BLAST Analysis of Monkeypox PT0001 against Influenza H1N1

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1 Introduction

The study conducted blastn analysis on the sequence of Monkeypox virus (PT0001) against influenza virus H1N1. Considering there is no hitting when blast analysis with whole length of Monkeypox virus, we spliced the Monkeypox virus genome sequence into segments of 1,000bp with sliding windows of 50bp, and then conducted blast analysis on these segments against sequences of influenza virus.

2 Methods

2.1 Monkeypox sequence splicing

The sequence of Monkeypox virus (strain PT0001, collected on Portgual on 5/4/2022) were spliced into segments of 1,000bp length, with starting positions shifting from 1 to 95 at interval of 50bp. In total 20 sets of segments were created.

2.2 Blast analysis

The 20 sets of Monkeypox genome segments were compared against sequences of influenza downloaded from NCBI (https://ftp.ncbi.nih.gov/genomes/INFLUENZA/) with blastn tools (2.13.0+) on a linux server, respectively.

2.3 Results retrieving and sorting

The hits/alignments on variants of influenza H1N1 viruses reported by the blast analysis were retrieved with customized python scripts. Common hits across different sets of Monkeypox genome segments were merged.

3 Results

There are 238 hits reported by blast analysis between 16 Monkeypox segments and 232 Influenza sequences, after merging all the blast results from 20 sets of Monkeypox genome segments.

Table 1: Number of hits by segments of Monkeypox virus genome sequences

Monkeypox	sequence	hits
Monkeypox/PT0001/2022 | sampling date 2022-05-04 106451-106481	CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT	132
Monkeypox/PT0001/2022 | sampling date 2022-05-04 159286-159310	CAATTCCATTATTCTCTTAGCTGCC	36
Monkeypox/PT0001/2022 | sampling date 2022-05-04 167616-167657	GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG	27
Monkeypox/PT0001/2022 | sampling date 2022-05-04 172714-172740	TGAAGACCATCCCACTAGTAA-CAGTCT	10
Monkeypox/PT0001/2022 | sampling date 2022-05-04 167610-167657	TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG	9
Monkeypox/PT0001/2022 | sampling date 2022-05-04 76555-76579	TGGGAATAGAAACCAGATTAAAACA	5
Monkeypox/PT0001/2022 | sampling date 2022-05-04 77698-77733	GAATGCCATTTACGGATTCACCAATAAAAATAAACT	3
Monkeypox/PT0001/2022 | sampling date 2022-05-04 168709-168753	AAACACGTCTTGGATCATCNCATACATATATTAAATTCAGTAACA	3
Monkeypox/PT0001/2022 | sampling date 2022-05-04 77701-77733	TGCCATTTACGGATTCACCAATAAAAATAAACT	3
Monkeypox/PT0001/2022 | sampling date 2022-05-04 167630-167657	ATTTTGATTCCNAAATTGAATGGACTGG	2
Monkeypox/PT0001/2022 | sampling date 2022-05-04 167616-167658	GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGGG	2
Monkeypox/PT0001/2022 | sampling date 2022-05-04 152962-152991	ATATAAAGAAAAATCTAAATTAATTAGAGA	2
Monkeypox/PT0001/2022 | sampling date 2022-05-04 29666-29690	CTTCCCCTATAATCTTCGTCTATTA	1
Monkeypox/PT0001/2022 | sampling date 2022-05-04 167614-167657	AAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG	1
Monkeypox/PT0001/2022 | sampling date 2022-05-04 78655-78693	ATATATTAAAGTCGAATAAAGTTGAAAAATAATTAATTC	1
Monkeypox/PT0001/2022 | sampling date 2022-05-04 168213-168243	AGAAG-ATGTTCCCAATTTCAAGGACAAAATA	1

Table 2: Number of hits by influenza sequences

Influenza	hits
> gi|1060099600|gb|KX651622|Influenza A virus (A/France/556-P2T/2009(H1N1)) segment 6 neuraminidase (NA) gene, partial cds Length=1288	2
> gi|1243281195|gb|MF768483|Influenza A virus (A/swine/Saskatchewan/SD0094/2015(H1N1)) segment 4 hemagglutinin (HA) gene, partial cds	2
> gi|1060099598|gb|KX651621|Influenza A virus (A/France/556-1T/2009(H1N1)) segment 6 neuraminidase (NA) gene, partial cds Length=1246	2
> gi|300217057|gb|HM598355|Influenza A virus (A/Thailand/CU-MV52/2010(H1N1)) segment 6 neuraminidase (NA) gene, partial cds Length=1288	2
> gi|1253893475|gb|CY245721|Influenza A virus (A/swine/Saskatchewan/SD0082/2015(H1N1)) hemagglutinin (HA) gene, complete cds Length=1701	2
> gi|974752620|gb|CY195455|Influenza A virus (A/swine/Saskatchewan/SD0056/2014(H1N1)) hemagglutinin (HA) gene, complete cds Length=1701	2
> gi|323696882|gb|CY084089|Influenza A virus (A/Puerto Rico/8-JV2/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|392357030|gb|CY121667|Influenza A virus (A/reassortant/NYMC X-177A(Hong Kong/1870/2008 x Puerto Rico/8/1934)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|323695999|gb|CY083993|Influenza A virus (A/Puerto Rico/8-9VMC2/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|459681168|gb|CY138623|Influenza A virus (A/American black duck/Nova Scotia/00096/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|323696075|gb|CY084025|Influenza A virus (A/Puerto Rico/8-CV2/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|1177505|gb|Z54291|Influenza A virus (Mongolia/153/88 (H1N1)) nucleoprotein gene Length=1518	1
> gi|298853453|gb|CY065101|Influenza A virus (A/New York/7426/2009(H1N1)) segment 6, complete sequence Length=1420	1
> gi|339518872|gb|JN185138|Influenza A virus (A/Tula/CRIE-LMV/2011(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|268507374|gb|CY050422|Influenza A virus (A/Wisconsin/629-D02206/2009(H1N1)) segment 6, complete sequence Length=1420	1
> gi|392350173|gb|CY121392|Influenza A virus (A/reassortant/X-139(X-31B x New Caledonia/20/1999)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|1356470707|gb|MH031338|Influenza A virus (A/swine/Iowa/A01785439/2018(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|1366793715|gb|MH085242|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone OP7-5 segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|268634439|gb|CY051145|Influenza A virus (A/Wisconsin/629-D01734/2009(H1N1)) segment 6, complete sequence Length=1417	1
> gi|523511807|gb|CY147529|Influenza A virus (A/Puerto Rico/8-SV13/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|662496441|gb|KJ942635|Influenza A virus (A/reassortant/NYMC X-179(NYMC X-157 x A/California/07/2009)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|563408536|gb|KF840466|Influenza A virus (A/swine/London/Scholtissek lab(H1N1)) segment 2 polymerase PB1 (PB1) and putative PB1-F2 protein (PB1-F2) genes, complete cds	1
> gi|459681308|gb|CY138679|Influenza A virus (A/American black duck/New Brunswick/00328/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1

Table 2: Number of hits by influenza sequences *(continued)*

Influenza	hits
> gi|1366793691|gb|MH085233|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone OP7-1 segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|339736825|gb|JN193423|Influenza A virus (A/swine/MN/25618/2011(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|1177501|gb|Z54292|Influenza A virus (A/Mongolia/111/91 (H1N1)) nucleoprotein gene Length=1518	1
> gi|1366793723|gb|MH085245|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone PP-1 segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|512248800|gb|CY146860|Influenza A virus (A/Puerto Rico/8-SV40/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|596604082|gb|CY180795|Influenza A virus (A/green-winged teal/Wisconsin/535/1976(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|189230379|gb|CY032219|Influenza A virus (A/swine/Wisconsin/1/1961(H1N1)) segment 2, complete sequence Length=2298	1
> gi|392356627|gb|CY121627|Influenza A virus (A/reassortant/NYMC X-173C(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|585479340|gb|KJ206107|Influenza A virus (A/swine/North Carolina/A01410044/2013(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|323697256|gb|CY084121|Influenza A virus (A/Puerto Rico/8-KV1/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|745991135|gb|AB910573|Influenza A virus (A/swine/Kagoshima/23/2012(H1N1)) viral cRNA, segment 6, complete sequence, strain: A/swine/Kagoshima/23/2012(H1N1)	1
> gi|459680849|gb|CY138567|Influenza A virus (A/mallard/Nova Scotia/00088/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds Length=2307	1
> gi|323695942|gb|CY083969|Influenza A virus (A/Puerto Rico/8-9NMC2/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|292495973|gb|CY058512|Influenza A virus (A/reassortant/NYMC X-179(California/07/2009 x NYMC X-157)(H1N1)) segment 5 sequence Length=1550	1
> gi|1366793731|gb|MH085248|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone PP-5 segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|208344071|gb|CY035121|Influenza A virus (A/NYMC X-163B(NYMC X-157-St. Petersburg/8/2006)(H1N1)) segment 5, complete sequence Length=1530	1
> gi|459680013|gb|CY138287|Influenza A virus (A/blue-winged teal/Nova Scotia/00121/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|459681509|gb|CY138760|Influenza A virus (A/mallard/New Brunswick/00340/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|257165112|gb|CY045767|Influenza A virus (A/Puerto Rico/8-1/1934(H1N1)) segment 5, complete sequence Length=1501	1
> gi|523511767|gb|CY147513|Influenza A virus (A/Puerto Rico/8-SV10/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|910269612|gb|KT314335|Influenza A virus (A/Puerto Rico/8HY/1934(H1N1)) segment 5 nucleoprotein (NP) gene, complete cds Length=1565	1
> gi|125976187|gb|CY019958|Influenza A virus (A/Alaska/1935(H1N1)) segment 5, complete sequence Length=1528	1
> gi|1366793747|gb|MH085254|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone PR8-RKI segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|523511547|gb|CY147425|Influenza A virus (A/New Jersey/Wistar/1976(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|712040567|gb|KP019768|Influenza A virus (A/FuZhou/SWL129/2013(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|459681268|gb|CY138663|Influenza A virus (A/mallard/New Brunswick/00324/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|746645839|gb|KP288107|Influenza A virus (A/swine/North Carolina/A01476912/2014(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|392357104|gb|CY121699|Influenza A virus (A/reassortant/NYMC X-181A(A/NYMC X-157 x California/07/2009)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|512252239|gb|CY146892|Influenza A virus (A/Puerto Rico/8-KV20/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|323696113|gb|CY084041|Influenza A virus (A/Puerto Rico/8-CV6/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|404502817|gb|CY116396|Influenza A virus (A/swine/OMS/2111/1995(H1N1)) hemagglutinin (HA) gene, complete cds Length=1701	1
> gi|1352367018|gb|MH006711|Influenza A virus (A/swine/Michoacan/MichDMZC10/2015(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|323695720|gb|CY083953|Influenza A virus (A/Puerto Rico/8-MC/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|158426703|gb|CY026433|Influenza A virus (A/swine/Jamesburg/1942(H1N1)) segment 2, complete sequence Length=2297	1
> gi|323697408|gb|CY084185|Influenza A virus (A/Puerto Rico/8-V24/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|372349484|gb|CY105899|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1524	1
> gi|392356608|gb|CY121619|Influenza A virus (A/reassortant/NYMC X-173B(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|392357122|gb|CY121707|Influenza A virus (A/reassortant/NYMC X-181B(A/NYMC X-157 x California/07/2009)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|260593826|gb|CY047401|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 5 sequence Length=1564	1
> gi|1717351649|gb|MN254405|Influenza A virus (A/Lesser Snow Goose/Arkansas/AH0085499S.3.A/2016(H1N1)) clone A segment 3 polymerase PA (PA) and PA-X protein (PA-X) genes, partial cds	1
> gi|528917074|gb|KF424231|Influenza A virus (A/blue winged teal/Alberta/212/1984(H1N1)) segment 1 polymerase PB2 (PB2) gene, complete cds	1
> gi|523511827|gb|CY147537|Influenza A virus (A/Puerto Rico/8-SV14/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|145322854|gb|EF190983|Influenza A virus (A/lvPR8/34(H1N1)) segment 5, complete sequence Length=1565	1
> gi|323695980|gb|CY083985|Influenza A virus (A/Puerto Rico/8-9VMC1/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|284027628|gb|GU471692|Influenza A virus (A/Guangdong/1104/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1415	1
> gi|324969|gb|M55472|Influenza A virus (A/swine/1976/1931(H1N1)) polymerase gene, complete cds Length=2317	1
> gi|89779327|gb|CY009447|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1537	1
> gi|323696056|gb|CY084017|Influenza A virus (A/Puerto Rico/8-CV1/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|425786331|gb|CY128453|Influenza A virus (A/Viet Nam/001-1880/2009(H1N1)) neuraminidase (NA) gene, complete cds Length=1432	1
> gi|291264370|gb|GU983255|Influenza A virus (A/Eastern India/2493/2009(H1N1)) segment 6 neuraminidase (NA) gene, partial cds Length=1356	1

Table 2: Number of hits by influenza sequences *(continued)*

Influenza	hits
> gi|459681669|gb|CY138824|Influenza A virus (A/American black duck/New Brunswick/00385/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|523511647|gb|CY147465|Influenza A virus (A/Puerto Rico/8-LVD4/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|323696920|gb|CY084105|Influenza A virus (A/Puerto Rico/8-JV9/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|194304809|gb|CY033580|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 5, complete sequence Length=1524	1
> gi|291264376|gb|GU983258|Influenza A virus (A/Eastern India/2503/2009(H1N1)) segment 6 neuraminidase (NA) gene, partial cds Length=1349	1
> gi|512249910|gb|CY146868|Influenza A virus (A/Puerto Rico/8-SV60/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|459680829|gb|CY138559|Influenza A virus (A/American black duck/Nova Scotia/00086/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|459681489|gb|CY138752|Influenza A virus (A/mallard/New Brunswick/00339/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|320006586|gb|HQ877025|Influenza A virus (A/swine/Guangdong/L3/2009(H1N1)) segment 2 polymerase PB1 (PB1) gene, complete cds	1
> gi|587680786|gb|KJ397940|Influenza A virus (A/swine/North Carolina/A01410047/2013(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|400315883|gb|JX416721|Influenza A virus (A/reassortant/IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|459681228|gb|CY138647|Influenza A virus (A/American black duck/New Brunswick/00321/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|512250611|gb|CY146876|Influenza A virus (A/Puerto Rico/8-SV120/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|89941395|gb|CY009634|Influenza A virus (A/swine/1931(H1N1)) segment 2, complete sequence Length=2302	1
> gi|323697294|gb|CY084137|Influenza A virus (A/Puerto Rico/8-KV3/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|392357086|gb|CY121691|Influenza A virus (A/reassortant/NYMC X-181(A/NYMC X-157 x California/07/2009)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|372349519|gb|CY105915|Influenza A virus (A/Puerto Rico/8-SV4/1934(H1N1)) nucleocapsid protein (NP) gene, partial cds Length=1495	1
> gi|323696423|gb|CY084073|Influenza A virus (A/Puerto Rico/8-CV10/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|1366793699|gb|MH085236|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone OP7-3 segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|78096033|gb|CY004599|Influenza A virus (A/mallard duck/ALB/127/1977(H1N1)) segment 1, complete sequence Length=2341	1
> gi|392345391|gb|CY121272|Influenza A virus (A/reassortant/X-83(Chile/1/1983 x X-31)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|459681469|gb|CY138744|Influenza A virus (A/mallard/New Brunswick/00337/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|225733652|gb|CY037929|Influenza A virus (A/swine/France/WVL13/1995(H1N1)) segment 4 sequence Length=1701	1
> gi|484849244|gb|KC866598|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|459681731|gb|CY138849|Influenza A virus (A/American black duck/New Brunswick/00410/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|338220961|gb|CY092720|Influenza A virus (A/Sydney/DD3-52/2010(H1N1)) neuraminidase (NA) gene, complete cds Length=1420	1
> gi|546236506|gb|KF612138|Influenza A virus (A/Santa Cruz/87212/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1458	1
> gi|474456754|gb|KC780561|Influenza A virus (A/Minnesota/15/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|323695923|gb|CY083961|Influenza A virus (A/Puerto Rico/8-9NMC1/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|474456305|gb|KC780371|Influenza A virus (A/Florida/30/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|479284794|gb|KC815515|Influenza A virus (A/Puerto Rico/8-RG001C/1934(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|523511727|gb|CY147497|Influenza A virus (A/Puerto Rico/8-SV8/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|459680889|gb|CY138583|Influenza A virus (A/American black duck/Nova Scotia/00090/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|307069302|gb|HQ247714|Influenza A virus (A/Finland/687/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|1069560153|gb|LC120392|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) RNA, segment 5, complete sequence Length=1565	1
> gi|538118479|gb|CY148246|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|372349503|gb|CY105907|Influenza A virus (A/Puerto Rico/8-SV2/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1524	1
> gi|523511787|gb|CY147521|Influenza A virus (A/Puerto Rico/8-SV11/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|304420504|gb|CY072672|Influenza A virus (A/Managua/1054.02/2009(H1N1)) segment 6, complete sequence Length=1420	1
> gi|323696132|gb|CY084049|Influenza A virus (A/Puerto Rico/8-CV7/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|523511687|gb|CY147481|Influenza A virus (A/Puerto Rico/8-SV5/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|459680033|gb|CY138295|Influenza A virus (A/blue-winged teal/Nova Scotia/00126/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|156536590|gb|CY025063|Influenza A virus (A/swine/Tennessee/48/1977(H1N1)) segment 2, complete sequence Length=2299	1
> gi|284027641|gb|GU470881|Influenza A virus (A/swine/Indiana/27007/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|433680166|gb|CY130013|Influenza A virus (A/duck/Alberta/35/1976(H1N1)) polymerase PB2 (PB2) gene, complete cds Length=2316	1
> gi|218875175|gb|CY036922|Influenza A virus (A/NYMC X-163A(NYMC X-157-St. Petersburg/8/2006)(H1N1)) segment 5, complete sequence Length=1523	1
> gi|523511627|gb|CY147457|Influenza A virus (A/Puerto Rico/8-LVD2/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|392357479|gb|CY121859|Influenza A virus (A/reassortant/NYMC X-205A(NYMC X-157 x South Carolina/10/2010)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|459681589|gb|CY138792|Influenza A virus (A/mallard/New Brunswick/00349/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1

Table 2: Number of hits by influenza sequences *(continued)*

Influenza	hits
> gi|323696901|gb|CY084097|Influenza A virus (A/Puerto Rico/8-JV3/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|523511516|gb|CY147412|Influenza A virus (A/swine/JY2/1931(H1N1)) polymerase PB1 (PB1) gene, complete cds; and PB1-F2 gene, complete sequence	1
> gi|343787293|gb|CY096838|Influenza A virus (A/X-139(X-31B-New Caledonia/20/1999)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|662496878|gb|KJ942811|Influenza A virus (A/reassortant/X-139(X-31B x New Caledonia/20/1999)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|662494957|gb|KM029681|Influenza A virus (A/swine/Guangdong/NS2434/2012(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|474459290|gb|KC781642|Influenza A virus (A/California/35/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|60750|gb|V01084|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) gene for nucleoprotein, genomic RNA Length=1565	1
> gi|297595768|gb|CY064435|Influenza A virus (A/Guangdong/1240/2009(H1N1)) segment 6 sequence Length=1410	1
> gi|552055568|gb|KF687932|Influenza A virus (A/Cyprus/504/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|146759958|gb|CY021960|Influenza A virus (A/New Jersey/1976(H1N1)) segment 5, complete sequence Length=1532	1
> gi|326987189|gb|JF714030|Influenza A virus (A/swine/MB/46/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|698321881|gb|KM596716|Influenza A virus (A/swine/Japan/KU-YG5/2013(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|523511747|gb|CY147505|Influenza A virus (A/Puerto Rico/8-SV9/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|1366793739|gb|MH085251|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone PP-6 segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|662496680|gb|KJ942731|Influenza A virus (A/reassortant/NYMC X-179A(NYMC X-157 x A/California/07/2009)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|323697313|gb|CY084145|Influenza A virus (A/Puerto Rico/8-KV4/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|133754138|gb|CY020448|Influenza A virus (A/Henry/1936(H1N1)) segment 5, complete sequence Length=1530	1
> gi|304422849|gb|CY072984|Influenza A virus (A/Managua/5273.02/2009(H1N1)) segment 6, complete sequence Length=1420	1
> gi|766554047|gb|KP765783|Influenza A virus (A/NanChang/08/2010(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|323696404|gb|CY084065|Influenza A virus (A/Puerto Rico/8-CV9/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|459681288|gb|CY138671|Influenza A virus (A/American black duck/New Brunswick/00326/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|323697370|gb|CY084169|Influenza A virus (A/Puerto Rico/8-KV7/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|253584644|gb|GQ369418|Influenza A virus (A/swine/Alberta/OTH-33-21/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|237689099|gb|CY040173|Influenza A virus (A/Puerto Rico/8-SV14/1934(H1N1)) segment 5, complete sequence Length=1500	1
> gi|208343881|gb|CY035033|Influenza A virus (A/X-53A(Puerto Rico/8/1934-New Jersey/11/1976)(H1N1)) segment 5, complete sequence Length=1526	1
> gi|324691|gb|M38279|Influenza A virus (A/Puerto Rico/8/34(H1N1)) nucleoprotein gene, complete cds Length=1565	1
> gi|400315828|gb|JX416729|Influenza A virus (A/reassortant/IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|61197035|gb|AY936882|Influenza A virus (A/Puerto Rico/8/34(H1N1)) clone NP3-aPR8-34 nucleoprotein gene, partial cds Length=1494	1
> gi|323697389|gb|CY084177|Influenza A virus (A/Puerto Rico/8-KV8/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|459680909|gb|CY138591|Influenza A virus (A/American black duck/Nova Scotia/00091/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|78095797|gb|CY004481|Influenza A virus (A/pintail duck/ALB/219/1977(H1N1)) segment 1, complete sequence Length=2341	1
> gi|686690865|gb|KM409531|Influenza A virus (A/swine/North Carolina/A01476197/2014(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|662494977|gb|KM029689|Influenza A virus (A/swine/Guangdong/2481/2012(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|324709|gb|J02147|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 5, complete sequence Length=1565	1
> gi|323696018|gb|CY084001|Influenza A virus (A/Puerto Rico/8-9VMC3/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|21693170|gb|AF389119|Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1)) segment 5, complete sequence Length=1565	1
> gi|459680809|gb|CY138551|Influenza A virus (A/mallard/Nova Scotia/00085/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds Length=2316	1
> gi|392357461|gb|CY121851|Influenza A virus (A/reassortant/NYMC X-205(NYMC X-157 x South Carolina/10/2010)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|317016255|gb|HQ840310|Influenza A virus (A/swine/Minnesota/130A/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|705550511|gb|KM985433|Influenza A virus (A/Kottayam/MCVR6946/2011(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|1027918528|gb|KX135815|Influenza A virus (A/California/04-183-MA/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|372349536|gb|CY105923|Influenza A virus (A/Puerto Rico/8-SV7/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1530	1
> gi|459681208|gb|CY138639|Influenza A virus (A/American black duck/Nova Scotia/00099/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|392357049|gb|CY121675|Influenza A virus (A/reassortant/NYMC X-177B(Hong Kong/1870/2008 x Puerto Rico/8/1934)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|256385423|gb|CY044312|Influenza A virus (A/X-127(Puerto Rico/8/1934-Beijing/262/1995)(H1N1)) segment 5, complete sequence Length=1500	1
> gi|323697351|gb|CY084161|Influenza A virus (A/Puerto Rico/8-KV6/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|226954791|gb|CY038898|Influenza A virus (A/Puerto Rico/8-SV1/1934(H1N1)) segment 5, complete sequence Length=1500	1
> gi|226954810|gb|CY038906|Influenza A virus (A/Puerto Rico/8-SV3/1934(H1N1)) segment 5, complete sequence Length=1507	1
> gi|323696094|gb|CY084033|Influenza A virus (A/Puerto Rico/8-CV5/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|269315113|gb|GU186639|Influenza A virus (A/duck/Alberta/35/1976(H1N1)) segment 1 polymerase PB2 (PB2) gene, complete cds Length=2316	1
> gi|400315797|gb|JX416737|Influenza A virus (A/reassortant/IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1

Table 2: Number of hits by influenza sequences *(continued)*

Influenza	hits
> gi|459680969|gb|CY138615|Influenza A virus (A/American black duck/Nova Scotia/00094/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|194352358|gb|CY034127|Influenza A virus (A/NYMC X-163(NYMC X-157-St. Petersburg/8/2006)(H1N1)) segment 5, complete sequence Length=1527	1
> gi|323697332|gb|CY084153|Influenza A virus (A/Puerto Rico/8-KV5/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|596592631|gb|CY180010|Influenza A virus (A/mallard/Wisconsin/216/1979(H1N1)) polymerase PB2 (PB2) gene, complete cds Length=2316	1
> gi|512245169|gb|CY146828|Influenza A virus (A/Puerto Rico/8-LVD1/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|512246971|gb|CY146844|Influenza A virus (A/Puerto Rico/8-SV20/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|523511667|gb|CY147473|Influenza A virus (A/Puerto Rico/8-SV1/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|662494937|gb|KM029673|Influenza A virus (A/swine/Guangdong/NS2433/2012(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|649787197|gb|KJ856423|Influenza A virus (A/swine/Sri Lanka/72/2011(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|699978054|gb|KM821559|Influenza A virus (A/swine/North Carolina/A01476345/2014(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|459680929|gb|CY138599|Influenza A virus (A/American black duck/Nova Scotia/00092/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|323696385|gb|CY084057|Influenza A virus (A/Puerto Rico/8-CV8/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|1366793707|gb|MH085239|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) clone OP7-4 segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|512246232|gb|CY146836|Influenza A virus (A/Puerto Rico/8-LVD3/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|662496361|gb|KJ942603|Influenza A virus (A/reassortant/X-53(Puerto Rico/8/1934 x New Jersey/11/1976)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|392356570|gb|CY121603|Influenza A virus (A/reassortant/NYMC X-173(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|126599284|gb|EF467822|Influenza A virus (A/Puerto Rico/8/34(H1N1)) segment 5, complete sequence Length=1565	1
> gi|400315749|gb|JX414013|Influenza A virus (A/reassortant/IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|523511707|gb|CY147489|Influenza A virus (A/Puerto Rico/8-SV7/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|392343956|gb|CY121240|Influenza A virus (A/reassortant/X-65(USSR/90/1977 x Puerto Rico/8/1934)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|308269726|gb|CY075526|Influenza A virus (A/Boston/606/2009(H1N1)) segment 6, complete sequence Length=1420	1
> gi|1377224805|gb|MH201215|Influenza A virus (A/PR/8__RGCDC-4,6/34(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|705550525|gb|KM985440|Influenza A virus (A/Udupi/MCVR7048/2011(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|479284825|gb|KC815527|Influenza A virus (A/Puerto Rico/8-RG001A/1934(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|259017832|gb|CY046982|Influenza A virus (A/Puerto Rico/8-1-MA/1934(H1N1)) segment 5, complete sequence Length=1506	1
> gi|317016257|gb|HQ840318|Influenza A virus (A/swine/Minnesota/136B/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|317016253|gb|HQ840305|Influenza A virus (A/swine/Minnesota/130A/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds	1
> gi|1473283053|gb|MH879780|Influenza A virus (A/mallard/Wisconsin/A00751454/2009(H1N1)) segment 1 polymerase PB2 (PB2) gene, complete cds	1
> gi|512251480|gb|CY146884|Influenza A virus (A/Puerto Rico/8-CV10/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|323695961|gb|CY083977|Influenza A virus (A/Puerto Rico/8-9NMC3/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|323697275|gb|CY084129|Influenza A virus (A/Puerto Rico/8-KV2/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|372349587|gb|CY105946|Influenza A virus (A/Puerto Rico/8-SV13/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1519	1
> gi|307087791|gb|HQ256653|Influenza A virus (A/Myanmar/M535/2009(H1N1)) segment 6 neuraminidase (NA) gene, complete cds Length=1410	1
> gi|372477405|gb|CY105938|Influenza A virus (A/Puerto Rico/8-SV11/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1502	1
> gi|459681409|gb|CY138720|Influenza A virus (A/green-winged teal/New Brunswick/00333/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|78095835|gb|CY004497|Influenza A virus (A/mallard duck/ALB/965/1979(H1N1)) segment 1, complete sequence Length=2341	1
> gi|323696037|gb|CY084009|Influenza A virus (A/Puerto Rico/8-WG/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|459681569|gb|CY138784|Influenza A virus (A/mallard/Nova Scotia/00346/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds Length=2316	1
> gi|145559567|gb|EF190975|Influenza A virus (A/hvPR8/34(H1N1)) segment 5, complete sequence Length=1565	1
> gi|323696939|gb|CY084113|Influenza A virus (A/Puerto Rico/8-JV18/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1
> gi|22218187|gb|AF510857|Influenza A virus (A/Puerto Rico/8/34/Mount Sinai(H1N1)) nucleoprotein gene, partial cds Length=1025	1
> gi|1177513|gb|Z54290|Influenza A virus (Mongolia/231/85 (H1N1)) nucleoprotein gene Length=1518	1
> gi|392340012|gb|CY121112|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|157829262|gb|CY026289|Influenza A virus (A/swine/Wisconsin/1/1957(H1N1)) segment 2, complete sequence Length=2298	1
> gi|459680869|gb|CY138575|Influenza A virus (A/American black duck/Nova Scotia/00089/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1
> gi|1480163912|gb|MH785014|Influenza A virus (A/Puerto Rico/8/1934(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|392356589|gb|CY121611|Influenza A virus (A/reassortant/NYMC X-173A(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|158344942|gb|CY026425|Influenza A virus (A/swine/Tennessee/23/1976(H1N1)) segment 2, complete sequence Length=2299	1
> gi|512248015|gb|CY146852|Influenza A virus (A/Puerto Rico/8-SV30/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1540	1
> gi|323696442|gb|CY084081|Influenza A virus (A/Puerto Rico/8-JV1/1934(H1N1)) nucleocapsid protein (NP) gene, complete cds Length=1552	1

Table 2: Number of hits by influenza sequences *(continued)*

Influenza	hits
> gi|392356918|gb|CY121659|Influenza A virus (A/reassortant/NYMC X-177(Hong Kong/1870/2008 x Puerto Rico/8/1934)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|292495142|gb|CY058542|Influenza A virus (A/Managua/462.01/2009(H1N1)) segment 6, complete sequence Length=1420	1
> gi|459680949|gb|CY138607|Influenza A virus (A/mallard/Nova Scotia/00093/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds Length=2293	1
> gi|292495991|gb|CY058520|Influenza A virus (A/reassortant/NYMC X-179A(California/07/2009 x NYMC X-157)(H1N1)) segment 5 sequence Length=1524	1
> gi|982220222|gb|KU518835|Influenza A virus (A/swine/North Carolina/B58223/2014(H1N1)) segment 5 nucleocapsid protein (NP) gene, complete cds	1
> gi|299781723|gb|CY062630|Influenza A virus (A/X-53(Puerto Rico/8/1934-New Jersey/11/1976)(H1N1)) nucleocapsid protein (NP) gene, complete cds	1
> gi|914294355|gb|KT313551|Influenza A virus (A/swine/Pennsylvania/A01432180/2012(H1N1)) segment 2 polymerase PB1 (PB1) and PB1-F2 protein (PB1-F2) genes, complete cds	1
> gi|459680789|gb|CY138543|Influenza A virus (A/mallard/Nova Scotia/00084/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds Length=2307	1
> gi|459681188|gb|CY138631|Influenza A virus (A/American black duck/Nova Scotia/00098/2010(H1N1)) polymerase PB2 (PB2) gene, complete cds	1

3.1 Hits/Alignments

3.1.1 Monkeypox/PT0001/2022 | sampling date 2022-05-04 106451-106481:

CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT

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> gi|1480163912|gb|MH785014|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
segment 5 nucleocapsid protein (NP) gene, complete
cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|1377224805|gb|MH201215|Influenza A virus (A/PR/8_RGCDC-4,6/34(H1N1))
segment 5 nucleocapsid protein (NP) gene, complete
cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|1366793747|gb|MH085254|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone PR8-RKI segment 5 nucleocapsid protein (NP)
gene, complete cds
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Length=1561
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1366793739|gb|MH085251|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone PP-6 segment 5 nucleocapsid protein (NP) gene,
complete cds
Length=1561
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1366793731|gb|MH085248|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone PP-5 segment 5 nucleocapsid protein (NP) gene,
complete cds
Length=1561
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1366793723|gb|MH085245|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone PP-1 segment 5 nucleocapsid protein (NP) gene,
complete cds
Length=1561
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
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Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1366793715|gb|MH085242|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone OP7-5 segment 5 nucleocapsid protein (NP)
gene, complete cds
Length=1561
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1366793707|gb|MH085239|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone OP7-4 segment 5 nucleocapsid protein (NP)
gene, complete cds
Length=1561
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1366793699|gb|MH085236|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone OP7-3 segment 5 nucleocapsid protein (NP)
gene, complete cds
Length=1561
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1366793691|gb|MH085233|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
clone OP7-1 segment 5 nucleocapsid protein (NP)
gene, complete cds
Length=1561
```

```
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  767  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  736


> gi|1352367018|gb|MH006711|Influenza A virus (A/swine/Michoacan/
MichDMZC10/2015(H1N1)) segment 5 nucleocapsid protein (NP)
gene, complete cds
Length=1576
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|1069560153|gb|LC120392|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
RNA, segment 5, complete sequence
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|982220222|gb|KU518835|Influenza A virus (A/swine/North Carolina/
B58223/2014(H1N1)) segment 5 nucleocapsid protein (NP)
gene, complete cds
Length=1497
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693
```

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> gi|910269612|gb|KT314335|Influenza A virus (A/Puerto Rico/8HY/1934(H1N1))
segment 5 nucleoprotein (NP) gene, complete cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|766554047|gb|KP765783|Influenza A virus (A/NanChang/08/2010(H1N1))
segment 5 nucleocapsid protein (NP) gene, complete
cds
Length=1567
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  770  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  739


> gi|662496878|gb|KJ942811|Influenza A virus (A/reassortant/X-139(X-31B
x New Caledonia/20/1999)(H1N1)) segment 5 nucleocapsid
protein (NP) gene, complete cds
Length=1559
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|662496680|gb|KJ942731|Influenza A virus (A/reassortant/NYMC
X-179A(NYMC X-157 x A/California/07/2009)(H1N1)) segment 5
nucleocapsid protein (NP) gene, complete cds
Length=1556
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
```

```
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|662496441|gb|KJ942635|Influenza A virus (A/reassortant/NYMC
X-179(NYMC X-157 x A/California/07/2009)(H1N1)) segment 5
nucleocapsid protein (NP) gene, complete cds
Length=1558
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|662496361|gb|KJ942603|Influenza A virus (A/reassortant/X-53(Puerto
Rico/8/1934 x New Jersey/11/1976)(H1N1)) segment 5
nucleocapsid protein (NP) gene, complete cds
Length=1549
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  759  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  728


> gi|538118479|gb|CY148246|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511827|gb|CY147537|Influenza A virus (A/Puerto Rico/8-SV14/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
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Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511807|gb|CY147529|Influenza A virus (A/Puerto Rico/8-SV13/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511787|gb|CY147521|Influenza A virus (A/Puerto Rico/8-SV11/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511767|gb|CY147513|Influenza A virus (A/Puerto Rico/8-SV10/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

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> gi|523511747|gb|CY147505|Influenza A virus (A/Puerto Rico/8-SV9/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511727|gb|CY147497|Influenza A virus (A/Puerto Rico/8-SV8/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511707|gb|CY147489|Influenza A virus (A/Puerto Rico/8-SV7/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511687|gb|CY147481|Influenza A virus (A/Puerto Rico/8-SV5/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

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> gi|523511667|gb|CY147473|Influenza A virus (A/Puerto Rico/8-SV1/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511647|gb|CY147465|Influenza A virus (A/Puerto Rico/8-LVD4/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511627|gb|CY147457|Influenza A virus (A/Puerto Rico/8-LVD2/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|523511547|gb|CY147425|Influenza A virus (A/New Jersey/Wistar/1976(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
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            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512252239|gb|CY146892|Influenza A virus (A/Puerto Rico/8-KV20/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512251480|gb|CY146884|Influenza A virus (A/Puerto Rico/8-CV10/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512250611|gb|CY146876|Influenza A virus (A/Puerto Rico/8-SV120/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512249910|gb|CY146868|Influenza A virus (A/Puerto Rico/8-SV60/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
```

```
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512248800|gb|CY146860|Influenza A virus (A/Puerto Rico/8-SV40/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512248015|gb|CY146852|Influenza A virus (A/Puerto Rico/8-SV30/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512246971|gb|CY146844|Influenza A virus (A/Puerto Rico/8-SV20/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512246232|gb|CY146836|Influenza A virus (A/Puerto Rico/8-LVD3/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
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Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|512245169|gb|CY146828|Influenza A virus (A/Puerto Rico/8-LVD1/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|484849244|gb|KC866598|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
segment 5 nucleocapsid protein (NP) gene, complete
cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|479284825|gb|KC815527|Influenza A virus (A/Puerto Rico/8-RG001A/1934(H1N1))
segment 5 nucleocapsid protein (NP) gene,
complete cds
Length=1497
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693
```

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> gi|479284794|gb|KC815515|Influenza A virus (A/Puerto Rico/8-RG001C/1934(H1N1))
segment 5 nucleocapsid protein (NP) gene,
complete cds
Length=1497
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693


> gi|400315883|gb|JX416721|Influenza A virus (A/reassortant/
IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid
protein (NP) gene, complete cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|400315828|gb|JX416729|Influenza A virus (A/reassortant/
IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid
protein (NP) gene, complete cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|400315797|gb|JX416737|Influenza A virus (A/reassortant/
IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid
protein (NP) gene, complete cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
```

```
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|400315749|gb|JX414013|Influenza A virus (A/reassortant/
IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1N1)) segment 5 nucleocapsid
protein (NP) gene, complete cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|392357479|gb|CY121859|Influenza A virus (A/reassortant/NYMC
X-205A(NYMC X-157 x South Carolina/10/2010)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392357461|gb|CY121851|Influenza A virus (A/reassortant/NYMC
X-205(NYMC X-157 x South Carolina/10/2010)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392357122|gb|CY121707|Influenza A virus (A/reassortant/NYMC
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X-181B(A/NYMC X-157 x California/07/2009)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392357104|gb|CY121699|Influenza A virus (A/reassortant/NYMC
X-181A(A/NYMC X-157 x California/07/2009)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392357086|gb|CY121691|Influenza A virus (A/reassortant/NYMC
X-181(A/NYMC X-157 x California/07/2009)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392357049|gb|CY121675|Influenza A virus (A/reassortant/NYMC
X-177B(Hong Kong/1870/2008 x Puerto Rico/8/1934)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
```

```
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

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> gi|392357030|gb|CY121667|Influenza A virus (A/reassortant/NYMC
X-177A(Hong Kong/1870/2008 x Puerto Rico/8/1934)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

```
> gi|392356918|gb|CY121659|Influenza A virus (A/reassortant/NYMC
X-177(Hong Kong/1870/2008 x Puerto Rico/8/1934)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

```
> gi|392356627|gb|CY121627|Influenza A virus (A/reassortant/NYMC
X-173C(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

```
> gi|392356608|gb|CY121619|Influenza A virus (A/reassortant/NYMC
X-173B(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid
```

```
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392356589|gb|CY121611|Influenza A virus (A/reassortant/NYMC
X-173A(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392356570|gb|CY121603|Influenza A virus (A/reassortant/NYMC
X-173(NYMC X-157 x South Dakota/06/2007)(H1N1)) nucleocapsid
protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392350173|gb|CY121392|Influenza A virus (A/reassortant/X-139(X-31B
x New Caledonia/20/1999)(H1N1)) nucleocapsid protein
(NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
```

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            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392345391|gb|CY121272|Influenza A virus (A/reassortant/X-83(Chile/1/1983
x X-31)(H1N1)) nucleocapsid protein (NP) gene,
complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392343956|gb|CY121240|Influenza A virus (A/reassortant/X-65(USSR/90/1977
x Puerto Rico/8/1934)(H1N1)) nucleocapsid protein
(NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|392340012|gb|CY121112|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1540
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|372477405|gb|CY105938|Influenza A virus (A/Puerto Rico/8-SV11/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1502
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
```

```
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  726  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  695


> gi|372349587|gb|CY105946|Influenza A virus (A/Puerto Rico/8-SV13/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1519
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  740  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  709


> gi|372349536|gb|CY105923|Influenza A virus (A/Puerto Rico/8-SV7/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1530
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  753  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  722


> gi|372349519|gb|CY105915|Influenza A virus (A/Puerto Rico/8-SV4/1934(H1N1))
nucleocapsid protein (NP) gene, partial cds
Length=1495
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  726  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  695


> gi|372349503|gb|CY105907|Influenza A virus (A/Puerto Rico/8-SV2/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
```

```
Length=1524
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  747  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  716


> gi|372349484|gb|CY105899|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1524
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  747  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  716


> gi|343787293|gb|CY096838|Influenza A virus (A/X-139(X-31B-New
Caledonia/20/1999)(H1N1)) nucleocapsid protein (NP) gene, complete
cds
Length=1530
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  753  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  722


> gi|323697408|gb|CY084185|Influenza A virus (A/Puerto Rico/8-V24/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

```
> gi|323697389|gb|CY084177|Influenza A virus (A/Puerto Rico/8-KV8/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323697370|gb|CY084169|Influenza A virus (A/Puerto Rico/8-KV7/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323697351|gb|CY084161|Influenza A virus (A/Puerto Rico/8-KV6/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323697332|gb|CY084153|Influenza A virus (A/Puerto Rico/8-KV5/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
```

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Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323697313|gb|CY084145|Influenza A virus (A/Puerto Rico/8-KV4/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323697294|gb|CY084137|Influenza A virus (A/Puerto Rico/8-KV3/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323697275|gb|CY084129|Influenza A virus (A/Puerto Rico/8-KV2/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323697256|gb|CY084121|Influenza A virus (A/Puerto Rico/8-KV1/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
```

```
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696939|gb|CY084113|Influenza A virus (A/Puerto Rico/8-JV18/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696920|gb|CY084105|Influenza A virus (A/Puerto Rico/8-JV9/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696901|gb|CY084097|Influenza A virus (A/Puerto Rico/8-JV3/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696882|gb|CY084089|Influenza A virus (A/Puerto Rico/8-JV2/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
```

```
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696442|gb|CY084081|Influenza A virus (A/Puerto Rico/8-JV1/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696423|gb|CY084073|Influenza A virus (A/Puerto Rico/8-CV10/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696404|gb|CY084065|Influenza A virus (A/Puerto Rico/8-CV9/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696385|gb|CY084057|Influenza A virus (A/Puerto Rico/8-CV8/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
```

```
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696132|gb|CY084049|Influenza A virus (A/Puerto Rico/8-CV7/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696113|gb|CY084041|Influenza A virus (A/Puerto Rico/8-CV6/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696094|gb|CY084033|Influenza A virus (A/Puerto Rico/8-CV5/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696075|gb|CY084025|Influenza A virus (A/Puerto Rico/8-CV2/1934(H1N1))
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nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696056|gb|CY084017|Influenza A virus (A/Puerto Rico/8-CV1/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696037|gb|CY084009|Influenza A virus (A/Puerto Rico/8-WG/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323696018|gb|CY084001|Influenza A virus (A/Puerto Rico/8-9VMC3/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726
```

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> gi|323695999|gb|CY083993|Influenza A virus (A/Puerto Rico/8-9VMC2/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323695980|gb|CY083985|Influenza A virus (A/Puerto Rico/8-9VMC1/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323695961|gb|CY083977|Influenza A virus (A/Puerto Rico/8-9NMC3/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323695942|gb|CY083969|Influenza A virus (A/Puerto Rico/8-9NMC2/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
```

```
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323695923|gb|CY083961|Influenza A virus (A/Puerto Rico/8-9NMC1/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|323695720|gb|CY083953|Influenza A virus (A/Puerto Rico/8-MC/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1552
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  757  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  726


> gi|299781723|gb|CY062630|Influenza A virus (A/X-53(Puerto Rico/8/1934-New
Jersey/11/1976)(H1N1)) nucleocapsid protein (NP)
gene, complete cds
Length=1517
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  740  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  709


> gi|292495991|gb|CY058520|Influenza A virus (A/reassortant/NYMC
X-179A(California/07/2009 x NYMC X-157)(H1N1)) segment 5 sequence
Length=1524
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
```

```
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  749  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  718


> gi|292495973|gb|CY058512|Influenza A virus (A/reassortant/NYMC
X-179(California/07/2009 x NYMC X-157)(H1N1)) segment 5 sequence
Length=1550
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|260593826|gb|CY047401|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
segment 5 sequence
Length=1564
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|259017832|gb|CY046982|Influenza A virus (A/Puerto Rico/8-1-MA/1934(H1N1))
segment 5, complete sequence
Length=1506
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693


> gi|257165112|gb|CY045767|Influenza A virus (A/Puerto Rico/8-1/1934(H1N1))
segment 5, complete sequence
Length=1501
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
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Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693


> gi|256385423|gb|CY044312|Influenza A virus (A/X-127(Puerto Rico/8/1934-
Beijing/262/segment 5, complete sequence
Length=1500
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693


> gi|237689099|gb|CY040173|Influenza A virus (A/Puerto Rico/8-SV14/1934(H1N1))
segment 5, complete sequence
Length=1500
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693


> gi|226954810|gb|CY038906|Influenza A virus (A/Puerto Rico/8-SV3/1934(H1N1))
segment 5, complete sequence
Length=1507
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  729  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  698


> gi|226954791|gb|CY038898|Influenza A virus (A/Puerto Rico/8-SV1/1934(H1N1))
segment 5, complete sequence
```

```
Length=1500
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693


> gi|218875175|gb|CY036922|Influenza A virus (A/NYMC X-163A(NYMC
X-157-St. Petersburg/8/2006)(H1N1)) segment 5, complete sequence
Length=1523
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  746  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  715


> gi|208344071|gb|CY035121|Influenza A virus (A/NYMC X-163B(NYMC
X-157-St. Petersburg/8/2006)(H1N1)) segment 5, complete sequence
Length=1530
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  753  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  722


> gi|208343881|gb|CY035033|Influenza A virus (A/X-53A(Puerto Rico/8/1934-New
Jersey/11/1976)(H1N1)) segment 5, complete sequence
Length=1526
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  750  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  719
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> gi|194352358|gb|CY034127|Influenza A virus (A/NYMC X-163(NYMC
X-157-St. Petersburg/8/2006)(H1N1)) segment 5, complete sequence
Length=1527
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  750  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  719


> gi|194304809|gb|CY033580|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
segment 5, complete sequence
Length=1524
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  749  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  718


> gi|146759958|gb|CY021960|Influenza A virus (A/New Jersey/1976(H1N1))
segment 5, complete sequence
Length=1532
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  751  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  720


> gi|145559567|gb|EF190975|Influenza A virus (A/hvPR8/34(H1N1))
segment 5, complete sequence
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738
```

```
> gi|145322854|gb|EF190983|Influenza A virus (A/lvPR8/34(H1N1))
segment 5, complete sequence
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|133754138|gb|CY020448|Influenza A virus (A/Henry/1936(H1N1))
segment 5, complete sequence
Length=1530
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  749  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  718


> gi|126599284|gb|EF467822|Influenza A virus (A/Puerto Rico/8/34(H1N1))
segment 5, complete sequence
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|125976187|gb|CY019958|Influenza A virus (A/Alaska/1935(H1N1))
segment 5, complete sequence
Length=1528
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
```

```
            |||| ||||| |||||||||||| ||| ||||
Sbjct  747  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  716


> gi|89779327|gb|CY009447|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
nucleocapsid protein (NP) gene, complete cds
Length=1537
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  756  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  725


> gi|61197035|gb|AY936882|Influenza A virus (A/Puerto Rico/8/34(H1N1))
clone NP3-aPR8-34 nucleoprotein gene, partial cds
Length=1494
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  724  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  693


> gi|22218187|gb|AF510857|Influenza A virus (A/Puerto Rico/8/34/Mount
Sinai(H1N1)) nucleoprotein gene, partial cds
Length=1025
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|21693170|gb|AF389119|Influenza A virus (A/Puerto Rico/8/34/Mount
Sinai(H1N1)) segment 5, complete sequence
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
```

```
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|1177513|gb|Z54290|Influenza A virus (Mongolia/231/85 (H1N1))
nucleoprotein gene
Length=1518
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  745  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  714


> gi|1177505|gb|Z54291|Influenza A virus (Mongolia/153/88 (H1N1))
nucleoprotein gene
Length=1518
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  745  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  714


> gi|1177501|gb|Z54292|Influenza A virus (A/Mongolia/111/91 (H1N1))
nucleoprotein gene
Length=1518
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  745  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  714


> gi|324709|gb|J02147|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
segment 5, complete sequence
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
```

```
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|324691|gb|M38279|Influenza A virus (A/Puerto Rico/8/34(H1N1))
nucleoprotein gene, complete cds
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738


> gi|60750|gb|V01084|Influenza A virus (A/Puerto Rico/8/1934(H1N1))
gene for nucleoprotein, genomic RNA
Length=1565
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  106451-106481
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  451  CTTGTTCCATTATTGCTTTTTGT-CAGTAGTT  481
            |||| ||||| |||||||||||| ||| ||||
Sbjct  769  CTTGATCCATCATTGCTTTTTGTGCAGCAGTT  738
```

3.1.2 Monkeypox/PT0001/2022 | sampling date 2022-05-04 159286-159310:

CAATTCCATTATTCTCTTAGCTGCC

```
> gi|1473283053|gb|MH879780|Influenza A virus (A/mallard/Wisconsin/A00751454/2009(H1N1))
segment 1 polymerase PB2 (PB2) gene,
complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186
```

```
> gi|596604082|gb|CY180795|Influenza A virus (A/green-winged teal/Wisconsin/535/1976(
polymerase PB2 (PB2) gene, complete
cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|596592631|gb|CY180010|Influenza A virus (A/mallard/Wisconsin/216/1979(H1N1))
polymerase PB2 (PB2) gene, complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|528917074|gb|KF424231|Influenza A virus (A/blue winged teal/Alberta/212/1984(H1N1))
segment 1 polymerase PB2 (PB2) gene,
complete cds
Length=2314
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  198  CATTTCCATTATTCTCTTATCTGCC  174


> gi|459681731|gb|CY138849|Influenza A virus (A/American black
duck/New Brunswick/00410/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
```

```
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459681669|gb|CY138824|Influenza A virus (A/American black
duck/New Brunswick/00385/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459681589|gb|CY138792|Influenza A virus (A/mallard/New Brunswick/00349/2010(H1N1))
polymerase PB2 (PB2) gene, complete
cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459681569|gb|CY138784|Influenza A virus (A/mallard/Nova Scotia/00346/2010(H1N1))
polymerase PB2 (PB2) gene, complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459681509|gb|CY138760|Influenza A virus (A/mallard/New Brunswick/00340/2010(H1N1))
```

```
       polymerase PB2 (PB2) gene, complete
       cds
       Length=2307
       Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
       Score = 37.4 bits (40),  Expect = 7.0
        Identities = 23/25 (92%), Gaps = 0/25 (0%)
        Strand=Plus/Minus
       Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
                    || ||||||||||||||| |||||
       Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


 > gi|459681489|gb|CY138752|Influenza A virus (A/mallard/New Brunswick/00339/2010(H1N1))
 polymerase PB2 (PB2) gene, complete
 cds
 Length=2307
 Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
 Score = 37.4 bits (40),  Expect = 7.0
        Identities = 23/25 (92%), Gaps = 0/25 (0%)
        Strand=Plus/Minus
       Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
                    || ||||||||||||||| |||||
       Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459681469|gb|CY138744|Influenza A virus (A/mallard/New Brunswick/00337/2010(H1N1))
polymerase PB2 (PB2) gene, complete
cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
        Identities = 23/25 (92%), Gaps = 0/25 (0%)
        Strand=Plus/Minus
       Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
                    || ||||||||||||||| |||||
       Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


       > gi|459681409|gb|CY138720|Influenza A virus (A/green-winged teal/New
       Brunswick/00333/2010(H1N1)) polymerase PB2 (PB2) gene,
       complete cds
       Length=2307
       Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
       Score = 37.4 bits (40),  Expect = 7.0
        Identities = 23/25 (92%), Gaps = 0/25 (0%)
        Strand=Plus/Minus
```

```
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459681308|gb|CY138679|Influenza A virus (A/American black
duck/New Brunswick/00328/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459681288|gb|CY138671|Influenza A virus (A/American black
duck/New Brunswick/00326/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459681268|gb|CY138663|Influenza A virus (A/mallard/New Brunswick/00324/2010(H1N1))
polymerase PB2 (PB2) gene, complete
cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459681228|gb|CY138647|Influenza A virus (A/American black
duck/New Brunswick/00321/2010(H1N1)) polymerase PB2 (PB2) gene,
```

```
complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459681208|gb|CY138639|Influenza A virus (A/American black
duck/Nova Scotia/00099/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459681188|gb|CY138631|Influenza A virus (A/American black
duck/Nova Scotia/00098/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459681168|gb|CY138623|Influenza A virus (A/American black
duck/Nova Scotia/00096/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
```

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            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459680969|gb|CY138615|Influenza A virus (A/American black
duck/Nova Scotia/00094/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459680949|gb|CY138607|Influenza A virus (A/mallard/Nova Scotia/00093/2010(H1N1))
polymerase PB2 (PB2) gene, complete cds
Length=2293
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  199  CATTTCCATTATTCTCTTATCTGCC  175


> gi|459680929|gb|CY138599|Influenza A virus (A/American black
duck/Nova Scotia/00092/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459680909|gb|CY138591|Influenza A virus (A/American black
duck/Nova Scotia/00091/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
```

```
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459680889|gb|CY138583|Influenza A virus (A/American black
duck/Nova Scotia/00090/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459680869|gb|CY138575|Influenza A virus (A/American black
duck/Nova Scotia/00089/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459680849|gb|CY138567|Influenza A virus (A/mallard/Nova Scotia/00088/2010(H1N1))
polymerase PB2 (PB2) gene, complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186
```

```
> gi|459680829|gb|CY138559|Influenza A virus (A/American black
duck/Nova Scotia/00086/2010(H1N1)) polymerase PB2 (PB2) gene,
complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459680809|gb|CY138551|Influenza A virus (A/mallard/Nova Scotia/00085/2010(H1N1))
polymerase PB2 (PB2) gene, complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|459680789|gb|CY138543|Influenza A virus (A/mallard/Nova Scotia/00084/2010(H1N1))
polymerase PB2 (PB2) gene, complete cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459680033|gb|CY138295|Influenza A virus (A/blue-winged teal/Nova
Scotia/00126/2010(H1N1)) polymerase PB2 (PB2) gene, complete
cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
```

```
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|459680013|gb|CY138287|Influenza A virus (A/blue-winged teal/Nova
Scotia/00121/2010(H1N1)) polymerase PB2 (PB2) gene, complete
cds
Length=2307
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  210  CATTTCCATTATTCTCTTATCTGCC  186


> gi|433680166|gb|CY130013|Influenza A virus (A/duck/Alberta/35/1976(H1N1))
polymerase PB2 (PB2) gene, complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|269315113|gb|GU186639|Influenza A virus (A/duck/Alberta/35/1976(H1N1))
segment 1 polymerase PB2 (PB2) gene, complete cds
Length=2316
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  213  CATTTCCATTATTCTCTTATCTGCC  189


> gi|78096033|gb|CY004599|Influenza A virus (A/mallard duck/ALB/127/1977(H1N1))
segment 1, complete sequence
Length=2341
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
```

```
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  225  CATTTCCATTATTCTCTTATCTGCC  201


> gi|78095835|gb|CY004497|Influenza A virus (A/mallard duck/ALB/965/1979(H1N1))
segment 1, complete sequence
Length=2341
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  225  CATTTCCATTATTCTCTTATCTGCC  201


> gi|78095797|gb|CY004481|Influenza A virus (A/pintail duck/ALB/219/1977(H1N1))
segment 1, complete sequence
Length=2341
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  159286-159310
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  286  CAATTCCATTATTCTCTTAGCTGCC  310
            || ||||||||||||||| |||||
Sbjct  225  CATTTCCATTATTCTCTTATCTGCC  201
```

3.1.3 Monkeypox/PT0001/2022 | sampling date 2022-05-04 167616-167657:

GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG

```
> gi|1060099600|gb|KX651622|Influenza A virus (A/France/556-P2T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  88   GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50
```

```
> gi|1060099598|gb|KX651621|Influenza A virus (A/France/556-1T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1246
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  86   GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  48


> gi|745991135|gb|AB910573|Influenza A virus (A/swine/Kagoshima/23/2012(H1N1))
viral cRNA, segment 6, complete sequence, strain:
A/swine/Kagoshima/23/2012(H1N1)
Length=1425
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  151  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  113


> gi|712040567|gb|KP019768|Influenza A virus (A/FuZhou/SWL129/2013(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|705550511|gb|KM985433|Influenza A virus (A/Kottayam/MCVR6946/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
```

```
            |||| ||||||   |||||||||||  || ||||||  || |||
Sbjct  143  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|474456754|gb|KC780561|Influenza A virus (A/Minnesota/15/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||||  |||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|474456305|gb|KC780371|Influenza A virus (A/Florida/30/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||||  |||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|425786331|gb|CY128453|Influenza A virus (A/Viet Nam/001-1880/2009(H1N1))
neuraminidase (NA) gene, complete cds
Length=1432
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||||  |||||||| |||
Sbjct  151  GTTTCAATCTG---ATTTTGATTCCCAAGTTGAATGGAGTGG  113


> gi|317016257|gb|HQ840318|Influenza A virus (A/swine/Minnesota/136B/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
```

```
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|317016255|gb|HQ840310|Influenza A virus (A/swine/Minnesota/130A/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|317016253|gb|HQ840305|Influenza A virus (A/swine/Minnesota/130A/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|307069302|gb|HQ247714|Influenza A virus (A/Finland/687/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| ||||||   |||||||||| || |||||| || |||
Sbjct  143  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|304422849|gb|CY072984|Influenza A virus (A/Managua/5273.02/2009(H1N1))
```

```
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  145  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  107


> gi|300217057|gb|HM598355|Influenza A virus (A/Thailand/CU-MV52/2010(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  88   GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50


> gi|298853453|gb|CY065101|Influenza A virus (A/New York/7426/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| ||||||   |||||||||| || |||||| || |||
Sbjct  145  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|297595768|gb|CY064435|Influenza A virus (A/Guangdong/1240/2009(H1N1))
segment 6 sequence
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105
```

```
> gi|292495142|gb|CY058542|Influenza A virus (A/Managua/462.01/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  145  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  107


> gi|291264376|gb|GU983258|Influenza A virus (A/Eastern India/2503/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1349
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  115  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  77


> gi|291264370|gb|GU983255|Influenza A virus (A/Eastern India/2493/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1356
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  116  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  78


> gi|284027641|gb|GU470881|Influenza A virus (A/swine/Indiana/27007/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
```

```
             |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|284027628|gb|GU471692|Influenza A virus (A/Guangdong/1104/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1415
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
             |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  148  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  110


> gi|268634439|gb|CY051145|Influenza A virus (A/Wisconsin/629-D01734/2009(H1N1))
segment 6, complete sequence
Length=1417
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
             |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|253584644|gb|GQ369418|Influenza A virus (A/swine/Alberta/OTH-33-21/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
             |||| ||||||   |||||||||| || |||||| || |||
Sbjct  163  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|268507374|gb|CY050422|Influenza A virus (A/Wisconsin/629-D02206/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167614-167657
Score = 39.2 bits (42),  Expect = 2.0
```

```
 Identities = 35/44 (80%), Gaps = 3/44 (7%)
 Strand=Plus/Minus
Query  614  AAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||||| |||| |   |||||||||||| || |||||| || |||
Sbjct  147  AAGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|1027918528|gb|KX135815|Influenza A virus (A/California/04-183-MA/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  169  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|705550525|gb|KM985440|Influenza A virus (A/Udupi/MCVR7048/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|698321881|gb|KM596716|Influenza A virus (A/swine/Japan/KU-YG5/2013(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|546236506|gb|KF612138|Influenza A virus (A/Santa Cruz/87212/2009(H1N1))
```

```
segment 6 neuraminidase (NA) gene, complete cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  169  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|474459290|gb|KC781642|Influenza A virus (A/California/35/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|339736825|gb|JN193423|Influenza A virus (A/swine/MN/25618/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|339518872|gb|JN185138|Influenza A virus (A/Tula/CRIE-LMV/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105
```

```
> gi|308269726|gb|CY075526|Influenza A virus (A/Boston/606/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  151  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|307087791|gb|HQ256653|Influenza A virus (A/Myanmar/M535/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|304420504|gb|CY072672|Influenza A virus (A/Managua/1054.02/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 33/42 (79%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  145  GTTTCAATCTG---ATTTTGATTCCCAARTTGAATTGAGTGG  107


> gi|1060099600|gb|KX651622|Influenza A virus (A/France/556-P2T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  16  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  57
```

```
           |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  88  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50


> gi|1060099598|gb|KX651621|Influenza A virus (A/France/556-1T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1246
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  16  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  57
           |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  86  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  48


> gi|300217057|gb|HM598355|Influenza A virus (A/Thailand/CU-MV52/2010(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  16  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  57
           |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  88  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50
```

3.1.4 Monkeypox/PT0001/2022 | sampling date 2022-05-04 172714-172740:

TGAAGACCATCCCACTAGTAA-CAGTCT

```
> gi|563408536|gb|KF840466|Influenza A virus (A/swine/London/Scholtissek
lab(H1N1)) segment 2 polymerase PB1 (PB1) and putative
PB1-F2 protein (PB1-F2) genes, complete cds
Length=2341
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
              |||||||||||||| ||||| ||||||
Sbjct  1349  TGAAGACCATCCCACCAGTAAGCAGTCT  1322


> gi|523511516|gb|CY147412|Influenza A virus (A/swine/JY2/1931(H1N1))
polymerase PB1 (PB1) gene, complete cds; and PB1-F2 gene,
```

```
complete sequence
Length=2304
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             |||||||||||||| ||||| ||||||
Sbjct  1325  TGAAGACCATCCCACCAGTAAGCAGTCT  1298


> gi|320006586|gb|HQ877025|Influenza A virus (A/swine/Guangdong/L3/2009(H1N1))
segment 2 polymerase PB1 (PB1) gene, complete
cds
Length=2274
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             |||||||||||||| ||||| ||||||
Sbjct  1325  TGAAGACCATCCCACCAGTAAGCAGTCT  1298


> gi|189230379|gb|CY032219|Influenza A virus (A/swine/Wisconsin/1/1961(H1N1))
segment 2, complete sequence
Length=2298
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             |||||||||||||| ||||| ||||||
Sbjct  1326  TGAAGACCATCCCACCAGTAAGCAGTCT  1299


> gi|158426703|gb|CY026433|Influenza A virus (A/swine/Jamesburg/1942(H1N1))
segment 2, complete sequence
Length=2297
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             |||||||||||||| ||||| ||||||
Sbjct  1325  TGAAGACCATCCCACCAGTAAGCAGTCT  1298
```

```
> gi|158344942|gb|CY026425|Influenza A virus (A/swine/Tennessee/23/1976(H1N1))
segment 2, complete sequence
Length=2299
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             |||||||||||||| ||||| ||||||
Sbjct  1327  TGAAGACCATCCCACCAGTAAGCAGTCT  1300


> gi|157829262|gb|CY026289|Influenza A virus (A/swine/Wisconsin/1/1957(H1N1))
segment 2, complete sequence
Length=2298
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             |||||||||||||| ||||| ||||||
Sbjct  1326  TGAAGACCATCCCACCAGTAAGCAGTCT  1299


> gi|156536590|gb|CY025063|Influenza A virus (A/swine/Tennessee/48/1977(H1N1))
segment 2, complete sequence
Length=2299
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             |||||||||||||| ||||| ||||||
Sbjct  1327  TGAAGACCATCCCACCAGTAAGCAGTCT  1300


> gi|89941395|gb|CY009634|Influenza A virus (A/swine/1931(H1N1))
segment 2, complete sequence
Length=2302
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
```

```
             ||||||||||||||| ||||| ||||||
Sbjct  1327  TGAAGACCATCCCACCAGTAAGCAGTCT  1300


> gi|324969|gb|M55472|Influenza A virus (A/swine/1976/1931(H1N1))
polymerase gene, complete cds
Length=2317
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  172714-172740
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 26/28 (93%), Gaps = 1/28 (4%)
 Strand=Plus/Minus
Query  714   TGAAGACCATCCCACTAGTAA-CAGTCT  740
             ||||||||||||||| ||||| ||||||
Sbjct  1325  TGAAGACCATCCCACCAGTAAGCAGTCT  1298
```

3.1.5 Monkeypox/PT0001/2022 | sampling date 2022-05-04 167610-167657:

TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG

```
> gi|1027918528|gb|KX135815|Influenza A virus (A/California/04-183-MA/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||| || |||||| || |||
Sbjct  169  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|705550525|gb|KM985440|Influenza A virus (A/Udupi/MCVR7048/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|698321881|gb|KM596716|Influenza A virus (A/swine/Japan/KU-YG5/2013(H1N1))
segment 6 neuraminidase (NA) gene, complete
```

```
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|546236506|gb|KF612138|Influenza A virus (A/Santa Cruz/87212/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  169  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|474459290|gb|KC781642|Influenza A virus (A/California/35/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|339736825|gb|JN193423|Influenza A virus (A/swine/MN/25618/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105
```

```
> gi|339518872|gb|JN185138|Influenza A virus (A/Tula/CRIE-LMV/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|308269726|gb|CY075526|Influenza A virus (A/Boston/606/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  151  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|307087791|gb|HQ256653|Influenza A virus (A/Myanmar/M535/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105
```

3.1.6 Monkeypox/PT0001/2022 | sampling date 2022-05-04 76555-76579:

TGGGAATAGAAACCAGATTAAAACA

```
> gi|746645839|gb|KP288107|Influenza A virus (A/swine/North Carolina/A01476912/2014(
segment 6 neuraminidase (NA) gene,
complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  76555-76579
Score = 37.4 bits (40),  Expect = 7.0
```

```
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Plus
Query  555  TGGGAATAGAAACCAGATTAAAACA  579
            |||||||| ||| ||||||||||||
Sbjct  120  TGGGAATAAAAATCAGATTAAAACA  144


> gi|699978054|gb|KM821559|Influenza A virus (A/swine/North Carolina/A01476345/2014(
segment 6 neuraminidase (NA) gene,
complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  76555-76579
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Plus
Query  555  TGGGAATAGAAACCAGATTAAAACA  579
            |||||||| ||| ||||||||||||
Sbjct  120  TGGGAATAAAAATCAGATTAAAACA  144


> gi|686690865|gb|KM409531|Influenza A virus (A/swine/North Carolina/A01476197/2014(
segment 6 neuraminidase (NA) gene,
complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  76555-76579
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Plus
Query  555  TGGGAATAGAAACCAGATTAAAACA  579
            |||||||| ||| ||||||||||||
Sbjct  120  TGGGAATAAAAATCAGATTAAAACA  144


> gi|587680786|gb|KJ397940|Influenza A virus (A/swine/North Carolina/A01410047/2013(H1N1))
segment 6 neuraminidase (NA) gene,
complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  76555-76579
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Plus
Query  555  TGGGAATAGAAACCAGATTAAAACA  579
            |||||||| ||| ||||||||||||
Sbjct  120  TGGGAATAAAAATCAGATTAAAACA  144
```

```
> gi|585479340|gb|KJ206107|Influenza A virus (A/swine/North Carolina/A01410044/2013(H1N1))
segment 6 neuraminidase (NA) gene,
complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  76555-76579
Score = 37.4 bits (40),  Expect = 7.0
          Identities = 23/25 (92%), Gaps = 0/25 (0%)
          Strand=Plus/Plus
         Query  555  TGGGAATAGAAACCAGATTAAAACA  579
                      |||||||| ||| ||||||||||||
         Sbjct  120  TGGGAATAAAAATCAGATTAAAACA  144
```

3.1.7 Monkeypox/PT0001/2022 | sampling date 2022-05-04 77698-77733:

GAATGCCATTTACGGATTCACCAATAAAAATAAACT

```
> gi|1253893475|gb|CY245721|Influenza A virus (A/swine/Saskatchewan/SD0082/2015(H1N1))
hemagglutinin (HA) gene, complete cds
Length=1701
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77698-77733
Score = 44.6 bits (48),  Expect = 0.047
       Identities = 32/36 (89%), Gaps = 1/36 (3%)
       Strand=Plus/Plus
      Query  698   GAATGCCATTTACGGATTCACCAATAAAAATAAACT  733
                    |||||||||| ||||| |||||||| ||| ||||||
      Sbjct  1158  GAATGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192


> gi|1243281195|gb|MF768483|Influenza A virus (A/swine/Saskatchewan/SD0094/2015(H1N1))
segment 4 hemagglutinin (HA) gene, partial
cds
Length=1700
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77698-77733
Score = 44.6 bits (48),  Expect = 0.047
       Identities = 32/36 (89%), Gaps = 1/36 (3%)
       Strand=Plus/Plus
      Query  698   GAATGCCATTTACGGATTCACCAATAAAAATAAACT  733
                    |||||||||| ||||| |||||||| ||| ||||||
      Sbjct  1158  GAATGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192


> gi|974752620|gb|CY195455|Influenza A virus (A/swine/Saskatchewan/SD0056/2014(H1N1))
hemagglutinin (HA) gene, complete cds
Length=1701
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77698-77733
Score = 44.6 bits (48),  Expect = 0.047
```

```
 Identities = 32/36 (89%), Gaps = 1/36 (3%)
 Strand=Plus/Plus
Query  698   GAATGCCATTTACGGATTCACCAATAAAAATAAACT  733
              |||||||||| ||||| |||||||| ||| ||||||
Sbjct  1158  GAATGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192
```

3.1.8 Monkeypox/PT0001/2022 | sampling date 2022-05-04 168709-168753:

AAACACGTCTTGGATCATCNCATACATATATTAAATTCAGTAACA

```
> gi|662494977|gb|KM029689|Influenza A virus (A/swine/Guangdong/2481/2012(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  168709-168753
Score = 38.3 bits (41),  Expect = 7.0
 Identities = 36/45 (80%), Gaps = 1/45 (2%)
 Strand=Plus/Plus
Query  709  AAACACGTCTTGGATCATCNCATACATATATTAAATTCAGTAACA  753
             |||||   ||||||||| | || ||||||||||  |||| ||||
Sbjct  171  AAACAACACTTGGATCAAC-CAGACATATATTAACATCAGCAACA  214


> gi|662494957|gb|KM029681|Influenza A virus (A/swine/Guangdong/NS2434/2012(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  168709-168753
Score = 38.3 bits (41),  Expect = 7.0
 Identities = 36/45 (80%), Gaps = 1/45 (2%)
 Strand=Plus/Plus
Query  709  AAACACGTCTTGGATCATCNCATACATATATTAAATTCAGTAACA  753
             |||||   ||||||||| | || ||||||||||  |||| ||||
Sbjct  171  AAACAACACTTGGATCAAC-CAGACATATATTAACATCAGCAACA  214


> gi|662494937|gb|KM029673|Influenza A virus (A/swine/Guangdong/NS2433/2012(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  168709-168753
Score = 38.3 bits (41),  Expect = 7.0
 Identities = 36/45 (80%), Gaps = 1/45 (2%)
 Strand=Plus/Plus
Query  709  AAACACGTCTTGGATCATCNCATACATATATTAAATTCAGTAACA  753
             |||||   ||||||||| | || ||||||||||  |||| ||||
```

```
Sbjct  171  AAACAACACTTGGATCAAC-CAGACATATATTAACATCAGCAACA  214
```

3.1.9 Monkeypox/PT0001/2022 | sampling date 2022-05-04 77701-77733:

TGCCATTTACGGATTCACCAATAAAAATAAACT

```
> gi|1253893475|gb|CY245721|Influenza A virus (A/swine/Saskatchewan/SD0082/2015(H1N1))
hemagglutinin (HA) gene, complete cds
Length=1701
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77698-77733
Score = 44.6 bits (48),  Expect = 0.047
      Identities = 32/36 (89%), Gaps = 1/36 (3%)
      Strand=Plus/Plus
     Query  698   GAATGCCATTTACGGATTCACCAATAAAAATAAACT  733
                  |||||||||| ||||| |||||||| ||| ||||||
     Sbjct  1158  GAATGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192


> gi|1243281195|gb|MF768483|Influenza A virus (A/swine/Saskatchewan/SD0094/2015(H1N1))
segment 4 hemagglutinin (HA) gene, partial
cds
Length=1700
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77698-77733
Score = 44.6 bits (48),  Expect = 0.047
      Identities = 32/36 (89%), Gaps = 1/36 (3%)
      Strand=Plus/Plus
     Query  698   GAATGCCATTTACGGATTCACCAATAAAAATAAACT  733
                  |||||||||| ||||| |||||||| ||| ||||||
     Sbjct  1158  GAATGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192


> gi|974752620|gb|CY195455|Influenza A virus (A/swine/Saskatchewan/SD0056/2014(H1N1))
hemagglutinin (HA) gene, complete cds
Length=1701
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77698-77733
Score = 44.6 bits (48),  Expect = 0.047
      Identities = 32/36 (89%), Gaps = 1/36 (3%)
      Strand=Plus/Plus
     Query  698   GAATGCCATTTACGGATTCACCAATAAAAATAAACT  733
                  |||||||||| ||||| |||||||| ||| ||||||
     Sbjct  1158  GAATGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192


> gi|1253893475|gb|CY245721|Influenza A virus (A/swine/Saskatchewan/SD0082/2015(H1N1))
hemagglutinin (HA) gene, complete cds
Length=1701
```

```
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77701-77733
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 29/33 (88%), Gaps = 1/33 (3%)
 Strand=Plus/Plus
Query  1     TGCCATTTACGGATTCACCAATAAAAATAAACT  33
             ||||||| ||||| |||||||| ||| ||||||
Sbjct  1161  TGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192
```

```
> gi|1243281195|gb|MF768483|Influenza A virus (A/swine/Saskatchewan/SD0094/2015(H1N1))
segment 4 hemagglutinin (HA) gene, partial
cds
Length=1700
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77701-77733
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 29/33 (88%), Gaps = 1/33 (3%)
 Strand=Plus/Plus
Query  1     TGCCATTTACGGATTCACCAATAAAAATAAACT  33
             ||||||| ||||| |||||||| ||| ||||||
Sbjct  1161  TGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192
```

```
> gi|974752620|gb|CY195455|Influenza A virus (A/swine/Saskatchewan/SD0056/2014(H1N1))
hemagglutinin (HA) gene, complete cds
Length=1701
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  77701-77733
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 29/33 (88%), Gaps = 1/33 (3%)
 Strand=Plus/Plus
Query  1     TGCCATTTACGGATTCACCAATAAAAATAAACT  33
             ||||||| ||||| |||||||| ||| ||||||
Sbjct  1161  TGCCATTGACGGAATCACCAAT-AAAGTAAACT  1192
```

3.1.10 Monkeypox/PT0001/2022 | sampling date 2022-05-04 167630-167657:

ATTTTGATTCCNAAATTGAATGGACTGG

```
> gi|1060099600|gb|KX651622|Influenza A virus (A/France/556-P2T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
             |||| |||| |   |||||||||| ||||||||| || |||
```

```
Sbjct  88   GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50


> gi|1060099598|gb|KX651621|Influenza A virus (A/France/556-1T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1246
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  86   GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  48


> gi|745991135|gb|AB910573|Influenza A virus (A/swine/Kagoshima/23/2012(H1N1))
viral cRNA, segment 6, complete sequence, strain:
A/swine/Kagoshima/23/2012(H1N1)
Length=1425
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  151  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  113


> gi|712040567|gb|KP019768|Influenza A virus (A/FuZhou/SWL129/2013(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|705550511|gb|KM985433|Influenza A virus (A/Kottayam/MCVR6946/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
```

```
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| ||||||   |||||||||||| || |||||| || |||
Sbjct  143  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|474456754|gb|KC780561|Influenza A virus (A/Minnesota/15/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|474456305|gb|KC780371|Influenza A virus (A/Florida/30/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|425786331|gb|CY128453|Influenza A virus (A/Viet Nam/001-1880/2009(H1N1))
neuraminidase (NA) gene, complete cds
Length=1432
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| || ||||||||| |||
Sbjct  151  GTTTCAATCTG---ATTTTGATTCCCAAGTTGAATGGAGTGG  113


> gi|317016257|gb|HQ840318|Influenza A virus (A/swine/Minnesota/136B/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
```

```
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|317016255|gb|HQ840310|Influenza A virus (A/swine/Minnesota/130A/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|317016253|gb|HQ840305|Influenza A virus (A/swine/Minnesota/130A/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|307069302|gb|HQ247714|Influenza A virus (A/Finland/687/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| ||||||   |||||||||| || |||||| || |||
Sbjct  143  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105
```

```
> gi|304422849|gb|CY072984|Influenza A virus (A/Managua/5273.02/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  145  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  107


> gi|300217057|gb|HM598355|Influenza A virus (A/Thailand/CU-MV52/2010(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  88   GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50


> gi|298853453|gb|CY065101|Influenza A virus (A/New York/7426/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| ||||||   |||||||||| || |||||| || |||
Sbjct  145  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|297595768|gb|CY064435|Influenza A virus (A/Guangdong/1240/2009(H1N1))
segment 6 sequence
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
```

```
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|292495142|gb|CY058542|Influenza A virus (A/Managua/462.01/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  145  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  107


> gi|291264376|gb|GU983258|Influenza A virus (A/Eastern India/2503/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1349
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  115  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  77


> gi|291264370|gb|GU983255|Influenza A virus (A/Eastern India/2493/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1356
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  116  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  78


> gi|284027641|gb|GU470881|Influenza A virus (A/swine/Indiana/27007/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
```

```
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|284027628|gb|GU471692|Influenza A virus (A/Guangdong/1104/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1415
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  148  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  110


> gi|268634439|gb|CY051145|Influenza A virus (A/Wisconsin/629-D01734/2009(H1N1))
segment 6, complete sequence
Length=1417
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|253584644|gb|GQ369418|Influenza A virus (A/swine/Alberta/OTH-33-21/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| ||||||   |||||||||| || |||||| || |||
Sbjct  163  GTTTCAATCCG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|552055568|gb|KF687932|Influenza A virus (A/Cyprus/504/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
```

```
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167630-167657
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 25/28 (89%), Gaps = 0/28 (0%)
 Strand=Plus/Minus
Query  630  ATTTTGATTCCNAAATTGAATGGACTGG  657
            |||||||||||| ||||||||| || |||
Sbjct  132  ATTTTGATTCCCAAATTGAATTGAGTGG  105


> gi|338220961|gb|CY092720|Influenza A virus (A/Sydney/DD3-52/2010(H1N1))
neuraminidase (NA) gene, complete cds
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167630-167657
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 25/28 (89%), Gaps = 0/28 (0%)
 Strand=Plus/Minus
Query  630  ATTTTGATTCCNAAATTGAATGGACTGG  657
            |||||||||||| ||||||||| || |||
Sbjct  134  ATTTTGATTCCCAAATTGAATTGAGTGG  107


> gi|268507374|gb|CY050422|Influenza A virus (A/Wisconsin/629-D02206/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167614-167657
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 35/44 (80%), Gaps = 3/44 (7%)
 Strand=Plus/Minus
Query  614  AAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||||| |||| |   |||||||||||| || |||||| || |||
Sbjct  147  AAGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|1027918528|gb|KX135815|Influenza A virus (A/California/04-183-MA/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  169  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125
```

```
> gi|705550525|gb|KM985440|Influenza A virus (A/Udupi/MCVR7048/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|698321881|gb|KM596716|Influenza A virus (A/swine/Japan/KU-YG5/2013(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|546236506|gb|KF612138|Influenza A virus (A/Santa Cruz/87212/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  169  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|474459290|gb|KC781642|Influenza A virus (A/California/35/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||||| || |||||| || |||
```

```
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|339736825|gb|JN193423|Influenza A virus (A/swine/MN/25618/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   ||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|339518872|gb|JN185138|Influenza A virus (A/Tula/CRIE-LMV/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   ||||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|308269726|gb|CY075526|Influenza A virus (A/Boston/606/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   ||||||||||| || |||||| || |||
Sbjct  151  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|307087791|gb|HQ256653|Influenza A virus (A/Myanmar/M535/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
```

```
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|304420504|gb|CY072672|Influenza A virus (A/Managua/1054.02/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 33/42 (79%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||| |||| |   |||||||||| || |||||| || |||
Sbjct  145  GTTTCAATCTG---ATTTTGATTCCCAARTTGAATTGAGTGG  107



> gi|1060099600|gb|KX651622|Influenza A virus (A/France/556-P2T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  16  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  57
           |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  88  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50


> gi|1060099598|gb|KX651621|Influenza A virus (A/France/556-1T/2009(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1246
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  16  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  57
           |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  86  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  48


> gi|300217057|gb|HM598355|Influenza A virus (A/Thailand/CU-MV52/2010(H1N1))
segment 6 neuraminidase (NA) gene, partial cds
Length=1288
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167657
```

```
Score = 40.1 bits (43),  Expect = 2.0
 Identities = 34/42 (81%), Gaps = 3/42 (7%)
 Strand=Plus/Minus
Query  16  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  57
           |||| |||| |   |||||||||| ||||||||| || |||
Sbjct  88  GTTTCAATCTG---ATTTTGATTCCCAAATTGAATTGAGTGG  50
```

3.1.11 Monkeypox/PT0001/2022 | sampling date 2022-05-04 167616-167658:

GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGGG

```
> gi|649787197|gb|KJ856423|Influenza A virus (A/swine/Sri Lanka/72/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167658
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 34/43 (79%), Gaps = 3/43 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGGG  658
            |||| |||| |   |||||||||| || |||||| || ||||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAGTTGAATCGAGTGGG  104


> gi|326987189|gb|JF714030|Influenza A virus (A/swine/MB/46/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167616-167658
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 34/43 (79%), Gaps = 3/43 (7%)
 Strand=Plus/Minus
Query  616  GTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGGG  658
            |||| |||| |   |||||||||| || |||||| || ||||
Sbjct  143  GTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGGG  104
```

3.1.12 Monkeypox/PT0001/2022 | sampling date 2022-05-04 152962-152991:

ATATAAAGAAAAATCTAAATTAATTAGAGA

```
> gi|404502817|gb|CY116396|Influenza A virus (A/swine/OMS/2111/1995(H1N1))
hemagglutinin (HA) gene, complete cds
Length=1701
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  152962-152991
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 26/30 (87%), Gaps = 0/30 (0%)
 Strand=Plus/Plus
Query  962   ATATAAAGAAAAATCTAAATTAATTAGAGA  991
```

```
             ||||  |||| |||||||||||| ||||||
Sbjct  1515  ATATTCAGAAGAATCTAAATTAAATAGAGA  1544


> gi|225733652|gb|CY037929|Influenza A virus (A/swine/France/WVL13/1995(H1N1))
segment 4 sequence
Length=1701
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  152962-152991
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 26/30 (87%), Gaps = 0/30 (0%)
 Strand=Plus/Plus
Query  962   ATATAAAGAAAAATCTAAATTAATTAGAGA  991
             ||||  |||| |||||||||||| ||||||
Sbjct  1515  ATATTCAGAAGAATCTAAATTAAATAGAGA  1544
```

3.1.13 Monkeypox/PT0001/2022 | sampling date 2022-05-04 29666-29690:

CTTCCCCTATAATCTTCGTCTATTA

```
> gi|914294355|gb|KT313551|Influenza A virus (A/swine/Pennsylvania/A01432180/2012(H1N1))
segment 2 polymerase PB1 (PB1) and
PB1-F2 protein (PB1-F2) genes, complete cds
Length=2274
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  29666-29690
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 23/25 (92%), Gaps = 0/25 (0%)
 Strand=Plus/Minus
Query  666   CTTCCCCTATAATCTTCGTCTATTA  690
             ||||||| |||||||||||| ||||
Sbjct  1868  CTTCCCCGATAATCTTCGTCCATTA  1844
```

3.1.14 Monkeypox/PT0001/2022 | sampling date 2022-05-04 167614-167657:

AAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG

```
> gi|268507374|gb|CY050422|Influenza A virus (A/Wisconsin/629-D02206/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167614-167657
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 35/44 (80%), Gaps = 3/44 (7%)
 Strand=Plus/Minus
Query  614  AAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            |||||| |||| |   |||||||||| || |||||| || |||
Sbjct  147  AAGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107
```

```
> gi|1027918528|gb|KX135815|Influenza A virus (A/California/04-183-MA/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1458
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
    Identities = 37/48 (77%), Gaps = 3/48 (6%)
    Strand=Plus/Minus
  Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
              || || |||| |||| |   |||||||||| || |||||| || |||
  Sbjct  169  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


  > gi|705550525|gb|KM985440|Influenza A virus (A/Udupi/MCVR7048/2011(H1N1))
  segment 6 neuraminidase (NA) gene, complete cds
  Length=1410
  Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
  Score = 37.4 bits (40),  Expect = 7.0
   Identities = 37/48 (77%), Gaps = 3/48 (6%)
   Strand=Plus/Minus
  Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
              || || |||| |||| |   |||||||||| || |||||| || |||
  Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


  > gi|698321881|gb|KM596716|Influenza A virus (A/swine/Japan/KU-YG5/2013(H1N1))
  segment 6 neuraminidase (NA) gene, complete
  cds
  Length=1410
  Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
  Score = 37.4 bits (40),  Expect = 7.0
   Identities = 37/48 (77%), Gaps = 3/48 (6%)
   Strand=Plus/Minus
  Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
              ||| | |||| |||| |   |||||||||| || |||||| || |||
  Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


  > gi|546236506|gb|KF612138|Influenza A virus (A/Santa Cruz/87212/2009(H1N1))
  segment 6 neuraminidase (NA) gene, complete cds
  Length=1458
  Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
  Score = 37.4 bits (40),  Expect = 7.0
   Identities = 37/48 (77%), Gaps = 3/48 (6%)
   Strand=Plus/Minus
  Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
```

```
            ||| | |||| |||| |   |||||||||| || |||||| || |||
Sbjct  169  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  125


> gi|474459290|gb|KC781642|Influenza A virus (A/California/35/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            || || |||| |||| |   |||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|339736825|gb|JN193423|Influenza A virus (A/swine/MN/25618/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|339518872|gb|JN185138|Influenza A virus (A/Tula/CRIE-LMV/2011(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
            ||| | |||| |||| |   |||||||||| || |||||| || |||
Sbjct  149  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105


> gi|308269726|gb|CY075526|Influenza A virus (A/Boston/606/2009(H1N1))
segment 6, complete sequence
Length=1420
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
```

```
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
             ||| | |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  151  TTACATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  107


> gi|307087791|gb|HQ256653|Influenza A virus (A/Myanmar/M535/2009(H1N1))
segment 6 neuraminidase (NA) gene, complete cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  167610-167657
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 37/48 (77%), Gaps = 3/48 (6%)
 Strand=Plus/Minus
Query  610  TTATAAGTTTGAATCCGTCAATTTTGATTCCNAAATTGAATGGACTGG  657
             || || |||| |||| |   |||||||||||| || |||||| || |||
Sbjct  149  TTGTATGTTTCAATCTG---ATTTTGATTCCCAAGTTGAATTGAGTGG  105
```

3.1.15 Monkeypox/PT0001/2022 | sampling date 2022-05-04 78655-78693:

ATATATTAAAGTCGAATAAAGTTGAAAAATAATTAATTC

```
> gi|1356470707|gb|MH031338|Influenza A virus (A/swine/Iowa/A01785439/2018(H1N1))
segment 6 neuraminidase (NA) gene, complete
cds
Length=1410
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  78655-78693
Score = 39.2 bits (42),  Expect = 2.0
 Identities = 34/39 (87%), Gaps = 4/39 (10%)
 Strand=Plus/Plus
Query  655  ATATATTAAAGTCGAATAAAGTTGAAAAATAATTAATTC  693
             |||| ||||||| ||| ||||  ||||||||||||||||
Sbjct  763  ATAT-TTAAAGTGGAA-AAAG--GAAAAATAATTAATTC  797
```

3.1.16 Monkeypox/PT0001/2022 | sampling date 2022-05-04 168213-168243:

AGAAG-ATGTTCCCAATTTCAAGGACAAAATA

```
> gi|1717351649|gb|MN254405|Influenza A virus (A/Lesser Snow Goose/Arkansas/AH0085499S.
clone A segment 3 polymerase
PA (PA) and PA-X protein (PA-X) genes, partial cds
Length=2180
Query = Monkeypox/PT0001/2022 | sampling date 2022-05-04  168213-168243
Score = 37.4 bits (40),  Expect = 7.0
 Identities = 28/32 (88%), Gaps = 1/32 (3%)
 Strand=Plus/Minus
Query  213   AGAAG-ATGTTCCCAATTTCAAGGACAAAATA  243
              ||||| |||| ||| ||||||||||| ||||
```

```
Sbjct  1621  AGAAGCATGTCCCCTATTTCAAGGACACAATA  1590
```