

COVID-19 is an emerging, rapidly evolving situation.
 Get the latest public health information from CDC: <https://www.coronavirus.gov>.
 Get the latest research from NIH: <https://www.nih.gov/coronavirus>.
 Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>.

BLAST® >> **blastn suite** >> results for RID-RT74V342016

Your search parameters were adjusted to search for a short input sequence.
 Your search is limited to records that include: HCoV-NL63 (taxid:277944), Human coronavirus NL63 (taxid:277944), NL63-related bat coronavirus (taxid:1920748), NL63-related bat coronavirus strain BtKYNL63-9b (taxid:2501929), SARSr-CoV (taxid:694009), SARS-CoV-2 (taxid:2697049)

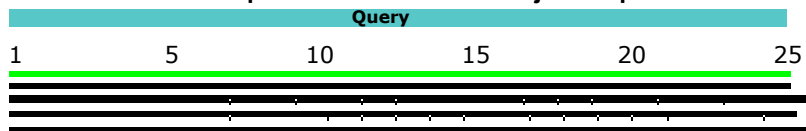
Job Title [Nucleotide Sequence ...](#)
 RID [RT74V342016](#) Search expires on 10-08 00:34 am
 Program BLASTN
 Database ref_viruses_rep_genomes
 Query ID lcl|Query_34821
 Description [None ...](#)
 Molecule type dna
 Query Length 25

Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome	50.1	826	100%	2e-09	100.00%	NC_045512.2
SARS coronavirus Tor2, complete genome	26.3	1007	100%	0.027	88.00%	NC_004718.3
NL63-related bat coronavirus strain BtKYNL63-9a, complete genome	20.3	629	100%	1.7	100.00%	NC_032107.1
NL63-related bat coronavirus strain BtKYNL63-9b, complete genome	18.3	924	96%	6.5	100.00%	NC_048216.1
Human Coronavirus NL63, complete genome	16.4	467	100%	26	100.00%	NC_005831.2

Graphic Summary

Distribution of the top 255 Blast Hits on 5 subject sequences



Alignments

Alignment view CDS feature

Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome
 Sequence ID: **NC_045512.2** Length: 29903 Number of Matches: 53
 Range 1: 15470 to 15494

Score	Expect	Identities	Gaps	Strand	Frame
50.1 bits(25)	2e-09()	25/25(100%)	0/25(0%)	Plus/Plus	
Query 1	CAGGTGGAACCTCATCAGGAGATGC	25			
Sbjct 15470	CAGGTGGAACCTCATCAGGAGATGC	15494			

Range 2: 3283 to 3295

Score	Expect	Identities	Gaps	Strand	Frame
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18.3 bits(9) 6.5() 12/13(92%) 0/13(0%) Plus/Minus

```
Query 2      AGGTGGAACCTCA 14
           ||||| |||||
Sbjct 3295   AGGTTGAACCTCA 3283
```

Range 3: 1534 to 1541

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 4	GTGGAACC	11			
Sbjct 1541	GTGGAACC	1534			

Range 4: 3042 to 3053

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	11/12(92%)	0/12(0%)	Plus/Minus	
Query 10	CCTCATCAGGAG	21			
Sbjct 3053	CCTCATCTGGAG	3042			

Range 5: 4895 to 4902

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 2	AGGTGGAA	9			
Sbjct 4902	AGGTGGAA	4895			

Range 6: 5338 to 5345

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 1	CAGGTGGA	8			
Sbjct 5345	CAGGTGGA	5338			

Range 7: 9458 to 9465

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 8	AACCTCAT	15			
Sbjct 9465	AACCTCAT	9458			

Range 8: 21149 to 21156

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 6	GGAACCTC	13			
Sbjct 21156	GGAACCTC	21149			

Range 9: 25122 to 25129

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 8	AACCTCAT	15			
Sbjct 25129	AACCTCAT	25122			

Range 10: 26228 to 26235

Score	Expect	Identities	Gaps	Strand	Frame
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16.4 bits(8) 26() 8/8(100%) 0/8(0%) Plus/Minus

Query 11 CTCATCAG 18
 |||||
 Sbjct 26235 CTCATCAG 26228

Range 11: 5088 to 5095

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 8	AACCTCAT	15			
Sbjct 5088	AACCTCAT	5095			

Range 12: 16061 to 16068

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 14	ATCAGGAG	21			
Sbjct 16061	ATCAGGAG	16068			

Range 13: 26580 to 26587

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 5	TGGAACCT	12			
Sbjct 26580	TGGAACCT	26587			

Range 14: 27301 to 27308

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 8	AACCTCAT	15			
Sbjct 27301	AACCTCAT	27308			

Range 15: 28830 to 28837

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 10	CCTCATCA	17			
Sbjct 28830	CCTCATCA	28837			

Range 16: 842 to 848

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 13	CATCAGG	19			
Sbjct 848	CATCAGG	842			

Range 17: 1588 to 1594

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 6	GGAACCT	12			
Sbjct 1594	GGAACCT	1588			

Range 18: 2989 to 2995

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 11 CTCATCA 17
 |||||
 Sbjct 2995 CTCATCA 2989

Range 19: 3525 to 3531

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 12 TCATCAG 18
 |||||
 Sbjct 3531 TCATCAG 3525

Range 20: 4703 to 4709

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 13 CATCAGG 19
 |||||
 Sbjct 4709 CATCAGG 4703

Range 21: 5693 to 5699

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 1 CAGGTGG 7
 |||||
 Sbjct 5699 CAGGTGG 5693

Range 22: 6078 to 6084

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 12 TCATCAG 18
 |||||
 Sbjct 6084 TCATCAG 6078

Range 23: 7760 to 7766

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 5 TGAACC 11
 |||||
 Sbjct 7766 TGAACC 7760

Range 24: 12756 to 12762

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 12 TCATCAG 18
 |||||
 Sbjct 12762 TCATCAG 12756

Range 25: 15751 to 15757

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 19 GAGATGC 25
 |||||
 Sbjct 15757 GAGATGC 15751

Range 26: 16116 to 16122

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 11 CTCATCA 17
 |||||
 Sbjct 16122 CTCATCA 16116

Range 27: 17083 to 17089

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 17089	CAGGTGG	17083			

Range 28: 21753 to 21759

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 5	TGGAACC	11			
Sbjct 21759	TGGAACC	21753			

Range 29: 26103 to 26109

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 26109	CTCATCA	26103			

Range 30: 26454 to 26460

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 14	ATCAGGA	20			
Sbjct 26460	ATCAGGA	26454			

Range 31: 28080 to 28086

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 10	CCTCATC	16			
Sbjct 28086	CCTCATC	28080			

Range 32: 28889 to 28895

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 16	CAGGAGA	22			
Sbjct 28895	CAGGAGA	28889			

Range 33: 29400 to 29406

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 29406	TCATCAG	29400			

Range 34: 221 to 227

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

```
Query 12 TCATCAG 18
      |||
Sbjct 221 TCATCAG 227
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Range 35: 502 to 508

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 9	ACCTCAT	15			
Sbjct 502	ACCTCAT	508			

Range 36: 2070 to 2076

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 1	CAGGTGG	7			
Sbjct 2070	CAGGTGG	2076			

Range 37: 3291 to 3297

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 8	AACCTCA	14			
Sbjct 3291	AACCTCA	3297			

Range 38: 10702 to 10708

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 1	CAGGTGG	7			
Sbjct 10702	CAGGTGG	10708			

Range 39: 10772 to 10778

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 7	GAACCTC	13			
Sbjct 10772	GAACCTC	10778			

Range 40: 12891 to 12897

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 5	TGGAACC	11			
Sbjct 12891	TGGAACC	12897			

Range 41: 14507 to 14513

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 14	ATCAGGA	20			
Sbjct 14507	ATCAGGA	14513			

Range 42: 15864 to 15870

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 9 ACCTCAT 15
 Sbjct 15864 ACCTCAT 15870

Range 43: 16188 to 16194

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 6 GGAACCT 12
 Sbjct 16188 GGAACCT 16194

Range 44: 18482 to 18488

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 9 ACCTCAT 15
 Sbjct 18482 ACCTCAT 18488

Range 45: 19889 to 19895

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 19 GAGATGC 25
 Sbjct 19889 GAGATGC 19895

Range 46: 22408 to 22414

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 5 TGGAACC 11
 Sbjct 22408 TGGAACC 22414

Range 47: 23397 to 23403

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 14 ATCAGGA 20
 Sbjct 23397 ATCAGGA 23403

Range 48: 24105 to 24111

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 9 ACCTCAT 15
 Sbjct 24105 ACCTCAT 24111

Range 49: 24730 to 24736

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 9 ACCTCAT 15
 Sbjct 24730 ACCTCAT 24736

Range 50: 26171 to 26177

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 5 TGGAACC 11
 |||||
 Sbjct 26171 TGGAACC 26177

Range 51: 26754 to 26760

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 3 GGTGGAA 9
 |||||
 Sbjct 26754 GGTGGAA 26760

Range 52: 27653 to 27659

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 12 TCATCAG 18
 |||||
 Sbjct 27653 TCATCAG 27659

Range 53: 28166 to 28172

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	

Query 6 GGAACCT 12
 |||||
 Sbjct 28166 GGAACCT 28172

SARS coronavirus Tor2, complete genome

Sequence ID: **NC_004718.3** Length: 29751 Number of Matches: 66

Range 1: 15400 to 15424

Score	Expect	Identities	Gaps	Strand	Frame
26.3 bits(13)	0.027()	22/25(88%)	0/25(0%)	Plus/Plus	

Query 1 CAGGTGGAACCTCATCAGGAGATGC 25
 |||||
 Sbjct 15400 CAGGTGGAACATCATCCGGTGATGC 15424

Range 2: 3900 to 3909

Score	Expect	Identities	Gaps	Strand	Frame
20.3 bits(10)	1.7()	10/10(100%)	0/10(0%)	Plus/Minus	

Query 8 AACCTCATCA 17
 |||||
 Sbjct 3909 AACCTCATCA 3900

Range 3: 22419 to 22428

Score	Expect	Identities	Gaps	Strand	Frame
20.3 bits(10)	1.7()	10/10(100%)	0/10(0%)	Plus/Plus	

Query 15 TCAGGAGATG 24
 |||||
 Sbjct 22419 TCAGGAGATG 22428

Range 4: 21617 to 21625

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	6.5()	9/9(100%)	0/9(0%)	Plus/Minus	

Query 12 TCATCAGGA 20
 |||||
 Sbjct 21625 TCATCAGGA 21617

Range 5: 1183 to 1190

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 18	GGAGATGC	25			
Sbjct 1190	GGAGATGC	1183			

Range 6: 3044 to 3055

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	11/12(92%)	0/12(0%)	Plus/Minus	
Query 10	CCTCATCAGGAG	21			
Sbjct 3055	CCTCATCTGGAG	3044			

Range 7: 4839 to 4846

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 7	GAACCTCA	14			
Sbjct 4846	GAACCTCA	4839			

Range 8: 13772 to 13779

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 10	CCTCATCA	17			
Sbjct 13779	CCTCATCA	13772			

Range 9: 14332 to 14339

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 2	AGGTGGAA	9			
Sbjct 14339	AGGTGGAA	14332			

Range 10: 25205 to 25212

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 10	CCTCATCA	17			
Sbjct 25212	CCTCATCA	25205			

Range 11: 5018 to 5025

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 8	AACCTCAT	15			
Sbjct 5018	AACCTCAT	5025			

Range 12: 9237 to 9244

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 14	ATCAGGAG	21			
Sbjct 9237	ATCAGGAG	9244			

Range 13: 15836 to 15843

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 17	AGGAGATG	24			
Sbjct 15836	AGGAGATG	15843			

Range 14: 15991 to 15998

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 14	ATCAGGAG	21			
Sbjct 15991	ATCAGGAG	15998			

Range 15: 18866 to 18873

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 17	AGGAGATG	24			
Sbjct 18866	AGGAGATG	18873			

Range 16: 26452 to 26459

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 5	TGGAACCT	12			
Sbjct 26452	TGGAACCT	26459			

Range 17: 27331 to 27338

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 14	ATCAGGAG	21			
Sbjct 27331	ATCAGGAG	27338			

Range 18: 27379 to 27386

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 13	CATCAGGA	20			
Sbjct 27379	CATCAGGA	27386			

Range 19: 27858 to 27865

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 8	AACCTCAT	15			
Sbjct 27858	AACCTCAT	27865			

Range 20: 28679 to 28686

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 10	CCTCATCA	17			
Sbjct 28679	CCTCATCA	28686			

Range 21: 1610 to 1616

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 17	AGGAGAT	23			
Sbjct 1616	AGGAGAT	1610			

Range 22: 1941 to 1947

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 14	ATCAGGA	20			
Sbjct 1947	ATCAGGA	1941			

Range 23: 2671 to 2677

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 16	CAGGAGA	22			
Sbjct 2677	CAGGAGA	2671			

Range 24: 2930 to 2936

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 17	AGGAGAT	23			
Sbjct 2936	AGGAGAT	2930			

Range 25: 2958 to 2964

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 2964	CTCATCA	2958			

Range 26: 4158 to 4164

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 4164	CTCATCA	4158			

Range 27: 5109 to 5115

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 5115	CTCATCA	5109			

Range 28: 5623 to 5629

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 5629	CAGGTGG	5623			

Range 29: 6008 to 6014

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 6014	TCATCAG	6008			

Range 30: 8663 to 8669

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 8669	TCATCAG	8663			

Range 31: 9070 to 9076

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 5	TGGAACC	11			
Sbjct 9076	TGGAACC	9070			

Range 32: 11326 to 11332

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 11332	TCATCAG	11326			

Range 33: 12364 to 12370

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 4	GTGGAAC	10			
Sbjct 12370	GTGGAAC	12364			

Range 34: 12686 to 12692

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 12692	TCATCAG	12686			

Range 35: 13548 to 13554

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 10	CCTCATC	16			
Sbjct 13554	CCTCATC	13548			

Range 36: 15646 to 15652

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 15652	TCATCAG	15646			

Range 37: 16046 to 16052

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 16052	CTCATCA	16046			

Range 38: 17013 to 17019

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 17019	CAGGTGG	17013			

Range 39: 19365 to 19371

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 4	GTGGAAC	10			
Sbjct 19371	GTGGAAC	19365			

Range 40: 22875 to 22881

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 13	CATCAGG	19			
Sbjct 22881	CATCAGG	22875			

Range 41: 22896 to 22902

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 22902	CAGGTGG	22896			

Range 42: 24034 to 24040

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 24040	TCATCAG	24034			

Range 43: 24997 to 25003

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 9	ACCTCAT	15			
Sbjct 25003	ACCTCAT	24997			

Range 44: 25337 to 25343

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 16	CAGGAGA	22			
Sbjct 25343	CAGGAGA	25337			

Range 45: 26056 to 26062

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 26062	CTCATCA	26056			

Range 46: 26329 to 26335

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 14	ATCAGGA	20			
Sbjct 26335	ATCAGGA	26329			

Range 47: 27546 to 27552

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 7	GAACCTC	13			
Sbjct 27552	GAACCTC	27546			

Range 48: 28738 to 28744

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 16	CAGGAGA	22			
Sbjct 28744	CAGGAGA	28738			

Range 49: 29249 to 29255

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 29255	TCATCAG	29249			

Range 50: 220 to 226

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	TCATCAG	18			
Sbjct 220	TCATCAG	226			

Range 51: 4123 to 4129

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 19	GAGATGC	25			
Sbjct 4123	GAGATGC	4129			

Range 52: 7268 to 7274

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	TCATCAG	18			
Sbjct 7268	TCATCAG	7274			

Range 53: 10049 to 10055

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 4	GTGGAAC	10			
Sbjct 10049	GTGGAAC	10055			

Range 54: 10931 to 10937

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 11	CTCATCA	17			
Sbjct 10931	CTCATCA	10937			

Range 55: 12821 to 12827

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 5	TGGAACC	11			
Sbjct 12821	TGGAACC	12827			

Range 56: 13539 to 13545

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 16	CAGGAGA	22			
Sbjct 13539	CAGGAGA	13545			

Range 57: 13996 to 14002

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 14	ATCAGGA	20			
Sbjct 13996	ATCAGGA	14002			

Range 58: 14437 to 14443

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 14	ATCAGGA	20			
Sbjct 14437	ATCAGGA	14443			

Range 59: 15083 to 15089

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	TCATCAG	18			
Sbjct 15083	TCATCAG	15089			

Range 60: 16118 to 16124

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 6	GGAACCT	12			
Sbjct 16118	GGAACCT	16124			

Range 61: 18262 to 18268

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 19	GAGATGC	25			
Sbjct 18262		GAGATGC			18268

Range 62: 18627 to 18633

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	TCATCAG	18			
Sbjct 18627		TCATCAG			18633

Range 63: 22662 to 22668

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 18	GGAGATG	24			
Sbjct 22662		GGAGATG			22668

Range 64: 24648 to 24654

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 16	CAGGAGA	22			
Sbjct 24648		CAGGAGA			24654

Range 65: 26021 to 26027

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 15	TCAGGAG	21			
Sbjct 26021		TCAGGAG			26027

Range 66: 27532 to 27538

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	TCATCAG	18			
Sbjct 27532		TCATCAG			27538

NL63-related bat coronavirus strain BtKYNL63-9a, complete genome

Sequence ID: **NC_032107.1** Length: 28363 Number of Matches: 42

Range 1: 27447 to 27456

Score	Expect	Identities	Gaps	Strand	Frame
20.3 bits(10)	1.7()	10/10(100%)	0/10(0%)	Plus/Minus	
Query 7	GAACCTCATC	16			
Sbjct 27456		GAACCTCATC			27447

Range 2: 305 to 313

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	6.5()	9/9(100%)	0/9(0%)	Plus/Minus	
Query 17	AGGAGATGC	25			

Sbjct 313 AGGAGATGC 305

Range 3: 1237 to 1245

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	6.5()	9/9(100%)	0/9(0%)	Plus/Minus	
Query 9	ACCTCATCA	17			
Sbjct 1245	ACCTCATCA	1237			

Range 4: 5486 to 5493

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 4	GTGGAACC	11			
Sbjct 5493	GTGGAACC	5486			

Range 5: 16530 to 16537

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 13	CATCAGGA	20			
Sbjct 16537	CATCAGGA	16530			

Range 6: 22760 to 22767

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 13	CATCAGGA	20			
Sbjct 22767	CATCAGGA	22760			

Range 7: 11815 to 11822

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 2	AGGTGGAA	9			
Sbjct 11815	AGGTGGAA	11822			

Range 8: 16481 to 16488

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 5	TGGAACCT	12			
Sbjct 16481	TGGAACCT	16488			

Range 9: 25613 to 25620

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 5	TGGAACCT	12			
Sbjct 25613	TGGAACCT	25620			

Range 10: 865 to 871

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			

Sbjct 871 CTCATCA 865

Range 11: 2844 to 2850

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 2850	TCATCAG	2844			

Range 12: 3232 to 3238

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 8	AACCTCA	14			
Sbjct 3238	AACCTCA	3232			

Range 13: 3343 to 3349

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 8	AACCTCA	14			
Sbjct 3349	AACCTCA	3343			

Range 14: 3706 to 3712

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 3712	CTCATCA	3706			

Range 15: 3909 to 3915

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 7	GAACCTC	13			
Sbjct 3915	GAACCTC	3909			

Range 16: 5954 to 5960

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 5960	CAGGTGG	5954			

Range 17: 6761 to 6767

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 4	GTGGAAC	10			
Sbjct 6767	GTGGAAC	6761			

Range 18: 14424 to 14430

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 8	AACCTCA	14			

Sbjct 14430 AACCTCA 14424

Range 19: 14708 to 14714

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 14714	TCATCAG	14708			

Range 20: 16078 to 16084

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 16084	CAGGTGG	16078			

Range 21: 21130 to 21136

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 21136	TCATCAG	21130			

Range 22: 21912 to 21918

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 13	CATCAGG	19			
Sbjct 21918	CATCAGG	21912			

Range 23: 23130 to 23136

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 4	GTGGAAC	10			
Sbjct 23136	GTGGAAC	23130			

Range 24: 23534 to 23540

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 8	AACCTCA	14			
Sbjct 23540	AACCTCA	23534			

Range 25: 25164 to 25170

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 7	GAACCTC	13			
Sbjct 25170	GAACCTC	25164			

Range 26: 26645 to 26651

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 8	AACCTCA	14			

Sbjct 26651 AACCTCA 26645

Range 27: 27396 to 27402

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 27402	CAGGTGG	27396			

Range 28: 27420 to 27426

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 5	TGGAACC	11			
Sbjct 27426	TGGAACC	27420			

Range 29: 6382 to 6388

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 19	GAGATGC	25			
Sbjct 6382	GAGATGC	6388			

Range 30: 9911 to 9917

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 4	GTGGAAC	10			
Sbjct 9911	GTGGAAC	9917			

Range 31: 11030 to 11036

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 19	GAGATGC	25			
Sbjct 11030	GAGATGC	11036			

Range 32: 11218 to 11224

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 11	CTCATCA	17			
Sbjct 11218	CTCATCA	11224			

Range 33: 11379 to 11385

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	TCATCAG	18			
Sbjct 11379	TCATCAG	11385			

Range 34: 16248 to 16254

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 3	GGTGGAA	9			

Sbjct 16248 GGTGGAA 16254

Range 35: 17582 to 17588

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 1	CAGGTGG	7			
Sbjct 17582	CAGGTGG	17588			

Range 36: 18054 to 18060

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 1	CAGGTGG	7			
Sbjct 18054	CAGGTGG	18060			

Range 37: 21149 to 21155

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 11	CTCATCA	17			
Sbjct 21149	CTCATCA	21155			

Range 38: 21438 to 21444

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 8	AACCTCA	14			
Sbjct 21438	AACCTCA	21444			

Range 39: 22724 to 22730

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 6	GGAACCT	12			
Sbjct 22724	GGAACCT	22730			

Range 40: 23466 to 23472

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 16	CAGGAGA	22			
Sbjct 23466	CAGGAGA	23472			

Range 41: 26030 to 26036

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 1	CAGGTGG	7			
Sbjct 26030	CAGGTGG	26036			

Range 42: 26726 to 26732

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 8	AACCTCA	14			

Sbjct 26726 AACCTCA 26732

NL63-related bat coronavirus strain BtKYNL63-9b, complete genome
 Sequence ID: **NC_048216.1** Length: 28679 Number of Matches: 62
 Range 1: 27584 to 27592

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	6.5()	9/9(100%)	0/9(0%)	Plus/Minus	
Query 8	AACCTCATC	16			
Sbjct 27592	AACCTCATC	27584			

Range 2: 20941 to 20949

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	6.5()	9/9(100%)	0/9(0%)	Plus/Plus	
Query 2	AGGTGGAAC	10			
Sbjct 20941	AGGTGGAAC	20949			

Range 3: 809 to 816

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 5	TGGAACCT	12			
Sbjct 816	TGGAACCT	809			

Range 4: 2519 to 2526

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 6	GGAACCTC	13			
Sbjct 2526	GGAACCTC	2519			

Range 5: 2955 to 2962

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 9	ACCTCATC	16			
Sbjct 2962	ACCTCATC	2955			

Range 6: 3912 to 3919

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 4	GTGGAACC	11			
Sbjct 3919	GTGGAACC	3912			

Range 7: 4357 to 4364

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 8	AACCTCAT	15			
Sbjct 4364	AACCTCAT	4357			

Range 8: 8484 to 8491

Score	Expect	Identities	Gaps	Strand	Frame
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16.4 bits(8) 26() 8/8(100%) 0/8(0%) Plus/Minus

Query 4 GTGGAACC 11
 Sbjct 8491 GTGGAACC 8484

Range 9: 9628 to 9635

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 6	GGAACCTC	13			
Sbjct 9635	GGAACCTC	9628			

Range 10: 9656 to 9663

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 16	CAGGAGAT	23			
Sbjct 9663	CAGGAGAT	9656			

Range 11: 12931 to 12938

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 7	GAACCTCA	14			
Sbjct 12938	GAACCTCA	12931			

Range 12: 23763 to 23770

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 17	AGGAGATG	24			
Sbjct 23770	AGGAGATG	23763			

Range 13: 168 to 175

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 5	TGGAACCT	12			
Sbjct 168	TGGAACCT	175			

Range 14: 14143 to 14150

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 7	GAACCTCA	14			
Sbjct 14143	GAACCTCA	14150			

Range 15: 26473 to 26480

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 2	AGGTGGAA	9			
Sbjct 26473	AGGTGGAA	26480			

Range 16: 1239 to 1245

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 10 CCTCATC 16
 Sbjct 1245 CCTCATC 1239

Range 17: 2845 to 2851

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 12 TCATCAG 18
 Sbjct 2851 TCATCAG 2845

Range 18: 3233 to 3239

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 11 CTCATCA 17
 Sbjct 3239 CTCATCA 3233

Range 19: 3526 to 3532

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 12 TCATCAG 18
 Sbjct 3532 TCATCAG 3526

Range 20: 4118 to 4124

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 8 AACCTCA 14
 Sbjct 4124 AACCTCA 4118

Range 21: 4529 to 4535

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 8 AACCTCA 14
 Sbjct 4535 AACCTCA 4529

Range 22: 5114 to 5120

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 11 CTCATCA 17
 Sbjct 5120 CTCATCA 5114

Range 23: 6619 to 6625

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 8 AACCTCA 14
 Sbjct 6625 AACCTCA 6619

Range 24: 7161 to 7167

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 7 GAACCTC 13
 Sbjct 7167 GAACCTC 7161

Range 25: 10094 to 10100

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 8 AACCTCA 14
 Sbjct 10100 AACCTCA 10094

Range 26: 10955 to 10961

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 3 GGTGGAA 9
 Sbjct 10961 GGTGGAA 10955

Range 27: 11171 to 11177

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 11 CTCATCA 17
 Sbjct 11177 CTCATCA 11171

Range 28: 11203 to 11209

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 4 GTGGAAC 10
 Sbjct 11209 GTGGAAC 11203

Range 29: 11301 to 11307

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 5 TGGAACC 11
 Sbjct 11307 TGGAACC 11301

Range 30: 11612 to 11618

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 14 ATCAGGA 20
 Sbjct 11618 ATCAGGA 11612

Range 31: 12466 to 12472

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 9 ACCTCAT 15
 Sbjct 12472 ACCTCAT 12466

Range 32: 12916 to 12922

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 11 CTCATCA 17
 |||||
 Sbjct 12922 CTCATCA 12916

Range 33: 13668 to 13674

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	

Query 18 GGAGATG 24
 |||||
 Sbjct 13674 GGAGATG 13668

Range 34: 14793 to 14799

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	

Query 12 TCATCAG 18
 |||||
 Sbjct 14799 TCATCAG 14793

Range 35: 16615 to 16621

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	

Query 14 ATCAGGA 20
 |||||
 Sbjct 16621 ATCAGGA 16615

Range 36: 17687 to 17693

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	

Query 9 ACCTCAT 15
 |||||
 Sbjct 17693 ACCTCAT 17687

Range 37: 20793 to 20799

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	

Query 4 GTGGAAC 10
 |||||
 Sbjct 20799 GTGGAAC 20793

Range 38: 22656 to 22662

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	

Query 8 AACCTCA 14
 |||||
 Sbjct 22662 AACCTCA 22656

Range 39: 23988 to 23994

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	

Query 1 CAGGTGG 7
 |||||
 Sbjct 23994 CAGGTGG 23988

Range 40: 24016 to 24022

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 13 CATCAGG 19
 Sbjct 24022 CATCAGG 24016

Range 41: 26062 to 26068

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 17 AGGAGAT 23
 Sbjct 26068 AGGAGAT 26062

Range 42: 27268 to 27274

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Minus

Query 3 GGTGGAA 9
 Sbjct 27274 GGTGGAA 27268

Range 43: 1581 to 1587

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 14 ATCAGGA 20
 Sbjct 1581 ATCAGGA 1587

Range 44: 2409 to 2415

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 3 GGTGGAA 9
 Sbjct 2409 GGTGGAA 2415

Range 45: 2934 to 2940

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 3 GGTGGAA 9
 Sbjct 2934 GGTGGAA 2940

Range 46: 4225 to 4231

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 1 CAGGTGG 7
 Sbjct 4225 CAGGTGG 4231

Range 47: 7998 to 8004

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 13 CATCAGG 19
 Sbjct 7998 CATCAGG 8004

Range 48: 11675 to 11681

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 4 GTGGAAC 10
 |||||
 Sbjct 11675 GTGGAAC 11681

Range 49: 11725 to 11731

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 17	AGGAGAT 23				
Sbjct 11725	AGGAGAT 11731				

Range 50: 12371 to 12377

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 9	ACCTCAT 15				
Sbjct 12371	ACCTCAT 12377				

Range 51: 14941 to 14947

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 9	ACCTCAT 15				
Sbjct 14941	ACCTCAT 14947				

Range 52: 15777 to 15783

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 17	AGGAGAT 23				
Sbjct 15777	AGGAGAT 15783				

Range 53: 16041 to 16047

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 14	ATCAGGA 20				
Sbjct 16041	ATCAGGA 16047				

Range 54: 16566 to 16572

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 5	TGGAACC 11				
Sbjct 16566	TGGAACC 16572				

Range 55: 16960 to 16966

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 8	AACCTCA 14				
Sbjct 16960	AACCTCA 16966				

Range 56: 17664 to 17670

Score	Expect	Identities	Gaps	Strand	Frame
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14.4 bits(7) 102() 7/7(100%) 0/7(0%) Plus/Plus

Query 1 CAGGTGG 7
 Sbjct 17664 CAGGTGG 17670

Range 57: 18508 to 18514

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 2	AGGTGGA	8			
Sbjct 18508	AGGTGGA	18514			

Range 58: 20159 to 20165

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 16	CAGGAGA	22			
Sbjct 20159	CAGGAGA	20165			

Range 59: 20848 to 20854

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 4	GTGGAAC	10			
Sbjct 20848	GTGGAAC	20854			

Range 60: 21829 to 21835

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 8	AACCTCA	14			
Sbjct 21829	AACCTCA	21835			

Range 61: 25682 to 25688

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 4	GTGGAAC	10			
Sbjct 25682	GTGGAAC	25688			

Range 62: 27111 to 27117

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 14	ATCAGGA	20			
Sbjct 27111	ATCAGGA	27117			

Human Coronavirus NL63, complete genome

Sequence ID: **NC_005831.2** Length: 27553 Number of Matches: 32

Range 1: 9091 to 9098

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 2	AGGTGGAA	9			
Sbjct 9098	AGGTGGAA	9091			

Range 2: 21192 to 21199

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 4	GTGGAACC	11			
Sbjct 21199	GTGGAACC	21192			

Range 3: 19634 to 19641

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 5	TGGAACCT	12			
Sbjct 19634	TGGAACCT	19641			

Range 4: 26384 to 26395

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	26()	11/12(92%)	0/12(0%)	Plus/Plus	
Query 9	ACCTCATCAGGA	20			
Sbjct 26384	ACCTCATAAGGA	26395			

Range 5: 2997 to 3003

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 3003	TCATCAG	2997			

Range 6: 7040 to 7046

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 7	GAACCTC	13			
Sbjct 7046	GAACCTC	7040			

Range 7: 7317 to 7323

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 7323	TCATCAG	7317			

Range 8: 9070 to 9076

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 2	AGGTGGA	8			
Sbjct 9076	AGGTGGA	9070			

Range 9: 9539 to 9545

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 16	CAGGAGA	22			
Sbjct 9545	CAGGAGA	9539			

Range 10: 9958 to 9964

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CTCATCA	17			
Sbjct 9964	CTCATCA	9958			

Range 11: 12303 to 12309

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 6	GGAACCT	12			
Sbjct 12309	GGAACCT	12303			

Range 12: 12922 to 12928

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 19	GAGATGC	25			
Sbjct 12928	GAGATGC	12922			

Range 13: 13411 to 13417

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 4	GTGGAAC	10			
Sbjct 13417	GTGGAAC	13411			

Range 14: 14675 to 14681

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 14681	TCATCAG	14675			

Range 15: 15993 to 15999

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 5	TGGAACC	11			
Sbjct 15999	TGGAACC	15993			

Range 16: 16498 to 16504

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 13	CATCAGG	19			
Sbjct 16504	CATCAGG	16498			

Range 17: 19325 to 19331

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 19331	TCATCAG	19325			

Range 18: 22219 to 22225

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CAGGTGG	7			
Sbjct 22225		CAGGTGG			22219

Range 19: 25077 to 25083

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 7	GAACCTC	13			
Sbjct 25083		GAACCTC			25077

Range 20: 27005 to 27011

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 8	AACCTCA	14			
Sbjct 27011		AACCTCA			27005

Range 21: 27016 to 27022

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 27022		TCATCAG			27016

Range 22: 27217 to 27223

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 12	TCATCAG	18			
Sbjct 27223		TCATCAG			27217

Range 23: 3530 to 3536

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 19	GAGATGC	25			
Sbjct 3530		GAGATGC			3536

Range 24: 6562 to 6568

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	TCATCAG	18			
Sbjct 6562		TCATCAG			6568

Range 25: 14429 to 14435

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 1	CAGGTGG	7			
Sbjct 14429		CAGGTGG			14435

Range 26: 15350 to 15356

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 13	CATCAGG	19			
Sbjct 15350		CATCAGG			15356

Range 27: 18823 to 18829

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 9	ACCTCAT	15			
Sbjct 18823		ACCTCAT			18829

Range 28: 19516 to 19522

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 2	AGGTGGA	8			
Sbjct 19516		AGGTGGA			19522

Range 29: 19752 to 19758

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 9	ACCTCAT	15			
Sbjct 19752		ACCTCAT			19758

Range 30: 24616 to 24622

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 9	ACCTCAT	15			
Sbjct 24616		ACCTCAT			24622

Range 31: 26074 to 26080

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 15	TCAGGAG	21			
Sbjct 26074		TCAGGAG			26080

Range 32: 26500 to 26506

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	102()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 5	TGGAACC	11			
Sbjct 26500		TGGAACC			26506

Taxonomy

Reports

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Lineage

Organism	Blast Name	Score	Number of Hits	Description

Orthocoronavirinae	viruses		<u>5</u>	
.Severe acute respiratory syndrome-related coronavirus	viruses		<u>2</u>	
..Severe acute respiratory syndrome coronavirus 2	viruses	50.1	<u>1</u>	Severe acute respiratory syndrome coronavirus 2 hits
..SARS coronavirus Tor2	viruses	26.3	<u>1</u>	SARS coronavirus Tor2 hits
.NL63-related bat coronavirus	viruses	20.3	<u>2</u>	NL63-related bat coronavirus hits
.Human coronavirus NL63	viruses	16.4	<u>1</u>	Human coronavirus NL63 hits

Organism

Description	Score	E value	Accession
Wuhan seafood market pneumonia virus [viruses]			
Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome	50.1	2e-09	NC_045512
SARS coronavirus Tor2 [viruses]			
SARS coronavirus Tor2, complete genome	26.3	0.027	NC_004718
NL63-related bat coronavirus [viruses]			
NL63-related bat coronavirus strain BtKYNL63-9a, complete genome	20.3	1.7	NC_032107
NL63-related bat coronavirus strain BtKYNL63-9b, complete genome	18.3	6.5	NC_048216
Human coronavirus NL63 [viruses]			
Human Coronavirus NL63, complete genome	16.4	26	NC_005831

Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
Orthocoronavirinae	<u>5</u>	4	
. Severe acute respiratory syndrome-related coronavirus	<u>2</u>	2	
.. Severe acute respiratory syndrome coronavirus 2	<u>1</u>	1	Severe acute respiratory syndrome coronavirus 2 hits
.. SARS coronavirus Tor2	<u>1</u>	1	SARS coronavirus Tor2 hits
. Setracovirus	<u>3</u>	2	
.. NL63-related bat coronavirus	<u>2</u>	1	NL63-related bat coronavirus hits
.. Human coronavirus NL63	<u>1</u>	1	Human coronavirus NL63 hits

Top