

# A

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## B

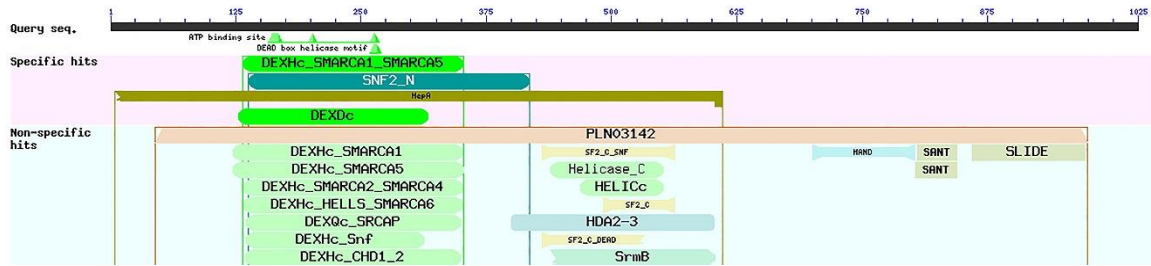
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580    M T K A E D R G E L L K K F N C K D S E Y F L F L L S T R A G G L G L N Q S A
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1020   Y I S D D E D Y E E D
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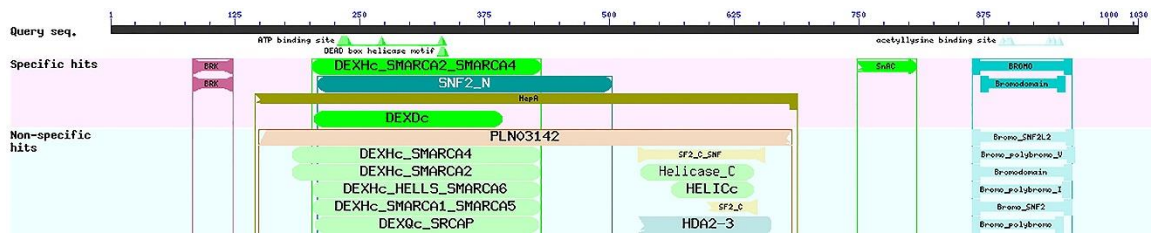
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**Figure S1.** (A) Full-length cDNA sequence of *TaISWI* and its deduced amino acid sequence. (B) Partial-length *TaBRM* cDNA sequence and its deduced aa sequence.

A

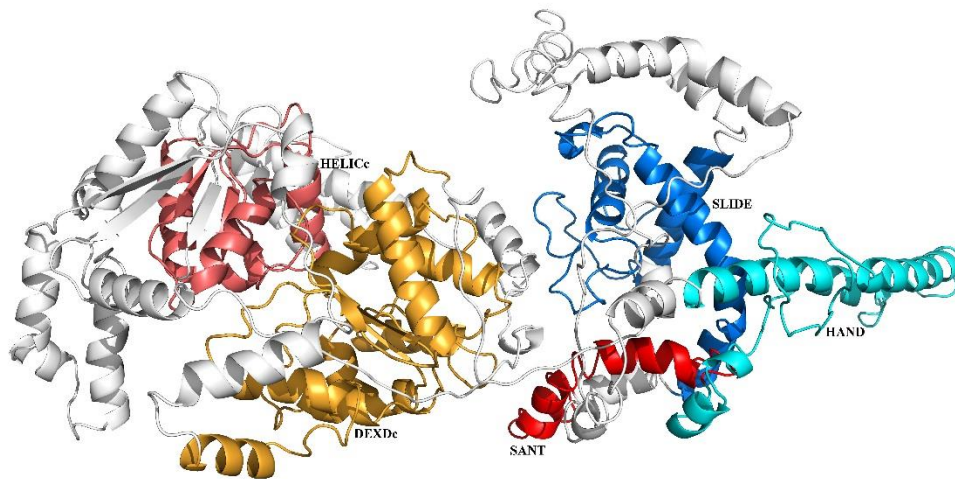


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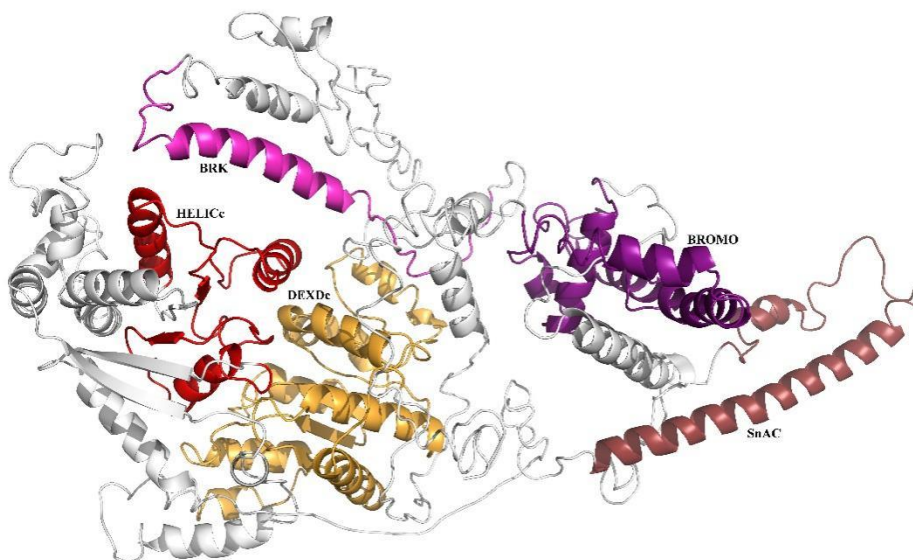


**Figure S2.** Conserved domain prediction of ISWI (A) and BRM (B) proteins in *Tuta absoluta*. The domains were analysed with the online NCBI Conserved Domains Database (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>).

**A**



**B**



**Figure S3.** Predicted 3D structure of ISWI (A) and BRM (B) proteins in *Tuta absoluta*.

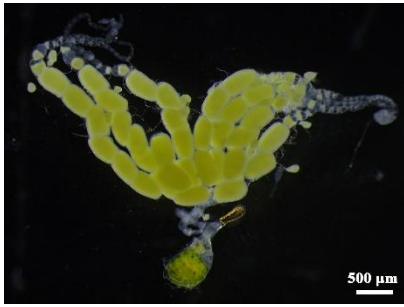
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B.mori	.MACSDAMDVADIGDNGSSDSSSGREGIFESKQDORSRRHLLKQTEIESHFMNTHSGS..SEPRKQGRHGVKELFEQSEDSANHRHRRTEQEEELLAEINAKINPIRFEZSP	124
T.ni	.MSQDEPMVAADVGVENSSDSSSGREGIFESKQDORSRRHLLKQTEIESHFMNTHSGS..SEPRKQGRHGVKELFEQSEDSANHRHRRTEQEEELLAEINAKINPIRFEZSP	125
H.armigera	MSQTEPMVAADVGVENSSDSSSGREGIFESKQDORSRRHLLKQTEIESHFMNTHSGS..SEPRKQGRHGVKELFEQSEDSANHRHRRTEQEEELLAEINAKINPIRFEZSP	127
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D.melanogaster	MSQTDAVAVATENSGTTCDAHSSGREGIFESKQDORSRRHLLKQTEIESHFMNTHSGS.....TSPGGRHGVKELFEQSEDSANHRHRRTEQEEELLAEINAKINPIRFEZSP	120
T.absoluta	FVFNCGVRYCVRGLNWMISLYE GINGILADEMGLGKTLQTSILGVMRRNVGPHIVIVPKSTLNNNEFRKNCPSIRAVCLIGDQTRTFIRVVMFGWVQVTSYEMIRDSVFKKFW	257
B.mori	FVFNCGVRYCVRGLNWMISLYE GINGILADEMGLGKTLQTSILGVMRRNVGPHIVIVPKSTLNNNEFRKNCPSIRAVCLIGDQTRTFIRVVMFGWVQVTSYEMIRDSVFKKFW	254
T.ni	FVFNCGVRYCVRGLNWMISLYE GINGILADEMGLGKTLQTSILGVMRRNVGPHIVIVPKSTLNNNEFRKNCPSIRAVCLIGDQTRTFIRVVMFGWVQVTSYEMIRDSVFKKFW	255
H.armigera	FVFNCGVRYCVRGLNWMISLYE GINGILADEMGLGKTLQTSILGVMRRNVGPHIVIVPKSTLNNNEFRKNCPSIRAVCLIGDQTRTFIRVVMFGWVQVTSYEMIRDSVFKKFW	257
A.mellifera	FVFNCGVRYCVRGLNWMISLYE GINGILADEMGLGKTLQTSILGVMRRNVGPHIVIVPKSTLNNNEFRKNCPSIRAVCLIGDQTRTFIRVVMFGWVQVTSYEMIRDSVFKKFW	253
D.melanogaster	FVFNCGVRYCVRGLNWMISLYE GINGILADEMGLGKTLQTSILGVMRRNVGPHIVIVPKSTLNNNEFRKNCPSIRAVCLIGDQTRTFIRVVMFGWVQVTSYEMIRDSVFKKFW	250
T.absoluta	RYVIDEABRIKNEKSKLSELRFRFNNRLLTGTPLONNLHEMLNLLFLPDVNSSDDFSWNTNARLGNQSRLEBAVLPFLLRLRKEVBRKLEPKKEDRYVGLSKMCRGWYTKVLMKDI	387
B.mori	RYVIDEABRIKNEKSKLSELRFRFNNRLLTGTPLONNLHEMLNLLFLPDVNSSDDFSWNTNARLGNQSRLEBAVLPFLLRLRKEVBRKLEPKKEDRYVGLSKMCRGWYTKVLMKDI	384
T.ni	RYVIDEABRIKNEKSKLSELRFRFNNRLLTGTPLONNLHEMLNLLFLPDVNSSDDFSWNTNARLGNQSRLEBAVLPFLLRLRKEVBRKLEPKKEDRYVGLSKMCRGWYTKVLMKDI	385
H.armigera	RYVIDEABRIKNEKSKLSELRFRFNNRLLTGTPLONNLHEMLNLLFLPDVNSSDDFSWNTNARLGNQSRLEBAVLPFLLRLRKEVBRKLEPKKEDRYVGLSKMCRGWYTKVLMKDI	387
A.mellifera	RYVIDEABRIKNEKSKLSELRFRFNNRLLTGTPLONNLHEMLNLLFLPDVNSSDDFSWNTNARLGNQSRLEBAVLPFLLRLRKEVBRKLEPKKEDRYVGLSKMCRGWYTKVLMKDI	383
D.melanogaster	RYVIDEABRIKNEKSKLSELRFRFNNRLLTGTPLONNLHEMLNLLFLPDVNSSDDFSWNTNARLGNQSRLEBAVLPFLLRLRKEVBRKLEPKKEDRYVGLSKMCRGWYTKVLMKDI	380
T.absoluta	LVVNGAGVEKMRQLNIMCLRKCNHPLYFDGAEPGPPYTTIHLVYNGGKMLDKLPLKLCQSRVLFSQCMTRMLDILEYCHWQVYCYRLDGTHEEDRCQIDENAGSSEKFMFLSTRAG	517
B.mori	LVVNGAGVEKMRQLNIMCLRKCNHPLYFDGAEPGPPYTTIHLVYNGGKMLDKLPLKLCQSRVLFSQCMTRMLDILEYCHWQVYCYRLDGTHEEDRCQIDENAGSSEKFMFLSTRAG	514
T.ni	LVVNGAGVEKMRQLNIMCLRKCNHPLYFDGAEPGPPYTTIHLVYNGGKMLDKLPLKLCQSRVLFSQCMTRMLDILEYCHWQVYCYRLDGTHEEDRCQIDENAGSSEKFMFLSTRAG	515
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A.mellifera	LVVNGAGVEKMRQLNIMCLRKCNHPLYFDGAEPGPPYTTIHLVYNGGKMLDKLPLKLCQSRVLFSQCMTRMLDILEYCHWQVYCYRLDGTHEEDRCQIDENAGSSEKFMFLSTRAG	513
D.melanogaster	LVVNGAGVEKMRQLNIMCLRKCNHPLYFDGAEPGPPYTTIHLVYNGGKMLDKLPLKLCQSRVLFSQCMTRMLDILEYCHWQVYCYRLDGTHEEDRCQIDENAGSSEKFMFLSTRAG	510
T.absoluta	GLGINLADVVIIYDSNNFQMCQAMDRAHRIGCKQCVRVFPIITITVEEKIVERAEVKRLDQVIGGRVLVQSNLNKDEMLNIRGANVVSQDSATTEIDIITLAGEVHTEDRCQI	646
B.mori	GLGINLADVVIIYDSNNFQMCQAMDRAHRIGCKQCVRVFPIITITVEEKIVERAEVKRLDQVIGGRVLVQSNLNKDEMLNIRGANVVSQDSATTEIDIITLAGEVHTEDRCQI	643
T.ni	GLGINLADVVIIYDSNNFQMCQAMDRAHRIGCKQCVRVFPIITITVEEKIVERAEVKRLDQVIGGRVLVQSNLNKDEMLNIRGANVVSQDSATTEIDIITLAGEVHTEDRCQI	644
H.armigera	GLGINLADVVIIYDSNNFQMCQAMDRAHRIGCKQCVRVFPIITITVEEKIVERAEVKRLDQVIGGRVLVQSNLNKDEMLNIRGANVVSQDSATTEIDIITLAGEVHTEDRCQI	646
A.mellifera	GLGINLADVVIIYDSNNFQMCQAMDRAHRIGCKQCVRVFPIITITVEEKIVERAEVKRLDQVIGGRVLVQSNLNKDEMLNIRGANVVSQDSATTEIDIITLAGEVHTEDRCQI	643
D.melanogaster	GLGINLADVVIIYDSNNFQMCQAMDRAHRIGCKQCVRVFPIITITVEEKIVERAEVKRLDQVIGGRVLVQSNLNKDEMLNIRGANVVSQDSATTEIDIITLAGEVHTEDRCQI	640
T.absoluta	LSISESSLRPFMSDTGAT..DSVYCFEGEDIREKQKSHLPGSIEFFPKRRKANYAVDAYFREALRVSEPKARVQCAPRPPKQIVQDFQFFPPFLFELLDCETINSGRTGKYKVRNEELGEDAKAQ	774
B.mori	LSISESSLRPFMSDTGAT..DSVYCFEGEDIREKQKSHLPGSIEFFPKRRKANYAVDAYFREALRVSEPKARVQCAPRPPKQIVQDFQFFPPFLFELLDCETINSGRTGKYKVRNEELGEDAKAQ	772
T.ni	LSISESSLRPFMSDTGAT..DSVYCFEGEDIREKQKSHLPGSIEFFPKRRKANYAVDAYFREALRVSEPKARVQCAPRPPKQIVQDFQFFPPFLFELLDCETINSGRTGKYKVRNEELGEDAKAQ	773
H.armigera	LSISESSLRPFMSDTGAT..DSVYCFEGEDIREKQKSHLPGSIEFFPKRRKANYAVDAYFREALRVSEPKARVQCAPRPPKQIVQDFQFFPPFLFELLDCETINSGRTGKYKVRNEELGEDAKAQ	775
A.mellifera	LSISESSLRPFMSDTGAT..DSVYCFEGEDIREKQKSHLPGSIEFFPKRRKANYAVDAYFREALRVSEPKARVQCAPRPPKQIVQDFQFFPPFLFELLDCETINSGRTGKYKVRNEELGEDAKAQ	767
D.melanogaster	LSISESSLRPFMSDTGAT..DSVYCFEGEDIREKQKSHLPGSIEFFPKRRKANYAVDAYFREALRVSEPKARVQCAPRPPKQIVQDFQFFPPFLFELLDCETINSGRTGKYKVRNEELGEDAKAQ	768
T.absoluta	FEQRKILAEPLTEPVEKEKLLQGFTWTKRDFNQFIKANERYGRDDINIAKVEGKTPEEVYSAVWERCQELQIDIRMGQIERGEKICRRACIKKALDPMARYRAPPHOLRISYGNK	904
B.mori	FEQRKILAEPLTEPVEKEKLLQGFTWTKRDFNQFIKANERYGRDDINIAKVEGKTPEEVYSAVWERCQELQIDIRMGQIERGEKICRRACIKKALDPMARYRAPPHOLRISYGNK	902
T.ni	FEQRKILAEPLTEPVEKEKLLQGFTWTKRDFNQFIKANERYGRDDINIAKVEGKTPEEVYSAVWERCQELQIDIRMGQIERGEKICRRACIKKALDPMARYRAPPHOLRISYGNK	903
H.armigera	FEQRKILAEPLTEPVEKEKLLQGFTWTKRDFNQFIKANERYGRDDINIAKVEGKTPEEVYSAVWERCQELQIDIRMGQIERGEKICRRACIKKALDPMARYRAPPHOLRISYGNK	905
A.mellifera	FEQRKILAEPLTEPVEKEKLLQGFTWTKRDFNQFIKANERYGRDDINIAKVEGKTPEEVYSAVWERCQELQIDIRMGQIERGEKICRRACIKKALDPMARYRAPPHOLRISYGNK	897
D.melanogaster	FEQRKILAEPLTEPVEKEKLLQGFTWTKRDFNQFIKANERYGRDDINIAKVEGKTPEEVYSAVWERCQELQIDIRMGQIERGEKICRRACIKKALDPMARYRAPPHOLRISYGNK	898
T.absoluta	GRNNVDEDRFLVCMHLGFDKENVYEELRAVHAPCFRFDWHKSRTAELQRCRNTLITLIERENLELEPERGKRRKESANQNTIPGAASKGAGAGRRADAAQDSACKQKRRK.....	1025
B.mori	GRNNVDEDRFLVCMHLGFDKENVYEELRAVHAPCFRFDWHKSRTAELQRCRNTLITLIERENLELEPERGKRRKESANQNTIPGAASKGAGAGRRADAAQDSACKQKRRK.....	1026
T.ni	GRNNVDEDRFLVCMHLGFDKENVYEELRAVHAPCFRFDWHKSRTAELQRCRNTLITLIERENLELEPERGKRRKESANQNTIPGAASKGAGAGRRADAAQDSACKQKRRK.....	1027
H.armigera	GRNNVDEDRFLVCMHLGFDKENVYEELRAVHAPCFRFDWHKSRTAELQRCRNTLITLIERENLELEPERGKRRKESANQNTIPGAASKGAGAGRRADAAQDSACKQKRRK.....	1028
A.mellifera	GRNNVDEDRFLVCMHLGFDKENVYEELRAVHAPCFRFDWHKSRTAELQRCRNTLITLIERENLELEPERGKRRKESANQNTIPGAASKGAGAGRRADAAQDSACKQKRRK.....	1009
D.melanogaster	GRNNVDEDRFLVCMHLGFDKENVYEELRAVHAPCFRFDWHKSRTAELQRCRNTLITLIERENLELEPERGKRRKESANQNTIPGAASKGAGAGRRADAAQDSACKQKRRK.....	1026

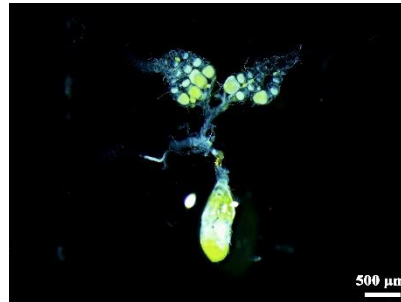


**Figure S4.** (A) Multiple alignments of the ISWI protein sequences from *Tuta absoluta* and other insects. The results revealed that the deduced protein sequence of *TaISWI* was highly conserved when compared to previously identified ISWI protein sequences. *T. absoluta*: *Tuta absoluta*; *B. mori*: *Bombyx mori* (XP\_012547334.1); *T. ni*: *Trichoplusia ni* (XP\_026747092.1); *H. armigera*: *Helicoverpa armigera* (XP\_021184575.1); *A. mellifera*: *Apis mellifera* (XP\_006565266.1); *D. melanogaster*: *Drosophila melanogaster* (NP\_523719.1). (B) Multiple alignments of the BRM protein sequences from *Tuta absoluta* and other insects. *B. mori* (XP\_037871728.1); *T. ni* (XP\_026725796.1); *P. rapae*: *Pieris rapae* (XP\_022130779.1); *D. melanogaster* (NP\_536745.4).

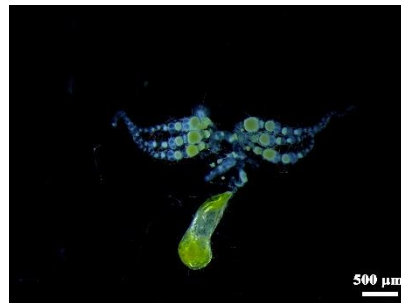
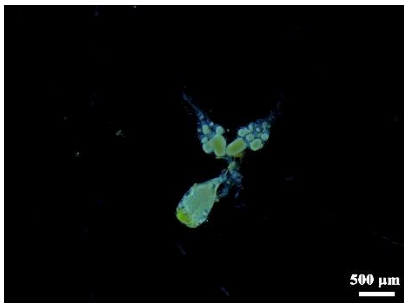
A



B



C



**Figure S5.** More pictures of the effects of dsISWI and dsBRM on *Tuta absoluta* ovary development. (A) Ovaries of uninjected 4-d females. (B) Abnormal ovaries of 4-d females injected with dsISWI. (C) Abnormal ovaries of 4-d females injected with dsBRM.

**Table S1.** Details of protein sequences used for phylogenetic analysis.

ISWI			
Insect species	GenBank accession number	Insect species	GenBank accession number
<i>Polistes canadensis</i>	XP_014609868.1	<i>Ooceraea biroi</i>	XP_011352072.1
<i>Ceratina calcarata</i>	XP_017890682.1	<i>Camponotus floridanus</i>	XP_011254438.1
<i>Linepithema humile</i>	XP_012220642.1	<i>Bombus impatiens</i>	XP_024221024.1
<i>Apis mellifera</i>	XP_006565266.1	<i>Apis florea</i>	XP_012344097.1
<i>Rhopalosiphum maidis</i>	XP_026823151.1	<i>Myzus persicae</i>	XP_022171705.1
<i>Aphis gossypii</i>	XP_027848482.1	<i>Acyrtosiphon pisum</i>	XP_001945595.1
<i>Sipha flava</i>	XP_025406176.1	<i>Diuraphis noxia</i>	XP_015375778.1
<i>Trichoplusia ni</i>	XP_026747092.1	<i>Helicoverpa armigera</i>	XP_021184575.1
<i>Spodoptera litura</i>	XP_022829094.1	<i>Agrilus planipennis</i>	XP_025836927.1
<i>Nicrophorus vespilloides</i>	XP_017778534.1	<i>Bombyx mandarina</i>	XP_028037570.1
<i>Onthophagus taurus</i>	XP_022908972.1	<i>Aethina tumida</i>	XP_019866350.1
<i>Papilio machaon</i>	XP_014355986.1	<i>Papilio xuthus</i>	XP_013175309.1
<i>Papilio polytes</i>	XP_013135016.1	<i>Galleria mellonella</i>	XP_026765070.1
<i>Bombyx mori</i>	XP_012547334.1	<i>Bicyclus anynana</i>	XP_023952043.1
<i>Leptinotarsa decemlineata</i>	XP_023014233.1	<i>Diabrotica virgifera</i>	XP_028129819.1
<i>Plutella xylostella</i>	XP_011555157.1	<i>Ostrinia furnacalis</i>	XP_028158215.1
<i>Dendroctonus ponderosae</i>	XP_019754255.1	<i>Bactrocera dorsalis</i>	XP_011197903.1
<i>Drosophila melanogaster</i>	NP_523719.1	<i>Ceratitis capitata</i>	XP_004517436.1
<i>Anoplophora glabripennis</i>	XP_018572974.1	<i>Bactrocera latifrons</i>	XP_018803107.1
BRM			
Insect species	GenBank accession number	Insect species	GenBank accession number
<i>Bombyx mori</i>	XP_037871728.1	<i>Pararge aegeria</i>	XP_039765300.1
<i>Leptinotarsa decemlineata</i>	XP_023029618.1	<i>Bombyx mandarina</i>	XP_028033541.1
<i>Hyposmocoma kahamanoa</i>	XP_026323568.1	<i>Pieris rapae</i>	XP_022130779.1
<i>Maniola hyperantus</i>	XP_034841481.1	<i>Ostrinia furnacalis</i>	XP_028176736.1
<i>Spodoptera litura</i>	XP_022824228.1	<i>Trichoplusia ni</i>	XP_026725796.1
<i>Manduca sexta</i>	XP_037300295.1	<i>Drosophila busckii</i>	ALC44792.1
<i>Drosophila melanogaster</i>	NP_536745.4	<i>Bactrocera tryoni</i>	XP_039964134.1
<i>Cyphomyrmex costatus</i>	XP_018396747.1	<i>Sipha flava</i>	XP_025423084.1
<i>Vollenhovia emeryi</i>	XP_011868917.1	<i>Myzus persicae</i>	XP_022166801.1
<i>Trachymyrmex septentrionalis</i>	XP_018355410.1	<i>Bombus terrestris</i>	XP_012166376.1



<b>Insect species</b>	<b>GenBank accession number</b>	<b>Insect species</b>	<b>GenBank accession number</b>
<i>Camponotus floridanus</i>	XP_011257142.2	<i>Nylanderia fulva</i>	XP_029162796.1
<i>Apis mellifera</i>	XP_026300357.1	<i>Apis florea</i>	XP_012343937.1
<i>Melanaphis sacchari</i>	XP_025204346.1	<i>Apis dorsata</i>	XP_006622867.1
<i>Rhopalosiphum maidis</i>	XP_026814829.1	<i>Photinus pyralis</i>	XP_031335174.1
<i>Acyrtosiphon pisum</i>	XP_001947872.2	<i>Polistes dominula</i>	XP_015191338.1
<i>Sitophilus oryzae</i>	XP_030758143.1	<i>Tribolium castaneum</i>	EEZ97706.2
<i>Anoplophora glabripennis</i>	XP_018562326.2	<i>Agrilus planipennis</i>	XP_025830418.1