

Sequence	Gene	Top BLAST hit nt	Top BLAST hit aa	% identity/coverage top BLAST nt	% identity/coverage top BLAST aa	accession number of top BLAST nt	accession number of top BLAST aa
<b>OQ818316</b>	Full sequence	Bat picornavirus 1 strain LMH22A	polyprotein [African bat icavirus]	93.18/0	46.51/81	HQ595341.1	YP_009121743.1
<b>OQ818317</b>	Full sequence	Kunsagivirus B clone Bat/CAM/KuV-P2/2013 polyprotein gene, complete cds	polyprotein [Kunsagivirus B]	81.93/95	91.61/90	NC_033818.1	YP_009345896.1
<b>OQ818318</b>	Full sequence	Bat picornavirus 1 strain LMH22A	polyprotein [Teschovirus A]	81.95/1	44.42/90	HQ595341.1	AYD75972.1
<b>OQ818319</b>	Full sequence	NA	polyprotein [Bat sapovirus]	NA/NA	67.15/99	NA	AQQ78883.1
<b>OQ818320</b>	Full sequence	Bat sapelovirus clone Bat/CAM/Sap-P24/2013 polyprotein gene, complete cds	polyprotein [Bat sapelovirus]	94.37/99	98.95/96	KX644938.1	YP_009345901.1
<b>OQ818321</b>	Full sequence	Bat sapelovirus clone Bat/CAM/Sap-P24/2013 polyprotein gene, complete cds	polyprotein [Bat sapelovirus]	73.31/96	75.75/95	KX644938.1	YP_009345901.1
<b>OQ818322</b>	Full sequence	Eidolon dupreanum kobuvirus, complete genome	polyprotein [Eidolon dupreanum kobuvirus]	99.42/98	99.88/87	OP287812.1	WBP49885.1
<b>OQ818323</b>	Full sequence	Sapelovirus-like porcine picornavirus Japan Pig/Isi-lm1/JPN/2015 genomic RNA, nearly complete genome	polyprotein [teschovirus A6]	77.36/89.90	44.26/88	LC386162.1	QWS67609.1
<b>OQ818324</b>	Full sequence	Feline picornavirus	polyprotein [Porcine teschovirus 16]	78.74/1	43/89	NC_016156.1	BBE37019.1
<b>OQ818325</b>	Full sequence	Marmot sapelovirus 2 strain HT6, complete genome	polyprotein [Bat picornavirus 3]	78.86/3	59.57/91	KY855433.1	YP_004782204.1
<b>OQ818326</b>	Full sequence	NA	polyprotein 1 [Mulberry mosaic leaf roll associated virus]	NA/NA	39.51/77	NA	QIK02125.1
<b>OQ818327</b>	Full sequence	NA	polyprotein P2-V [Arabis mosaic virus]	NA/NA	28.50/62	NA	ADJ39333.1
<b>OQ818328</b>	Full sequence	Marmot sapelovirus 2 strain HT6, complete genome	polyprotein [Bat picornavirus 3]	78.86/3	59.90/91	KY855433.1	YP_004782204.1
<b>OQ818329</b>	Full sequence	Bat sapelovirus clone Bat/CAM/Sap-P24/2013 polyprotein gene, complete cds	polyprotein [Bat sapelovirus]	84.34/4	64.02/96	KX644938.1	YP_009345901.1