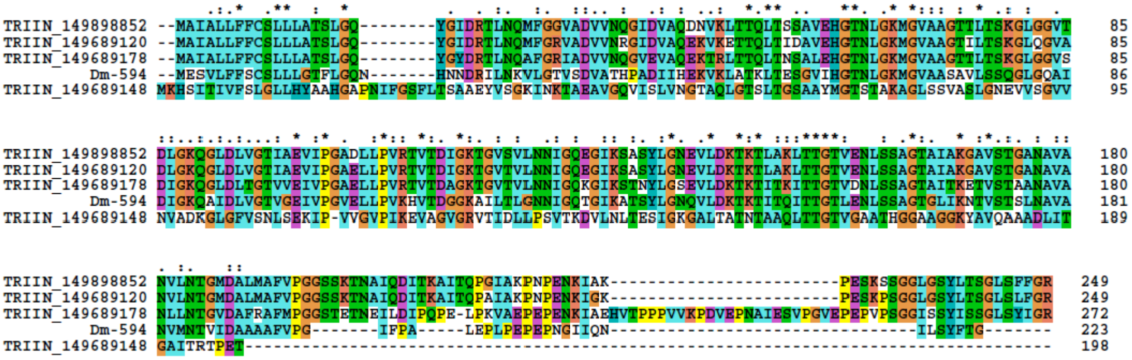
Supplemental figure 1 – Clustal alignment of the Hemolysin-domain containing protein with other hemolysin-like secreted salivary proteins from *T. infestans*. The symbols above the alignment indicate: (*) identical sites; (:) conserved sites; (.) less conserved sites.



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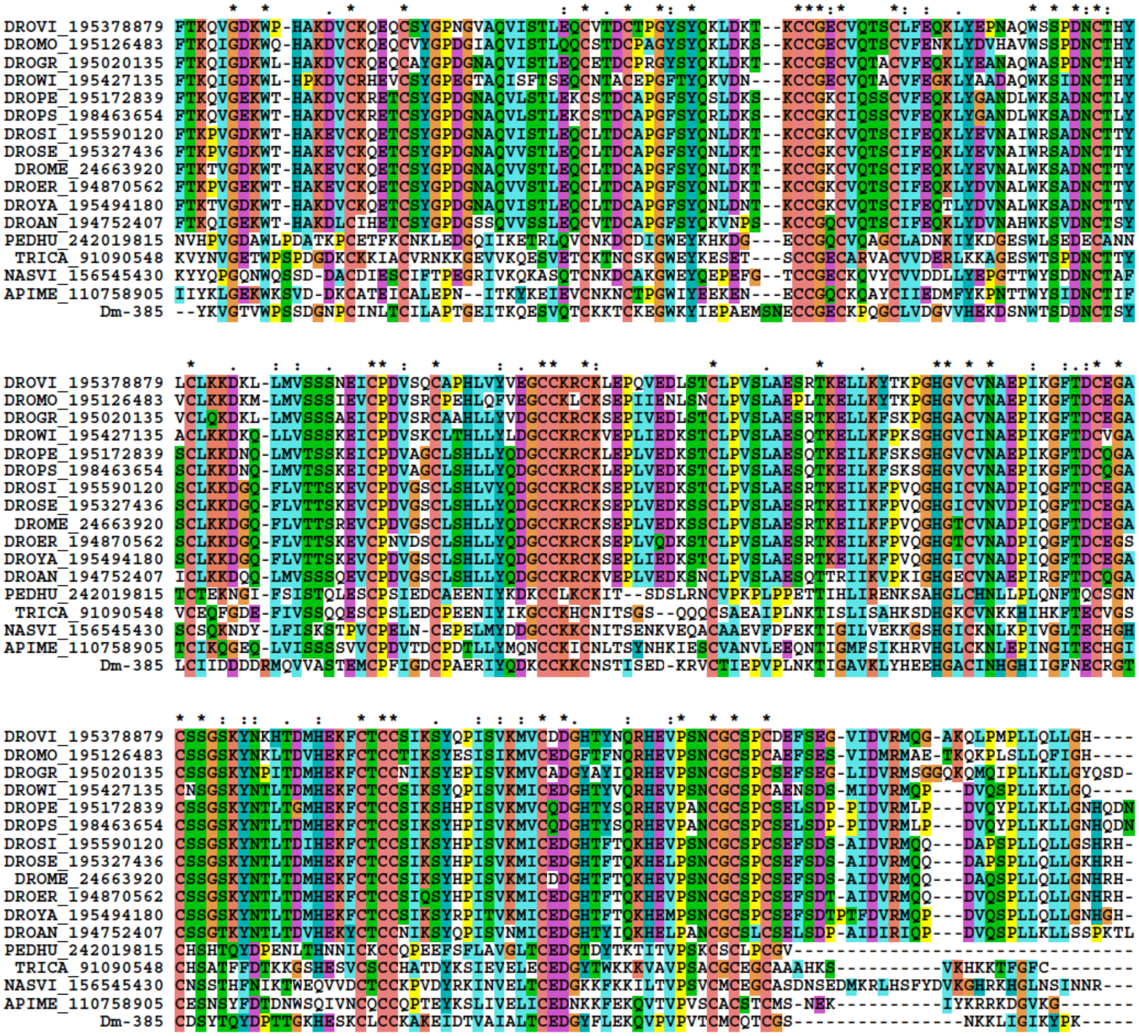
                     .:.*  .**  :  *          .  . :.  :.  ::.. :  .: : ..:  *.** ..   **. .* *::: : * .: :  .
TRIIN_149898852 --MAIALLFFCSLLLATSLGQ--------YGIDRTLNQMFGGVADVVNQGIDVAQDNVKLTTQLTSSAVEHGTNLGKMGVAAGTTLTSKGLGGVT    85
TRIIN_149689120 --MAIALLFFCSLLLATSLGQ--------YGIDRTLNQMFGRVADVVNRGIDVAQEKVKETTQLTIDAVEHGTNLGKMGVAAGTILTSKGLQGVA    85
TRIIN_149689178 --MAIALLFFCSLLLATSLGQ--------YGYDRTLNQAFGRIADVVNQGVEVAQEKTRLTTQLTNSALEHGTNLGKMGVAAGTTLTSKGLGGVS    85
         Dm-594 --MESVLFFSCSLLLGTFLGQN-------HNNDRILNKVLGTVSDVATHPADIIHEKVKLATKLTESGVIHGTNLGKMGVAASAVLSSQGLGQAI    86
TRIIN_149689148 MKHSITIVFSLGLLHYAAHGAPNIFGSFLTSAAEYVSGKINKTAEAVGQVISLVNGTAQLGTSLTGSAAYMGTSTAKAGLSSVASLGNEVVSGVV    95

                ::..:.:.:...: * :* .  :*:: *:. *:. : :  .: :  :: :. :*. .*  *:* :::****:   : .*:.  * :*.:. : ::
TRIIN_149898852 DLGKQGLDLVGTIAEVIPGADLLPVRTVTDIGKTGVSVLNNIGQEGIKSASYLGNEVLDKTKTLAKLTTGTVENLSSAGTAIAKGAVSTGANAVA   180
TRIIN_149689120 DLGKQGLDLVGTIAEVIPGAELLPVRTVTDIGKTGVTVLNNIGQEGIKSASYLGNEVLDKTKTLAKLTTGTVENLSSAGTAIAKGAVSTGANAVA   180
TRIIN_149689178 DIGKQGLDLTGTVVEIVPGAELLPVRTVTDAGKTGVTVLNNIGQKGIKSTNYLGSEVLDKTKTITKITTGTVDNLSSAGTAITKETVSTAANAVA   180
         Dm-594 DIGKQAIDLVGTVGEIVPGVELLPVKHVTDGGKAILTLGNNIGQTGIKATSYLGNQVLDKTKTITQITTGTLENLSSAGTGLIKNTVSTSLNAVA   181
TRIIN_149689148 NVADKGLGFVSNLSEKIP-VVGVPIKEVAGVGRVTIDLLPSVTKDVLNLTESIGKGALTATNTAAQLTTGTVGAATHGGAAGGKYAVQAAADLIT   189

                . :.   ::
TRIIN_149898852 NVLNTGMDALMAFVPGGSSKTNAIQDITKAITQPGIAKPNPENKIAK------------------------PESKSSGGLGSYLTSGLSFFGR   249
TRIIN_149689120 NVLNTGMDALMAFVPGGSSKTNAIQDITKAITQPAIAKPNPENKIGK------------------------PESKPSGGLGSYLTSGLSLFGR   249
TRIIN_149689178 NLLNTGVDAFRAFMPGGSTETNEILDIPQPE-LPKVAEPEPENKIAEHVTPPPVVKPDVEPNAIESVPGVEPEPVPSGGISSYISSGLSYIGR   272
         Dm-594 NVMNTVIDAAAAFVPG-------IFPA-----LEPLPEPEPNGIIQN--------------------------------ILSYFTG-------   223
TRIIN_149689148 GAITRTPET------------------------------------------------------------------------------------   198
```

Supplemental figure 2 – Clustal alignment of members of the Hemolectin family protein. The *D. maxima* protein is indicated by Dm-385. The remaining sequences are named with the first three letters from the genus name followed by two letters from the species name and by their NCBI protein accession number. Only the carboxy-terminal region is shown. The symbols above the alignment indicate: (*) identical sites; (:) conserved sites; (.) less conserved sites.



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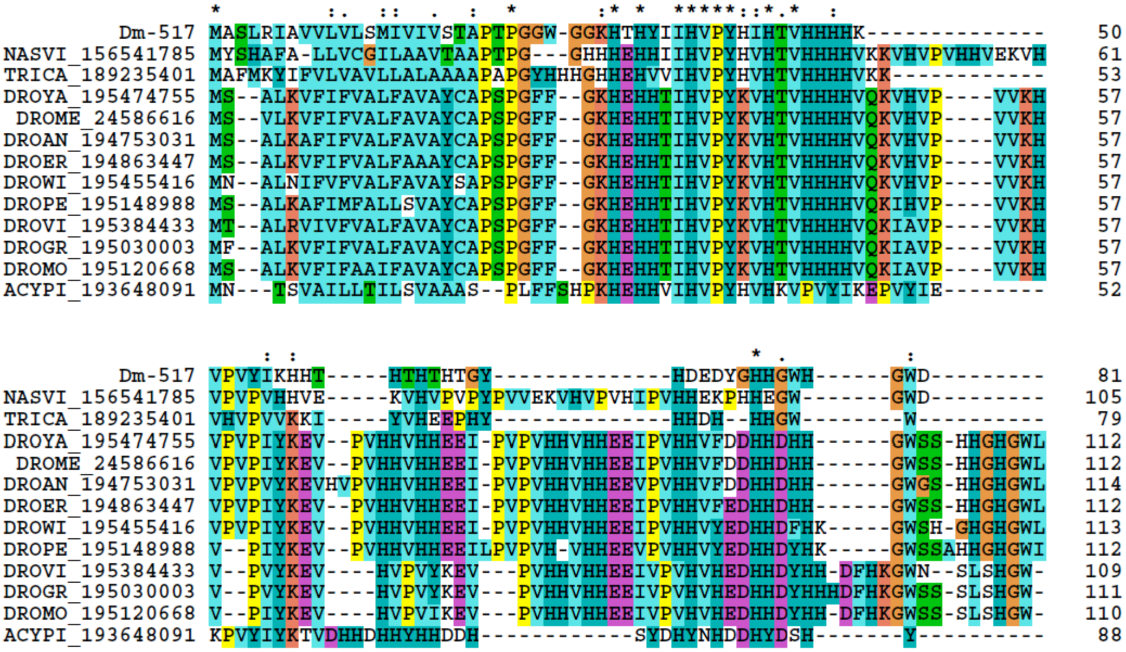
                     *  *     . *    *              : * . *  *: *         ***:*    *: :  .      * * *:*:
DROVI_195378879 FTKQVGDKWP-HAKDVCKQEQCSYGPNGVAQVISTLEQCVTDCTPGYSYQKLDKT--KCCGECVQTSCLFEQKLYEPNAQWSSPDNCTHY
DROMO_195126483 FTKQIGDKWQ-HAKDVCKQEQCVYGPDGIAQVISTLQQCSTDCPAGYSYQKLDKS--KCCGECVQTSCVFENKLYDVHAVWSSPDNCTHY
DROGR_195020135 FTKQIGDKWL-HAKDVCKQEQCAYGPDGNAQVISTLEQCETDCPRGYSYQKLDKT--KCCGECVQTACVFEQKLYEANAQWASPDNCTHY
DROWI_195427135 FTKQIGDKWL-HPKDVCRHEVCSYGPEGTAQISFTSEQCNTACEPGFTYQKVDN---KCCGECVQTACVFEGKLYAADAQWKSIDNCTHY
DROPE_195172839 FTKQVGEKWT-HAKDVCKRETCSYGPDGNAQVLSTLEKCSTDCAPGFSYQSLDKS--KCCGKCIQSSCVFEQKLYGANDLWKSADNCTLY
DROPS_198463654 FTKQVGEKWT-HAKDVCKRETCSYGPDGNAQVLSTLEKCSTDCAPGFSYQRLDKS--KCCGKCIQSSCVFEQKLYGANDLWKSADNCTLY
DROSI_195590120 FTKPVGDKWT-HAKEVCKQETCSYGPDGNAQVISTLEQCLTDCAPGFSYQNLDKT--KCCGKCVQTSCIFEQKLYEVNAIWRSADNCTTY
DROSE_195327436 FTKPVGDKWT-HAKEVCKQETCSYGPDGNAQVVSTLEQCLTDCAPGFSYQNLDKT--KCCGKCVQTSCIFEQKLYEVNAIWRSADNCTTY
 DROME_24663920 FTKTVGDKWT-HAKEVCKQETCSYGPDGNAQVVSTLEQCLTDCAPGFSYQNLDKT--KCCGKCVQTSCIFEQKLYEVNALWKSADNCTTY
DROER_194870562 FTKPVGEKWT-HAKEVCKQETCSYGPDGNAQVVSTLEQCLTDCAPGFSYQNLDKT--KCCGKCVQTSCIFEQKLYDVNALWKSADNCTTY
DROYA_195494180 FTKTVGDKWT-HAKDVCKQETCSYGPDGNAQVISTLEQCLTDCAPGFSYQNLDNT--KCCGKCVQTSCIFEQTLYDVNALWKSADNCTTY
DROAN_194752407 FTKQIGEKWT-HAKDLCIHETCSYGPDGSSQVVSSLEQCVTDCAPGFSYQKVNPS--KCCGQCVQTSCIFEQKLYDVNAHWKSVDNCTSY
PEDHU_242019815 NVHPVGDAWLPDATKPCETFKCNKLEDGQIIKETRLQVCNKDCDIGWEYKHKDG---ECCGQCVQAGCLADNKIYKDGESWLSEDECANN
 TRICA_91090548 KVYNVGETWPSPDGDKCKKIACVRNKKGEVVKQESVETCKTNCSKGWEYKESET---SCCGECARVACVVDERLKKAGESWTSPDNCTTY
NASVI_156545430 KYYQPGQNWQSSD-DACDIESCIFTPEGRIVKQKASQTCNKDCAKGWEYQEPEFG--TCCGECKQVYCVVDDLLYEPGTTWYSDDNCTAF
APIME_110758905 IIYKLGEKWKSVD-DKCATEICALEPN--ITKYKEIEVCNKNCTPGWIYEEKEN---ECCGQCKQAYCIIEDMFYKPNTTWYSIDNCTIF
         Dm-385 --YKVGTVWPSSDGNPCINLTCILAPTGEITKQESVQTCKKTCKEGWKYIEPAEMSNECCGECKPQGCLVDGVVHEKDSNWTSDDNCTSY

                 *   .   : :  .   ** :  *     : . **  *:          *    .    *   .      ** * *   :  :.:* *
DROVI_195378879 LCLKKDKL-LMVSSSNEICPDVSQCAPHLVYVEGCCKRCKLEPQVEDLSTCLPVSLAESRTKELLKYTKPGHGVCVNAEPIKGFTDCEGA
DROMO_195126483 VCLKKDKM-LMVSSSIEVCPDVSRCPEHLQFVEGCCKLCKSEPIIENLSNCLPVSLAEPLTKELLKYTKPGHGVCVNAEPIKGFTDCEGA
DROGR_195020135 VCLQKDKL-LMVSSSAEICPDVSRCAAHLLYVDGCCKRCKSEPIVEDLSTCLPVSLAESRTKELLKFSKPGHGACVNAEPIKGFTDCEGA
DROWI_195427135 ACLKKDKQ-LLVSSSKEICPDVSKCLTHLLYLDGCCKRCKVEPLIEDKSTCLPVSLAESQTKELLKFPKSGHGVCINAEPIKGFTDCVGA
DROPE_195172839 SCLKKDNQ-LMVTSSKEICPDVAGCLSHLLYQDGCCKRCKLEPLVEDKSTCLPVSLAESQTKEILKFSKSGHGVCVNAEPIKGFTDCQGA
DROPS_198463654 SCLKKDNQ-LMVTSSKEICPDVAGCLSHLLYQDGCCKRCKLEPLVEDKSTCLPVSLAESQTKEILKFSKSGHGVCVNAEPIKGFTDCQGA
DROSI_195590120 SCLKKDGQ-FLVTTSKEVCPDVGSCLSHLVYQDGCCKRCKSEPLVEDKSTCLPVSLAESRTKEILKFPVQGHGICVNADPIQGFTDCEGA
DROSE_195327436 SCLKKDGQ-FLVTTSKEVCPDVGSCLSHLLYQDGCCKRCKSEPLVEDKSSCLPVSLAESRTKEIIKFPVQGHGICVNVDPIQGFTDCEGA
 DROME_24663920 SCLKKDGQ-FLVTTSREVCPDVGSCLSHLLYQDGCCKRCKSEPLVEDKSSCLPVSLAESRTKEILKFPVQGHGTCVNADPIQGFTDCEGA
DROER_194870562 SCLKKDGQ-FLVTTSKEVCPNVDSCLSHLLYQDGCCKRCKSEPLVQDKSTCLPVSLAESRTKEILKFPVQGHGTCVNADPIQGFTDCEGS
DROYA_195494180 SCLKKDGQ-FLVTTSKEVCPDVGSCLSHLLYQDGCCKRCKSEPLIEDKSTCLPVSLAESRTKEILKFPVQGHGICVNADPIQGFTDCEGA
DROAN_194752407 ICLKKDQQ-LMVSSSQEVCPDVGSCLSHLLYQDGCCKRCKVEPLVEDKSNCLPVSLAESQTTRIIKVPKIGHGECVNAEPIRGFTDCQGA
PEDHU_242019815 TCTEKNGI-FSISTQLESCPSIEDCAEENIYKDKCCLKCKIT--SDSLRNCVPKPLPPETTIHLIRENKSAHGLCHNLLPLQNFTQCSGN
 TRICA_91090548 VCEQFGDE-FIVSSQQESCPSLEDCPEENIYIKGCCKHCNITSGS--QQQCSAEAIPLNKTISLISAHKSDHGKCVNKKHIHKFTECVGS
NASVI_156545430 SCSQKNDY-LFISKSTPVCPELN-CEPELMYDDGCCKKCNITSENKVEQACAAEVFDFEKTIGILVEKKGSHGICKNLKPIVGLTECHGH
APIME_110758905 TCIKQGEQ-LVISSSSVVCPDVTDCPDTLLYMQNCCKICNLTSYNHKIESCVANVLEEQNTIGMFSIKHRVHGLCKNLEPINGITECHGI
         Dm-385 LCIIDDDDRMQVVASTEMCPFIGDCPAERIYQDKCCKKCNSTISED-KRVCTIEPVPLNKTIGAVKLYHEEHGACINHGHIIGFNECRGT

                * * : ::  .  :   * **   .   : : : * *.    :   :*  * *  *
DROVI_195378879 CSSGSKYNKHTDMHEKFCTCCSIKSYQPISVKMVCDDGHTYNQRHEVPSNCGCSPCDEFSEG-VIDVRMQG-AKQLPMPLLQLLGH----
DROMO_195126483 CSSGSKYNKLTDVHEKFCTCCTIKSYESISIKMVCEDGFTFNQRHEVPSNCGCSPCAEFSES-VIDMRMAE-TKQKPLSLLQFIGH----
DROGR_195020135 CSSGSKYNPITDMHEKFCTCCNIKSYEPISVKMVCADGYAYIQRHEVPSNCGCSPCSEFSEG-LIDVRMSGGQKQMQIPLLKLLGYQSD-
DROWI_195427135 CNSGSKYNTLTDMHEKFCTCCSIKSYQPISVKMICEDGHTYVQRHEVPSNCGCSPCAENSDS-MIDVRMQP---DVQSPLLKLLGQ----
DROPE_195172839 CSSGSKYNTLTGMHEKFCTCCSIKSHHPISVKMVCQDGHTYSQRHEVPANCGCSPCSELSDP-PIDVRMLP---DVQYPLLKLLGNHQDN
DROPS_198463654 CSSGSKYNTLTDMHEKFCTCCSIKSYHPISVKMVCQDGHTYSQRHEVPANCGCSPCSELSDP-PIDVRMLP---DVQYPLLKLLGNHQDN
DROSI_195590120 CSSGSKYNTLTDIHEKFCTCCSIKSYHPISVKMICEDGHTFTQKHEVPSNCGCSPCSEFSDS-AIDVRMQQ---DAPSPLLQLLGSHRH-
DROSE_195327436 CSSGSKYNTLTDMHEKFCTCCSIKSYHPISVKMICEDGHTFTQKHELPSNCGCSPCSEFSDS-AIDVRMQQ---DAPSPLLQLLGKHRH-
 DROME_24663920 CSSGSKYNTLTDMHEKFCTCCSIKSYHPISVKMICDDGHTFTQKHEVPSNCGCSPCSEFSDS-AIDVRMQQ---DAQSPLLQLLGNHRH-
DROER_194870562 CSSGSKYNTLTDMHEKFCTCCSIQSYHPISVKMICEDGHTFTQKHEVPSNCGCSPCSEFSDT-AIDVRMQQ---DVQSPLLQLLGNHRH-
DROYA_195494180 CSSGSKYNTLTDMHEKFCTCCSIKSYRPITVKMICEDGHTFTQKHEMPSNCGCSPCSEFSDTPTFDVRMQP---DVQSPLLQLLGNHGH-
DROAN_194752407 CSSGTKYNTLTDVHEKYCTCCNIKSYQPISVNMICEDGHTYIQKHELPANCGCSLCSELSDP-AIDIRIQP---DVQSPLLKLLSSPKTL
PEDHU_242019815 CHSHTQYDPENLTHNNICKCCQPEEFSFLAVGLTCEDGTDYTKTITVPSKCSCLPCGV--------------------------------
 TRICA_91090548 CHSATFFDTKKGSHESVCSCCHATDYKSIEVELECEDGYTWKKKVAVPSACGCEGCAAAHKS----------VKHKKTFGFC--------
NASVI_156545430 CNSSTHFNIKTWEQVVDCTCCKPVDYRKINVELTCEDGKKFKKILTVPSVCMCEGCASDNSEDMKRLHSFYDVKGHRKHGLNSINNR---
APIME_110758905 CESNSYFDTDNWSQIVNCQCCQPTEYKSLIVELICEDNKKFEKQVTVPVSCACSTCMS-NEK----------IYKRRKDGVKG-------
         Dm-385 CDSYTQYDPTTGKHESKCLCCKAKEIDTVAIALTCEDGYFLEKQVPVPVTCMCQTCGS----------------NKKLIGIKYPK-----
```

Supplemental figure 3 – Clustal alignment of a predicted sequence from a contig of *D. maxima* library with similarity to a secreted Histidine rich peptide precursor. The symbols above the alignment indicate: (*) identical sites; (:) conserved sites; (.) less conserved sites.



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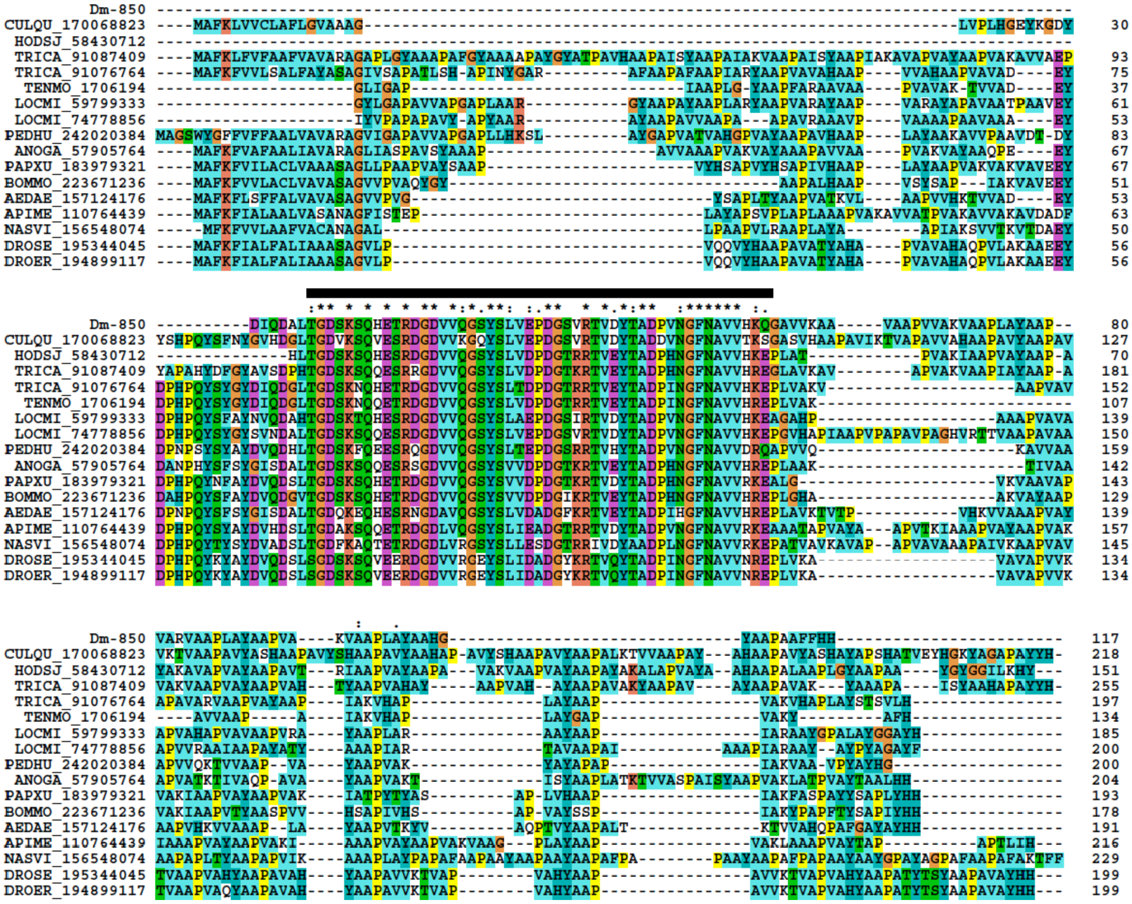
                *        :.  ::  .  :  *      :* *  *****::*.*  :
         Dm-517 MASLRIAVVLVLSMIVIVSTAPTPGGW-GGKHTHYIIHVPYHIHTVHHHHK--------------    50
NASVI_156541785 MYSHAFA-LLVCGILAAVTAAPTPG---GHHHEHHIIHVPYHVHTVHHHHVKKVHVPVHHVEKVH    61
TRICA_189235401 MAFMKYIFVLVAVLLALAAAAPAPGYHHHGHHEHVVIHVPYHVHTVHHHHVKK------------    53
DROYA_195474755 MS--ALKVFIFVALFAVAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKVHVP----VVKH    57
 DROME_24586616 MS--VLKVFIFVALFAVAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKVHVP----VVKH    57
DROAN_194753031 MS--ALKAFIFVALFAVAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKVHVP----VVKH    57
DROER_194863447 MS--ALKVFIFVALFAAAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKVHVP----VVKH    57
DROWI_195455416 MN--ALNIFVFVALFAVAYSAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKVHVP----VVKH    57
DROPE_195148988 MS--ALKAFIMFALLSVAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKIHVP----VVKH    57
DROVI_195384433 MT--ALRVIVFVALFAVAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKIAVP----VVKH    57
DROGR_195030003 MF--ALKVFIFVALFAVAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKIAVP----VVKH    57
DROMO_195120668 MS--ALKVFIFAAIFAVAYCAPSPGFF--GKHEHHTIHVPYKVHTVHHHHVQKIAVP----VVKH    57
ACYPI_193648091 MN---TSVAILLTILSVAAAS--PLFFSHPKHEHHVIHVPYHVHKVPVYIKEPVYIE--------    52

                    : :                                   * .         :
         Dm-517 VPVYIKHHT-----HTHTHTGY--------------HDEDYGHHGWH------GWD---------    81
NASVI_156541785 VPVPVHHVE-----KVHVPVPYPVVEKVHVPVHIPVHHEKPHHEGW-------GWD---------   105
TRICA_189235401 VHVPVVKKI-----YVHEEPHY--------------HHDH--HHGW--------W----------    79
DROYA_195474755 VPVPIYKEV--PVHHVHHEEI-PVPVHHVHHEEIPVHHVFDDHHDHH------GWSS-HHGHGWL   112
 DROME_24586616 VPVPIYKEV--PVHHVHHEEI-PVPVHHVHHEEIPVHHVFDDHHDHH------GWSS-HHGHGWL   112
DROAN_194753031 VPVPVYKEVHVPVHHVHHEEI-PVPVHHVHHEEVPVHHVFDDHHDHH------GWGS-HHGHGWL   114
DROER_194863447 VPVPIYKEV--PVHHVHHEEI-PVPVHHVHHEEIPVHHVFEDHHDHH------GWSS-HHGHGWL   112
DROWI_195455416 VPVPIYKEV--PVHHVHHEEI-PVPVHHVHHEEIPVHHVYEDHHDFHK-----GWSH-GHGHGWL   113
DROPE_195148988 V--PIYKEV--PVHHVHHEEILPVPVH-VHHEEVPVHHVYEDHHDYHK-----GWSSAHHGHGWI   112
DROVI_195384433 V--PVYKEV----HVPVYKEV---PVHHVHHEEIVPVHVHEDHHDYHH-DFHKGWN--SLSHGW-   109
DROGR_195030003 V--PVYKEV----HVPVYKEV---PVHHVHHEEIVPVHVHEDHHDYHHHDFHKGWSS-SLSHGW-   111
DROMO_195120668 V--PIYKEV----HVPVIKEV---PVHHVHHEEIVPVHVHEDHHDYHH-DFHKGWSS-SLSHGW-   110
ACYPI_193648091 KPVYIYKTVDHHDHHYHHDDH------------SYDHYNHDDHYDSH-------Y----------    88
```

Supplemental figure 4 – Clustal alignment of a predicted sequence from a contig of *D. maxima* library that showed similarity to a larval cuticle protein. The thick bar indicates the chitin-binding domain region. The symbols above the alignment indicate: (*) identical sites; (:) conserved sites; (.) less conserved sites.



Supplemental Table 1. Identification of Proteins of *Dipetalogaster maxima* Saliva by Peptide Mass Fingerprinting

Spot [a]	Identity [b]	Accession number (cDNA library) [c]	Score [d]	Coverage (%) [e]	Mol. Mass (kDa) [f]		Isoelectric Point [g]	
					Exp.	Theor.	Exp.	Theor.
1	Apyrase	Dm-68	74 > 48	31	94.4	25.0	4.8	4.8
2	Apyrase	Dm-68	53 > 48	17	94.0	25.0	5.0	4.8
3	Apyrase	Dm-68	70 > 48	26	95.7	25.0	5.1	4.8
4	Apyrase	Dm-68	49 > 48	16	95.0	25.0	5.2	4.8
5	Lipocalin	Dm-96	68 > 48	28	83.1	17.7	7.6	5.2
6	Lipocalin	Dm-96	51 > 48	25	53.5	17.7	5.0	5.2
7	Lipocalin	Dm-105	84 > 48	42	44.6	16.0	5.9	5.4
8	Lipocalin	Dm-45	60 > 48	24	43.3	19.8	6.6	6.9
9	Lipocalin	Dm-272	95 > 48	46	42.5	17.6	8.4	7.7
10	Lipocalin	Dm-270	77 > 48	29	40.0	17.3	8.4	7.7
11	Lipocalin	Dm-270	129 >48	50	38.5	17.3	8.4	7.7
12	Lipocalin	Dm-96	61 > 48	31	33.6	17.7	5.0	5.2
13	Antigen-5	Dm-124	53 > 48	18	31.1	28.3	8.4	8.6
14	Antigen-5	Dm-124	88 > 48	38	31.4	28.3	8.6	8.7
15	Antigen-5	Dm-124	136 >48	38	30.4	28.3	8.2	8.6
16	Antigen-5	Dm-124	58 > 48	14	30.4	28.3	8.4	8.6
17	Antigen-5	Dm-79	80 > 48	46	30.0	21.2	8.6	8.5
18	Lipocalin	Dm-105	60 > 48	28	28.7	16.0	5.9	5.4
19	Lipocalin	Dm-75	58 > 48	34	27.3	14.9	5.9	5.2
20	Lipocalin	Dm-78	90 > 48	31	25.7	18.1	7.0	6.6

					Mol. Mass (kDa) [f]		Isoelectric Point [g]	
Spot [a]	Identity [b]	Accession number (cDNA library) [c]	Score [d]	Coverage (%) [e]	Exp.	Theor.	Exp.	Theor.
21	Lipocalin	Dm-99	97 > 48	48	25.7	14.3	9.4	8.9
22 Mixture	Lipocalin	Dm-1189 Dm-288	196 >48	77 36	25.0	11.4 21.4	9.5	9.6 7.5
23	Pallidipin	Dm-1049	72 > 48	40	24.6	20.3	6.8	6.5
24	Pallidipin	Dm-1049	66 > 48	33	24.1	20.3	7.0	6.5
25	Pallidipin	Dm-1049	85 > 48	32	24.3	20.3	7.2	6.5
26	Unknown	M_ASB-722_FR2	52 > 48	13	24.2	31.8	8.4	10.4
27	Lipocalin	Dm-346	118 >48	47	23.8	20.2	8.8	8.7
28 Mixture	Pallidipin Lipocalin	M_ASB-1047_FR1 Dm-78	116 >48	18 26	23.0	39.4 18.1	7.0	9.9 6.6
29	Lipocalin	Dm-49	261 >48	68	23.0	20.2	8.4	8.1
30	Lipocalin	Dm-346	70 > 48	35	22.5	20.2	8.8	8.7
31	Lipocalin	Dm-240	65 > 48	28	22.0	17.9	6.7	7.0
32	Lipocalin	Dm-270	175 >48	43	21.5	17.3	8.5	7.7
33	Lipocalin	Dm-270	95 > 48	26	21.5	17.3	8.8	7.7
34	Lipocalin	Dm-96	70 > 48	35	22.1	17.7	5.0	5.2
35	Lipocalin	Dm-270	122 >48	43	21.2	17.3	7.7	7.7
36	Lipocalin	Dm-96	64 > 48	40	20.6	17.7	5.0	5.2
37	Lipocalin	Dm-96	89 > 48	40	20.7	17.7	5.3	5.2
38	Lipocalin	Dm-171	68 > 48	36	20.3	8.2	6.2	8.6
39 Mixture	Lipocalin	Dm-278 Dm-78	102 >48	28 26	20.4	16.3 18.0	7.0	5.6 6.6
40 Mixture	Lipocalin	Dm-237 Dm-278	158 >48	42 37	20.0	15.2 16.3	7.7	6.1 5.6

Spot [a]	Identity [b]	Accession number (cDNA library) [c]	Score [d]	Coverage (%) [e]	Mol. Mass (kDa) [f] Exp.	Mol. Mass (kDa) [f] Theor.	Isoelectric Point [g] Exp.	Isoelectric Point [g] Theor.
41 Mixture	Lipocalin	Dm-270 Dm-346	131 >48	45 40	20.3	17.3 20.1	8.8	7.7 8.7
42	Lipocalin	Dm-96	69 > 48	33	19.7	17.7	5.0	5.2
43	Lipocalin	Dm-270	124 >48	49	18.8	17.3	7.7	7.7
44	Lipocalin	Dm-272	139 >48	46	19.4	17.6	8.4	7.7
45 Mixture	Lipocalin	Dm-278 Dm-258	123 >48	32 27	19.8	16.3 17.7	8.8	5.6 7.7
46	Lipocalin	Dm-270	93 > 48	26	19.5	17.3	9.5	7.7
47	Lipocalin	Dm-278	94 > 48	36	19.1	16.4	9.8	5.6

[a] Spot numbers are indicated in Figure 2.
[b] Results obtained by MASCOT software against partial predicted proteins library.
[c] Accession number in predicted proteins library.
[d] Probability-based Mowse score of MASCOT software. The numbers after the symbol ">" represent the minimum statistically significant score calculated by the software.
[e] Percentage of predicted protein sequences covered by matched peptides via MASCOT.
[f] Experimental and theoretical molecular masses of proteins visualized on gels and calculated from amino acid sequences, respectively.