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          10      20      30      40      50      60      70
C.finmarchicus 22  DHFLQDPFFNSWSDMDKVRDHFAGQOTQMSKRFDNWSKRESSLNADNRNFSITVPASDPPMFKNLLM
A.franciscana 22  MITLVFW.TDQWT..DPWEDEPADLFEVETFTGRWRDPPFAA.....DVKPYGLPR.THLHR
C.quinquefasciatus 22 MSIIPIIF.RDSFM.....DDFMR.PSIMEKSLFDEFPA.....NLLVANIETR.RG...

          80      90      100     110     120     130     140
C.finmarchicus 22  PRKWMPKLFDDNFGSMLKMKDSNLLSMKNDITKMEISLDTAGYKPSSELTVNVSDGEISIEGKHEEKs..
A.franciscana 22  RRRRRRIRTVQRFES.....RKGTDVTRREDDKEWELITMQLPGFLPSDITVNSTDKELIVEGVHKEKRPDY
C.quinquefasciatus 22 EKRRRCCTCVTEN.....QQNNAVQKKSRES.FEVSIDVQNFKPEEISVVKMVDNYIITVEGKHEEKOD.

          150     160     170     180     190     200     210
C.finmarchicus 22  ..EEGHTMVSRQFSKKYTLPAEAKLIEVASNL.....
A.franciscana 22  EGEEGY..VSRREIRRFVPPKTIINPGEISSIFSSDCELRITAPKAIKPGE..PRQRRIQIMPAPIGSRFEG
C.quinquefasciatus 22 ..EEGF..VSRHFVRKYRLPEGHDIKVASLSSDCEVLTTRAPRLALPEVPAKERITPIIVRTEQIAEDFP

          ....|..
C.finmarchicus 22  .....
A.franciscana 22  ENEEEWP
C.quinquefasciatus 22 KSQKTAD

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Fig. A.4: Alignment of translated *Hsp22* sequences from *Calanus finmarchicus* (this study), *Artemia franciscana* (ABD19713), and *Culex quinquefasciatus* (XP_001847194). The *Hsp22*-like sequence identified in this study represents 168 amino acids aligned towards the 5' end of an approximately 200 amino acid long *Hsp22* protein.