CLUSTAL O(1.2.4) multiple sequence alignment

PB2_NCBI PB2_pHW2000	MERIKELRNLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPSLRMKWMM SESRSIIFSMERIKELRNLMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPSLRMKWMM	51 60

PB2_NCBI PB2_pHW2000	AMKYPITADKRITEMVPERNEQGQTLWSKMSDAGSDRVMVSPLAVTWWNRNGPVTSTVHY AMKYPITADKRITEMVPERNEQGQTLWSKMSDAGSDRVMVSPLAVTWWNRNGPVTSTVHY	111 120
PB2_NCBI	PKVYKTYFDKVERLKHGTFGPVHFRNQVKIRRRVDINPGHADLSAKEAQDVIMEVVFPNE	171
PB2_pHW2000	PKVYKTYFDKVERLKHGTFGPVHFRNQVKIRRRVDINPGHADLSAKEAQDVIMEVVFPNE ************************************	180
PB2 NCBI	VGARILTSESQLTITKEKKEELRDCKISPLMVAYMLERELVRKTRFLPVAGGTSSIYIEV	231
PB2_pHW2000	VGARILTSESQLTITKEKKEELRDCKISPLMVAYMLERELVRKTRFLPVAGGTSSIYIEV ************************************	240
PB2 NCBI	LHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRAAVSADPLASLLEMCHSTQIGG	291
PB2_pHW2000	LHLTQGTCWEQMYTPGGEVRNDDVDQSLIIAARNIVRRAAVSADPLASLLEMCHSTQIGG	300
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PB2 NCBI	TRMVDILRQNPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQT	351
PB2 pHW2000	TRMVDILRQNPTEEQAVDICKAAMGLRISSSFSFGGFTFKRTSGSSVKREEEVLTGNLQT	360

PB2 NCBI	LKIRVHEGYEEFTMVGKRATAILRKATRRLVQLIVSGRDEQSIAEAIIVAMVFSQEDCMI	411
PB2_pHW2000	LKIRVHEGYEEFTMVGKRATAILRKATRRLVQLIVSGRDEQSIAEAIIVAMVFSQEDCMI	420

PB2 NCBI	KAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWGIEHIDSVMGMVGVLPDMTPST	471
PB2_pHW2000	KAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWGIEHIDSVMGMVGVLPDMTPST	480

PB2_NCBI	EMSMRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTERLTITY	531
PB2_pHW2000	EMSMRGIRVSKMGVDEYSSTERVVVSIDRFLRVRDQRGNVLLSPEEVSETQGTERLTITY	540

PB2_NCBI	SSSMMWEINGPESVLVNTYQWIIRNWEAVKIQWSQNPAMLYNKMEFEPFQSLVPKAIRGQ	591
PB2_pHW2000	SSSMMWEINGPESVLVNTYQWIIRNWEAVKIQWSQNPAMLYNKMEFEPFQSLVPKAIRGQ ************************************	600
PB2_NCBI	YSGFVRTLFQQMRDVLGTFDTTQIIKLLPFAAAPPKQSRMQFSSLTVNVRGSGMRILVRG	651
PB2_pHW2000	YSGFVRTLFQQMRDVLGTFDTTQIIKLLPFAAAPPKQSRMQFSSLTVNVRGSGMRILVRG ************************************	660
PB2 NCBI	NSPVFNYNKTTKRLTILGKDAGTLIEDPDESTSGVESAVLRGFLIIGKEDRRYGPALSIN	711
 PB2_pHW2000	NSPVFNYNKTTKRLTILGKDAGTLIEDPDESTSGVESAVLRGFLIIGKEDRRYGPALSIN	720

PB2_NCBI	ELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTATKRIRMAIN	759
	ELSNLAKGEKANVLIGQGDVVLVMKRKRDSSILTDSQTATKRIRMAIN*C*IV*KRPCFY	777
