Major ORFs

GLV-1h68	WR	COP		Annotation
GL001 |290	VACWR001 |218	GI:335318 |577	C23L |B29R	chemokine-binding protein
/-	/-	GI:335320		Putative C ORF G, - nonsense mutation in GLV-1h68, WR, considered as pseudogenes
GL003 |289*	4714..4556 |189998..190156	5347..5189 |186391..186549		fragment of Tumor necrosis factor receptor, * a frame shift mutation in GLV-1h68, leads to a longer ORF (63aa) in 1h68 than the ORF(52aa) in WR(4714..4524, 189998..190188) |COP(5347..5157, 186391..186581), using a premature start codon. We consider GL003|288 as a pseudo strain-specific (low orthology), due to the length difference.
/*	VACWR002 |217	/*		TNF-alpha-receptor-like protein, * a frame shift mutation in GLV-1h68 (2446..2241) |COP(5627..5422, 186111..186316), in addition, with another start codon, two peptides (30aa and 34aa) might be translated instead of a 61aa-protein in WR
/*	VACWR003 |216	/*		Unknown protein (gene fragment) * a frame shift mutation in GLV-1h68 (2371..2606)| COP(5552..5787, 186186..185951), the original ORF is completely disrupted in COP and 1h68
GL004 |288	VACWR004 |215	GI:335321 |576	C22L |B28R	TNF-alpha-receptor-like protein
GL004.5 |287.5	VACWR005 |214	6377..6231 |185361..185507		ankyrin-like protein
/	VACWR006 |213	GI:335322 |575	C21L|B27R	putative C21L, ankyrin-like protein
/	VACWR007 |212	GI:335323 |574	C20L|B26R	putative C20L, ankyrin-like protein
/	VACWR008 |211*-	GI:335324 |573	C19L|B25R	putative C19L ankyrin-like protein, *- a frame shift mutation. 103aa segment of (112aa in WR008/211) is identical with C19L/B25R(259aa in COP)
/	6914..7126* |187798..187586*	GI:335325 |572		putative C ORF F, * a frame shift mutation at the late location (in low complex region), the alignment has good identity, but the end 20aa is totally novel, thus we consider it as pseudo strain-specific due to the low identity.
GL005 |287	/	/		ankyrin-like protein [Vaccinia virus]
GL006 |286*	/	GI:335326 |571	C18L|B24R	putative; host range protein [Vaccinia virus] * a frame shift mutation occurs, GL006 is identical to the early fragment (49aa) of C18L, B24R(150aa).
/				putative C18L, B24R
GL007 |285* GL008 |284*	/	GI:335327 |570	C17L|B23R	putative host range polypeptide * a frame-shift mutation
/	/	GI:335328 |569	C16L|B22R	putative C16L
/	/	GI:335329 |568	C15L|B21R	putative C15L

GL009 |283	VACWR205	GI:335332	C12L	serine protease inhibitor-like SPI-1
GL009.5 |282.5	VACWR204.5	264		very short ORF, well conserved putative early and late promoter
GL010 |282	VACWR009 |210	GI:335333	C11R	secreted epidermal growth factor
GL011 |280	VACWR010 |209	GI:335334	C10L	fragment of IL-1 receptor antagonist
GL013 |279	VACWR011 |208	/		zinc finger-like protein
GL014 |278	VACWR012 |207	/		zinc finger-like protein
GL015 |277	VACWR013	/		interleukin-18-binding protein
GL016-	VACWR014	/		ankyrin-like protein
GL017-		/		ankyrin-like protein - nonsense mutation, but with a closely-later start codon, the rest fragment might be translated
GL018	VACWR015	/		ankyrin-like protein
GL019	VACWR016*	/		ankyrin-like protein * frame shift mutation
	VACWR017*	/		ankyrin-like protein * frame shift mutation
/	VACWR018	/		unknown
GL020	/	/		unknown, orthologous to TC10L [Tian tan strain]
GL021	VACWR019	GI:335336	C9L	ankyrin-like protein
GL023	VACWR020	GI:335338	C8L	unknown protein
GL023.5	15121..15369	GI:335339		putative C ORF C,
/				- nonsense mutation in GLV-1h68, ORF translates a 45aa protein instead of 82aa in WR|COP
GL025	VACWR021	GI:335341	C7L	host-range related protein
GL026	VACWR022	GI:335342	C6L	unknown protein with epitope hits
GL027	VACWR023	GI:335343	C5L	unknown protein with epitope hits
GL028	VACWR024	GI:335344	C4L	unknown protein with epitope hits
GL029	VACWR025	GI:335345	C3L	secreted complement binding
GL030	19411..19620	GI:335346		similar to putative C ORF A[COP]
GL031	VACWR026	GI:335347	C2L	kelch-like protein
GL032	VACWR027	GI:335348	C1L	unknown
GL033	VACWR028	GI:335349	N1L	virokine
GL034	VACWR029	GI:335350	N2L	alpha-amanitin sensitive protein
GL035	VACWR030	GI:335351	M1L	ankyrin-like protein
GL036	VACWR031	GI:335352	M2L	unknown
GL037	VACWR032	GI:335353	K1L	ankyrin-like protein
GL038	VACWR033	GI:335354	K2L	serine protease inhibitor-like
GL041*	27312..27491	30369..30554		hypothetical protein, orthologous to m0036R[Vaccinia],

				* a frame shift mutation, causes GL041 has to use another start codon (earlier than which in WR|COL), it may translate a 78aa protein instead of the 61aa protein by WR|COL (78% coverage), (pseudo-specific)
GL042	VACWR034	GI:335357	K3L	interferon resistance protein
GL043	VACWR035	GI:335358	K4L	phospholipase-D-like protein
GL044	VACWR036	32117..31983		putative monoglyceride lipase[Vaccinia]
GL045	VACWR037	GI:335359	K5L	putative monoglyceride lipase
GL046	VACWR038	GI:335360	K6L	putative monoglyceride lipase
GL047	VACWR039	GI:335361	K7R	unknown protein
GL049	VACWR040	GI:335362	F1L	putative protein localizes exclusively tot he mitchondira where it functions to inhibit apoptosis
GL050	VACWR041	GI:335363	F2L	dUTPase
GL051	VACWR042	GI:335364	F3L	kelch-like protein
GL053	VACWR043	GI:335366	F4L	ribonucleotide reductase small subunit
GL056	VACWR044	GI:335369	F5L	Major membrane protein
GL057	VACWR045	GI:335370	F6L	unknown
GL058	VACWR046	GI:335371	F7L	unknown
GL059	VACWR047	GI:335372	F8L	protein with iActA-like proline repeats
GL060	VACWR048	GI:335373	F9L	S-S bond formation pathway protein (membrane)
GL061	VACWR049	GI:335374	F10L	ser/thr kinase
GL062	37757..37993	GI:335375		similar to putative F ORF D [COP]
GL063	VACWR050	GI:335376	F11L	unknown
GL064	VACWR051	GI:335377	F12L	involved in plaque and EEV formation
GL066	VACWR052	GI:335379	F13L	palmytilated EEV membrane protein
GL067	VACWR053	GI:335380	F14L	unknown protein
/*	/*	GI:335381		putative F ORF F, * a frame shift mutation at the very early position; causing disfunctional proteins (if translated) in WR(42554..42664) |GLV-1h68
GL068-	VACWR053.5	F14.5L		hypothetical 49aa protein in LIVP wt, WR and COP with Epitope database hit: 1072792, orthologous to m0062L[Vac] - in GLV-1h68, the corresponding ORF is disrupted by a foreign insertion of Ruc-GFP and can not be translated, but the nucleotide sequence is intact after removing the insertion.
Ruc-GFP				*Ruc-GFP insertion*
GL069	VACWR054	GI:335382	F15L	unknown
GL070	VACWR055	GI:335383	F16L	unknown
GL071	VACWR056	GI:335384	F17R	putative DNA-binding phosphoprotein
GL073	VACWR057	GI:335386	E1L	poly-A polymerase catalytic subunit VP55

GL074	VACWR058	GI:335387	E2L	unknown protein
GL075	VACWR059	GI:335388	E3L	double-stranded RNA binding protein
GL076	VACWR060	GI:335389	E4L	DNA-dependent RNA polymerase subunit rpo30
GL077	VACWR061	GI:335390	E5R	abundant component of virosome
GL079	VACWR062	GI:335392	E6R	unknown
GL080	VACWR063	GI:335393	E7R	soluble myristyl-protein
GL082	VACWR064	GI:335395	E8R	membrane protein
GL084	VACWR065	GI:335397	E9L	DNA polymerase
GL086	VACWR066	GI:335399	E10R	sulfhydryl oxidase
GL087	VACWR067	GI:335400	E11L	virion core protein
GL088	VACWR068	GI:335401	O1L	Unknown protein
GL090	59356..59544	62487..62675		unknown protein, orthologous to CPXV078A[Cowpox virus]
GL091	VACWR069	GI:335403	O2L	nonessential glutaredoxin
GL091.5	VACWR069.5	266		Extremely short(35aa), well conserved ORF with a good, well conserved putative early and late promoters
GL092	VACWR070	GI:335404	I1L	DNA-binding core protein
GL093^	VACWR071	GI:335405	I2L	I2L(Cop), hypothetical protein (similar to m0086L[Vac]), ^ two amino acids deletion in the low complex region, still orthologous
GL094	VACWR072	GI:335406	I3L	ssDNA-binding phosphoprotein
GL095	VACWR073	GI:335407	I4L	ribonucleotide reductase large subunit
GL098	VACWR074	GI:335409	I5L	IMV protein VP13
GL099	VACWR075	GI:335410	I6L	Protein binding to viral telomers and directing genome encapsidation
GL100	VACWR076	GI:335411	I7L	viral core cysteine proteinase
GL101	VACWR077	GI:335412	I8R	RNA-helicase, DExH-NPH-II
GL102	VACWR078	GI:335413	G1L	insulin metalloproteinase-like protein
GL103	VACWR079	GI:335414	G3L	unknown
GL104	VACWR080	GI:335415	G2R	late transcription elongation factor
GL105	VACWR081	GI:335416	G4L	thioredoxin-like protein
GL106	VACWR082	GI:335417	G5R	Viral membrane formation protein, expressed early in infection, becomes incorporated in the viral core
GL107	VACWR083	G5.5R		DNA-dependent RNA polymerase subunit rpo7
GL108	VACWR084	GI:335418	G6R	unknown
GL109	VACWR085	GI:335419	G7L	virion structural protein
GL111	75339..75130	GI:335421		similar to (COP) putative G ORF B
GL112	VACWR086	GI:335422	G8R	late gene transcription factor VLTF-1 (replication related)
GL113	VACWR087	GI:335423	G9R	myristylprotein

GL114	VACWR088	GI:335424	L1R	IMV membrane protein
GL115	VACWR089	GI:335425	L2R	unknown
GL116	VACWR090	GI:335426	L3L	unknown
GL117	VACWR091	GI:335427	L4R	core protein vp8
GL118	VACWR092	GI:335428	L5R	putative membrane protein
GL119	VACWR093	GI:335429	J1R	virion protein
GL120- GL121-	VACWR094	GI:335430	J2R	thymidine kinase - in GLV-1h68 the gene is disrupted by a nonsense mutation GAA (Lister strain) -> TAA (stop codon), forming two fragments, this latter one is likely not present.
lacZ				*LacZ insertion*
GL122	VACWR095	GI:335431	J3R	multifunctional poly-A polymerase subunit
GL123	VACWR096	GI:335432	J4R	DNA-dependent RNA polymerase subunit rpo22
GL124	VACWR097	GI:335433	J5L	late 16kDa putative membrane protein
GL125	VACWR098	GI:335434	J6R	DNA-dependent RNA polymerase subunit rpo147
GL127	VACWR099	GI:335436	H1L	tyr/ser protein phosphatase
GL128	VACWR100	GI:335437	H2R	unknown
GL129	VACWR101	GI:335438	H3L	IMV heparin binding surface protein
GL130	VACWR102	GI:335439	H4L	RAP94, RNA polymerase associated transcription specificity factor
GL131	VACWR103	GI:335440	H5R	morphogenesis-related, substrate of B1R kinase
GL132	VACWR104	GI:335441	H6R	topoisomerase type IB
GL133	93582..93400	96727..96545		unknown, orthologous to CPXV116[CPV: Cowpox virus]
GL134	VACWR105	GI:335442	H7R	unknown
GL135	VACWR106	GI:335443	D1R	large subunit of mRNA capping enzyme
GL137	VACWR107	GI:335445	D2L	virion core protein
GL139	VACWR108	GI:335447	D3R	virion core protein
GL140	VACWR109	GI:335448	D4R	uracil-DNA glycosylase
GL141	98480..98271	GI:335449		unknown protein, similar to putative D ORF C (COP)
GL142	VACWR110	GI:335450	D5R	NTPase interacts with A20R
GL145	VACWR111	GI:335453	D6R	70kDa small subunit of early gene transcription factor VETF
GL147	VACWR112	GI:335454	D7R	DNA-dependent RNA polymerase subunit rpo18
GL148	VACWR113	GI:335455	D8L	IMV membrane protein
GL149	VACWR114	GI:335456	D9R	contains mutT-like motif of NTP-phosphohydrolase for DNA repair
GL150	VACWR115	GI:335457	D10R	contains mutT-like motif of NTP-phosphohydrolase for DNA repair
GL151	VACWR116	GI:335458	D11L	ATPase, nucleoside triphosphate phosphohydrolase-I, NPH-I
GL155	VACWR117	GI:335461	D12L	small subunit of mRNA capping enzyme
GL157	108157..108375	111302..111520		unknown, orthologous to unknown protein[Tian tan]

GL158	VACWR118	GI:335462	D13L	Rifampicin resistance protein
GL160	VACWR119	GI:335464	A1L	late gene transcription factor VLTF-2
GL161	VACWR120	GI:335465	A2L	late gene transcription factor VLTF-3
GL162	VACWR121	A2.5L		S-S bond formation pathway
GL163	VACWR122	GI:335466	A3L	p4b precursor of core protein 4b
GL165	VACWR123	GI:335468	A4L	39kDa core protein
GL167	VACWR124	GI:335470	A5R	DNA-dependent RNA polymerase subunit rpo19
GL168	VACWR125	GI:335471	A6L	virion core protein required for formation of mature virion
GL169	VACWR126	GI:335472	A7L	82kDa large subunit of early gene transcription factor VETF
GL172	VACWR127	GI:335475	A8R	32kDa small subunit of transcription factor VITF-3
GL173	VACWR128	GI:335476	A9L	IMV membrane protein
GL174	VACWR129	GI:335477	A10L	precursor p4a of core protein 4a
GL178	VACWR130	GI:335481	A11R	Viral membrames formation
GL179	VACWR131	GI:335482	A12L	core protein
GL180	VACWR132	GI:335483	A13L	IMV membrane protein
GL181	VACWR133	GI:335484	A14L	phosphorylated IMV membrane protein
GL182	VACWR134	A14.5L		hydrophobic IV and IMV membrane protein
GL183	VACWR135	GI:335485	A15L	unknown
GL184	VACWR136	GI:335486	A16L	soluble myristylprotein
GL185	VACWR137	GI:335487	A17L	IMV membrane protein
GL186	VACWR138	GI:335488	A18R	DNA helicase
GL187	VACWR139	GI:335489	A19L	unknown
GL188	VACWR140	GI:335490	A21L	Component of poxvirus multiprotein entry-fusion complex
GL189	VACWR141	GI:335491	A20R	viral DNA polymerase processivity factor
GL192	VACWR142	GI:335494	A22R	cleaving virual DANN concatamers to yield unit-length virual genome (DNA holilday-junction resolvase)
GL193	VACWR143	GI:335495	A23R	45kDa large subunit of intermediate gene transcription factor VITF-3
GL194	VACWR144	GI:335496	A24R	DNA-dependent RNA polymerase subunit rpo132
GL196	VACWR145*	GI:335498	A25L	cowpox A-type inclusion protein* frame shift muation
	VACWR146*			cowpox A-type inclusion protein* frame shift muation
GL197	VACWR147	/		cowpox A-type inclusion protein
GL199	VACWR148	/		cowpox A-type inclusion protein
/	/	GI:335499^	A26L	putative A26L, ^ sequence segment rearrangement, the early 197aa of 332aa(COP) is identical with the early part of WR149, GL201, the rest sequence is derived from other region. GL201, WR149 are much longer (500aa), they can not

				be considered as orthologs.
GL201	VACWR149	/		cowpox A-type inclusion protein
GL203	VACWR150	GI:335500	A27L	IMV surface protein
GL204	VACWR151	GI:335501	A28L	Membrane component of IMV
GL205	VACWR152	GI:335502	A29L	DNA-dependent RNA polymerase rpo35
GL206	141520..141732	GI:335503		similar to (COP) putative A ORF K
GL207	VACWR153	GI:335504	A30L	IMV protein
GL207.5	VACWR153.5	A30.5L		42aa short ORF, late promoter element in infected cells
GL208	VACWR154	GI:335505	A31R	unknown
GL209	VACWR155	GI:335506	A32L	putative ATPase
GL211	VACWR156	GI:335508	A33R	EEV membrane phosphoglycoprotein
GL212	VACWR157	GI:335509	A34R	EEV glycoprotein
GL213	144622..144392	GI:335510		similar to (COP) putative A ORF M
GL214	VACWR158	GI:335511	A35R	intracellular protein of virulence
GL215	VACWR159	GI:335512	A36R	IEV transmembrane phosphoprotein
GL216	VACWR160	GI:335513	A37R	unknown
GL218	VACWR161	/		unknown
GL220	VACWR162	GI:335516	A38L	CD47-like antigen/integrin association membrane protein
GL221	VACWR163* VACWR164*	GI:335517	A39R	similar to putative A39R[COP] * frame shift mutation semaphorin-like protein * frame shift mutation
GL223	VACWR165	GI:335519	A40R	C-type lectin-like type-II membrane protein
GL224	VACWR166	GI:335520	A41L	secreted glycoprotein
GL225	VACWR167	GI:335521	A42R	profilin-like protein
GL226	VACWR168	GI:335522	A43R	putative type-I membrane glycoprotein
GL227	VACWR169	268*		Unknown, with epitope hit ID:1086349, *a frame shift mutation induces the generation of 268, bringing a novel stop codon in GL227|WR169, thus only the early 38aa (COP) of 78aa (WR, GLV-1h68) can be translated.
				hypothetical protein, orthologous to m0215
GL228	VACWR170	GI:335523	A44L	hydroxysteroid dehydrogenase
GL229	VACWR171	GI:335524	A45R	Cu-Zn superoxide dismutase-like in virion, nonessential for replication or virulence
GL230	VACWR172	GI:335525	A46R	Toll/IL1-receptor
GL232	VACWR173	GI:335527	A47L	Unknown protein
GL233*	154848..154711	153862..153683		unknown, orthologous to unknown protein[monkeypox virus]

				* frame shift mutation at stop codon location in GLV-1h68, extends the ORF length (till new stop codon), coding a slightly longer protein (59aa) in comparison with (45aa protein) in WR and Copenhagen. Due to 76% coverage, it is considered as pseudo-strain-specific
GL234	VACWR174	GI:335528	A48R	thymidylate kinase
GL235	VACWR175	GI:335529	A49R	unknown
GL236	VACWR176	GI:335530	A50R	DNA ligase
GL239	VACWR177	GI:335533	A51R	unknown protein
GL240	VACWR178	GI:335534	A52R	Toll/IL1-receptor
/-	159729..159457	GI:335535	A54L	putative A54L, in GLV-1h68, - original start codon and multiple nonsense mutations are involved in GLV-1h68 sequence, interrupting the ORF
GL241	159637..159882*	GI:335537*	A53R	putative A ORF T, * frame shift mutation in WR, GLV-1h68, sharing the early 25aa fragment of GL241(186aa)
	VACWR179*	GI:335536*		secretory TNF-receptor-like protein, putative A53R; CrmC, intact in some VAC strains; host defence modulator, sharing the part sequence (coding: 34..84th aa) of region of GL241 * frame shift mutation
	/	/		Tumor necrosis factor receptor[Vaccinia], 186aa intact in GLV-1h68
GL243	160068..160247	159082..159258		putative protein orthologous to CPXV192[Camelpox virus]
GL244	VACWR180	GI:335538	A55R	kelch-like protein
GL245-	VACWR181	GI:335539	A56R	hemagglutinin - fragmented by a foreign insertion, however in wt this ORF is intact
gusA				*gusA: foreign insertion*
/-	/-	GI:335540		putative A ORF U, - start codon mutation in WR |GLV-1h68, however, with another start codon, the rest sequence can be translated into a very short protein of (35aa), which is potentially a lack-of-function fragment of GI:335540 (72aa), thus we treat them as absent
GL245.5	VACWR181.5	269		Unknown protein
GL246	VACWR182	GI:335541	A57R	guanylate kinase
GL247	VACWR183	GI:335542	B1R	ser/thr kinase
GL249	VACWR184	GI:335544	B2R	unknown
GL251	165660..165373	GI:335546		similar to (COP) putative B ORF C
GL252	VACWR185	GI:335547	B3R	unknown
GL253	/	/		unknown
GL255	VACWR186	GI:335548	B4R	ankyrin-like protein
GL256	VACWR187	GI:335549	B5R	EEV type-I membrane glycoprotein

GL257	VACWR188	GI:335550	B6R	ankyrin-like protein
GL259	VACWR189	GI:335552	B7R	21kDa precursor protein
GL260	VACWR190	GI:335553	B8R	soluble interferon-gamma receptor-like protein
GL261	171634..171461	170657..170484		Potential protein orthologous to RPXV171[Rabbitpox virus]
GL262	VACWR191	GI:335554	B9R	6kDa intracellular viral protein
GL263	VACWR192	GI:335555	B10R	unknown kelch-like protein
GL264	VACWR193	GI:335556	B11R	unknown
GL265	VACWR194	GI:335557	B12R	ser/thr protein kinase-like protein
GL266*	VACWR195	GI:335558*	B13R	SPI-2/CrmA inhibits Fas-mediated apoptosis, IL-1 convertase, lipoxygenase pathway * a frame shift mutation presents a new stop codon
GL267*		GI:335559*	B14R	SPI-2/CrmA inhibits Fas-mediated apoptosis, IL-1 convertase, lipoxygenase pathway * a frame shift mutation splits the ORF(WR195) into 2 fragments in GLV-1h68|COP, same in Lister strain
GL268	VACWR196	GI:335560	B15R	IL-1 binding B15R protein
GL270	VACWR197	270-		Extremely short (30aa), Immune Epitope Database hits, well conserved late promoter - nonsense mutation COP, forming a short ORF(30aa)
		GI:335562-	B16R-	IL-1-beta-receptor - non-sense mutation (forming 270), with a later start codon, the rest ORF may be translated.
GL272	VACWR198	GI:335564	B17L	unknown protein
GL273	VACWR199	GI:335565	B18R	ankyrin-like protein
GL274	VACWR200	GI:335566	B19R	IFN-alpha/beta-receptor-like secreted glycoprotein
GL275	VACWR202^	GI:335567	B20R	similar to (COP) putative B20R, ^ nucleotide sequence changes near the start codon, using a later start codon, WR202(53aa) can be translated as the late fragment of GL275(139aa).
/	VACWR203	/		unknown
/	VACWR204	/		unknown Kelch-like fragment
GL277 |015	VACWR013	/		interleukin18-binding protein, WR lacks the paralog duplicate of WR013
GL278 |014	VACWR207 |012	/		zinc finger-like protein
GL279 |013	VACWR208 |011	/		zinc finger-like protein
GL280 |011	VACWR209 |010	GI:335334	C10L	Fragment of IL-1 Ra (receptor antagonist)
GL282 |010	VACWR210 |009	GI:335333	C11R	secreted epidermal growth factor-like protein
GL282.5 |009.5	VACWR204.5	264		unknown short ORF(37aa), very well conserved, ORF with well conserved putative late promoter and putative early promoter
GL283 |009	VACWR205	GI:335332	C12L	serine protease inhibitor-like SPI-1
/	VACWR206	GI:335330	C14L	putative C14L
		GI:335331	C13L	putative C13L

<table>
<tr><td>/</td><td>/</td><td>GI:335568 |329</td><td>B21R |C15L</td><td>putative B21R</td></tr>
<tr><td>/</td><td>/</td><td>GI:335569 |328</td><td>B22R |C16L</td><td>putative B22R</td></tr>
<tr><td>GL284 |008
GL285 |007</td><td>/
/</td><td>GI:335570 |327</td><td>B23R |C17L</td><td>similar to (COP) putative C17L, putative host range polypeptide</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>GL286 |006*
/</td><td>/</td><td>GI:335571 |326</td><td>B24R |C18L</td><td>Putative host range protein. GL286 is the early fragment (49aa) of C18L, B24R (150aa) * a frame shift mutation occurs</td></tr>
<tr><td>GL287 |005</td><td>/</td><td>/</td><td></td><td>ankyrin-like protein</td></tr>
<tr><td>/</td><td>6914..7126*- |187798..187586*</td><td>GI:335572 |325</td><td></td><td>putative B ORF G
* a frame shift mutation at a later location (in a low complex region), causing the late 20 amino acids are totally novel, thus we consider them as pseudo-strain-specific due to the lower orthology</td></tr>
<tr><td>/</td><td>VACWR211 |008*</td><td>GI:335573 |324</td><td>B25R |C19L</td><td>putative B25R, ankyrin-like protein,
*- a frame shift mutation induced an early end and with a different start codon, 103aa of (112aa in WR008) are identical with B25R (259aa in COP)</td></tr>
<tr><td>/</td><td>VACWR212 |007</td><td>GI:335574 |323</td><td>B26R |C20L</td><td>putative B26R</td></tr>
<tr><td>/</td><td>VACWR213 |006</td><td>GI:335575 |322</td><td>B27R |C21L</td><td>putative B27R</td></tr>
<tr><td>GL287.5 |004.5</td><td>VACWR214 |005</td><td>6377..6231 |185361..185507</td><td></td><td>ankyrin-like protein</td></tr>
<tr><td>GL288 |004</td><td>VACWR215 |004</td><td>GI:335576 |321</td><td>B28R |C22L</td><td>TNF-alpha-receptor-like protein</td></tr>
<tr><td>/*</td><td>VACWR216 |003*</td><td>/*</td><td></td><td>Unknown protein (gene fragment)
* a frame shift mutation in GLV-1h68|COP, the original ORF is completely disrupted in COP and GLV-1h68</td></tr>
<tr><td>/*</td><td>VACWR217 |002</td><td>/*</td><td></td><td>TNF-alpha-receptor-like protein
* a frame shift mutation in GLV-1h68|COP</td></tr>
<tr><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>GL289 |003*</td><td>4714..4556 |189998..190156</td><td>5347..5189 |186391..186549</td><td></td><td>Tumor necrosis factor receptor fragment
* a frame shift mutation in GLV-1h68, leads to a longer ORF(63aa) in GLV-1h68 than (52aa) in WR(4714..4524, 189998..190188) |COP (5347..5157, 186391..186581). The alignment identity is relatively high, so that we have to assume they are pseudo specific due to their orthology.</td></tr>
<tr><td>GL290 |001</td><td>VACWR218 |001</td><td>GI:335577 |318</td><td>B29R |C23L</td><td>chemokine-binding protein</td></tr>
</table>

Table S1. Major ORFs

/ no ortholog present in a certain strain
* frame-shift mutations
- non-sense mutations, start codon mutation
^ sequence insertions, deletion and rearrangement events in larger scale
Italic locus_tag denotes the foreign gene insertions, in comparison with LIVPwt.

Minor ORFs

GLV-1h68	WR	COP	Annotation
GL002 |291	3857..4060 |190855..190652	GI:335319 |579	similar to putative C ORF H[COP]
GL012 |281	8700..8879 |186012..185815	GI:335335	putative C ORF E
GL039	26534..26779	GI:335355	similar to putative K ORF A[COP]
GL040	26664..26903-	GI:335356-	similar to putative K ORF B[COP] - start codon mutation, in WR at 26601, in COP at 29658 ATG->ATA
GL022	14662..14874	GI:335337	similar to putative C ORF D[COP]
GL024	15294..15518	GI:335340-	similar to putative C ORF B[COP], - nonsense mutation at 18578 in COP, shortening the translation product in comparison to WR, however still orthologous
GL048	30110..29916	33181..32987	hypothetical protein, orthologous to m0043L
GL052	31866..32069	GI:335365	similar to (COP) putative F ORF A
GL054	33229..33465	GI:335367	similar to (COP) putative F ORF B
GL055	33477..33767	GI:335368	similar to (COP) putative F ORF C
GL065	39572..39787	GI:335378	similar to (COP) putative F ORF E
GL072	43949..43737	GI:335385	similar to (COP) putative E ORF A
GL078	50113..49793	GI:335391	similar to (COP) putative E ORF B
GL081	52616..52404	GI:335394	similar to (COP) putative E ORF C
GL083	53208..53008	GI:335396	similar to (COP) putative E ORF D
GL085	56234..56431	GI:335398	similar to (COP) putative E ORF E
GL089	58064..58411	GI:335402	similar to (COP) putative E ORF F
GL096	62750..62983	GI:335408	similar to (COP) putative I ORF A
GL097	63272..63436	66403..66567	putative protein, orthologous to CMP70.56R[Camelpox]
GL110	74184..74582	GI:335420	similar to (COP) putative G ORF A
GL126	86543..86328	GI:335435	similar to (COP) putative H ORF A
GL136	96412..96158	GI:335444	hypothetical protein
GL138	96496..96738	GI:335446	similar to (COP) putative D ORF B
GL143	100076..99858	GI:335451	similar to (COP) putative D ORF D
GL144	100610..100368	GI:335452	similar to (COP) putative D ORF E
GL146	101751..101560	104896..104705	Hypothetical protein
GL152	105919..106128	GI:335459	similar to (COP) putative D ORF F

GL153	106711..106869	GI:335460	similar to (COP) putative D ORF G
GL154	106866..107051	110011..110196	hypothetical 7.2KDa protein
GL156	107612..107880	110757..110945	hypothetical 7.0KDa protein
GL159	/-	GI:335463	similar to (COP) putative D ORF I; - in WR, an early nonsense mutation disrupted it-
GL164	111873..112232	GI:335467	similar to (COP) putative A ORF A
GL166	113711..113451	GI:335469	Hypothetical protein orthologous to unkown protein [Tian tan] putative A ORF B [COP]
GL170	116881..117267	GI:335473	similar to (COP) putative A ORF C
GL171	117349..117615-	GI:335473-	similar to (COP) putative A ORF D, - in WR, Cop, an early nonsense mutation induces the protein shorter (88aa) than which in GLV-1h68 (101aa)
GL175	119512..120012	GI:335478	similar to (COP) putative A ORF E
GL176	120394..120621	GI:335479	similar to (COP) putative A ORF F
GL177	120888..121115	GI:335480	similar to (COP) putative A ORF G
GL190	129077..128691	GI:335492	similar to (COP) putative A ORF H, orthologs in WR, COP are shorter than which in GLV-1h68 with a later start codon
GL191	129380..129159	GI:335493	similar to (COP) putative A ORF I
GL195	134079..133858	GI:335497	putative A ORF J(COP)
GL198	135723..135896	/	unknown, orthologous to TAZ8R[Tian tan]
GL200	137325..137471	/	hypothetical protein
GL202	138689..139183	/	Hypothetical protein
GL210	142522..142788	GI:335507	putative A ORF L
GL217	146560..146309	GI:335515	similar to (COP) putative A ORF O
/-	146086..145874	GI:335514	putative A ORF N, in GLV-1h68, - nonsense mutation occurs at 155201, however, which may translate a 33aa fragment (145303..145202) instead of 70aa protein in COP
GL219	146851..146675	145842..145660	Unknown protein
GL222	148736..148467	GI:335518	similar to (COP) putative A ORF P
GL231	153790..153473	GI:335526*	putative A ORF Q * frame shift mutation at 152700 in Cop, using another start codon, the corresponding product is shorter (77aa) than WR, GLV-1h68 (105aa)
GL237	156827..156627	GI:335531	similar to (COP) putative A ORF R
GL238	156946..156745	GI:335532	similar to (COP) putative A ORF S
GL242	/-	/-	putative protein orthologous to CMP170.5L[Camelpox], - in WR, COP, start codon and nonsense mutation both shorten the translation product, we consider it has no ortholog in WR or COP
GL248	164701..164378	GI:335543	similar to (COP) putative B ORF A

GL250	165397..165197	GI:335545	similar to (COP) putative B ORF B
GL254	166151..166002	165158..165009	unknown protein, weakly orthologous to B5L[Variola]
GL258	169686..169471	GI:335551	similar to (COP) putative B ORF D
GL269-	175046..174771	GI:335561	similar to (COP) putative B ORF E - with a different start codon, the ORF is shorter than which in WR, COP
GL271	175659..175432	GI:335563	similar to (COP) putative B ORF F
GL276	VACWR201#	179400..179570	Unknown protein
GL281 |012	8700..8897 |186012..185815	GI:335335	similar to (COP) putative C ORF E
/-	/-	GI:335578	putative B ORF H - in GLV-1h68, WR, due to a nonsense mutation, the corresponding genes were disrupted-
GL291 |002	3857..4060 |190855..190652	GI:335579 |319	similar to (COP) putative B ORF I; C ORF H

Table S2. Minor ORFs

VACWR201 is not a significant minor ORF, since it is only slightly overlapped with a major ORF, however its orthologs (GL276, COP: 179400..179570) in GLV-1h68 and COP are both minor ORFs, we specially classified WR201 into minor group. Further investigation reveals the mutation event leads to this difference, which is located on its major ORF (WR202), shortens the corresponding ORF size.

No.	Len	Locus_tag	Annotation	Description
Major ORFs				
1)	48	GL004.5	ankyrin-like protein	
2)	49	GL006	fragment of putative C18L, B24R	Only early 40aa fragment present, induced by a frame shift mutation
3)	37	GL009.5	Unknown protein	very short ORF well conserved putative early and late promoter
4)	45	GL023.5	unknown protein	
5)	44	GL044	putative monoglyceride lipase	
6)	49	GL068*	hypothetical protein	orthologous to m0062L, WR53.5, F14.5L, epitope: 1072792
7)	35	GL091.5	extremely short, unknown protein	with well conserved putative early and late promoter
8)	42	GL207.5	unknown protein	42aa, late promoter element in transfected and infected cells, viral replication and packaging
9)	37	GL245.5	unknown protein	
10)	37	GL282.5	very short ORF	well conserved putative early and late promoter
11)	49	GL286	fragment putative C18L, B24R	Early 40aa fragment, induced by a frame shift mutation, Paralog of GL006
12)	48	GL287.5	ankyrin-like protein	Paralog of GL004.5
Minor ORF				
13)	49	GL254	unknown protein	weakly orthologous to B5L[Variola virus]

Table S3. Short ORFs present in GLV-1h68, defined by the coding protein length are shorter than 50 amino acids

* GL068 is recovered by removing the foreign insertion of Ruc-GFP, which is intact within its parental LIVPwt strain.

GLV-1h68	WR	COP	ANNOTATION
/	/	C ORF G	putative C ORF G
GL003 |289*	4714..4556 | 189998..190156	5347..5189 | 186391..186549	fragment of tumor necrosis factor receptor, * pseudo-specific
/*	WR002 |217	/*	TNF-alpha-receptor-like protein
/*	WR003 |216	/*	Unknown protein (gene fragment)
/	WR006 |213	C21L |B27R	putative C21L, ankyrin-like protein
/	WR007 |212	C20L |B26R	putative C20L, ankyrin-like protein
/	WR008 |211*-	C19L |B25R	putative C19L ankyrin-like protein
/	6914..7126* |187798..187586*	C ORF F | B ORF G	putative C ORF F, B ORF G
GL005 |287	/	/	ankyrin-like protein
GL006 |286*	/	C18L |B24R	putative; host range protein
GL007 |285*	/	C17L |B23R	fragment of putative C17L, putative host range polypeptide
GL008 |284*			
/	/	C16L |B22R	putative C16L
/	/	C15L |B21R	putative C15L
GL009 |283	WR205	C12L	serine protease inhibitor-like SPI-1
GL009.5 |282.5	WR204.5	264	very short, well conserved putative early and late promoter
GL010 |282	WR009 |210	C11R	secreted epidermal growth factor
GL011 |280	WR010 |209	C10L	Fragment of IL-1 Ra (receptor antagonist)
GL013 |279	WR011 |208	/	zinc finger-like protein
GL014 |278	WR012 |207	/	zinc finger-like protein
GL015 |277	WR013	/	interleukin-18-binding protein, no paralog in WR
GL016-	WR014	/	ankyrin-like protein, - nonsense mutation
GL017-		/	ankyrin-like protein, - with another start codon
GL018	WR015	/	ankyrin-like protein
GL019	WR016*	/	ankyrin-like protein
	WR017*	/	ankyrin-like protein
/	WR018	/	Unknown
GL020	/	/	unknown, orthologous to TC10L[Tian tan]
GL023.5-	15121..15369	C ORF C	- nonsense mutation inducing a 45aa protein
/			putative C ORF C,
GL041*	27312..27491	30369..30554	hypothetical protein
/*	/*	F ORF F	putative F ORF F
GL120-	WR094	J2R	thymidine kinase (TK) - fragmented by a nonsense mutation
GL121-			

GL196	WR145*	A25L	Cowpox A-type inclusion protein
	WR146*		
GL197	WR147	/	Cowpox A-type inclusion protein
GL199	WR148	/	Cowpox A-type inclusion protein
/	/	A26L	Putative protein
GL201	WR149	/	Cowpox A-type inclusion protein
GL218	WR161	/	unknown
GL221	WR163*	A39R	similar to (COP) putative A39R
	WR164*		semaphorin-like protein
GL227	WR169	268*	Unknown, with epitope hit ID:1086349
		/	hypothetical protein, orthologous to m0215[Vac]
GL233*	154848..154711	153862..153683	orthologous to unknown protein[monkeypox]
/-	159729..159457	A54L	putative A54L
GL241	159637..159882*	A ORF T*	putative A ORF T
	WR179*	A53R	secreted TNF-receptor-like protein, putative A53R; CrmC, host defence modulator
	/	/	Tumor necrosis factor receptor
/-	/-	A ORF U	putative A ORF U
GL253	/	/	Unknown
GL266*	WR195	B13R*	SPI-2/CrmA inhibits Fas-mediated apoptosis, IL-1 convertase, lipoxygenase pathway
GL267*		B14R*	
GL270	WR197	270-	Extremely short (30aa), Immune Epitope Database hits, well conserved late promoter
		B16R-	IL-1-beta-inhibitor
GL275	/	B20R	similar to (COP) putative B20R, ^(sequence changing) loses start codon, WR202 is shorter
	WR202^		
/	WR203	/	Unknown protein
/	WR204	/	Kelch-like fragment, unknown protein
/	WR206	C14L	putative C14L
		C13L	putative C13L
/	/	B21R |C15L	putative B21R
/	/	B22R |C16L	putative B22R
/	6914..7126*$^{-}$ |187798..187586*	B ORF G | C ORF F	putative B ORF G
/	WR211 |008*	B25R |C19L	putative B25R, ankyrin-like protein
/	WR212 |007	B26R |C20L	putative B26R
/	WR213 |006	B27R |C21L	putative B27R
/*	WR216 |003	/*	Unknown protein (gene fragment)
/*	WR217 |002	/*	TNF-alpha-receptor-like protein

Table S4. Major differences in the ORFs among GLV-1h68, WR and Copenhagen

*: frame shift mutation interfering the ORF

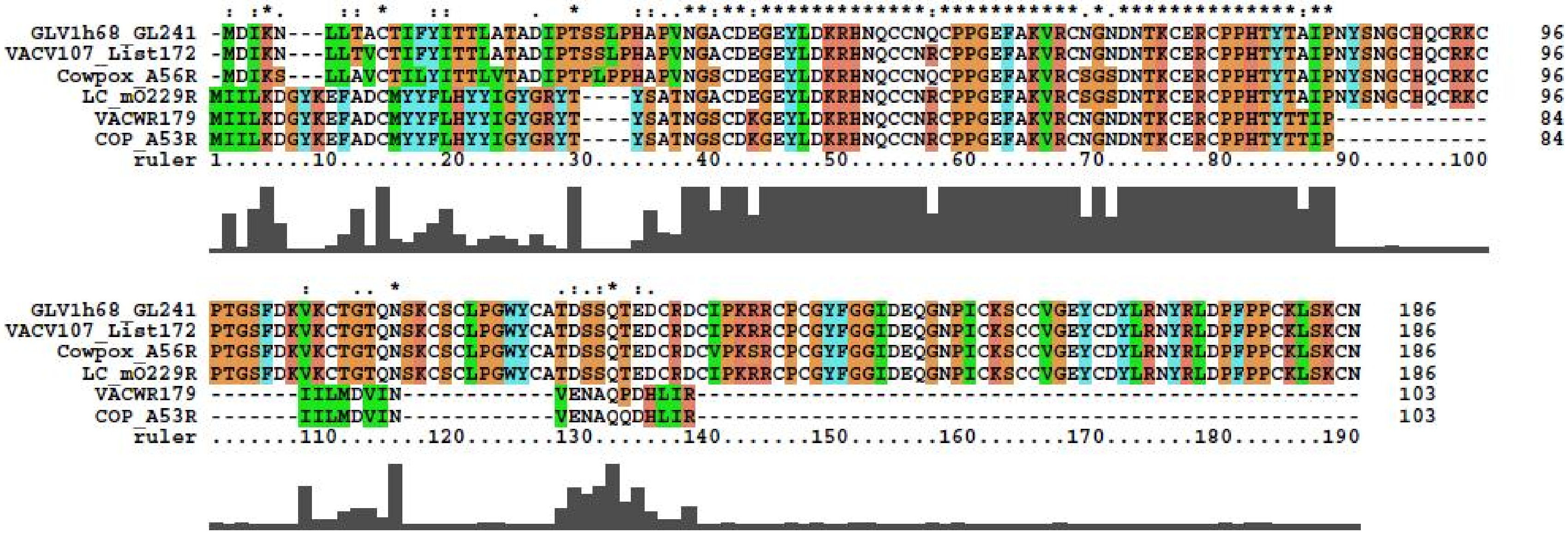
-: non-sense mutation

/: no corresponding orthologs present in the genome

ORF summary			
ORF category	**GLV-1h68**	**Western Reserve**	**Copenhagen**
Major ORF	238*	244	236
Minor ORF	61	60	59
Total	299	304	295

Table S5. Summary of the major, minor ORF number of different vaccinia strains (GLV-1h68, WR and COP).

Three foreign insertion genes are not counted, whereas the recovered gene (GL068) by eliminating those insertions has been taken account of.



```
                 : :*.    :: *   ::      .  *    ::..**:**:*************:***********.*.**************:**
  GLV1h68_GL241 -MDIKN---LLTACTIFYITTLATADIPTSSLPHAPVNGACDEGEYLDKRHNQCCNQCPPGEFAKVRCNGNDNTKCERCPPHTYTAIPNYSNGCHQCRKC    96
VACV107_List172 -MDIKN---LLTVCTIFYITTLATADIPTSSLPHAPVNGACDEGEYLDKRHNQCCNRCPPGEFAKVRCNGNDNTKCERCPPHTYTAIPNYSNGCHQCRKC    96
   Cowpox_A56R -MDIKS---LLAVCTILYITTLVTADIPTPLPPHAPVNGSCDEGEYLDKRHNQCCNQCPPGEFAKVRCSGSDNTKCERCPPHTYTAIPNYSNGCHQCRKC    96
     LC_mO229R MIILKDGYKEFADCMYYFLHYYIGYGRYT----YSATNGACDEGEYLDKRHNQCCNRCPPGEFAKVRCSGSDNTKCERCPPHTYTAIPNYSNGCHQCRKC    96
      VACWR179 MIILKDGYKEFADCMYYFLHYYIGYGRYT----YSATNGSCDKGEYLDKRHNQCCNRCPPGEFAKVRCNGNDNTKCERCPPHTYTTIP------------    84
      COP_A53R MIILKDGYKEFADCMYYFLHYYIGYGRYT----YSATNGSCDKGEYLDKRHNQCCNRCPPGEFAKVRCNGNDNTKCERCPPHTYTTIP------------    84
         ruler 1.......10........20........30........40........50........60........70........80........90.......100

                       :   .. *            .:.:* :.
  GLV1h68_GL241 PTGSFDKVKCTGTQNSKCSCLPGWYCATDSSQTEDCRDCIPKRRCPCGYFGGIDEQGNPICKSCCVGEYCDYLRNYRLDPFPPCKLSKCN   186
VACV107_List172 PTGSFDKVKCTGTQNSKCSCLPGWYCATDSSQTEDCRDCIPKRRCPCGYFGGIDEQGNPICKSCCVGEYCDYLRNYRLDPFPPCKLSKCN   186
   Cowpox_A56R PTGSFDKVKCTGTQNSKCSCLPGWYCATDSSQTEDCRDCVPKSRCPCGYFGGIDEQGNPICKSCCVGEYCDYLRNYRLDPFPPCKLSKCN   186
     LC_mO229R PTGSFDKVKCTGTQNSKCSCLPGWYCATDSSQTEDCRDCIPKRRCPCGYFGGIDEQGNPICKSCCVGEYCDYLRNYRLDPFPPCKLSKCN   186
      VACWR179 -------IILMDVIN------------VENAQPDHLIR----------------------------------------------------   103
      COP_A53R -------IILMDVIN------------VENAQQDHLIR----------------------------------------------------   103
         ruler .......110.......120.......130.......140.......150.......160.......170.......180.......190
```

Figure S1. Sequence alignment of crmC gene for selected poxvirus strains. The ORFs for *crmC* in selected poxvirus strains were translated into amino acids and their sequences were aligned using ClustalX. GLV-1h68 exhibits an intact *crmC* gene (GL241), which is highly identical to List172 in Lister isolate VACV107, and A56 gene in Cowpox virus, all of which contain a typical signal peptide sequence predicted by SignalP 3 software. Lister strain LC16mO seems to have a full length protein, but its N-terminal sequence suggests that this protein is not secreted. The *crmC* genes in VACV strains Copenhagen and WR are truncated.

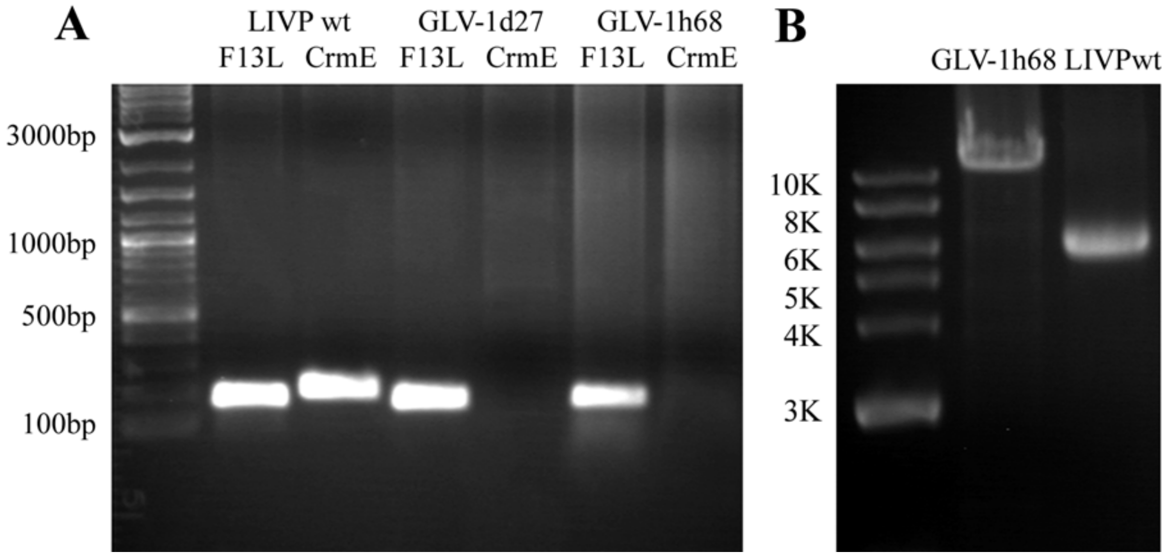


Figure S2. The PCR results indicate the parental strain of GLV-1h68 is a unique isolate from LIVP. (**A**) The genomic DNAs from LIVP wt, GLV-1d27 (the parental strain of GLV-1h68), and GLV-1h68 viruses were used as the templates for PCR amplification of the specific CrmE gene fragment and the conserved F13L gene fragment. The primer sequences for *crmE* were 5'-GTCCGAGTGACACATTCACG-3', and 5'-ACCCACGACCACATTTTGTT-3', corresponding to the *crmE* gene (mO259R) 181,487..181,506 and 181,677..181,696, respectively, in Lister isolate LC16mO (accession number AY678277). The primer sequences for F13L, serving as the positive control, were 5'-CGCGTCATTTACTGGAGGAT-3' and 5'-GCAGTGCTAACTGGCAAACA-3', corresponding to 40,770..40,789 and 40,613..40,632 respectively in the GLV-1h68 genome sequence, or 44,171..44,190 and 44,014..44,033 respectively in the LC16mO genome sequence. The PCR results indicate that while LIVP wild type population was CrmE positive, GLV-1d27 and GLV-1h68 were not. (**B**) The genomic DNAs from LIVP wt and GLV-1h68 were used as the templates for PCR with primer 5'-GCTATGATTAACTCCCACGATACTATGC-3', corresponding to 178,812..178,839 (mO257L) in LC16mO or 188,293..188,320 (GL272) in GLV-1h68, and primer 5'-CCTTACGACGTTTACATCGACGAG-3', corresponding to 184,655..185,678 (mORTR02R) in LC16mO or 199,241..199,264 (GL285) in GLV-1h68. The PCR product for GLV-1h68 was 10,971 bps as predicted. The PCR product for LIVP wt was much smaller, similar to the size predicted for LC16mO (5,866 bps), further confirming that GLV-1h68 was derived from a unique isolate of LIVP (a derivative of Lister strain).

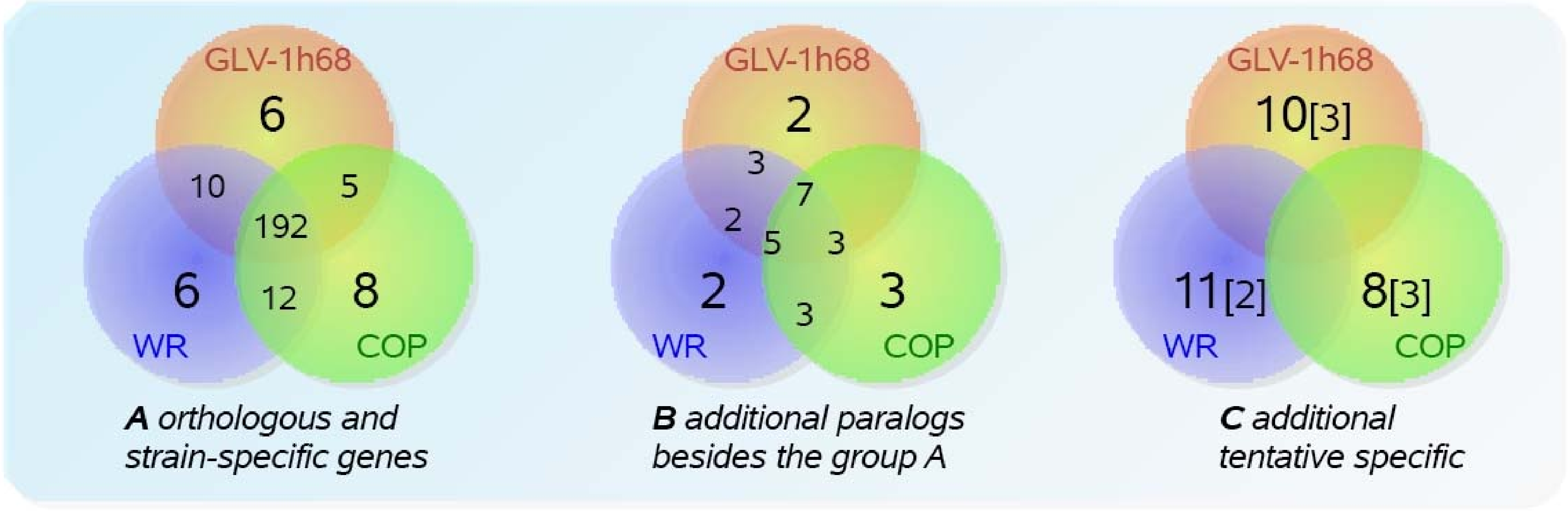


Fig. S3. Orthologous and strain-specific major genes among GLV-1h68, WR and COP. The three foreign insertion segments in GLV-1h68 were deleted before the genome comparison. Only major non-overlapping ORFs were counted. A red circle in the Venn diagram represents the ORFs in GLV-1h68, blue in WR and green in COP. (**A**) The orthologs shared by two or three VACV strains are indicated, with the central 192 ORFs highly conserved, which may be genes involved in basic vaccinia viral and survival functions. The numbers in bold specify putative virus strain-specific genes in comparison to the other twoVACV strains. In addition, there were 10 ORFs shared only by GLV-1h68 and WR, 12 shared only by WR and COP, and 5 shared only by GLV-1h68 and COP. (**B**) The paralogs in addition to the orthologs and strain-specific genes were counted, including 7 in GLV-1h68, 5 in WR and 3 in COP. (**C**) Genes of low orthology were counted as tentative specific genes. These genes still have above 50% alignment coverage or are fragmented into two in-frame ORFs. Numbers in square brackets represent the number of additional paralogs to those tentative specific genes.

List S1. Prosite protein motif hits: The translated protein sequence were analysed with a local Prosite program, the result is reorganized in the following list.

>GL001 | [gene=GL001] [protein=chemokine-binding protein]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS51257 PROKAR_LIPOPROTEIN Prokaryotic membrane lipoprotein lipid attachment site profile.
>GL002 | [gene=GL002] [protein=similar to putative C ORF H]
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
>GL003 | [gene=GL003] [protein=fragment of Tumor necrosis factor receptor]
>GL004 | [gene=GL004] [protein=TNF-alpha-receptor-like]
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS00009 AMIDATION Amidation site.
>GL004.5 | [gene=GL004.5] [protein=ankyrin-like protein]
>GL005 | [gene=GL005] [protein=ankyrin-like protein]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL006 | [gene=GL006] [protein=similar to putative C18L]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00008 MYRISTYL N-myristoylation site.
>GL007 | [gene=GL007] [protein=putative host range polypeptide, similar to putative C17L]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
>GL008 | [gene=GL008] [protein=similar to putative C17L]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
>GL009 | [gene=GL009] [protein=serine protease inhibitor-like SPI-1]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS00284 SERPIN Serpins signature.
>GL009.5 | [gene=GL009.5] [protein=very short ORF, well conserved putative early and late promoter]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL010 | [gene=GL010] [protein=secreted epidermal growth factor-like]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS00022 EGF_1 EGF-like domain signature 1.
| PS01186 EGF_2 EGF-like domain signature 2.
| PS50026 EGF_3 EGF-like domain profile.
>GL011 | [gene=GL011] [protein=fragment of IL-1Ra (receptor antagonist), C10L]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS00009 AMIDATION Amidation site.
>GL012 | [gene=GL012] [protein=similar to putative C ORF E]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
>GL013 | [gene=GL013] [protein=zinc finger-like protein]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS51301 KILA_N KilA-N domain profile.
>GL014 | [gene=GL014] [protein=zinc finger-like protein]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS00518 ZF_RING_1 Zinc finger RING-type signature.
| PS50089 ZF_RING_2 Zinc finger RING-type profile.
>GL015 | [gene=GL015] [protein=interleukin-18-binding protein]
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
>GL016 | [gene=GL016] [protein=ankyrin-like protein]
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL017 | [gene=GL017] [protein=ankyrin-like protein]
| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.
| PS50088 ANK_REPEAT Ankyrin repeat profile.
| PS50297 ANK_REP_REGION Ankyrin repeat region circular profile.
>GL018 | [gene=GL018] [protein=ankyrin-like protein]
| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
| PS00008 MYRISTYL N-myristoylation site.

```
>GL019 | [gene=GL019] [protein=ankyrin-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL020 | [gene=GL020] [protein=unknown, orthologous to TC10L]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS50315 GLY_RICH Glycine-rich region profile.
	| PS00342 MICROBODIES_CTER Microbodies C-terminal targeting signal.
>GL021 | [gene=GL021] [protein=ankyrin-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS50328 TYR_RICH Tyrosine-rich region profile.
	| PS50088 ANK_REPEAT Ankyrin repeat profile.
	| PS50297 ANK_REP_REGION Ankyrin repeat region circular profile.
>GL022 | [gene=GL022] [protein=similar to putative C ORF D]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL023 | [gene=GL023] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL023.5 | [gene=GL023.5] [protein=unknown protein]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL024 | [gene=GL024] [protein=similar to putative C ORF B]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL025 | [gene=GL025] [protein=host-range protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL026 | [gene=GL026] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL027 | [gene=GL027] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL028 | [gene=GL028] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL029 | [gene=GL029] [protein=secreted complement binding]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS51257 PROKAR_LIPOPROTEIN Prokaryotic membrane lipoprotein lipid attachment site profile.
	| PS50923 SUSHI Sushi/CCP/SCR domain profile.
>GL030 | [gene=GL030] [protein=similar to putative C ORF A]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00342 MICROBODIES_CTER Microbodies C-terminal targeting signal.
>GL031 | [gene=GL031] [protein=kelch-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS50097 BTB BTB domain profile.
>GL032 | [gene=GL032] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL033 | [gene=GL033] [protein=virokine ]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL034 | [gene=GL034] [protein=alpha-amanitin sensitive protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS50079 NLS_BP Bipartite nuclear localization signal profile.
>GL035 | [gene=GL035] [protein=ankyrin-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS50088 ANK_REPEAT Ankyrin repeat profile.
	| PS50297 ANK_REP_REGION Ankyrin repeat region circular profile.
>GL036 | [gene=GL036] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL037 | [gene=GL037] [protein=ankyrin-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS50088 ANK_REPEAT Ankyrin repeat profile.
```

```
        | PS50297 ANK_REP_REGION Ankyrin repeat region circular profile.
>GL038 | [gene=GL038] [protein=serine protease inhibitor-like]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL039 | [gene=GL039] [protein=similar to putative K ORF A]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL040 | [gene=GL040] [protein=similar to putative K ORF B]
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL041 | [gene=GL041] [protein=hypothetical protein, orthologous to m0036R]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL042 | [gene=GL042] [protein=interferon resistance protein]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL043 | [gene=GL043] [EC_number=3.1.1.3] [protein=phospholipase-D-like protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS50035 PLD Phospholipase D phosphodiesterase active site profile.
>GL044 | [gene=GL044] [protein=putative monoglyceride lipase]
>GL045 | [gene=GL045] [protein=putative monoglyceride lipase]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL046 | [gene=GL046] [protein=putative monoglyceride lipase]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL047 | [gene=GL047] [protein=unknown ]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL048 | [gene=GL048] [protein=hypothetical protein, orthologous to m0043L]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL049 | [gene=GL049] [protein=protein localizes exclusively to the mitochondia where it functions
to inhibit apoptosis]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00009 AMIDATION Amidation site.
>GL050 | [gene=GL050] [EC_number=3.6.1.23] [protein=dUTPase ]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00016 RGD Cell attachment sequence.
>GL051 | [gene=GL051] [protein=kelch-like protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00009 AMIDATION Amidation site.
        | PS50097 BTB BTB domain profile.
>GL052 | [gene=GL052] [protein=similar to  putative F ORF A]
        | PS00008 MYRISTYL N-myristoylation site.
>GL053 | [gene=GL053] [EC_number=1.17.4.1] [protein=ribonucleotide reductase small subunit]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00368 RIBORED_SMALL Ribonucleotide reductase small subunit signature.
>GL054 | [gene=GL054] [protein=similar to  putative F ORF B]
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL055 | [gene=GL055] [protein=similar to  putative F ORF C]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL056 | [gene=GL056] [protein=major membrane protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS51257 PROKAR_LIPOPROTEIN Prokaryotic membrane lipoprotein lipid attachment site
profile.
>GL057 | [gene=GL057] [protein=unknown ]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
>GL058 | [gene=GL058] [protein=unknown ]
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL059 | [gene=GL059] [protein=protein with iActA-like proline repeats]
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL060 | [gene=GL060] [protein=S-S bond formation pathway protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL061 | [gene=GL061] [EC_number=2.7.11.1] [protein=ser/thr kinase]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
```

```
	| PS00108 PROTEIN_KINASE_ST Serine/Threonine protein kinases active-site signature.
	| PS50011 PROTEIN_KINASE_DOM Protein kinase domain profile.
>GL062 | [gene=GL062] [protein=similar to  putative F ORF D]
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL063 | [gene=GL063] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL064 | [gene=GL064] [protein=involved in plaque and EEV formation]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL065 | [gene=GL065] [protein=similar to  putative F ORF E]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL066 | [gene=GL066] [protein=palmytilated EEV membrane protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
	| PS50035 PLD Phospholipase D phosphodiesterase active site profile.
>GL067 | [gene=GL067] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL068.5 | [gene=GL068.5] [protein=Renilla luciferase-Aequorea green fluorescent pro tein (GFP) fusion protein.]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
>GL069 | [gene=GL069] [protein=unknown]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00016 RGD Cell attachment sequence.
>GL070 | [gene=GL070] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL071 | [gene=GL071] [protein=putative DNA-binding phosphoprotein]
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL072 | [gene=GL072] [protein=similar to  putative E ORF A]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL073 | [gene=GL073] [EC_number=2.7.7.19] [protein=poly-A polymerase catalytic subunit VP55]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00009 AMIDATION Amidation site.
>GL074 | [gene=GL074] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL075 | [gene=GL075] [protein=double-stranded RNA binding protein]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS50137 DS_RBD Double stranded RNA-binding domain (dsRBD) profile.
	| PS50139 DRADA_REPEAT DRADA repeat profile.
>GL076 | [gene=GL076] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase subunit rpo30]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00466 ZF_TFIIS_1 Zinc finger TFIIS-type signature.
	| PS51133 ZF_TFIIS_2 Zinc finger TFIIS-type profile.
>GL077 | [gene=GL077] [protein=abundant component of virosome]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL078 | [gene=GL078] [protein=similar to  putative E ORF B]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL079 | [gene=GL079] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
```

```
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL080 | [gene=GL080] [protein=soluble, myristylprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL081 | [gene=GL081] [protein=similar to  putative E ORF C]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL082 | [gene=GL082] [protein=membrane protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL083 | [gene=GL083] [protein=similar to  putative E ORF D]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL084 | [gene=GL084] [EC_number=2.7.7.7] [protein=DNA polymerase]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00009 AMIDATION Amidation site.
      | PS00116 DNA_POLYMERASE_B DNA polymerase family B signature.
>GL085 | [gene=GL085] [protein=similar to  putative E ORF E]
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL086 | [gene=GL086] [protein=sulfhydryl oxidase]
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS51324 ERV_ALR ERV/ALR sulfhydryl oxidase domain profile.
>GL087 | [gene=GL087] [protein=virion core protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL088 | [gene=GL088] [protein=unknown ]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS50079 NLS_BP Bipartite nuclear localization signal profile.
      | PS00029 LEUCINE_ZIPPER Leucine zipper pattern.
>GL089 | [gene=GL089] [protein=similar to  putative E ORF F]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL090 | [gene=GL090] [protein=unknown protein, orthologous to CPXV078A]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL091 | [gene=GL091] [EC_number=1.8.4.-] [protein=nonessential glutaredoxin]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00195 GLUTAREDOXIN_1 Glutaredoxin active site.
      | PS51354 GLUTAREDOXIN_2 Glutaredoxin domain profile.
>GL091.5 | [gene=GL091.5] [protein=Extremely short, with well conserved putative early and late
promoter]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL092 | [gene=GL092] [protein=DNA-binding core protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00009 AMIDATION Amidation site.
>GL093 | [gene=GL093] [protein=hypothetical protein, orthologous to m0086L]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL094 | [gene=GL094] [protein=ssDNA-binding phosphoprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL095 | [gene=GL095] [EC_number=1.17.4.1] [protein=ribonucleotide reductase large subunit]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS51161 ATP_CONE ATP-cone domain profile.
      | PS00089 RIBORED_LARGE Ribonucleotide reductase large subunit signature.
>GL096 | [gene=GL096] [protein=similar to  putative I ORF A]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL097 | [gene=GL097] [protein=putative protein, orthologous to CMP70.56R]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL098 | [gene=GL098] [protein=IMV protein VP13]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL099 | [gene=GL099] [protein=protein binds to viral telomers and directs genome
encapsidation]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
```

```
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL100 | [gene=GL100] [protein=viral core cysteine proteinase]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL101 | [gene=GL101] [protein=RNA-helicase, DExH-NPH-II]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
	| PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
	| PS51192 HELICASE_ATP_BIND_1 Superfamilies 1 and 2 helicase ATP-binding type-1 domain profile.
	| PS51194 HELICASE_CTER Superfamilies 1 and 2 helicase C-terminal domain profile.
	| PS00690 DEAH_ATP_HELICASE DEAH-box subfamily ATP-dependent helicases signature.
>GL102 | [gene=GL102] [protein=insulin metalloproteinase-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL103 | [gene=GL103] [protein=unknown ]
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00009 AMIDATION Amidation site.
>GL104 | [gene=GL104] [protein=late transcription elongation factor]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL105 | [gene=GL105] [EC_number=1.8.4.-] [protein=thioredoxin-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL106 | [gene=GL106] [protein=viral membrane formation protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL107 | [gene=GL107] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase subunit rpo7]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL108 | [gene=GL108] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL109 | [gene=GL109] [protein=virion structural protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL110 | [gene=GL110] [protein=similar to  putative G ORF A]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL111 | [gene=GL111] [protein=similar to  putative G ORF B]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL112 | [gene=GL112] [protein=late gene transcription VLTF-1]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL113 | [gene=GL113] [protein=myristylprotein ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL114 | [gene=GL114] [protein=IMV membrane protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL115 | [gene=GL115] [protein=unknown ]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL116 | [gene=GL116] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00016 RGD Cell attachment sequence.
>GL117 | [gene=GL117] [protein=core protein vp8]
```

```
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00009 AMIDATION Amidation site.
>GL118 | [gene=GL118] [protein=putative membrane protein, component of poxvirus multiprotein entry-fusion complex]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL119 | [gene=GL119] [protein=virion protein]
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL120 | [gene=GL120] [EC_number=2.7.1.21] [protein=thymidine kinase]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
>GL120.5 | [gene=GL120.5] [EC_number=3.2.1.23] [protein=beta-D-galactosidase]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00016 RGD Cell attachment sequence.
        | PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
        | PS00719 GLYCOSYL_HYDROL_F2_1 Glycosyl hydrolases family 2 signature 1.
        | PS00608 GLYCOSYL_HYDROL_F2_2 Glycosyl hydrolases family 2 acid/base catalyst.
>GL121 | [gene=GL121] [EC_number=2.7.1.21] [protein=thymidine kinase]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00603 TK_CELLULAR_TYPE Thymidine kinase cellular-type signature.
>GL122 | [gene=GL122] [EC_number=2.1.1.57] [protein=multifunctional poly-A polymerase subunit]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL123 | [gene=GL123] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase subunit rpo22]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00009 AMIDATION Amidation site.
>GL124 | [gene=GL124] [EC_number=_no_value] [protein=late 16kDa putative membrane protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL125 | [gene=GL125] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase subunit rpo147]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL126 | [gene=GL126] [protein=similar to  putative H ORF A]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL127 | [gene=GL127] [EC_number=3.1.3.16] [protein=tyr/ser protein phosphatase]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00383 TYR_PHOSPHATASE_1 Tyrosine specific protein phosphatases active site.
        | PS50056 TYR_PHOSPHATASE_2 Tyrosine specific protein phosphatases family profile.
        | PS50054 TYR_PHOSPHATASE_DUAL Dual specificity protein phosphatase family profile.
>GL128 | [gene=GL128] [protein=component of poxvirus multiprotein entry-fusion complex]
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL129 | [gene=GL129] [protein=IMV heparin binding surface protein]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL130 | [gene=GL130] [protein=RAP94, transcription factor]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00016 RGD Cell attachment sequence.
>GL131 | [gene=GL131] [protein=morphogenesis-related, substrate of B1R kinase, late gene transscription factor VLTF-4]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL132 | [gene=GL132] [protein=topoisomerase type IB]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
```

```
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
	| PS00176 TOPOISOMERASE_I_EUK Eukaryotic DNA topoisomerase I active site.
>GL133 | [gene=GL133] [protein=unknown, orthologous to CPXV116]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL134 | [gene=GL134] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL135 | [gene=GL135] [protein=large subunit of mRNA capping enzyme]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL136 | [gene=GL136] [protein=hypothetical protein, orthologous to m0126L]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL137 | [gene=GL137] [protein=virion core protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL138 | [gene=GL138] [protein=similar to  putative D ORF B]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL139 | [gene=GL139] [protein=virion core protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL140 | [gene=GL140] [EC_number=3.2.2.-] [protein=uracil-DNA glycosylase]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00130 U_DNA_GLYCOSYLASE Uracil-DNA glycosylase signature.
>GL141 | [gene=GL141] [protein=similar to  putative D ORF C]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL142 | [gene=GL142] [EC_number=3.6.1.15] [protein=NTPase interacts with A20R]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00016 RGD Cell attachment sequence.
	| PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
	| PS51206 SF3_HELICASE_1 Superfamily 3 helicase of DNA viruses domain profile.
>GL143 | [gene=GL143] [protein=similar to  putative D ORF D]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL144 | [gene=GL144] [protein=similar to  putative D ORF E]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL145 | [gene=GL145] [EC_number=3.2.2.-] [protein=70kDa small subunit of early gene
transcription factor VETF]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
	| PS51192 HELICASE_ATP_BIND_1 Superfamilies 1 and 2 helicase ATP-binding type-1 domain
profile.
	| PS51194 HELICASE_CTER Superfamilies 1 and 2 helicase C-terminal domain profile.
	| PS00690 DEAH_ATP_HELICASE DEAH-box subfamily ATP-dependent helicases signature.
>GL146 | [gene=GL146] [protein=hypothetical protein, orthologous to m0136L]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00092 N6_MTASE N-6 Adenine-specific DNA methylases signature.
>GL147 | [gene=GL147] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase subunit
rpo18]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL148 | [gene=GL148] [protein=IMV membrane protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS51144 ALPHA_CA_2 Alpha-carbonic anhydrases profile.
>GL149 | [gene=GL149] [protein=contains mutT-like motif of NTP-phosphohydrolase for DNA
repair]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00893 NUDIX Nudix hydrolase signature.
```

```
>GL150 | [gene=GL150] [EC_number=3.6.1.-] [protein=contains mutT-like motif of NTP-phosphohydrolase for DNA repair]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00893 NUDIX Nudix hydrolase signature.
>GL151 | [gene=GL151] [EC_number=3.6.1.15] [protein=ATPase, nucleoside triphosphate phosphohydrolase-I, NPH-I]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS51192 HELICASE_ATP_BIND_1 Superfamilies 1 and 2 helicase ATP-binding type-1 domain profile.
        | PS51194 HELICASE_CTER Superfamilies 1 and 2 helicase C-terminal domain profile.
>GL152 | [gene=GL152] [protein=similar to  putative D ORF F]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL153 | [gene=GL153] [protein=similar to  putative D ORF G]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL154 | [gene=GL154] [protein=hypothetical 7.2KDa protein]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL155 | [gene=GL155] [EC_number=2.1.1.56] [protein=small subunit of mRNA capping enzyme]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL156 | [gene=GL156] [protein=hypothetical 7.0KDa protein, orthologous to m0145R]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00029 LEUCINE_ZIPPER Leucine zipper pattern.
>GL157 | [gene=GL157] [protein=unknown, orthologous to unknown protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL158 | [gene=GL158] [EC_number=_no_value] [protein=rifampicin resistance protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL159 | [gene=GL159] [protein=similar to  putative D ORF I]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL160 | [gene=GL160] [protein=late gene transcription factor VLTF-2]
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL161 | [gene=GL161] [protein=late gene transcription factor VLTF-3]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL162 | [gene=GL162] [EC_number=_no_value] [protein=S-S bond formation pathway]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL163 | [gene=GL163] [protein=p4b precursor of core protein 4b]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL164 | [gene=GL164] [protein=similar to  putative A ORF A]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL165 | [gene=GL165] [protein=39kDa core protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS50325 THR_RICH Threonine-rich region profile.
>GL166 | [gene=GL166] [protein=unknown, orthologous to unknown protein]
        | PS00342 MICROBODIES_CTER Microbodies C-terminal targeting signal.
        | PS00029 LEUCINE_ZIPPER Leucine zipper pattern.
>GL167 | [gene=GL167] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase subunit rpo19]
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL168 | [gene=GL168] [protein=virion core protein required for virus formation]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
```

```
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL169 | [gene=GL169] [protein=82kDa large subunit of early gene transcription factor VETF]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
>GL170 | [gene=GL170] [protein=similar to  putative A ORF C]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL171 | [gene=GL171] [protein=similar to  putative A ORF D]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL172 | [gene=GL172] [protein=32kDa small subunit of transcription factor VITF-3]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL173 | [gene=GL173] [protein=IMV membrane protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS50321 ASN_RICH Asparagine-rich region profile.
>GL174 | [gene=GL174] [protein=precursor p4a of core protein 4a]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL175 | [gene=GL175] [protein=similar to  putative A ORF E]
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL176 | [gene=GL176] [protein=similar to  putative A ORF F]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL177 | [gene=GL177] [protein=similar to  putative A ORF G]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL178 | [gene=GL178] [protein=viral membranes formation]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL179 | [gene=GL179] [protein=core protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
>GL180 | [gene=GL180] [protein=IMV membrane protein]
	| PS00008 MYRISTYL N-myristoylation site.
>GL181 | [gene=GL181] [protein=phosphorylated IMV membrane protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL182 | [gene=GL182] [protein=nonessential hydrophobic IV amd IMV membrane protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL183 | [gene=GL183] [protein=unknown ]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL184 | [gene=GL184] [EC_number=_no_value] [protein=soluble myristylprotein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL185 | [gene=GL185] [protein=IMV membrane protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL186 | [gene=GL186] [EC_number=3.1.21.5] [protein=DNA helicase]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
	| PS51192 HELICASE_ATP_BIND_1 Superfamilies 1 and 2 helicase ATP-binding type-1 domain profile.
>GL187 | [gene=GL187] [protein=unknown ]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL188 | [gene=GL188] [protein=Component of poxvirus multiprotein entry-fusion complex]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
```

```
>GL189 | [gene=GL189] [protein=viral DNA polymerase processivity factor]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00009 AMIDATION Amidation site.
>GL190 | [gene=GL190] [protein=similar to  putative A ORF H]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL191 | [gene=GL191] [protein=similar to  putative A ORF I]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL192 | [gene=GL192] [EC_number=3.1.-.-] [protein=late protein essential for concatemer resolution cleaing DNA concatamers to yield unit-length genome, DNA holiday junction (HJ) resolvase]
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL193 | [gene=GL193] [protein=45kDa large subunit of intermediate gene transcription factor VITF-3]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00009 AMIDATION Amidation site.
>GL194 | [gene=GL194] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase subunit rpo132]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS00009 AMIDATION Amidation site.
        | PS00029 LEUCINE_ZIPPER Leucine zipper pattern.
        | PS01166 RNA_POL_BETA RNA polymerases beta chain signature.
>GL195 | [gene=GL195] [protein=similar to  putative A ORF J]
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL196 | [gene=GL196] [EC_number=_no_value] [protein=Cow-pox A-type inclusion protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL197 | [gene=GL197] [protein=cowpox A-type inclusion protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL198 | [gene=GL198] [protein=unknown, orthologous to TAZ8R]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL199 | [gene=GL199] [protein=cowpox A-type inclusion protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL200 | [gene=GL200] [protein=hypothetical protein, orthologous to m0188R]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL201 | [gene=GL201] [protein=cowpox A-type inclusion protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
        | PS50099 PRO_RICH Proline-rich region profile.
>GL202 | [gene=GL202] [protein=hypothetical protein, orthologous to m0190R]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00009 AMIDATION Amidation site.
        | PS50317 ILE_RICH Isoleucine-rich region profile.
>GL203 | [gene=GL203] [protein=IMV surface protein]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00009 AMIDATION Amidation site.
>GL204 | [gene=GL204] [protein=membrane component of IMV]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
>GL205 | [gene=GL205] [EC_number=2.7.7.6] [protein=DNA-dependent RNA polymerase rpo35]
        | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
        | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
        | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
        | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
        | PS00008 MYRISTYL N-myristoylation site.
```

```
      | PS00342 MICROBODIES_CTER Microbodies C-terminal targeting signal.
>GL206 | [gene=GL206] [protein=similar to  putative A ORF K]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL207 | [gene=GL207] [protein=IMV protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL207.5 | [gene=GL207.5] [protein=late promoter element in transfected cell]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL208 | [gene=GL208] [protein=unknown ]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL209 | [gene=GL209] [protein=putative ATPase]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00009 AMIDATION Amidation site.
      | PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
>GL210 | [gene=GL210] [protein=putative A ORF L]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL211 | [gene=GL211] [protein=EEV membrane phosphoglycoprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL212 | [gene=GL212] [protein=EEV glycoprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
>GL213 | [gene=GL213] [protein=similar to  putative A ORF M]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL214 | [gene=GL214] [protein=intracellular protein of virulence]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL215 | [gene=GL215] [protein=IEV transmembrane phosphoprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL216 | [gene=GL216] [protein=unknown ]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL217 | [gene=GL217] [protein=similar to  putative A ORF O]
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL218 | [gene=GL218] [protein=unknown ]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00342 MICROBODIES_CTER Microbodies C-terminal targeting signal.
>GL219 | [gene=GL219] [protein=unknown, othologous to unknown protein]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL220 | [gene=GL220] [protein=CD47-like antigen/integrin-associated protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL221 | [gene=GL221] [protein=similar to  putative A39R]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS51004 SEMA Sema domain profile.
>GL222 | [gene=GL222] [protein=similar to  putative A ORF P]
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL223 | [gene=GL223] [protein=C-type lectin-like type-II membrane protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS50041 C_TYPE_LECTIN_2 C-type lectin domain profile.
>GL224 | [gene=GL224] [protein=secreted glycoprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL225 | [gene=GL225] [protein=profilin-like protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00414 PROFILIN Profilin signature.
>GL226 | [gene=GL226] [protein=putative type-I membrane glycoprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
```

```
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL227 | [gene=GL227] [protein=hypothetical protein, orthologous to m0215]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL228 | [gene=GL228] [EC_number=5.3.3.1, 1.1.1.145] [protein=hydroxysteroid dehydrogenase]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL229 | [gene=GL229] [EC_number=1.15.1.1] [protein=Cu-Zn superoxide dismutase-like in
virion, non- essential for replication or virulence]
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL230 | [gene=GL230] [protein=Toll/IL1-receptor ]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL231 | [gene=GL231] [protein=hypothetical protein, orthologous to m0219L]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL232 | [gene=GL232] [protein=unknown ]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL233 | [gene=GL233] [protein=unknown, orthologs to unknown protein]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL234 | [gene=GL234] [protein=thymidylate kinase]
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
    | PS01331 THYMIDYLATE_KINASE Thymidylate kinase signature.
>GL235 | [gene=GL235] [protein=unknown ]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL236 | [gene=GL236] [protein=DNA ligase]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00009 AMIDATION Amidation site.
    | PS00697 DNA_LIGASE_A1 ATP-dependent DNA ligase AMP-binding site.
    | PS00333 DNA_LIGASE_A2 ATP-dependent DNA ligase signature 2.
    | PS50160 DNA_LIGASE_A3 ATP-dependent DNA ligase family profile.
>GL237 | [gene=GL237] [protein=similar to  putative A ORF R]
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL238 | [gene=GL238] [protein=similar to  putative A ORF S]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL239 | [gene=GL239] [protein=unknown ]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00009 AMIDATION Amidation site.
>GL240 | [gene=GL240] [protein=Toll/IL1-receptor]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL241 | [gene=GL241] [protein=Tumor necrosis factor receptor]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS50311 CYS_RICH Cysteine-rich region profile.
    | PS00652 TNFR_NGFR_1 TNFR/NGFR family cysteine-rich region signature.
    | PS50050 TNFR_NGFR_2 TNFR/NGFR family cysteine-rich region domain profile.
>GL242 | [gene=GL242] [protein=putative protein orthologous to CMP170.5L]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL243 | [gene=GL243] [protein=putative protein orthologous to CPXV192]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
>GL244 | [gene=GL244] [protein=kelch-like protein]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation
site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS50097 BTB BTB domain profile.
>GL245 | [gene=GL245] [protein=hemagglutinin fragment]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS50835 IG_LIKE Ig-like domain profile.
>GL245.2 | [gene=GL245.2] [protein=beta-D-glucuronidase]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
```

```
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00009 AMIDATION Amidation site.
    | PS00719 GLYCOSYL_HYDROL_F2_1 Glycosyl hydrolases family 2 signature 1.
    | PS00608 GLYCOSYL_HYDROL_F2_2 Glycosyl hydrolases family 2 acid/base catalyst.
>GL245.5 | [gene=GL245.5] [protein=Unknown]
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00017 ATP_GTP_A ATP/GTP-binding site motif A (P-loop).
>GL246 | [gene=GL246] [protein=guanylate kinase]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS50052 GUANYLATE_KINASE_2 Guanylate kinase-like domain profile.
>GL247 | [gene=GL247] [EC_number=2.7.11.1] [protein=ser/thr kinase]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00016 RGD Cell attachment sequence.
    | PS00108 PROTEIN_KINASE_ST Serine/Threonine protein kinases active-site signature.
    | PS50011 PROTEIN_KINASE_DOM Protein kinase domain profile.
>GL248 | [gene=GL248] [protein=similar to  putative B ORF A]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL249 | [gene=GL249] [protein=unknown ]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL250 | [gene=GL250] [protein=similar to  putative B ORF B]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL251 | [gene=GL251] [protein=similar to  putative B ORF C]
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL252 | [gene=GL252] [protein=unknown ]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL253 | [gene=GL253] [protein=unknown]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL254 | [gene=GL254] [protein=unknown protein, weakly orthologous to B5L]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00009 AMIDATION Amidation site.
>GL255 | [gene=GL255] [protein=ankyrin-like protein]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00009 AMIDATION Amidation site.
    | PS50088 ANK_REPEAT Ankyrin repeat profile.
    | PS50297 ANK_REP_REGION Ankyrin repeat region circular profile.
    | PS00036 BZIP_BASIC Basic-leucine zipper (bZIP) domain signature.
>GL256 | [gene=GL256] [protein=EEV type-I membrane glycoprotein]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS50923 SUSHI Sushi/CCP/SCR domain profile.
>GL257 | [gene=GL257] [protein=ankyrin-like protein]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL258 | [gene=GL258] [protein=similar to  putative B ORF D]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00029 LEUCINE_ZIPPER Leucine zipper pattern.
>GL259 | [gene=GL259] [protein=21kDa precursor protein]
    | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL260 | [gene=GL260] [protein=soluble interferon-gamma receptor-like protein]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
    | PS00016 RGD Cell attachment sequence.
>GL261 | [gene=GL261] [protein=Potential protein orthologous to RPXV171-Rabbitpox]
    | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL262 | [gene=GL262] [protein=6kDa intracellular viral protein]
    | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
    | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
    | PS00008 MYRISTYL N-myristoylation site.
>GL263 | [gene=GL263] [protein=unknown protein, kelch-like ]
```

```
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL264 | [gene=GL264] [protein=unknown ]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL265 | [gene=GL265] [EC_number=2.7.11.1] [protein=ser/thr protein kinase-like protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00009 AMIDATION Amidation site.
      | PS00016 RGD Cell attachment sequence.
      | PS50011 PROTEIN_KINASE_DOM Protein kinase domain profile.
>GL266 | [gene=GL266] [protein=SPI-2/CrmA inhibits Fas-mediated apoptosis, IL-1 convertase, lipoxygenase pathway]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL267 | [gene=GL267] [protein=SPI-2/CrmA inhibits Fas-mediated apoptosis, IL-1 convertase, lipoxygenase pathway]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00284 SERPIN Serpins signature.
>GL268 | [gene=GL268] [protein=IL-1 binding B15R protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL269 | [gene=GL269] [protein=similar to  putative B ORF E]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL270 | [gene=GL270] [protein=IL-1-beta-inhibitor ]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS50835 IG_LIKE Ig-like domain profile.
>GL271 | [gene=GL271] [protein=similar to  putative B ORF F]
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL272 | [gene=GL272] [protein=unknown ]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL273 | [gene=GL273] [protein=ankyrin-like protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00342 MICROBODIES_CTER Microbodies C-terminal targeting signal.
      | PS50088 ANK_REPEAT Ankyrin repeat profile.
      | PS50297 ANK_REP_REGION Ankyrin repeat region circular profile.
      | PS50181 FBOX F-box domain profile.
>GL274 | [gene=GL274] [protein=IFN-alpha/beta-receptor-like secreted glycoprotein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS50835 IG_LIKE Ig-like domain profile.
>GL275 | [gene=GL275] [protein=similar to  putative B20R]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS50328 TYR_RICH Tyrosine-rich region profile.
>GL276 | [gene=GL276] [protein=unknown]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
>GL277 | [gene=GL277] [protein=interleukin-18-binding protein]
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
>GL278 | [gene=GL278] [protein=zinc finger-like protein]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00518 ZF_RING_1 Zinc finger RING-type signature.
      | PS50089 ZF_RING_2 Zinc finger RING-type profile.
>GL279 | [gene=GL279] [protein=zinc finger-like; apoptosis]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS51301 KILA_N KilA-N domain profile.
>GL280 | [gene=GL280] [protein=fragment of IL-1Ra]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
      | PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
      | PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
      | PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
      | PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
      | PS00008 MYRISTYL N-myristoylation site.
      | PS00009 AMIDATION Amidation site.
>GL281 | [gene=GL281] [protein=similar to  putative C ORF E]
      | PS00001 ASN_GLYCOSYLATION N-glycosylation site.
>GL282 | [gene=GL282] [protein=secreted epidermal growth factor-like protein]
```

```
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00022 EGF_1 EGF-like domain signature 1.
	| PS01186 EGF_2 EGF-like domain signature 2.
	| PS50026 EGF_3 EGF-like domain profile.
>GL282.5 | [gene=GL282.5] [protein=very short ORF, well conserved putative early and late promoter]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL283 | [gene=GL283] [protein=serine protease inhibitor-like SPI-1]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00284 SERPIN Serpins signature.
>GL284 | [gene=GL284] [protein=putative host-range protein, similar to C17L]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL285 | [gene=GL285] [protein=putative host-range protein, similar to C17L]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL286 | [gene=GL286] [protein=similar to  putative C18L]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00008 MYRISTYL N-myristoylation site.
>GL287 | [gene=GL287] [protein=ankyrin-like protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
>GL287.5 | [gene=GL287.5] [protein=ankyrin-like protein]
>GL288 | [gene=GL288] [protein=TNF-alpha-receptor-like protein]
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS00009 AMIDATION Amidation site.
>GL289 | [gene=GL289] [protein=fragement of tumor necrosis factor receptor II-Cowpox-]
>GL290 | [gene=GL290] [protein=chemokine-binding protein]
	| PS00001 ASN_GLYCOSYLATION N-glycosylation site.
	| PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.
	| PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
	| PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.
	| PS00008 MYRISTYL N-myristoylation site.
	| PS51257 PROKAR_LIPOPROTEIN Prokaryotic membrane lipoprotein lipid attachment site profile.
>GL291 | [gene=GL291] [protein=similar to putative C ORF H]
```

	Abbreviation	Locations	Description (accession numer)
1	GLV-1h68	54190..144462	vaccinia virus strain GLV-1h68 (EU410304)
2	DUKE	58159..139791	vaccinia virus strain DUKE (DQ439815)
3	COP	56141..137787	vaccinia virus strain Copenhagen (M35027)
4	MVA	47897..129414	vaccinia virus strain Ankara (U94848)
5	CP_GRI	69243..150930	cowpox virus strain GRI-90 (X94355)
6	ACAM	55854..137498	accinia virus strain ACAM2000 (AY313847)
7	WR	53010..134667	vaccinia virus strain Western Reserve (AY243312)
8	MP_SL	52741..134378	monkeypox virus isolate Sierra Leone (AY741551)
9	ECT_MOS	61822..143478	ectromelia virus strain Moscow (AF012825)
10	VAR_IND	43828..125446	variola virus India-1967 (X69198)
11	VAR_GAR	44823..126451	variola virus Garcia-1966 (Y16780)
12	CAM_CMS	54089..135765	camelpox virus CMS (AY009089)
13	LIST	55511..137189	vaccinia Lister major strain (AY678276)
14	MP_ZAI	53064..134679	monkeypox virus strain Zaire-96-I-16 (AF380138)
15	VAR_BSH	44460..126076	variola virus Bangladesh-1975 (L22578)
16	LC	55632..137303	vaccinia Lister isolate LC16mO (AY678277)

List S2. Highly conserved region across poxvirus strains on which the phylogenetic analysis was performed.