Supplementary Material: Transcriptome of the Australian Mollusc *Dicathais orbita* Provides Insights into the Biosynthesis of Indoles and Choline Esters

Abdul Baten, Ajit Kumar Ngangbam, Daniel L. E. Waters and Kirsten Benkendorff

Table S1. Analysis of KEGG pathway showing the top 20 metabolic pathway involving the largest number of contigs in *D. orbita* trancriptome.

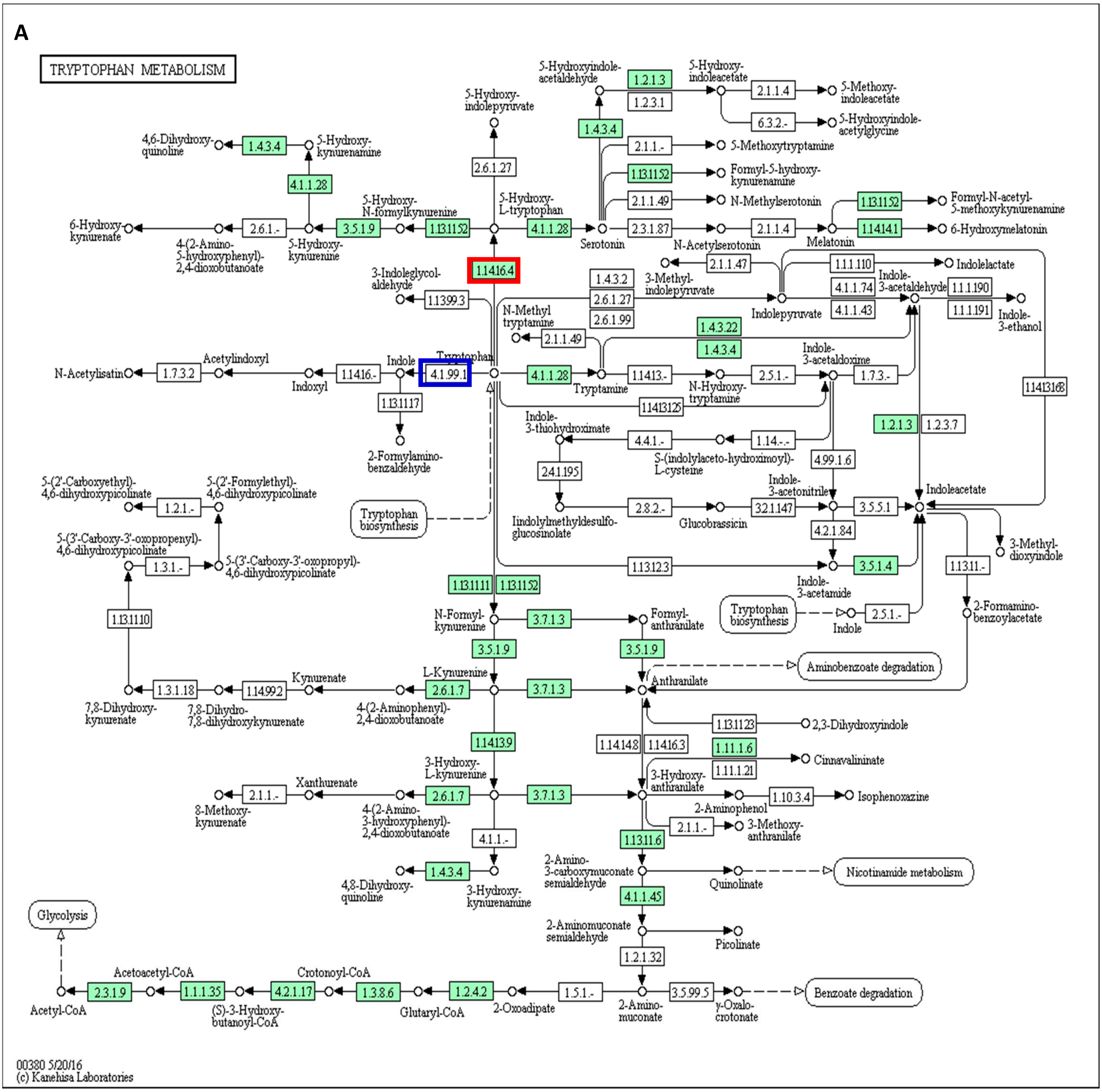
Sl. No.	Top 20 Metabolic Pathway
1	ko01100 Metabolic pathways (914)
2	ko01110 Biosynthesis of secondary metabolites (304)
3	ko01130 Biosynthesis of antibiotics (211)
4	ko01120 Microbial metabolism in diverse environments (173)
5	ko00230 Purine metabolism (120)
6	ko03013 RNA transport (118)
7	ko04144 Endocytosis (1118)
8	ko03010 Ribosome (117)
9	ko01200 Carbon metabolism (113)
10	ko05016 Huntington's disease (112)
11	ko03040 Spliceosome (106)
12	ko00190 Oxidative phosphorylation (105)
13	ko04141 Protein processing in endoplasmic reticulum (103)
14	ko00240 Pyrimidine metabolism (98)
15	ko05010 Alzheimer's disease (92)
16	ko01230 Biosynthesis of amino acids (91)
17	ko04120 Ubiquitin mediated proteolysis (88)
18	ko05169 Epstein-Barr virus infection (88)
19	ko05166 HTLV-I infection (86)
20	ko04142 Lysosome (80)

Table S2. List of the 28 mapped contigs and with the KEGG orthology assignment in *D. orbita* trancriptome for tryptophan metabolism.

Sl. No.	List of the Enzymes in *D. orbita* Trancriptome for Tryptophan Metabolism
1	ko:K00022 HADH; 3-hydroxyacyl-CoA dehydrogenase [EC:1.1.1.35]
2	ko:K00128 E1.2.1.3; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]
3	ko:K00149 ALDH9A1; aldehyde dehydrogenase family 9 member A1 [EC:1.2.1.47 1.2.1.3]
4	ko:K00164 OGDH; 2-oxoglutarate dehydrogenase E1 component [EC:1.2.4.2]
5	ko:K00252 GCDH; glutaryl-CoA dehydrogenase [EC:1.3.8.6]
6	ko:K00274 MAO; monoamine oxidase [EC:1.4.3.4]
7	ko:K00452 HAAO; 3-hydroxyanthranilate 3,4-dioxygenase [EC:1.13.11.6]
8	ko:K00453 E1.13.11.11; tryptophan 2,3-dioxygenase [EC:1.13.11.11]
9	ko:K00463 INDO; indoleamine 2,3-dioxygenase [EC:1.13.11.52]
10	ko:K00486 KMO; kynurenine 3-monooxygenase [EC:1.14.13.9]
11	ko:K00626 E2.3.1.9; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]
12	ko:K00816 CCBL; kynurenine—oxoglutarate transaminase/cysteine-S-conjugate beta-lyase/glutamine—phenylpyruvate transaminase [EC:2.6.1.7 4.4.1.13 2.6.1.64]
13	ko:K00825 AADAT; kynurenine/2-aminoadipate aminotransferase [EC:2.6.1.7 2.6.1.39]
14	ko:K01426 E3.5.1.4; amidase [EC:3.5.1.4]
15	ko:K01432 AFMID; arylformamidase [EC:3.5.1.9]
16	ko:K01556 KYNU; kynureninase [EC:3.7.1.3]
17	ko:K01593 DDC; aromatic-L-amino-acid decarboxylase [EC:4.1.1.28]
18	ko:K01667 tnaA; tryptophanase [EC:4.1.99.1]
19	ko:K01692 paaF; enoyl-CoA hydratase [EC:4.2.1.17]
20	ko:K01782 fadJ; 3-hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase/3-hydroxybutyryl-CoA epimerase [EC:1.1.1.35 4.2.1.17 5.1.2.3]
21	ko:K03781 katE; catalase [EC:1.11.1.6]
22	ko:K07408 CYP1A1; cytochrome P450, family 1, subfamily A, polypeptide 1 [EC:1.14.14.1]
23	ko:K07511 ECHS1; enoyl-CoA hydratase [EC:4.2.1.17]
24	ko:K07514 EHHADH; enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase/3,2-trans-enoyl-CoA isomerase [EC:4.2.1.17 1.1.1.35 5.3.3.8]
25	ko:K07515 HADHA; enoyl-CoA hydratase/long-chain 3-hydroxyacyl-CoA dehydrogenase [EC:4.2.1.17 1.1.1.211]
26	ko:K11182 AOC1; diamine oxidase [EC:1.4.3.22]
27	ko:K11818 CYP83B1; cytochrome P450, family 83, subfamily B, polypeptide 1 [EC:1.14.-.-]
28	ko:K14085 ALDH7A1; aldehyde dehydrogenase family 7 member A1 [EC:1.2.1.31 1.2.1.8 1.2.1.3]

Table S3. List of known bromoperoxidsae genes available in NCBI GenBank used for BLAST against *D. orbita*.

Accession Numbers	**Source Species**
AJ491786.1	*Laminaria digitata*
JX128092.1	*Gracilaria changii*
AF218810.1	*Corallina officinalis*
XM_001822243.2	*Aspergillus oryzae*
XM_003234475.1	*Trichophyton rubrum*
XM_002679630.1	*Naegleria gruberi*
NM_001157259.1	*Zea mays*
KLO55315.1	*Mycobacterium haemophilum*
AKJ56790.1	*Bacillus thuringiensis*
KLI98717.1	*Luteimonas* sp. FCS-9
YP_029199.1	*Bacillus anthracis* str. Sterne
KKM37545.1	*Bacillus anthracis*
KKI91829.1	*Bacillus* sp. SA1-12
KXH89531	*Bacillus* sp. JH7
KXI43580	*Bacillus cereus*
ALQ29400.1	*Arthrobacter* sp. YC-RL1
KND40451.1	*Streptomyces stelliscabiei*
WP_046733028	*Streptomyces* sp. MUSC119T


A
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
4,6-Dihydroxy-quinoline
5-Hydroxy-kynurenamine
2.6.1.27
1.13.11.52
Formyl-5-hydroxy-kynurenamine
4.1.1.28
2.1.1.49
N-Methylserotonin
Formyl-N-acetyl-5-methoxykynurenamine
5-Hydroxy-N-formylkynurenine
5-Hydroxy-L-tryptophan
6-Hydroxy-kynurenate
2.6.1.-
3.5.1.9
2.3.1.87
Melatonin
1.14.14.1
6-Hydroxymelatonin
4-(2-Amino-5-hydroxyphenyl)-2,4-dioxobutanoate
5-Hydroxy-kynurenine
Serotonin
N-Acetylserotonin
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
1.4.3.22
2.1.1.49
1.4.3.4
Acetylindoxyl
Indole
Tryptophan
Indole-3-acetaldoxime
N-Acetylisatin
1.7.3.2
1.14.16.-
4.1.99.1
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
4.4.1.-
1.14.-.-
1.2.1.3
1.2.3.7
2-Formylamino-benzaldehyde
S-(indolylaceto-hydroximoyl)-L-cysteine
4.99.1.6
2.4.1.195
Indole-3-acetonitrile
Indoleacetate
5-(2'-Carboxyethyl)-4,6-dihydroxypicolinate
5-(2'-Formylethyl)-4,6-dihydroxypicolinate
1.2.1.-
Tryptophan biosynthesis
2.8.2.-
3.2.1.147
3.5.5.1
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
N-Formyl-kynurenine
3.7.1.3
Formyl-anthranilate
Tryptophan biosynthesis
2.5.1.-
Indole
2-Formamino-benzoylacetate
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
1.13.11.23
2,3-Dihydroxyindole
1.14.13.9
1.14.14.8
1.14.16.3
1.11.1.6
Cinnavalininate
3-Hydroxy-L-kynurenine
1.11.1.21
3-Hydroxy-anthranilate
Xanthurenate
8-Methoxy-kynurenate
2.1.1.-
2.6.1.7
3.7.1.3
1.10.3.4
Isophenoxazine
4-(2-Amino-3-hydroxyphenyl)-2,4-dioxobutanoate
2-Aminophenol
4.1.1.-
2.1.1.-
3-Methoxy-anthranilate
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
Glycolysis
2-Aminomuconate semialdehyde
Picolinate
1.2.1.32
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
γ-Oxalo-crotonate
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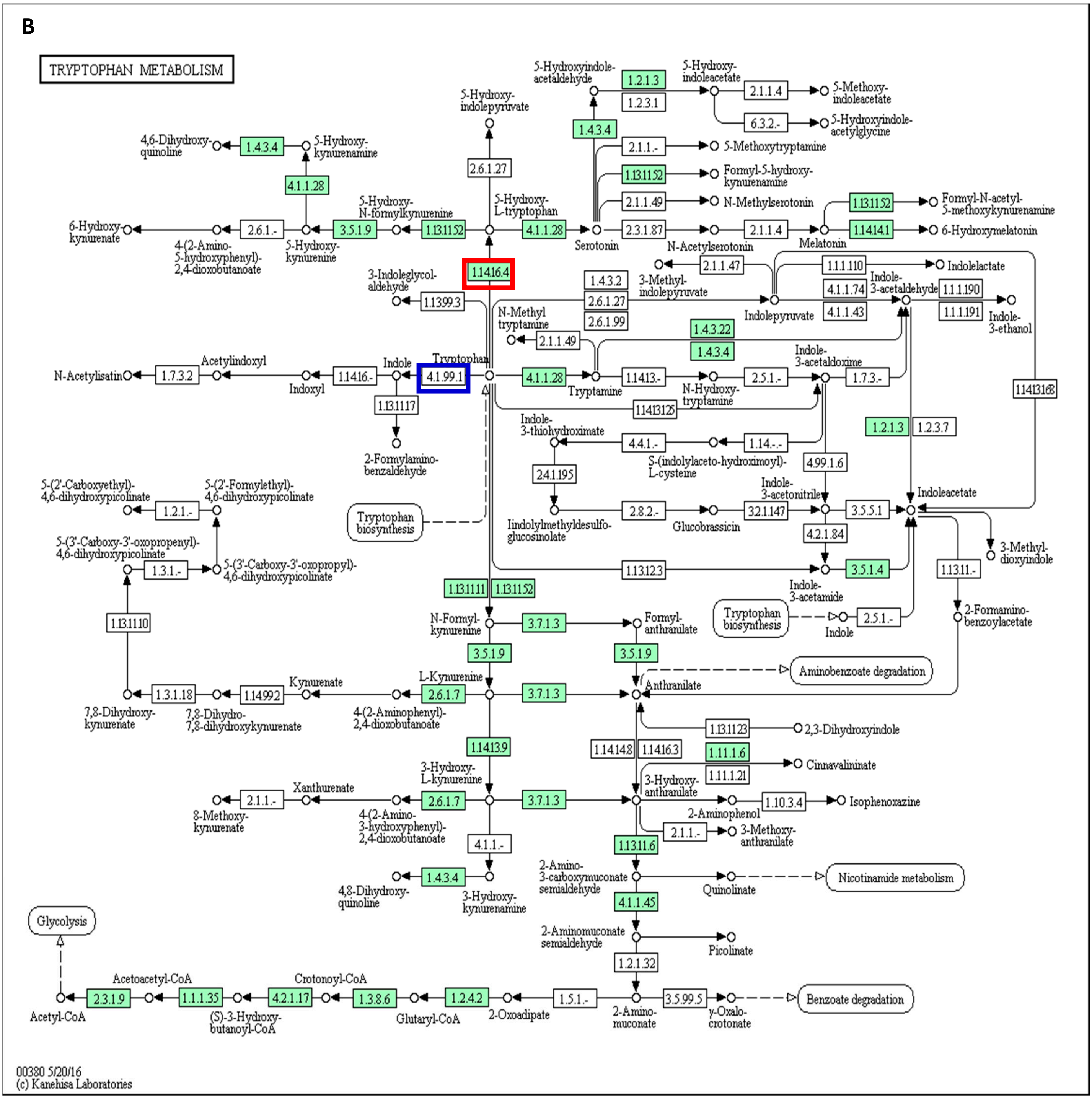
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1.7.3.2
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Indoxyl
1.14.16.-
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4.1.99.1
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1.13.12.3
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1.13.11.-
Indole-3-acetamide
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1.13.11.11
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3.7.1.3
2-Aminophenol
1.10.3.4
Isophenoxazine
2.1.1.-
3-Methoxy-anthranilate
4.1.1.-
1.13.11.6
4,8-Dihydroxy-quinoline
1.4.3.4
3-Hydroxy-kynurenamine
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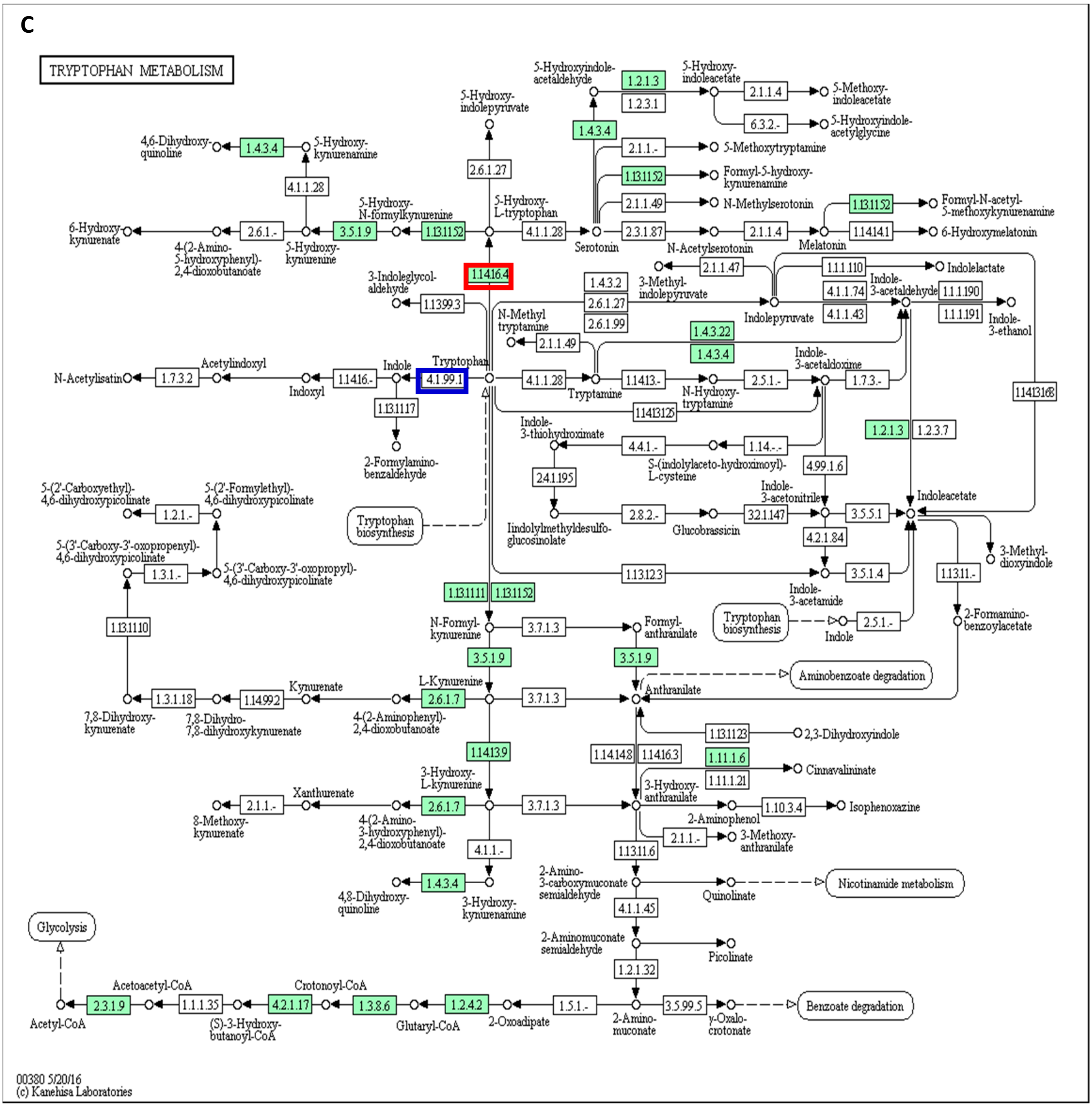
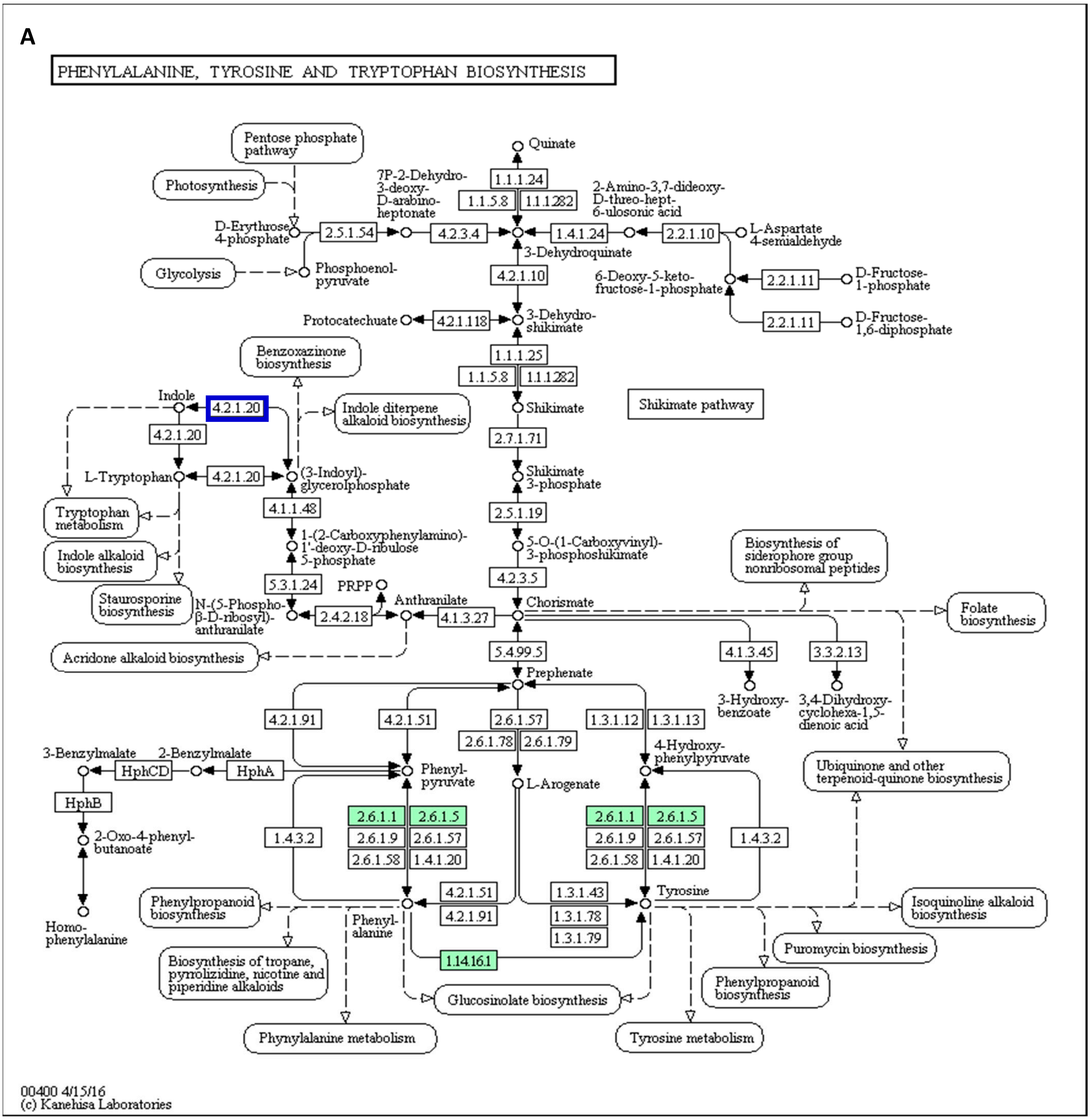


Figure S1. Tryptophan metabolism pathways for (**A**) *Crassostrea gigas*, (**B**) *Lottia gigantea* and, (**C**) *Octopus bimaculoides* showing enzyme matches in green including tryptophan 5-monoxygenase (red box), which was missing form *Dicathais orbita*, but no match to tryptophanase (blue box).


A
PHENYLALANINE, TYROSINE AND TRYPTOPHAN BIOSYNTHESIS
Pentose phosphate pathway
Photosynthesis
Glycolysis
D-Erythrose 4-phosphate
Phosphoenol-pyruvate
2.5.1.54
7P-2-Dehydro-3-deoxy-D-arabino-heptonate
4.2.3.4
Quinate
1.1.1.24
1.1.5.8
1.1.1.282
2-Amino-3,7-dideoxy-D-threo-hept-6-ulosonic acid
1.4.1.24
2.2.1.10
L-Aspartate 4-semialdehyde
3-Dehydroquinate
4.2.1.10
6-Deoxy-5-keto-fructose-1-phosphate
2.2.1.11
D-Fructose-1-phosphate
2.2.1.11
D-Fructose-1,6-diphosphate
Protocatechuate
4.2.1.118
3-Dehydro-shikimate
1.1.1.25
1.1.5.8
1.1.1.282
Shikimate
Shikimate pathway
Benzoxazinone biosynthesis
Indole
4.2.1.20
4.2.1.20
Indole diterpene alkaloid biosynthesis
L-Tryptophan
4.2.1.20
(3-Indoyl)-glycerolphosphate
2.7.1.71
Shikimate 3-phosphate
Tryptophan metabolism
4.1.1.48
2.5.1.19
Indole alkaloid biosynthesis
1-(2-Carboxyphenylamino)-1'-deoxy-D-ribulose 5-phosphate
5-O-(1-Carboxyvinyl)-3-phosphoshikimate
Biosynthesis of siderophore group nonribosomal peptides
5.3.1.24
PRPP
4.2.3.5
Staurosporine biosynthesis
N-(5-Phospho-β-D-ribosyl)-anthranilate
2.4.2.18
Anthranilate
4.1.3.27
Chorismate
Folate biosynthesis
Acridone alkaloid biosynthesis
5.4.99.5
4.1.3.45
3.3.2.13
Prephenate
3-Hydroxy-benzoate
3,4-Dihydroxy-cyclohexa-1,5-dienoic acid
4.2.1.91
4.2.1.51
2.6.1.57
1.3.1.12
1.3.1.13
2.6.1.78
2.6.1.79
3-Benzylmalate
2-Benzylmalate
HphCD
HphA
Phenyl-pyruvate
4-Hydroxy-phenylpyruvate
Ubiquinone and other terpenoid-quinone biosynthesis
HphB
L-Arogenate
2.6.1.1
2.6.1.5
2.6.1.9
2.6.1.57
2.6.1.58
1.4.1.20
1.4.3.2
2.6.1.1
2.6.1.5
2.6.1.9
2.6.1.57
2.6.1.58
1.4.1.20
1.4.3.2
2-Oxo-4-phenyl-butanoate
Homo-phenylalanine
Phenylpropanoid biosynthesis
4.2.1.51
4.2.1.91
1.3.1.43
1.3.1.78
1.3.1.79
Tyrosine
Isoquinoline alkaloid biosynthesis
Phenyl-alanine
1.14.16.1
Puromycin biosynthesis
Biosynthesis of tropane, pyrrolizidine, nicotine and piperidine alkaloids
Phenylpropanoid biosynthesis
Glucosinolate biosynthesis
Phynylalanine metabolism
Tyrosine metabolism
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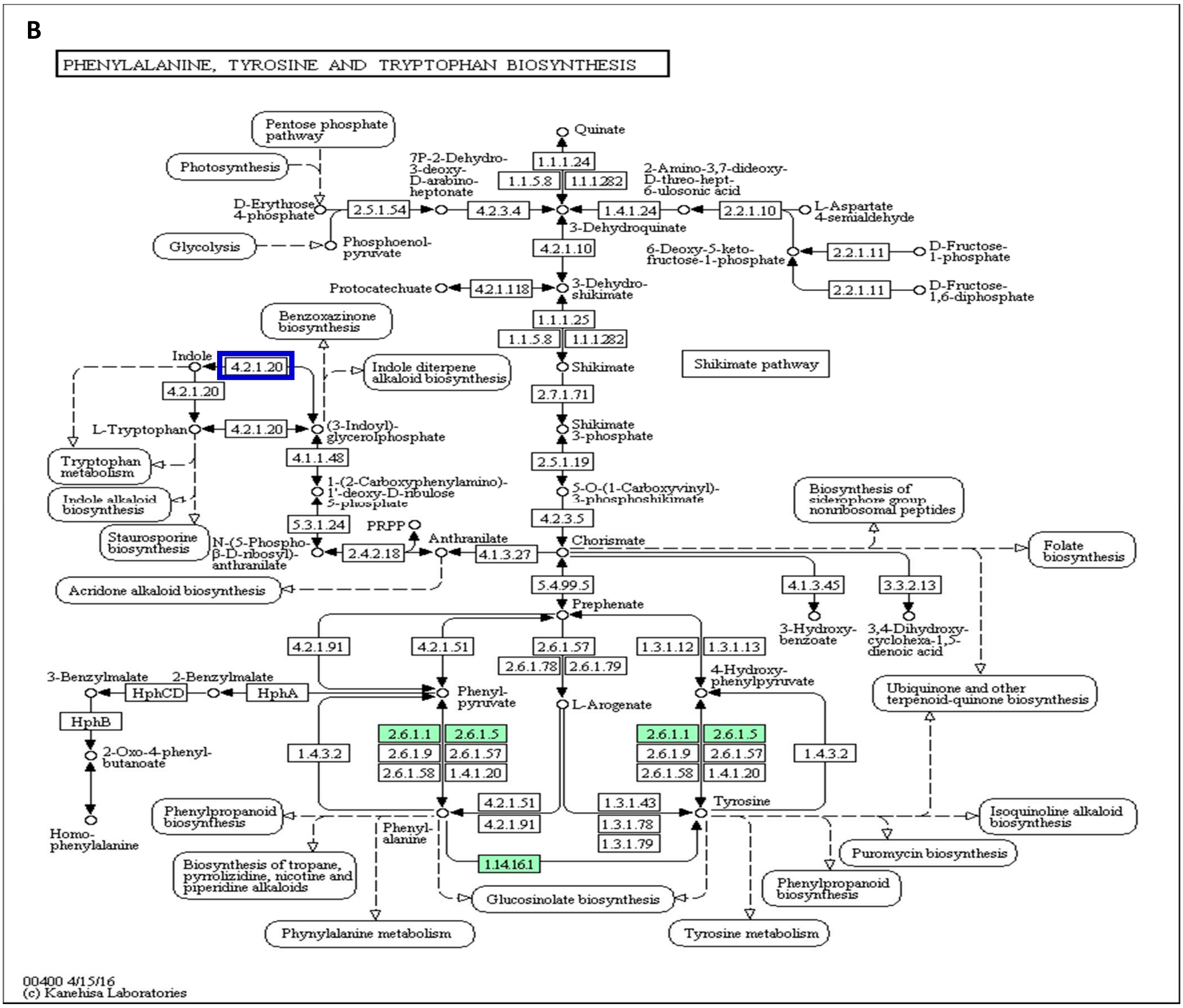
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Quinate
1.1.1.24
1.1.5.8
1.1.1.282
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1.4.1.24
2.2.1.10
L-Aspartate 4-semialdehyde
3-Dehydroquinate
4.2.1.10
6-Deoxy-5-keto-fructose-1-phosphate
2.2.1.11
D-Fructose-1-phosphate
2.2.1.11
D-Fructose-1,6-diphosphate
Protocatechuate
4.2.1.118
3-Dehydro-shikimate
1.1.1.25
1.1.5.8
1.1.1.282
Shikimate
Shikimate pathway
2.7.1.71
Shikimate 3-phosphate
2.5.1.19
5-O-(1-Carboxyvinyl)-3-phosphoshikimate
4.2.3.5
Chorismate
Benzoxazinone biosynthesis
Indole
4.2.1.20
Indole diterpene alkaloid biosynthesis
4.2.1.20
L-Tryptophan
4.2.1.20
(3-Indoyl)-glycerolphosphate
4.1.1.48
Tryptophan metabolism
Indole alkaloid biosynthesis
1-(2-Carboxyphenylamino)-1'-deoxy-D-ribulose 5-phosphate
5.3.1.24
PRPP
Staurosporine biosynthesis
N-(5-Phospho-β-D-ribosyl)-anthranilate
2.4.2.18
Anthranilate
4.1.3.27
Acridone alkaloid biosynthesis
Biosynthesis of siderophore group nonribosomal peptides
Folate biosynthesis
4.1.3.45
3.3.2.13
3-Hydroxy-benzoate
3,4-Dihydroxy-cyclohexa-1,5-dienoic acid
5.4.99.5
Prephenate
4.2.1.91
4.2.1.51
2.6.1.57
2.6.1.78
2.6.1.79
1.3.1.12
1.3.1.13
L-Arogenate
4-Hydroxy-phenylpyruvate
Ubiquinone and other terpenoid-quinone biosynthesis
3-Benzylmalate
2-Benzylmalate
HphCD
HphA
Phenyl-pyruvate
HphB
2-Oxo-4-phenyl-butanoate
Homo-phenylalanine
1.4.3.2
2.6.1.1
2.6.1.5
2.6.1.9
2.6.1.57
2.6.1.58
1.4.1.20
2.6.1.1
2.6.1.5
2.6.1.9
2.6.1.57
2.6.1.58
1.4.1.20
1.4.3.2
4.2.1.51
4.2.1.91
1.3.1.43
1.3.1.78
1.3.1.79
Tyrosine
Phenylpropanoid biosynthesis
Phenyl-alanine
1.14.16.1
Isoquinoline alkaloid biosynthesis
Puromycin biosynthesis
Phenylpropanoid biosynthesis
Biosynthesis of tropane, pyrrolizidine, nicotine and piperidine alkaloids
Glucosinolate biosynthesis
Phynylalanine metabolism
Tyrosine metabolism
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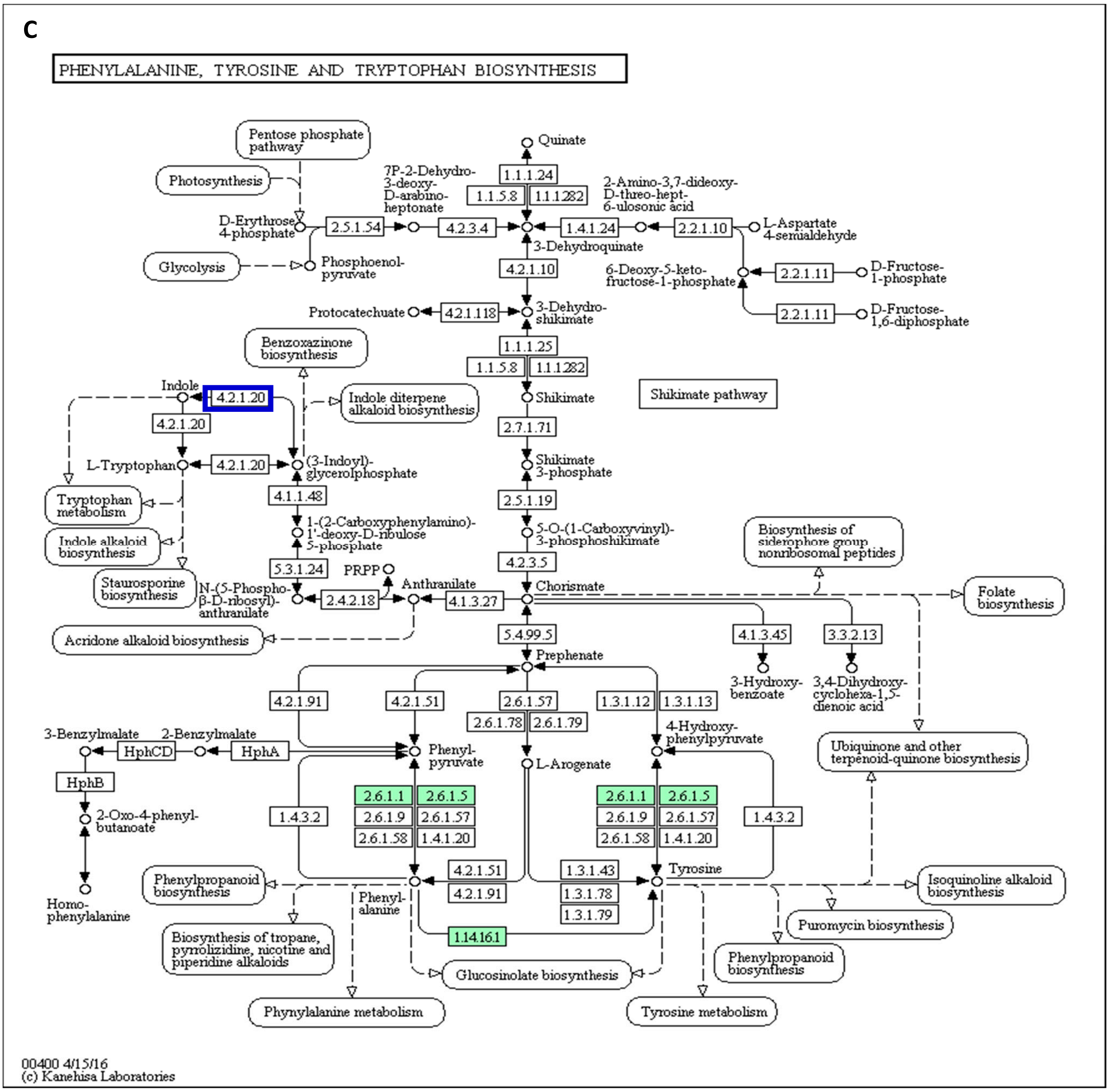
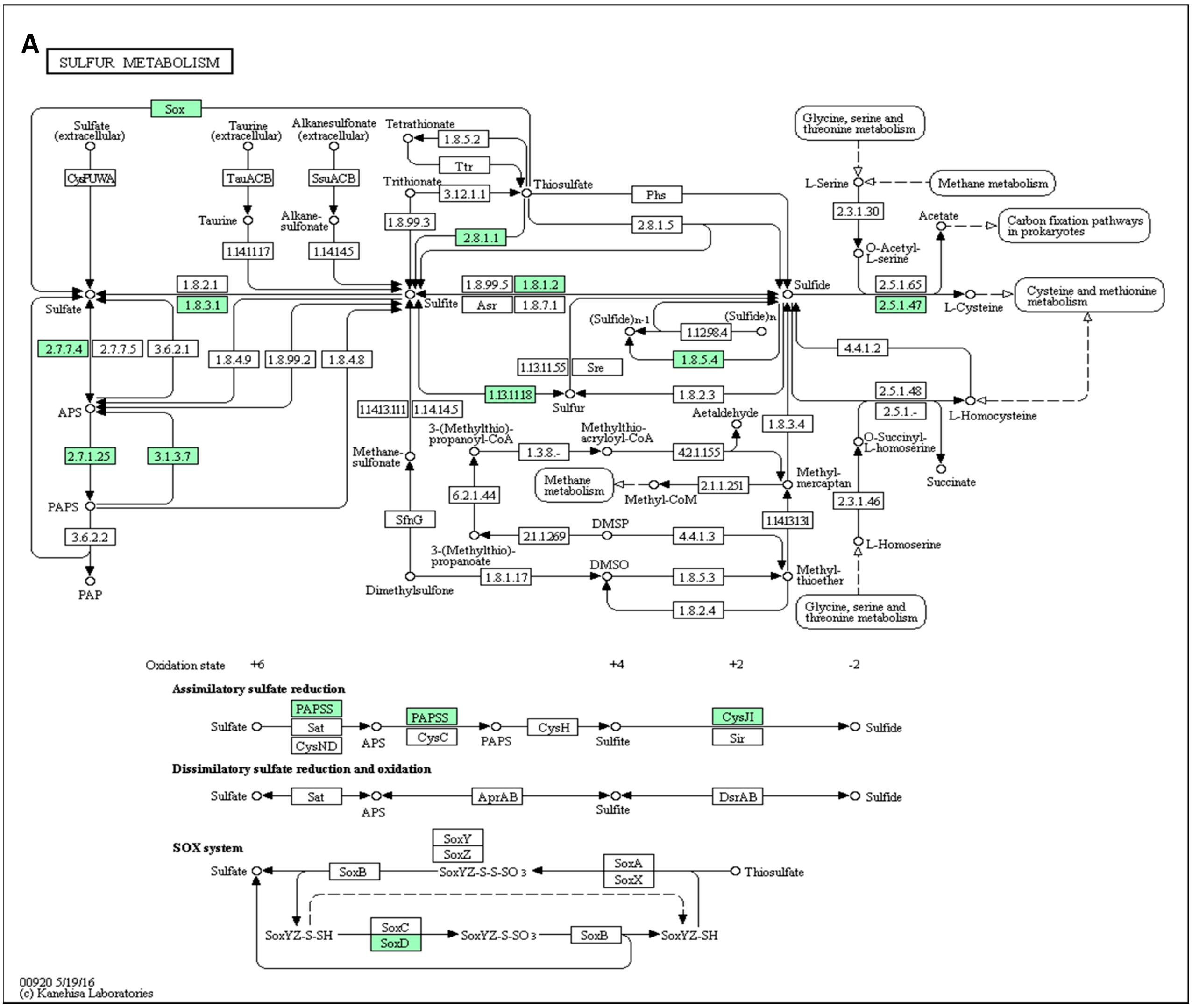


Figure S2. Phenylalanine, tyrosine and tryptophan biosynthetic pathways for (**A**) *Crassostrea gigas*, (**B**) *Lottia gigantea* and, (**C**) *Octopus bimaculoides* with enzyme matches in green, but with no match to tryptophan synthase highlighted in the blue box.


A
SULFUR METABOLISM
Sox
Sulfate (extracellular)
CysPUWA
Taurine (extracellular)
TauACB
Taurine
1.14.11.17
Alkanesulfonate (extracellular)
SsuACB
Alkane-sulfonate
1.14.14.5
Tetrathionate
1.8.5.2
Ttr
Trithionate
3.12.1.1
Thiosulfate
1.8.99.3
2.8.1.1
Phs
2.8.1.5
Sulfate
1.8.2.1
1.8.3.1
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
Sulfite
1.8.99.5
1.8.1.2
Asr
1.8.7.1
Sulfide
(Sulfide)n-1
(Sulfide)n
1.12.98.4
1.8.5.4
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
3-(Methylthio)-propanoyl-CoA
1.3.8.-
Methylthio-acryloyl-CoA
4.2.1.155
Aetaldehyde
1.8.3.4
6.2.1.44
Methane metabolism
Methyl-CoM
2.1.1.251
Methyl-mercaptan
3-(Methylthio)-propanoate
2.1.1.269
DMSP
4.4.1.3
1.14.13.131
1.8.1.17
DMSO
1.8.5.3
1.8.2.4
Methyl-thioether
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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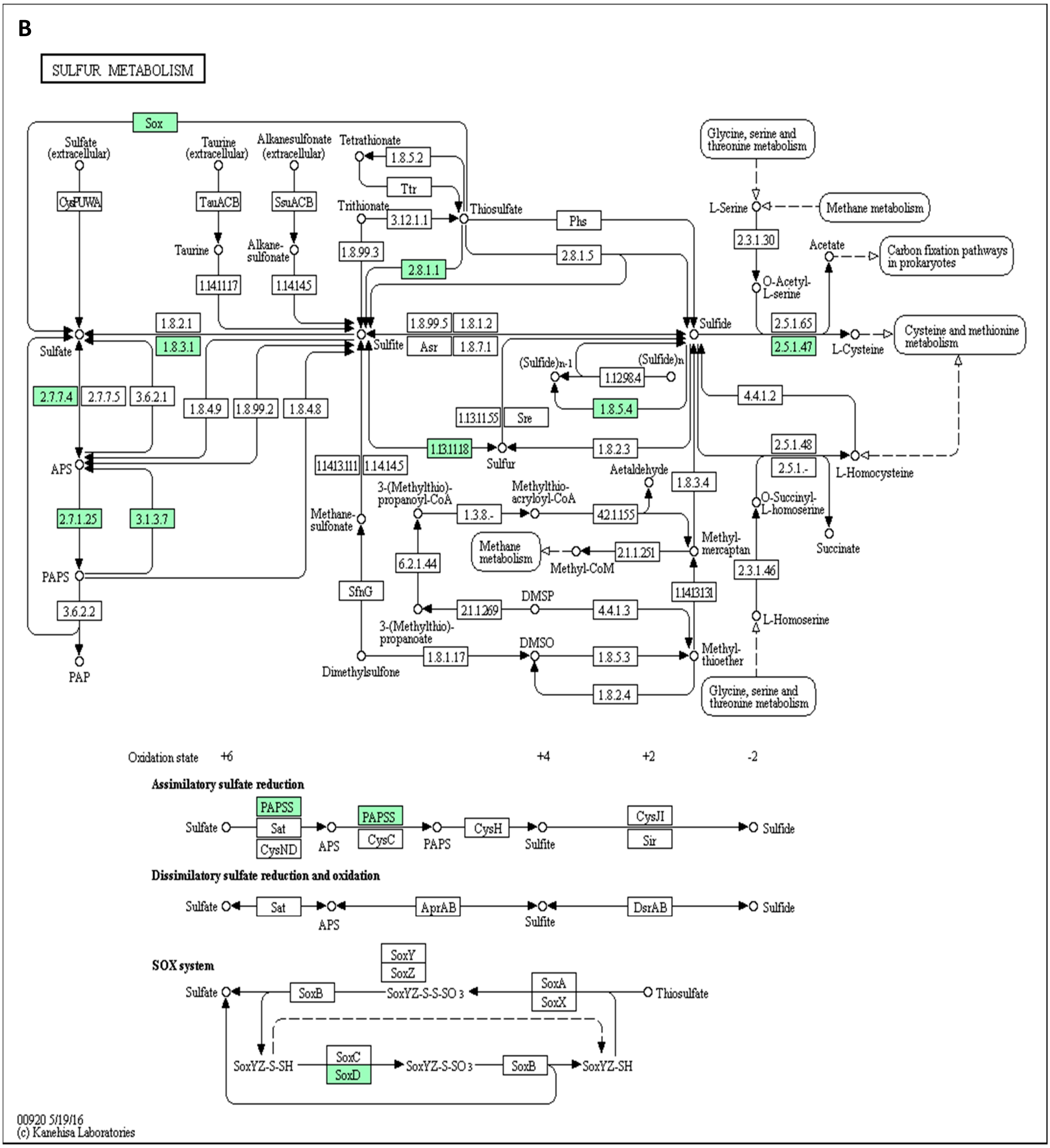
B
SULFUR METABOLISM
Sox
Sulfate (extracellular)
Taurine (extracellular)
Alkanesulfonate (extracellular)
Tetrathionate
1.8.5.2
Ttr
Trithionate
3.12.1.1
Thiosulfate
Phs
CysPUWA
TauACB
SsuACB
Taurine
Alkane-sulfonate
1.8.99.3
2.8.1.1
2.8.1.5
1.14.11.17
1.14.14.5
Glycine, serine and threonine metabolism
L-Serine
Methane metabolism
2.3.1.30
Acetate
Carbon fixation pathways in prokaryotes
O-Acetyl-L-serine
1.8.2.1
1.8.3.1
Sulfate
1.8.99.5
1.8.1.2
Asr
1.8.7.1
Sulfite
Sulfide
2.5.1.65
2.5.1.47
L-Cysteine
Cysteine and methionine metabolism
(Sulfide)n-1
(Sulfide)n
1.12.98.4
1.8.5.4
4.4.1.2
2.7.7.4
2.7.7.5
3.6.2.1
1.8.4.9
1.8.99.2
1.8.4.8
1.13.11.55
Sre
1.13.11.18
Sulfur
1.8.2.3
2.5.1.48
2.5.1.-
L-Homocysteine
APS
1.14.13.111
1.14.14.5
3-(Methylthio)-propanoyl-CoA
Methylthio-acryloyl-CoA
Aetaldehyde
1.8.3.4
O-Succinyl-L-homoserine
2.7.1.25
3.1.3.7
Methane-sulfonate
1.3.8.-
4.2.1.155
Succinate
Methane metabolism
2.1.1.251
Methyl-mercaptan
Methyl-CoM
PAPS
6.2.1.44
2.3.1.46
SfnG
1.14.13.131
DMSP
3.6.2.2
2.1.1.269
4.4.1.3
L-Homoserine
3-(Methylthio)-propanoate
DMSO
PAP
Dimethylsulfone
1.8.1.17
1.8.5.3
Methyl-thioether
1.8.2.4
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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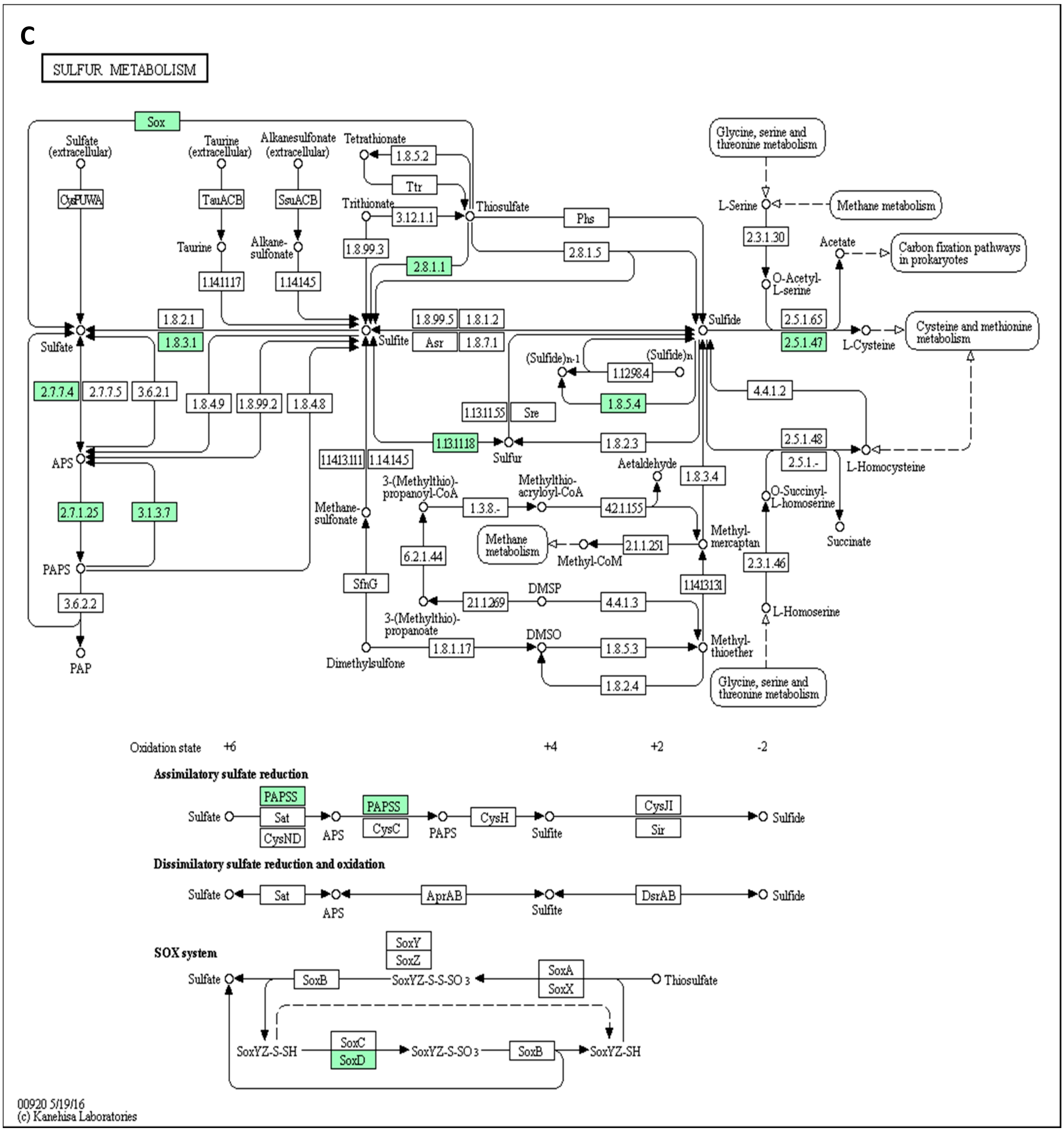
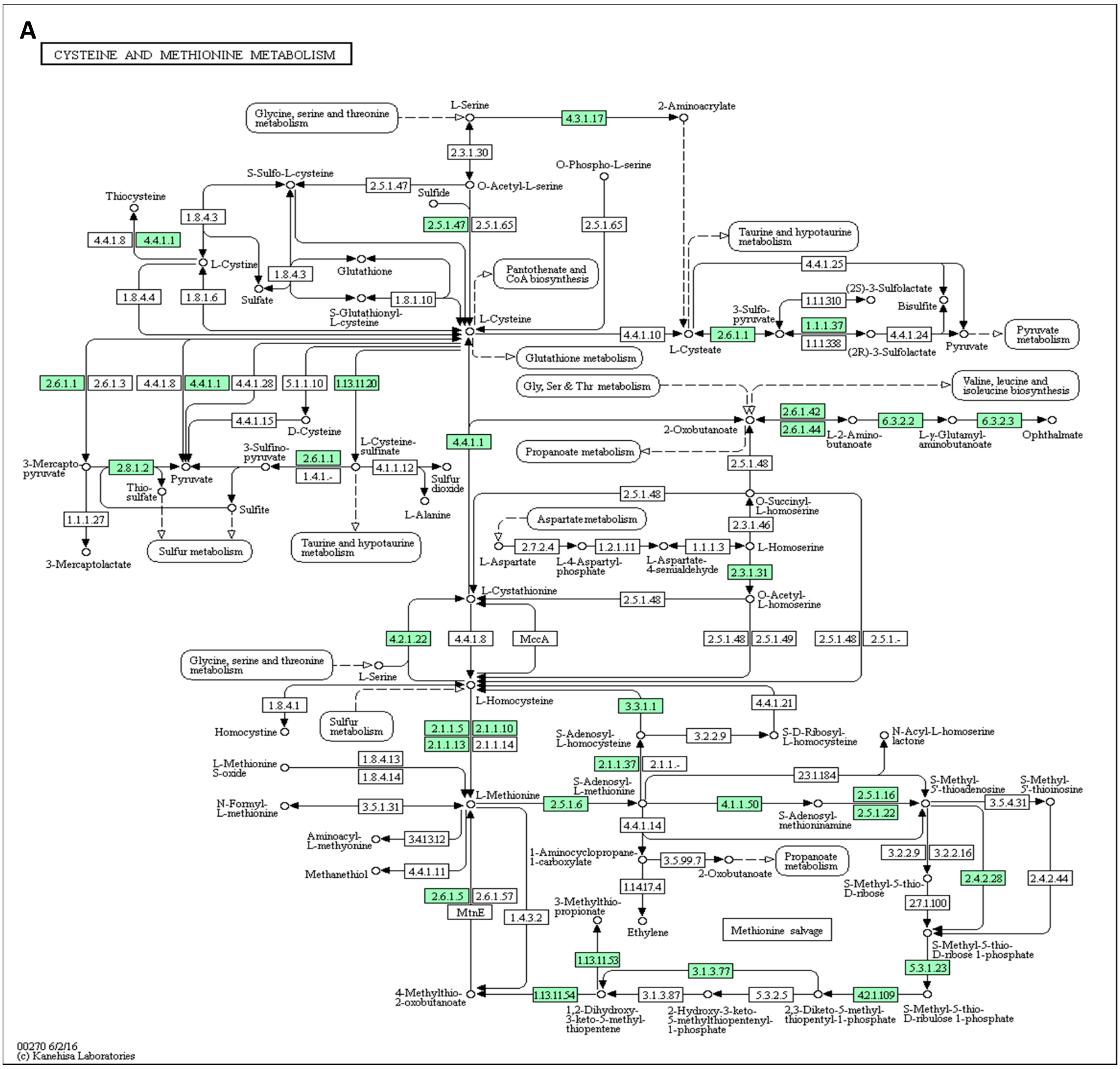


Figure S3. Sulfur metabolism pathways for (**A**) *Crassostrea gigas*, (**B**) *Lottia gigantea* and, (**C**) *Octopus bimaculoides*.


A
CYSTEINE AND METHIONINE METABOLISM
Glycine, serine and threonine metabolism
L-Serine
4.3.1.17
2-Aminoacrylate
2.3.1.30
O-Phospho-L-serine
S-Sulfo-L-cysteine
2.5.1.47
Sulfide
O-Acetyl-L-serine
Thiocysteine
1.8.4.3
4.4.1.8
4.4.1.1
2.5.1.47
2.5.1.65
2.5.1.65
Taurine and hypotaurine metabolism
L-Cystine
1.8.4.3
Glutathione
Pantothenate and CoA biosynthesis
4.4.1.25
1.8.4.4
1.8.1.6
Sulfate
1.8.1.10
S-Glutathionyl-L-cysteine
L-Cysteine
(2S)-3-Sulfolactate
1.1.1.310
Bisulfite
3-Sulfo-pyruvate
1.1.1.37
4.4.1.10
2.6.1.1
4.4.1.24
Pyruvate metabolism
1.1.1.338
L-Cysteate
(2R)-3-Sulfolactate
Pyruvate
Glutathione metabolism
2.6.1.1
2.6.1.3
4.4.1.8
4.4.1.1
4.4.1.28
5.1.1.10
1.13.11.20
Gly, Ser & Thr metabolism
Valine, leucine and isoleucine biosynthesis
2.6.1.42
6.3.2.2
6.3.2.3
4.4.1.15
D-Cysteine
2-Oxobutanoate
2.6.1.44
L-2-Amino-butanoate
L-γ-Glutamyl-aminobutanoate
Ophthalmate
4.4.1.1
Propanoate metabolism
3-Sulfino-pyruvate
L-Cysteine-sulfinate
3-Mercapto-pyruvate
2.8.1.2
Pyruvate
2.6.1.1
4.1.1.12
2.5.1.48
1.4.1.-
Sulfur dioxide
Thio-sulfate
Sulfite
L-Alanine
2.5.1.48
O-Succinyl-L-homoserine
1.1.1.27
Aspartate metabolism
2.3.1.46
Sulfur metabolism
Taurine and hypotaurine metabolism
2.7.2.4
1.2.1.11
1.1.1.3
L-Homoserine
3-Mercaptolactate
L-Aspartate
L-4-Aspartyl-phosphate
L-Aspartate-4-semialdehyde
2.3.1.31
L-Cystathionine
2.5.1.48
O-Acetyl-L-homoserine
4.2.1.22
4.4.1.8
MccA
2.5.1.48
2.5.1.49
2.5.1.48
2.5.1.-
Glycine, serine and threonine metabolism
L-Serine
L-Homocysteine
1.8.4.1
3.3.1.1
4.4.1.21
Homocystine
Sulfur metabolism
2.1.1.5
2.1.1.10
S-Adenosyl-L-homocysteine
3.2.2.9
S-D-Ribosyl-L-homocysteine
N-Acyl-L-homoserine lactone
2.1.1.13
2.1.1.14
L-Methionine S-oxide
1.8.4.13
1.8.4.14
2.1.1.37
2.1.1.-
2.3.1.184
S-Adenosyl-L-methionine
S-Methyl-5'-thioadenosine
S-Methyl-5'-thioinosine
N-Formyl-L-methionine
3.5.1.31
L-Methionine
2.5.1.6
4.1.1.50
2.5.1.16
3.5.4.31
S-Adenosyl-methioninamine
2.5.1.22
Aminoacyl-L-methyonine
3.4.13.12
4.4.1.14
1-Aminocyclopropane-1-carboxylate
3.2.2.9
3.2.2.16
Methanethiol
4.4.1.11
3.5.99.7
2-Oxobutanoate
Propanoate metabolism
S-Methyl-5-thio-D-ribose
2.4.2.28
2.4.2.44
2.6.1.5
2.6.1.57
1.14.17.4
2.7.1.100
MtnE
1.4.3.2
3-Methylthio-propionate
Ethylene
Methionine salvage
S-Methyl-5-thio-D-ribose 1-phosphate
1.13.11.53
5.3.1.23
3.1.3.77
4-Methylthio-2-oxobutanoate
1.13.11.54
3.1.3.87
5.3.2.5
4.2.1.109
1,2-Dihydroxy-3-keto-5-methyl-thiopentene
2-Hydroxy-3-keto-5-methylthiopentenyl-1-phosphate
2,3-Diketo-5-methyl-thiopentyl-1-phosphate
S-Methyl-5-thio-D-ribulose 1-phosphate
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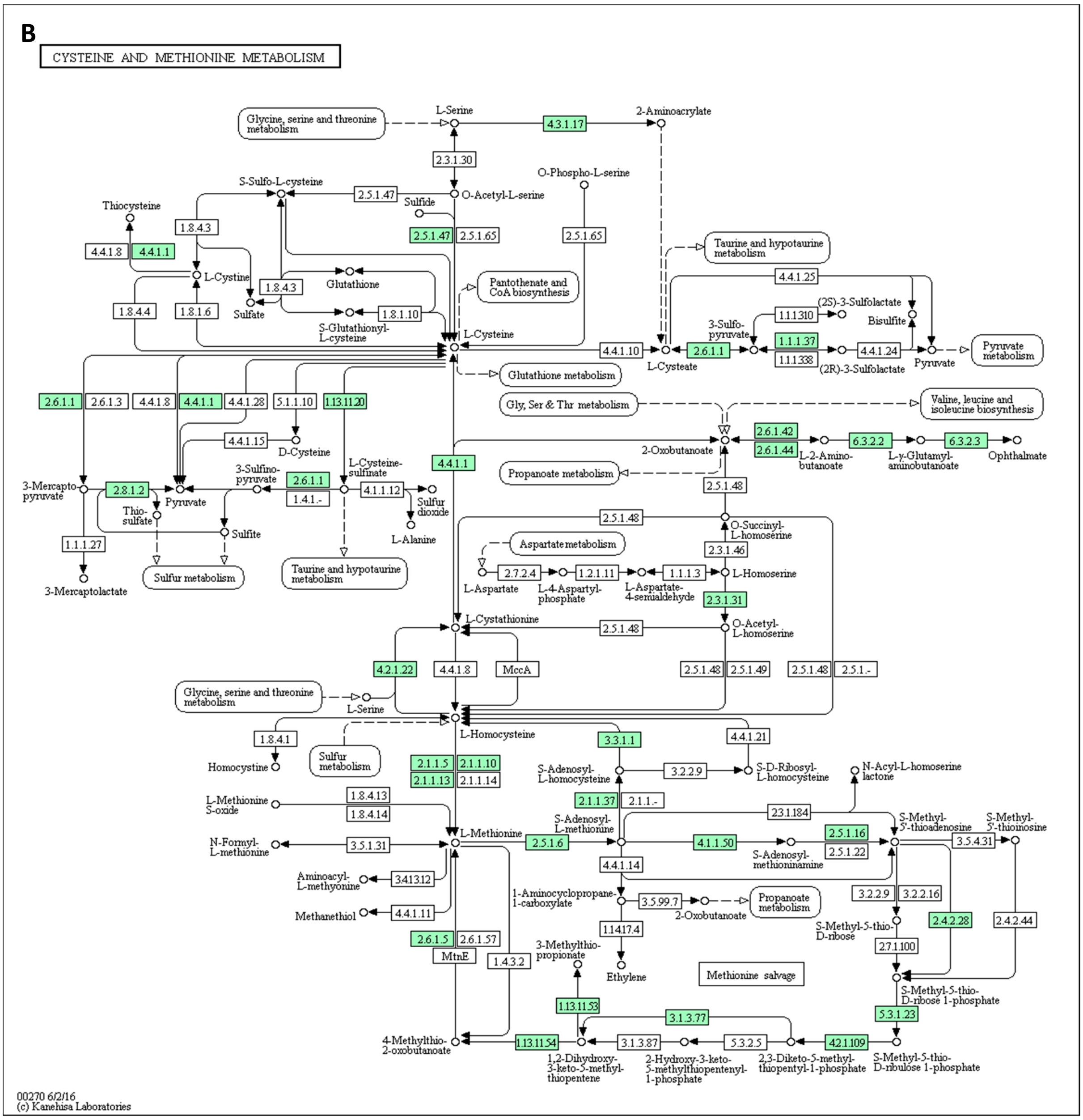
B
CYSTEINE AND METHIONINE METABOLISM
Glycine, serine and threonine metabolism
L-Serine
4.3.1.17
2-Aminoacrylate
2.3.1.30
O-Phospho-L-serine
S-Sulfo-L-cysteine
2.5.1.47
O-Acetyl-L-serine
Sulfide
Thiocysteine
1.8.4.3
4.4.1.8
4.4.1.1
2.5.1.47
2.5.1.65
2.5.1.65
Taurine and hypotaurine metabolism
L-Cystine
1.8.4.3
Glutathione
Pantothenate and CoA biosynthesis
4.4.1.25
Sulfate
(2S)-3-Sulfolactate
1.8.4.4
1.8.1.6
S-Glutathionyl-L-cysteine
1.8.1.10
1.1.1.310
Bisulfite
L-Cysteine
3-Sulfo-pyruvate
1.1.1.37
4.4.1.10
2.6.1.1
4.4.1.24
Pyruvate metabolism
L-Cysteate
1.1.1.338
(2R)-3-Sulfolactate
Pyruvate
Glutathione metabolism
2.6.1.1
2.6.1.3
4.4.1.8
4.4.1.1
4.4.1.28
5.1.1.10
1.13.11.20
Gly, Ser & Thr metabolism
Valine, leucine and isoleucine biosynthesis
4.4.1.15
D-Cysteine
2.6.1.42
2-Oxobutanoate
2.6.1.44
6.3.2.2
6.3.2.3
L-2-Amino-butanoate
L-γ-Glutamyl-aminobutanoate
Ophthalmate
4.4.1.1
3-Sulfino-pyruvate
L-Cysteine-sulfinate
Propanoate metabolism
3-Mercapto-pyruvate
2.8.1.2
Pyruvate
2.6.1.1
4.1.1.12
Sulfur dioxide
2.5.1.48
1.4.1.-
Thio-sulfate
Sulfite
L-Alanine
2.5.1.48
O-Succinyl-L-homoserine
1.1.1.27
Aspartate metabolism
2.3.1.46
3-Mercaptolactate
Sulfur metabolism
Taurine and hypotaurine metabolism
2.7.2.4
1.2.1.11
1.1.1.3
L-Homoserine
L-Aspartate
L-4-Aspartyl-phosphate
L-Aspartate-4-semialdehyde
2.3.1.31
L-Cystathionine
2.5.1.48
O-Acetyl-L-homoserine
4.2.1.22
4.4.1.8
MccA
2.5.1.48
2.5.1.49
2.5.1.48
2.5.1.-
Glycine, serine and threonine metabolism
L-Serine
L-Homocysteine
1.8.4.1
3.3.1.1
4.4.1.21
Homocystine
Sulfur metabolism
2.1.1.5
2.1.1.10
2.1.1.13
2.1.1.14
S-Adenosyl-L-homocysteine
3.2.2.9
S-D-Ribosyl-L-homocysteine
N-Acyl-L-homoserine lactone
L-Methionine S-oxide
1.8.4.13
1.8.4.14
2.1.1.37
2.1.1.-
2.3.1.184
S-Adenosyl-L-methionine
S-Methyl-5'-thioadenosine
S-Methyl-5'-thioinosine
N-Formyl-L-methionine
3.5.1.31
L-Methionine
2.5.1.6
4.1.1.50
2.5.1.16
3.5.4.31
S-Adenosyl-methioninamine
2.5.1.22
Aminoacyl-L-methionine
3.4.13.12
4.4.1.14
Methanethiol
4.4.1.11
1-Aminocyclopropane-1-carboxylate
3.5.99.7
2-Oxobutanoate
Propanoate metabolism
3.2.2.9
3.2.2.16
1.14.17.4
2.4.2.28
2.4.2.44
S-Methyl-5-thio-D-ribose
2.6.1.5
2.6.1.57
3-Methylthio-propionate
2.7.1.100
MtnE
1.4.3.2
Ethylene
Methionine salvage
S-Methyl-5-thio-D-ribose 1-phosphate
1.13.11.53
3.1.3.77
5.3.1.23
4-Methylthio-2-oxobutanoate
1.13.11.54
3.1.3.87
5.3.2.5
4.2.1.109
1,2-Dihydroxy-3-keto-5-methyl-thiopentene
2-Hydroxy-3-keto-5-methylthiopentenyl-1-phosphate
2,3-Diketo-5-methyl-thiopentyl-1-phosphate
S-Methyl-5-thio-D-ribulose 1-phosphate
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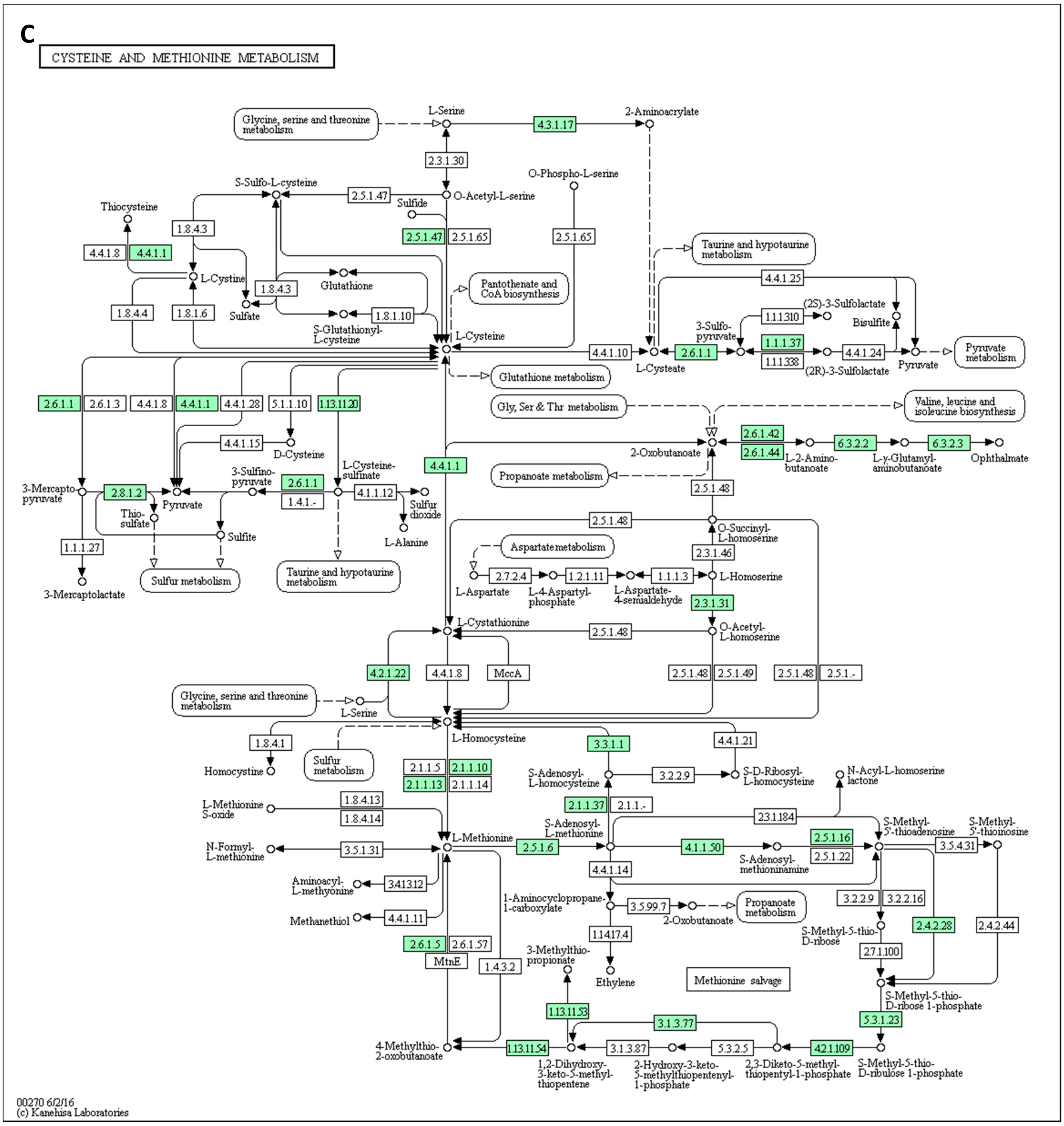
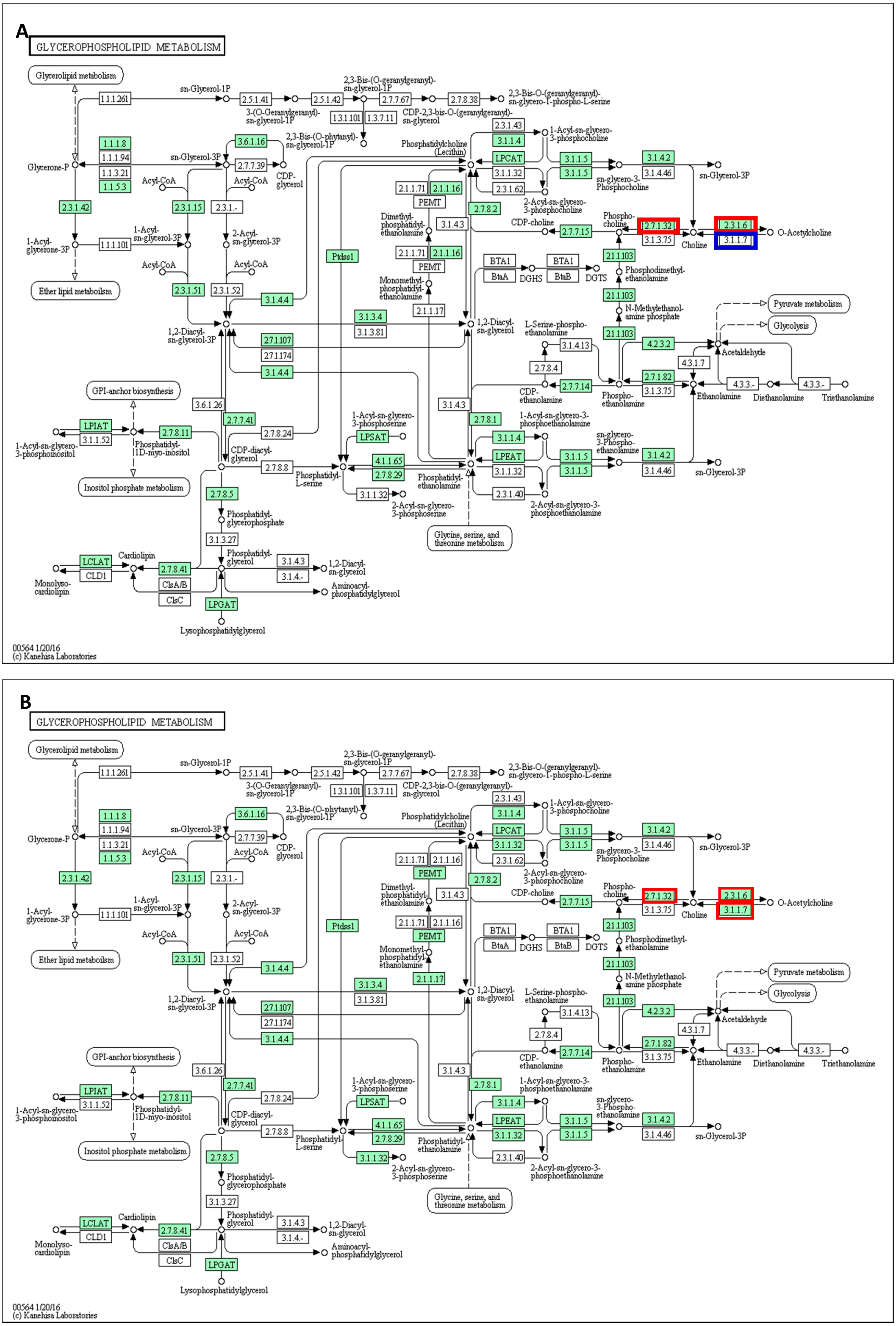


Figure S4. Cysteine and methionine metabolism pathway of (**A**) *Crassostrea gigas*, (**B**) *Lottia gigantea* and, (**C**) *Octopus bimaculoides*.


A
GLYCEROPHOSPHOLIPID METABOLISM
Glycerolipid metabolism
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
1.1.1.261
3-(O-Geranylgeranyl)-sn-glycerol-1P
1.3.1.101
1.3.7.11
CDP-2,3-bis-O-(geranylgeranyl)-sn-glycerol
2.3.1.43
1-Acyl-sn-glycero-3-phosphocholine
1.1.1.8
1.1.1.94
1.1.3.21
1.1.5.3
3.6.1.16
2,3-Bis-(O-phytanyl)-sn-glycerol-1P
Phosphatidylcholine (Lecithin)
3.1.1.4
LPCAT
3.1.1.32
3.1.1.5
3.1.4.2
3.1.4.46
sn-Glycerol-3P
sn-glycero-3-Phosphocholine
Glycerone-P
sn-Glycerol-3P
2.7.7.39
CDP-glycerol
Acyl-CoA
2.1.1.71
2.1.1.16
2.3.1.62
2-Acyl-sn-glycero-3-phosphocholine
2.3.1.42
2.3.1.15
2.3.1.-
PEMT
2.7.8.2
Dimethyl-phosphatidyl-ethanolamine
3.1.4.3
CDP-choline
2.7.7.15
Phospho-choline
2.7.1.32
2.3.1.6
O-Acetylcholine
3.1.3.75
Choline
3.1.1.7
1-Acyl-glycerone-3P
1.1.1.101
1-Acyl-sn-glycerol-3P
2-Acyl-sn-glycerol-3P
Ptdss1
BTA1
BtaA
DGHS
BtaB
DGTS
2.1.1.103
Phosphodimethyl-ethanolamine
Ether lipid metabolism
2.3.1.51
2.3.1.52
3.1.4.4
Monomethyl-phosphatidyl-ethanolamine
2.1.1.17
N-Methylethanol-amine phosphate
Pyruvate metabolism
Glycolysis
3.1.3.4
3.1.3.81
1,2-Diacyl-sn-glycerol
L-Serine-phospho-ethanolamine
1,2-Diacyl-sn-glycerol-3P
2.7.1.107
2.7.1.174
3.1.4.13
4.2.3.2
Acetaldehyde
2.7.8.4
4.3.1.7
2.7.1.82
4.3.3.-
GPI-anchor biosynthesis
3.6.1.26
CDP-ethanolamine
2.7.7.14
Phospho-ethanolamine
Ethanolamine
Diethanolamine
Triethanolamine
LPIAT
2.7.8.11
2.7.7.41
1-Acyl-sn-glycero-3-phosphoserine
1-Acyl-sn-glycero-3-phosphoethanolamine
3.1.1.52
1-Acyl-sn-glycero-3-phosphoinositol
Phosphatidyl-1D-myo-inositol
2.7.8.24
LPSAT
LPEAT
sn-glycero-3-Phospho-ethanolamine
CDP-diacyl-glycerol
2.7.8.8
4.1.1.65
2.7.8.29
Phosphatidyl-L-serine
Phosphatidyl-ethanolamine
Inositol phosphate metabolism
2.7.8.5
2.3.1.40
2-Acyl-sn-glycero-3-phosphoserine
2-Acyl-sn-glycero-3-phosphoethanolamine
Phosphatidyl-glycerophosphate
Glycine, serine, and threonine metabolism
3.1.3.27
LCLAT
Cardiolipin
Phosphatidyl-glycerol
1,2-Diacyl-sn-glycerol
CLD1
2.7.8.41
3.1.4.-
Monolyso-cardiolipin
ClsA/B
ClsC
Aminoacyl-phosphatidylglycerol
LPGAT
Lysophosphatidylglycerol
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(c) Kanehisa Laboratories
B
GLYCEROPHOSPHOLIPID METABOLISM
00564 1/20/16
(c) Kanehisa Laboratories

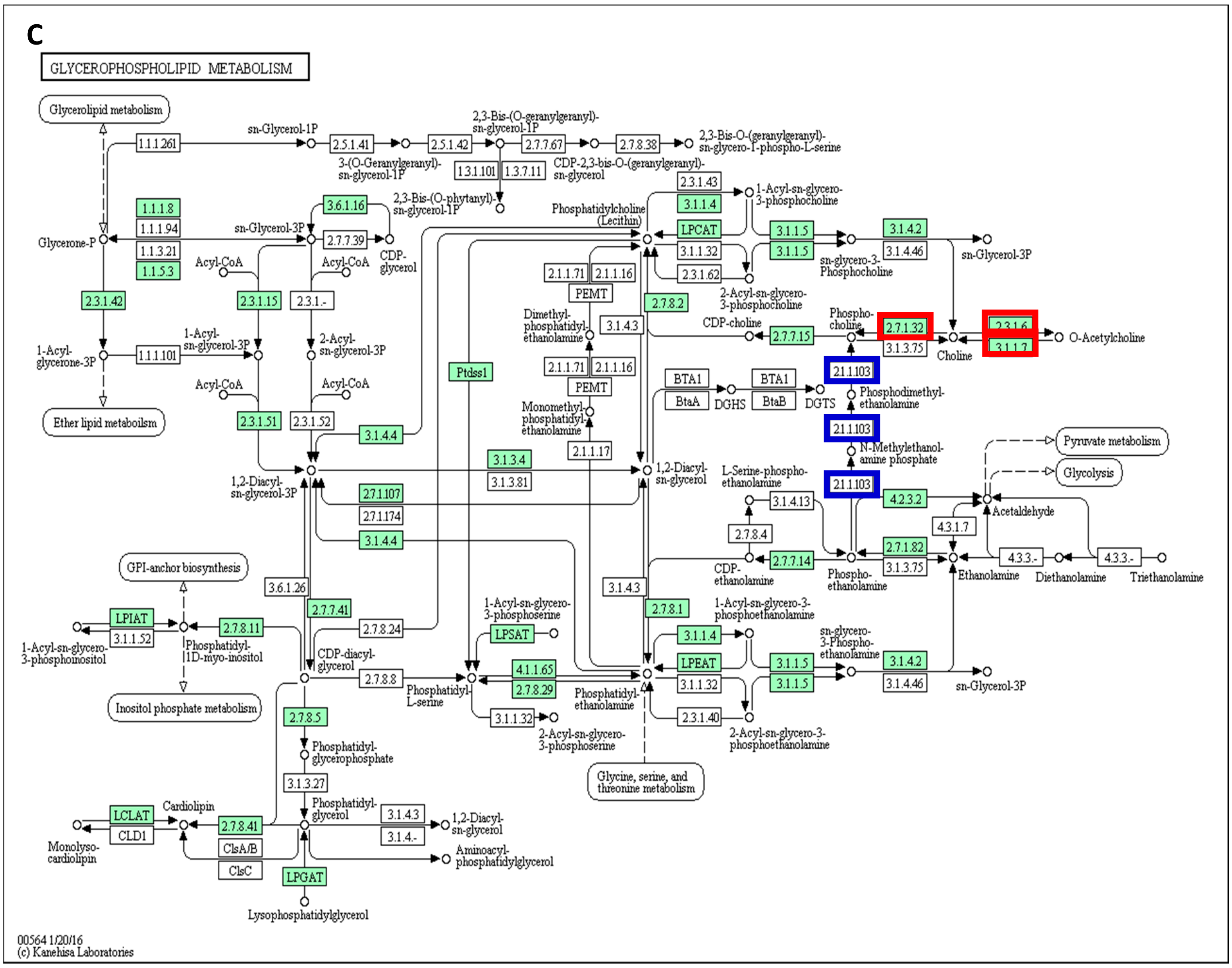
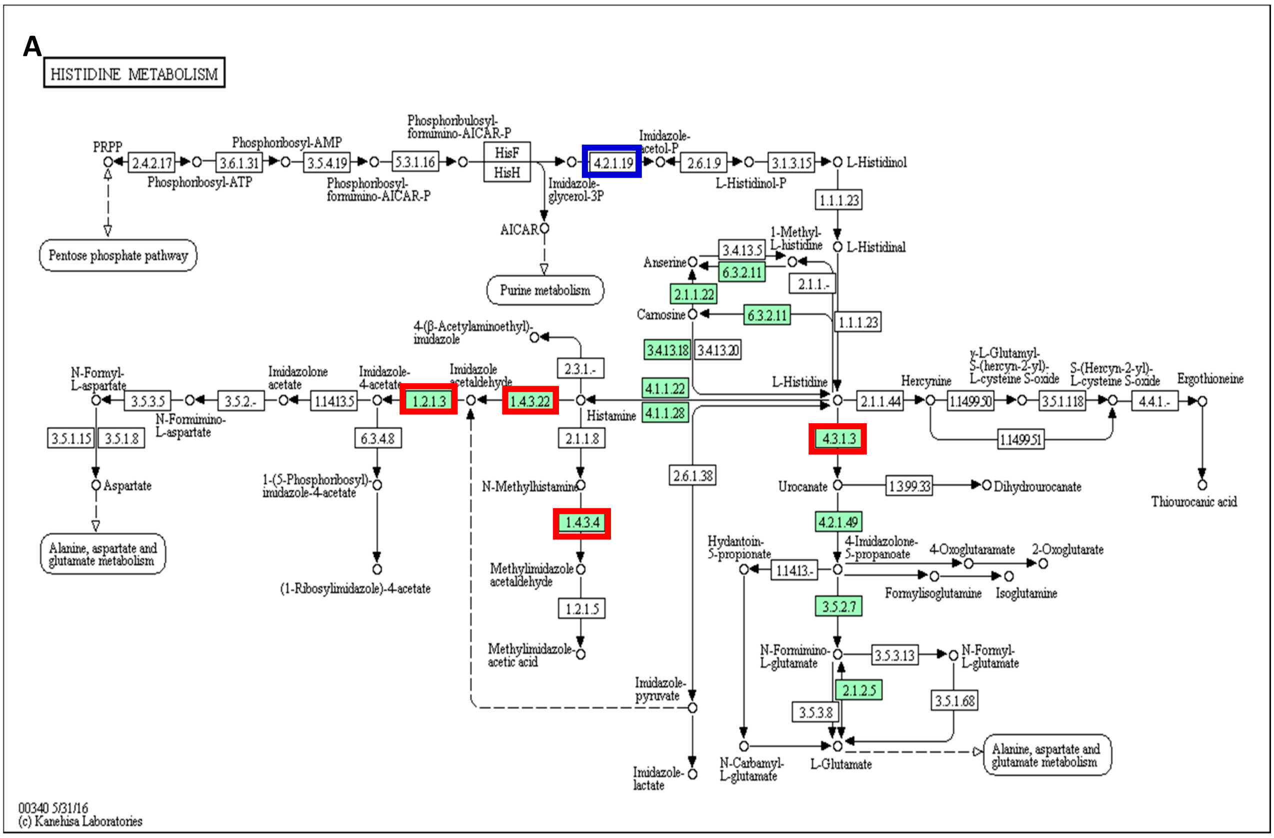


Figure S5. Glycerophospholipid metabolism pathway of (**A**) *Crassostrea gigas*, (**B**) *Lottia gigantea* and, (**C**) *Octopus bimaculoides* showing enzyme matches in green with those relevant to choline ester synthesis highlighted in red (present) and blue (absent).


A
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
AICAR
Purine metabolism
4.2.1.19
Imidazole-glycerol-3P
Imidazole-acetol-P
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
Anserine
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
3.5.2.-
N-Formimino-L-aspartate
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
L-Histidine
2.1.1.44
Hercynine
1.14.99.50
γ-L-Glutamyl-S-(hercyn-2-yl)-L-cysteine S-oxide
3.5.1.118
S-(Hercyn-2-yl)-L-cysteine S-oxide
4.4.1.-
Ergothioneine
1.14.99.51
Thiourocanic acid
3.5.1.15
3.5.1.8
Aspartate
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
Hydantoin-5-propionate
1.14.13.-
4-Imidazolone-5-propanoate
4-Oxoglutaramate
2-Oxoglutarate
Formylisoglutamine
Isoglutamine
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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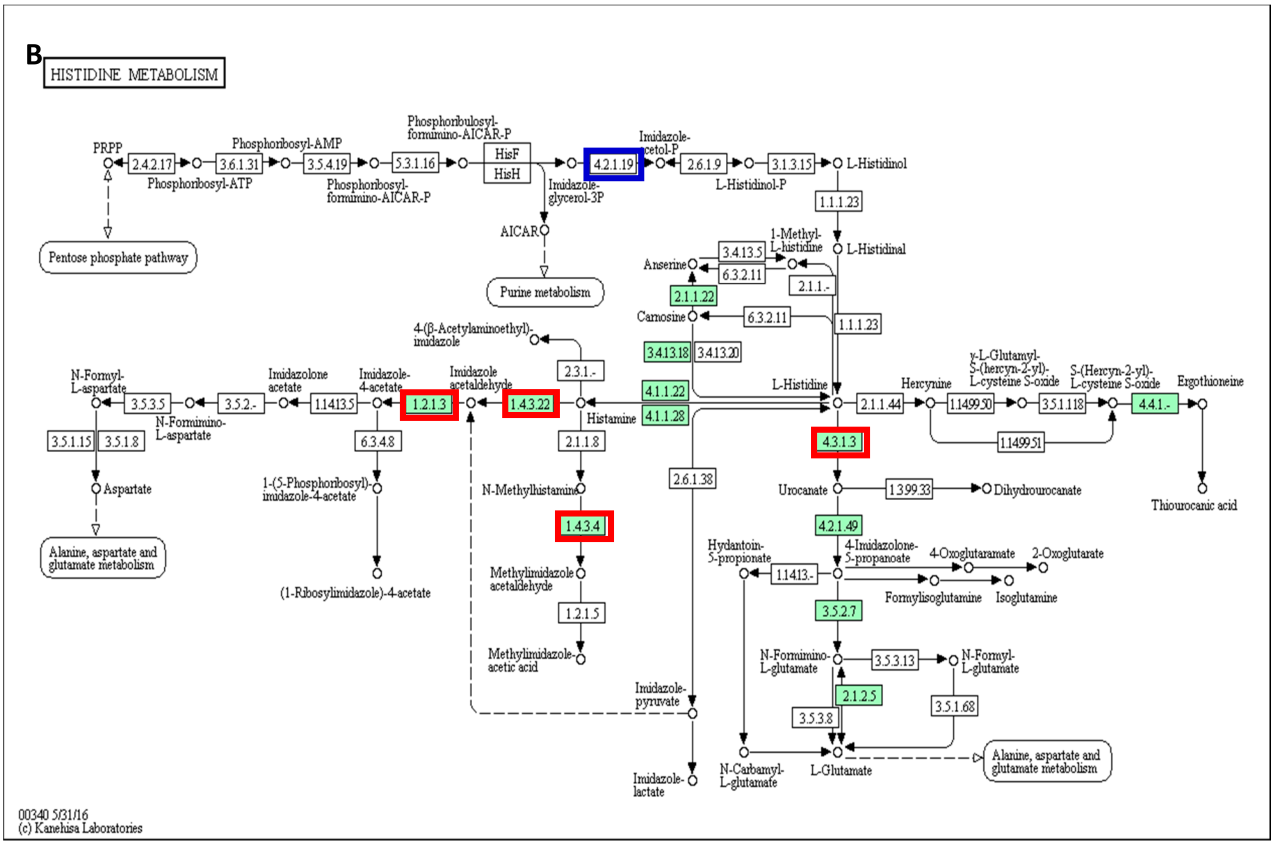
B
HISTIDINE METABOLISM
PRPP
2.4.2.17
Phosphoribosyl-ATP
3.6.1.31
Phosphoribosyl-AMP
3.5.4.19
Phosphoribosyl-formimino-AICAR-P
5.3.1.16
Phosphoribulosyl-formimino-AICAR-P
HisF
HisH
AICAR
Purine metabolism
4.2.1.19
Imidazole-glycerol-3P
Imidazole-acetol-P
2.6.1.9
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3.1.3.15
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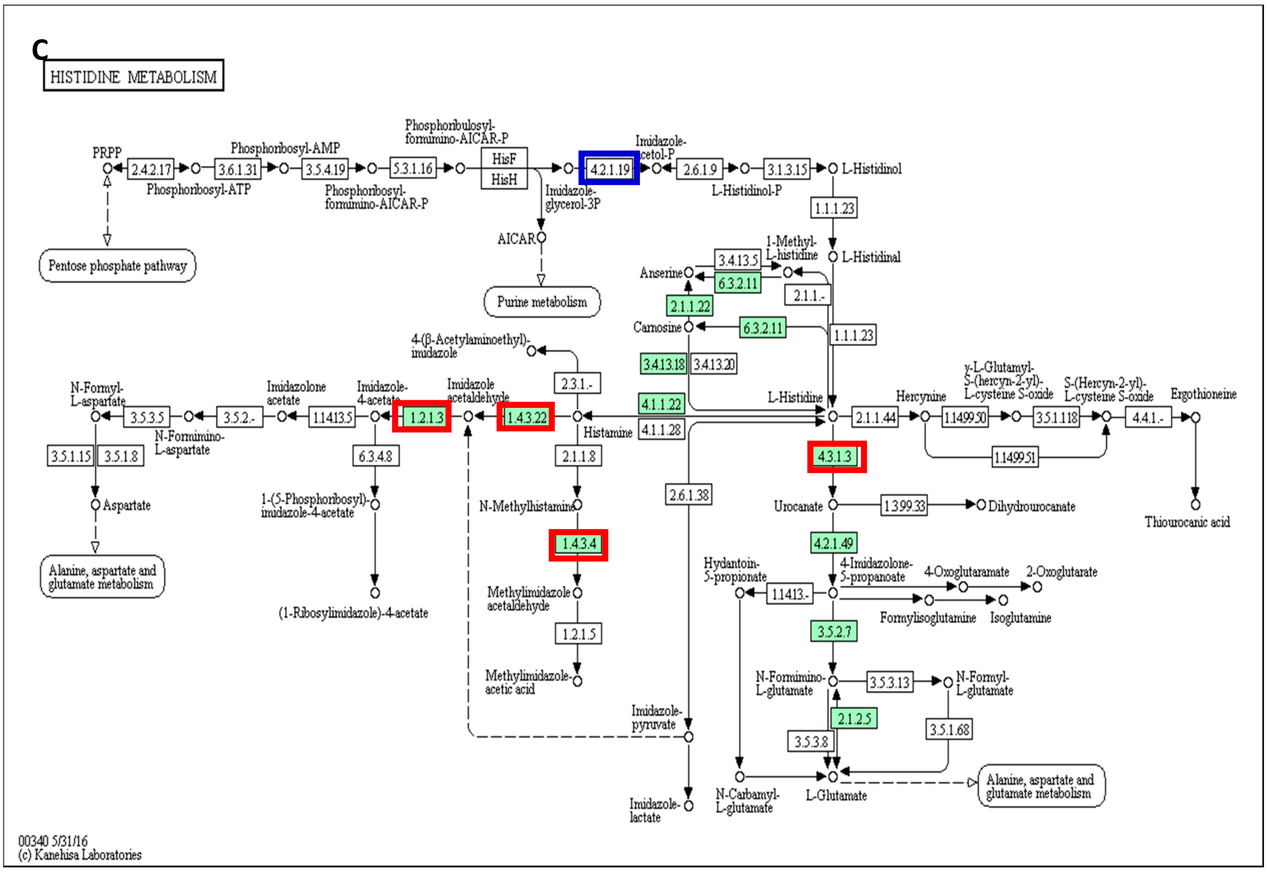

Figure S6. Histidine metabolism pathway of (**A**) *Crassostrea gigas*, (**B**) *Lottia gigantea* and, (**C**) *Octopus bimaculoides* showing matching enzymes in green, including several enzymes that convert histidine into imidazole (red boxes) but not imidazoleglycerol-phosphate dehydratase (blue box).