CLUSTAL O(1.2.4) multiple sequence alignment

NA_NCBI NA_pHW2000	MNPNQKIITIGSVSLTIATICFLMQIAILVTTVTLHFKQYECNSPPNNQVMLCEPTIIER (
NA_NCBI NA_pHW2000	NITEIVYLTNTTIEKEICPKLAKYRNWSKPQCNITGFAPFSKDNSIRLSAXGDIWSRSKDESKSKDNNDWLCFSH ** *** * .: *
NA_NCBI NA_pHW2000	VTREPYVSCDPDKCYQFALGQGT-TLNNGHSNDTVHDRTPYRTL HCHNMLPYANCHPGNYCNIAFQAI*MQLPPKQPSDAV*TNNNRKKHNRDSVSDQHHHREG . ***.*: :: *: *: :: :: :: :: :: :: :: :: :: :
NA_NCBI NA_pHW2000	LMNELGVPFHLGTKQVCIAWSSSSCHDGKAWLHVCVTGDDENATASFIYNGRLVD NMPQTSRIQKLVKAAM*HYRICTFF*GQFDSAFRWWGHLGDKRTLCVMRS*QVL *:. *:. *: *:. *
NA_NCBI NA_pHW2000	SIGSWSKKILRTQESECVCINGTCTVVMTDGSASGKADTKILFIEEGKIVHTSPL-SGSA SICPWTGNNTKQRAFK*HST**DPLSDP-IDE*VGCSISFGNQASVHSMVQLKLSRW ** *:: : : : : : : : : : : : : : : : :
NA_NCBI NA_pHW2000	QHVEECSCYPRYPGVRCVCRDNWKGSNRPIVDINVKDYSIVSSYVCSGLVGDTPRKNDSS KSMAACLCNGG**KCNC*LHLQWEACR*YWFM
NA_NCBI NA_pHW2000	SSSHCLDPNNEEGGHGVKGWAFDDGNDVWMGRTISEKLRSGYETFK
NA_NCBI NA_pHW2000	VIEGWSKPNSKLQINRQVIVDRGNRSGYSGIFSVEGKSCINRCFYVELIRGRKQ RGMLLLSSISWCQMCLQRQLERLQ*AHRRYKCKGL*HCFQLCVLRTCWR .*.: : *::** .* .* ::**:::* :
NA_NCBI NA_pHW2000	ETEVLWTSNSIVVFCGTSGTYGTGSWPDGADINLMPI
NA_NCBI NA_pHW2000	*RLVQTQLQIADK*ASHS*QR**VRLFWYFLC*RQKLHQSVLLCGVDKGKETGN*SLVDL
NA_NCBI NA_pHW2000	469 KQYCCVLWHLRYIWNRLMA*WGGHQSHAYISFRNFRKNSLFL 453