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          10      20      30      40      50      60      70
C.finmarchicus 21 QMGSMQSMGQMGAVGGMOSQQTOSAKATQSVQAQOSILOTOQQAVESRQDVEDQDFFVPLKHTIAKVKKNA
A.franciscana 21 MSGMRLARSLLL.LGRPOSRLFWGR.....RLWDPFELR..MIMREMENQEQONINQNVFKA
B.mori 21      MADSGIKRNIPIKLGDFSVIDTEFSSIRERFDAE..MRKMEEEMSKFRSELMNRESNNPFKSTTTSTTSS

          80      90      100     110     120     130     140
C.finmarchicus 21 LS.....EATAMAKMRD...GVFELVNIHGFEPELVKIVCVQAVFVKAKH..VTAECF.V
A.franciscana 21 LPSSFK.....EETAVEVVISSKGDDNMYRLVLDLSEKPELVKIDLMDRNLRVTKCEOKTSDGCRM
B.mori 21      QHSDSRQLAEP SHWDSLNSPLIQDEGDGKTLKLRFDVSOYTPETVVKTVLNKLLVHAKHEEKSDTKS.V

          150     160     170     180     190     200
C.finmarchicus 21 NNVMQKFNLPEDVDTGKLTSGMSRDGILLIRVPRR..ASPERITAIKRDVQI.....DAVKKA
A.franciscana 21 YHETQREYLLPENVNLNELKSAFTDSGYLITEAPME.GMKPKETPINRGAQIESESKESKRED
B.mori 21      YREYNREFLLPKGTNPEATKSSLSRDGVLTVEAPLPQALITDRNIPLOKH.....

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Fig. A.3: Alignment of translated *Hsp21* sequences from *Calanus finmarchicus* (this study), *Artemia franciscana* (ABD19712), and *Bombyx mori* (BAD74197.1). The *Hsp21*-like sequence identified in this study represents 181 amino acids aligned towards the middle of an approximately 200 amino acid long Hsp21 protein.