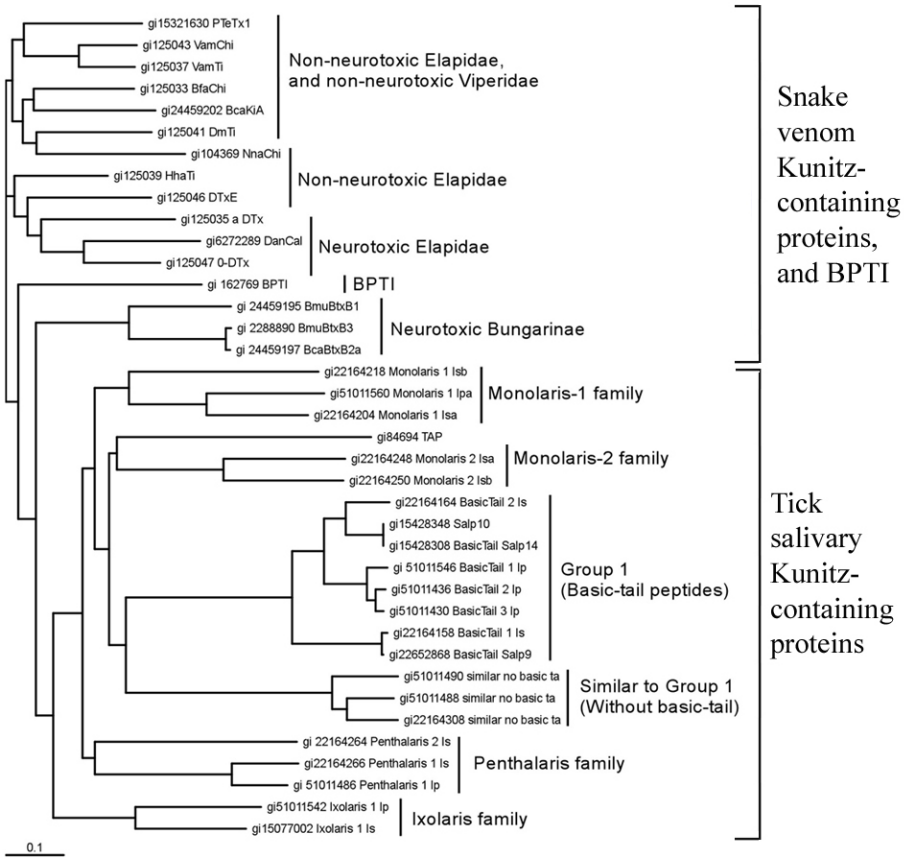
(A)

```
                   1                                                  60                                                  89
gi15321630_PTeT    -----------KDRPDFCELPAD-TGPCRV---RFPSFYYNPDEKKCLEFIYG-GCEGNANNFITKEECESTCAA--------------
gi125033_BfaChi    -----------KNRPTFCNLLPE-TGRCNA---LIPAFYYNSHLHKCQKFNYG-GCGGNANNFKTIDECQRTCAAKYGRSS--------
gi24459202_BcaK    -----------KDRPKFCNVPPE-PGRCNA---NVRAFYYNPRLRKCIEFTYG-GCGGNANNFKSRGECKRTCAE--------------
gi125043_VamChi    -----------RDRPKFCYLPAD-PGRCLA---YMPRFYYNPASNKCEKFIYG-GCRGNANNFKTWDECRHTCVASGIQPR--------
gi125041_DmTi      -----------HDRPTFCNLAPE-SGRCRG---HLRRIYYNLESNKCKVFFYG-GCGGNANNFETRDECRETCGGK-------------
gi125037_VamTi     -----------QDHPKFCYLPAD-PGRCKA---HIPRFYYDSASNKCNKFIYG-GCPGNANNFKTWDECRQTCGASA------------
gi104369_NnaChi    -------------RPRFCELAPS-AGSCFG---FVSSYYYNRYSNTCHSFTYS-GCGKNANRFRTIDECNRTCVV--------------
gi125046_DTxE      -----------LQHRTFCKLPAE-PGPCKA---SIPAFYYNWAAKKCQLFHYG-GCKGNANRFSTIEKCRHACVG--------------
gi125039_HhaTi     -------------RPDFCELPAE-TGLCKA---YIRSFHYNLAAQQCLQFIYG-GCGGNANRFKTIDECRRTCVG--------------
gi125035_a_DTx     -----------QPRRKLCILHRN-PGRCYD---KIPAFYYNQKKKQCERFDWS-GCGGNSNRFKTIEECRRTCIG--------------
gi6272289_DanCa    -----------WQPPWYCKEPVR-IGSCKK---QFSSFYFKWTAKKCLPFLFS-GCGGNANRFQTIGECRKKCLGK-------------
gi125047_0-DTx     -------------AAKYCKLPVR-YGPCKK---KIPSFYYKWKAKQCLPFDYS-GCGGNANRFKTIEECRRTCVG--------------
gi_2288890_BmuB    -----------RKRHPDCDKPPD-TKICQT---VVRAFYYKPSAKRCVQFRYG-GCNGNGNHFKSDHLCRCECLEYR------------
gi_24459195_Bmu    -----------RQRHRDCDKPPD-KGNCGS---VRRAFYYDTRLKTCKAFPYR-GCNGNGNHFKTETLCRCECLVYP------------
gi_24459197_Bca    -----------RKRHPDCDKPPD-TKICQT---VVRAFYYKPSAKRCVQFRYG-GCNGNGNHFKSDHLCRCECLEYP------------
gi_162769_BPTI     -------------RPDFCLEPPY-TGPCKA---RIIRYFYNAKAGLCQTFVYG-GCRAKRNNFKSAEDCMRTCGGAIGPWENL------
gi51011560_Mono    ------------LSKEDCEAPHA-TPQCAPNAILVTTYYNNGTHKCEEDY---NCAKGPMDFTTEEECKKACPYGIYASDR-------
gi22164204_Mono    ------------LSREVCEAPHA-MPQCAPGVTPRVTYYFNNGTGRCESDY---GCGNGRNDFPTAEKCRDACPYGIYASSG-------
gi22164218_Mono    -----------TLTEDECRAQLA-FSSCEANSTRVFYSFFNN-TNQCESYT---GCDTGKNRFPSLGKCINECPYGNHHPPGMRVRGTY
gi22164248_Mono    IVVEARMASQPIDNDALNGRCVK-PKECPG---NSKTVYYYDPKSGCQHIQLGADCTDNGN-YRTLAECNQYCLTPPGK----------
gi22164250_Mono    ---------TIIDNGELNPRCEK-PNDCPG---NQRTVFYYNRTAGCQQIRLGAGCSDNGN-YQTLDECLTKCAPPPGKQV--------
gi84694_TAP        -------------YNRLCIKPRDWIDECDSNE-GGERAYFRNGKGGCDSFWICPEDHTGADYYSSYRDCFNACI---------------
```

(B)



(C)

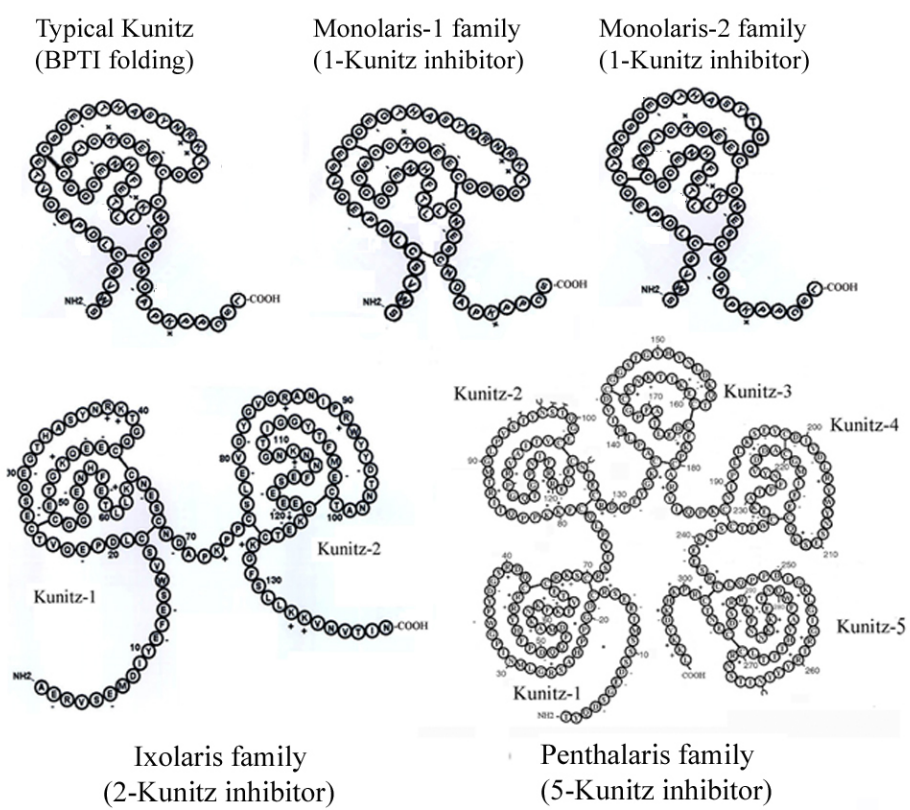


Figure 4