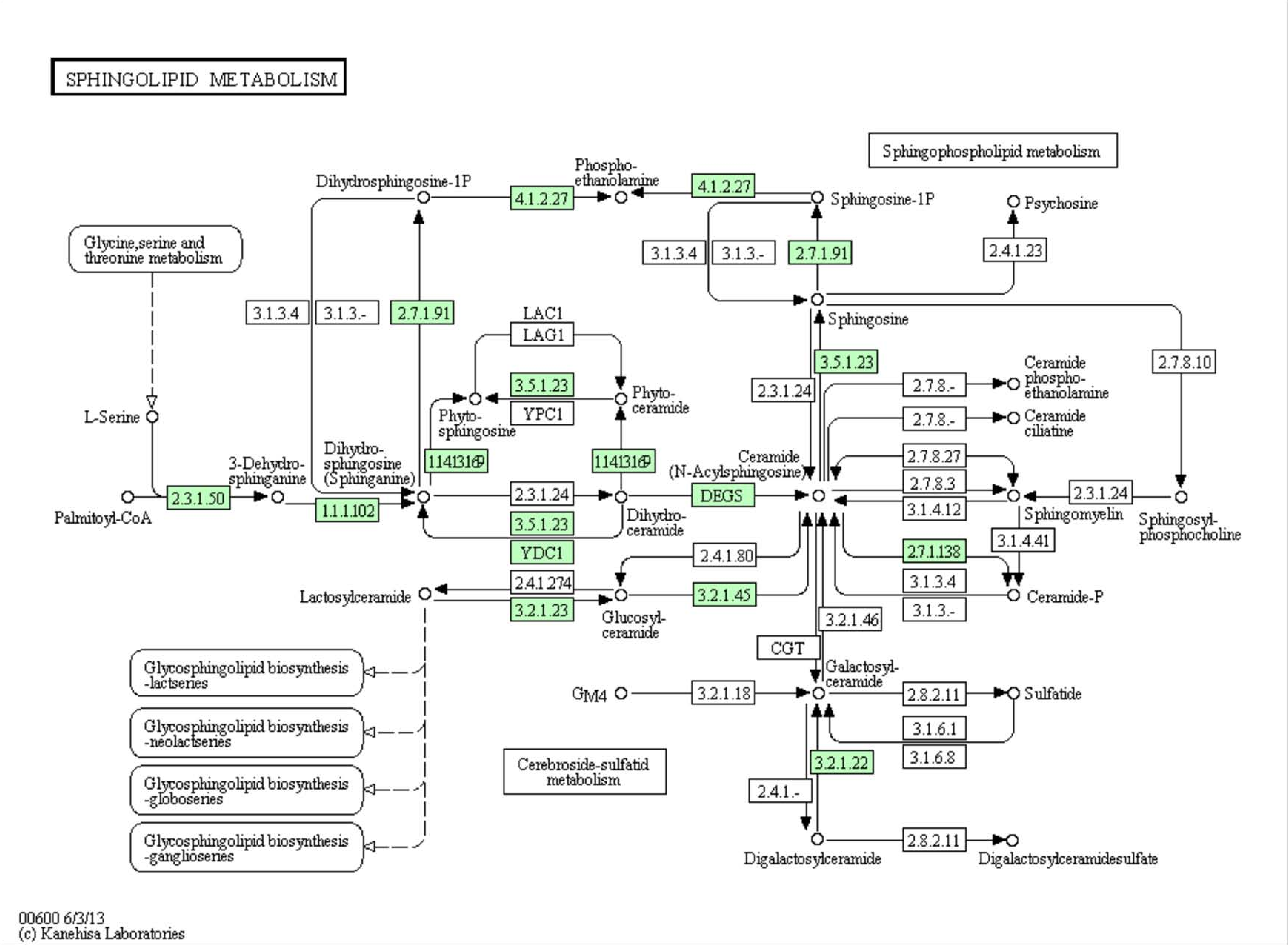
SPHINGOLIPID METABOLISM
Sphingophospholipid metabolism
Glycine,serine and threonine metabolism
Dihydrosphingosine-1P
4.1.2.27
Phospho-ethanolamine
4.1.2.27
Sphingosine-1P
Psychosine
3.1.3.4
3.1.3.-
2.7.1.91
2.4.1.23
3.1.3.4
3.1.3.-
2.7.1.91
Sphingosine
LAC1
LAG1
3.5.1.23
Phyto-ceramide
YPC1
Phyto-sphingosine
3.5.1.23
2.3.1.24
2.7.8.10
2.7.8.-
Ceramide phospho-ethanolamine
2.7.8.-
Ceramide ciliatine
L-Serine
Dihydro-sphingosine (Sphinganine)
1.14.13.169
1.14.13.169
Ceramide (N-Acylsphingosine)
2.7.8.27
2.7.8.3
3-Dehydro-sphinganine
Palmitoyl-CoA
2.3.1.50
1.1.1.102
2.3.1.24
Dihydro-ceramide
DEGS
3.1.4.12
Sphingomyelin
2.3.1.24
Sphingosyl-phosphocholine
3.5.1.23
YDC1
3.1.4.41
2.4.1.80
2.7.1.138
Lactosylceramide
2.4.1.274
3.2.1.23
Glucosyl-ceramide
3.2.1.45
3.1.3.4
Ceramide-P
3.1.3.-
3.2.1.46
CGT
Galactosyl-ceramide
Glycosphingolipid biosynthesis -lactseries
GM4
3.2.1.18
2.8.2.11
Sulfatide
3.1.6.1
Glycosphingolipid biosynthesis -neolactseries
3.1.6.8
Cerebroside-sulfatid metabolism
3.2.1.22
Glycosphingolipid biosynthesis -globoseries
2.4.1.-
Glycosphingolipid biosynthesis -ganglioseries
2.8.2.11
Digalactosylceramide
Digalactosylceramidesulfate
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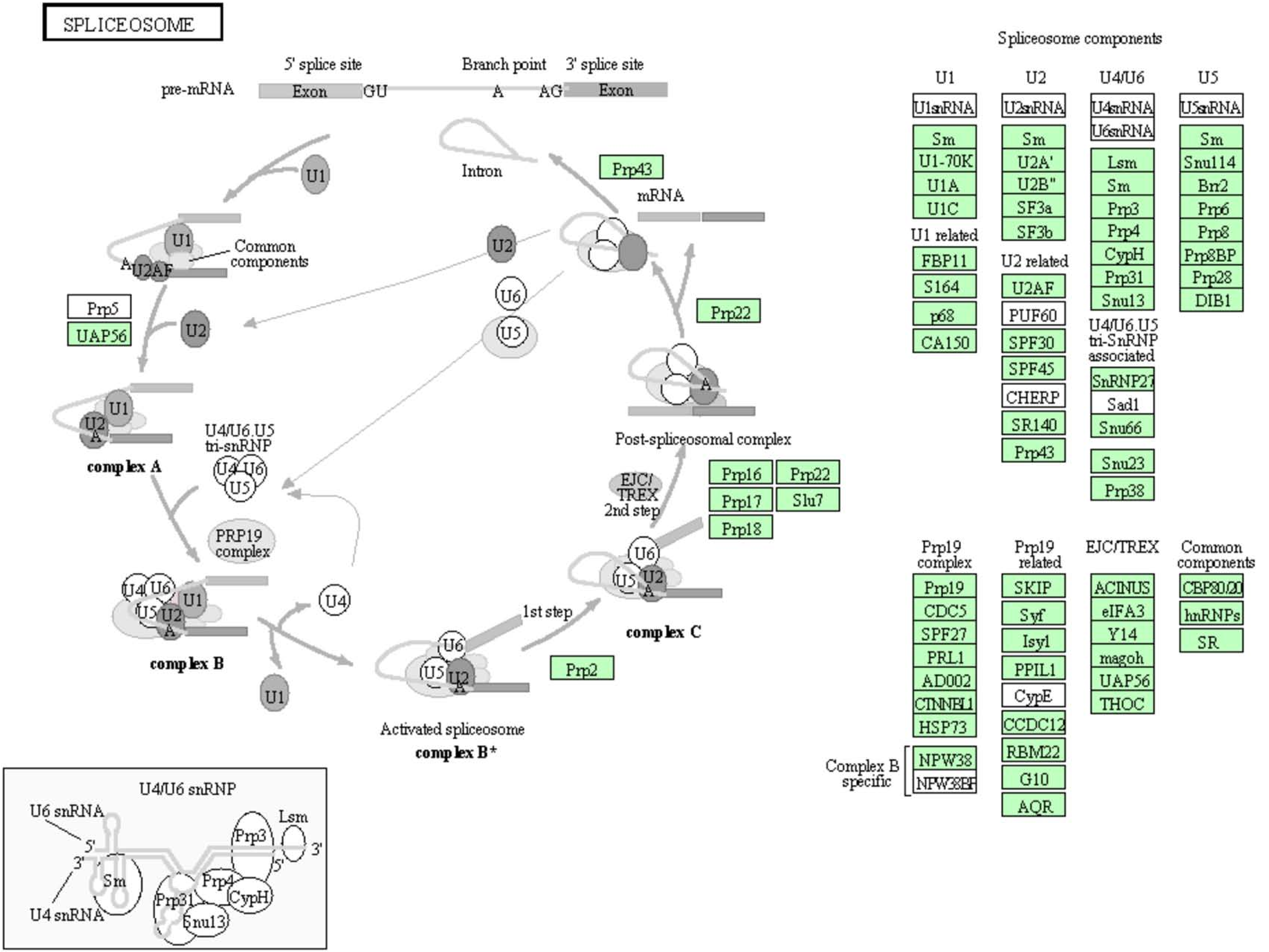

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STARCH AND SUCROSE METABOLISM
Amino sugar and nucleotide sugar metabolism
UDP-D-galacturonate
2.4.1.43
Pectin
3.1.1.11
Pectate
3.2.1.15
3.2.1.67
D-Galacturonate
5.1.3.6
Pentose and glucuronate interconversions
D-Xylose
3.2.1.37
1,4-β-D-Xylan
2.4.2.24
UDP-D-xylose
4.1.1.35
UDP-D-glucuronate
2.4.1.17
β-D-Glucuronoside
3.2.1.31
D-Glucuronate
Ascorbate metabolism
Retinol metabolism
Sucrose-6P
2.7.1.69
Sucrose (extracellular)
3.2.1.26
(2,6-β-D-Fructosyl)n
3.2.1.65
2.4.1.10
(2,6-β-D-Fructosyl)m+n
α-D-Glucose-6P
1.1.1.22
Sucrose-6'P
2.4.1.14
3.1.3.24
1.1.99.13
3-Ketosucrose
β-D-Fructose
3.2.1.20
3.2.1.26
3.2.1.48
Sucrose
2.4.1.13
UDP-glucose
2.4.1.11
2.4.1.10
2.4.1.4
2.4.1.5
D-Fructose
2.7.7.9
D-Glucose
3.2.1.39
1,3-β-Glucan
2.4.1.34
3.2.1.58
α-D-Glucose
3.2.1.21
Glucoside
2.4.1.35
2.4.1.12
2.7.1.1
2.7.1.4
Cellobiose
3.2.1.21
3.2.1.4
3.2.1.91
3.6.1.9
GDP-glucose
2.4.1.29
2.7.7.34
Cellulose
β-D-Glucose
3.2.1.21
1,4-β-D-Glucan
3.6.1.21
Amino sugar and nucleotide sugar metabolism
2.7.7.33
CDP-glucose
2.7.1.41
2.7.1.10
2.7.1.106
α-D-Glucose-1,6P2
5.4.2.2
α-D-Glucose-6P
3.1.3.9
2.7.1.1
2.7.1.2
α-D-Glucose
5.3.1.9
β-D-Fructose-6P
D-Fructose
2.4.1.7
Sucrose
2.7.7.27
ADP-glucose
2.4.1.21
3.6.1.21
α-D-Glucose-1P
Glycolysis / Gluconeogenesis
Glycogen; Amylose
2.4.1.18
3.2.1.33
2.4.1.15
2.4.1.245
Trehalose
3.2.1.28
2.4.1.64
D-Glucose
β-D-Glucose-6P
5.4.2.6
β-D-Glucose-1P
3.1.3.12
Trehalose-6P
3.2.1.122
3.2.1.93
D-Glucose-6P
TreXYZ
2.7.1.69
α,α-Trehalose (extracellular)
3.2.1.122
Maltose-6'P
2.7.1.69
Maltose (extracellular)
2.4.1.8
5.4.99.16
Cyclomaltodextrin
3.2.1.54
Maltodextrin
Starch; Glycogen
2.4.1.1
3.2.1.2
Maltose
3.2.1.1
Dextrin
2.4.1.25
3.2.1.20
3.2.1.3
3.2.1.10
3.2.1.3
α-D-Glucose
2.7.1.175
2.4.99.16
α-Maltose-1-P
3.2.1.74
3.2.1.10
Isomaltose
2.4.1.20
Celloheptaose
3.2.1.74
Cellohexaose
3.2.1.74
Cellopentaose
3.2.1.74
Cellotetraose
3.2.1.74
Cellotriose
3.2.1.74
Cellobiose

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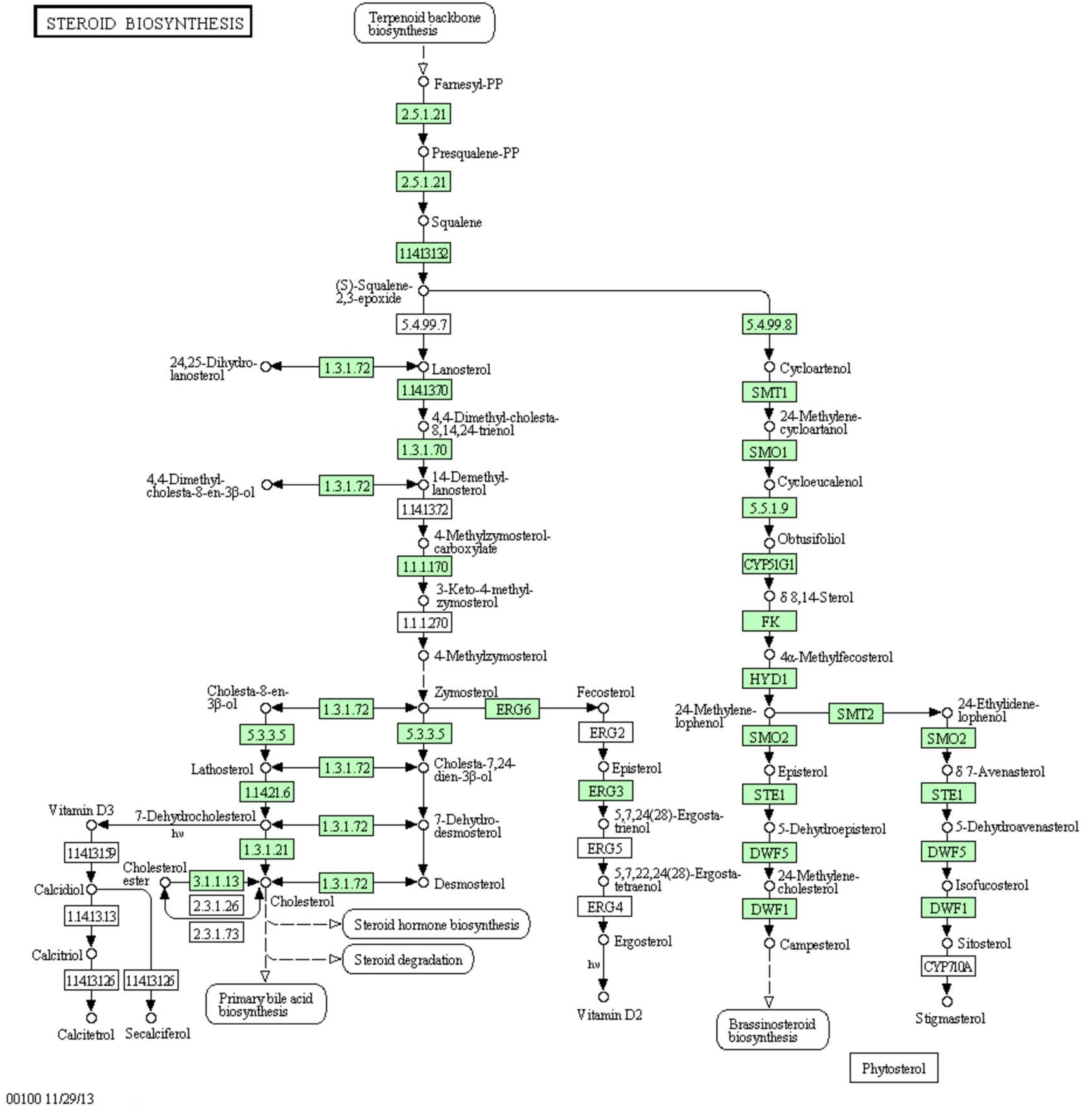
STEROID BIOSYNTHESIS
Terpenoid backbone biosynthesis
Farnesyl-PP
2.5.1.21
Presqualene-PP
2.5.1.21
Squalene
1.14.13.132
(S)-Squalene-2,3-epoxide
5.4.99.7
5.4.99.8
24,25-Dihydro-lanosterol
1.3.1.72
Lanosterol
1.14.13.70
4,4-Dimethyl-cholesta-8,14,24-trienol
1.3.1.70
4,4-Dimethyl-cholesta-8-en-3β-ol
1.3.1.72
14-Demethyl-lanosterol
1.14.13.72
4-Methylzymosterol-carboxylate
1.1.1.170
3-Keto-4-methyl-zymosterol
1.1.1.270
4-Methylzymosterol
Cholesta-8-en-3β-ol
1.3.1.72
Zymosterol
ERG6
Fecosterol
5.3.3.5
5.3.3.5
ERG2
Lathosterol
1.3.1.72
Cholesta-7,24-dien-3β-ol
Episterol
1.14.21.6
ERG3
Vitamin D3
7-Dehydrocholesterol
hν
1.3.1.72
7-Dehydro-desmosterol
5,7,24(28)-Ergosta-trienol
1.14.13.159
1.3.1.21
ERG5
Cholesterol ester
3.1.1.13
1.3.1.72
Desmosterol
5,7,22,24(28)-Ergosta-tetraenol
Calcidiol
2.3.1.26
Cholesterol
ERG4
1.14.13.13
2.3.1.73
Steroid hormone biosynthesis
Ergosterol
Calcitriol
Steroid degradation
hν
1.14.13.126
1.14.13.126
Primary bile acid biosynthesis
Vitamin D2
Calcitetrol
Secalciferol
Cycloartenol
SMT1
24-Methylene-cycloartanol
SMO1
Cycloeucalenol
5.5.1.9
Obtusifoliol
CYP51G1
δ 8,14-Sterol
FK
4α-Methylfecosterol
HYD1
24-Methylene-lophenol
SMT2
24-Ethylidene-lophenol
SMO2
SMO2
Episterol
δ 7-Avenasterol
STE1
STE1
5-Dehydroepisterol
5-Dehydroavenasterol
DWF5
DWF5
24-Methylene-cholesterol
Isofucosterol
DWF1
DWF1
Campesterol
Sitosterol
CYP710A
Brassinosteroid biosynthesis
Stigmasterol
Phytosterol
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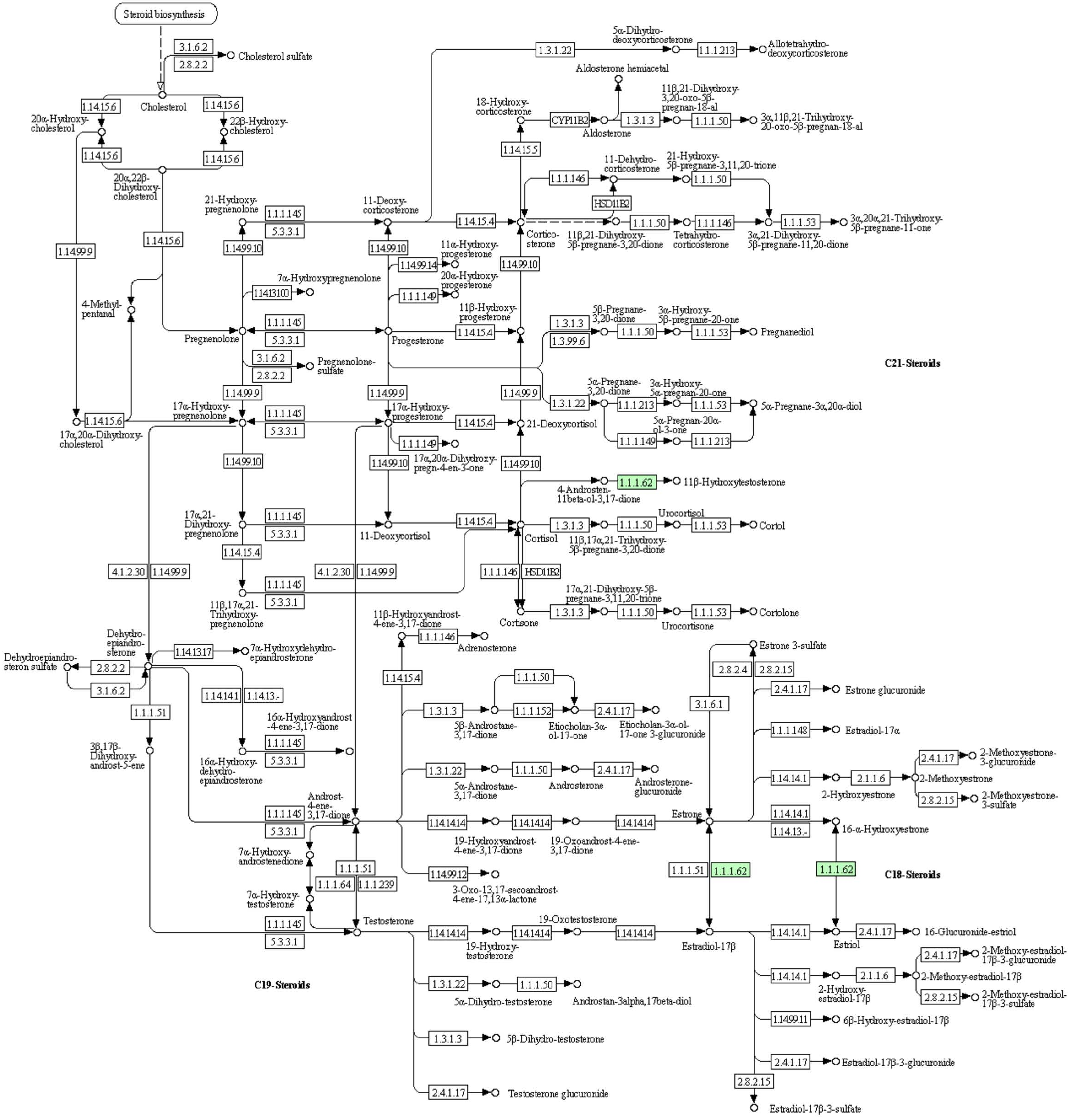
STEROID HORMONE BIOSYNTHESIS



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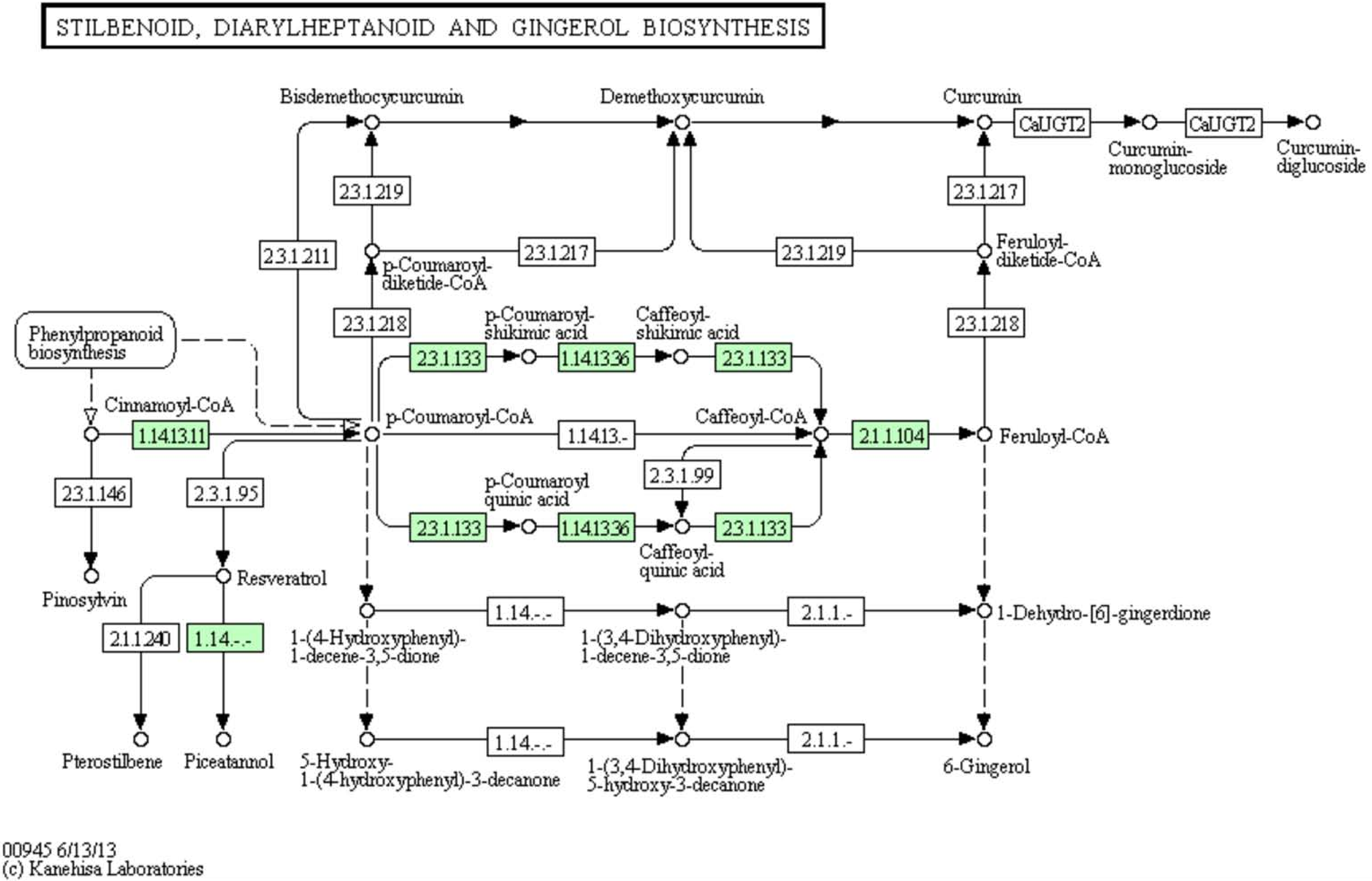
STILBENOID, DIARYLHEPTANOID AND GINGEROL BIOSYNTHESIS
Bisdemethocycurcumin
Demethoxycurcumin
Curcumin
CaUGT2
CaUGT2
Curcumin-monoglucoside
Curcumin-diglucoside
2.3.1.219
2.3.1.217
2.3.1.211
2.3.1.217
2.3.1.219
p-Coumaroyl-diketide-CoA
Feruloyl-diketide-CoA
2.3.1.218
2.3.1.218
Phenylpropanoid biosynthesis
p-Coumaroyl-shikimic acid
Caffeoyl-shikimic acid
2.3.1.133
1.14.13.36
2.3.1.133
Cinnamoyl-CoA
1.14.13.11
p-Coumaroyl-CoA
1.14.13.-
Caffeoyl-CoA
2.1.1.104
Feruloyl-CoA
2.3.1.146
2.3.1.95
2.3.1.99
p-Coumaroyl quinic acid
2.3.1.133
1.14.13.36
2.3.1.133
Caffeoyl-quinic acid
Pinosylvin
Resveratrol
2.1.1.240
1.14.-.-
1.14.-.-
2.1.1.-
1-Dehydro-[6]-gingerdione
1-(4-Hydroxyphenyl)-1-decene-3,5-dione
1-(3,4-Dihydroxyphenyl)-1-decene-3,5-dione
1.14.-.-
2.1.1.-
Pterostilbene
Piceatannol
5-Hydroxy-1-(4-hydroxyphenyl)-3-decanone
1-(3,4-Dihydroxyphenyl)-5-hydroxy-3-decanone
6-Gingerol
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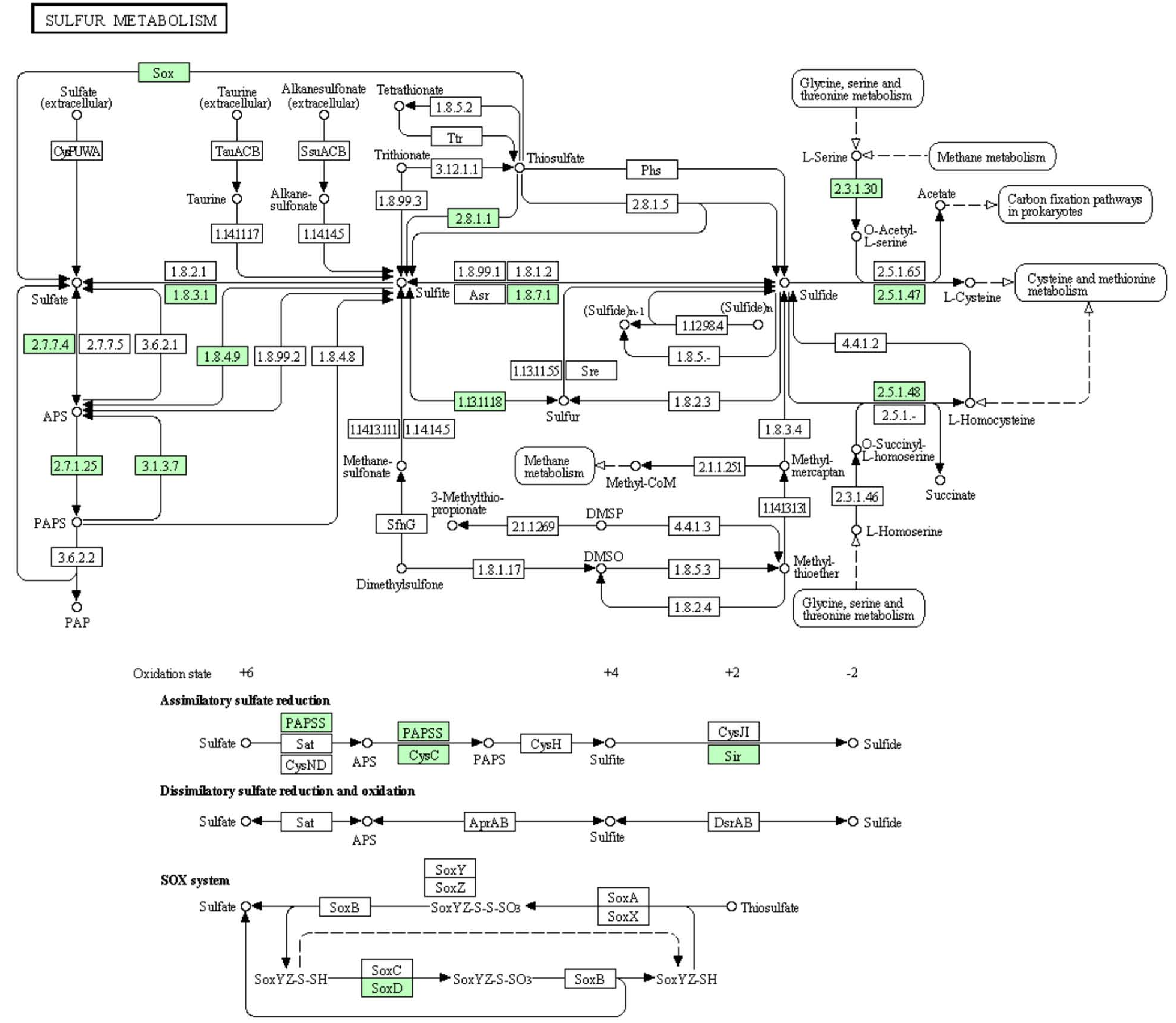
SULFUR METABOLISM
Sox
Sulfate (extracellular)
CysPUWA
Taurine (extracellular)
TauACB
Alkanesulfonate (extracellular)
SsuACB
Tetrathionate
1.8.5.2
Ttr
Trithionate
3.12.1.1
Thiosulfate
Phs
2.8.1.5
1.8.99.3
2.8.1.1
Taurine
Alkane-sulfonate
1.14.11.17
1.14.14.5
1.8.2.1
1.8.3.1
Sulfate
Sulfite
1.8.99.1
1.8.1.2
Asr
1.8.7.1
Sulfide
2.7.7.4
2.7.7.5
3.6.2.1
1.8.4.9
1.8.99.2
1.8.4.8
APS
2.7.1.25
3.1.3.7
PAPS
3.6.2.2
PAP
(Sulfide)n-1
(Sulfide)n
1.12.98.4
1.8.5.-
1.13.11.55
Sre
1.13.11.18
Sulfur
1.8.2.3
1.14.13.111
1.14.14.5
Methane-sulfonate
SfnG
Dimethylsulfone
1.8.1.17
DMSO
1.8.5.3
1.8.2.4
3-Methylthio-propionate
2.1.1.269
DMSP
4.4.1.3
Methyl-thioether
Methane metabolism
Methyl-CoM
2.1.1.251
Methyl-mercaptan
1.8.3.4
1.14.13.131
Glycine, serine and threonine metabolism
L-Serine
Methane metabolism
2.3.1.30
O-Acetyl-L-serine
Acetate
Carbon fixation pathways in prokaryotes
2.5.1.65
2.5.1.47
L-Cysteine
Cysteine and methionine metabolism
4.4.1.2
2.5.1.48
2.5.1.-
L-Homocysteine
O-Succinyl-L-homoserine
Succinate
2.3.1.46
L-Homoserine
Glycine, serine and threonine metabolism
Oxidation state
+6
+4
+2
-2
Assimilatory sulfate reduction
Sulfate
PAPSS
Sat
CysND
APS
PAPSS
CysC
PAPS
CysH
Sulfite
CysJI
Sir
Sulfide
Dissimilatory sulfate reduction and oxidation
Sulfate
Sat
APS
AprAB
Sulfite
DsrAB
Sulfide
SOX system
Sulfate
SoxB
SoxY
SoxZ
SoxYZ-S-S-SO3
SoxA
SoxX
Thiosulfate
SoxYZ-S-SH
SoxC
SoxD
SoxYZ-S-SO3
SoxB
SoxYZ-SH
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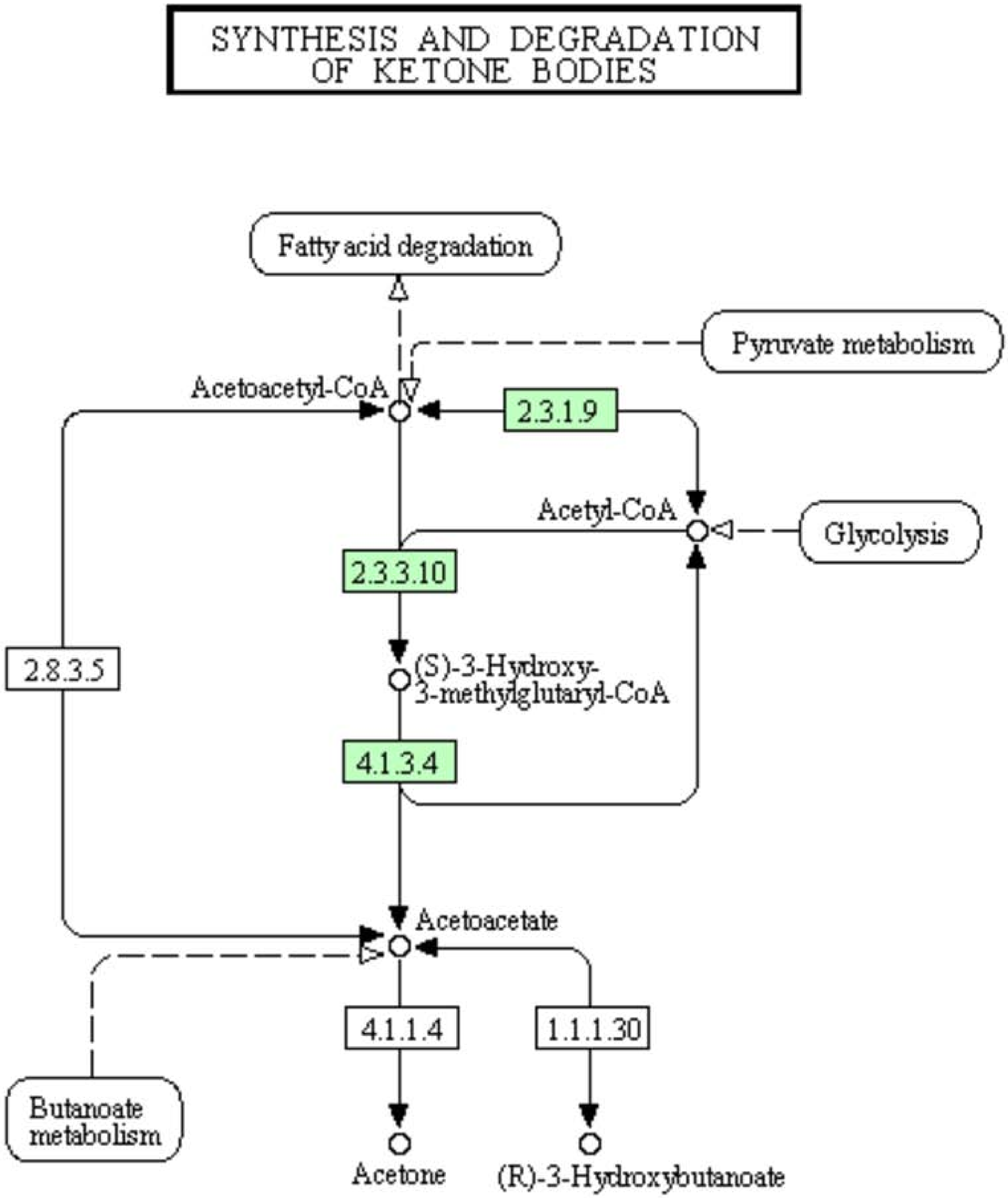

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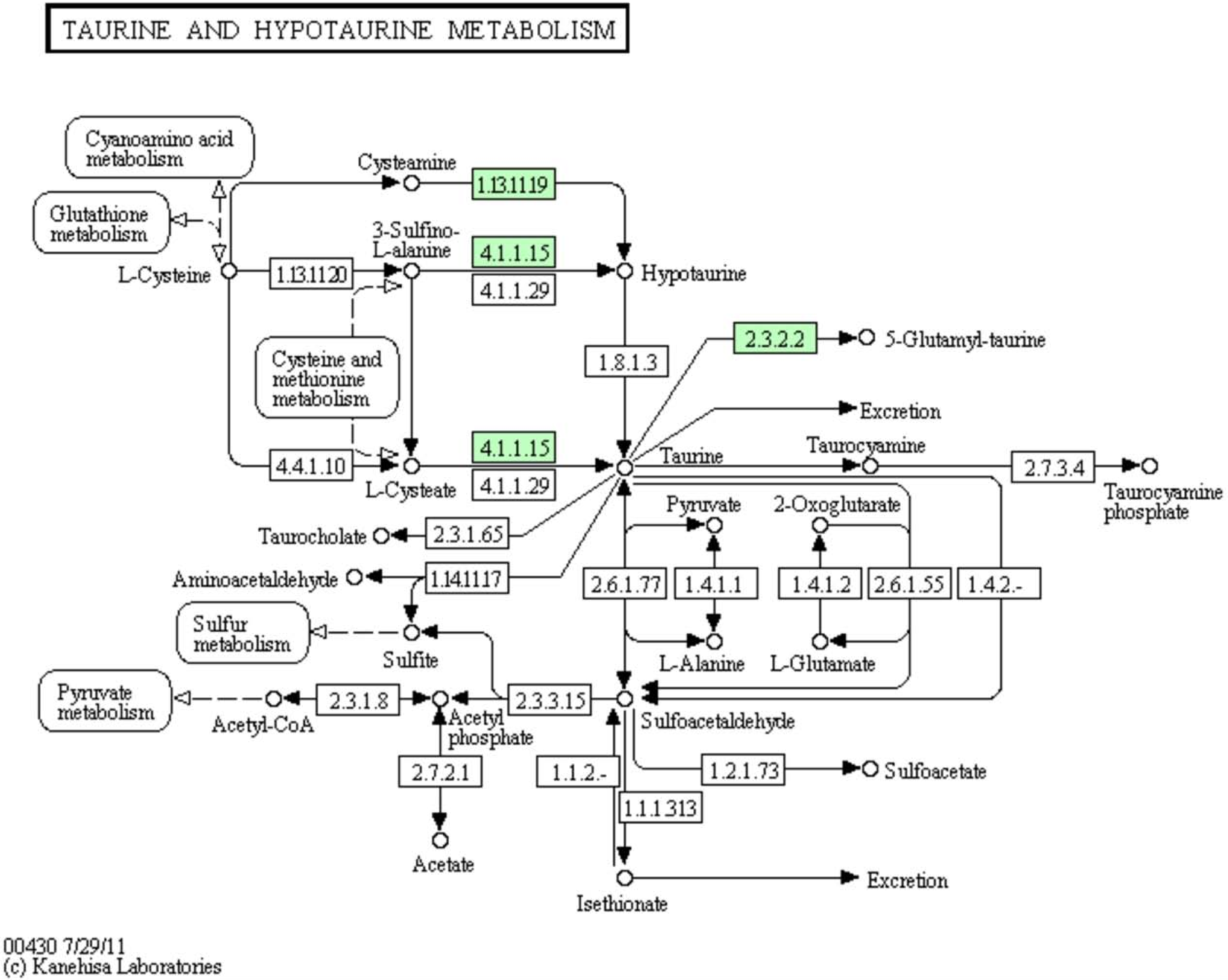
TAURINE AND HYPOTAURINE METABOLISM
Cyanoamino acid metabolism
Glutathione metabolism
L-Cysteine
Cysteamine
1.13.11.19
3-Sulfino-L-alanine
1.13.11.20
4.1.1.15
4.1.1.29
Hypotaurine
Cysteine and methionine metabolism
1.8.1.3
2.3.2.2
5-Glutamyl-taurine
Excretion
4.4.1.10
4.1.1.15
4.1.1.29
L-Cysteate
Taurine
Taurocyamine
2.7.3.4
Taurocyamine phosphate
Taurocholate
2.3.1.65
Aminoacetaldehyde
1.14.11.17
Pyruvate
2-Oxoglutarate
2.6.1.77
1.4.1.1
1.4.1.2
2.6.1.55
1.4.2.-
Sulfur metabolism
Sulfite
L-Alanine
L-Glutamate
Pyruvate metabolism
Acetyl-CoA
2.3.1.8
Acetyl phosphate
2.3.3.15
Sulfoacetaldehyde
2.7.2.1
Acetate
1.1.2.-
1.2.1.73
Sulfoacetate
1.1.1.313
Isethionate
Excretion
00430 7/29/11
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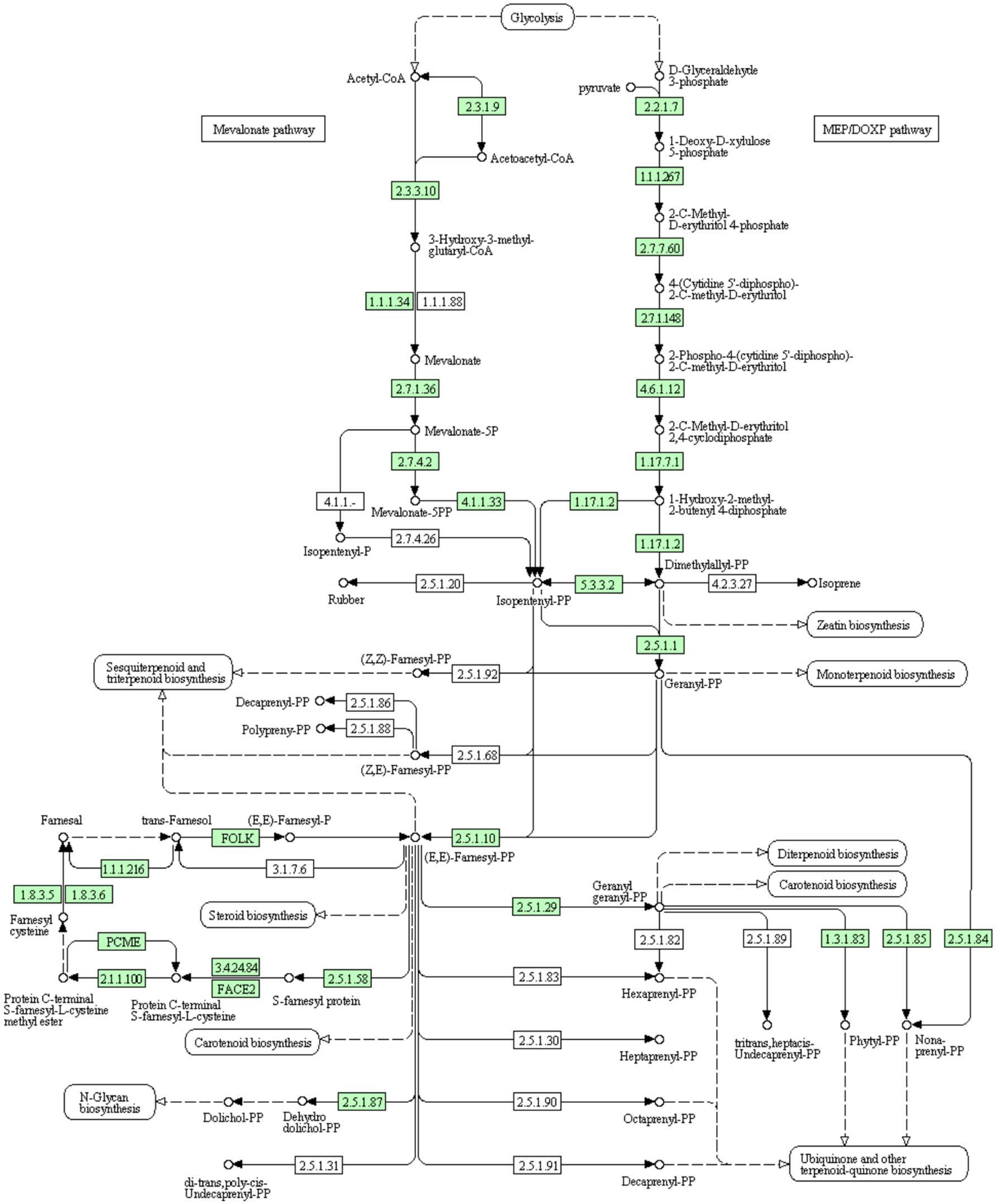
TERPENOID BACKBONE BIOSYNTHESIS



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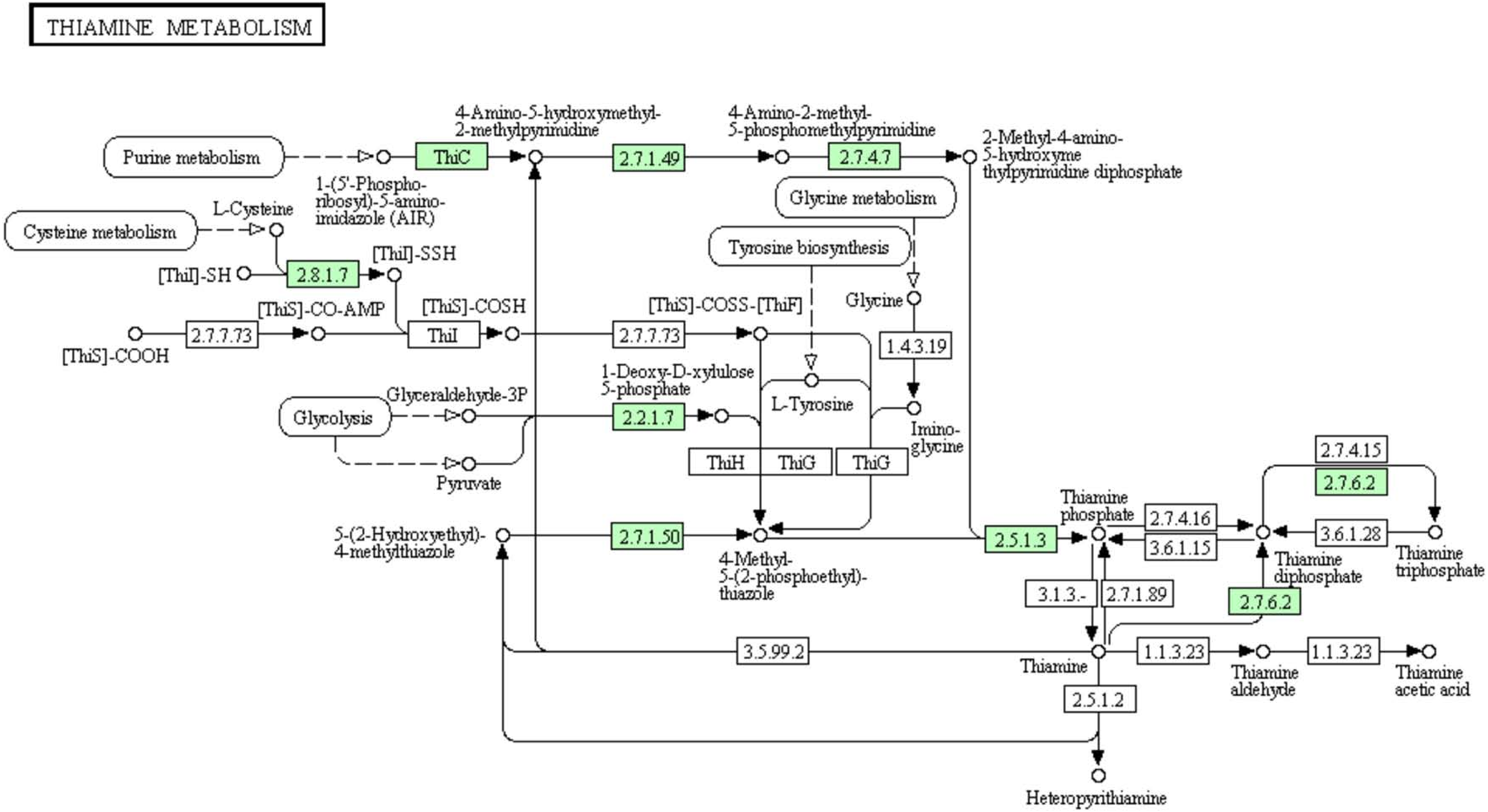

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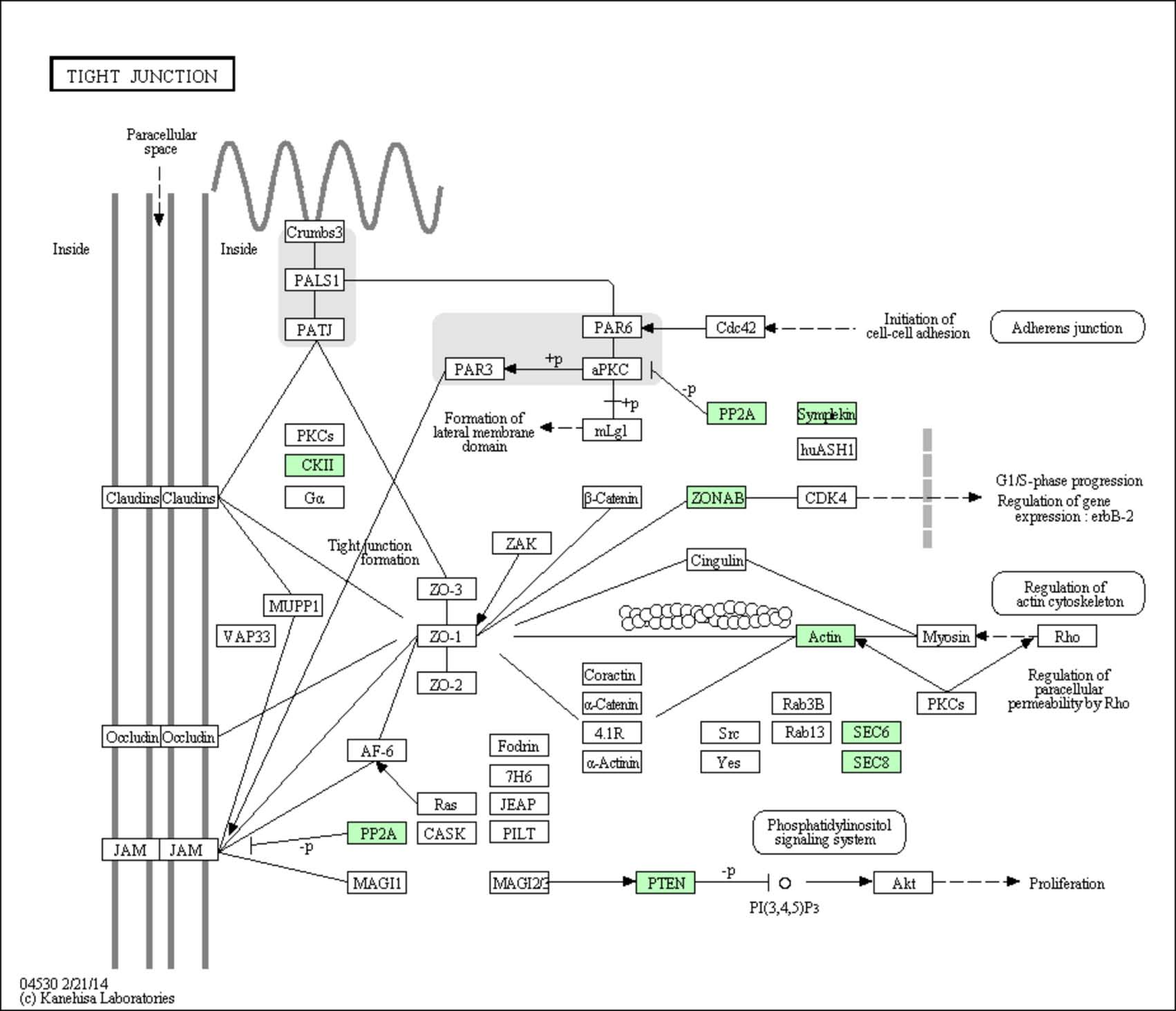
TIGHT JUNCTION
Paracellular space
Inside
Inside
Crumbs3
PALS1
PATJ
PAR6
Cdc42
Initiation of cell-cell adhesion
Adherens junction
PAR3
+p
aPKC
-p
PP2A
Symplekin
+p
Formation of lateral membrane domain
mLgl
huASH1
PKCs
CKII
Gα
Claudins
Claudins
β-Catenin
ZONAB
CDK4
G1/S-phase progression
Regulation of gene expression : erbB-2
ZAK
Tight junction formation
Cingulin
ZO-3
Regulation of actin cytoskeleton
MUPP1
VAP33
ZO-1
Actin
Myosin
Rho
ZO-2
Coractin
α-Catenin
Rab3B
PKCs
Regulation of paracellular permeability by Rho
Occludin
Occludin
4.1R
Src
Rab13
SEC6
AF-6
Fodrin
α-Actinin
Yes
SEC8
7H6
Ras
JEAP
PP2A
CASK
PILT
Phosphatidylinositol signaling system
JAM
JAM
-p
MAGI1
MAGI2/3
PTEN
-p
Akt
Proliferation
PI(3,4,5)P3
04530 2/21/14
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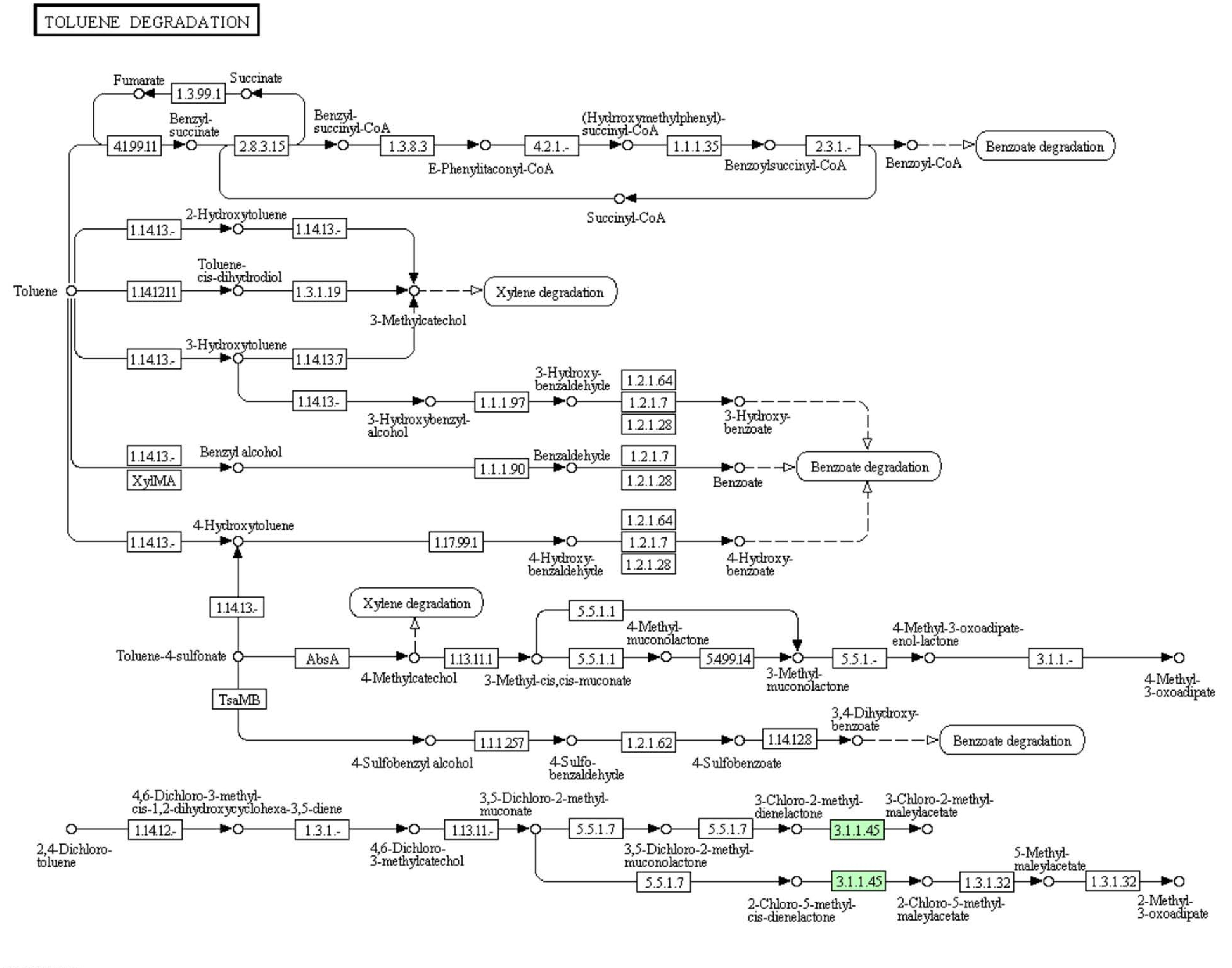
TOLUENE DEGRADATION
Fumarate
1.3.99.1
Succinate
Benzyl-
succinate
4.1.99.11
2.8.3.15
Benzyl-
succinyl-CoA
1.3.8.3
E-Phenylitaconyl-CoA
4.2.1.-
(Hydroxymethylphenyl)-
succinyl-CoA
1.1.1.35
Benzoylsuccinyl-CoA
2.3.1.-
Benzoyl-CoA
Benzoate degradation
Succinyl-CoA
1.14.13.-
2-Hydroxytoluene
1.14.13.-
Toluene
1.14.12.11
Toluene-
cis-dihydrodiol
1.3.1.19
Xylene degradation
3-Methylcatechol
1.14.13.-
3-Hydroxytoluene
1.14.13.7
1.14.13.-
3-Hydroxybenzyl-
alcohol
1.1.1.97
3-Hydroxy-
benzaldehyde
1.2.1.64
1.2.1.7
1.2.1.28
3-Hydroxy-
benzoate
1.14.13.-
XylMA
Benzyl alcohol
1.1.1.90
Benzaldehyde
1.2.1.7
1.2.1.28
Benzoate
Benzoate degradation
1.14.13.-
4-Hydroxytoluene
1.17.99.1
4-Hydroxy-
benzaldehyde
1.2.1.64
1.2.1.7
1.2.1.28
4-Hydroxy-
benzoate
1.14.13.-
Xylene degradation
Toluene-4-sulfonate
AbsA
4-Methylcatechol
1.13.11.1
3-Methyl-cis,cis-muconate
5.5.1.1
5.5.1.1
4-Methyl-
muconolactone
5.4.99.14
3-Methyl-
muconolactone
5.5.1.-
4-Methyl-3-oxoadipate-
enol-lactone
3.1.1.-
4-Methyl-
3-oxoadipate
TsaMB
4-Sulfobenzyl alcohol
1.1.1.257
4-Sulfo-
benzaldehyde
1.2.1.62
4-Sulfobenzoate
1.14.12.8
3,4-Dihydroxy-
benzoate
Benzoate degradation
2,4-Dichloro-
toluene
1.14.12.-
4,6-Dichloro-3-methyl-
cis-1,2-dihydroxycyclohexa-3,5-diene
1.3.1.-
4,6-Dichloro-
3-methylcatechol
1.13.11.-
3,5-Dichloro-2-methyl-
muconate
5.5.1.7
3,5-Dichloro-2-methyl-
muconolactone
5.5.1.7
3-Chloro-2-methyl-
dienelactone
3.1.1.45
3-Chloro-2-methyl-
maleylacetate
5.5.1.7
2-Chloro-5-methyl-
cis-dienelactone
3.1.1.45
2-Chloro-5-methyl-
maleylacetate
1.3.1.32
5-Methyl-
maleylacetate
1.3.1.32
2-Methyl-
3-oxoadipate
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TROPANE, PIPERIDINE AND PYRIDINE ALKALOID BIOSYNTHESIS

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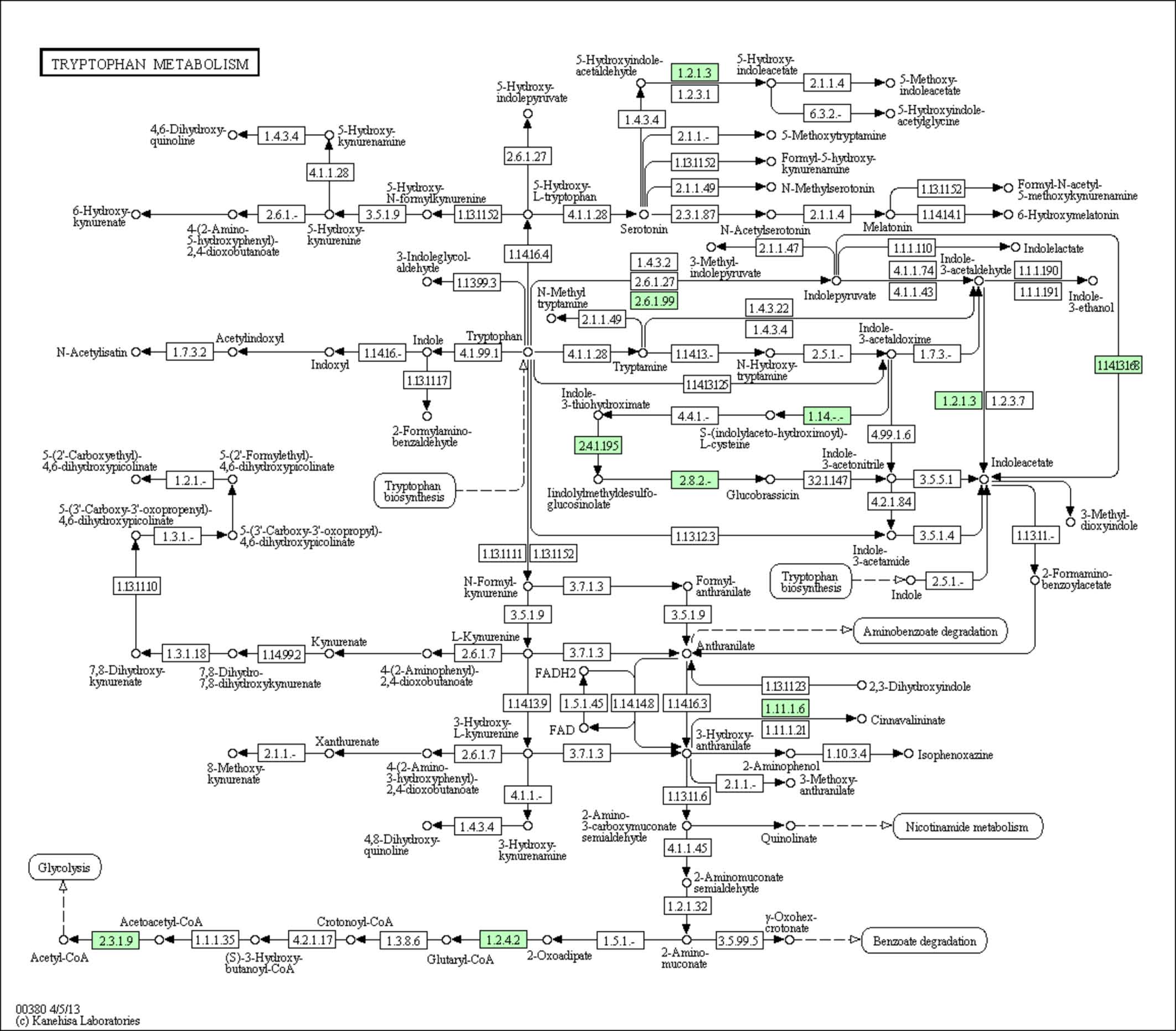
TRYPTOPHAN METABOLISM
5-Hydroxyindole-acetaldehyde
1.2.1.3
1.2.3.1
5-Hydroxy-indoleacetate
2.1.1.4
5-Methoxy-indoleacetate
6.3.2.-
5-Hydroxyindole-acetylglycine
5-Hydroxy-indolepyruvate
1.4.3.4
2.1.1.-
5-Methoxytryptamine
1.13.11.52
Formyl-5-hydroxy-kynurenamine
2.1.1.49
N-Methylserotonin
1.13.11.52
Formyl-N-acetyl-5-methoxykynurenamine
4,6-Dihydroxy-quinoline
1.4.3.4
5-Hydroxy-kynurenamine
2.6.1.27
4.1.1.28
5-Hydroxy-N-formylkynurenine
5-Hydroxy-L-tryptophan
6-Hydroxy-kynurenate
2.6.1.-
3.5.1.9
1.13.11.52
4.1.1.28
2.3.1.87
2.1.1.4
1.14.14.1
6-Hydroxymelatonin
4-(2-Amino-5-hydroxyphenyl)-2,4-dioxobutanoate
5-Hydroxy-kynurenine
Serotonin
N-Acetylserotonin
Melatonin
1.14.16.4
2.1.1.47
1.1.1.110
Indolelactate
3-Indoleglycol-aldehyde
1.4.3.2
3-Methyl-indolepyruvate
4.1.1.74
Indole-3-acetaldehyde
1.1.1.190
1.13.99.3
2.6.1.27
Indolepyruvate
4.1.1.43
1.1.1.191
Indole-3-ethanol
N-Methyl tryptamine
2.6.1.99
2.1.1.49
1.4.3.22
1.4.3.4
Indole-3-acetaldoxime
Acetylindoxyl
Indole
Tryptophan
N-Acetylisatin
1.7.3.2
1.14.16.-
4.1.99.1
4.1.1.28
1.14.13.-
2.5.1.-
1.7.3.-
1.14.13.168
Indoxyl
Tryptamine
N-Hydroxy-tryptamine
1.13.11.17
1.14.13.125
Indole-3-thiohydroximate
2-Formylamino-benzaldehyde
4.4.1.-
1.14.-.-
1.2.1.3
1.2.3.7
S-(indolylaceto-hydroximoyl)-L-cysteine
4.99.1.6
5-(2'-Carboxyethyl)-4,6-dihydroxypicolinate
5-(2'-Formylethyl)-4,6-dihydroxypicolinate
2.4.1.195
Indole-3-acetonitrile
Indoleacetate
1.2.1.-
2.8.2.-
3.2.1.147
3.5.5.1
Tryptophan biosynthesis
Indolylmethyldesulfo-glucosinolate
Glucobrassicin
4.2.1.84
3-Methyl-dioxyindole
5-(3'-Carboxy-3'-oxopropenyl)-4,6-dihydroxypicolinate
1.3.1.-
5-(3'-Carboxy-3'-oxopropyl)-4,6-dihydroxypicolinate
1.13.12.3
3.5.1.4
1.13.11.-
1.13.11.11
1.13.11.52
Indole-3-acetamide
1.13.11.10
Tryptophan biosynthesis
2.5.1.-
2-Formamino-benzoylacetate
N-Formyl-kynurenine
3.7.1.3
Formyl-anthranilate
Indole
3.5.1.9
3.5.1.9
Aminobenzoate degradation
Kynurenate
L-Kynurenine
Anthranilate
1.3.1.18
1.14.99.2
2.6.1.7
3.7.1.3
7,8-Dihydroxy-kynurenate
7,8-Dihydro-7,8-dihydroxykynurenate
4-(2-Aminophenyl)-2,4-dioxobutanoate
FADH2
1.13.11.23
2,3-Dihydroxyindole
1.14.13.9
1.5.1.45
1.14.14.8
1.14.16.3
1.11.1.6
3-Hydroxy-L-kynurenine
FAD
Cinnavalininate
1.11.1.21
3-Hydroxy-anthranilate
Xanthurenate
2.1.1.-
2.6.1.7
3.7.1.3
1.10.3.4
Isophenoxazine
8-Methoxy-kynurenate
4-(2-Amino-3-hydroxyphenyl)-2,4-dioxobutanoate
2-Aminophenol
2.1.1.-
3-Methoxy-anthranilate
4.1.1.-
1.13.11.6
2-Amino-3-carboxymuconate semialdehyde
1.4.3.4
Quinolinate
Nicotinamide metabolism
4,8-Dihydroxy-quinoline
3-Hydroxy-kynurenamine
4.1.1.45
2-Aminomuconate semialdehyde
Glycolysis
1.2.1.32
γ-Oxohex-crotonate
Acetoacetyl-CoA
Crotonoyl-CoA
Acetyl-CoA
2.3.1.9
1.1.1.35
4.2.1.17
1.3.8.6
1.2.4.2
1.5.1.-
3.5.99.5
Benzoate degradation
(S)-3-Hydroxy-butanoyl-CoA
Glutaryl-CoA
2-Oxoadipate
2-Amino-muconate
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TWO-COMPONENT SYSTEM
OmpR family
Phosphate limitation
PhoR
PhoB
PhoP
PhoA
PhoD
Phosphate assimilation
SenX3
RegX3
PstS
Mg2+ starvation
Antimicrobial peptide
PhoQ
PagC
PagO
PagD
PagK
PgtE
PhoN
Virulence, antimicrobial peptide resistance
Osmotic upshift (K+)
EnvZ
OmpR
OmpC
OmpF
Outer membrane
smaller hole
larger hole
Stress
RstB
RstA
Misfolded proteins
CpxA
CpxR
HtrA
Cell envelope protein folding, and protein degradation
Secretion stress
Misfolded proteins
CssS
CssR
Serine protease
CreC
CreB
BaeS
BaeR
Multidrug efflux
MdtA
MdtB
MdtC
Ferric ion
BasS
BasR
ArnB
Modification of lipopolysaccharides
Copper ions
CusS
CusR
Copper / silver efflux
CusC
CusF
CusB
CusA
Hormone-like molecules
Quorum sensing
QseC
QseB
Flagella regulon
FlhD
FlhC
FliC
FliA
MotA
K+ limitation
KdpD
KdpE
Potassium transport
KdpA
KdpB
KdpC
KdpF
Trimethylamine N-oxide
TorS
TorR
Trimethylamine N-oxide respiration
TorC
TorA
TorD
Quinone electron carriers
ArcB
ArcA
Anaerobic respiration
Catabolite repression
TctE
TctD
Tricarboxylates transport
TctA
TctB
TctC
Oxygen limitation
ResE
ResD
CtaA
Aerobic and anaerobic respiration
Temperature
VicK
VicR
Bacterial cell wall, membrane composition
GtfB
GtfC
GtfD
FtF
MprB
MprA
PepD
Serine protease
MtrB
MtrA
DnaA
DNA replication
Cell envelope stress, osmoprotection, cell division
Low oxygen condition
PrrB
PrrA
Photosynthesis
TrcS
TrcR
Intracellular multiplication
Ni2+ ions
Changes in the PQ redox poise
NrsS
NrsR
NrsB
NrsA
NrsC
NrsD
Photosystem I, II genes
Mn2+ starvation
ManS
ManR
Manganese transport
MntC
MntA
MntB
High light exposure
Nutrient deprivation
NblS
NblR
Photosynthesis and metabolic process regulation
Circadian timing signal
SasA
RpaA
RpaB
Energy transfer from phycobilisomes to photosystem II
agr quorum sensing signal
SaeS
SaeR
Virulence genes
Bacitracin
BceS
BceR
Bacitracin efflux
BceA
BceB
Cationic antimicrbial peptide
YxdK
YxdJ
YxdL
YxdM
Acidic condition
ChvG
ChvI
Virulence genes
CiaH
CiaR
CiaX
CiaI
Stress resistance and pathogenesis
Cationic antimicrobial peptide
ParS
ParR
OprD
MexX
MexY
β-Lactam resistance
Sporulation family
KinA
KinB
KapB
KinC
KinD
KinE
Spo0F
Spo0B
Spo0A
Environmental conditions
Sporulation
Biofilm formation
CitB family
Citrate
CitA
CitB
Citrate fermentation
CitC
CitD
CitE
CitF
CitX
CitG
CitT
AppY
Anaerobic metabolism
Mg2+-Citrate complex
CitS
CitT
CitM
Citrate transport
Fumarate
DcuS
DcuR
DcuB
Anaerobic fumarate respiratory system
C4-Dicarboxyrate
DctS
DctR
DctP
C4-Dicarboxyrate transport
DctB
Malate
MalK
MalR
Malate utilization
MaeA
MaeN
YflS
LytT family
LytS
LytR
LrgA
LrgB
Autolysis
Murein hydrolase activity
AlgZ
AlgR
AlgD
Alginate biosynthesis
NatK
NatR
Sodium extrusion
NatA
NatB
AgrA family
AgrB
AgrD
Autoinducing peptide
Quorum sensing
AgrC
AgrA
Exoproteins
Cell wall proteins
ComA
ComB
ComC
Competence stimulating peptide
ComD
ComE
Early com genes
ComA
ComB
ComC
ComD
ComE
ComX
Late com genes
Competence
NarL family
Nitrate / Nitrite
NarX
NarQ
NarL
NarP
Nitrate reductase
NarG
NarH
NarJ
NarI
Formate dehydrogenase
FdnG
FdnH
FdnI
Fumarate reductase
FrdA
FrdB
FrdC
FrdD
Nitrogen metabolism
Glucose 6-P
UhpC
UhpB
UhpA
UhpT
Hexose phosphate uptake
Glucose
RcsF
RcsC
RcsD
RcsA
RcsB
cps genes (Capsular polysaccharide synthesis)
SdiA
BarA
UvrY
CsrB
CsrA
Carbon storage regulator
Pheromone
ComX
Quorum sensing
ComP
ComA
ComS
Competence
EvgS
EvgA
EmrK
EmrY
Antibiotic resistance
FimZ
AmpC
beta-lactam resistance
Salt stress
DegS
DegU
Degradative enzymes
Low temperature
DesK
DesR
Des
Membrane phospholipid desaturase
Cell wall stress stimulon
VraS
VraR
Cell wall biosynthesis
Peptidoglycan biosynthesis
Cell wall-active antibiotics
Cationic antimicrobial peptide
LiaS
LiaR
LiaI
LiaH
LiaG
LiaF
LiaS
LiaR
Hypoxia
DevS
DevR
Oxygen
NreB
NreC
NreA
NreB
NreC
NarG
NarH
NarJ
NarI
NarT
Nitrogen assimilation
YdfH
YdfI
YdfJ
NtrC family
GlnD
GlnB
Nitrogen assimilation
Nitrogen availability low
GlnL
NtrY
GlnG
GlnA
Glutamate metabolism
NtrX
NifA
Zn / Pb
HydH
HydG
ZraP
Zinc / lead efflux
Labile hydrogenase activity
Acetoacetate
AtoS
AtoC
AtoD
AtoA
AtoE
AtoB
Short chain fatty acid metabolism
PgtC
PgtB
PgtA
PgtP
Phosphoglycerate transport
C4-Dicarboxyrate
DctB
DctD
DctA
C4-Dicarboxyrate transport
PilS
PilR
RpoN
PilA
KinB
AlgB
AlgD
Alginate biosynthesis
Stationary phase
Hormone-like molecules
QseC
QseF/GlrK
QseF/GlrR
RpoN
GlmY
Amino sugar metabolism
Attaching and effacing (AE) lesions
SalK
SalR
Virulence genes
Chemotaxis family
Bacterial chemotaxis
Attractant / Repellent
MCP
CheW
CheA
CheR
CheY
CheV
CheB
Flageller motor switch
Adaptation
Flageller assembly
ChpC
PilI
PilJ
ChpA
PilK
PilG
PilH
ChpB
Twitching motility
PixI
PixJ
PixL
PixG
PixH
Positive phototactic motility
Surfaces or cell contact
WspB/D
WspA
WspE
WspR
WspF
WspC
c-di-GMP
Extracellular polysaccharide production
Red/Far-red light
Cph1
Rcp1
Phytocrome
Growth and development
Cell cycle family
PleC
PleD
c-di-GMP
Pole morphogenesis
DivJ
DivK
Cell cycle progression and development
Cell cycle - Caulobacter
CckA
ChpT
CtrA
CpdR
Cell cycle progression
Lux family
Autoinducer
AI-2
LuxP
LuxQ
CAI-1
CqsS
AI-1/HAI-1
LuxN
LuxU
LuxO
sRNAs
Qrr
LuxR
Luciferase operon
LuxC
LuxD
LuxA
LuxB
LuxE
LuxR family
C4-Dicarboxyrate
DctS
DctR
DctP
DctQ
DctM
C4-Dicarboxyrate transport
Tetrathionate
TtrS
TtrR
TtrA
TtrB
TtrC
Tetrathionate respiration
Oxygen limitation
FixL
FixJ
NifA
FixK
nif genes
fix genes
Respiration and nitrogen fixation
SsrA/SpiR
SsrB
SPI-2 genes
Bacterial secretion system
Other families
FlrA
σ54
FlrB
FlrC
Class III flagellar system genes
Flageller assembly
Glutamate
σ54
AauS
AauR
AatP
AatM
AatQ
AatJ
AnsA
Acidic amino acid uptake and metabolism
Hyperosmotic stress
Sln1
Ypd1
Ssk1
Ssk2
Osmolyte synthesis
MAPK signaling pathway - yeast
Skn7
Heat shock genes
Diffusible signaling factor (DSF)
RpfC
RpfG
RpfF
c-di-GMP
Clp
σ54
Biofilm formation, motility, and virulence
DSF synthesis
Glutamine
GlnK
GlnL
GlsA
GlnT
Glutamine utilization
YesM
YesN
CikA
Circadian genes
Redox signal
RegB
RegA
Puc
Puf
Puh
Photosystem
PetA
PetB
PetC
CycA/Y
Electron transfer system
Oxidative phosphorylation
CcoN
CcoO
CcoQ
CcoP
CydA
CydB
Aerobic respiration
NifA
Nitrogen assimilation
+p
-p
e
?
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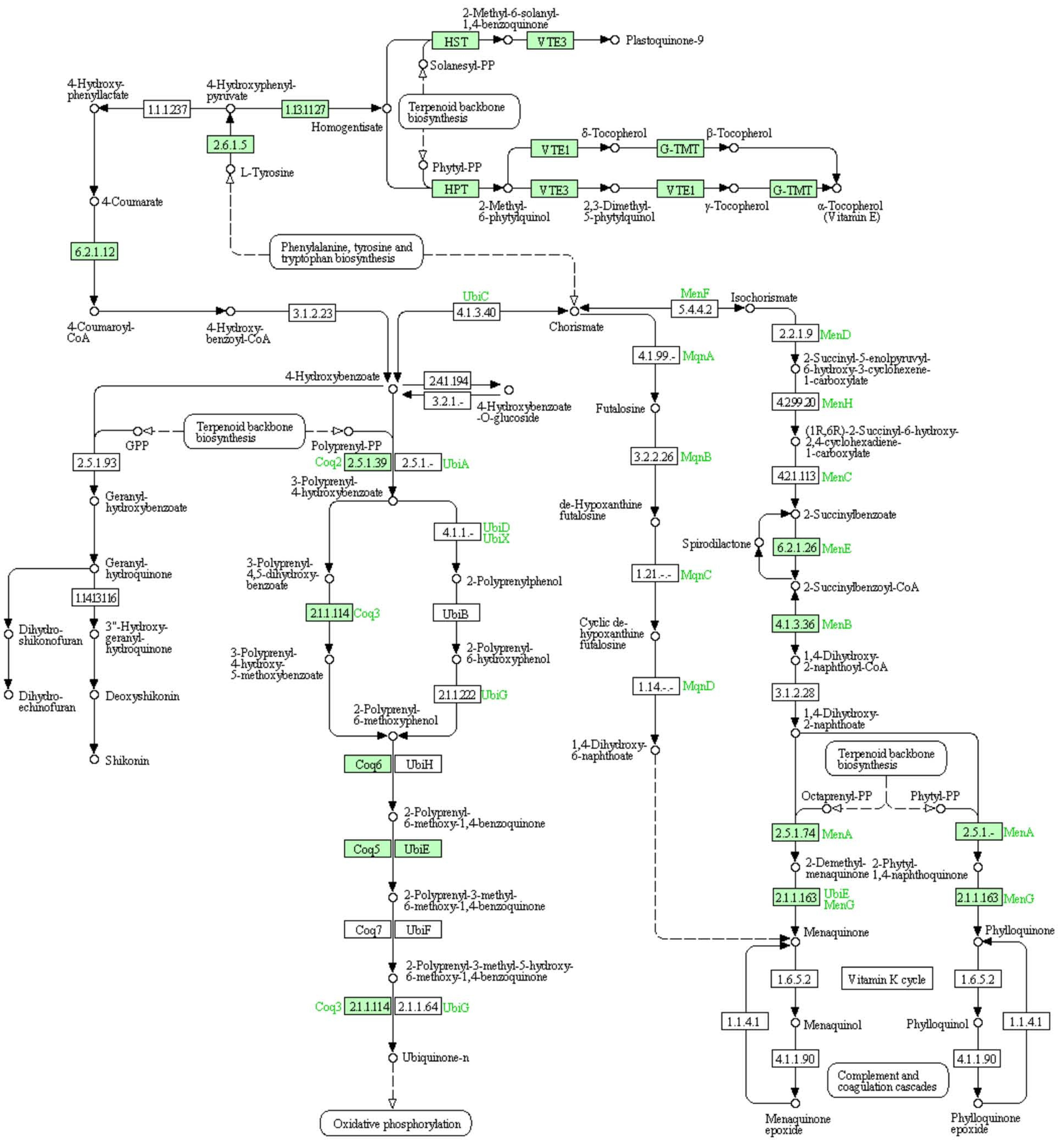
UBIQUINONE AND OTHER TERPENOID-QUINONE BIOSYNTHESIS



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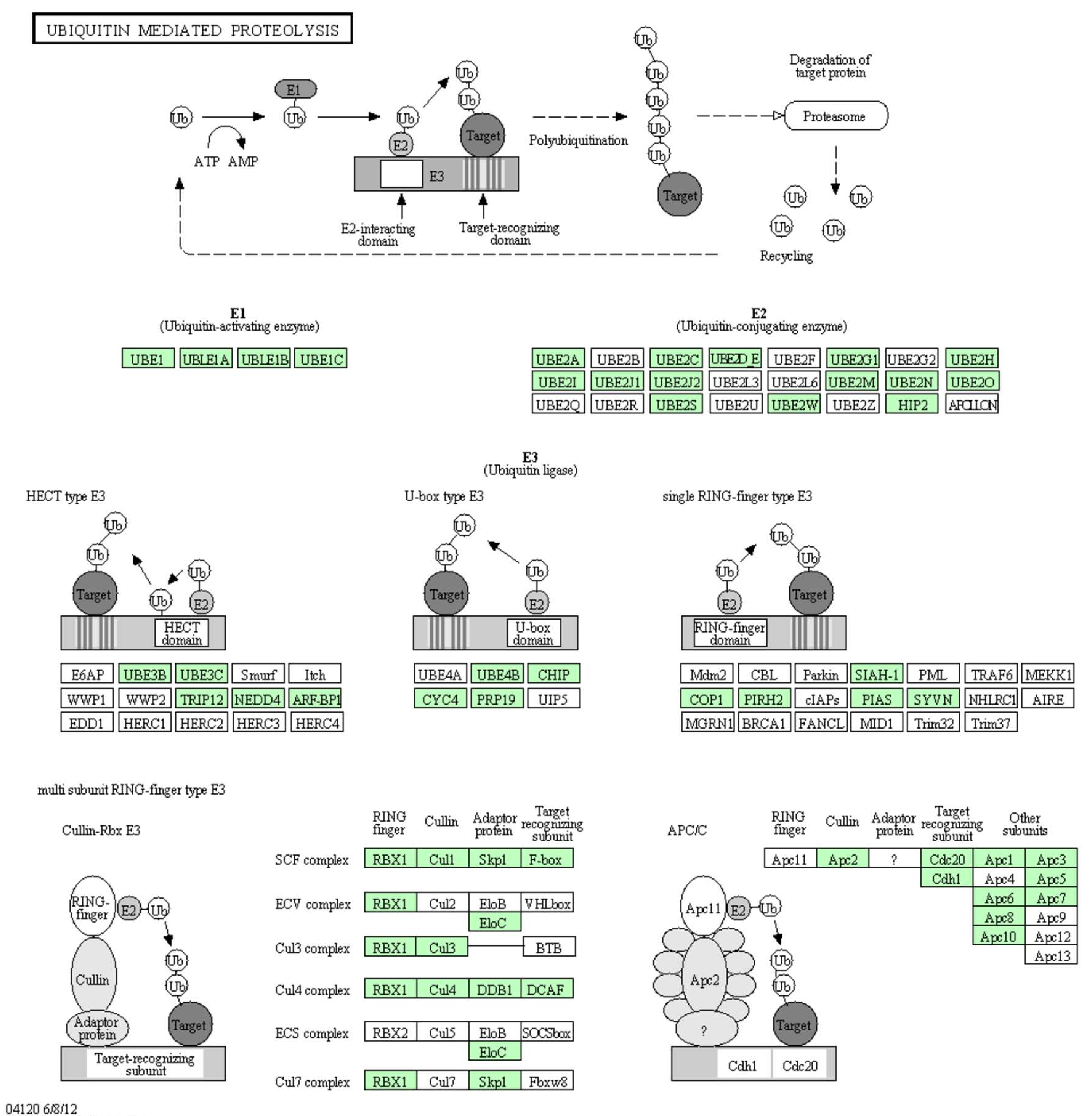
UBIQUITIN MEDIATED PROTEOLYSIS
Ub
ATP AMP
E1
E2
E3
Target
E2-interacting domain
Target-recognizing domain
Polyubiquitination
Degradation of target protein
Proteasome
Recycling
E1
(Ubiquitin-activating enzyme)
UBE1
UBLE1A
UBLE1B
UBE1C
E2
(Ubiquitin-conjugating enzyme)
UBE2A
UBE2B
UBE2C
UBE2D_E
UBE2F
UBE2G1
UBE2G2
UBE2H
UBE2I
UBE2J1
UBE2J2
UBE2L3
UBE2L6
UBE2M
UBE2N
UBE2O
UBE2Q
UBE2R
UBE2S
UBE2U
UBE2W
UBE2Z
HIP2
APOLLON
E3
(Ubiquitin ligase)
HECT type E3
HECT domain
E6AP
UBE3B
UBE3C
Smurf
Itch
WWP1
WWP2
TRIP12
NEDD4
ARF-BP1
EDD1
HERC1
HERC2
HERC3
HERC4
U-box type E3
U-box domain
UBE4A
UBE4B
CHIP
CYC4
PRP19
UIP5
single RING-finger type E3
RING-finger domain
Mdm2
CBL
Parkin
SIAH-1
PML
TRAF6
MEKK1
COP1
PIRH2
cIAPs
PIAS
SYVN
NHLRC1
AIRE
MGRN1
BRCA1
FANCL
MID1
Trim32
Trim37
multi subunit RING-finger type E3
Cullin-Rbx E3
RING-finger
Cullin
Adaptor protein
Target-recognizing subunit
RING finger
Cullin
Adaptor protein
Target recognizing subunit
SCF complex
RBX1
Cul1
Skp1
F-box
ECV complex
RBX1
Cul2
EloB
VHLbox
EloC
Cul3 complex
RBX1
Cul3
BTB
Cul4 complex
RBX1
Cul4
DDB1
DCAF
ECS complex
RBX2
Cul5
EloB
SOCSbox
EloC
Cul7 complex
RBX1
Cul7
Skp1
Fbxw8
APC/C
Apc11
Apc2
?
Cdh1
Cdc20
RING finger
Cullin
Adaptor protein
Target recognizing subunit
Other subunits
Apc11
Apc2
?
Cdc20
Apc1
Apc3
Cdh1
Apc4
Apc5
Apc6
Apc7
Apc8
Apc9
Apc10
Apc12
Apc13
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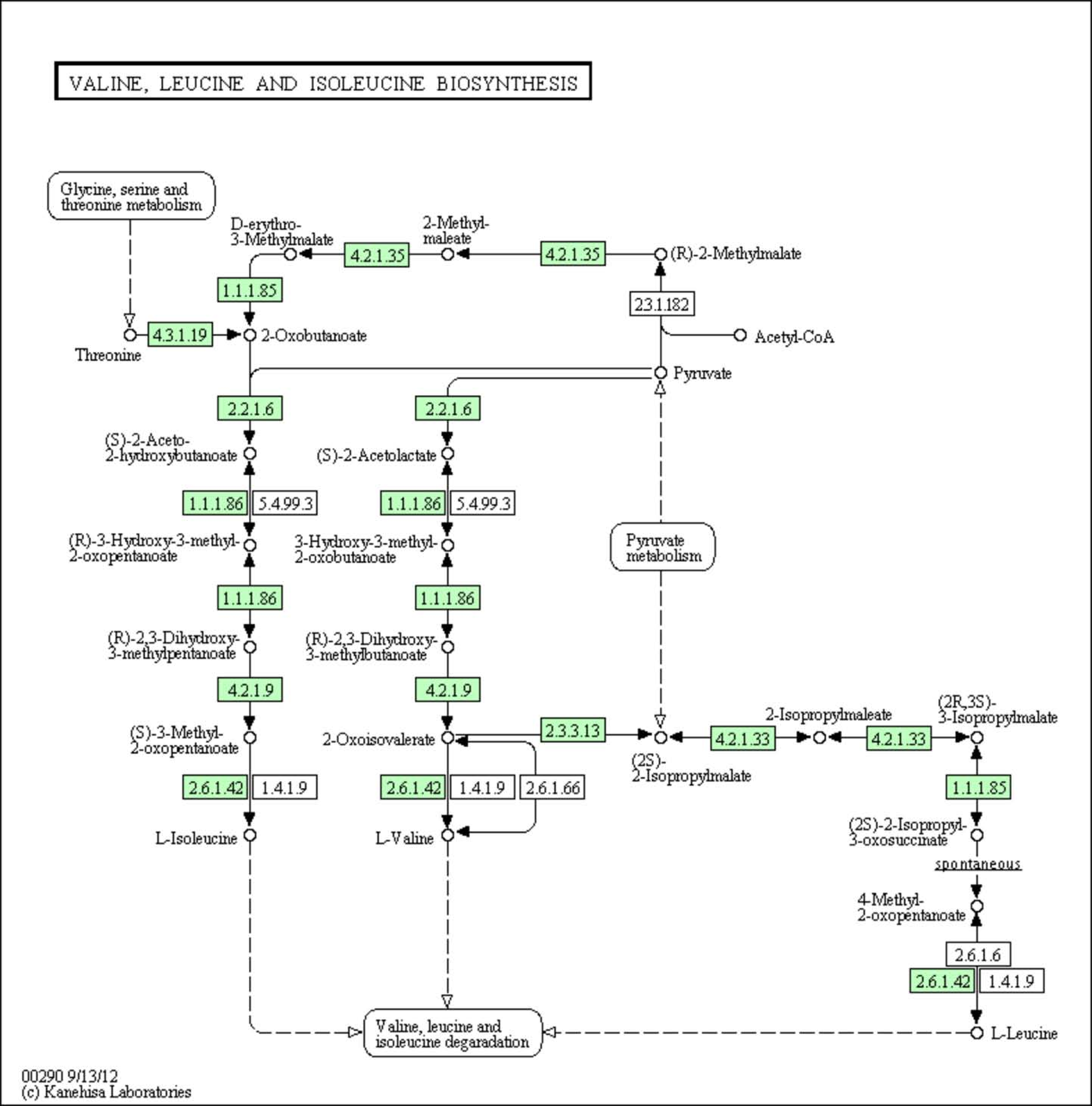
VALINE, LEUCINE AND ISOLEUCINE BIOSYNTHESIS
Glycine, serine and threonine metabolism
D-erythro-3-Methylmalate
4.2.1.35
2-Methylmaleate
4.2.1.35
(R)-2-Methylmalate
1.1.1.85
2.3.1.182
Threonine
4.3.1.19
2-Oxobutanoate
Acetyl-CoA
Pyruvate
2.2.1.6
2.2.1.6
(S)-2-Aceto-2-hydroxybutanoate
(S)-2-Acetolactate
1.1.1.86
5.4.99.3
1.1.1.86
5.4.99.3
(R)-3-Hydroxy-3-methyl-2-oxopentanoate
3-Hydroxy-3-methyl-2-oxobutanoate
Pyruvate metabolism
1.1.1.86
1.1.1.86
(R)-2,3-Dihydroxy-3-methylpentanoate
(R)-2,3-Dihydroxy-3-methylbutanoate
4.2.1.9
4.2.1.9
(S)-3-Methyl-2-oxopentanoate
2-Oxoisovalerate
2.3.3.13
(2S)-2-Isopropylmalate
4.2.1.33
2-Isopropylmaleate
4.2.1.33
(2R,3S)-3-Isopropylmalate
2.6.1.42
1.4.1.9
2.6.1.42
1.4.1.9
2.6.1.66
1.1.1.85
L-Isoleucine
L-Valine
(2S)-2-Isopropyl-3-oxosuccinate
spontaneous
4-Methyl-2-oxopentanoate
2.6.1.6
2.6.1.42
1.4.1.9
Valine, leucine and isoleucine degaradation
L-Leucine
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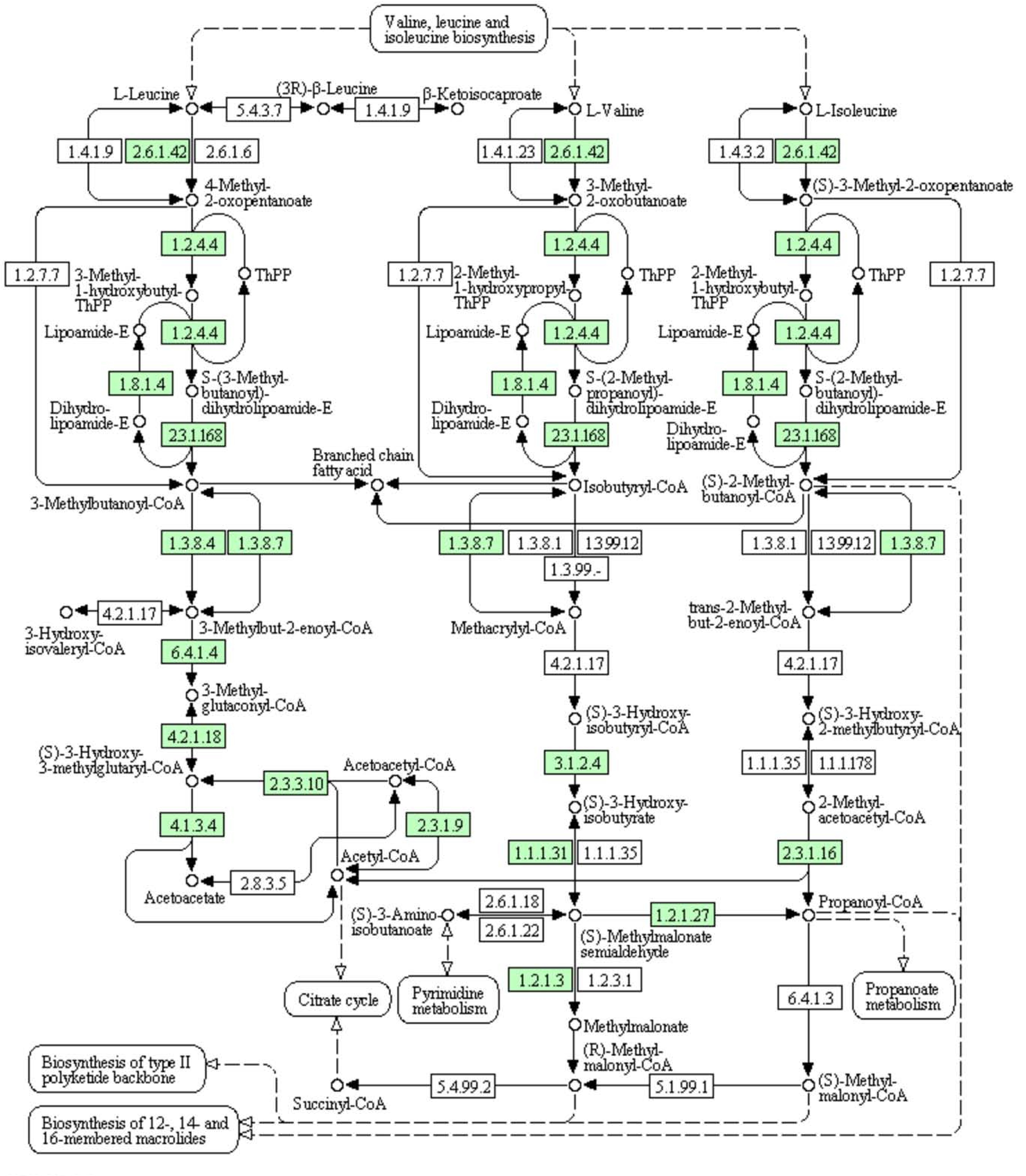
VALINE, LEUCINE AND ISOLEUCINE DEGRADATION



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VARIOUS TYPES OF N-GLYCAN BIOSYNTHESIS
High-mannose type (Yeast)
N-Glycan biosynthesis
MAN1
OCH1
2.4.1.-
MNN1
MNN9
VAN1
MNN10
MNN11
ANP1
HOC1
MNN2
MNN5
MNN6
Man α1 — 6Manα1
Man α1 — 3Manα1 — 2Manα1
Manα1 — 3Manα1 — 2Manα1
Manα1 — 3Man1 — P
Manα1 — 3Manα1
6/2 Manα1
6Manα1
6/3 Manα1
6/2 Manα1
Manα1 — 3Manα1 — 2Manα1
6/3 Manβ1 — 4 GlcNAcβ1 — 4 GlcNAcβ1 — Asn
Complex type (Plant)
MGAT1
MAN2
MGAT2
XYLT
FUT11
GALT1
FUT13
Fucα1
Galβ1
4/3 GlcNAcβ1 — 2Manα1
6/3 Manβ1 2
Xyl β1
4 GlcNAcβ1
4/3 GlcNAcβ1 — Asn
Paucimannose type (Nematode)
FUT8
GALT-1
HEX-2
FUT-1
Manα1
6/3 Manβ1 — 4GlcNAcβ1
Galβ1 — 4 Fucα1
6/4/3 GlcNAcβ1 — Asn
Glycohormone
2.4.1.38
2.4.99.6
2.4.1.244
CHST8/9
S — GalNAcβ1
Neu5Acα2 — 3Galβ1
4/4 GlcNAcβ1 — 2 Manα1
Neu5Acα2 — 3 Galβ1 — 4 GlcNAcβ1
S — 4GalNAcβ1
Neu5Acα2 — 3 Galβ1
4/2 Manα1
6/3 Manβ1 — 4 GlcNAcβ1
Fucα1
6/4 GlcNAcβ1 — Asn
00513 11/20/12
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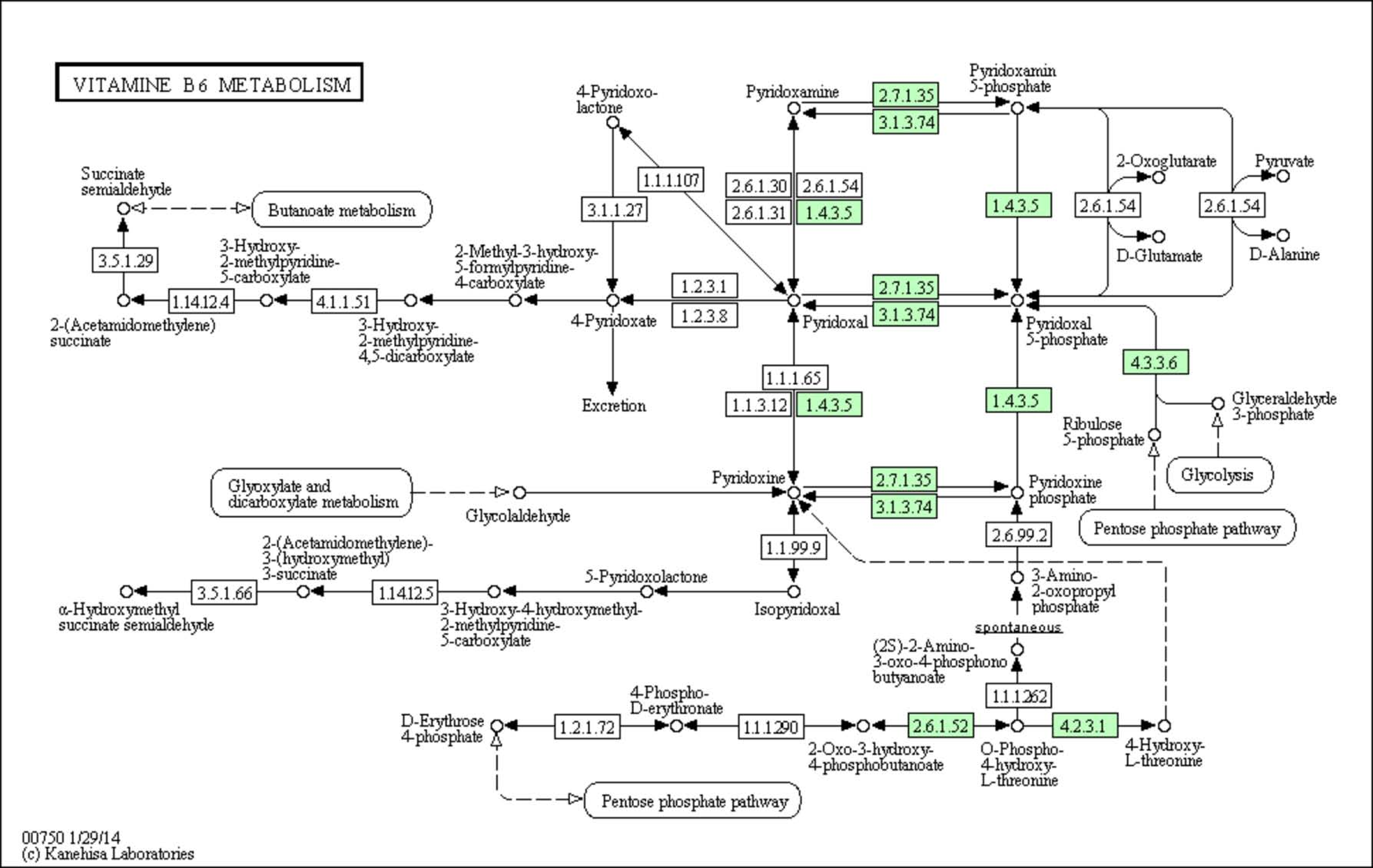

00750 1/29/14
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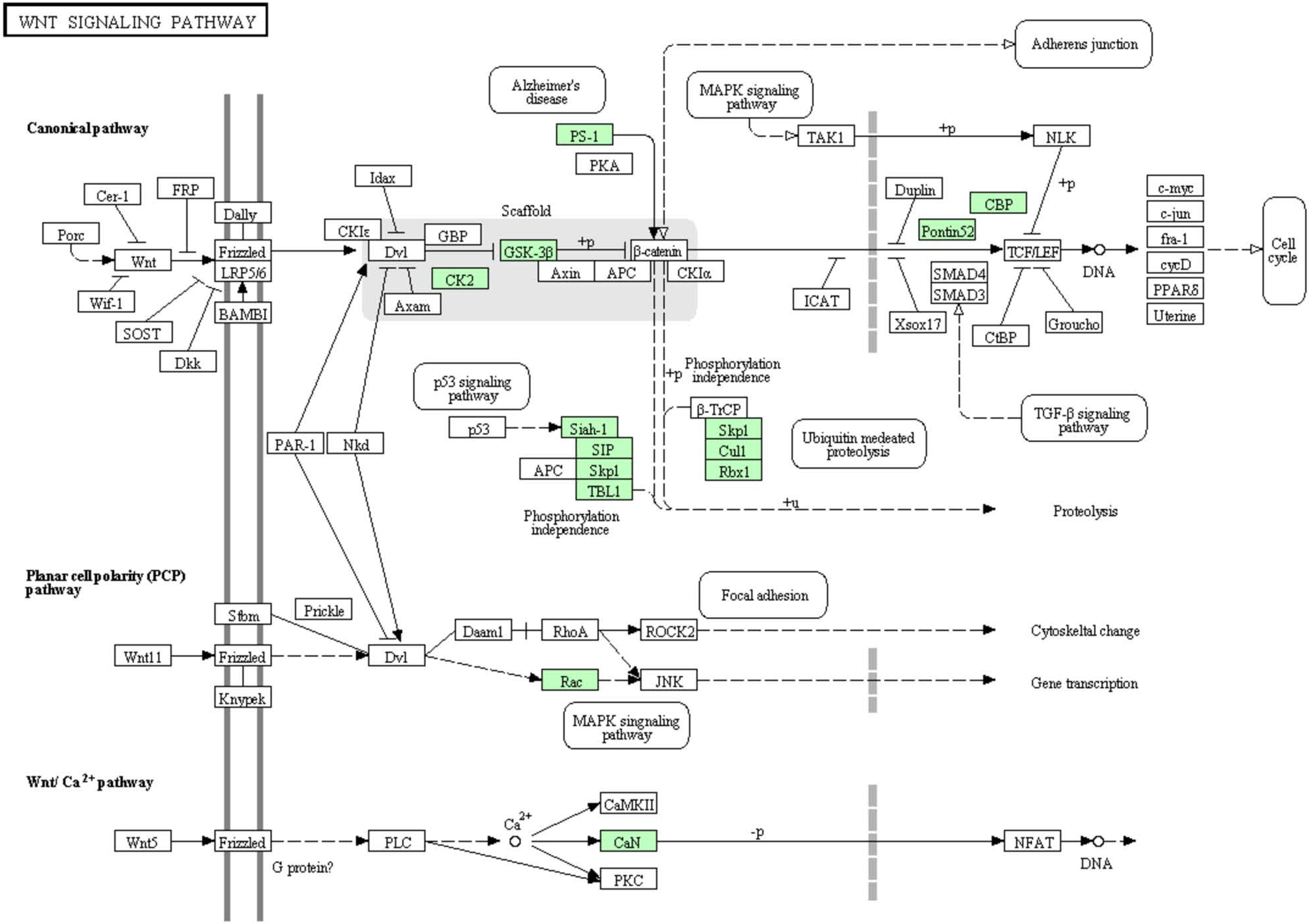

04310 7/26/13
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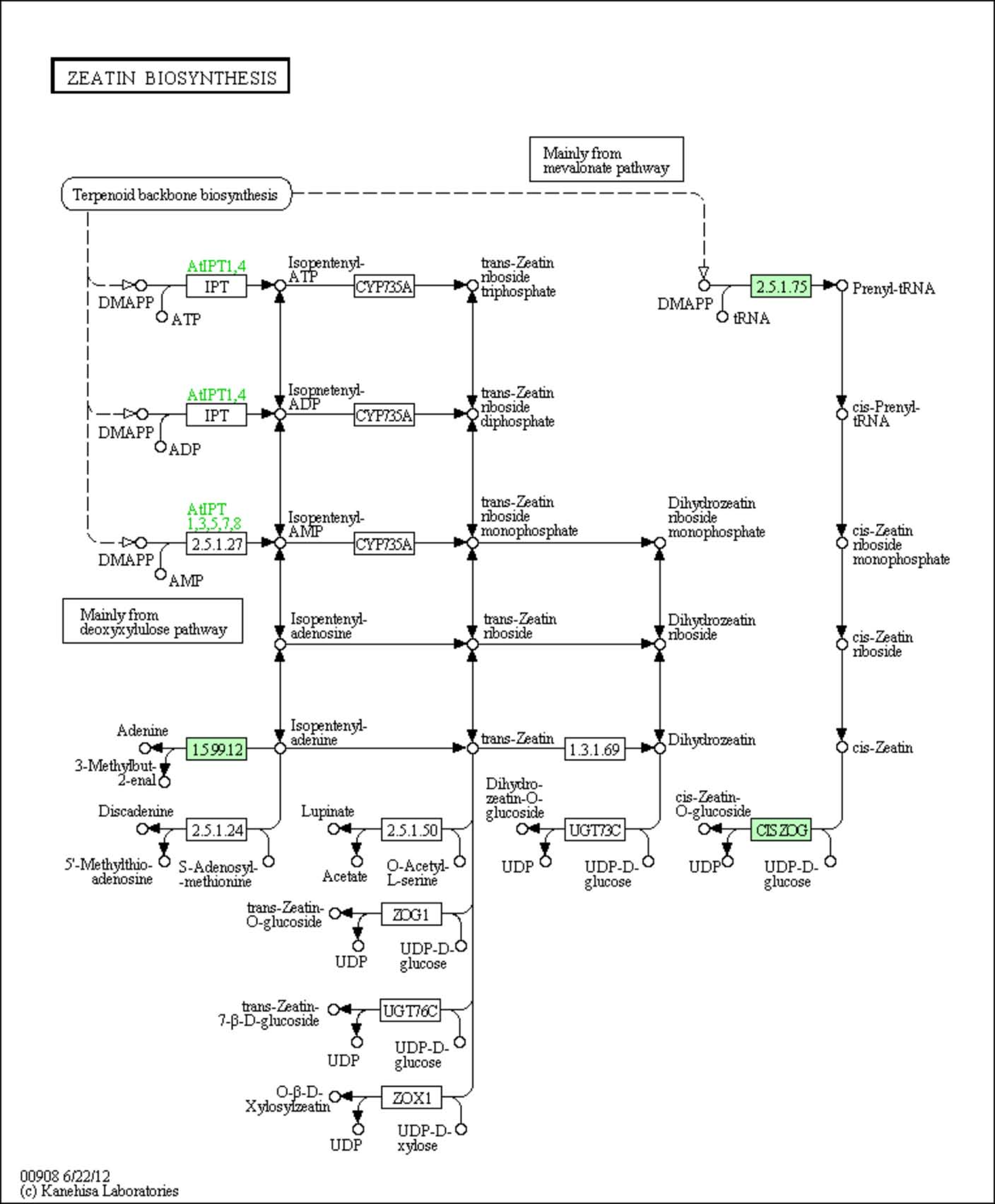
ZEATIN BIOSYNTHESIS
Mainly from mevalonate pathway
Terpenoid backbone biosynthesis
AtIPT1,4
IPT
DMAPP
ATP
Isopentenyl-ATP
CYP735A
trans-Zeatin riboside triphosphate
DMAPP
2.5.1.75
Prenyl-tRNA
tRNA
AtIPT1,4
IPT
DMAPP
ADP
Isopnetenyl-ADP
CYP735A
trans-Zeatin riboside diphosphate
cis-Prenyl-tRNA
AtIPT 1,3,5,7,8
2.5.1.27
DMAPP
AMP
Isopentenyl-AMP
CYP735A
trans-Zeatin riboside monophosphate
Dihydrozeatin riboside monophosphate
cis-Zeatin riboside monophosphate
Mainly from deoxyxylulose pathway
Isopentenyl-adenosine
trans-Zeatin riboside
Dihydrozeatin riboside
cis-Zeatin riboside
Adenine
1.5.99.12
3-Methylbut-2-enal
Isopentenyl-adenine
trans-Zeatin
1.3.1.69
Dihydrozeatin
cis-Zeatin
Discadenine
2.5.1.24
5'-Methylthio-adenosine
S-Adenosyl--methionine
Lupinate
2.5.1.50
Acetate
O-Acetyl-L-serine
Dihydro-zeatin-O-glucoside
UGT73C
UDP
UDP-D-glucose
cis-Zeatin-O-glucoside
CISZOG
UDP
UDP-D-glucose
trans-Zeatin-O-glucoside
ZOG1
UDP
UDP-D-glucose
trans-Zeatin-7-β-D-glucoside
UGT76C
UDP
UDP-D-glucose
O-β-D-Xylosylzeatin
ZOX1
UDP
UDP-D-xylose
00908 6/22/12
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