

Supporting Information Results 1: SeqAPASS Evaluation Results for Nicotinic Acetylcholine Receptor $\alpha 1$ Subunit

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

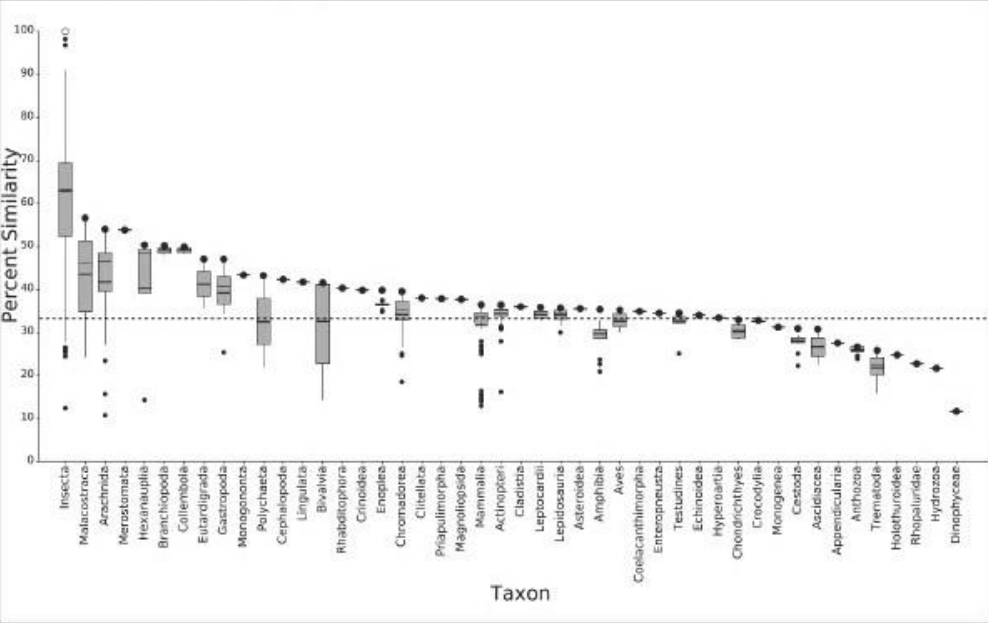
Level 1 Query Protein Information

SeqAPASS ID: 2323
Query Species: *Apis mellifera*
Query Protein: nicotinic acetylcholine receptor alpha1 subunit
Query Accession: NP_001091690.1
Ortholog Count: 110
Protein and Taxonomy Data: 06/08/2020
BLAST Version: 2.10.0
Software Version: 4.1

Report Settings

Report Type: Primary
E-value: 0.01
Sorted By Taxonomic Group: CLASS
Common Domains: 1
Species Read-Across: Y
Cut-off %: 33.12
Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2323

Query Species: *Apis mellifera*

Query Domain: (21) pfam02931, Neur_chan_LBD,
Neurotransmitter-gated ion-channel ligand binding domain

Query Accession: NP_001091690.1

Ortholog Count: 110

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 4.1

Report Settings

Report Type: Primary

E-value: 10.0

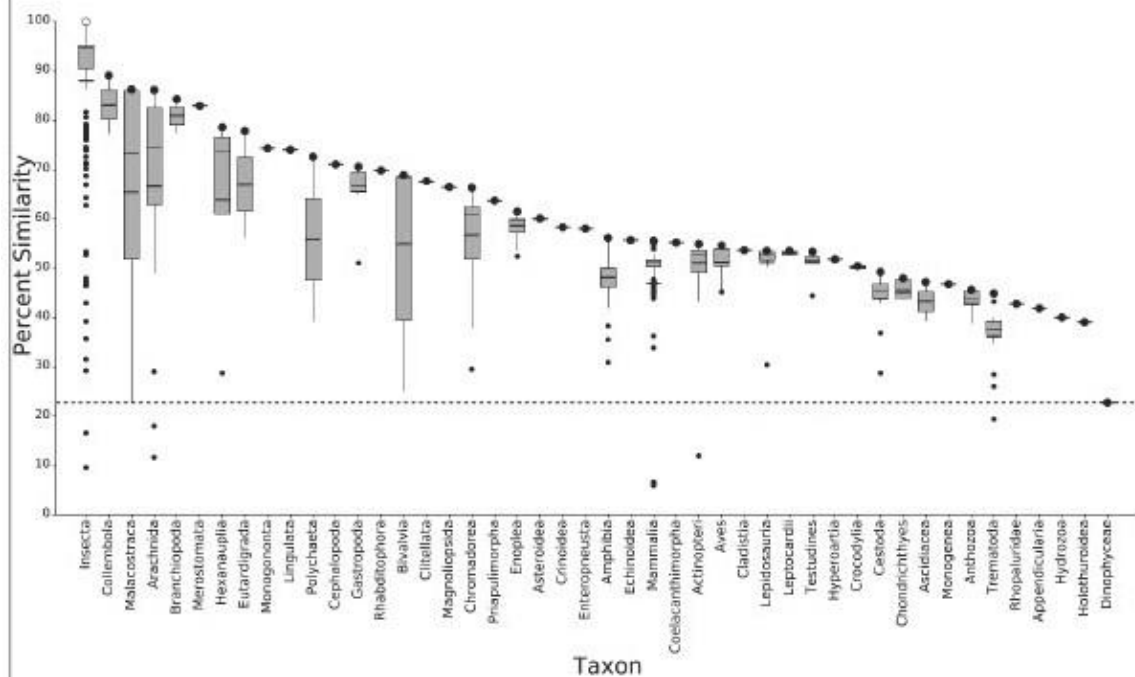
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 22.72

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Level 3

Selected Amino Acids

57R, 78E, 140K, 170W, 220Y, 221S, 227Y

Level 3 Template Protein Information

SeqAPASS ID: 2323

Template Species: *Drosophila melanogaster*

Template Protein: [NP_524481.2] nicotinic acetylcholine receptor alpha1, isoform A

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 4.1

Level 3 Visualization

Total Match	
Partial Match	
Not a Match	
Susceptible Yes	
Susceptible No	

Scientific Name	Similar Susceptibility	Amino Acid 1	Amino Acid 2	Amino Acid 3	Amino Acid 4	Amino Acid 5	Amino Acid 6	Amino Acid 7
<i>Drosophila melanogaster</i>	Y	57R	78E	140K	170W	220Y	221S	227Y
<i>Apis mellifera</i>	Y	53R	74E	176K	166W	216Y	217I	221Y
<i>Apis cerana</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Apis florea</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Habropoda labonosa</i>	Y	53R	74E	176K	166W	216Y	217I	223Y
<i>Osmia bicornis bicornis</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Osmia lignaria</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Bombus buxatus</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Bombus vancouverensis nearcticus</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Bombus vosnesenskii</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Bombus terrestris</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Megachile rotundata</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Dufourea novaeangliae</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Bombus impatiens</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Nomia melanderi</i>	Y	59R	100E	162K	192W	242Y	243I	249F
<i>Eufriesca mexicana</i>	Y	59R	100E	162K	192W	242Y	243I	249Y
<i>Megalopta genalis</i>	N	--	8E	70K	100W	150Y	151I	157F
<i>Apis dorsata</i>	Y	57K	78E	140K	170W	220Y	221T	227Y
<i>Ceratina calcarata</i>	Y	61K	82E	144K	174W	224Y	225T	231Y

Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(21) pfam02931, Neur_chan_LBD, Neurotransmitter-gated ion-channel ligand binding domain	Level 3 Template	Level 3 Amino Acids (Y/N)
Apis mellifera	nicotinic acetylcholine receptor alpha1 subunit	Y	Y	Drosophila melanogaster	Y
Apis cerana	acetylcholine receptor subunit alpha-like 1 isoform X2	Y	Y	Drosophila melanogaster	Y
Apis florea	acetylcholine receptor subunit alpha-like 1 isoform X2	Y	Y	Drosophila melanogaster	Y
Habropoda laboriosa	PREDICTED: acetylcholine receptor subunit alpha-like 1 isoform X3	Y	Y	Drosophila melanogaster	Y
Osmia bicornis bicornis	acetylcholine receptor subunit alpha-like 1 isoform X1	Y	Y	Drosophila melanogaster	Y
Osmia lignaria	acetylcholine receptor subunit alpha-like 1 isoform X1	Y	Y	Drosophila melanogaster	Y
Bombus bifarius	acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	Y
Bombus vancouverensis nearcticus	acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	Y
Bombus vosnesenskii	acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	Y
Bombus terrestris	acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	Y
Megachile rotundata	PREDICTED: acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	Y
Dufourea novaeangliae	PREDICTED: acetylcholine receptor subunit alpha-like 1 isoform X1	Y	Y	Drosophila melanogaster	Y

Bombus impatiens	acetylcholine receptor subunit alpha-like 1 isoform X2	Y	Y	Drosophila melanogaster	Y
Nomia melanderi	acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	Y
Eufriesea mexicana	PREDICTED: acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	Y
Megalopta genalis	acetylcholine receptor subunit alpha-like 1	Y	Y	Drosophila melanogaster	N
Apis dorsata	acetylcholine receptor subunit alpha-like isoform X7	Y	Y	Drosophila melanogaster	Y
Ceratina calcarata	acetylcholine receptor subunit alpha-like isoform X1	Y	Y	Drosophila melanogaster	Y

Supporting Information Results 2: SeqAPASS Evaluation Results for Nicotinic Acetylcholine
Receptor $\alpha 2$ Subunit

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

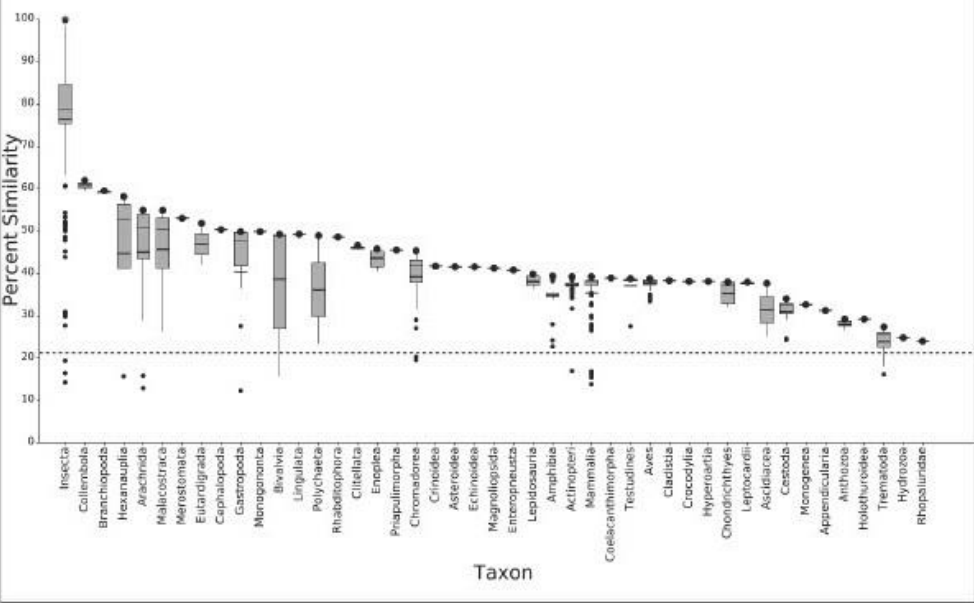
Level 1 Query Protein Information

SeqAPASS ID: 2323
Query Species: *Apis mellifera*
Query Protein: nicotinic acetylcholine receptor alpha2 subunit
Query Accession: AJE70260.1
Ortholog Count: 228
Protein and Taxonomy Data: 06/08/2020
BLAST Version: 2.10.0
Software Version: 5.0

Report Settings

Report Type: Primary
E-value: 0.01
Sorted By Taxonomic Group: CLASS
Common Domains: 1
Species Read-Across: Y
Cut-off %: 21.23
Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2323

Query Species: *Apis mellifera*

Query Domain: (21) pfam02931, Neur_chan_LBD,
Neurotransmitter-gated ion-channel ligand binding domain

Query Accession: AJE70260.1

Ortholog Count: 227

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

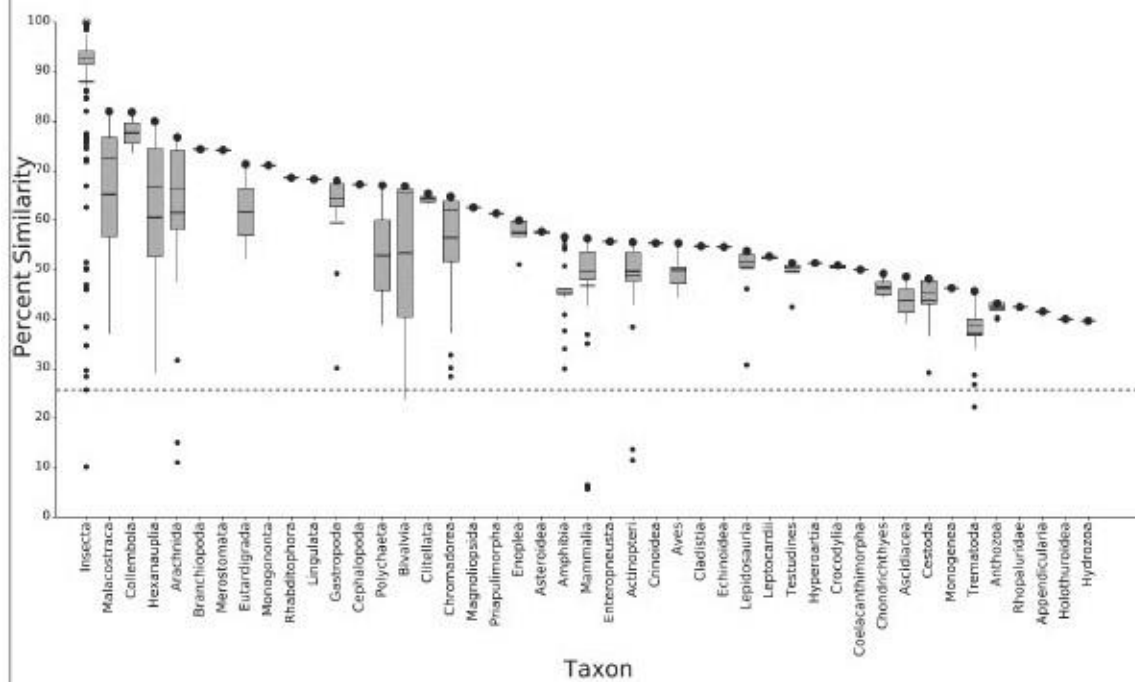
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 25.58

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Level 3

Selected Amino Acids

190W,241Y,242P,248Y

Level 3 Template Protein Information

SeqAPASS ID: 2323

Template Species: *Drosophila melanogaster*






Template Protein: [NP_524482.1] nicotinic acetylcholine receptor alpha2, isoform A

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Level 3 Visualization

	Total Match		Susceptible Yes
	Partial Match		Susceptible No
	Not a Match		

Scientific Name	Similar Susceptibility	Amino Acid 1	Amino Acid 2	Amino Acid 3	Amino Acid 4
<i>Drosophila melanogaster</i>	Y	190W	241Y	242P	248Y
<i>Apis mellifera</i>	Y	166W	215Y	216P	222Y
<i>Apis florea</i>	Y	166W	215Y	216P	222Y
<i>Apis cerana</i>	Y	166W	215Y	216P	222Y
<i>Apis dorsata</i>	Y	166W	215Y	216P	222Y
<i>Habropoda laboriosa</i>	Y	166W	215Y	216P	222Y
<i>Bombus vosnesenskii</i>	Y	166W	215Y	216P	222Y
<i>Bombus vancouverensis nearcticus</i>	Y	166W	215Y	216P	222Y
<i>Bombus bifarius</i>	Y	166W	215Y	216P	222Y
<i>Bombus impatiens</i>	Y	166W	215Y	216P	222Y
<i>Bombus terrestris</i>	Y	166W	215Y	216P	222Y
<i>Osmia bicornis bicornis</i>	Y	166W	215Y	216P	222Y
<i>Nomia melanderi</i>	Y	166W	217Y	218P	224Y
<i>Eufriesea mexicana</i>	Y	166W	215Y	216P	222Y
<i>Dufourea novaeangliae</i>	Y	166W	215Y	216P	222Y
<i>Osmia lignaria</i>	Y	166W	215Y	216P	222Y
<i>Megachile rotundata</i>	Y	183W	234Y	235P	241Y
<i>Megalopta genalis</i>	Y	166W	215Y	216P	222Y
<i>Ceratina calcarata</i>	Y	264W	314Y	315P	321Y
<i>Melipona quadrifasciata</i>	Y	166W	215Y	216P	222Y

Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(21) pfam02931, Neur_chan_LBD, Neurotransmitter-gated ion-channel ligand binding domain	Level 3 Template	Level 3 Amino Acids (Y/N)
Apis mellifera	nicotinic acetylcholine receptor alpha2 subunit	Y	Y	Drosophila melanogaster	Y
Apis florea	acetylcholine receptor subunit alpha-L1	Y	Y	Drosophila melanogaster	Y
Apis cerana	acetylcholine receptor subunit alpha-L1 isoform X1	Y	Y	Drosophila melanogaster	Y
Apis dorsata	acetylcholine receptor subunit alpha-L1 isoform X2	Y	Y	Drosophila melanogaster	Y
Habropoda laboriosa	PREDICTED: acetylcholine receptor subunit alpha-L1	Y	Y	Drosophila melanogaster	Y
Bombus vosnesenskii	acetylcholine receptor subunit alpha-L1 isoform X2	Y	Y	Drosophila melanogaster	Y
Bombus vancouverensis nearcticus	acetylcholine receptor subunit alpha-L1 isoform X2	Y	Y	Drosophila melanogaster	Y
Bombus bifarius	acetylcholine receptor subunit alpha-L1 isoform X2	Y	Y	Drosophila melanogaster	Y
Bombus impatiens	acetylcholine receptor subunit alpha-L1 isoform X2	Y	Y	Drosophila melanogaster	Y
Bombus terrestris	acetylcholine receptor subunit alpha-L1 isoform X2	Y	Y	Drosophila melanogaster	Y
Osmia bicornis bicornis	acetylcholine receptor subunit alpha-L1	Y	Y	Drosophila melanogaster	Y
Nomia melanderi	acetylcholine receptor subunit alpha-L1	Y	Y	Drosophila melanogaster	Y
Eufriesea mexicana	PREDICTED: acetylcholine receptor subunit alpha-L1	Y	Y	Drosophila melanogaster	Y
Dufourea novaeangliae	PREDICTED: acetylcholine receptor subunit	Y	Y	Drosophila melanogaster	Y

	alpha-L1 isoform X3				
Osmia lignaria	acetylcholine receptor subunit alpha-L1 isoform X2	Y	Y	Drosophila melanogaster	Y
Megachile rotundata	PREDICTED: acetylcholine receptor subunit alpha-L1	Y	Y	Drosophila melanogaster	Y
Megalopta genalis	acetylcholine receptor subunit alpha-L1 isoform X1	Y	Y	Drosophila melanogaster	Y
Ceratina calcarata	LOW QUALITY PROTEIN: acetylcholine receptor subunit alpha-L1-like	Y	Y	Drosophila melanogaster	Y
Melipona quadrifasciata	Acetylcholine receptor subunit alpha-L1	Y	Y	Drosophila melanogaster	Y

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

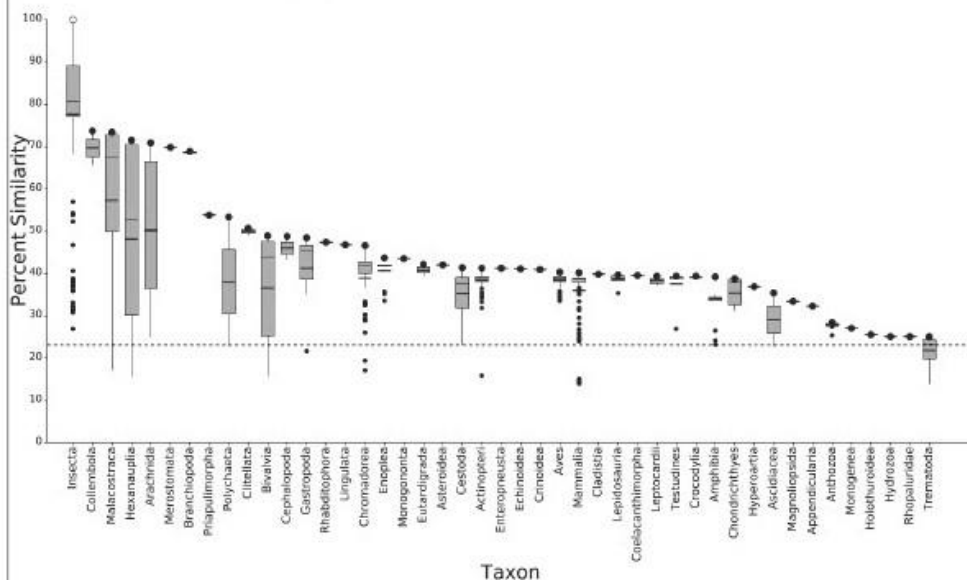
Level 1 Query Protein Information

SeqAPASS ID: 2323
Query Species: *Apis mellifera*
Query Protein: nicotinic acetylcholine receptor beta1 subunit
Query Accession: AAY87897.1
Ortholog Count: 296
Protein and Taxonomy Data: 06/08/2020
BLAST Version: 2.10.0
Software Version: 5.0

Report Settings

Report Type: Primary
E-value: 0.01
Sorted By Taxonomic Group: CLASS
Common Domains: 1
Species Read-Across: Y
Cut-off %: 23.01
Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2323

Query Species: *Apis mellifera*

Query Domain: (27) pfam02931, Neur_chan_LBD,
Neurotransmitter-gated ion-channel ligand binding domain

Query Accession: AAY87897.1

Ortholog Count: 295

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

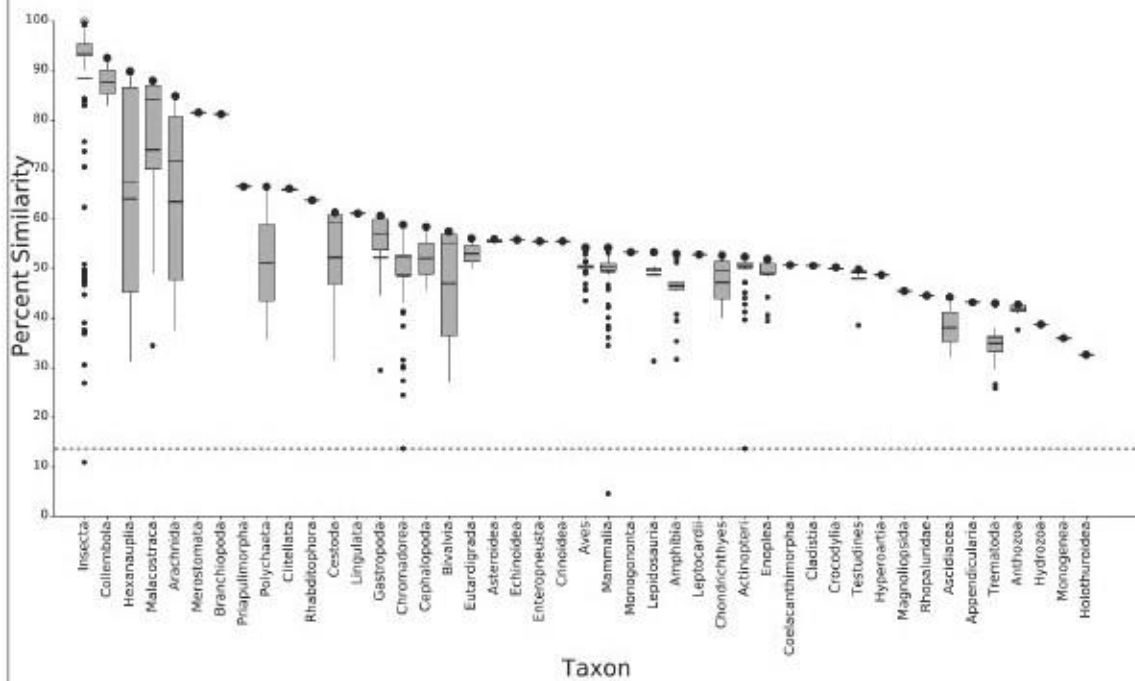
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 13.67

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Level 3

Selected Amino Acids

81R,141L,143V

Level 3 Template Protein Information

SeqAPASS ID: 2323

Template Species: *Drosophila melanogaster*






Template Protein: [NP_523927.2] nicotinic acetylcholine receptor beta1, isoform A

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Level 3 Visualization

	Total Match		Susceptible Yes
	Partial Match		Susceptible No
	Not a Match		

Scientific Name	Similar Susceptibility	Amino Acid 1	Amino Acid 2	Amino Acid 3
<i>Drosophila melanogaster</i>	Y	81R	141L	143V
<i>Apis mellifera</i>	Y	80R	140L	142V
<i>Apis cerana cerana</i>	Y	79R	139L	141V
<i>Apis dorsata</i>	Y	115R	175L	177V
<i>Apis florea</i>	Y	114R	174L	176V
<i>Apis cerana</i>	Y	115R	175L	177V
<i>Bombus impatiens</i>	Y	79R	139L	141V
<i>Bombus bifarius</i>	Y	79R	139L	141V
<i>Bombus vosnesenskii</i>	Y	79R	139L	141V
<i>Bombus vancouverensis nearcticus</i>	Y	79R	139L	141V
<i>Bombus terrestris</i>	Y	79R	139L	141V
<i>Nomia melanderi</i>	Y	79R	139L	141V
<i>Megalopta genalis</i>	Y	79R	139L	141V
<i>Ceratina calcarata</i>	Y	79R	139L	141V
<i>Dufourea novaeangliae</i>	Y	79R	139L	141V
<i>Habropoda laboriosa</i>	Y	79R	139L	141V
<i>Megachile rotundata</i>	Y	79R	139L	141V
<i>Osmia lignaria</i>	Y	79R	139L	141V
<i>Osmia bicornis bicornis</i>	Y	79R	139L	141V
<i>Eufriesea mexicana</i>	Y	91R	151L	153V

Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(27) pfam02931, Neur_chan_LBD, Neurotransmitter-gated ion-channel ligand binding domain	Level 3 Template	Level 3 Amino Acids (Y/N)
Apis mellifera	nicotinic acetylcholine receptor beta 1 subunit	Y	Y	Drosophila melanogaster	Y
Apis cerana cerana	nicotinic acetylcholine receptor beta 1	Y	Y	Drosophila melanogaster	Y
Apis dorsata	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Apis florea	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Apis cerana	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Bombus impatiens	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Bombus bifarius	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Bombus vosnesenskii	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Bombus vancouverensis nearcticus	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Bombus terrestris	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Nomia melanderi	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Megalopta genalis	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Ceratina calcarata	acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Dufourea novaeangliae	PREDICTED: acetylcholine receptor subunit beta-like 1	Y	Y	Drosophila melanogaster	Y
Habropoda laboriosa	PREDICTED:	Y	Y	Drosophila	Y

	acetylcholine receptor subunit beta- like 1			melanogaster	
Megachile rotundata	PREDICTED: acetylcholine receptor subunit beta- like 1	Y	Y	Drosophila melanogaster	Y
Osmia lignaria	acetylcholine receptor subunit beta- like 1	Y	Y	Drosophila melanogaster	Y
Osmia bicornis bicornis	acetylcholine receptor subunit beta- like 1	Y	Y	Drosophila melanogaster	Y
Eufriesea mexicana	PREDICTED: acetylcholine receptor subunit beta- like 1	Y	Y	Drosophila melanogaster	Y

Supporting Information Results 4: SeqAPASS Evaluation Results for Calmodulin

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

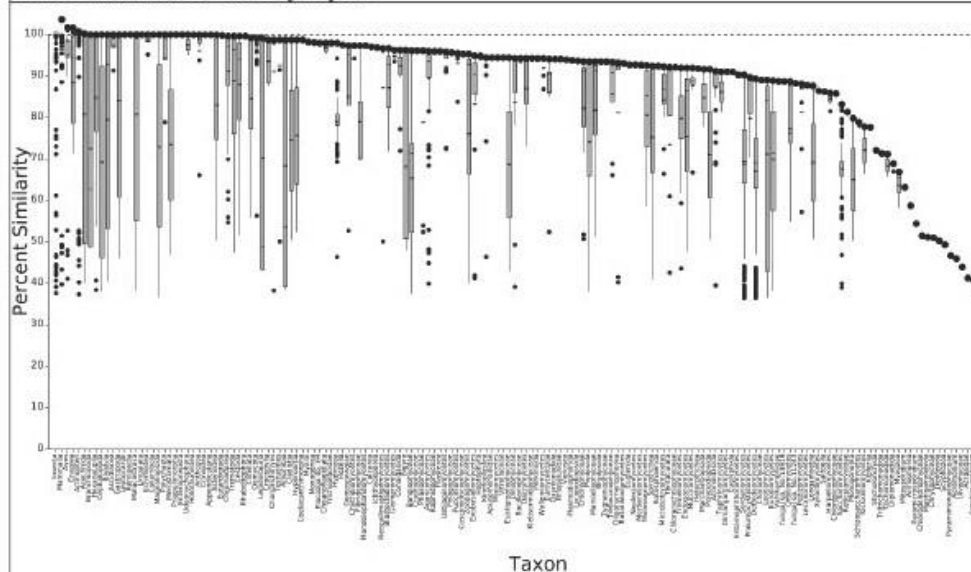
Level 1 Query Protein Information

SeqAPASS ID: 2281
Query Species: *Apis mellifera*
Query Protein: calmodulin
Query Accession: XP_006565317.1
Ortholog Count: 229
Protein and Taxonomy Data: 06/08/2020
BLAST Version: 2.10.0
Software Version: 5.0

Report Settings

Report Type: Primary
E-value: 0.01
Sorted By Taxonomic Group: CLASS
Common Domains: 1
Species Read-Across: Y
Cut-off %: 100.00
Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2281

Query Species: *Apis mellifera*

Query Domain: (12) cd00051, EFh, EF-hand, calcium binding motif, A diverse superfamily of calcium sensors and calcium signal modulators; most examples in this alignment model have 2 active canonical EF hands

Query Accession: XP_006565317.1

Ortholog Count: 229

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

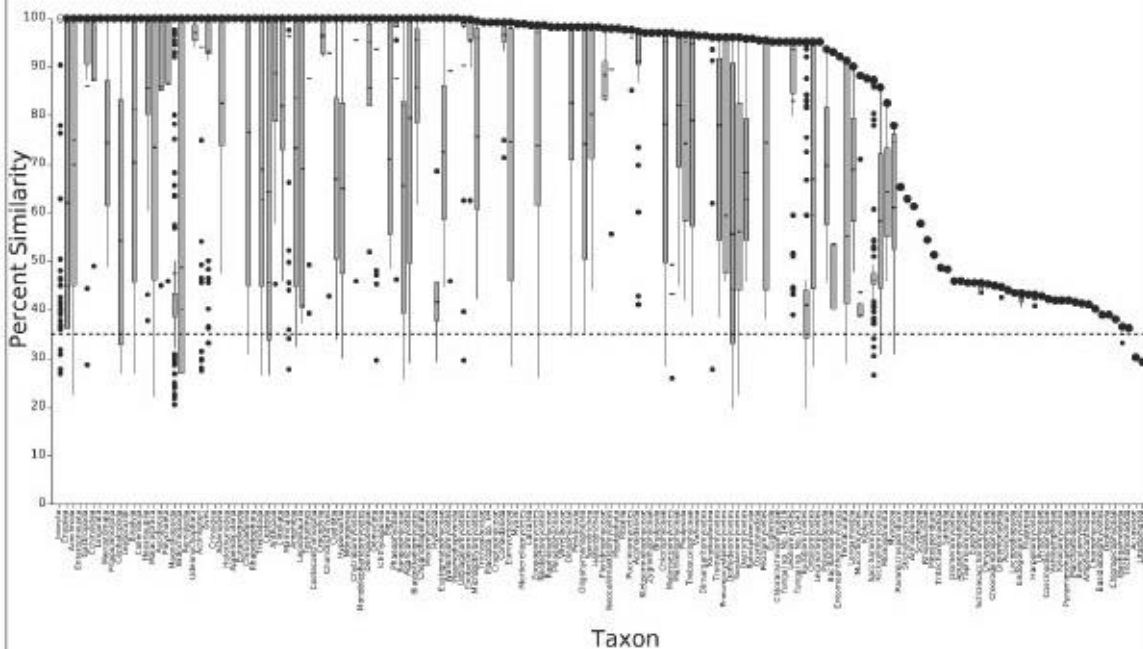
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 35.00

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Level 3

Selected Amino Acids

21D, 23D, 25D, 27T, 32E

Level 3 Template Protein Information

SeqAPASS ID: 2281

Template Species: *Rattus norvegicus*

Template Protein: [P0DP29.1] RecName:

Full=Calmodulin-1

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Level 3 Visualization

	Total Match		Susceptible Yes
	Partial Match		Susceptible No
	Not a Match		

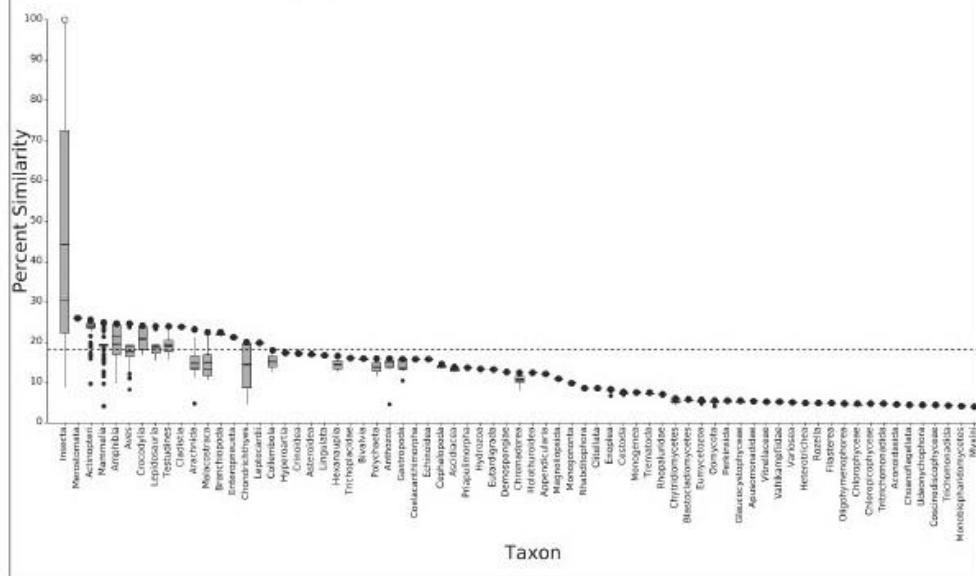
Scientific Name	Similar Susceptibility	Amino Acid 1	Amino Acid 2	Amino Acid 3	Amino Acid 4	Amino Acid 5
<i>Rattus norvegicus</i>	Y	21D	23D	25D	27T	32E
<i>Apis mellifera</i>	Y	21D	23D	25D	27T	32E
<i>Apis dorsata</i>	Y	21D	23D	25D	27T	32E
<i>Bombus terrestris</i>	Y	21D	23D	25D	27T	32E
<i>Bombus vancouverensis nearcticus</i>	Y	21D	23D	25D	27T	32E
<i>Nomia melanderi</i>	Y	21D	23D	25D	27T	32E
<i>Bombus vosgesensis</i>	Y	21D	23D	25D	27T	32E
<i>Dufourea novaeangliae</i>	Y	21D	23D	25D	27T	32E
<i>Apis cerana</i>	Y	21D	23D	25D	27T	32E
<i>Bombus bifarius</i>	Y	21D	23D	25D	27T	32E
<i>Bombus impatiens</i>	Y	21D	23D	25D	27T	32E
<i>Apis florea</i>	Y	21D	23D	25D	27T	32E
<i>Osmia bicornis bicornis</i>	Y	21D	23D	25D	27T	32E
<i>Habropoda laboriosa</i>	Y	21D	23D	25D	27T	32E
<i>Osmia lignaria</i>	Y	21D	23D	25D	27T	32E
<i>Megalopta genalis</i>	Y	21D	23D	25D	27T	32E
<i>Megachile rotundata</i>	Y	21D	23D	25D	27T	32E
<i>Eufriesen mexicana</i>	Y	21D	23D	25D	27T	32E
<i>Ceratina calcarata</i>	Y	21D	23D	25D	27T	32E
<i>Apis cerana cerana</i>	Y	21D	23D	25D	27T	32E

Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(12) cd00051, EFh, EF-hand, calcium binding motif; A diverse superfamily of calcium sensors and calcium signal modulators; most examples in this alignment model have 2 active canonical EF hands	Level 3 Template	Level 3 Amino Acids (Y/N)
<i>Apis mellifera</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Apis dorsata</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus terrestris</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus vancouverensis nearcticus</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Nomia melanderi</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus vosnesenskii</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Dufourea novaeangliae</i>	PREDICTED: calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Apis cerana</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Ceratina calcarata</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus bifarius</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus impatiens</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Apis florea</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Osmia bicornis bicornis</i>	calmodulin isoform X2	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Habropoda laboriosa</i>	PREDICTED: calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Osmia lignaria</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Megalopta genalis</i>	calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Megachile rotundata</i>	PREDICTED: calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Eufriesea mexicana</i>	PREDICTED: calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Apis cerana cerana</i>	Calmodulin	Y	Y	<i>Rattus norvegicus</i>	Y

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Level 1



Level 3

Selected Amino Acids

381D, 425D, 1117K, 1193D

Level 3 Template Protein Information

SeqAPASS ID: 2283

Template Species: *Apis mellifera*






Template Protein: [CCE60554.1] adenylyl cyclase

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Level 3 Visualization

 Total Match	 Partial Match	 Susceptible Yes
 Not a Match	 Susceptible No	

Scientific Name	Similar Susceptibility	Amino Acid 1	Amino Acid 2	Amino Acid 3	Amino Acid 4
<i>Apis mellifera</i>	Y	381D	425D	1117K	1193D
<i>Apis cerana</i>	Y	389D	433D	1125K	1201D
<i>Apis cerana cerana</i>	Y	380D	424D	1116K	1193D
<i>Apis dorsata</i>	Y	389D	433D	1125K	1201D
<i>Apis florea</i>	Y	389D	433D	1125K	1201D
<i>Bombus vosnesenskii</i>	Y	389D	433D	1128K	1204D
<i>Bombus bifarius</i>	Y	389D	433D	1128K	1204D
<i>Bombus impatiens</i>	Y	389D	433D	1128K	1204D
<i>Bombus vancouverensis nearcticus</i>	Y	389D	433D	1128K	1204D
<i>Eufriesea mexicana</i>	Y	389D	433D	1128K	1204D
<i>Bombus terrestris</i>	Y	389D	433D	1128K	1204D
<i>Habropoda laboriosa</i>	Y	403D	447D	1139K	1215D
<i>Megachile rotundata</i>	Y	389D	433D	1120K	1196D
<i>Osmia lignaria</i>	Y	382D	426D	1113K	1189D
<i>Osmia bicornis bicornis</i>	Y	390D	434D	1121K	1197D
<i>Ceratina calcarata</i>	Y	391D	435D	1122K	1198D
<i>Nomia melanderi</i>	Y	389D	433D	1122K	1198D
<i>Dufourea novaeangliae</i>	Y	389D	433D	1145K	1221D
<i>Megalopta genalis</i>	Y	389D	433D	1121K	1197D
<i>Melipona quadrifasciata</i>	Y	390D	434D	1034K	1110D

Final Decision Summary Report					
Species	Protein	Level 1 Susceptible (Y/N)	(367) pfam00211, Guanylate_cyc, Adenylate and Guanylate cyclase catalytic domain	Level 3 Template	Level 3 Amino Acids (Y/N)
<i>Apis mellifera</i>	adenylyl cyclase	Y	Y	<i>Apis mellifera</i>	Y
<i>Apis cerana</i>	adenylyl cyclase 78C isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Apis dorsata</i>	adenylyl cyclase 78C-like isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Apis florea</i>	adenylyl cyclase 78C isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus vosnesenskii</i>	adenylyl cyclase 78C-like isoform X5	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus impatiens</i>	adenylyl cyclase 78C isoform X5	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus bifarius</i>	adenylyl cyclase 78C-like isoform X5	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus vancouverensis nearcticus</i>	adenylyl cyclase 78C-like isoform X5	Y	Y	<i>Apis mellifera</i>	Y
<i>Eufriesea mexicana</i>	PREDICTED: adenylate cyclase type 8-like isoform X4	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus terrestris</i>	adenylate cyclase type 8 isoform X2	Y	Y	<i>Apis mellifera</i>	Y
<i>Habropoda laboriosa</i>	Adenylate cyclase type 8	Y	Y	<i>Apis mellifera</i>	Y
<i>Megachile rotundata</i>	PREDICTED: adenylate cyclase type 8 isoform X2	Y	Y	<i>Apis mellifera</i>	Y
<i>Osmia lignaria</i>	adenylyl cyclase 78C-like isoform X4	Y	Y	<i>Apis mellifera</i>	Y
<i>Osmia bicornis bicornis</i>	adenylyl cyclase 78C-like isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Ceratina calcarata</i>	adenylate cyclase type 8 isoform X6	Y	Y	<i>Apis mellifera</i>	Y
<i>Nomia melanderi</i>	adenylyl cyclase 78C-like isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Dufourea novaeangliae</i>	PREDICTED: LOW QUALITY PROTEIN: adenylate cyclase type 8-like	Y	Y	<i>Apis mellifera</i>	Y
<i>Megalopta genalis</i>	adenylyl cyclase 78C isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Melipona quadrifasciata</i>	Adenylate cyclase type 8	Y	Y	<i>Apis mellifera</i>	Y

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Level 1

Show Only Eukaryotes: Y

Figure 1 is a dot plot showing the percent similarity of 16S rDNA sequences for various taxa. The y-axis represents 'Percent Similarity' from 0 to 100. The x-axis represents 'Taxon' with labels for various species. A horizontal dashed line at 25% similarity indicates the threshold for species-level identification. Most taxa show similarity values above 25%, with some outliers below.

Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2452

Query Species: *Apis mellifera*

Query Domain: (143) pfam00027, cNMP_binding, Cyclic nucleotide-binding domain

Query Accession: XP_392905.2

Ortholog Count: 839

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

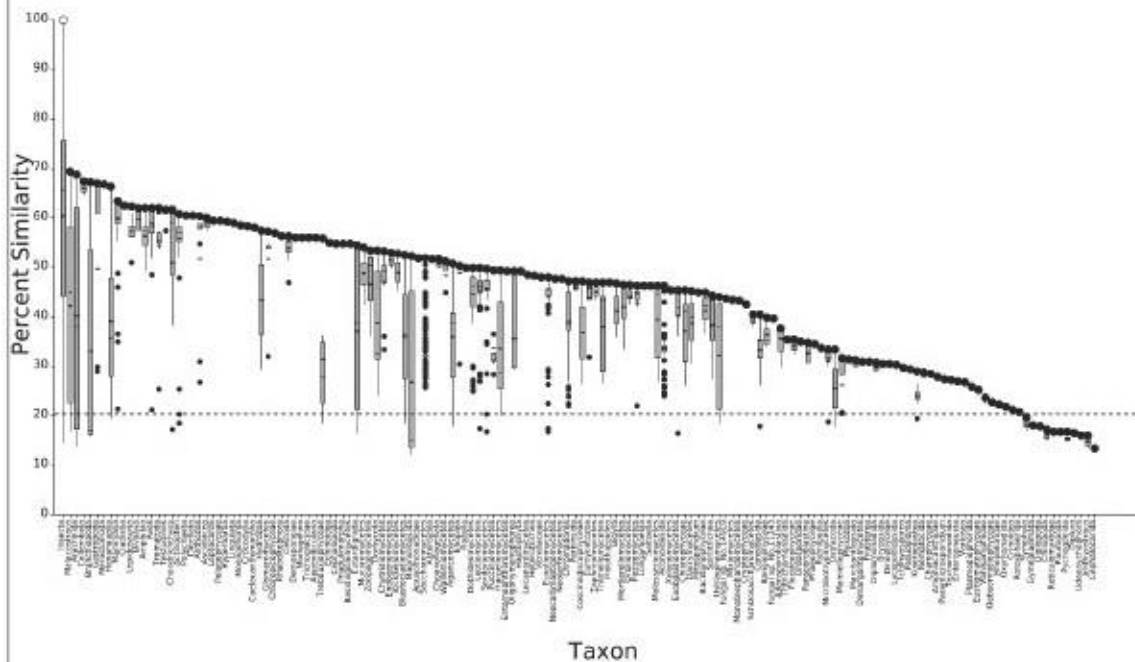
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 20.22

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Level 3

Selected Amino Acids

194G,195E,197A,204R,205A,317G,318E,320A,327R,328A

Level 3 Template Protein Information

SeqAPASS ID: 2452

Template Species: *Apis mellifera*

Template Protein: [CAG27571.1] cAMP-dependent protein kinase type II regulatory chain

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Level 3 Visualization

Sequence Name	Residue	Amino Acid 1	Amino Acid 2	Amino Acid 3	Amino Acid 4	Amino Acid 5	Amino Acid 6	Amino Acid 7	Amino Acid 8	Amino Acid 9	Amino Acid 10	Amino Acid 11
<i>Apis mellifera</i>	194	G	E	A	R	A	G	E	A	R	A	G
<i>Apis mellifera</i>	195	E	A	R	A	G	E	A	R	A	G	E
<i>Apis mellifera</i>	197	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	204	R	A	G	E	A	R	A	G	E	A	R
<i>Apis mellifera</i>	205	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	317	G	E	A	R	A	G	E	A	R	A	G
<i>Apis mellifera</i>	318	E	A	R	A	G	E	A	R	A	G	E
<i>Apis mellifera</i>	320	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	327	R	A	G	E	A	R	A	G	E	A	R
<i>Apis mellifera</i>	328	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	329	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	330	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	331	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	332	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	333	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	334	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	335	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	336	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	337	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	338	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	339	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	340	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	341	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	342	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	343	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	344	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	345	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	346	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	347	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	348	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	349	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	350	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	351	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	352	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	353	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	354	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	355	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	356	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	357	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	358	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	359	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	360	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	361	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	362	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	363	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	364	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	365	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	366	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	367	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	368	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	369	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	370	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	371	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	372	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	373	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	374	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	375	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	376	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	377	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	378	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	379	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	380	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	381	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	382	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	383	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	384	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	385	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	386	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	387	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	388	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	389	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	390	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	391	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	392	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	393	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	394	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	395	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	396	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	397	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	398	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	399	A	R	A	G	E	A	R	A	G	E	A
<i>Apis mellifera</i>	400	A	R	A	G	E	A	R	A	G	E	A

Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(143) pfam00027, cNMP_binding, Cyclic nucleotide-binding domain	Level 3 Template	Level 3 Amino Acids (Y/N)
Apis mellifera	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Apis mellifera carnica	cAMP-dependent protein kinase type II regulatory chain	Y	Y	Apis mellifera	Y
Apis cerana	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Apis cerana cerana	cAMP-dependent protein kinase type II regulatory subunit	Y	Y	Apis mellifera	Y
Apis dorsata	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Apis florea	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Eufriesea mexicana	PREDICTED: cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Bombus terrestris	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Bombus bifarius	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Bombus impatiens	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Bombus vosnesenskii	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Bombus vancouverensis nearcticus	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	Apis mellifera	Y
Megachile rotundata	PREDICTED:	Y	Y	Apis mellifera	Y

	cAMP-dependent protein kinase type II regulatory subunit isoform X1				
<i>Osmia bicornis bicornis</i>	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Osmia lignaria</i>	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Ceratina calcarata</i>	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Habropoda laboriosa</i>	PREDICTED: cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	<i>Apis mellifera</i>	Y
<i>Nomia melanderi</i>	cAMP-dependent protein kinase type II regulatory subunit, partial	Y	Y	<i>Apis mellifera</i>	Y
<i>Dufourea novaeangliae</i>	PREDICTED: LOW QUALITY PROTEIN: cAMP-dependent protein kinase type II regulatory subunit	Y	Y	<i>Apis mellifera</i>	Y
<i>Melipona quadrifasciata</i>	cAMP-dependent protein kinase type II regulatory subunit	Y	Y	<i>Apis mellifera</i>	Y
<i>Megalopta genalis</i>	cAMP-dependent protein kinase type II regulatory subunit isoform X1	Y	Y	<i>Apis mellifera</i>	Y

Supporting Information Results 7: SeqAPASS Evaluation Results for Calcium-Calmodulin-Dependent Protein Kinase II

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

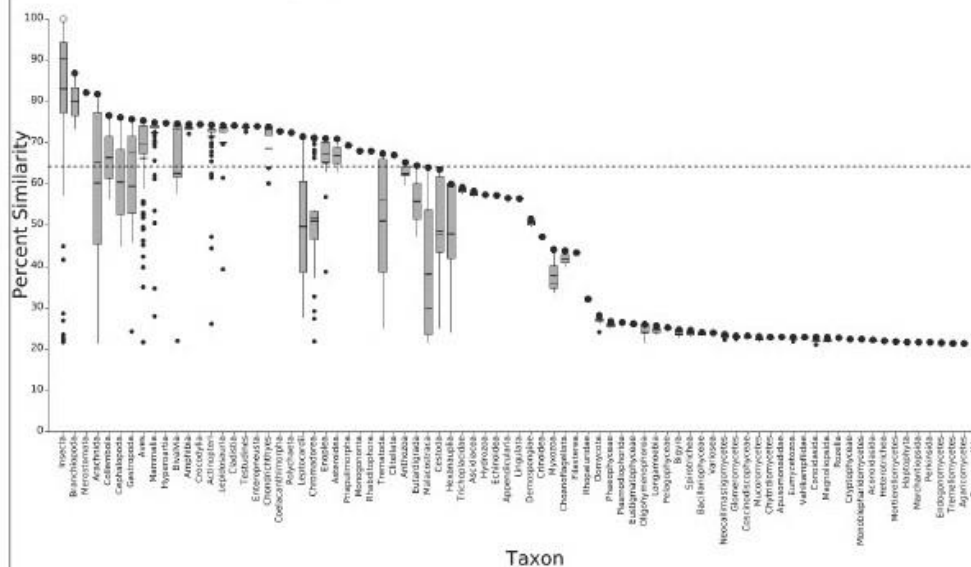
Level 1 Query Protein Information

SeqAPASS ID: 2283
Query Species: *Apis mellifera*
Query Protein: calcium/calmodulin-dependent protein kinase II
Query Accession: NP_001128422.1
Ortholog Count: 191
Protein and Taxonomy Data: 06/08/2020
BLAST Version: 2.10.0
Software Version: 5.0

Report Settings

Report Type: Primary
E-value: 0.01
Sorted By Taxonomic Group: CLASS
Common Domains: 1
Species Read-Across: Y
Cut-off %: 64.26
Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2283

Query Species: *Apis mellifera*

Query Domain: (12) cd14086, STKc_CaMKII, Catalytic domain of the Serine/Threonine kinase, Calcium/calmodulin-dependent protein kinase Type II

Query Accession: NP_001128422.1

Ortholog Count: 193

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

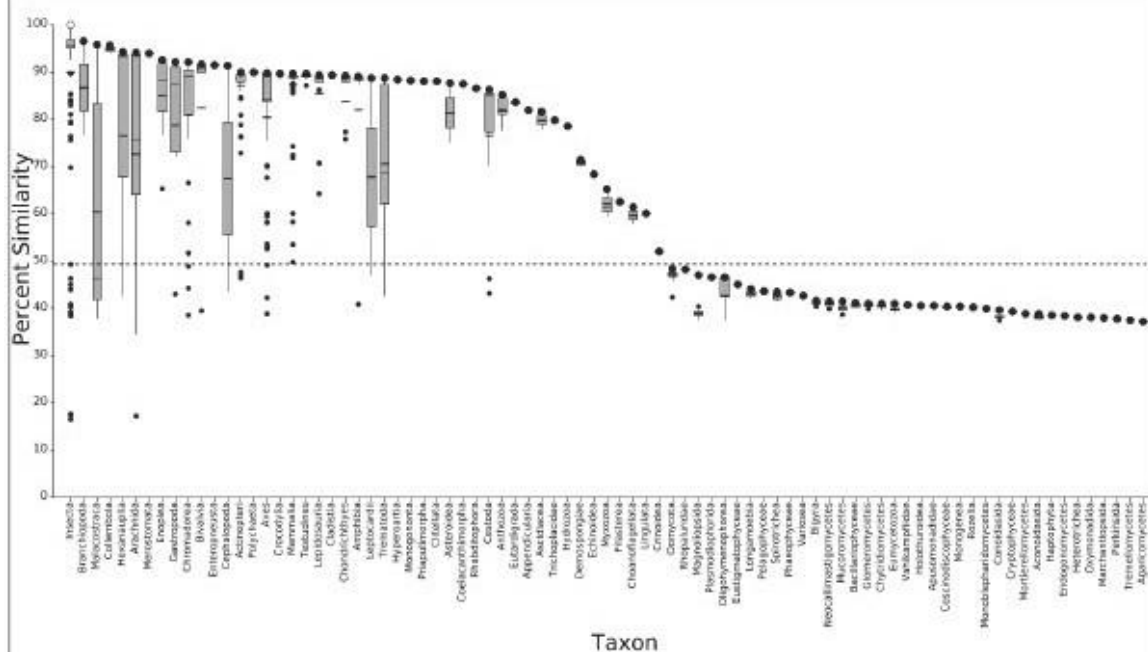
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 49.34

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Level 3

Selected Amino Acids

43K,254T,287T,306T,307T,315S

Level 3 Template Protein Information

SeqAPASS ID: 2283

Template Species: *Apis mellifera*

Template Protein: [NP_001128422.1]
calcium/calmodulin-dependent protein kinase II

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Level 3 Visualization

<div> <div>Total Match</div> <div>Partial Match</div> <div>Not a Match</div> </div> <div> <div>Susceptible Yes</div> <div>Susceptible No</div> </div>		Scientific Name	Similar Susceptibility	Amino Acid 1	Amino Acid 2	Amino Acid 3	Amino Acid 4	Amino Acid 5	Amino Acid 6
		<i>Apis mellifera</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Apis dorsata</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Apis florea</i>	Y	43K	234T	287T	306T	307T	313S
		<i>Osmia lignaria</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Eufriesea mexicana</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Megachile rotundata</i>	Y	43K	234T	287T	306T	307T	313S
		<i>Bombus vancouverensis nearcticus</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Bombus bifarius</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Bombus impatiens</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Bombus vosnesenskii</i>	Y	43K	234T	287T	306T	307T	313S
		<i>Bombus terrestris</i>	Y	43K	234T	287T	306T	307T	313S
		<i>Megalopta genalis</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Notrisa melanderi</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Dufourea novaeangliae</i>	Y	43K	234T	287T	306T	307T	313S
		<i>Ceratina calcarata</i>	Y	43K	233T	286T	305T	306T	314S
		<i>Habropoda laboriosa</i>	Y	43K	254T	287T	306T	307T	315S
		<i>Osmia bicornis bicornis</i>	Y	21K	232T	265T	294T	285T	293S
		<i>Apis cerana</i>	N	43K	254T	287T	--	--	306P

Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(12) cd14086, STKc_CaMKII, Catalytic domain of the Serine/Threonine kinase, Calcium/calmodulin-dependent protein kinase Type II	Level 3 Template	Level 3 Amino Acids (Y/N)
<i>Apis mellifera</i>	calcium/calmodulin-dependent protein kinase II	Y	Y	<i>Apis mellifera</i>	Y
<i>Apis dorsata</i>	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X24	Y	Y	<i>Apis mellifera</i>	Y
<i>Apis florea</i>	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X37	Y	Y	<i>Apis mellifera</i>	Y
<i>Osmia lignaria</i>	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X28	Y	Y	<i>Apis mellifera</i>	Y
<i>Eufriesea mexicana</i>	PREDICTED: calcium/calmodulin-dependent protein kinase type II alpha chain isoform X14	Y	Y	<i>Apis mellifera</i>	Y
<i>Megachile rotundata</i>	PREDICTED: calcium/calmodulin-dependent protein kinase type II alpha chain isoform X9	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus bifarius</i>	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X18	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus impatiens</i>	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X17	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus vosnesenskii</i>	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X17	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus vancouverensis nearcticus</i>	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X18	Y	Y	<i>Apis mellifera</i>	Y
<i>Bombus terrestris</i>	calcium/calmodulin-dependent protein	Y	Y	<i>Apis mellifera</i>	Y

	kinase type II alpha chain isoform X13				
Megalopta genalis	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X21	Y	Y	Apis mellifera	Y
Nomia melanderi	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X16	Y	Y	Apis mellifera	Y
Dufourea novaeangliae	PREDICTED: calcium/calmodulin-dependent protein kinase type II alpha chain isoform X8	Y	Y	Apis mellifera	Y
Ceratina calcarata	calcium/calmodulin-dependent protein kinase type II alpha chain isoform X19	Y	Y	Apis mellifera	Y
Habropoda laboriosa	PREDICTED: calcium/calmodulin-dependent protein kinase type II alpha chain isoform X8	Y	Y	Apis mellifera	Y
Osmia bicornis bicornis	calcium/calmodulin-dependent protein kinase type II alpha chain, partial	Y	Y	Apis mellifera	Y
Apis cerana	calcium/calmodulin-dependent protein kinase type II alpha chain	Y	Y	Apis mellifera	N

Supporting Information Results 8: SeqAPASS Evaluation Results for cAMP-Responsive Element Binding Protein

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

Level 1 Query Protein Information

SeqAPASS ID: 2306

Query Species: *Apis mellifera*

Query Protein: cyclic AMP-responsive element-binding protein 1 isoform X1

Query Accession: XP_006570112.1

Ortholog Count: 423

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 0.01

Sorted By Taxonomic Group: CLASS

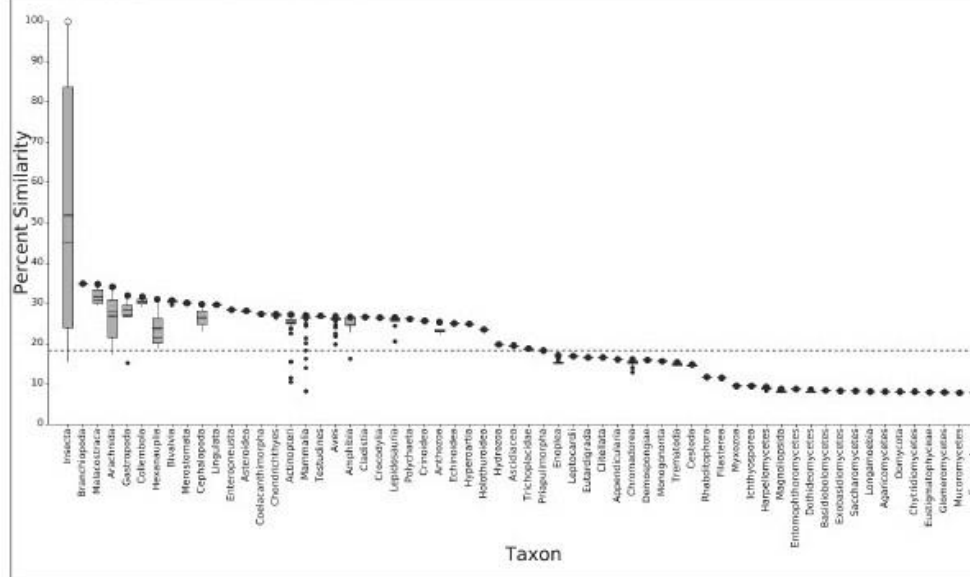
Common Domains: 1

Species Read-Across: Y

Cut-off %: 18.25

Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

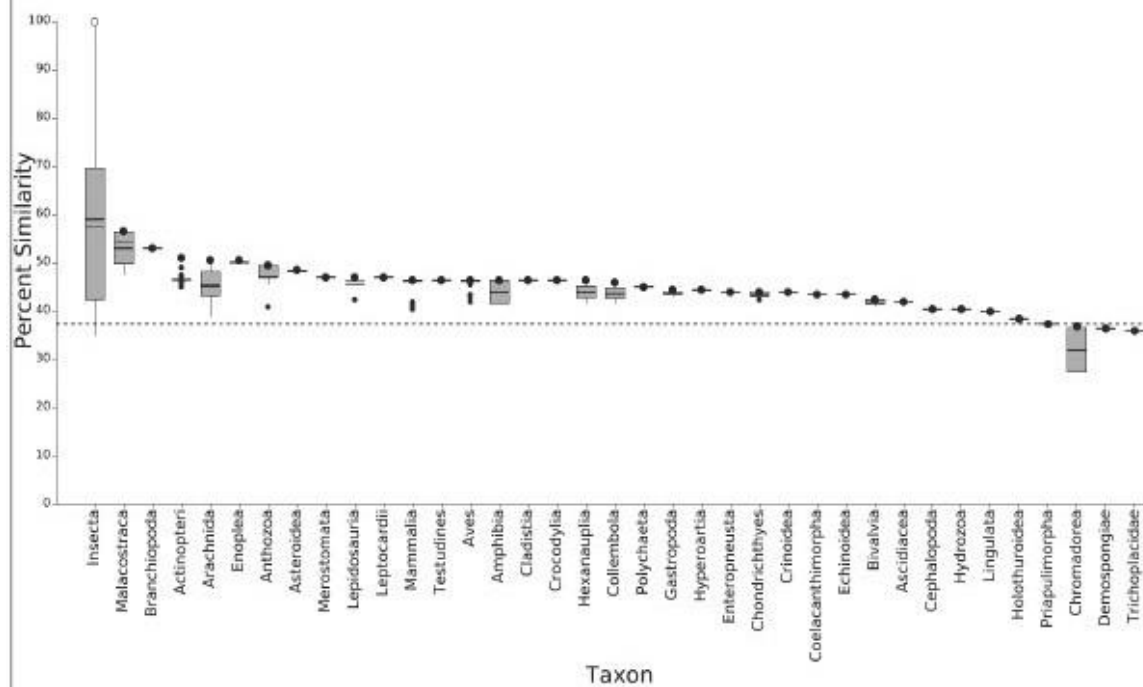
Level 2 Query Protein Information

SeqAPASS ID: 2306
 Query Species: *Apis mellifera*
 Query Domain: (124) pfam02173, pKID, pKID domain
 Query Accession: XP_006570112.1
 Ortholog Count: 420
 Protein and Taxonomy Data: 06/08/2020
 BLAST Version: 2.10.0
 Software Version: 5.0

Report Settings

Report Type: Primary
 E-value: 10.0
 Sorted By Taxonomic Group: CLASS
 Species Read-Across: Y
 Cut-off %: 37.36
 Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Level 3

Selected Amino Acids

130R,131R,132P,133S,134Y

Level 3 Template Protein Information

SeqAPASS ID: 2306

Template Species: *Rattus norvegicus*


Template Protein: [P15337.1] RecName:
Full=Cyclic AMP-responsive element-binding
protein 1; Short=CREB-1; Short=cAMP-responsive
element-binding protein 1

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Level 3 Visualization

	Total Match		Susceptible Yes
	Partial Match		Susceptible No
	Not a Match		

Scientific Name	Similar Susceptibility	Amino Acid 1	Amino Acid 2	Amino Acid 3	Amino Acid 4	Amino Acid 5
<i>Rattus norvegicus</i>	Y	130R	131R	132P	133S	134Y
<i>Megalopta genalis</i>	Y	140R	141R	142P	143S	144Y
<i>Megachile rotundata</i>	Y	140R	141R	142P	143S	144Y
<i>Apis mellifera</i>	Y	139R	140R	141P	142S	143Y
<i>Apis dorsata</i>	Y	139R	140R	141P	142S	143Y
<i>Apis florea</i>	Y	139R	140R	141P	142S	143Y
<i>Bombus vosnesenskii</i>	Y	139R	140R	141P	142S	143Y
<i>Bombus impatiens</i>	Y	139R	140R	141P	142S	143Y
<i>Bombus vancouverensis nearcticus</i>	Y	139R	140R	141P	142S	143Y
<i>Bombus terrestris</i>	Y	139R	140R	141P	142S	143Y
<i>Bombus bifarius</i>	Y	139R	140R	141P	142S	143Y
<i>Eufriesea mexicana</i>	Y	139R	140R	141P	142S	143Y
<i>Dufourea novaeangliae</i>	Y	140R	141R	142P	143S	144Y
<i>Nomia melanderi</i>	Y	140R	141R	142P	143S	144Y
<i>Osmia lignaria</i>	Y	140R	141R	142P	143S	144Y
<i>Osmia bicornis bicornis</i>	Y	140R	141R	142P	143S	144Y
<i>Apis cerana cerana</i>	Y	139R	140R	141P	142S	143Y
<i>Ceratina calcarata</i>	Y	140R	141R	142P	143S	144Y
<i>Habropoda laboriosa</i>	Y	139R	140R	141P	142S	143Y
<i>Apis cerana</i>	Y	139R	140R	141P	142S	143Y
<i>Melipona quadrifasciata</i>	N	141I	142L	143S	144F	145W

Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(124) pfam02173, pKID, pKID domain	Level 3 Template	Level 3 Amino Acids (Y/N)
<i>Apis mellifera</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Apis florea</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Apis dorsata</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus vosnesenskii</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus impatiens</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus vancouverensis nearcticus</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus terrestris</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Bombus bifarius</i>	cyclic AMP-responsive element-binding protein 1-like isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Eufriesea mexicana</i>	PREDICTED: cyclic AMP-responsive element-binding protein 1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Dufourea novaeangliae</i>	PREDICTED: cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Nomia melanderi</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Osmia lignaria</i>	cyclic AMP-responsive element-binding protein 1 isoform X1	Y	Y	<i>Rattus norvegicus</i>	Y
<i>Osmia bicornis</i>	cyclic AMP-	Y	Y	<i>Rattus norvegicus</i>	Y

bicornis	responsive element-binding protein 1 isoform X1				
Apis cerana cerana	Cyclic AMP-responsive element-binding protein	Y	Y	Rattus norvegicus	Y
Ceratina calcarata	cyclic AMP-responsive element-binding protein 1 isoform X2	Y	Y	Rattus norvegicus	Y
Habropoda laboriosa	Cyclic AMP-responsive element-binding protein 1	Y	Y	Rattus norvegicus	Y
Apis cerana	cyclic AMP-responsive element-binding protein 1	Y	Y	Rattus norvegicus	Y
Melipona quadrifasciata	Cyclic AMP-responsive element-binding protein 1	Y	N/A	Rattus norvegicus	N

Supporting Information Results 9: SeqAPASS Evaluation Results for Vitellogenin

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

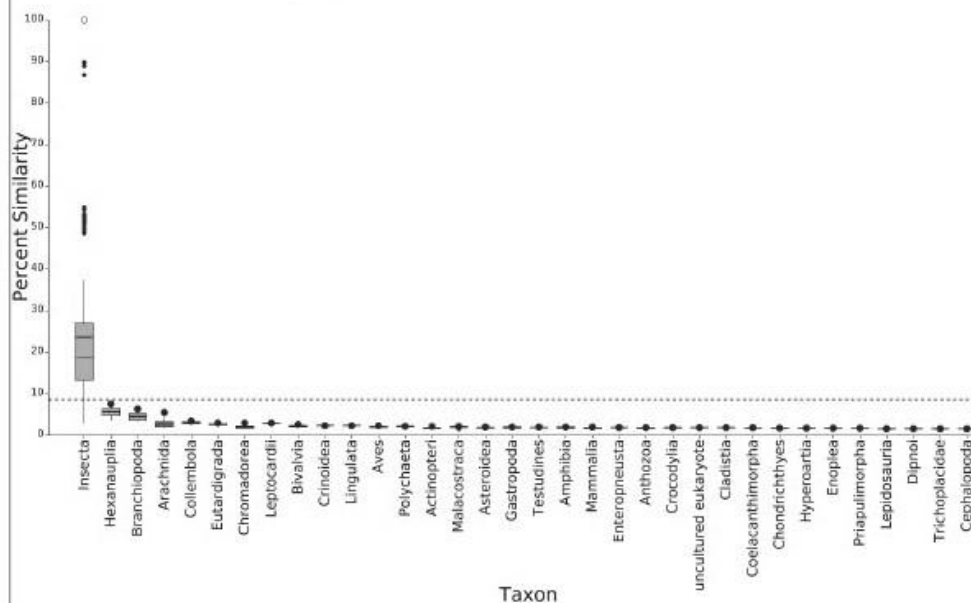
Level 1 Query Protein Information

SeqAPASS ID: 2454
 Query Species: *Apis mellifera*
 Query Protein: vitellogenin precursor
 Query Accession: NP_001011578.1
 Ortholog Count: 304
 Protein and Taxonomy Data: 06/08/2020
 BLAST Version: 2.10.0
 Software Version: 5.0

Report Settings

Report Type: Primary
 E-value: 0.01
 Sorted By Taxonomic Group: CLASS
 Common Domains: 1
 Species Read-Across: Y
 Cut-off %: 8.51
 Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2454

Query Species: *Apis mellifera*

Query Domain: (22) pfam01347, Vitellogenin_N, Lipoprotein amino terminal region

Query Accession: NP_001011578.1

Ortholog Count: 310

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

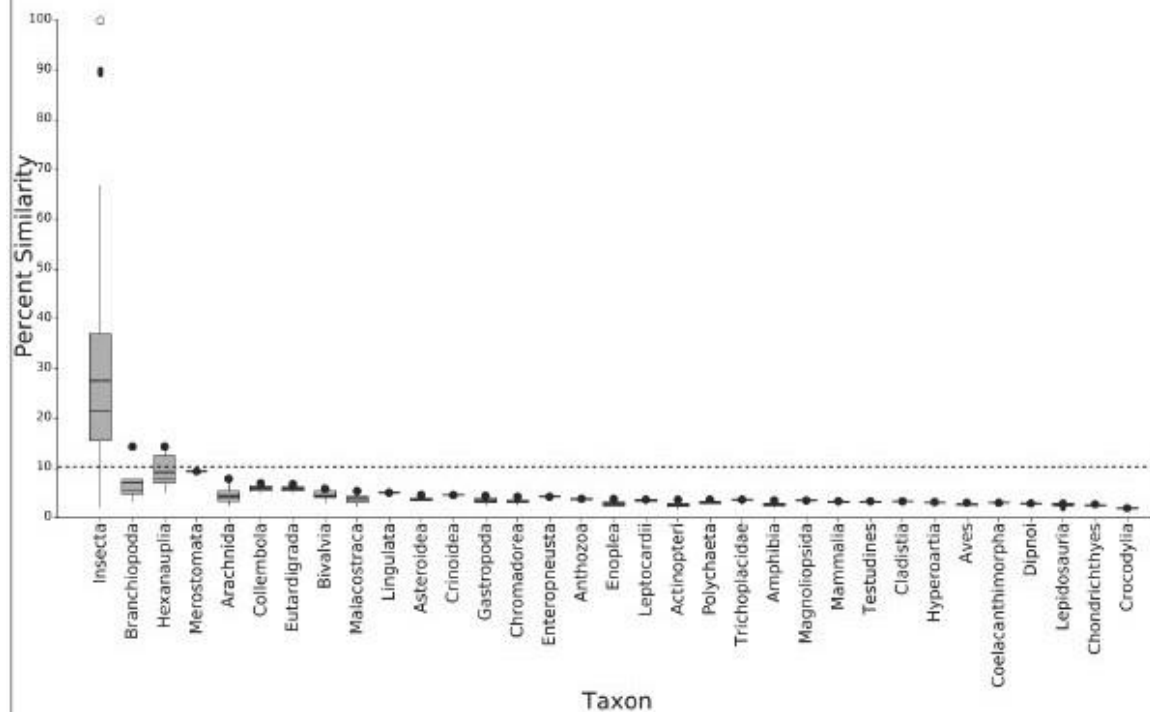
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 10.18

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(22) pfam01347, Vitellogenin_N, Lipoprotein amino terminal region
<i>Apis mellifera</i>	vitellogenin precursor	Y	Y
<i>Apis dorsata</i>	vitellogenin	Y	Y
<i>Apis cerana</i>	vitellogenin precursor	Y	Y
<i>Apis cerana cerana</i>	Vg	Y	Y
<i>Apis florea</i>	LOW QUALITY PROTEIN: vitellogenin	Y	Y
<i>Dufourea novaeangliae</i>	PREDICTED: vitellogenin-like	Y	Y
<i>Habropoda laboriosa</i>	Vitellogenin, partial	Y	Y
<i>Osmia cornifrons</i>	vitellogenin	Y	Y
<i>Osmia bicornis bicornis</i>	vitellogenin-like	Y	Y
<i>Osmia lignaria</i>	vitellogenin-like	Y	Y
<i>Bombus vancouverensis nearcticus</i>	vitellogenin-like	Y	Y
<i>Bombus bifarius</i>	vitellogenin-like	Y	Y
<i>Bombus vosnesenskii</i>	LOW QUALITY PROTEIN: vitellogenin-like	Y	Y
<i>Bombus impatiens</i>	vitellogenin	Y	Y
<i>Megachile rotundata</i>	PREDICTED: vitellogenin-like	Y	Y
<i>Bombus hypocrita</i>	vitellogenin	Y	Y
<i>Nomia melanderi</i>	vitellogenin-like	Y	Y
<i>Bombus lantschouensis</i>	Vitellogenin	Y	Y
<i>Bombus terrestris</i>	LOW QUALITY PROTEIN: vitellogenin	Y	Y
<i>Bombus ignitus</i>	vitellogenin	Y	Y
<i>Ceratina calcarata</i>	vitellogenin-like	Y	Y
<i>Melipona quadrifasciata</i>	Vitellogenin, partial	Y	Y
<i>Eufriesea mexicana</i>	PREDICTED: vitellogenin-like	Y	Y
<i>Megalopta genalis</i>	vitellogenin-like isoform X2	Y	Y

Supporting Information Results 10: SeqAPASS Evaluation Results for Methyl Farnesoate
Epoxidase

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

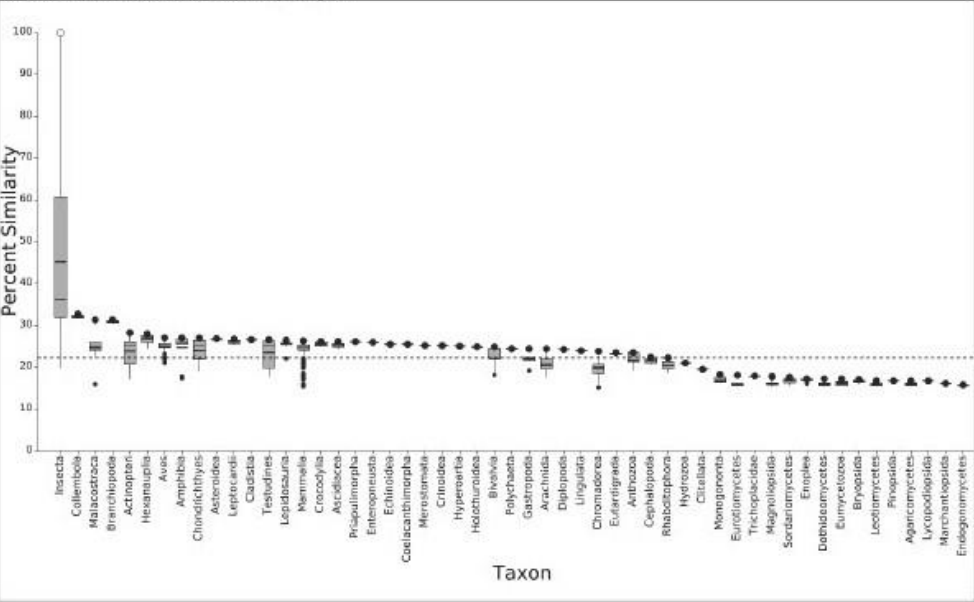
Level 1 Query Protein Information

SeqAPASS ID: 2456
Query Species: *Apis mellifera*
Query Protein: methyl farnesoate epoxidase precursor
Query Accession: NP_001314895.1
Ortholog Count: 258
Protein and Taxonomy Data: 06/08/2020
BLAST Version: 2.10.0
Software Version: 5.0

Report Settings

Report Type: Primary
E-value: 0.01
Sorted By Taxonomic Group: CLASS
Common Domains: 1
Species Read-Across: Y
Cut-off %: 22.23
Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2456

Query Species: *Apis mellifera*

Query Domain: (28) pfam00067, p450, Cytochrome P450

Query Accession: NP_001314895.1

Ortholog Count: 263

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

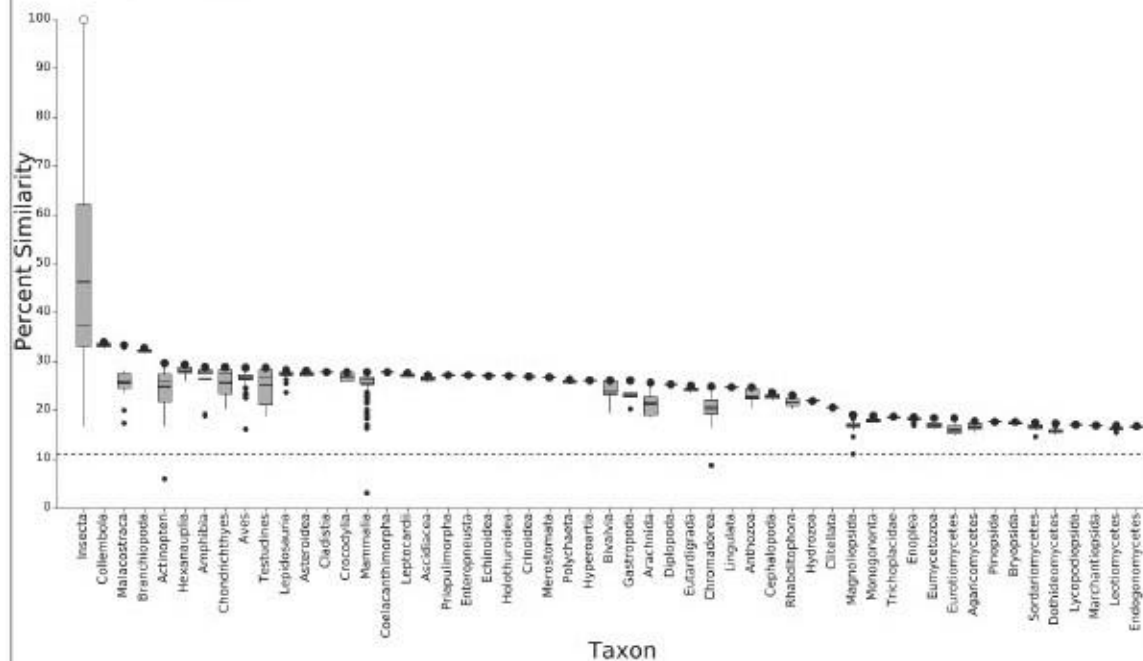
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 11.01

Show Only Eukaryotes: Y

Level 2 Visualization - Primary Report



Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(28) pfam00067, p450, Cytochrome P450
<i>Apis mellifera</i>	methyl farnesoate epoxidase precursor	Y	Y
<i>Apis mellifera ligustica</i>	cytochrome P450 15A1	Y	Y
<i>Apis cerana</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Apis cerana cerana</i>	cytochrome P450-like protein	Y	Y
<i>Apis florea</i>	methyl farnesoate epoxidase-like isoform X1	Y	Y
<i>Apis dorsata</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Eufriesea mexicana</i>	PREDICTED: methyl farnesoate epoxidase-like	Y	Y
<i>Bombus vosnesenskii</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Bombus impatiens</i>	methyl farnesoate epoxidase	Y	Y
<i>Bombus vancouverensis nearcticus</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Bombus bifarius</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Bombus terrestris</i>	methyl farnesoate epoxidase	Y	Y
<i>Habropoda laboriosa</i>	PREDICTED: methyl farnesoate epoxidase-like	Y	Y
<i>Osmia bicornis bicornis</i>	methyl farnesoate epoxidase-like isoform X2	Y	Y
<i>Osmia lignaria</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Megalopta genalis</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Ceratina calcarata</i>	methyl farnesoate epoxidase-like	Y	Y
<i>Dufourea novaeangliae</i>	PREDICTED: methyl farnesoate epoxidase-like	Y	Y
<i>Nomia melanderi</i>	methyl farnesoate epoxidase-like	Y	Y

Supporting Information Results 11: SeqAPASS Evaluation Results for Juvenile Hormone Acid O-Methyltransferase

Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS)

Decision Summary Report

Level 1

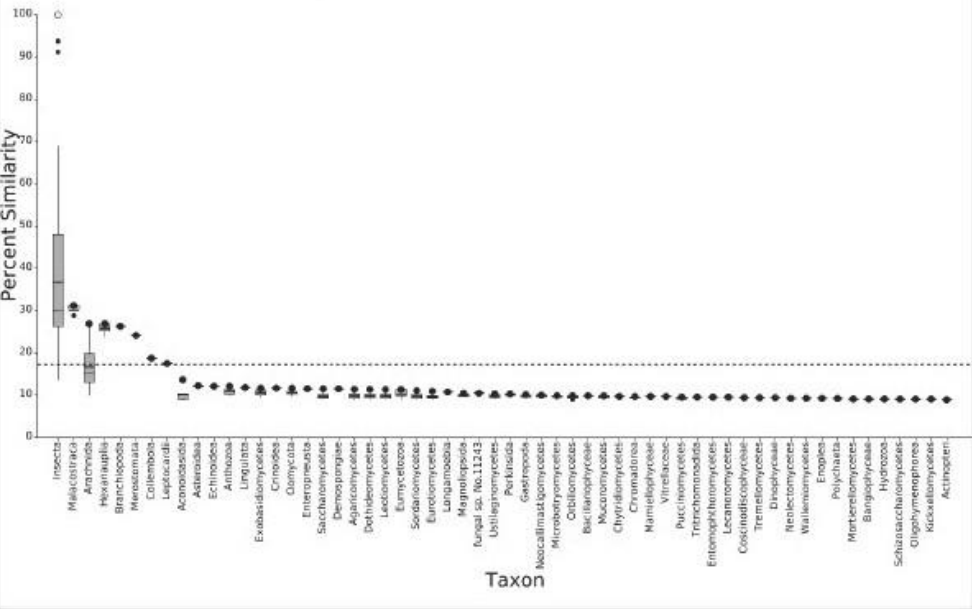
Level 1 Query Protein Information

SeqAPASS ID: 2506
Query Species: Apis mellifera
Query Protein: juvenile hormone acid O-methyltransferase
Query Accession: NP_001314896.1
Ortholog Count: 434
Protein and Taxonomy Data: 06/08/2020
BLAST Version: 2.10.0
Software Version: 5.0

Report Settings

Report Type: Primary
E-value: 0.01
Sorted By Taxonomic Group: CLASS
Common Domains: 1
Species Read-Across: Y
Cut-off %: 17.12
Show Only Eukaryotes: Y

Level 1 Visualization - Primary Report



Level 2

Level 2 Query Protein Information

SeqAPASS ID: 2506

Query Species: *Apis mellifera*

Query Domain: (37) pfam13649, Methyltransf_25, Methyltransferase domain

Query Accession: NP_001314896.1

Ortholog Count: 438

Protein and Taxonomy Data: 06/08/2020

BLAST Version: 2.10.0

Software Version: 5.0

Report Settings

Report Type: Primary

E-value: 10.0

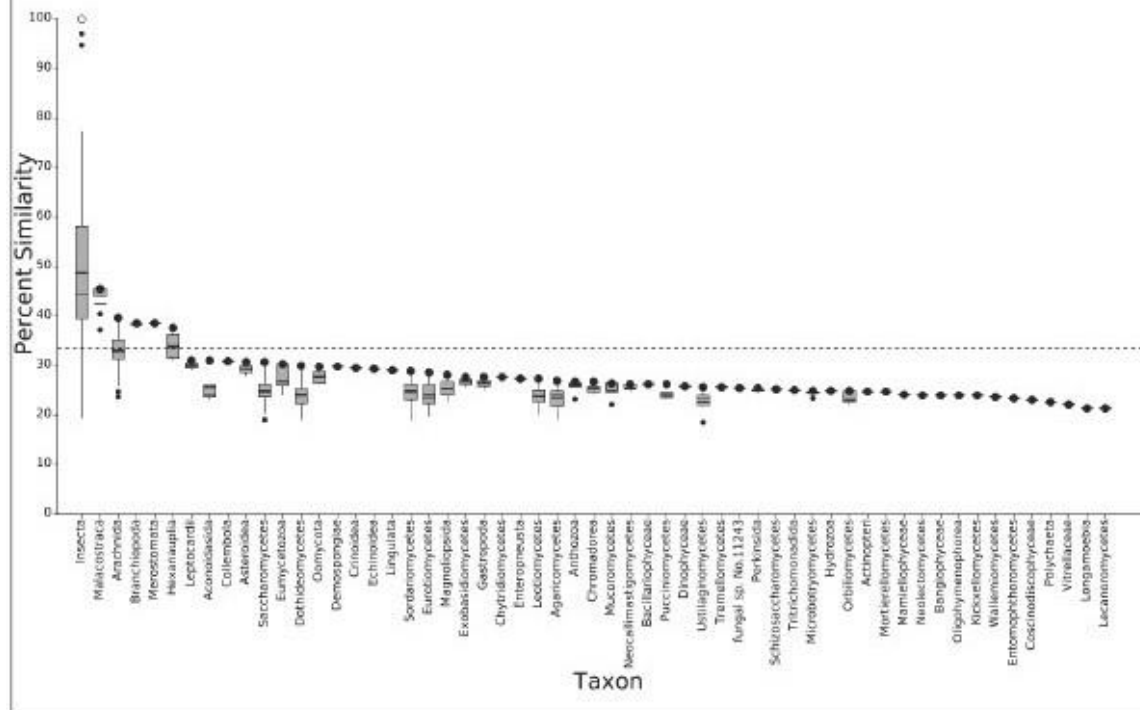
Sorted By Taxonomic Group: CLASS

Species Read-Across: Y

Cut-off %: 33.45

Show Only Eukaryotes: Y

Level 2 Visualization - Full Report



Final Decision Summary Report

Species	Protein	Level 1 Susceptible (Y/N)	(37) pfam13649, Methyltransf_25, Methyltransferase domain
<i>Apis mellifera</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Apis mellifera ligustica</i>	juvenile hormone acid methyltransferase	Y	Y
<i>Apis cerana</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Apis dorsata</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Apis cerana cerana</i>	Putative methyltransferase 235L	Y	Y
<i>Ceratina calcarata</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Bombus terrestris</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Eufriesea mexicana</i>	PREDICTED: juvenile hormone acid O-methyltransferase	Y	Y
<i>Bombus bifarius</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Habropoda laboriosa</i>	PREDICTED: juvenile hormone acid O-methyltransferase	Y	Y
<i>Bombus vancouverensis nearcticus</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Bombus impatiens</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Bombus vosnesenskii</i>	juvenile hormone acid O-methyltransferase	Y	Y
<i>Osmia lignaria</i>	juvenile hormone acid O-methyltransferase isoform X1	Y	Y
<i>Osmia bicornis bicornis</i>	juvenile hormone acid O-methyltransferase isoform X1	Y	Y
<i>Megachile rotundata</i>	PREDICTED: uncharacterized protein LOC100877526	Y	Y
<i>Megalopta genalis</i>	juvenile hormone acid O-methyltransferase isoform X1	Y	Y
<i>Dufourea novaeangliae</i>	PREDICTED: juvenile hormone acid O-methyltransferase	Y	Y
<i>Nomia melanderi</i>	juvenile hormone acid O-methyltransferase isoform X1	Y	Y
<i>Melipona quadrifasciata</i>	hypothetical protein WN51_13199	Y	Y
<i>Apis florea</i>	juvenile hormone acid O-methyltransferase	Y	Y