```
CLUSTAL O(1.2.4) multiple sequence alignment


HA_NCBI        MKTIIALSYILCLVFAQKLPGNDNSTATLCLGHHAVPNGTLVKTITNDQIEVTNATELVQ    60
HA_pHW2000     -----------------------------------------------------------     0


HA_NCBI        SSSTGRICDSPHQILDGENCTLIDALLGDPHCDGFQNKEWDLFVERSKAYSNCYPYDVPD   120
HA_pHW2000     SKSRG*FY*P*R-------LSLL*----------------------ATFYVW---FSLKN    24
               *.* * :     :         :*:                     :. *     :.: :


HA_NCBI        YASLRSLVASSGTLEFNNESFNWTGVAQNGTSSAC-KRRSIKSFFSRLNWLHQLEN-RYP   178
HA_pHW2000     FPE----------MTTARQRCAWDTMQCQTER**KQSRMTKLK*LMLLSWFRVPQQVEYA    71
               :  .          :   .:    * : :      .* : . : *.*:: :: .*


HA_NCBI        -ALNVTMPNNDKFDKLYIWGVHHPSTDSVQTSVYVQASGRVTVSTKRSQQTVIPNIG---   234
HA_pHW2000     TVLTKSLMEKTAH**MLYWETHIVMASKIRNGTFLLNAAKPTATVTLMMCRIMPPLGH*L   128
                .*. :: ::  . :  * .*   :..::...:: :.: *.:..      ::* :*


HA_NCBI        --SRPWVRGVSS------------------------------------------------   244
HA_pHW2000     PHPAPWSLTMKASIGLESLRMEQALLAKGDLLTVSLVD*IGCTN*NTDIQH*T*LCQTMT   184
                  **    :.:


HA_NCBI        ------------------------------------------------------------   244
HA_pHW2000     NLTNCTFGGFTTRVRTVTKPAYIPHQGESQSLPKEANKL*SRISDPDPG*GVSPAE*ASI   241


HA_NCBI        ----RISIYWTIVKPGDILLINSTGNLIAPRGYFKIRSGKSSIMRSDAPIGKCNSECITP   300
HA_pHW2000     GQ**NRETYF*LTAQGI*LLLGVTSKY---------EVGKAQ**GQMHPLTNAILNASLQ   286
                   . . *: :. *  **:. *.:        . **:.   . *: :. :.


HA_NCBI        NGSIPNDKPFQNVNRITYGACPRYVKQNTLKLATGMRNVPEKQTRGIFGAIA-----GFI   355
HA_pHW2000     MEAFPMTNHFKM*TGSHMGPVPDMLSKTL*NWQQGCGMYQRNK-LEAYSAQSRVS*KMVG   342
                ::* : *: .     * * :.:. :  *    .::    :.* :       .


HA_NCBI        ENGWE-GMMDGWYGFRHQNSEGTGQAADLKSTQAAINQINGKLNRL--IEKTNEKFHQIE   412
HA_pHW2000     RE*WTVGTVSGIKILRAQDKQQILKALKQQSTKSTGN*IG*SRKRTRNSIKLKKNSQK*K   398
               .: *  * * :.*    :* *:.:    :* . :**::: * *. . :*     * ::: :: :


HA_NCBI        KEFSEVEGRIQDLEK---YVEDTKIDLWSYNAELLVALENQH-TIDLTDSE---MNKLFE   465
HA_pHW2000     GEFRTSRNMLRTLK*ISGRTTRSFLLPWRTNIQLI*LTQK*TNCLKEQGSN*EKMLRIWA   454
                 **    .. :: *:      .  : :  *   * *:*:    ::    :.  .*:    * :::


HA_NCBI        RTRKQLRENA--EDMGNGCF----KIYHKCDNACIGSIRNGTYDHDVYRDEALNNRFQIK   519
HA_pHW2000     MVVSKYTTNVTMPA*GQSEMELMTMMYTETKH*TTG-----------------SRSKVL   494
                . .:   *.       *:. :     :* : .:   *                 .* ::


HA_NCBI        GVELKSGYKDWILWISFAISCFLLCVVLLGF---------------IMWACQKGNIRCNI   564
HA_pHW2000     S*SQDTKIGSYGFPLPYHVICF----VLFCWGSLCGPAKKATLGATFAFECIN*KHPCFY   548
               . . .:   .: : : : : **    **: :                 : : * :: *


HA_NCBI        CI     566
HA_pHW2000     --     548
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