

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
OQ818330	NA	<i>Arracacha virus B</i>	NA/NA	57.24/87	NA	QCY50806.1
OQ818331	NA	<i>Tetnovirus 1</i>	NA/NA	62.75/83	NA	ADK97708.1
OQ818332	<i>Victoria bee virus 2</i>	<i>Victoria bee virus 2</i>	89.41/99	92.14/99	MG995724.1	AWK77887.1
OQ818333	NA	<i>Rondonia picorna-like virus</i>	NA/NA	22.87/34	NA	QHI42122.1
OQ818334	<i>Victoria bee virus 2</i>	<i>Victoria bee virus 2</i>	97.83/100	97.64/99	MG995724.1	AWK77887.1
OQ818335	<i>Bat felisavirus</i>	<i>Bat felisavirus</i>	80.99/97	91.01/56	KX644943.1	AQP31140.1
OQ818336	<i>Victoria bee virus 2</i>	<i>Victoria bee virus 2</i>	90.63/100	93.03/98	MG995724.1	AWK77887.1
OQ818337	<i>Hepatovirus H2</i>	<i>Hepatovirus H2</i>	82.40/97	94.75/87	NC_028366.1	YP_009179216.1
OQ818338	<i>Aphid lethal paralysis virus</i>	<i>Aphid lethal paralysis virus</i>	93.86/100	98.34/99	MF458893.1	QFI36301.1
OQ818339	<i>Eotetranychus kankitus picorna-like virus</i>	<i>Picornavirales sp.</i>	73.35/14	45.56/99	MN745092.1	ULF99664.1
OQ818340	<i>Bat sapovirus</i>	<i>Bat sapovirus</i>	71.40/63	67.97/99	KX759619.1	AQQ78883.1
OQ818341	<i>Bat felisavirus</i>	<i>Bat felisavirus</i>	85.33/99	95.74/97	KX644943.1	AQP31140.1
OQ818342	<i>Bat sapelovirus</i>	<i>Bat sapelovirus</i>	94.73/99	98.47/99	KX644938.1	YP_009345901.1
OQ818343	<i>Bat sapelovirus</i>	<i>Bat sapelovirus</i>	92.28/100	98.67/99	KX644938.1	YP_009345901.1
OQ818344	<i>Bat sapelovirus</i>	<i>Bat sapelovirus</i>	94.57/99	99.15/99	KX644938.1	YP_009345901.1
OQ818345	NA	<i>Bat sapovirus BtSY3</i>	NA/NA	54.97/97	NA	WBV74435.1
OQ818346	Bat picornavirus	<i>Wilde virus 3</i>	81.94/15	57.23/93	ON168930.1	QQR34440.1
OQ818347	<i>Sapovirus Hu/GI.6/Nichinan/FP05284/2005/JPN</i>	<i>Bat sapovirus BtSY2</i>	72.44/11	75.80/99	LC380411.1	WBV74378.1
OQ818348	NA	<i>Bat sapovirus BtSY1</i>	NA/NA	59.91/99	NA	WBV74377.1