NA (1466 bp)

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AGCAAAAGCAGGAGTAAAGATGAATCCAAATCAAAAGATAATAACGATTGGCTCTGTTTCTCTCACCATT
GCCACAATATGCTTCCTTATGCAAATTGCCATCCTGGTAACTACTGTAACATTGCATTTCAAGCAATATG
AATGCAACTCCCCCCCAAACAACCAAGTGATGCTGTGTGAACCAACAATAATAGAAAGAAACATAACAGA
GATAGTGTATCTGACCAACACCACCATAGAGAAGGAAATATGCCCCAAACTAGCAAAATACAGAAATTGG
TCAAAGCCGCAATGTAACATTACAGGATTTGCACCTTTTTCTAAGGACAATTCGATTCGGCTTTCCGCTR
GTGGGGACATCTGGGTGACAAGAGAACCTTATGTGTCATGCGATCCTGACAAGTGTTATCAATTTGCCCT
TGGACAGGGAACAACACTAAACAACGGGCATTCAAATGACACAGTACATGATAGGACCCCTTATCGGACC
CTATTGATGAATGAGTTGGGTGTTCCATTTCATTTGGGAACCAAACAAGTGTGCATAGCATGGTCCAGCT
CAAGTTGTCACGATGGAAAAGCATGGCTGCATGTTTGTGTAACGGGGGATGATGAAAATGCAACTGCTAG
CTTCATTTACAATGGGAGGCTTGTAGATAGTATTGGTTCATGGTCCAAAAAAATCCTCAGGACCCAGGAG
TCGGAATGCGTTTGTATCAATGGAACTTGTACAGTAGTAATGACTGATGGGAGTGCTTCAGGAAAAGCTG
ATACTAAAATACTATTCATTGAGGAGGGGAAAATCGTTCATACTAGCCCATTGTCAGGAAGTGCTCAGCA
TGTCGAGGARTGCTCCTGTTATCCTCGATATCCTGGTGTCAGATGTGTCTGCAGAGACAACTGGAAAGGC
TCCAATAGGCCCATCGTAGATATAAATGTAAAGGATTATAGCATTGTTTCCAGTTATGTGTGCTCAGGAC
TTGTTGGAGACACACCCAGAAAAAACGACAGCTCCAGCAGTAGCCATTGCTTGGATCCTAACAATGAGGA
AGGTGGTCATGGAGTGAAAGGCTGGGCCTTTGATGATGGAAATGACGTGTGGATGGGAAGAACGATCAGC
GAGAAGTTACGCTCAGGATATGAAACCTTCAAAGTCATTGAAGGCTGGTCCAAACCYAACTCCAAATTGC
AGATAAATAGGCAAGTCATAGTTGACAGAGGTAATAGGTCCGGTTATTCTGGTATTTTCTCTGTTGAAGG
CAAAAGCTGCATCAATCGGTGCTTTTATGTGGAGTTGATAAGGGGAAGGAAACAGGAAACTGAAGTCTTG
TGGACCTCAAACAGTATTGTTGTGTTTTGTGGCACCTCAGGTACATATGGAACAGGCTCATGGCCTGATG
GGGCGGACATCAATCTCATGCCTATATAAGCTTTCGCAATTTTAGAAAAAAMTCCTTGTTTCTACT
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NA protein

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MNPNQKIITIGSVSLTIATICFLMQIAILVTTVTLHFKQYECNSPPNNQVMLCEPTIIERNITEIVYLTN
TTIEKEICPKLAKYRNWSKPQCNITGFAPFSKDNSIRLSAXGDIWVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVHDRTPYRTLLMNELGVPFHLGTKQVCIAWSSSSCHDGKAWLHVCVTGDDENATASFIYNGR
LVDSIGSWSKKILRTQESECVCINGTCTVVMTDGSASGKADTKILFIEEGKIVHTSPLSGSAQHVEECSC
YPRYPGVRCVCRDNWKGSNRPIVDINVKDYSIVSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVWMGRTISEKLRSGYETFKVIEGWSKPNSKLQINRQVIVDRGNRSGYSGIFSVEGKSCINR
CFYVELIRGRKQETEVLWTSNSIVVFCGTSGTYGTGSWPDGADINLMPI
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NA (1466 bp)

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NNNNNNAGCAGGAGTAAAGATGAATCCAAATCAAAAGATAATAACGATTGGCTCTGTTTCTC
TCACCATTGCCACAATATGCTTCCTTATGCAAATTGCCATCCTGGTAACTACTGTAACATTG
CATTTCAAGCAATATGAATGCAACTCCCCCCCAAACAACCAAGTGATGCTGTGTGAACCAAC
AATAATAGAAAGAAACATAACAGAGATAGTGTATCTGACCAACACCACCATAGAGAAGGAAA
TATGCCCCAAACTAGCAGAATACAGAAATTGGTCAAAGCCGCAATGTAACATTACAGGATTT
GCACCTTTTTCTAAGGACAATTCGATTCGGCTTTCCGCTGGTGGGGACATCTGGGTGACAAG
AGAACCTTATGTGTCATGCGATCCTGACAAGTGTTATCAATTTGCCCTTGGACAGGGAACAA
CACTAAACAACGGGCATTCAAATGACACAGTACATGATAGGACCCCTTATCGGACCCTATTG
ATGAATGAGTTGGGTGTTCCATTTCATTTGGGAACCAAGCAAGTGTGCATAGCATGGTCCAG
CTCAAGTTGTCACGATGGAAAAGCATGGCTGCATGTTTGTGTAACGGGGGATGATGAAAATG
CAACTGCTAGCTTCATTTACAATGGGAGGCTTGTAGATAGTATTGGTTCATGGTCCAAAAAA
ATCCTCAGGACCCAGGAGTCGGAATGCGTTTGTATCAATGGAACTTGTACAGTAGTAATGAC
TGATGGGAGTGCTTCAGGAAAGCTGATACTAAAATACTATTCATTGAGGAGGGGAAAATCG
TTCATACTAGCCCATTGTCAGGAAGTGCTCAGCATGTCGAGGAATGCTCCTGTTATCCTCGA
TATCCTGGTGTCAGATGTGTCTGCAGAGACAACTGGAAAGGCTCCAATAGGCCCATCGTAGA
TATAAATGTAAAGGATTATAGCATTGTTTCCAGTTATGTGTGCTCAGGACTTGTTGGAGACA
CACCCAGAAAAAACGACAGCTCCAGCAGTAGCCATTGCTTGGATCCTAACAATGAGGAAGGT
GGTCATGGAGTGAAAGGCTGGGCCTTTGATGATGGAAATGACGTGTGGATGGGAAGAACGAT
CAGCGAGAAGTTACGCTCAGGATATGAAACCTTCAAAGTCATTGAAGGCTGGTCCAAACCCA
ACTCCAAATTGCAGATAAATAGGCAAGTCATAGTTGACAGAGGTAATAGGTCCGGTTATTCT
GGTATTTTCTCTGTTGAAGGCAAAAGCTGCATCAATCGGTGCTTTTATGTGGAGTTGATAAG
GGGAAGGAAACAGGAAACTGAAGTCTTGTGGACCTCAAACAGTATTGTTGTGTTTTGTGGCA
CCTCAGGTACATATGGAACAGGCTCATGGCCTGATGGGGCGGACATCAATCTCATGCCTATA
TAAGCTTTCGCAATTTTAGAAAAAACTNNNNNNNNNNNN
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NA (1466 bp)

AGCAAAAGCAGGAGTAAAG**ATG**AATCCAAATCAAAAGATAATAACGATTGGCTCTGTTTCTC
TCACCATTGCCACAATATGCTTCCTTATGCAAATTGCCATCCTGGTAACTACTGTAACATTG
CATTTCAAGCAATATGAATGCAACTCCCCCCCAAACAACCAAGTGATGCTGTGTGAACCAAC
AATAATAGAAAGAAACATAACAGAGATAGTGTATCTGACCAACACCACCATAGAGAAGGAAA
TATGCCCCAAACTAGCAGAATACAGAAATTGGTCAAAGCCGCAATGTAACATTACAGGATTT
GCACCTTTTTCTAAGGACAATTCGATTCGGCTTTCCGCTGGTGGGGACATCTGGGTGACAAG
AGAACCTTATGTGTCATGCGATCCTGACAAGTGTTATCAATTTGCCCTTGGACAGGGAACAA
CACTAAACAACGGGCATTCAAATGACACAGTACATGATAGGACCCCTTATCGGACCCTATTG
ATGAATGAGTTGGGTGTTCCATTTCATTTGGGAACCAAGCAAGTGTGCATAGCATGGTCCAG
CTCAAGTTGTCACGATGGAAAAGCATGGCTGCATGTTTGTGTAACGGGGGATGATGAAAATG
CAACTGCTAGCTTCATTTACAATGGGAGGCTTGTAGATAGTATTGGTTCATGGTCCAAAAAA
ATCCTCAGGACCCAGGAGTCGGAATGCGTTTGTATCAATGGAACTTGTACAGTAGTAATGAC
TGATGGGAGTGCTTCAGGAAAAGCTGATACTAAAATACTATTCATTGAGGAGGGGAAAATCG
TTCATACTAGCCCATTGTCAGGAAGTGCTCAGCATGTCGAGGAATGCTCCTGTTATCCTCGA
TATCCTGGTGTCAGATGTGTCTGCAGAGACAACTGGAAAGGCTCCAATAGGCCCATCGTAGA
TATAAATGTAAAGGATTATAGCATTGTTTCCAGTTATGTGTGCTCAGGACTTGTTGGAGACA
CACCCAGAAAAAACGACAGCTCCAGCAGTAGCCATTGCTTGGATCCTAACAATGAGGAAGGT
GGTCATGGAGTGAAAGGCTGGGCCTTTGATGATGGAAATGACGTGTGGATGGGAAGAACGAT
CAGCGAGAAGTTACGCTCAGGATATGAAACCTTCAAAGTCATTGAAGGCTGGTCCAAACCCA
ACTCCAAATTGCAGATAAATAGGCAAGTCATAGTTGACAGAGGTAATAGGTCCGGTTATTCT
GGTATTTTCTCTGTTGAAGGCAAAAGCTGCATCAATCGGTGCTTTTATGTGGAGTTGATAAG
GGGAAGGAAACAGGAAACTGAAGTCTTGTGGACCTCAAACAGTATTGTTGTGTTTTGTGGCA
CCTCAGGTACATATGGAACAGGCTCATGGCCTGATGGGGCGGACATCAATCTCATGCCTATA
TAAGCTTTCGCAATTTTAGAAAAAACTCCTTGTTTCTACT

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CLUSTAL O(1.2.4) multiple sequence alignment


MO_NA_Virus      NNNNNNAGCAGGAGTAAAGATGAATCCAAATCAAAAGATAATAACGATTGGCTCTGTTTC 60
MO_NA_NCBI       AGCAAAAGCAGGAGTAAAGATGAATCCAAATCAAAAGATAATAACGATTGGCTCTGTTTC 60
MO_NA_pHW2000    AGCAAAAGCAGGAGTAAAGATGAATCCAAATCAAAAGATAATAACGATTGGCTCTGTTTC 60
                         *********************************************************

MO_NA_Virus      TCTCACCATTGCCACAATATGCTTCCTTATGCAAATTGCCATCCTGGTAACTACTGTAAC 120
MO_NA_NCBI       TCTCACCATTGCCACAATATGCTTCCTTATGCAAATTGCCATCCTGGTAACTACTGTAAC 120
MO_NA_pHW2000    TCTCACCATTGCCACAATATGCTTCCTTATGCAAATTGCCATCCTGGTAACTACTGTAAC 120
                 ************************************************************

MO_NA_Virus      ATTGCATTTCAAGCAATATGAATGCAACTCCCCCCCAAACAACCAAGTGATGCTGTGTGA 180
MO_NA_NCBI       ATTGCATTTCAAGCAATATGAATGCAACTCCCCCCCAAACAACCAAGTGATGCTGTGTGA 180
MO_NA_pHW2000    ATTGCATTTCAAGCAATATGAATGCAACTCCCCCCCAAACAACCAAGTGATGCTGTGTGA 180
                 ************************************************************

MO_NA_Virus      ACCAACAATAATAGAAAGAAACATAACAGAGATAGTGTATCTGACCAACACCACCATAGA 240
MO_NA_NCBI       ACCAACAATAATAGAAAGAAACATAACAGAGATAGTGTATCTGACCAACACCACCATAGA 240
MO_NA_pHW2000    ACCAACAATAATAGAAAGAAACATAACAGAGATAGTGTATCTGACCAACACCACCATAGA 240
                 ************************************************************

MO_NA_Virus      GAAGGAAATATGCCCCAAACTAGCAGAATACAGAAATTGGTCAAAGCCGCAATGTAACAT 300
MO_NA_NCBI       GAAGGAAATATGCCCCAAACTAGCAAAATACAGAAATTGGTCAAAGCCGCAATGTAACAT 300
MO_NA_pHW2000    GAAGGAAATATGCCCCAAACTAGCAGAATACAGAAATTGGTCAAAGCCGCAATGTAACAT 300
                 *************************  *********************************

MO_NA_Virus      TACAGGATTTGCACCTTTTTCTAAGGACAATTCGATTCGGCTTTCCGCTGGTGGGGACAT 360
MO_NA_NCBI       TACAGGATTTGCACCTTTTTCTAAGGACAATTCGATTCGGCTTTCCGCTRGTGGGGACAT 360
MO_NA_pHW2000    TACAGGATTTGCACCTTTTTCTAAGGACAATTCGATTCGGCTTTCCGCTGGTGGGGACAT 360
                 ************************************************* *********

MO_NA_Virus      CTGGGTGACAAGAGAACCTTATGTGTCATGCGATCCTGACAAGTGTTATCAATTTGCCCT 420
MO_NA_NCBI       CTGGGTGACAAGAGAACCTTATGTGTCATGCGATCCTGACAAGTGTTATCAATTTGCCCT 420
MO_NA_pHW2000    CTGGGTGACAAGAGAACCTTATGTGTCATGCGATCCTGACAAGTGTTATCAATTTGCCCT 420
                 ************************************************************

MO_NA_Virus      TGGACAGGGAACAACACTAAACAACGGGCATTCAAATGACACAGTACATGATAGGACCCC 480
MO_NA_NCBI       TGGACAGGGAACAACACTAAACAACGGGCATTCAAATGACACAGTACATGATAGGACCCC 480
MO_NA_pHW2000    TGGACAGGGAACAACACTAAACAACGGGCATTCAAATGACACAGTACATGATAGGACCCC 480
                 ************************************************************

MO_NA_Virus      TTATCGGACCCTATTGATGAATGAGTTGGGTGTTCCATTTCATTTGGGAACCAAGCAAGT 540
MO_NA_NCBI       TTATCGGACCCTATTGATGAATGAGTTGGGTGTTCCATTTCATTTGGGAACCAAACAAGT 540
MO_NA_pHW2000    TTATCGGACCCTATTGATGAATGAGTTGGGTGTTCCATTTCATTTGGGAACCAAGCAAGT 540
                 ******************************************************  *****

MO_NA_Virus      GTGCATAGCATGGTCCAGCTCAAGTTGTCACGATGGAAAAGCATGGCTGCATGTTTGTGT 600
MO_NA_NCBI       GTGCATAGCATGGTCCAGCTCAAGTTGTCACGATGGAAAAGCATGGCTGCATGTTTGTGT 600
MO_NA_pHW2000    GTGCATAGCATGGTCCAGCTCAAGTTGTCACGATGGAAAAGCATGGCTGCATGTTTGTGT 600
                 ************************************************************

MO_NA_Virus      AACGGGGGATGATGAAAATGCAACTGCTAGCTTCATTTACAATGGGAGGCTTGTAGATAG 660
MO_NA_NCBI       AACGGGGGATGATGAAAATGCAACTGCTAGCTTCATTTACAATGGGAGGCTTGTAGATAG 660
MO_NA_pHW2000    AACGGGGGATGATGAAAATGCAACTGCTAGCTTCATTTACAATGGGAGGCTTGTAGATAG 660
                 ************************************************************

MO_NA_Virus      TATTGGTTCATGGTCCAAAAAAATCCTCAGGACCCAGGAGTCGGAATGCGTTTGTATCAA 720
MO_NA_NCBI       TATTGGTTCATGGTCCAAAAAAATCCTCAGGACCCAGGAGTCGGAATGCGTTTGTATCAA 720
MO_NA_pHW2000    TATTGGTTCATGGTCCAAAAAAATCCTCAGGACCCAGGAGTCGGAATGCGTTTGTATCAA 720
                 ************************************************************

MO_NA_Virus      TGGAACTTGTACAGTAGTAATGACTGATGGGAGTGCTTCAGGAAAAGCTGATACTAAAAT 780
MO_NA_NCBI       TGGAACTTGTACAGTAGTAATGACTGATGGGAGTGCTTCAGGAAAAGCTGATACTAAAAT 780
MO_NA_pHW2000    TGGAACTTGTACAGTAGTAATGACTGATGGGAGTGCTTCAGGAAAAGCTGATACTAAAAT 780
                 ************************************************************

MO_NA_Virus      ACTATTCATTGAGGAGGGGAAAATCGTTCATACTAGCCCATTGTCAGGAAGTGCTCAGCA 840
MO_NA_NCBI       ACTATTCATTGAGGAGGGGAAAATCGTTCATACTAGCCCATTGTCAGGAAGTGCTCAGCA 840
MO_NA_pHW2000    ACTATTCATTGAGGAGGGGAAAATCGTTCATACTAGCCCATTGTCAGGAAGTGCTCAGCA 840
                 ************************************************************

MO_NA_Virus      TGTCGAGGAATGCTCCTGTTATCCTCGATATCCTGGTGTCAGATGTGTCTGCAGAGACAA 900
MO_NA_NCBI       TGTCGAGGARTGCTCCTGTTATCCTCGATATCCTGGTGTCAGATGTGTCTGCAGAGACAA 900
MO_NA_pHW2000    TGTCGAGGAATGCTCCTGTTATCCTCGATATCCTGGTGTCAGATGTGTCTGCAGAGACAA 900
                 ********* **************************************************

MO_NA_Virus      CTGGAAAGGCTCCAATAGGCCCATCGTAGATATAAATGTAAAGGATTATAGCATTGTTTC 960
MO_NA_NCBI       CTGGAAAGGCTCCAATAGGCCCATCGTAGATATAAATGTAAAGGATTATAGCATTGTTTC 960
MO_NA_pHW2000    CTGGAAAGGCTCCAATAGGCCCATCGTAGATATAAATGTAAAGGATTATAGCATTGTTTC 960
                 ************************************************************

MO_NA_Virus      CAGTTATGTGTGCTCAGGACTTGTTGGAGACACACCCAGAAAAAACGACAGCTCCAGCAG 1020
MO_NA_NCBI       CAGTTATGTGTGCTCAGGACTTGTTGGAGACACACCCAGAAAAAACGACAGCTCCAGCAG 1020
MO_NA_pHW2000    CAGTTATGTGTGCTCAGGACTTGTTGGAGACACACCCAGAAAAAACGACAGCTCCAGCAG 1020
                 ************************************************************

MO_NA_Virus      TAGCCATTGCTTGGATCCTAACAATGAGGAAGGTGGTCATGGAGTGAAAGGCTGGGCCTT 1080
MO_NA_NCBI       TAGCCATTGCTTGGATCCTAACAATGAGGAAGGTGGTCATGGAGTGAAAGGCTGGGCCTT 1080
MO_NA_pHW2000    TAGCCATTGCTTGGATCCTAACAATGAGGAAGGTGGTCATGGAGTGAAAGGCTGGGCCTT 1080
                 ************************************************************

MO_NA_Virus      TGATGATGGAAATGACGTGTGGATGGGAAGAACGATCAGCGAGAAGTTACGCTCAGGATA 1140
MO_NA_NCBI       TGATGATGGAAATGACGTGTGGATGGGAAGAACGATCAGCGAGAAGTTACGCTCAGGATA 1140
MO_NA_pHW2000    TGATGATGGAAATGACGTGTGGATGGGAAGAACGATCAGCGAGAAGTTACGCTCAGGATA 1140
                 ************************************************************

MO_NA_Virus      TGAAACCTTCAAAGTCATTGAAGGCTGGTCCAAACCCAACTCCAAATTGCAGATAAATAG 1200
MO_NA_NCBI       TGAAACCTTCAAAGTCATTGAAGGCTGGTCCAAACCYAACTCCAAATTGCAGATAAATAG 1200
MO_NA_pHW2000    TGAAACCTTCAAAGTCATTGAAGGCTGGTCCAAACCCAACTCCAAATTGCAGATAAATAG 1200
                 ************************************ ***********************

MO_NA_Virus      GCAAGTCATAGTTGACAGAGGTAATAGGTCCGGTTATTCTGGTATTTTCTCTGTTGAAGG 1260
MO_NA_NCBI       GCAAGTCATAGTTGACAGAGGTAATAGGTCCGGTTATTCTGGTATTTTCTCTGTTGAAGG 1260
MO_NA_pHW2000    GCAAGTCATAGTTGACAGAGGTAATAGGTCCGGTTATTCTGGTATTTTCTCTGTTGAAGG 1260
                 ************************************************************

MO_NA_Virus      CAAAAGCTGCATCAATCGGTGCTTTTATGTGGAGTTGATAAGGGGAAGGAAACAGGAAAC 1320
MO_NA_NCBI       CAAAAGCTGCATCAATCGGTGCTTTTATGTGGAGTTGATAAGGGGAAGGAAACAGGAAAC 1320
MO_NA_pHW2000    CAAAAGCTGCATCAATCGGTGCTTTTATGTGGAGTTGATAAGGGGAAGGAAACAGGAAAC 1320
                 ************************************************************

MO_NA_Virus      TGAAGTCTTGTGGACCTCAAACAGTATTGTTGTGTTTTGTGGCACCTCAGGTACATATGG 1380
MO_NA_NCBI       TGAAGTCTTGTGGACCTCAAACAGTATTGTTGTGTTTTGTGGCACCTCAGGTACATATGG 1380
MO_NA_pHW2000    TGAAGTCTTGTGGACCTCAAACAGTATTGTTGTGTTTTGTGGCACCTCAGGTACATATGG 1380
                 ************************************************************

MO_NA_Virus      AACAGGCTCATGGCCTGATGGGGCGGACATCAATCTCATGCCTATATAAGCTTTCGCAAT 1440
MO_NA_NCBI       AACAGGCTCATGGCCTGATGGGGCGGACATCAATCTCATGCCTATATAAGCTTTCGCAAT 1440
MO_NA_pHW2000    AACAGGCTCATGGCCTGATGGGGCGGACATCAATCTCATGCCTATATAAGCTTTCGCAAT 1440
                 ************************************************************

MO_NA_Virus      TTTAGAAAAAACTNNNNNNNNNNNNN    1466
MO_NA_NCBI       TTTAGAAAAAAMTCCTTGTTTCTACT    1466
MO_NA_pHW2000    TTTAGAAAAAACTCCTTGTTTCTACT    1466
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CLUSTAL O(1.2.4) multiple sequence alignment


NA_NCBI          MNPNQKIITIGSVSLTIATICFLMQIAILVTTVTLHFKQYECNSPPNNQVMLCEPTIIER     60
NA_pHW2000       ------------------------------------------------------------      0


NA_NCBI          NITEIVYLTNTTIEKEICPKLAKYRNWSKPQCNITGFAPFSKDNSIRLSAXGDIW-----    115
NA_pHW2000       --------------------------SK---------SRSKD--ESKSKDNNDWLCFSH     22
                                           **         ***      *  .: *

NA_NCBI          --VTREPYVSCDPDKCYQFALGQGT-TL--------------NNGHSNDTVHDRTPYRTL    158
NA_pHW2000       HCHNMLPYANCHPGNYCNIAFQAI*MQLPPKQPSDAV*TNNNRKKHNRDSVSDQHHHREG     80
                   .  **..*.*.:  ::*:      *          .: *..*:* *:  :*

NA_NCBI          LMNELG-----VPFHLGTKQVCIAWSSSSCHDGKAWLHVCVTGDDENATASFIYNGRLVD    213
NA_pHW2000       NMPQTSRIQKLVKAAM*HYRICTFF*GQFDSAFRWWGHL---GDKR---TLCVMRS*QVL    131
                    * : .      *    :   ::*  : ..     : * *:   **..   :  :.. *

NA_NCBI          SIGSWSKKILRTQESECVCINGTCTVVMTDGSASGKADTKILFIEEGKIVHTSPL-SGSA    272
NA_pHW2000       SICPWTGNNTKQRAFK*---HST**DPLSDP-IDE*VGCSISFGNQASVHSMVQLKLSRW    183
                 **  *: :  : :  :      :.*      ::*   .  .. .* * ::..:    *  .

NA_NCBI          QHVEECSCYPRYPGVRCVCRDNWKGSNRPIVDINVKDYSIVSSYVCSGLVGDTPRKNDSS    332
NA_pHW2000       KSMAACLCNGG**KCNC*LHLQWEACR*YWFM----------------------------    211
                  : :  * *      .*  : :*:...   .

NA_NCBI          SSSHCLDPNNEEGGHGVKGWAFDDGNDVWMGRTISEK---LRSGYET--FK---------    378
NA_pHW2000       ---VQKNPQDPGVGMRLYQWNLYSSND*WECFRKS*Y*NTIH*GGENRSY*PIVRKCSAC    263
                    :*::    *  :  * :..** *      *    ::  * *.  :

NA_NCBI          ------VIEGWSKPNSKLQINRQVIVDRGNRSGYSGIFSVEGKSCINRCFYVELIRGRKQ    432
NA_pHW2000       RGMLLLSSISWCQMCLQRQLERLQ*AH--RRYKCKG---------L*HCFQLCVLRTCWR    310
                       .*.:  :  * *::*   ..  .*   .*        : :** : ::*   :

NA_NCBI          ETEVLWTSNSIVVFCGTSGTYGTGSWPDGADINLMPI-----------------------    469
NA_pHW2000       HTQKK----RQLQQ*PLLGS*Q*GRWSWSERLGL**WK*RVDGKNDQREVTLRI*NLQSH    359
                 .*:       :      *:   * *  . :.*

NA_NCBI          ------------------------------------------------------------    469
NA_pHW2000       *RLVQTQLQIADK*ASHS*QR**VRLFWYFLC*RQKLHQSVLLCGVDKGKETGN*SLVDL    412


NA_NCBI          ----------------------------------------     469
NA_pHW2000       KQYCCVLWHLRYIWNRLMA*WGGHQSHAYISFRNFRKNSLFL    453
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