CLUSTAL O(1.2.4) multiple sequence alignment

NA_NCBI NA_pHW2000	MNPNQKIITIGSICLVVGLISLILQIGNIISIWISHSIQTGSQNHTGICNSKSRSLK*IQIRK**PLDQSVW*SD*LA*YCK*GI*SQYGLAIQFKLEV .* .: *:: * .: * :: *::	50 41
NA_NCBI NA_pHW2000	QNIITYKNSTWVKDTTSVILTGNSSLCPIRGWAIYSKDNSIRIGSKGDVFV KTILEYATKTSLPIKIAPG*RTQLQ*Y*PAIHLFVPSVGGLYTAKTIA*ELV :.*: ** : * * : * * : * * : *	101 89
NA_NCBI NA_pHW2000	<pre>IREPFISCSHLECRTFFLTQGALLNDRHSNGTVKDRSPYRALMSCPVGEA PKETFLS*ESPLFHVLTWNAGPFF*PKVPY*MTSIQVGLLRTEALIGP**AALSVKLR :* *:*</pre>	151 142
NA_NCBI NA_pHW2000	PSPYNSRFESVAWSAS PRTIQDLNRLLGQQVHVMMAWAG*QSEFQVQIMEQWLY*NTTA**LKP*KVGGRKY*GHK * * :**:.	167 196
NA_NCBI NA_pHW2000	ACHDGMGWLTIGISGPDNGAVAVLKYNGIITETIKSWRKKILRTQ SLNVPV*MVHVLL**LMARVMGWPRTKFSRSKRGRLLNQ*S*MHLILTMRNVPVTLIP *** :** : : :::: :	212 249
NA_NCBI NA_pHW2000	ESECACVNGSCFTIMTDGPSDGLASYKIFKIEKGKVTKSIELNAPNSHYEECSCYPDT AK*CVCAETIGMVRTGHGCLSIKTWIIK*DTSAVGFSVTTRVPKMEQA . *.*.:* * * :* : ::	270 295
NA_NCBI NA_pHW2000	GKVMCVCRDNWHGSNRPWVSFDQNLDYQIGYICSGVFGDNPRPKDGTGSCGPVYVDGANG AVVQCMLMEQTE*RDFHIGMVMVFG*EGPKVTVPDMG . * *: : *::**: ***: ** . *	330 330
NA_NCBI NA_pHW2000	VKGFSYRYGNGVWIGRTKSHSSRHGFEMIWDPNGWTETDSK LR*FGILMDGQRLIVSSL*GKMLWQ*LIGQGIAEVSFNILS*QG*TV*GRASGLN*SGDD :: *.	371 383
NA_NCBI NA_pHW2000	FSVRQDVVAMTDWSGYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEKTIWTSA LKKKQSGLVRAAFL-FVA*IVIL*IGLGQTVLSCHSALTSSLFKKLLVST : : : : : : : : : : : : : : : : :	425 430
NA_NCBI NA_pHW2000	SSISFCGVNSDTVDWSWPDGAELPFTIDK 454 430	