

ANRY8_COR : SPA-LQTRMFSEKTKWANGLF SKIPGIGPTFADTVSQAMF SVLNLQPKRMMEYRNR
 Q7VS08_BOR : GTA-RLPRLFAIKARIDSF CERVPLL PKYLSDRV LQFASRLF PDHLPRRLREYRDA
 Q4BKK3_BUR : GTK-RMPMLFGEKSKCDAWFDR LGE LPRHLSDRV MQAVSNLF PNHLPPRIRDYGKR
 Q5NQX4_ZYM : GTD-RLPQLFAMKGWFDG LNNRVSEL PRYLSDRV MQFASTLF PHHLPKRMDDFRDR
 Q6WB82_ALC : GTA-KVPSAFAMKSRIDGFEFERE G---RGVTD RVIQAVM NRLPSHL PARMRQRDR
 Q6FFS0_ACI : GTA-NVPKAFAMKDKIDGVLEK LKI---KGLTDHLLQALTE CLP SHLPKRMTEFRDL
 Q7N371_PHO : GTD-KMPTYFTLKG RMDAIFNRVPEL PVNLIDRIMQGLSRLLPSHLPKRLKEYRDR
 Q6D2B5_ERW : GTD-KLPLFFNLKGVQD TIFSKVPEL PSHLVDRTMQFLGRLLPSHL PARMKTYRNR
 DLD_ECOLI/ : GTD-KMPEFFNLKGR TDAMLEKVKV EFRPHETDRAMQKFGHLF PSHLP PARMKNWRDK
 Q66D31_YER : GTN-NMPEFFTLK GKIDARLNKI PHLVDH LTRD RVMQGF SQILPNHLPKRLKTYRNQ
 Q5F898_NEI : GTH-QLBKLEFDL KARVDRE GKKVSELPKHESDRAMQFVSKFLPDHLPKSMRDYRDK
 LDHD_HAEIN : GTH-WLPKLFSLKSNVDRI GKKFEFLPOHLSDKFMQTVSKFIPEHLPQSLWDYRDK
 Q5FRI2_GLU : GTK-YLPMFFF SMKSREDFVAORLP ELS DHE SDRAMQFLSRFLPKQLPQRMCDYRDR
 Q1NHT9_9SP : GTA-RLPRLFAAKSWVD----NLPCIRPGWSDRMMQRFGRLLPDHLPEMRRFRDR
 Q2BK95_9GA : GTD-PLBKLEFAIKGKIAAYLNKISELPKDI PDRVMQFACKLWENIIPKMRDFREK
 Q1UCB0_9GA : GTD-TLBRLEFSIKG AIDAKLNKWSMPKHE TDKVMQFIANIFPNHLPKRMTQYRDK
 Q1YWQ9_PHO : GTE-SLPKFFALKAKVENFLGRIPYVNKYLPDTILYYVSKLFPQHLPKRMLDFRDK
 Q1VBS3_VIB : GTD-KLPKMFALKAKVENFLERIPVSKYLPDTILYYASKLFPQHLPERMLDFRDK
 Q2VHK1_9LA : GTG-HLPQMFALKAKVENFLKHIPEFKPYE PDRLLQTL SNLF PNQMPKRLDDYIEK
 Q7V9S2_PRO : GTK-YLBPKLEAKRYIDQITGQVTEFLPENISDRLLMQFIADILENHLPIRLLSFRKK
 GBV_C_BAA2 : GTTTWLNRLLTTLERSS-CIPDSYEQQADYCDKISAMLRRLSLTRTVVALVNRPEK
 GBV_C_2210 : GTTTWLNRLLTTLERSS-CIPDSYEQQADYCDKVSATVRRSLTRTVVALVNRPEK
 GBV_C_BAA2 : GTTTWLNRLLTTLERSS-CIPDSYEQQADYCDKVSAMLRRLSLTRTVVALVNRPEK
 GBV_C_VARI : GTTTWLNRLLTTLPPSS-CIPDSYEQQVDYCDKVNATVRRSLTRTVVALVNRPEK
 GBV_C_AAD3 : GATTWLNRLLTTLERSS-VIPDTYPEQEADYCDRVSALLRRLSLTRLIVGAVTHQPR
 GBV_A_T088 : GOD-WVNRLLTLLERSS-VIPDDYEVKDEEVVQVSSILRRMSLSRWVMTLVDKREA
 GBV_A_AAB7 : GHD-WVNRLLTVLERSS-VMPDDEFVKDEYVNRVSSVLRKMSLSRWILT LVDKREA
 GBV_A_AAC4 : GED-WVNRLLTLLERSS-VLPDGEFVKSEETERVSTILRKMMSLSRWVMTLVERREL
 GBV_A_AAC5 : GOD-WVNRLLTMPERSS-VMPDDEFKDEFEVTKVSTVLRKLSRWIMTLVDKREM
 GBV_B_CAC3 : GEDHWLNRLTTLARSNTPVCEYFIATRDIRRKILGLEASTPWSVISA CIRLHHT
 HCV_CAA728 : GANQWMNRLIABASRGNHVSPTHYVPETDASKNVITQILTSLTITSLLRRLHQWVNE
 HCV_AAP556 : GAVQWMNRLIABASRGNHVAPTHYVAESDASQVMQMLSSLTITSLLRRLHTTWITE
 HCV_BAA326 : GATQWMNRLIABASRGNHVSPTHYVPETDTSRQIMTILSSLTITVTSLLRKLHEWINT
 HCV_D84263 : GATQWMNRLIABASRGNHVSPTHYVPETDASRAVTILSSLTITVTSLLRRLHEWISG
 HCV_AAF599 : GAVQWMNRLIABASRGNHVAPTHYVTESDASQVITQLLGS LTITVTSLLRRLHWNWITE
 HCV_AAR224 : GAVQWMNRLIABASRGNHVSPTHYVPESDAAARVTQILSSLTITVTSLLRRLHQWINE
 HCV_AAT006 : GAVQWMNRLIABASRGNHVSPTHYVPESDAAARVTQILSSLTITVTSLLRRLHQWINE
 HCV_AAT699 : GAVQWMNRLIABASRGNHVSPTHYVPESDASARVTPILTRLTVTQLLKGLHVWISS
 HCV_AAV755 : GAAQWMNRLIABASRGNHVSPTHYVPETDASRAVTNILSSLTITVTSLLRKLHQWINE
 HCV_BAA083 : GAVQWMNRLIABASRGNHVSPTHYVPESDAAAKVTALLS LTITVTSLLRRLHQWINE
 HCV_BAA098 : GAAQWMNRLIABASRGNHVSPTHYVPETDASRAVTNILSSLTITVTSLLRKLHWHWITE
 HCV_O39928 : GAVQWMNRLIABASRGNHVSPTHYVPETDASAKVTQILSSLTITVTSLLRKLHTTWIGE
 HCV_Y11604 : GAVQWMNRLIABASRGNHVSPTHYVPESDAAARVTILSSLTITVTSLLRRLHKWINE
 HCV_ABP888 : GATQWMNRLIABASRGNHVSPTHYVPETDASKNVTILSSLTITVTSLLRKLHEWINS
 HCV_VARI1 : GEVHWNRMIABASIGNHDSPRHYVVENDTAVRVT HVL SRLTITHLLKRLHAWIHE
 HCV_VARI2 : GTVQWVNRLIANTSRGNHISPAHYVPEGE PALRVTEILENGTITVTSLLRKLHWHWINE
 HCV_VARI3 : GAAQWMNRLIABASRGNHVSPTHYVPESDAAARVTIKLPNLTITVTSLLRRLHAWINE
 HCV_VARI4 : GAVQWMNRLIABASRGNHVSPTHYVPESDAAAGPVTQILSSLTITVTSLLRRLHQWINE

Lact-deh-mem

Hepaci-virus
NS4B-CTD