Figure S4

SP|P06477|GH_HHV11 MGNGLWFVGVIILGVAWGQVHDWTEQTDPWFLDGLGMDRMYWRDTNTGRLWLPNTPDPQKPPRGFLAP-PDE--------------LNLTTA--SLPLLRWYEERFCFVLVTTAEF--- 99
SP|P89445|GH_HHV2H MGPGLWVVMGVLVGVAGGHDTYWTEQIDPWFLHGLGLARTYWRDTNTGRLWLPNTPDASDPQRGRLAP-PGE--------------LNLTTA--SVPMLRWYAERFCFVLVTTAEF--- 99
SP|P09260|GH_VZVD ----MFA---LV--LAVVILPLWTTANKSY---------------------VT--PTPATRSIGHMSALLREYSDRNMSLKLEAFYPTGFDEE--LIKSLHWGNDRKHVFLVIVKVNPTT 86
SP|P17176|GH_HCMVT MRPGLPSYLIVL---AVCLLSHL---LSSRYGAEAISEPLDKAFHLLLNTYGRPIRFLRE-NTTQCTYNSSLRNSTV- 70
SP|Q1HVD2|GH_EBVA8 --------MQLL--CVFCLVLLWEVGAASLSEVK---LHLDIE---------------------------- 30
SP|P06477|GH_HHV11 -PRDPGQLLYIPKTYLLG-----RPPNASLPAPTTVEPTAQPPPSVAPLKGLLHNPAASVLLRSRAWVTFSAV-PDPEALTFPRGDNVATASHPSGPR----DTPPPRPPVGA-RRHPTT 207
SP|P89445|GH_HHV2H -PRDPGQLLYIPKTYLLG-----RPRNASLPELPEAGPTSRPPAEVTQLKGLSHNPGASALLRSRAWVTFAAA-PDREGLTFPRGDDGATERHPDGRR----NAPPPGPPAGT-PRHPTT 207
SP|P09260|GH_VZVD HEGDVGL-VIFP-KYLLSPYHFKAEHRAPFPAGR-FGFLSHP---VTPDVSFFD-SSFAPYLTTQHLVAFTTFPPNPLVWHLERAETAATAERPFGVS----LLPA-RPTV------PKN 188
SP|P17176|GH_HCMVT -VRENAISFNFFQSYN-QYYVFHM-PRCLFAGPLAEQFLNQVD--LTETLERYQQRLNTYALVSKDLASYRSFSQQ-LKAQDSLGEQPTTVPPPIDLSIPHVWMPPQTTPHGWTESHTTS 184
SP|Q1HVD2|GH_EBVA8 --G-HASHYTIPWTEL----------MAKVPGLSPEALWR--EANVTEDLASMLNRYKLIYKTSGTL--------------------GIALAEPVDIP--AVS--EGSMQVDASKVHPGV 111
SP|P06477|GH_HHV11 ELDITHLHNA--------STTWLATRGLLRSPGRYVYFSPSASTWPVGI-WTTGELVLGCDAALVRARYGREFMGLVISM---------------HDSPPVEVMVVPAGQTLDRVGDPAD 303
SP|P89445|GH_HHV2H NLSIAHLHNA--------SVTWLAARGLLRTPGRYVYLSPSASTWPVGV-WTTGGLAFGCDAALVRARYGKGFMGLVISM---------------RDSPPAEIIVVPADKTLARVGNPTD 303
SP|P09260|GH_VZVD --TILEHKAHFATWDALARHTFFSAEAIITNSTLRIHVPLFGSVWPIRY-WATGSVLLTSDSGRVEVNIGVGFMSSLISL---------------SSGPPIELIVVPHTVKLNAVTSDTT 290
SP|P17176|GH_HCMVT GLHRPHFNQT-----------------CIL-FDGHDLLFSTVTPCLHQGF-Y------LIDELRYVKITLTEDFFVVTVSI---------------DDDTPMLLIFGHLPRVLFKAPYQRD 265
SP|Q1HVD2|GH_EBVA8 ---ISG----------------LNSPACMLSAPLEKQLFYYIGTMLPNTRPHSYVFYQLRCHLSYVALSINGDKFQYTGAMTSKFLMGTYKRVTEKGDEHVLSLIFGKTKD-L-------- 204
SP|P06477|GH_HHV11 ENPPGALPGPPGGPRYRVFVLGSLTRADNGSALDALRRVGGYPEEGTNYAQFLS--------------RAYAEFFS-----GDAGAE-QGPRP--PLFWRLTGLLATSGFAFVNAAHANG 401
SP|P89445|GH_HHV2H ENAPAVLPGPPAGPRYRVFVLGAPTPADNGSALDALRRVAGYPEESTNYAQYMS--------------RAYAEFLG-----EDPGSG-TDARP--SLFWRLAGLLASSGFAFVNAAHAHD 401
SP|P09260|GH_VZVD -WFQLNPPGPDPGPSYRVYLLGRGLDMN--FSKHATVDICAYPEESLDYRYHLS--------------MAHTEALR-----MTTKADQHDINE--ESYYHIAARIATSIFALSEMGRTTE 386
SP|P17176|GH_HCMVT -NFILRQT-----EKHELLVLVKKDQLN----RHSYLKDPDFLDAALDFNYLDL---------SALLRNSFHRYAV-----DVLKSGRCQMLD--RRTVEMAFAYALALFAAARQEEAGA 359
SP|Q1HVD2|GH_EBVA8 --PD--LRGPFSYPSL--------TSAQSG--DYSLVIVTTFVHYANFHNYFVPNLKDMFSRAVTMTAASYARYVLQKLVLLEMKGG-CREPELDTETLTTMFEVSVAFF---KVGHA-- 304
SP|P06477|GH_HHV11 AVCLSDLLGFLAHSRALAGLAARGAAGC-------AADSVFFNVSVLDPTARLQLEARLQHLVAEILEREQSLALHALG-YQLAFVLDSPSAYDAVAPSAAHLIDALYAEFLGGRVL--- 510
SP|P89445|GH_HHV2H AIRLSDLLGFLAHSRVLAGLAARGAAGC-------AADSVFLNVSVLDPAARLRLEARLGHLVAAILEREQSLVAHALG-YQLAFVLDSPAAYGAVAPSAARLIDALYAEFLGGRAL--- 510
SP|P09260|GH_VZVD YFLLDEIVDVQYQLKFLNYILMRIGAGAHPNTISGTSDLIFADPSQLHDELSLLFGQVKPANVDYFISYDEARD----Q-LKTAYALSRGQDHVNALSLARRVIMSIYKGLLVKQNL--- 498
SP|P17176|GH_HCMVT QVSVPRALDRQAALLQIQEF----MITCLSQTPPRT--TLLLYPTAVDLAKRALWTP------------NQITDIT-SL-VRLVYILSKQNQQHLIPQWALRQIADF-ALKLHKTHLASF 458
SP|Q1HVD2|GH_EBVA8 --------------------VGETGNGCVDLR---WLAKSFFELTVLKDIIGICYGATVKGMQSYGLERLAAVLMATVKMEELGHLTTEKQEYALRLATVGYPKAGVYSGLIGGATSVLL 401
SP|P06477|GH_HHV11 -----------TTPVVHRALFYASAVLRQPFLAGVPSAVQRERARRSLLIASALCTSDVAAATNADLRTALARADHQKTLFWLPDHFSPCAASLRFDLDESVFILDALAQATRSETPVEV 619
SP|P89445|GH_HHV2H -----------TAPMVRRALFYATAVLRAPFLAGAPSAEQRERARRGLLITTALCTSDVAAATHADLRAALARTDHQKNLFWLPDHFSPCAASLRFDLAEGGFILDALAMATRSDIPADV 619
SP|P09260|GH_VZVD -----------NA-TERQALFFASMIL-LNFREGLENSSRVLDGRTTLLLMTSMCTAAHATQAALNIQEGLAYLNPSKHMFTIPNVYSPCMGSLRTDLTEEIHVMNLLSAIPTRPGLNEV 605
SP|P17176|GH_HCMVT -----------LSAFARQELYLMGSLVHSM-------LVHTTERREIFIVETGLCSLAELSH--------FTQLLAHPHHEYLSDLYTPCSSSGRRDHSLERLTRL----FPDATVPTTV 548
SP|Q1HVD2|GH_EBVA8 SAYNRHPLFQPLHTVMRETLFIGSHVVLRELRLNVT--TQGPNLALYQLLSTALCSALEIGEVL-----------RGLALGTESGLFSPCYLSLRFDLTRDKLLSM----APQ-----EA 499
SP|P06477|GH_HHV11 LAQQT---------HGLASTLTRWAHYNA-LIRAFVPEASHRCGGQSANVEPRILVPITHNASYVVTHSPLPRGI-GYKLTGVDVRRPLFLTYLT--ATCEGSTRDIES----KRLVRTQ 722
SP|P89445|GH_HHV2H MAQQT---------RGVASVLTRWAHYNA-LIRAFVPEATHQCSGPSHNAEPRILVPITHNASYVVTHTPLPRGI-GYKLTGVDVRRPLFITYLT--ATCEGHAREIEP----KRLVRTE 722
SP|P09260|GH_VZVD LHTQLDESEIFDAAFKTMMIFTTWTAKDLHILHTHVPEVFTCQDAAARNGEYVLILPAVQGHSYVITRNKPQRGL-VYSLADVDVYNPISVVYLSR-DTCVSEHGVIET----VALPHPD 719
SP|P17176|GH_HCMVT PA--------------ALSILSTMQPST---LE-TFPDLFCL-----PLGESFSALTVSEHVSYVVTNQYLIKGI-SYPVSTTVVGQSLIITQTDSQTKCELTRNMHTTH--SITAALNI 642
SP|Q1HVD2|GH_EBVA8 MLDQAAVSNAVDGFLGRLSLERE--DRD----AWHLPAYKCV-D---RLDKVLMIIP-LINVTFIISSDREVRGSALYEASTTYLSSSLFLSPVIM-NKCSQGAVAGEPRQIPKIQNFTR 607
SP|P06477|GH_HHV11 NQRDLGLVGAVFMRYTPAGEVMSVLLVDTDNTQQQIAAGPTEGAPSVF--SSDVPSTALLLFPNGTVIHLLAFDTQP---VAAIAPGFLAASALGVVMITAALAGIIKVLRT-------- 829
SP|P89445|GH_HHV2H NRRDLGLVGAVFLRYTPAGEVMSVLLVDTDATQQQLAQGPVAGTPNVF--SSDVPSVALLLFPNGTVIHLLAFDTLP---IATIAPGFLAASALGVVMITAALAGIIRVVRT-------- 829
SP|P09260|GH_VZVD NLKECLYCGSVFLRYLTTGAIMDIIIIDSKDTERQLAAMGNSTIPPFNPDMHGDDSKAVLLFPNGTVVTLLGFERRQ---AIRMSGQYLGASLGGAFLAVVG-FGIIGWMLCGNSRLREY 835
SP|P17176|GH_HCMVT SLENCAFCQSALLEYDDTQGVINIMYMHDSDDVL-FALDPYNEV-----VVSSPRTHYLMLLKNGTVLEVTDVVVDATDSRLLMMSVYALSAIIGIYL-------LYRMLKT-------- 741
SP|Q1HVD2|GH_EBVA8 TQKSCIFCGFALLSYDEKEGLETTTYITSQEVQNSILSSNY-------FDFDNLHVHYLLLTTNGTVMEIAGLYEERAHVVLAII-LYFIAFALGIFLVHKIVMFFL------------ 706
SP|P06477|GH_HHV11 -SVPFFWRRE 838
SP|P89445|GH_HHV2H -CVPFLWRRE 838
SP|P09260|GH_VZVD NKIPLT---- 841
SP|P17176|GH_HCMVT -C-------- 742
SP|Q1HVD2|GH_EBVA8 ----------