

Novel sequence	Top BLASTn hit	Top BLASTx hit	Identity/coverage top BLAST nt (%)	Identity/coverage top BLAST aa (%)	Accession number of top BLASTn hit	Accession number of top BLASTx hit
OQ818316	<i>Bat picornavirus 1 strain LMH22A</i>	polyprotein [<i>African bat icavirus</i>]	93.18/0	46.51/81	HQ595341.1	YP_009121743.1
OQ818317	<i>Kunsagivirus B clone Bat/CAM/KuV-P2/2013</i>	polyprotein [<i>Kunsagivirus B</i>]	81.93/95	91.61/90	NC_033818.1	YP_009345896.1
OQ818318	<i>Bat picornavirus 1 strain LMH22A</i>	polyprotein [<i>Teschovirus A</i>]	81.95/1	44.42/90	HQ595341.1	AYD75972.1
OQ818319	NA	polyprotein [<i>Bat sapovirus</i>]	NA/NA	67.15/99	NA	AQQ78883.1
OQ818320	<i>Bat sapelovirus clone Bat/CAM/Sap-P24/2013</i>	polyprotein [<i>Bat sapelovirus</i>]	94.37/99	98.95/96	KX644938.1	YP_009345901.1
OQ818321	<i>Bat sapelovirus clone Bat/CAM/Sap-P24/2013</i>	polyprotein [<i>Bat sapelovirus</i>]	73.31/96	75.75/95	KX644938.1	YP_009345901.1
OQ818322	<i>Eidolon dupreanum kobuvirus</i>	polyprotein [<i>Eidolon dupreanum kobuvirus</i>]	99.42/98	99.88/87	OP287812.1	WBP49885.1
OQ818323	<i>Sapelovirus-like porcine picornavirus</i>	polyprotein [<i>teschovirus A6</i>]	77.36/89.90	44.26/88	LC386162.1	QWS67609.1
OQ818324	<i>Feline picornavirus</i>	polyprotein [<i>Porcine teschovirus 16</i>]	78.74/1	43/89	NC_016156.1	BBE37019.1
OQ818325	<i>Marmot sapelovirus 2 strain HT6</i>	polyprotein [<i>Bat picornavirus 3</i>]	78.86/3	59.57/91	KY855433.1	YP_004782204.1
OQ818326	NA	polyprotein 1 [<i>Mulberry mosaic leaf roll associated virus</i>]	NA/NA	39.51/77	NA	QIK02125.1
OQ818327	NA	polyprotein P2-V [<i>Arabis mosaic virus</i>]	NA/NA	28.50/62	NA	ADJ39333.1
OQ818328	<i>Marmot sapelovirus 2 strain HT6</i>	polyprotein [<i>Bat picornavirus 3</i>]	78.86/3	59.90/91	KY855433.1	YP_004782204.1
OQ818329	<i>Bat sapelovirus clone Bat/CAM/Sap-P24/2013</i>	polyprotein [<i>Bat sapelovirus</i>]	84.34/4	64.02/96	KX644938.1	YP_009345901.1