```
MSRLIIVFIVVTMICSATALPSKKIIDEDEE-----DEKRSADVAGAVIDGASI
P61914 ACTP2 ACTEQ
                              1
                                                                                                      49
C9EIC7 ACTP1 URTCR
                              1
                                    -MNRLIVLCLFVAMIYATIALPKKEDISNDERSISVSKVPVKKSVAIAGAVIEGAKL
                                                                                                      56
Q93109 ACTP5 ACTEQ
                              1
                                 ----MSRLIIVFIVVTMICAATALSSKKSINEDEK-----DEKRSVAVAGAVIEGATI
                                                                                                      49
SEC-4-3103
                              1
                                 NFDEILRLSILYPATTGRV--IAIDVNDPLA-----PKPDGKP-----ENQF
                                                                                                      40
                                 SFDILKTVLEALGNVKRKIAVGVDNESGKTWTALNTYFRSGTSDIVLPHKVPHGKALLYN
P61914 ACTP2 ACTEQ
                             50
                                                                                                     109
                             57
                                 TEGILEKILTVLGDINRKIAIGVDNESGREWTAQNAYFFSGTSDVVLPASVPNTKAFLYN
                                                                                                     116
C9EIC7 ACTP1 URTCR
Q93109 ACTP5 ACTEQ
                             50
                                 TFNVLQTVLKALGDISRKIAVGIDNESGMTWTAMNTYFRSGTSDVILPHTVPHGKALLYN
                                                                                                     109
                                 AFSGEAKVL
                                                ----GIMALLDEGETDWKELGVDYFLE-
                                                                                                      72
SEC-4-3103
                             41
                                 GOKDRGPVATGAVGVLAYLMSDGNTLAVLESVPYDYNWYSIWWNVRIYKGKRRADORMYE
                           110
                                                                                                     169
P61914 ACTP2 ACTEQ
                                 AOKDRGPVATGVVGVLAYSLSNGNTLGILFSVPYDYNLYSNWWNIKLYKGIKRADRDMYN
C9EIC7 ACTP1 URTCR
                           117
                                                                                                     176
Q93109 ACTP5 ACTEQ
                           110
                                 GQKDRGPVATGVVGVLAYAMSDGNTLAVLFSIPFDYNLYSNWWNVKVYKGHRRADQRMYE
                                                                                                     169
                                 -RRELGVINIGGP---GFIEIDGAKLACS----VTHVWYLKFFSPRGFE---VFQNRKFS
SEC-4-3103
                            73
                                                                                                     121
                                 ELYYNLSPERGDNGWHTRNLGY--GLKSRGFMNSSGHAILEIHVSKA
P61914 ACTP2 ACTEQ
                           170
                                                                                                     214
                           177
                                 DLYYYAHPHKGDNGWHENSLGF--GLKSKGFMTSSGQTILQIRVSRA
                                                                                                     221
C9EIC7 ACTP1 URTCR
Q93109 ACTP5 ACTEQ
                           170
                                 ELYYNLSPERGDNGWHNRDLGY--GLKGRGFMNSSGQSILEIHVTKA
                                                                                                     214
                                 QIPYFSSY---DNVFRASDAGRKGGQHSGGNFK------
SEC-4-3103
                           122
                                                                                                     151
                                            ** ::
 Predicted cleavage site
    Cell attachment site motif
    Aromatic cluster
   ¬EqT II beta strand
 TEqT II helix
    Residues important for hemolytic activity
    Lipid binding site
```

Supplementary Figure 1. Alignments of the actinoporin-like protein from *M.complanata* (Spot 3103 SEC-4) and three model actinoporins. The accession numbers of the sequences used are as follows: DELTA-actitoxin-Aeq1a (Equinatoxin II from *Actinia equina*): P61914.; DELTA-actitoxin-Ucs1a (*Urticina crassicornis*): C9EIC7.; DELTA-actitoxin-Aeq1b (*Actinia equina*): Q93109. Sequences were aligned with ClustalW (default parameters). Identic (*), conserved(:) and, semi-conserved (.) amino acid residues are displayed.

🔨 Cysteine residue