

	10	20	30	40	50	60	70	80
ORF2 PA8 ORF2 PA (corrected)	MTGSNSHI TI LTL NVNGL NAPI KRHRL ANWI KSQDPSVCCI QETHL MCKDT HRL KI KGWRNI YQANGKQKAGVAI LVSD	80	MTGSNSHI TI LTL NVNGL NAPI KRHRL ANWI KSQDPSVCCI QETHL TCKDT HRL KI KGWRNI YQANGKQKAGVAI LVSD	80				
	90	100	110	120	130	140	150	160
ORF2 PA8 ORF2 PA (corrected)	KTDFKPTKI KKDKEGHYI MV NGS TQQEELTI LNI YAPNT GAPRFI KVQL RDL QRDL DSHTI I VGDFTNPLSI LDRSTRQK	160	KTDFKPTKI KKDKEGHYI MV KGS MQQEELTI LNI YAPNT GAPRFI KVQL RDL QRDL DSHTI I VGDFTNPLSI LDRSTRQK	160				
	170	180	190	200	210	220	230	240
ORF2 PA8 ORF2 PA (corrected)	I NKDI QDL NSAL DQVDLI DI YRTL HPKSTEYTF SAPHSTYSKI DHII GSCTLL SKCKRTEI ITNSL SDHSAI KLELRIK	240	I NKDI QDL NSAL DQVDLI DI YRTL HPKSTEYTF SAPHSTYSKI DHII GSCTLL SKCKRTEI ITNSL SDHSAI KLELRIK	240				
	250	260	270	280	290	300	310	320
ORF2 PA8 ORF2 PA (corrected)	KLTQNRTT TWKL NNLL NDYW WNEI KAEI KKFFETNENKETTYQNL WDTAKAVL RGKFIA LNAHI RKLERSQI DT LTSQ	320	KLTQNRTT TWKL NNLL NDYW WNEI KAEI KKFFETNENKETTYQNL WDTAKAVL RGKFIA LNAHI RKLERSQI DT LTSQ	320				
	330	340	350	360	370	380	390	400
ORF2 PA8 ORF2 PA (corrected)	LKELEKQEQ TNSKASRRQEITKIRAEVKEI ETRKTLQKINESRSWFFEKNKIDCPLARLKKREKNQIDTINKNDKGDI	400	LKELEKQEQ TNSKASRRQEITKIRAEVKEI ETRKTLQKINESRSWFFEKNKIDCPLARLKKREKNQIDTINKNDKGDI	400				
	410	420	430	440	450	460	470	480
ORF2 PA8 ORF2 PA (corrected)	TTDPTEI QTIREYYKHL YANKLENLEEMDKFLDTYTLPRLNQEEVESLNRPITSSEI EAVI NSLPTKKSPGPDGFTAEEF	480	TTDPTEI QTIREYYKHL YANKLENLEEMDKFLDTYTLPRLNQEEVESLNRPITSSEI EAVI NSLPTKKSPGPDGFTAEEF	480				
	490	500	510	520	530	540	550	560
ORF2 PA8 ORF2 PA (corrected)	YQRYKEELVPFLLKLFQTI EKEGLLPNSFYEASIILIPKPGRDTTKKENFRPISLMNIDAKILNKILANRIQHQIKKLIH	560	YQRYKEELVPFLLKLFQTI EKEGLLPNSFYEASIILIPKPGRDTTKKENFRPISLMNIDAKILNKILANRIQHQIKKLIH	560				
	570	580	590	600	610	620	630	640
ORF2 PA8 ORF2 PA (corrected)	HDQVGFI PGMQGWFNI RKSIVHII NRTNDKNHMIISI DAEKA FDKIQHPFMLKTLNKLIGIDGTYLKIRAIYDKPIAN	640	HDQVGFI PGMQGWFNI RKSIVHII NRTNDKNHMIISI DAEKA FDKIQHPFMLKTLNKLIGIDGTYLKIRAIYDKPIAN	640				
	650	660	670	680	690	700	710	720
ORF2 PA8 ORF2 PA (corrected)	ITLNGQKLEAFPLKTGTRQGCPLSPLLNFIVLEVLARAI RQEKEIKGIIQI GREEVKLSLFADDMIVYLENPIVSAPKLLK	720	ITLNGQKLEAFPLKTGTRQGCPLSPLLNFIVLEVLARAI RQEKEIKGIIQI GREEVKLSLFADDMIVYLENPIVSAQKLLK	720				
	730	740	750	760	770	780	790	800
ORF2 PA8 ORF2 PA (corrected)	LISNFSKVSGYKINVQKSQLYTNNRQAESQMELPFTIATKRYKLGQLTRDKLFDKLYKPLKEIREDTNKWK	800	LISNFSKVSGYKINVQKSQLYTNNRQAESQMELPFTIATKRYKLGQLTRDVKDFKLYKPLKEIREDTNKWK	800				
	810	820	830	840	850	860	870	880
ORF2 PA8 ORF2 PA (corrected)	NIPCSWGRINIVKMAILPKVIYRFNAIPIKLPLTFFAELEKTTLNFIWNQKRARIAKTILSKKNKAGGITLPDFKLYYK	880	NIPCSWGRINIVKMAILPKVIYRFNAIPIKLPLTFFAELEKTTLNFIWNQKRARIAKTILSKKNKAGGITLPDFKLYYK	880				
	890	900	910	920	930	940	950	960
ORF2 PA8 ORF2 PA (corrected)	ATVTKTAWWYQNRYIDQWNRTETSEITPHIYNHLIFNKPDKNQWGKDSL FNKWCWENWLAI CRKLKLDPLTPYTKIN	960	ATVTKTAWWYQNRYIDQWNRTETSEITPHIYNHLIFDKPDKNQWGKDSL FNKWCWENWLAI CRKLKLDPLTPYTKIN	960				
	970	980	990	1000	1010	1020	1030	1040
ORF2 PA8 ORF2 PA (corrected)	SRW KDLNVKPKTI KTLEENL GNTI QDI GMGKDFMTKTPKAMATKAKIDKWDLKLKSFCTAKETI IRVN RQPTEW EKI F	1040	SRW KDLNVKPKTI KTLEENL GNTI QDI GMGKDFMTKTPKAMATKAKIDKWDLKLKSFCTAKETI IRVN RQPTEW EKI F	1040				
	1050	1060	1070	1080	1090	1100	1110	1120
ORF2 PA8 ORF2 PA (corrected)	AIYPSDKGLISRYKELKQIYKKKTNNPICKWAKDMNRHFSKEDIYAANKHMKSSSLVIREMQUIKTTMRYHLT PVRMA	1120	AIYPSDKGLISRYKELKQIYKKKTNNPICKWAKDMNRHFSKEDIYAANKHMKSSSLVIREMQUIKTTMRYHLT PVRMA	1120				
	1130	1140	1150	1160	1170	1180	1190	1200
ORF2 PA8 ORF2 PA (corrected)	I I KKSGNNRCWRGCGEI GTL LHCWMECKLVQPLWKTWRFKLKDEPEIPFDPAIPLLGIYPKDYKSFYYKDTCTRMFI AA	1200	I I KKSGNNRCWRGCGEI GTL LHCWMECKLVQPLWKTWRFKLKDEPEIPFDPAIPLLGIYPKDYKSFYYKDTCTRMFI AA	1200				
	1210	1220	1230	1240	1250	1260	1270	
ORF2 PA8 ORF2 PA (corrected)	LFTI AKTNQPKCPMSIDWKKMWHIYTMEYYAAIKRNEFMSFAGTWMKLEAI ILSKLTQEOKTKHRMFSLISGS	1275	LFTI AKTNQPKCPMSIDWKKMWHIYTMEYYAAIKRNEFMSFAGTWMKLEAI ILSKLTQEOKTKHRMFSLISGS	1275				

Supplemental Figure S1. The alignment of the predicted amino acid sequence of the available consensus sequence of the L1PA8 ORF2 protein and the corrected L1PA8 ORF2 protein is shown. The amino acids selected for modification are highlighted by black boxes.