

A.

MDV-1	-----	0
MDV-2	-----	0
HVT	-----	0
HSV-1	MACRKFCRVYGGQGRKKEEAVPPETKPSRVFPHGPFYTPAEDACLDSPPPETPKPSHTTP	60
VZV	-----	0
MDV-1	-----MSSSPEAETMECGISSSKVHDSKTNTTY-----G	29
MDV-2	-----METNELSSKVSVDYNANRPY-----E	20
HVT	-----MEVDVLESSKVSAS-----NM-----G	16
HSV-1	PGDAERLCHLQEI LAQMYGNQDYP IEDDPSADAADDVE-DAPDDVAYPEEYAEELFLPG	119
VZV	-----MNDV-----DATDTF-----VGQG	14
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MDV-1	IIHNSINGTDT-----TL-F-----DTFPDSTDNAEVTGDVDDVKTESSPESQSE	73
MDV-2	TIRSDTS-----DTDPSVSCGTLSDKDGDDEESIDLKVPNA-TNVGAGE	64
HVT	IVCENIESGTT-----VAEPSMSPDTSNNSFDNEDFRGPEYDVEINTRKSANLD	65
HSV-1	DATGPLIGANDHIPPGRG-----ASPPGIRRRSRDEIGATG-----FTAEE-----LD	162
VZV	KFRGAISTSPSHIMQTCGFIQQMFPVEMSPGIESEDDPNYD-VN-----MDIQS-----FN	64
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MDV-1	DLSPFGNDGNESPETVTDIDAVSAVRMQYNIVSSLSPGSEGYIYVCTKRGDNTKRKVIVK	133
MDV-2	DCTSPNDGRTEL CRTTSVTGPASVVRMQYNIISPLPPSSEGRVVFCTRWDDVSNKKVIVK	124
HVT	RMESSCREQRAACELRKSCPTSAVRMQYSILSSLAPGSEGHVYICTRYGDADQKKCIVK	125
HSV-1	AMDRAARAISRGGKPPSTMAKLVTGMGFTIHGALTPGSEGCVFDDSSHPDY--PQRVIVK	220
VZV	IFDGVHETEAEASVALCAEARVGINKAGFVILKFTTPGAEGFAFACMSKT--CEHVVIVK	122
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MDV-1	AVTGGKTLGSEIDILKMSHRSIIRLVHAYRWKSTVCMVMPKYKCDLFTYIDIM-GPLPL	192
MDV-2	VVTGGRDPGREIEIVKTLSHCAIIQLIHAYSWKSTVCMVMPKYKCDLFTYVDRK-ESIPL	183
HVT	AVVGKKNPGREVDILKTI SHKSI IKLIHAYKWNVVCMMRVRYRDLFTYIDGV-GPMPL	184
HSV-1	AGW-YTSTSHEARLLRLRDHPAILPLLDLHVVSQVTCVLVLPKYQADLYTYSRRLNPLGR	279
VZV	AGQ-RQGTATEATVLRALTHPSVVQLKGTFTYNKMTCLILPRYRTDLYCYLAAKRN-LPI	180
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MDV-1	NQIITIERGLLGALAYIHEKGIIHRDVKTENIFLDPKENVVLGDFGAACKLDEHTDKPKC	252
MDV-2	KDVIVIERLLEALVYLHGKGVIIHRDVKTENIFLDYPGNAVVLGDFGAACKLDMHNSPKC	243
HVT	QQMIYIQRGLEALAYIHERGIIHRDVKTENIFLDNHENAVVLGDFGAACQLGDCIDTPQC	244
HSV-1	PQIAAVSRQLLSAVDYIHRQGIHRDIKTENIFINTPEDICLGDFGAACFVQGSRSSPFP	339
VZV	CDILAIQRSVLRALQYLHNNSSIHRDIKTENIFINHPGDVCGVDFGAACFPVDINAN-RY	239
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MDV-1	YGWSGTLETNSPELLALDPYCTKTDIWSAGLVLFEMSVKNITFFGKQV----NGSGSQRLR	308
MDV-2	YGWAGTMETNSPELLALDPYCAKTDIWSAGLVLFEMSAKRTLFGKQV----KTSSSQRLR	299
HVT	YGWSGTVETNSPELSALDPYCTKTDIWSAGLVLYEAMKNVPLFSKQV----KSSGSQRLR	300
HSV-1	YGIAGTIDTNAPEVLGDPYTTTVDIWSAGLVIFETAVHNASLFSAPRGPKRGPDCSQIT	399
VZV	YGWAGTIATNSPELLARDPYGPAVDIWSAGIVLFEMATGQNSLFRDGLDGNCDSERQIK	299
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MDV-1	SIIRCLQVHPLEFPQNNSTNLCKHFQYAI-QLRHPYAI PQIIRKSGMTMDELYAIAKML	367
MDV-2	ALIRCLQIHAEFPQDESTTLCKQFKQYAI-PLRPFSIPEVVRNIPSMDEVYTIKML	358
HVT	SIIRCMQVHELEFPNRDSTNLCKHFQYAV-RVRPPYTIPIRVIRNGGMPMDVEYVISKML	359
HSV-1	RIIRQAQVHVDEFSPHPESRLTSRYRSRAAGNNRPYTRPAWTRYKMDIDVEYLVCAL	459
VZV	LIIRRSRGTHPNEFPINPTSNLRQYIGLAKRSSRKPGSRPLWTLNLYELPIDLEYLICKML	359
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MDV-1	TFDQEFRPSAQDILMLPLFTKEPADALYTITAAHM	402
MDV-2	TFDQEFRPSAQDILAFPLFVKEAPQNLQALFVP--	391
HVT	TFDQEFRPSAKEILNMLPFTKAPINLLNITPDSV	394
HSV-1	TFDGA LRPSAAELLCLPLFQOK-----	481
VZV	SFDARHRPSAEVLLNHSVFQTLDPDPYPNPMVEVD-	393
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B.

	MDV-1	MDV-2	HVT	HSV-1	VZV
MDV-1	100				
MDV-2	59	100			
HVT	60	53	100		
HSV-1	36	33	36	100	
VZV	32	32	33	39	100

Figure S1. Comparative analysis of U_S3 from alphaherpesviruses. (A) Amino acid sequence alignment of U_S3 from MDV-1, MDV-2, HVT, herpes simplex virus type 1 (HSV-1), and varicella-zoster virus (VZV). The ATP binding site and catalytic active site are highlighted in yellow and green, respectively. (B) The amino acid percent identify matrix of U_S3 from MDV-1, MDV-2, HVT, HSV-1, and VZV.