

APPENDIX

Appendix 1

Multiple Sequence Alignment

HCV ----- 0
WNV ----- 0
JEV TDMWLERAADISWEMDAAITGSSRRLDVKLDGDFHLIDDPGVPWKGGGGSGGG-GGGV 59
DENV -----AGV 3
YFV DGLELKKLGEVSWEEEEAEISGSSARYDVALSEQGEFKLLSEEKVPWDGGGGSGGGGSDV 60

HCV -----MAPITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLA 46
WNV -----G-DTTTGVYRIMTRGLLGSY-----QAGAG 24
JEV FWDTPSPKPCSKG-DTTTGVYRIMARGILGTY-----QAGVG 95
DENV LWDVPSPPPVGKA-ELEDGAYRIKQKILGYS-----QIGAG 39
YFV LWDIPTPKIIIEECEHLEDGIYGIFQSTFLGAS-----QARGVG 97

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HCV TCVNGVCWTVYHGAGSKTLAGPKGPITQMYTINVQDLVGVWPAPPGARSMTPTCTCGSSDLY 106
WNV VMVEGVFHTLWHTTKGAALMSGEGRLDFYWGSVKEDRLOYGGPWKLQH---KWNHGDEVQ 81
JEV VMYENVEHTLWHTTRGAAIMSGEGKLTFFYWGSVKEDRIAYGGPWRFRD---KWNGTDDVQ 152
DENV VYKEGTFHTMWHVTRGAVLMHKGKRIEFSWADVKKDLISYGGGWKLEG---EWKEGEEVQ 96
YFV VAQGGVFHTMWHVTRGAFLVRNGKKLIFSASVKEDLVAYGGSWKLEG---RWDGEEEVQ 154

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HCV LVTR--HADVIPVRRRG----DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGI FRAAVC 160
WNV MIVVEPGKNVKNVQTKPGVFKTP-EGEIGAVTLDYPTGTS GSPIVDKNGDVIGLYGNGVI 140
JEV VIVVEPGKAAVNIQTKPGVFRTF- FGEVGAVSLDYPRGTS GSPILDSNGDIIGLYGNGVE 211
DENV VLALPEPGKNPRAVQTKPGLFKTN-TGTIGAVSLDFSPGTS GSPIVDKKGKVVIGLYGNGVV 155
YFV LIAAVPGKNVVNVQTKPSLFKVRNGGEIGAVALDYPSTGTS GSPIVNRNGEVIGLYGNGIL 214

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HCV	TRGVAKAVDFIPVESMETTMRA-----SKKKK	187
WNV	MPNGSYISAIVQGERMEEPAPAGFE-PEMLRKK-	172
JEV	LGDSYVSAIVQGDRQEEPVEAYT-----	236
DENV	TRSGAYVSAIANTEKSIEDNPEIEDD--IFRK--	185
YFV	VGDNSFVSAISQTEVKEEGKEELQEIPTMLK--	246
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