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                                 *           *                                                                             *
Human Igκ V-J    SPSSLSASVGDRVTITCRASQGISNYLAWFQ......................QKPGKAPELLIYAASGLQSG...VPSKFSGSGSGTDFTLTISSLQPEDFATYYCLQYNSYP
Pig Igκ V-J      SPASLAASLGDTVSITCRASQSISSSLGWYQ......................QQPGKAPKLLIYAASSLQSG...VPSRFKGSGSGTDFTLTISGLQAEDVATYYCLQHNSAP
Mouse Igκ V-J    SPSPMYASLGERVTITCKASQDINSHLSWFQ......................QKPGKSPKTLIHRADRLVDG...VPSRFSGSGSGQDYSLTISNLEYEDMGIYYCLQYDEFY

HCMV UL141       SPAPVLVAEGEQVTIPCTVM.....THSWPMVSIRARFCRS..HDGSDELILDAVKGHRLMNGLQYRLPYA......TWNFSQLHLGQIFSLTFN.VSMDTAGMYECVLRNYSH
CCMV UL141       SPAPMLVAEGERVTVPCTVM.....IHQWPLAVIRATFCLSPPTERSVELVFNLSRGGEVVVPLEEKLTESRLRGGVSYNFTDLHVAHLFSLTFR.ATASSAGVYECLLRNDSH
RhCMV UL141      SPAPLIMPIGSQVTVPCAFL.....PHSWPMVSIRARFCQSEY..GGYELKINATNGTVVDDDLTYRLINA......SWKFHDLAISHYVTLTMN.ISDNTTGMFDCVLRNATH
HCMV UL14        PGSPQLLPYGDRLEVACIFP.....AHDWPEVSIRVHLCYWP..EIVRSLVVDARSGQVLHNDASCYIAGG......RWRFEDGGAAQRLSLSFR.LITETAGTYTCVLGNETH
CCMV UL14        LSSPKMLPYGDRLDVSCIFP.....SHAWPEVSIHVRLCYWP..EIVRSLVVDAHSGQLLHNDVTCQISSG......RWSFEDGGAAQTLTLSFR.LITQTAGTYHCVLGNETH
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Supplementary Figure 2

Ig-like β sandwich domain encoded by HCMV UL141 (residues 15-114 in the mature protein), its orthologues in chimpanzee and rhesus cytomegalovirus (CCMV and RhCMV UL141), and the related UL14 gene in HCMV and CCMV. The domain was initially identified using the protein fold recognition program 3D-PSSM (http://www.sbg.bio.ic.ac.uk/~3dpssm/), and the alignment was derived from sequences in GenBank. Residues that are conserved in all the viral sequences and, in some instances, in cellular proteins containing the cognate domain, are in red. The central part of the alignment is predicated on the conserved W residue (asterisked) that is packed against the disulphide bond (C residues asterisked) in most Ig domains.