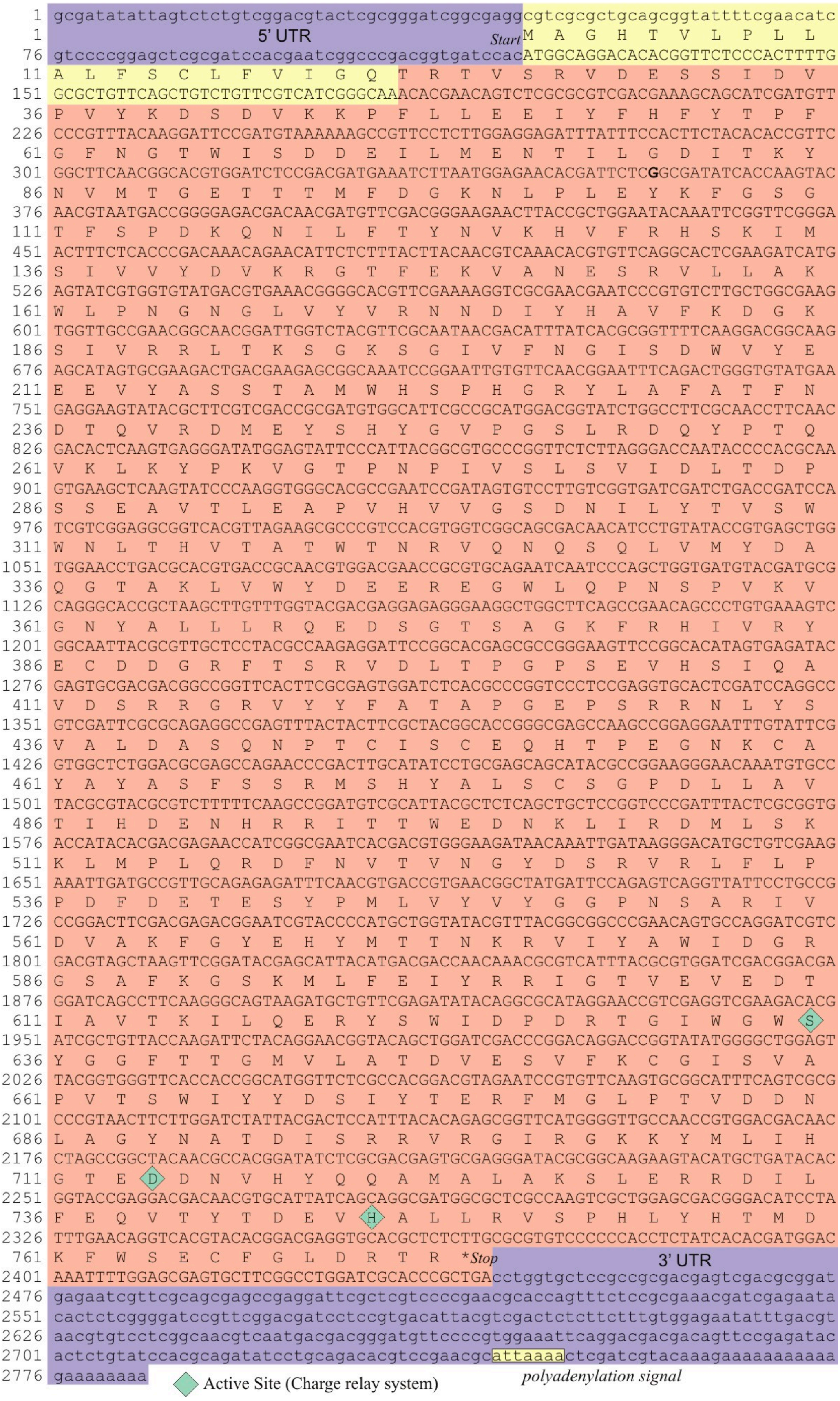
Supplementary Materials: Bottom-up Proteomic Analysis of Polypeptide Venom Components of the Giant Ant *Dinoponera quadriceps*

Douglas Oscar Ceolin Mariano, Úrsula Castro de Oliveira, André Junqueira Zaharenko, Daniel Carvalho Pimenta, Gandhi Rádis-Baptista and Álvaro Rossan de Brandão Prieto-da-Silva

Contig164_B2-2 *D. quadriceps* venom dipeptidyl peptidase 4
[Corrected] 5'3' Frame +1 insertion G position 359



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  61 G  F  N  G  T  W  I  S  D  D  E  I  L  M  E  N  T  I  L  G  D  I  T  K  Y
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  86 N  V  M  T  G  E  T  T  T  M  F  D  G  K  N  L  P  L  E  Y  K  F  G  S  G
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 636 Y  G  G  F  T  T  G  M  V  L  A  T  D  V  E  S  V  F  K  C  G  I  S  V  A
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 686 L  A  G  Y  N  A  T  D  I  S  R  R  V  R  G  I  R  G  K  K  Y  M  L  I  H
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 736 F  E  Q  V  T  Y  T  D  E  V  H  A  L  L  R  V  S  P  H  L  Y  H  T  M  D
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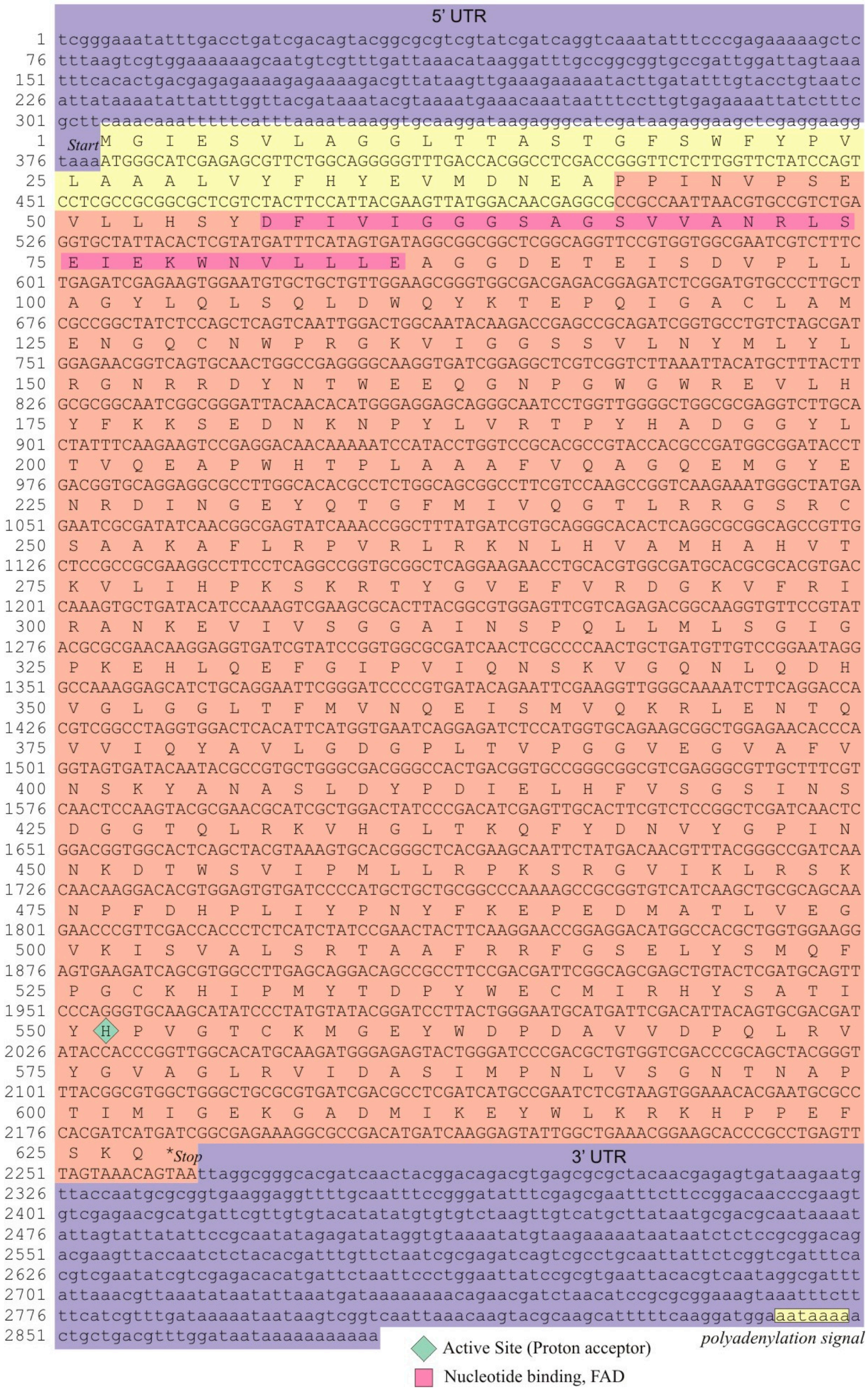
2626 aacgtgtcctcggcaacgtcaatgacgacgggatgttccccgtggaaattcaggacgacgacagttccgagatac
2701 actctgtatccacgcagatatcctgcagacacgtccgaacgcattaaaactcgatcgtacaaagaaaaaaaaaaa
2776 gaaaaaaaa                                  polyadenylation signal
```

◆ Active Site (Charge relay system)

Figure S1. Structural nucleotide organization of venom dipeptidyl peptidase-4 of *D. quadriceps* expressed transcript contig164_B2-2. The product of this transcript is found in SDS-PAGE, gel band 1. (Figure 2, in the main text). In purple, part of the 5'UTR is shown, followed by the start codon that initiates the signal peptide of 21 amino acids predicted by SignalP 5.0 (in yellow). Followed by the coding region of a mature protein with 752 amino acids (pink), the active site is indicated by the catalytic triad (green diamonds). Followed by the stop codon, the 3 'UTR region (purple) and the polyadenylation signal (ATTAAA), indicated by a yellow box.

Contig75_B2-2 *D. quadriceps* Glucose dehydrogenase [FAD, quinone] 3'5' Frame 2



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 500  V  K  I  S  V  A  L  S  R  T  A  A  F  R  R  F  G  S  E  L  Y  S  M  Q  F
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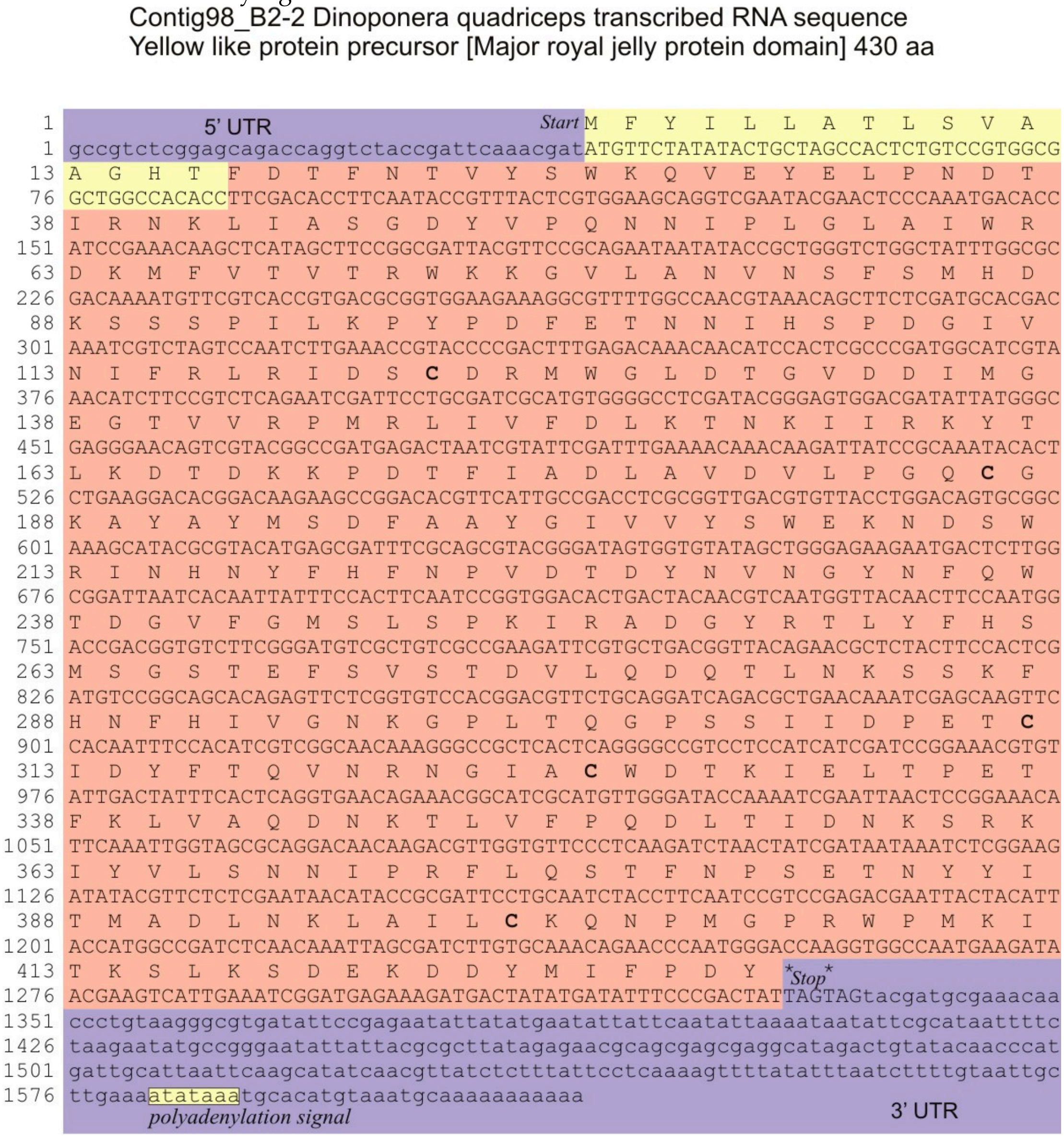
2776 ttcatcgtttgataaaaataataagtcggtcaattaaacaagtacgcaagcattttcaaggatggaaataaaaa
2851 ctgctgacgtttggataataaaaaaaaaaa
```

polyadenylation signal

◆ Active Site (Proton acceptor)

🟥 Nucleotide binding, FAD

Figure S2. Glucose dehydrogenase precursor [FAD, quinone] encoded by Contig75_B2-2. The mature peptide was found in the venom proteomics, according to explanation in the main text. The cDNA encodes a precursor with 627 amino acids, the mature part of which is indicated in salmon. The nucleotide binding site is indicated by the pink box. The 5 'and 3'-untranslated regions (UTRs) are indicated in purple. The polyadenylation signal is indicated by the yellow box. The proton acceptor of the active site indicated by a green diamond.



Contig98_B2-2 Dinoponera quadriceps transcribed RNA sequence
Yellow like protein precursor [Major royal jelly protein domain] 430 aa

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  13 A  G  H  T  F  D  T  F  N  T  V  Y  S  W  K  Q  V  E  Y  E  L  P  N  D  T
  76 GCTGGCCACACCTTCGACACCTTCAATACCGTTTACTCGTGGAAGCAGGTCGAATACGAACTCCCAAATGACACC
  38 I  R  N  K  L  I  A  S  G  D  Y  V  P  Q  N  N  I  P  L  G  L  A  I  W  R
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  63 D  K  M  F  V  T  V  T  R  W  K  K  G  V  L  A  N  V  N  S  F  S  M  H  D
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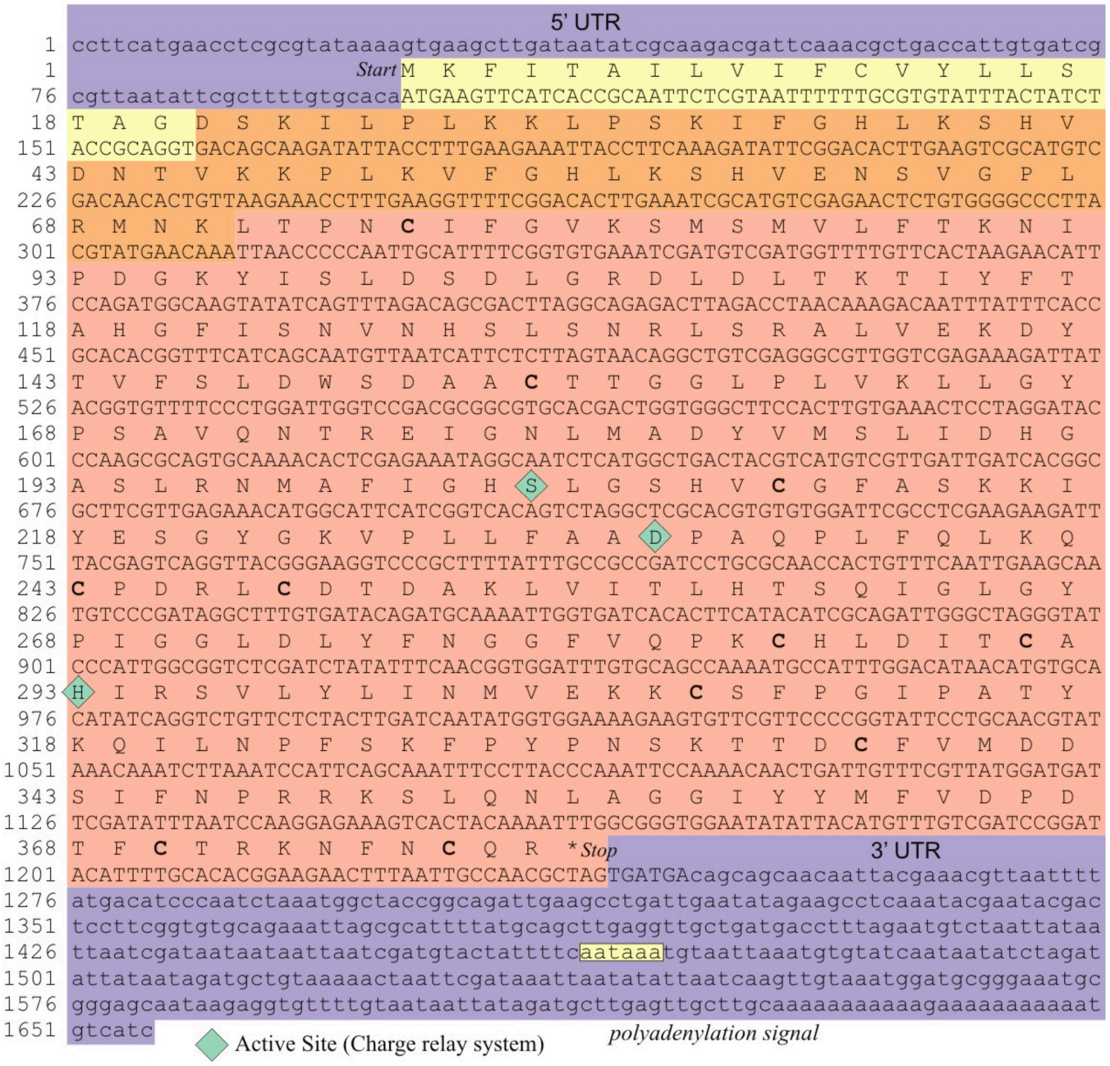
1126 ATATACGTTCTCTCGAATAACATACCGCGATTCCTGCAATCTACCTTCAATCCGTCCGAGACGAATTACTACATT
 388 T  M  A  D  L  N  K  L  A  I  L  C  K  Q  N  P  M  G  P  R  W  P  M  K  I
1201 ACCATGGCCGATCTCAACAAATTAGCGATCTTGTGCAAACAGAACCCAATGGGACCAAGGTGGCCAATGAAGATA
 413 T  K  S  L  K  S  D  E  K  D  D  Y  M  I  F  P  D  Y *Stop*
1276 ACGAAGTCATTGAAATCGGATGAGAAAGATGACTATATGATATTTCCCGACTATTAGTAGtacgatgcgaaacaa
1351 ccctgtaagggcgtgatattccgagaatattatatgaatattattcaatattaaaataatattcgcataattttc
1426 taagaatatgccgggaatattattacgcgcttatagagaacgcagcgagcgaggcatagactgtatacaacccat
1501 gattgcattaattcaagcatatcaacgttatctctttattcctcaaaagttttatatttaatcttttgtaattgc
1576 ttgaaaatataaatgcacatgtaaatgcaaaaaaaaaaa
           polyadenylation signal                                  3' UTR
```

Figure S3. Structural nucleotide organization of the precursor of *D. quadriceps* MRJP-like venom protein. The contig98_B2-2 cDNA code for major royal jelly protein-like in giant ant venom gland.The mature toxins were found in the venom by the proteomic analysis (this study). Non-coding regions 5 'and 3'-UTRs are indicated in purple. The predicted signal peptide is shown in yellow. The coding region for the mature protein (detailed in the main text) is indicated in beige/orange. Start and stop codons are indicated with asterisks. The putative polyadenylation site is indicated by the yellow box.

Contig27_B2-2 transcribed RNA sequence, phospholipase A1 2-like, Dinoponera quadriceps



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                                             5' UTR
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   1                         Start M  K  F  I  T  A  I  L  V  I  F  C  V  Y  L  L  S
  76 cgttaatattcgcttttgtgcacaATGAAGTTCATCACCGCAATTCTCGTAATTTTTTGCGTGTATTTACTATCT
  18 T  A  G  D  S  K  I  L  P  L  K  K  L  P  S  K  I  F  G  H  L  K  S  H  V
 151 ACCGCAGGTGACAGCAAGATATTACCTTTGAAGAAATTACCTTCAAAGATATTCGGACACTTGAAGTCGCATGTC
  43 D  N  T  V  K  K  P  L  K  V  F  G  H  L  K  S  H  V  E  N  S  V  G  P  L
 226 GACAACACTGTTAAGAAACCTTTGAAGGTTTTCGGACACTTGAAATCGCATGTCGAGAACTCTGTGGGGCCCTTA
  68 R  M  N  K  L  T  P  N  C  I  F  G  V  K  S  M  S  M  V  L  F  T  K  N  I
 301 CGTATGAACAAATTAACCCCCAATTGCATTTTCGGTGTGAAATCGATGTCGATGGTTTTGTTCACTAAGAACATT
  93 P  D  G  K  Y  I  S  L  D  S  D  L  G  R  D  L  D  L  T  K  T  I  Y  F  T
 376 CCAGATGGCAAGTATATCAGTTTAGACAGCGACTTAGGCAGAGACTTAGACCTAACAAAGACAATTTATTTCACC
 118 A  H  G  F  I  S  N  V  N  H  S  L  S  N  R  L  S  R  A  L  V  E  K  D  Y
 451 GCACACGGTTTCATCAGCAATGTTAATCATTCTCTTAGTAACAGGCTGTCGAGGGCGTTGGTCGAGAAAGATTAT
 143 T  V  F  S  L  D  W  S  D  A  A  C  T  T  G  G  L  P  L  V  K  L  L  G  Y
 526 ACGGTGTTTTCCCTGGATTGGTCCGACGCGGCGTGCACGACTGGTGGGCTTCCACTTGTGAAACTCCTAGGATAC
 168 P  S  A  V  Q  N  T  R  E  I  G  N  L  M  A  D  Y  V  M  S  L  I  D  H  G
 601 CCAAGCGCAGTGCAAAACACTCGAGAAATAGGCAATCTCATGGCTGACTACGTCATGTCGTTGATTGATCACGGC
 193 A  S  L  R  N  M  A  F  I  G  H  S  L  G  S  H  V  C  G  F  A  S  K  K  I
 676 GCTTCGTTGAGAAACATGGCATTCATCGGTCACAGTCTAGGCTCGCACGTGTGTGGATTCGCCTCGAAGAAGATT
 218 Y  E  S  G  Y  G  K  V  P  L  L  F  A  A  D  P  A  Q  P  L  F  Q  L  K  Q
 751 TACGAGTCAGGTTACGGGAAGGTCCCGCTTTTATTTGCCGCCGATCCTGCGCAACCACTGTTTCAATTGAAGCAA
 243 C  P  D  R  L  C  D  T  D  A  K  L  V  I  T  L  H  T  S  Q  I  G  L  G  Y
 826 TGTCCCGATAGGCTTTGTGATACAGATGCAAAATTGGTGATCACACTTCATACATCGCAGATTGGGCTAGGGTAT
 268 P  I  G  G  L  D  L  Y  F  N  G  G  F  V  Q  P  K  C  H  L  D  I  T  C  A
 901 CCCATTGGCGGTCTCGATCTATATTTCAACGGTGGATTTGTGCAGCCAAAATGCCATTTGGACATAACATGTGCA
 293 H  I  R  S  V  L  Y  L  I  N  M  V  E  K  K  C  S  F  P  G  I  P  A  T  Y
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 318 K  Q  I  L  N  P  F  S  K  F  P  Y  P  N  S  K  T  T  D  C  F  V  M  D  D
1051 AAACAAATCTTAAATCCATTCAGCAAATTTCCTTACCCAAATTCCAAAACAACTGATTGTTTCGTTATGGATGAT
 343 S  I  F  N  P  R  R  K  S  L  Q  N  L  A  G  G  I  Y  Y  M  F  V  D  P  D
1126 TCGATATTTAATCCAAGGAGAAAGTCACTACAAAATTTGGCGGGTGGAATATATTACATGTTTGTCGATCCGGAT
 368 T  F  C  T  R  K  N  F  N  C  Q  R  *Stop                 3' UTR
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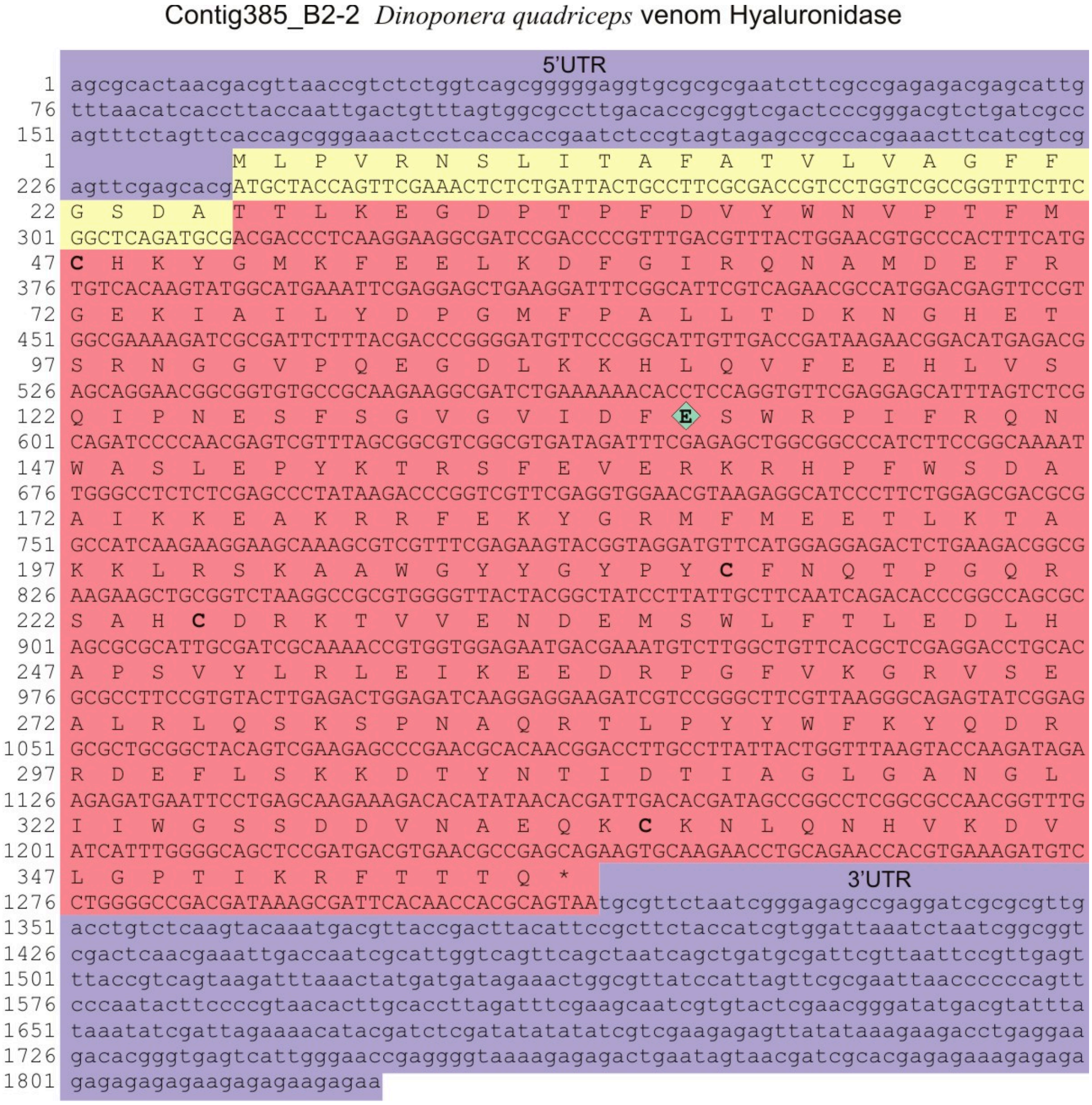
1576 gggagcaataagaggtgttttgtaataattatagatgcttgagttgcttgcaaaaaaaaaaagaaaaaaaaaaat
1651 gtcatc
```

Figure S4. Structural organization of the Contig27_B2-2 cDNA that code for phospholipase A1 in the *D. quadriceps* venom. The full-length precursor is 379-amino acid residues long. A signal peptide with 20 amino acids, as predicted by SignalP 5.0, is indicated in yellow. The 5 'and 3'-untranslated regions are indicated in purple. The mature sequence is indicated in light pink and the putative propeptide is visible in the region indicated in orange. The mature peptide has 11 cysteines of which 10 are conserved among the PLA1s from the venom of hymenopterans. The mature peptide is found in the venom as detected by proteomic analysis (this study). The amino acids in the active site are indicated by green diamonds. The predicted polyadenylation signal is indicated by a yellow box



Contig385_B2-2 *Dinoponera quadriceps* venom Hyaluronidase

```
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 151 agtttctagttcaccagcgggaaactcctcaccaccgaatctccgtagtagagccgccacgaaacttcatcgtcg
   1            M  L  P  V  R  N  S  L  I  T  A  F  A  T  V  L  V  A  G  F  F
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  22 G  S  D  A  T  T  L  K  E  G  D  P  T  P  F  D  V  Y  W  N  V  P  T  F  M
 301 GGCTCAGATGCGACGACCCTCAAGGAAGGCGATCCGACCCCGTTTGACGTTTACTGGAACGTGCCCACTTTCATG
  47 C  H  K  Y  G  M  K  F  E  E  L  K  D  F  G  I  R  Q  N  A  M  D  E  F  R
 376 TGTCACAAGTATGGCATGAAATTCGAGGAGCTGAAGGATTTCGGCATTCGTCAGAACGCCATGGACGAGTTCCGT
  72 G  E  K  I  A  I  L  Y  D  P  G  M  F  P  A  L  L  T  D  K  N  G  H  E  T
 451 GGCGAAAAGATCGCGATTCTTTACGACCCGGGGATGTTCCCGGCATTGTTGACCGATAAGAACGGACATGAGACG
  97 S  R  N  G  G  V  P  Q  E  G  D  L  K  K  H  L  Q  V  F  E  E  H  L  V  S
 526 AGCAGGAACGGCGGTGTGCCGCAAGAAGGCGATCTGAAAAAACACCTCCAGGTGTTCGAGGAGCATTTAGTCTCG
 122 Q  I  P  N  E  S  F  S  G  V  G  V  I  D  F  E  S  W  R  P  I  F  R  Q  N
 601 CAGATCCCCAACGAGTCGTTTAGCGGCGTCGGCGTGATAGATTTCGAGAGCTGGCGGCCCATCTTCCGGCAAAAT
 147 W  A  S  L  E  P  Y  K  T  R  S  F  E  V  E  R  K  R  H  P  F  W  S  D  A
 676 TGGGCCTCTCTCGAGCCCTATAAGACCCGGTCGTTCGAGGTGGAACGTAAGAGGCATCCCTTCTGGAGCGACGCG
 172 A  I  K  K  E  A  K  R  R  F  E  K  Y  G  R  M  F  M  E  E  T  L  K  T  A
 751 GCCATCAAGAAGGAAGCAAAGCGTCGTTTCGAGAAGTACGGTAGGATGTTCATGGAGGAGACTCTGAAGACGGCG
 197 K  K  L  R  S  K  A  A  W  G  Y  Y  G  Y  P  Y  C  F  N  Q  T  P  G  Q  R
 826 AAGAAGCTGCGGTCTAAGGCCGCGTGGGGTTACTACGGCTATCCTTATTGCTTCAATCAGACACCCGGCCAGCGC
 222 S  A  H  C  D  R  K  T  V  V  E  N  D  E  M  S  W  L  F  T  L  E  D  L  H
 901 AGCGCGCATTGCGATCGCAAAACCGTGGTGGAGAATGACGAAATGTCTTGGCTGTTCACGCTCGAGGACCTGCAC
 247 A  P  S  V  Y  L  R  L  E  I  K  E  E  D  R  P  G  F  V  K  G  R  V  S  E
 976 GCGCCTTCCGTGTACTTGAGACTGGAGATCAAGGAGGAAGATCGTCCGGGCTTCGTTAAGGGCAGAGTATCGGAG
 272 A  L  R  L  Q  S  K  S  P  N  A  Q  R  T  L  P  Y  Y  W  F  K  Y  Q  D  R
1051 GCGCTGCGGCTACAGTCGAAGAGCCCGAACGCACAACGGACCTTGCCTTATTACTGGTTTAAGTACCAAGATAGA
 297 R  D  E  F  L  S  K  K  D  T  Y  N  T  I  D  T  I  A  G  L  G  A  N  G  L
1126 AGAGATGAATTCCTGAGCAAGAAAGACACATATAACACGATTGACACGATAGCCGGCCTCGGCGCCAACGGTTTG
 322 I  I  W  G  S  S  D  D  V  N  A  E  Q  K  C  K  N  L  Q  N  H  V  K  D  V
1201 ATCATTTGGGGCAGCTCCGATGACGTGAACGCCGAGCAGAAGTGCAAGAACCTGCAGAACCACGTGAAAGATGTC
 347 L  G  P  T  I  K  R  F  T  T  T  Q  *                         3’UTR
1276 CTGGGGCCGACGATAAAGCGATTCACAACCACGCAGTAAtgcgttctaatcgggagagccgaggatcgcgcgttg
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1576 cccaatacttccccgtaacacttgcaccttagatttcgaagcaatcgtgtactcgaacgggatatgacgtattta
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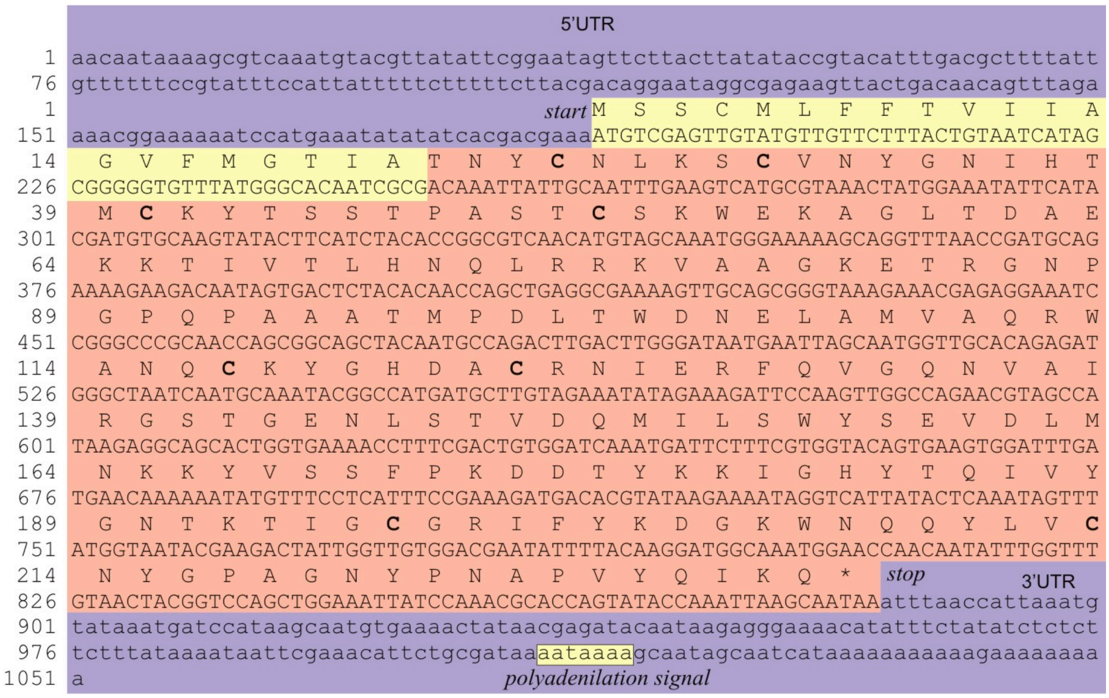
1726 gacacgggtgagtcattgggaaccgaggggtaaaagagagactgaatagtaacgatcgcacgagagaaagagaga
1801 gagagagagaagagagaagagaa
```

Figure S5. The venom hyaluronidase precursor, transcript contig385_B2-2, from *D. quadriceps* venom gland. Venom hyaluronidase was identified in proteomic analysis (this study) and confirmed the presence of the transcript product in the venom. Structurally, the untranslated regions, 5'-UTR and 3'-UTR, are indicated in purple. The coding region comprises a precursor of 368 amino acids, containing a signal peptide of 25 amino acids, as indicated in yellow, and a mature protein with 343 amino acids, as initiated in rose. This venom component belongs to the family of glycosyl hydrolases 56. The conserved cysteine residues, that form intramolecular disulfide bonds are indicated in bold and the proton donor of the active site is indicated by a green diamond. These characteristics are typical of a catalytically active hyaluronidase, in *D. quadriceps* venom.

Contig12_B2-2 *Dinoponera quadriceps* Major Allergen-3 Precursor (CAP/SPC)



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   1                                            M  S  S  C  M  L  F  F  T  V  I  I  A
 151 aaacggaaaaaatccatgaaatatatatcacgacgaaaATGTCGAGTTGTATGTTGTTCTTTACTGTAATCATAG
  14  G  V  F  M  G  T  I  A  T  N  Y  C  N  L  K  S  C  V  N  Y  G  N  I  H  T
 226 CGGGGGTGTTTATGGGCACAATCGCGACAAATTATTGCAATTTGAAGTCATGCGTAAACTATGGAAATATTCATA
  39  M  C  K  Y  T  S  S  T  P  A  S  T  C  S  K  W  E  K  A  G  L  T  D  A  E
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  64  K  K  T  I  V  T  L  H  N  Q  L  R  R  K  V  A  A  G  K  E  T  R  G  N  P
 376 AAAAGAAGACAATAGTGACTCTACACAACCAGCTGAGGCGAAAAGTTGCAGCGGGTAAAGAAACGAGAGGAAATC
  89  G  P  Q  P  A  A  A  T  M  P  D  L  T  W  D  N  E  L  A  M  V  A  Q  R  W
 451 CGGGCCCGCAACCAGCGGCAGCTACAATGCCAGACTTGACTTGGGATAATGAATTAGCAATGGTTGCACAGAGAT
 114  A  N  Q  C  K  Y  G  H  D  A  C  R  N  I  E  R  F  Q  V  G  Q  N  V  A  I
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 139  R  G  S  T  G  E  N  L  S  T  V  D  Q  M  I  L  S  W  Y  S  E  V  D  L  M
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 164  N  K  K  Y  V  S  S  F  P  K  D  D  T  Y  K  K  I  G  H  Y  T  Q  I  V  Y
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 189  G  N  T  K  T  I  G  C  G  R  I  F  Y  K  D  G  K  W  N  Q  Q  Y  L  V  C
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 214  N  Y  G  P  A  G  N  Y  P  N  A  P  V  Y  Q  I  K  Q  *
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 901 tataaatgatccataagcaatgtgaaaactataacgagatacaataagagggaaaacatatttctatatctctct
 976 tctttataaaataattcgaaacattctgcgataaaataaaagcaatagcaatcataaaaaaaaaaagaaaaaaaa
1051 a
```

Figure S6. Structural nucleotide organization of transcript contig12_B2-2 that code for major allergen-3 in *D. quadriceps*. The major allergen-3 was identified in the proteomic, in this study, as one of the predominant components in the crude venom. In orange, the mature polypeptide is evidenced with its conserved 8 cysteine residues (in bold). This protein structure is typical of the V5-SCP/CAP (CRISP) family. Highlighted in purple, is indicate the 5′- and 3′-untranslated regions. In yellow the putative signal peptide as predicted by SignalP5.0. In yellow, the polyadenylation signal is boxed.

Contig8_B2-2 Ant Venom Allergen 2/4 (OBP/PBP)precursor *Dinoponera quadriceps*

```
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 21 D  K  E  R  F  H  N  F  K  K  M  I  M  K  C  S  Q  K  F  D  E  V  H  T  K
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226 CCCTCTGTGAAAACAATATTGTGTCAAGAGGAAATGGAAGGTCGTATATTAAATAATAAAGGCGAATACATAAAG
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 96 K  C  Y  K  D  G  I  R  S  G  K  K  G  K  E  Q  S  R  Y  I  T  A  C  I  L
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121 T  A  W  P  L  I  D  F  R  G  I  *
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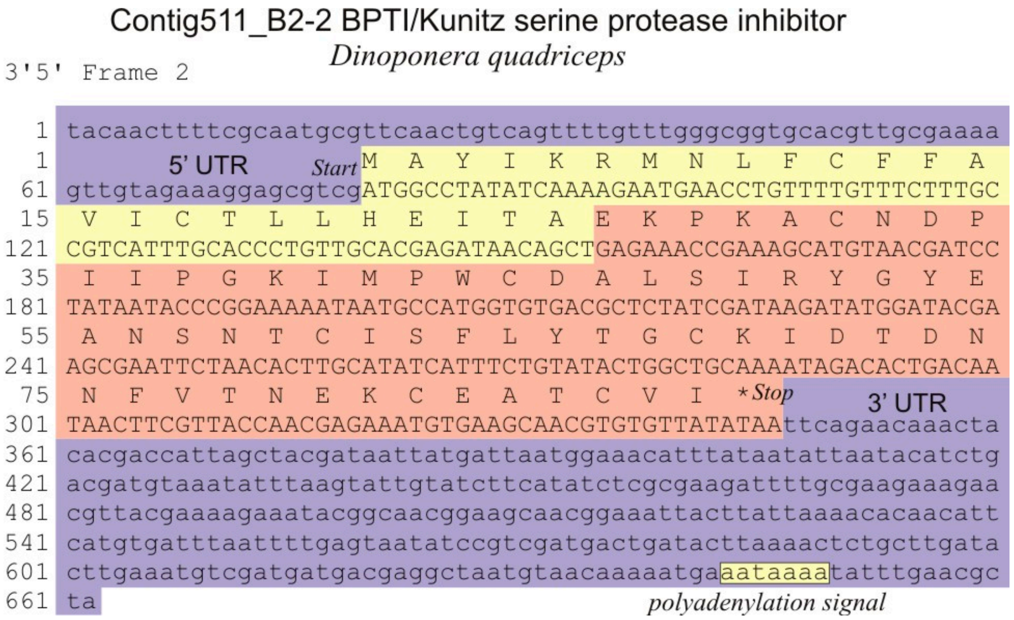
601 tctggtgaactctgtgtgtacatgatggtaattcaataaaatgaagttgatctgaaaaaaaaaaagaaaaaaaaa
```

Figure S7. Structural organization of *D. quadriceps* venom gland transcript for Venom allergen 2/4 (Contig29_B2-2) and respective protein precursor product. The sequence is 675 bp-long. In purple the untranslated regions (5 'and 3' UTRs) are shown. In yellow the signal peptide region predicted by SpecialP 5.0 (19aa) and in pink the mature peptide (112aa). A polyadenylation signal is indicated by a yellow box. Four conserved cysteines in the Ant venom Allergen 2/4 family are indicated in bold type and may form two disulfide bonds by similarity.



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3'5' Frame 2

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 61 gttgtagaaaggagcgtcgATGGCCTATATCAAAAGAATGAACCTGTTTTGTTTCTTTGC
 15  V  I  C  T  L  L  H  E  I  T  A  E  K  P  K  A  C  N  D  P
121 CGTCATTTGCACCCTGTTGCACGAGATAACAGCTGAGAAACCGAAAGCATGTAACGATCC
 35  I  I  P  G  K  I  M  P  W  C  D  A  L  S  I  R  Y  G  Y  E
181 TATAATACCCGGAAAAATAATGCCATGGTGTGACGCTCTATCGATAAGATATGGATACGA
 55  A  N  S  N  T  C  I  S  F  L  Y  T  G  C  K  I  D  T  D  N
241 AGCGAATTCTAACACTTGCATATCATTTCTGTATACTGGCTGCAAAATAGACACTGACAA
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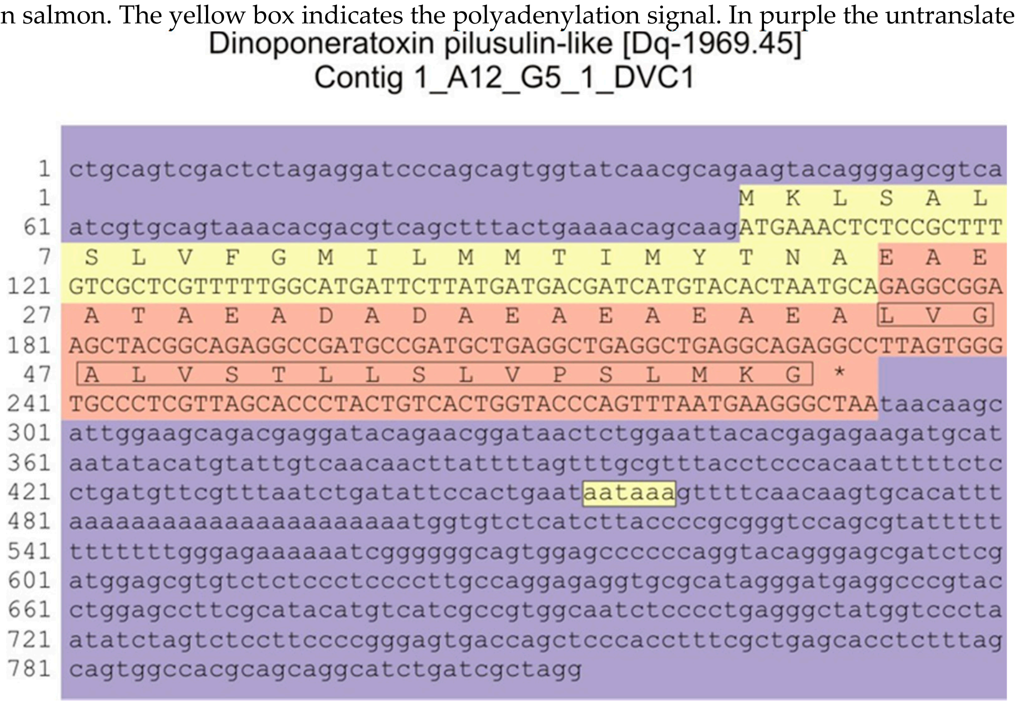
601 cttgaaatgtcgatgatgacgaggctaatgtaacaaaaatgaaataaaatatttgaacgc
661 ta                                    polyadenylation signal
```

Figure S8. The *D. quadriceps* venom component BPTI/Kunitz-serine protease inhibitor. The structural organization of transcript Contig511_B2-2 from the *D. quadriceps* venom gland, identified by peptide mass fingerprint mass spectrometry analysis is shown. The signal peptide is shown in yellow; The mature part in salmon. The yellow box indicates the polyadenylation signal. In purple the untranslated regions.



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  7  S  L  V  F  G  M  I  L  M  M  T  I  M  Y  T  N  A  E  A  E
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 27  A  T  A  E  A  D  A  D  A  E  A  E  A  E  A  E  A  L  V  G
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 47  A  L  V  S  T  L  L  S  L  V  P  S  L  M  K  G  *
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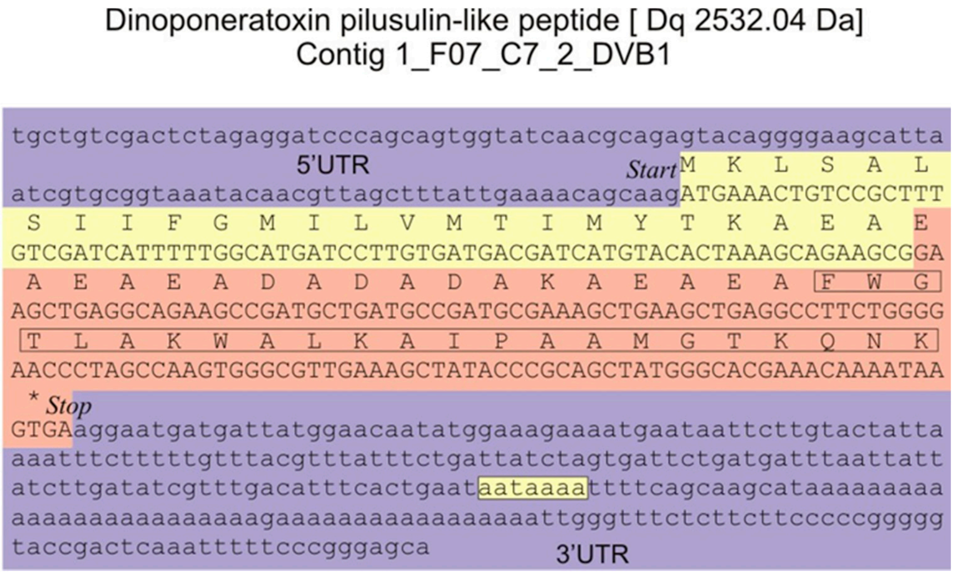
541 tttttttgggagaaaaaatcgggggcagtggagcccccaggtacagggagcgatctcg
601 atggagcgtgtctctccctccccttgccaggagaggtgcgcatagggatgaggcccgtac
661 ctggagccttcgcatacatgtcatcgccgtggcaatctcccctgagggctatggtcccta
721 atatctagtctccttccccgggagtgaccagctcccacctttcgctgagcacctctttag
781 cagtggccacgcagcaggcatctgatcgctagg
```

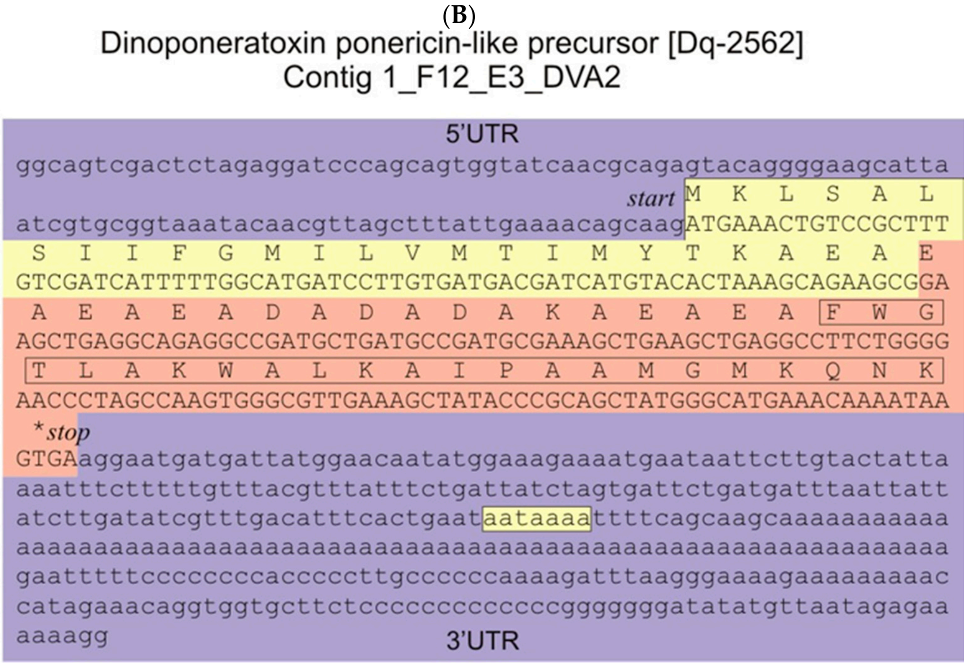
(**A**)



Dinoponeratoxin pilusulin-like peptide [Dq 2532.04 Da]
Contig 1_F07_C7_2_DVB1

```
  1 tgctgtcgactctagaggatcccagcagtggtatcaacgcagagtacaggggaagcatta
  1               5'UTR                        Start M  K  L  S  A  L
 61 atcgtgcggtaaatacaacgttagctttattgaaaacagcaagATGAAACTGTCCGCTTT
  7  S  I  I  F  G  M  I  L  V  M  T  I  M  Y  T  K  A  E  A  E
121 GTCGATCATTTTTGGCATGATCCTTGTGATGACGATCATGTACACTAAAGCAGAAGCGGA
 27  A  E  A  E  A  D  A  D  A  D  A  K  A  E  A  E  A  F  W  G
181 AGCTGAGGCAGAAGCCGATGCTGATGCCGATGCGAAAGCTGAAGCTGAGGCCTTCTGGGG
 47  T  L  A  K  W  A  L  K  A  I  P  A  A  M  G  T  K  Q  N  K
241 AACCCTAGCCAAGTGGGCGTTGAAAGCTATACCCGCAGCTATGGGCACGAAACAAAATAA
 67  * Stop
301 GTGAaggaatgatgattatggaacaatatggaaagaaaatgaataattcttgtactatta
361 aaatttctttttgtttacgtttatttctgattatctagtgattctgatgatttaattatt
421 atcttgatatcgtttgacatttcactgaataataaaattttcagcaagcataaaaaaaaa
481 aaaaaaaaaaaaaaaagaaaaaaaaaaaaaaaaaattgggtttctcttcttcccccggggg
541 taccgactcaaatttttcccgggagca                3'UTR
```

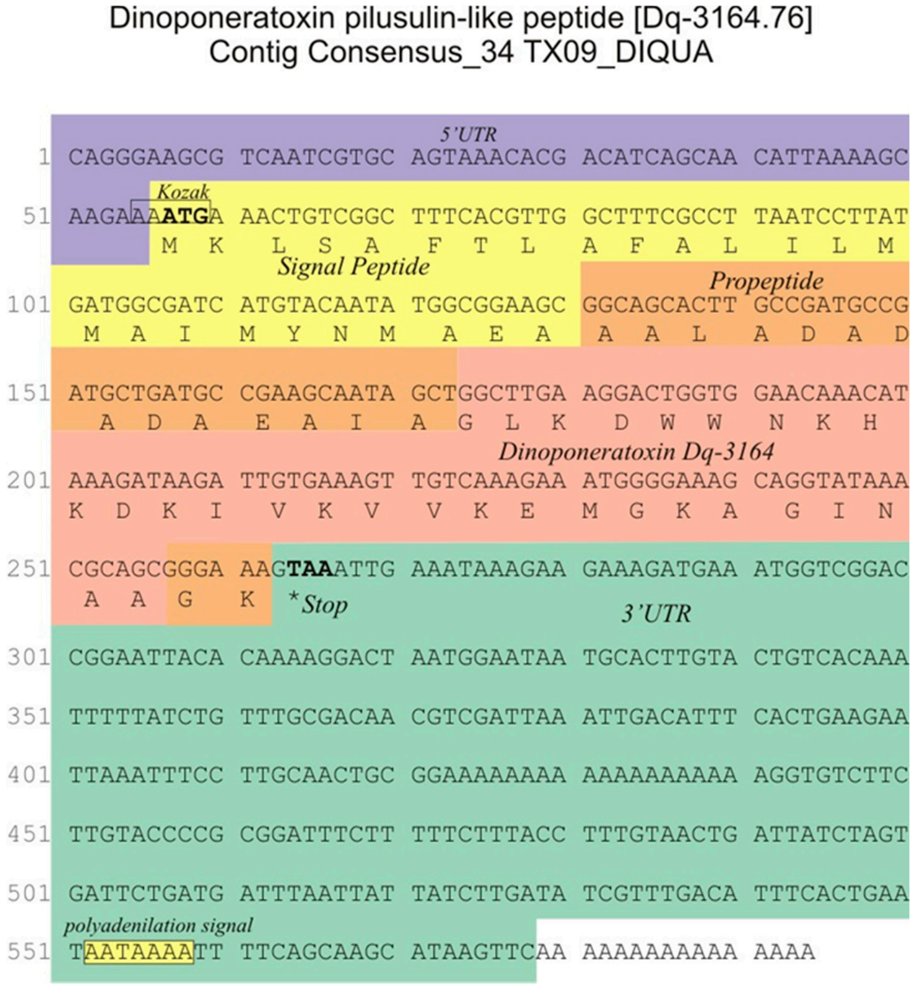
(**B**)



Dinoponeratoxin ponericin-like precursor [Dq-2562]
Contig 1_F12_E3_DVA2

```
                              5'UTR
  1 ggcagtcgactctagaggatcccagcagtggtatcaacgcagagtacaggggaagcatta
  1                                            start M  K  L  S  A  L
 61 atcgtgcggtaaatacaacgttagctttattgaaaacagcaagATGAAACTGTCCGCTTT
  7  S  I  I  F  G  M  I  L  V  M  T  I  M  Y  T  K  A  E  A  E
121 GTCGATCATTTTTGGCATGATCCTTGTGATGACGATCATGTACACTAAAGCAGAAGCGGA
 27  A  E  A  E  A  D  A  D  A  D  A  K  A  E  A  E  A  F  W  G
181 AGCTGAGGCAGAGGCCGATGCTGATGCCGATGCGAAAGCTGAAGCTGAGGCCTTCTGGGG
 47  T  L  A  K  W  A  L  K  A  I  P  A  A  M  G  M  K  Q  N  K
241 AACCCTAGCCAAGTGGGCGTTGAAAGCTATACCCGCAGCTATGGGCATGAAACAAAATAA
 67  *stop
301 GTGAaggaatgatgattatggaacaatatggaaagaaaatgaataattcttgtactatta
361 aaatttctttttgtttacgtttatttctgattatctagtgattctgatgatttaattatt
421 atcttgatatcgtttgacatttcactgaataataaaattttcagcaagcaaaaaaaaaaa
481 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
541 gaattttccccccccacccccttgccccccaaaagatttaagggaaaagaaaaaaaaac
601 catagaaacaggtggtgcttctccccccccccccgggggggatatatgttaatagagaa
661 aaaagg                         3'UTR
```

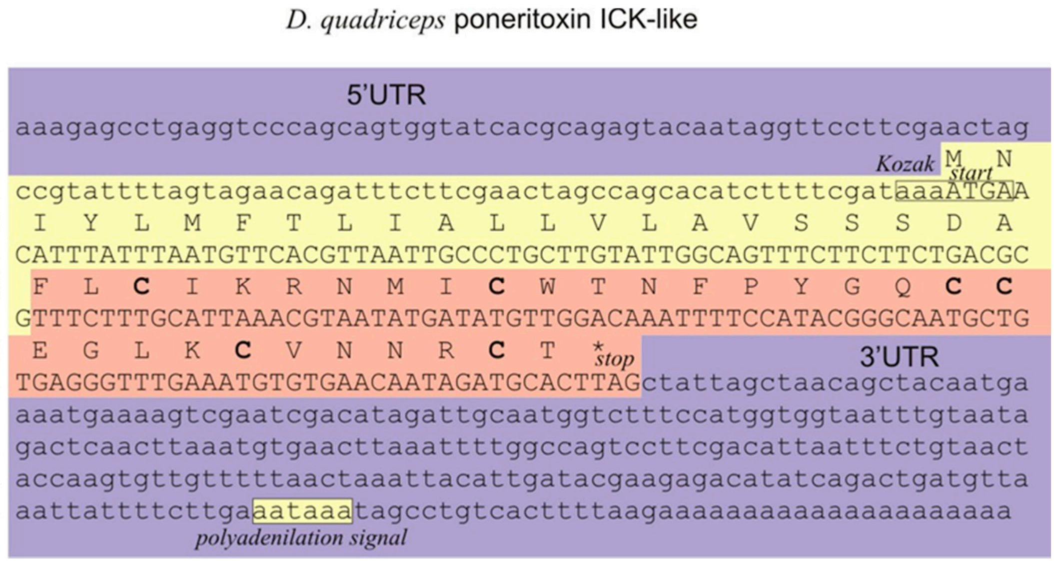
(**C**)



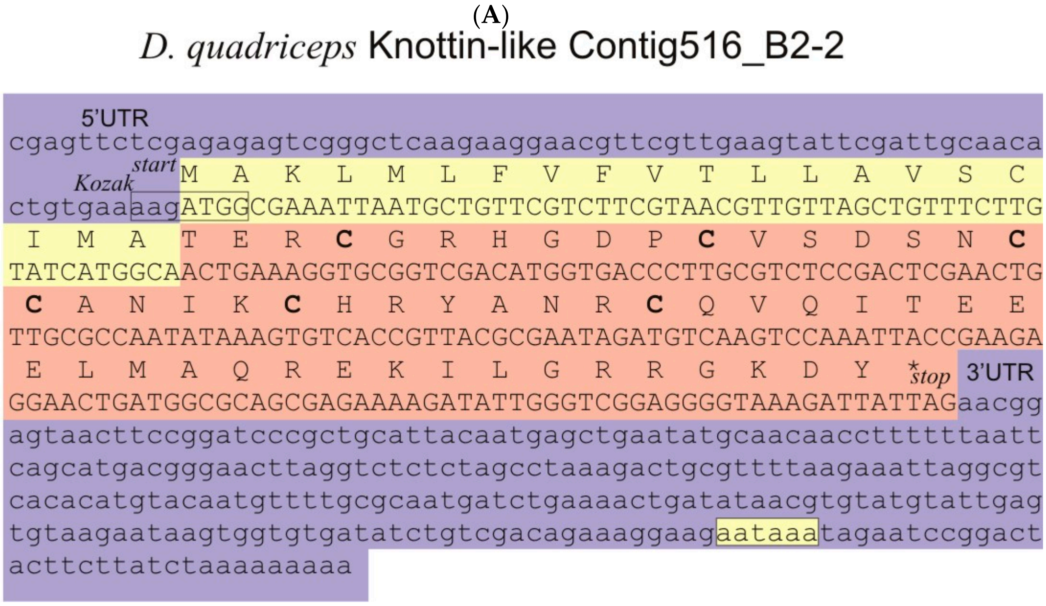
```
  1 CAGGGAAGCG TCAATCGTGC AGTAAACACG ACATCAGCAA CATTAAAAGC
 51 AAGAAAATGA AACTGTCGGC TTTCACGTTG GCTTTCGCCT TAATCCTTAT
          M  K   L  S  A   F  T  L   A  F  A  L   I  L  M
101 GATGGCGATC ATGTACAATA TGGCGGAAGC GGCAGCACTT GCCGATGCCG
     M  A  I   M  Y  N  M   A  E  A   A  A  L   A  D  A  D
151 ATGCTGATGC CGAAGCAATA GCTGGCTTGA AGGACTGGTG GAACAAACAT
      A  D  A   E  A  I   A  G  L  K   D  W  W   N  K  H
201 AAAGATAAGA TTGTGAAAGT TGTCAAAGAA ATGGGGAAAG CAGGTATAAA
    K  D  K  I   V  K  V   V  K  E   M  G  K  A   G  I  N
251 CGCAGCGGGA AAGTAAATTG AAATAAAGAA GAAAGATGAA ATGGTCGGAC
     A  A  G   K
301 CGGAATTACA CAAAAGGACT AATGGAATAA TGCACTTGTA CTGTCACAAA
351 TTTTTATCTG TTTGCGACAA CGTCGATTAA ATTGACATTT CACTGAAGAA
401 TTAAATTTCC TTGCAACTGC GGAAAAAAAA AAAAAAAAAA AGGTGTCTTC
451 TTGTACCCCG CGGATTTCTT TTTCTTTACC TTTGTAACTG ATTATCTAGT
501 GATTCTGATG ATTTAATTAT TATCTTGATA TCGTTTGACA TTTCACTGAA
551 TAATAAAATT TTCAGCAAGC ATAAGTTCAA AAAAAAAAAA AAAA
```

(**D**)

Figure S9. *D. quadriceps* venom gland transcript precursors for dinoponeratoxins (pilosulin- and ponericin-like peptides) with their respective peptide products, identified by proteomic analysis. The structural organization of transcrips and respective mature peptide, are as follow: **A.** Contig 1_A12_G5_1_DVC1 Pilosulin-like Precursor Peptide [Dq-1969]; **B**. Contig 1_F07_C7_2_DVB1 Pilosulin-like Precursor Peptide [Dq- 2532]; **C.** Contig Consensus 34 Pilosulin-like Precursor Peptide; **D.** Contig 1_F12_E3_DVA2 Pilosulin-like precursor peptide [Dq-2562]. In purple, the transcript untranslated regions (UTR) are shown; in yellow the signal of peptides as predicted by the SignalP 5.0 algorithm and in salmon the regions of the pro-peptide. A yellow box indicates the signal of polyadenylation convenience in every 3´-UTR sequence. The amino acid sequence of the mature peptide, of which fragments were identified by mass spectrometry analysis (this study) are indicated by open box or underlined.



(**A**)



(**B**)

Figure S10. Structural organization of transcripts encoding knottin (ICK)-like toxins from the venom gland of D. quadriceps, of which identifiers of mature peptides were found in the venom proteomics. A. Contig 1_D07_A11_4_DVB1 coding for an ICK-like toxin (U1-poneritoxin-Dq5a) similar to neurotoxins from honey bee and Conus sea snail. B. structural organization of the transcript contig516_B2-2 gi|578895399| encoding a toxin similar to neurotoxins from honey bee and the ponerine ant O. monticola. The 5 'and 3'-UTR transcript termini are shown in purple. The signal peptides were predicted by SignalP 5.0 and are indicated by yellow boxes. The mature peptides, of which the full sequences matched several peptide fragments identified by in-solution proteomics, are enlightened in pink color. The polyadenylation signal (AATAA) are indicated by yellow boxes. The start codon and the stop codon are indicated the conserved cysteines which may form disulfide bonds are indicated in bold.