CLUSTAL O(1.2.4) multiple sequence alignment

PA_NCBI PA_pHW2000	MEDFVRQCFNPMIVELAEKAMKEYGEDLKIETNKFAAICTHLEVCFMYSDFH SKSRY*FEMEDFVRQCFNPMIVELAEKAMKEYGEDLKIETNKFAAICTHLEVCFMYSDFH ************************************	52 59
PA_NCBI PA_pHW2000	FINEQGESIVVELDDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGAEKPKFLPDLYDY FINEQGESIVVELDDPNALLKHRFEIIEGRDRTMAWTVVNSICNTTGAEKPKFLPDLYDY **********************************	112 119
PA NCBI	KENRFIEIGVTRREVHIYYLEKANKIKSENTHIHIFSFTGEEMATKADYTLDEESRARIK	172
PA_pHW2000	KENRFIEIGVTRREVHIYYLEKANKIKSENTHIHIFSFTGEEMATKADYTLDEESRARIK ************************************	179
PA NCBI	TRLFTIRQEMANRGLWDSFRQSERGEETIEEKFEISGTMRRLADQSLPPNFSCLENFRAY	232
PA_pHW2000	TRLFTIRQEMANRGLWDSFRQSERGEETIEEKFEISGTMRRLADQSLPPNFSCLENFRAY ************************************	239
PA NCBI	VDGFEPNGCIEGKLSQMSKEVNAKIEPFLKTTPRPIKLPNGPPCYQRSKFLLMDALKLSI	292
PA_pHW2000	VDGFEPNGCIEGKLSQMSKEVNAKIEPFLKTTPRPIKLPNGPPCYQRSKFLLMDALKLSI	299

PA NCBI	EDPSHEGEGIPLYDAIKCIKTFFGWKEPYIVKPHEKGINSNYLLSWKQVLSELQDIENEE	352
PA_pHW2000	EDPSHEGEGIPLYDAIKCIKTFFGWKEPYIVKPHEKGINSNYLLSWKQVLSELQDIENEE **********************************	359
PA NCBI	KIPRTKNMKKTSQLKWALGENMAPEKVDFDNCRDISDLKQYDSDEPELRSLSSWIQNEFN	412
PA_pHW2000	KIPRTKNMKKTSQLKWALGENMAPEKVDFDNCRDISDLKQYDSDEPELRSLSSWIQNEFN ***********************************	419
PA NCBI	KACELTDSIWIELDEIGEDVAPIEYIASMRRNYFTAEVSHCRATEYIMKGVYINTALLNA	472
PA_pHW2000	KACELTDSIWIELDEIGEDVAPIEYIASMRRNYFTAEVSHCRATEYIMKGVYINTALLNA **********************************	479
PA NCBI	SCAAMDDFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRL	532
PA_pHW2000	SCAAMDDFQLIPMISKCRTKEGRRKTNLYGFIIKGRSHLRNDTDVVNFVSMEFSLTDPRL ************************************	539
PA NCBI	EPHKWEKYCVLEIGDMLLRSAIGQISRPMFLYVRTNGTSKVKMKWGMEMRRCLLQSLQQI	592
PA_pHW2000	EPHKWEKYCVLEIGDMLLRSAIGQISRPMFLYVRTNGTSKVKMKWGMEMRRCLLQSLQQI ***********************************	599
PA NCBI	ESMIEAESSVKEKDMTKEFFENKSEAWPIGESPKGVEEGSIGKVCRTLLAKSVFNSLYAS	652
PA_pHW2000	ESMIEAESSVKEKDMTKEFFENKSEAWPIGESPKGVEEGSIGKVCRTLLAKSVFNSLYAS ************************************	659
PA NCBI	PQLEGFSAESRKLLLVVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLT	712
PA_pHW2000	PQLEGFSAESRKLLLVVQALRDNLEPGTFDLGGLYEAIEECLINDPWVLLNASWFNSFLT ************************************	719
PA NCBI	HALK 716	
PA_pHW2000	HALK*LWQCYYLLSVLSKKVPCFY 742 ****	