



**A**

CgueCMV1.1	MNLLQKLCVVCCKNEYAMELECKLYCDPNVLAEESSPFKRNALAIAYLYRKYIYPEVVRQNRQTSLTLYMEMILKALYEDTELLDRALKAYCRPRDM	100
CgueCMV1.2	.....	100
	EYRTILRLDRCDRHHTVELTPTETVKFVSVTLATLNDIERFLCKMNYVYAILAPETGLEVCSQLLQLLRRLCGVSPVACQEAIVEGTTCQAQCYEELTIIP	200
	.....V.....	200
	NQGRSLNKRLLQGLLNHNHIVHRPSSQCDVNIQTVEQDLDDLTPRIPSLPGVLTALKNLFSSSSVYHSYIQEAEEALREYNLFTDIPARIYSLSDPTFYWSR	300
	.....	300
	TSEVIVKRVGISIQQLNVYHHLRCVLMNSLNSHLYGEDVEDIFVVGEKLSREERLFGVSVFAAPSRIDILITSLSIQAFEGNVPFNKLHESNEMYTKIK	400
	.....	400
	CILEEIRRPVDPGAAGEAGASGASRQDRPNTSNN-SDAQNEDDDFLDWRDARTMHNVTRVNMKRKAYLQKVSEVGYAKVIRCIKSQLRSLTKLIDVN	499
	.....L.....N.....	500
	LIGTVCLDFISKLMNGFIYRTQYLDNPDLDVAQLLSYDEHLYVNNI IHKSLPAESLPLLGQQIYQLCNGPLFTHCTDRYPLSHVDMAYACDNAGVLP	599
	.....E.....	600
	HIKDDLKCAKEGTYVPEWVVVYQGFNFSDQCQDLNMLQKEMKHWRELVLVSVLYNETFGKQLTIACLRDELTTDRDLLTYNKEVPLLRHREGTYLK	699
	.....	700
	SKDLYLLYRHLARPDEQRDVFQPD SACVPAAPRRVRAPKRPRNSLLLDLARDQDDQLVPGCLR	768
	.....C.....	769
	<b>UL56 (complete)</b>	
CgueCMV1.1	MTQIWFVACASLLTVNSATSTSNVSSPTPASSSSDRTPASSTAADNGTAPFIANTTVRTNEVSLDKARFPYRVCMSQGTDFLFRDNNIQCEAFK	100
CgueCMV1.2	..K.....V.....I.....A.....V.....N---TPTSTS.....GLVP...L...LD...RSKY.....A.....E.....	97
	PTKEDFDEGIMLVYKRDIRAYTFKVHVYQKVTQRQSYIYINVMGQTVEHLVPMWEVHYINKLRNCYNSILRVMGDKRTYYSYHKDSFVNETMVLVP	200
	.....N.....L.....ST.....K...E.....V.RI.....V.F.N.EP.....M.T.....L..Q	197
	DFPSNTHSSRFVTKQLWHKPGSTWLYTTSNVMCMVTVTARSRYPNFVTSAGEVVDISPPYNGSNDKHGFENRDKPHLKRNYTMVQYVYADNAPES	300
	..Y.....T.....K...A.....I.....AS.D.....T.G.....TK...VFN..S..E...RE.V.QV	297
	AHPLVAFPERADSLMSWDIVDESNNTCQYALWEVSEIRIRSEAEHTYHTSASMTATPLSKKETVNIISDPALECVREVEARLEKLFNTTYNETYAKSGN	400
	N..M.....L..A.....F...T.....D.....SK.S...T..I..E...T.IKD.ASEQ.Q.IY.Q...S..VQ...	397
	VTVYETGGLIVFWLVPEKSLLEMERLTKNSTNAT--VRSKRSLDNG--NSTEVLSHVVYAQLQPTDYDLRNYINRALRQIADAWCWDKQKRTAEVLKEL	496
	MSI.....Q.RAIW..KQ.NDGRQ.V.NSS.HR..T.SSLL.N.....QN.....K.....L..L	497
	SKINPSAMLSAIYDKPIAARHIGDVISLAKCEVVDQDSVQVVRDMHVKGQNDVCYSRPVVLFRPKNSSHVHYGQLEHNEILLGRHRETCEVPSLKIFI	596
	.....E.T...I...D.TG...T...Q...Y.....T.....	597
	AGNTSYEYVDYLFKGEIPLESIPTIDLIALDIDPLENTDFKALELYSQDELASNVDFLEEIMREFNSYRQRIVPMEDKVFDPVPSYLRGLDLDMSGLG	696
	...VY..R..S.D.....M.S.....E...S.....D.....T.G.....G.....	697
	AAGKALGVAIGAVGAVASIMDGIAGFLKNPFGSFTVVLFLAVLGVYIYIMRQRMYESPLQHLFPYVVPVAVHKETPPPPSYEESVYASIKKKSAS	796
	.....	796
	PTREFSVEDAYQMLLALQRLDQEKRNKSEDDVVEFPFADGADRGLDLRLRYRNRGKYLQNEYEV	862
	.....	862
	<b>Glycoprotein B (UL55; complete)</b>	
CgueCMV1.1	MFFNPYLSGGRKPSAPVAKRPVDKTFLEIVPRGAMVDGQSGLIKHKHKTGRGLMFYREIKHMLDNDMAWPCPLPPPPSIETFARRISGLPKFHTYDQVDG	100
CgueCMV1.2	.....T.....	100
	VLAHDTSEAVSPRYRPHIIPSGNVLRFFGATEQGYTICVNVFGQRSYFYCQYPDGDRDLRLDIASVSELVSEPRMAYALSIVQTKMSIYGYGTQVFPDLY	200
	.....D.....	200
	RVISNNSMAKIGEHLLDQGIPIVFEVRVDLTRLVIDKMTTFGWCNVRYDWRGYSKSSCTDFEVDVCDVADLIALADDTSWPVYRCLSPDIECMSCG	300
	.....T.....E.....	300
	GGFPVAEQVDDIVIQISVCVYETGGTGREGEESAVFGTSGHLFLTIGCCQGVGTADVVEFPSEYEMLLGFLIFPKRYAPCFVTGYNINSDFKYILTRL	400
	.....	400
	EFYVKVNPNPYKSLPCHGRFNATPVRKNHATTTATKVFISGCVVIDMPVCMKATNSPNYKLNMTMAELYLQKHKEDLSYKIEPVKFSVGAEGRAQVQYKY	500
	.....	500
	CVQDAVLKDLFNTINFHYEAGAIARLAKIPMRRVFDGQQIRIYTSLLDECACRDFVLPNHKGAETSSDATTEVSYQGATVFEPEVGYSDFPVVVFDA	600
	.....	600
	SLYPSIIMAHNLCYSTLVMPGGECPADDSQLFTVELENGVYTRFVKNTVRLSILSELLTKWVSQRRAVRETRMGCDPVRMLLDKEQLALKVTNCFYFG	700
	.....	700
	FTGVVNGMPCPIAASITRIGRDLMLRTSRFVNENFAEPCFLHNFNREDYSGDPVEVKV	761
	.....	761
	<b>DNA polymerase (UL54; partial)</b>	

**B**