

# Figure S5

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SP|P06487|GI_HHV11 ---MPCRPLQGLVLVGLWVCATSLVVRGPTVSLVSNFVDAGALGPDGVVEEDLLILGELRFVGDQVPHTTYDGGVELWHYPMGHKCPRVVHVVTACPRRPAVAFALCRATDSHSP 117
SP|P13291|GI_HHV2H ---MPGRSLQGLAIGLWVCATGLVVRGPTVSLVSDSLVDAGAVGPQGFVEEDLRVFGELHFVGAQVPHTNYDGIIELFHYPLGNHCPRVVHVVTLTACPRRPAVAFTLCRSTHHAHSP 117
SP|P09258|GI_VZVD MFLIQCLI--SAVI-FYIQVTNALIFKGDHVS LQVNSSLTSILIPM--QNDNYTEIKGQLVFIQEQLPTGTNYSGTLELLYADTVAFCFRSVQVIRYDGCPRIRTSAFISCRYKHSWHYG 115
      :      . . :      :..*.:.* *** : * : : :      : : : * : * * : * . * . : * :      * * * : . * * : * * * . . *

SP|P06487|GI_HHV11 AYP-TLELNLAQQPLLRVQRA1RDYAGVYVLRVWVGDPNASLFLVGMIAAEGTLA-YNGSAYGSCDPKLLPSSAPRLAPASVYQPAPN--QASTPSTTTSTPSTTIPAPSTTIPAPQA 233
SP|P13291|GI_HHV2H AYP-TLELGLARQPLLRVRTATRDYAGLYVLRVWVGSATNASRFLVGLVALSANGTFV-YNGSDYGSCDPAQLPFSAPRLGPPSSVYTPGAS--RPTPPR1TTT1PPSSPRD----PT1PAPG- 227
SP|P09258|GI_VZVD NSTDRISTEPDAGVMLKIKKPGINDAGVYVLLVRLDHSRSTDFILGVNVYTAGSHHNIHGVIYTS1PSLQ-NGY----STRALFQARLCLDLPAT1PKGSGT1SLFQHM--LDLRAGK1SL 226
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SP|P06487|GI_HHV11 STTPFFTGDPK1PD-----PPGVNHEPPSNATRATRDSRYALTVTQIIQ1IAIPASIIALVFLGSCICFIHRCQRRYRRSRRIYSPQMPTG--ISCAVNEAAMARLGAELKSHPTPPK 344
SP|P13291|GI_HHV2H -----DTGTP-----APASGEIAPPNSTRSASESRHRLTVAQVIQ1IAIPASIIAFVFLGSCICFIHRCQRRYRRPRGQIYNP--GG--VSCAVNEAAMARLGAELRSHPTPPK 327
SP|P09258|GI_VZVD EDNPWLHEDV1V1TE1TKSVVKEGIENHVY1TD1MS1TLPEKSLNDPPENLLIIPIVASVMI--LTAMVIVIVI1SVKRRRIK1KHPI1YRPNT1KTRRGIQNATPESDVM----- 328
      *      . * : :      . *      : * * * * : : * : : * . : * * : * * *      . . * . * :

SP|P06487|GI_HHV11 SRRRS-SRTPMPSLTAIAEESepAGAAGLPTPPVDPTTPTPPLL 390
SP|P13291|GI_HHV2H PRRRSSSTTMPSLTSAEESepGPVVLVSVPRRSGPTAPQEV-- 372
SP|P09258|GI_VZVD -----LEAAIAQLATIREESP1PHSVVNP1FK----- 354
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