

Informații despre COVID-19[Informații privind sănătatea publică \(CDC\)](#)[Informații de cercetare \(NIH\)](#)[Date SARS-CoV-2 \(NCBI\)](#)[Informații privind prevenirea și tratamentul \(HHS\)](#)[Español](#)**EXPLOZIE®** >> rezultatele **suitei de sablare** pentru RID-PB525NAF013 >>

Titlul postului [Secvență nucleotidică ...](#)
 SCĂPA [PB525NAF013](#) Căutarea expiră pe 10-13 21:57
 Program EXPLOZIE
 Bază de date nt
 ID interogare LCL|Query_5395
 Descriere [Niciunul ...](#)
 Tipul moleculei am
 Lungimea interogării 4200

Descrieri

Descriere	Denumire științifică	Scor maxim	Scor total	Copertă interogare	Valoarea E	Per. Ident	Acc. Len	Aderare
Clona sintetică construct E484K_Spike_del21aa gena spike_CD-uri complete	construcție sintetică	6746	6746	89%	0.0	99.07%	3759	MW816500.1
Sintetic construi clona rcVSV-CoV2-S gena glicoproteina de suprafata_CDS complet	construcție sintetică	6735	6735	89%	0.0	99.02%	3759	MZ771336.1
Construct sintetic SARS_CoV_2_ectoCSPP gena_CD-uri complete	construcție sintetică	6529	6529	86%	0.0	99.09%	3771	MT380725.1
Mutant rujeola tulpina morbillivirus MeVvac2-SARS2-S(H)_,genom complet	Morbillivirusul rujeolei	6037	6037	90%	0.0	95.21%	19800	MW090971.1
Construcție sintetică HCV1146 Moderna (ARNm-1273) Secvență de vaccin SARS-CoV-2	construcție sintetică	5060	5060	91%	0.0	90.56%	3828	OK120841.1
Sintetic construi himerică spike vaccin construi secvență	construcție sintetică	4289	4289	89%	0.0	87.22%	4257	MZ393690.1
Sintetic construi himerică spike vaccin construi secvență	construcție sintetică	4228	4228	89%	0.0	86.91%	4257	MZ393689.1
Vector recombinant AAVCOVID19-1_secvență completă	Recombinant vector AAVCOVID19-1	4215	4215	91%	0.0	86.57%	7488	MW408785.1
Vector de clonare pCDNA3.1.2S_secvență completă	Vector de clonare pCDNA3.1.2S	4185	4185	91%	0.0	86.42%	9209	MT613044.1
Vector expresie SARSCoV2SGFP_secvență completă	Vector de expresie SARSCoV2SGFP	4120	4120	89%	0.0	86.45%	11445	MW560963.1
Vector de expresie SARSCoV2S&SmBit_secvență completă	Vector de expresie SARSCoV2S&smBit	4120	4120	89%	0.0	86.45%	10752	MW560962.1
Vector de expresie SARSCoV2SP681H_secvență completă	Vector de expresie SARSCoV2SP681H	4120	4120	89%	0.0	86.45%	8586	MW560961.1
Vector de expresie SARSCoV2S_secvență completă	Vector de expresie SARSCoV2S	4120	4120	89%	0.0	86.45%	8586	MW560957.1
Vector de expresie SARSCoV2SD614G_secvență completă	Vector de expresie SARSCoV2SD614G	4115	4115	89%	0.0	86.42%	8586	MW560960.1
Vector expresie SARSCoV2SN501Y_secvență completă	Vector de expresie SARSCoV2SN501Y	4115	4115	89%	0.0	86.42%	8586	MW560959.1
Vector de expresie SARSCoV2SY453F_secvență completă	Vector de expresie SARSCoV2SY453F	4115	4115	89%	0.0	86.42%	8586	MW560958.1
Vector de expresie SARS-CoV-2-S-E484K_secvență completă	Vector de expresie SARS-CoV-2-S-E484K	4115	4115	89%	0.0	86.42%	8586	MW598454.1
Vector de expresie SARS-CoV-2-S-N439K_secvență completă	Vector de expresie SARS-CoV-2-S-N439K	4115	4115	89%	0.0	86.42%	8586	MW598453.1
Construcție sintetică HCV1147 Pfizer-BioNTech (BTN162b2) Secvența de vaccin SARS-CoV-2	construcție sintetică	3472	5993	79%	0.0	97.81%	3720	OK120842.1
Sintetic construi himerică spike vaccin construi secvență	construcție sintetică	3201	3201	72%	0.0	85.74%	4218	MZ393687.1
Sintetic construi himerică spike vaccin construi secvență	construcție sintetică	2918	2918	72%	0.0	84.11%	4215	MZ393688.1
Vector recombinant AAV-COVID19-06_secvență completă	Recombinant vector AAV-COVID19-06	2217	2217	48%	0.0	86.25%	3945	OK272511.1
Vector recombinant AAV-COVID19-05_secvență completă	Recombinant vector AAV-COVID19-05	2217	2217	48%	0.0	86.25%	3846	OK272510.1

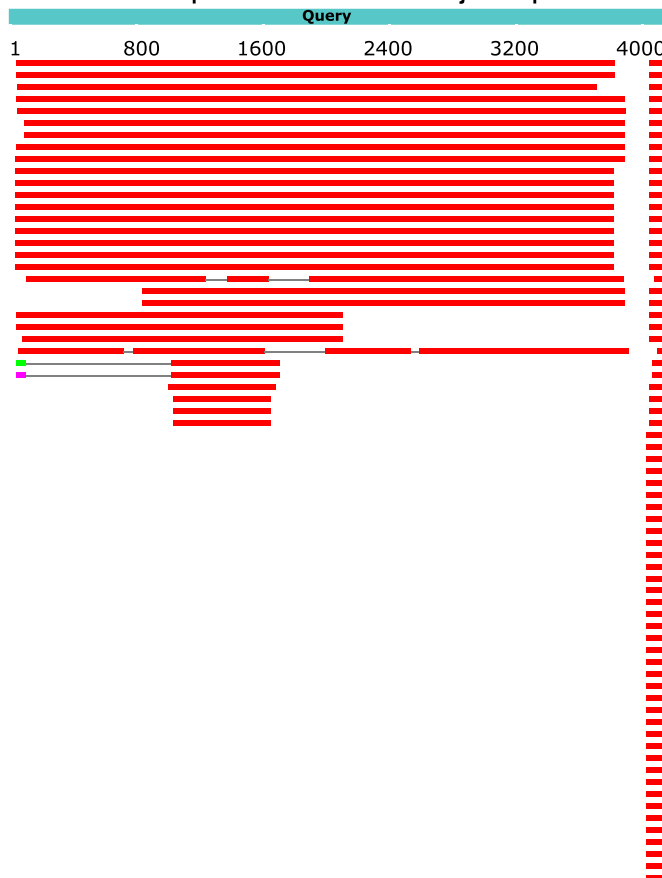
Descriere	Denumire științifică	Scor maxim	Scor total	Copertă interogare	Valoarea E	Per. Ident	Acc. Len	Aderare
Vector recombinant AAVCOVID19-3, secvență completă	Recombinant vector AAVCOVID19-3	2176	2176	47%	0.0	86.27%	6832	MW408786.1
Construcție sintetică HCV1101 Moderna (ARNm-1273) Secvență de vaccin SARS-CoV-2	construcție sintetică	1694	4321	78%	0.0	90.06%	3790	OK120840.1
Sintetic construi SARS CoV_2RBD his gena, CD-uri complete	construcție sintetică	1236	1309	16%	0.0	100.00%	732	MT380724.1
Construcție sintetică p1.1-Tr2-RBDv1, secvență completă	construcție sintetică	1236	1320	17%	0.0	99.85%	7575	MW187858.1
Construcție sintetică pTM-RBDv2, secvență completă	construcție sintetică	1208	1208	15%	0.0	99.55%	7513	MW187856.1
Sintetic construi SARS CoV-2 spike proteine receptorilor de legare gena domeniu, CD-uri complete	construcție sintetică	929	929	14%	0.0	94.80%	1746	MT649401.1
Sintetic construi SpyTag / RBD gena proteinei de fuziune, CD-uri complete	construcție sintetică	652	652	14%	0.0	86.41%	744	MT945427.1
Sintetic construi SARS CoV-1 spike proteine receptorilor de legare gena domeniu, CD-uri complete	construcție sintetică	472	472	14%	2e-127	81.23%	1743	MT649402.1
Homo sapiens izola CO41 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397878.1
Homo sapiens izola HAPLOGRUPUL CO39 D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397877.1
Homo sapiens izola HAPLOGRUPUL CO35 D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397876.1
Homo sapiens izola haplogrupul DE CO22 D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397875.1
Homo sapiens izola CO14 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397874.1
Homo sapiens izola haplogrupul DE CO1 D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397873.1
Homo sapiens izolat CHI92 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397872.1
Homo sapiens izolat CHI91 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397871.1
Homo sapiens izolat CHI35 haplogrup D1f mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397870.1
Homo sapiens izolat CHI29 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397869.1
Homo sapiens izolat CHI25 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397868.1
Homo sapiens izolat CHI24 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397867.1
Homo sapiens izolat CHI23 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397866.1
Homo sapiens izolat CHI20 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397865.1
Homo sapiens izolat CHI14 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397864.1
Homo sapiens izolat CHI13 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397863.1
Homo sapiens izolat CHI12 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397862.1
Homo sapiens izolat CHI11 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397861.1
Homo sapiens izolat CHI9 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397860.1
Homo sapiens izolat CHI4 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397859.1
Homo sapiens izolat CHI3 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397858.1
Homo sapiens izolat CHI2 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397857.1
Homo sapiens izolat CHI1 haplogrup D1 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397856.1
Homo sapiens izola CO44 haplogrup C1b mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397855.1
Homo sapiens izola CO34 haplogrup C1b mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397854.1
Homo sapiens izolează haplogrupul de CO29 C1b mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397853.1
Homo sapiens izolat CHI10 haplogrup C1b12 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397852.1
Homo sapiens izolat CHI7 haplogrup C1b12 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397851.1
Homo sapiens izola CO40 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397827.1
Homo sapiens izola CO38 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397826.1

Descriere	Denumire științifică	Scor maxim	Scor total	Copertă interogare	Valoarea E	Per. Ident	Acc. Len	Aderare
Homo sapiens izolat CO37 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397825.1
Homo sapiens izola CO36 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397824.1
Homo sapiens izola CO33 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397823.1
Homo sapiens izola HAPLOGRUPUL CO32 A2w mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397822.1
Homo sapiens izola CO31 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397821.1
Homo sapiens izola CO30 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397820.1
Homo sapiens izola CO13 haplogrup A2w mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397819.1
Homo sapiens izola CO7 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397818.1
Homo sapiens izolat CHI96 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397816.1
Homo sapiens izolat CHI93 haplogrup A2 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397815.1
Homo sapiens izolat CHI34 mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397814.1
Homo sapiens izolat CHI18 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397813.1
Homo sapiens izolat CHI15 haplogrup A2ac mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397812.1
Homo sapiens izolat CHI8 haplogrup A2k mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397811.1
Homo sapiens izolat CHI6 haplogrup A2k mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397810.1
Homo sapiens izolat CHI5 haplogrup A2k mitochondrion, genom complet	Umanitate	257	257	3%	6e-63	100.00%	16569	MZ397809.1
Homo sapiens isolate 1113002343_S91 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16569	MZ921390.1
Homo sapiens isolate 1113001817_S2 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16568	MZ921389.1
Homo sapiens isolate 1113001079_S53 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16568	MZ921388.1
Homo sapiens isolate ALP266 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16568	MZ921386.1
Homo sapiens isolate ALP129 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921385.1
Homo sapiens isolate ALP029 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921384.1
Homo sapiens isolate LBZ00057 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921383.1
Homo sapiens isolate LBZ00056 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921382.1
Homo sapiens isolate LBZ00055 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921381.1
Homo sapiens isolate LBN00097 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921380.1
Homo sapiens isolate LBG00337 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921379.1
Homo sapiens isolate LBG00336 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921378.1
Homo sapiens isolate LBG00335 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921377.1
Homo sapiens isolate LBG00334 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921376.1
Homo sapiens isolate LBG00333 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921375.1
Homo sapiens isolate PT-351-314 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16569	MZ921374.1
Homo sapiens isolate PT-351-283 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16569	MZ921373.1
Homo sapiens isolate PT-351-218 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16569	MZ921372.1
Homo sapiens isolate PT-351-160 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16569	MZ921371.1
Homo sapiens isolate PT-351-132 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921370.1
Homo sapiens isolate PT-351-124 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16569	MZ921369.1
Homo sapiens isolate PT-351-088 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16569	MZ921368.1

Descriere	Denumire științifică	Scor maxim	Scor total	Copertă interogare	Valoarea E	Per. Ident	Acc. Len	Aderare
Homo sapiens isolate PT-351-083 mitochondrion, complete genome	Homo sapiens	257	257	3%	6e-63	100.00%	16570	MZ921367.1

Rezumat grafic

Distribution of the top 107 Blast Hits on 100 subject sequences



Aliniamente

Alignment view CDS feature

Synthetic construct clone E484K_Spike_del21aa spike gene, complete cds
 Sequence ID: **MW816500.1** Length: 3759 Number of Matches: 1
 Range 1: 1 to 3758

Score	Expect	Identities	Gaps	Strand	Frame
6746 bits(3653)	0.0()	3724/3759(99%)	2/3759(0%)	Plus/Plus	
Query 55	ATGTTTCGTGTTCTCGGTGCTGCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACC	114			
Sbjct 1	ATGTTTCGTGTTCTCGGTGCTGCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACA	60			
Query 115	AGAACACAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTACTACCCCGAC	174			
Sbjct 61	AGAACCAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTACTACCCCGAC	120			
Query 175	AAGGTGTTTCAGATCCAGCGTGCCTGCACTTACCCAGGACCTGTTCTCGCCTTTCTTCAGC	234			
Sbjct 121	AAGGTGTTTCAGATCCAGCGTGCCTGCACTTACCCAGGACCTGTTCTCGCCTTTCTTCAGC	180			
Query 235	AACGTGACCTGGTTCACGCCATCCACGTGTCGGCACCAATGGCACCAAGAGATTCGAC	294			
Sbjct 181	AACGTGACCTGGTTCACGCCATCCACGTGTCGGCACCAATGGCACCAAGAGATTCGAC	240			
Query 295	AACCCCGTGCCTTCAACGACGGGGTGTACTTTGCCAGCACCGAGAAGTCCAACATC	354			
Sbjct 241	AACCCCGTGCCTTCAACGACGGGGTGTACTTTGCCAGCACCGAGAAGTCCAACATC	300			
Query 355	ATCAGAGGCTGGATCTTCGGCACCACTGGACAGCAAGACCCAGAGCCTGCTGATCGTG	414			
Sbjct 301	ATCAGAGGCTGGATCTTCGGCACCACTGGACAGCAAGACCCAGAGCCTGCTGATCGTG	360			
Query 415	AACAACGCCACCAACGTGGTCAACAAAGTGTGCGAGTTCAGTTCGCAACGACCCCTTC	474			
Sbjct 361	AACAACGCCACCAACGTGGTCAACAAAGTGTGCGAGTTCAGTTCGCAACGACCCCTTC	420			
Query 475	CTGGCGTCTACTACCACAAGAACAAAGAGCTGGATGGAAGCGAGTTCGGGTGTAC	534			
Sbjct 421	CTGGCGTCTACTATCACAAAGAACAAAGAGCTGGATGGAAGCGAGTTCGGGTGTAC	480			

```

Query 535 AGCAGCGCCAACTGCACCTTCGAGTACGTGCCAGCCTTCTCTGATGGACCTGGAA 594
Sbjct 481 AGCAGCGCCAACTGCACCTTCGAGTACGTGCCAGCCTTCTCTGATGGACCTGGAA 540

Query 595 GGC AAGCAGGGCACTTCAAGAACTCGCGAGTTCGTGTTTAAAGAACATCGACGGCTAC 654
Sbjct 541 GGC AAGCAGGGCACTTCAAGAACTCGCGAGTTCGTGTTTAAAGAACATCGACGGCTAC 600

Query 655 TTC AAGATCTACAGCAAGCACACCCCTATCAACCTCGTGC GGATCTGCCTCAGGGCTTC 714
Sbjct 601 TTC AAGATCTACAGCAAGCACACCCCTATCAACCTCGTGC GGATCTGCCTCAGGGCTTC 660

Query 715 TCTGCTCTGGAACCCCTGGTGGATCTGCCCATCGGCATCAACATCACCCGGTTTCAGACA 774
Sbjct 661 TCTGCTCTGGAACCCCTGGTGGATCTGCCCATCGGCATCAACATCACCCGGTTTCAGACA 720

Query 775 CTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT 834
Sbjct 721 CTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT 780

Query 835 GGTGCCCGCTTACTATGTGGGTACCTGCAGCCTAGAACCTTCTGCTGAAGTACAAC 894
Sbjct 781 GGTGCCCGCTTACTATGTGGGTACCTGCAGCCTAGAACCTTCTGCTGAAGTACAAC 840

Query 895 GAGAACGGCACCATCACCGACGCGTGGATTGTGCTCTGGATCTCTGAGCGAGACAAAG 954
Sbjct 841 GAGAACGGCACCATCACCGACGCGTGGATTGTGCTCTGGATCTCTGAGCGAGACAAAG 900

Query 955 TGCACCTGAAGTCTTACCCTGGAAAAGGGCATCTACCAGACCAGCAACTTCCGGGTG 1014
Sbjct 901 TGCACCTGAAGTCTTACCCTGGAAAAGGGCATCTACCAGACCAGCAACTTCCGGGTG 960

Query 1015 CAGCCCACCGAATCCATCGTGC GGTTCCCAATATCACCAATCTGTGCCCTTCGGCGAG 1074
Sbjct 961 CAGCCCACCGAATCCATCGTGC GGTTCCCAATATCACCAATCTGTGCCCTTCGGCGAG 1020

Query 1075 GTGTTCAATGCCACCAGATTGCTCTGTGTACGCCTGGAACCGAAGCGGATCAGCAAT 1134
Sbjct 1021 GTGTTCAATGCCACCAGATTGCTCTGTGTACGCCTGGAACCGAAGCGGATCAGCAAT 1080

Query 1135 TGC GTGGCCGACTACTCCGTGTGTACAACTCCGCAGCTTTCAGCACCTTCAAGTGTAC 1194
Sbjct 1081 TGC GTGGCCGACTACTCCGTGTGTACAACTCCGCAGCTTTCAGCACCTTCAAGTGTAC 1140

Query 1195 GGC GTGTCCTTACCAAGTGAACGACCTGTGCTTCAAAAGTGTACGCCGACAGCTTC 1254
Sbjct 1141 GGC GTGTCCTTACCAAGTGAACGACCTGTGCTTCAAAAGTGTACGCCGACAGCTTC 1200

Query 1255 GTGATCCGGGGAGATGAAGTGC GGAGATTGCCCTGGACAGACAGGCAAGATCGCCGAC 1314
Sbjct 1201 GTGATCCGGGGAGATGAAGTGC GGAGATTGCCCTGGACAGACAGGCAAGATCGCCGAC 1260

Query 1315 TACAATACAAGTGC CGGACGACTTACC GGCTGTGTGATTGCC TGGAACAGCAACAAC 1374
Sbjct 1261 TACAATACAAGTGC CGGACGACTTACC GGCTGTGTGATTGCC TGGAACAGCAACAAC 1320

Query 1375 CTGGACTCCAAGTGGCGGCAACTACAATTACCTGTACCGGTGTTCCGGAAAGTCCAAT 1434
Sbjct 1321 CTGGACTCCAAGTGGCGGCAACTACAATTACCTGTACCGGTGTTCCGGAAAGTCCAAT 1380

Query 1435 CTGAAGCCCTTCGAGCGGGACATCTCCACCGAGATCTATCAGGCCGGCAGCACCCCTTGT 1494
Sbjct 1381 CTGAAGCCCTTCGAGCGGGACATCTCCACCGAGATCTATCAGGCCGGCAGCACCCCTTGT 1440

Query 1495 AACGGCGTGAAGGCTTCAACTGCTACTTCCACTGCAGTCTTACGGCTTTCAGCCACA 1554
Sbjct 1441 AACGGCGTGAAGGCTTCAACTGCTACTTCCACTGCAGTCTTACGGCTTTCAGCCACA 1500

Query 1555 AATGGCGTGGGTATCAGCCCTACAGAGTGGTGGTGTGAGCTTCAAGTGTGATGCC 1614
Sbjct 1501 AATGGCGTGGGTATCAGCCCTACAGAGTGGTGGTGTGAGCTTCAAGTGTGATGCC 1560

Query 1615 CCTGCCACAGTGTGCGGCCCTAAGAAAAGCACCAATCTCGTGAAGAACAAATGCGTGAAC 1674
Sbjct 1561 CCTGCCACAGTGTGCGGCCCTAAGAAAAGCACCAATCTCGTGAAGAACAAATGCGTGAAC 1620

Query 1675 TTCAACTTCAACGGCTGACCGGCACCGCGTGTGACAGAGAGCAACAAGAAGTTCCTG 1734
Sbjct 1621 TTCAACTTCAACGGCTGACCGGCACCGCGTGTGACAGAGAGCAACAAGAAGTTCCTG 1680

Query 1735 CCATTTCAGCAGTTCGGCCGGGATATCGCCGATACCACAGACGCCGTTAGAGATCCCAG 1794
Sbjct 1681 CCATTTCAGCAGTTCGGCCGGGATATCGCCGATACCACAGACGCCGTTAGAGATCCCAG 1740

Query 1795 AACTGGAAATCCTGGACATCACCCCTTGCAGCTTGGCGGAGTGTCTGTGATCACCCCT 1854
Sbjct 1741 AACTGGAAATCCTGGACATCACCCCTTGCAGCTTGGCGGAGTGTCTGTGATCACCCCT 1800

Query 1855 GGCACCAACACCAGCAATCAGTGGCAGTGTGTACCAGGACGTGAATGTACC GAAGT 1914
Sbjct 1801 GGCACCAACACCAGCAATCAGTGGCAGTGTGTACCAGGACGTGAATGTACC GAAGT 1860

Query 1915 CCCGTGGCCATTACGCCGATCAGTGCACCTACATGGCGGGTACTCCACCGGCAGC 1974
Sbjct 1861 CCCGTGGCCATTACGCCGATCAGTGCACCTACATGGCGGGTACTCCACCGGCAGC 1920

Query 1975 AATGTGTTTTCAGACCAGAGCCGGCTGTGTGATCGGAGCCGAGCACGTGAACAATAGCTAC 2034
Sbjct 1921 AATGTGTTTTCAGACCAGAGCCGGCTGTGTGATCGGAGCCGAGCACGTGAACAATAGCTAC 1980

Query 2035 GAGTGCACATCCCCTCGGCCTGGAATCTGC CGCAGCTACAGACACAGACAAACAGC 2094
Sbjct 1981 GAGTGCACATCCCCTCGGCCTGGAATCTGC CGCAGCTACAGACACAGACAAACAGC 2040

Query 2095 CCTCGGA-GAGCCAGAAGCGTGGCCAGCCAGAGCATATTGCC TACACAATGTCTTGGG 2153
Sbjct 2041 CC-CAGACGGCCAGATCTGTGGCCAGCCAGAGCATATTGCC TACACAATGTCTTGGG 2099

Query 2154 CGCCGAGAACAGCGTGGCTACTCCAACAACCTATCGCTATCCCACCAACTTCACCAT 2213
Sbjct 2100 CGCCGAGAACAGCGTGGCTACTCCAACAACCTATCGCTATCCCACCAACTTCACCAT 2159

Query 2214 CAGCGTACCACAGAGATCTGCTGTGTCCATGACCAAGACAGCGTGGATGCACCAT 2273
Sbjct 2160 CAGCGTACCACAGAGATCTGCTGTGTCCATGACCAAGACAGCGTGGATGCACCAT 2219

Query 2274 GTACATCTGCGGGCATTCACCGAGTGTCCAACCTGCTGCTGCAGTACGGCAGCTTCTG 2333
Sbjct 2220 GTACATCTGCGGGCATTCACCGAGTGTCCAACCTGCTGCTGCAGTACGGCAGCTTCTG 2279

Query 2334 CACCCAGCTGAATAGACCCTGACAGGGATCGCGTGGAAACAGGACAAGAACCACCAAGA 2393

```

Sbjct 2280 CACCCAGCTGAATAGACCCCTGACAGGGATCGCCGTGGAACAGGACAAGAACACCCAAGA 2339
 Query 2394 GGTGTTTCGCCCAAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTT 2453
 Sbjct 2340 GGTGTTTCGCCCAAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTT 2399
 Query 2454 CAATTTTCAGCCAGATTCTGCCCGATCTAGCAAGCCAGCAAGCGGAGCTTCATCGAGGA 2513
 Sbjct 2400 CAATTTTCAGCCAGATTCTGCCCGATCTAGCAAGCCAGCAAGCGGAGCTTCATCGAGGA 2459
 Query 2514 CCTGCTGTTCAACAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2573
 Sbjct 2460 CCTGCTGTTCAACAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2519
 Query 2574 TCTGGGCGACATTGCCGCCAGGGATCTGATTTGCGCCAGAAAGTTTAAACGGACTGACAGT 2633
 Sbjct 2520 TCTGGGCGACATTGCCGCCAGGGATCTGATTTGCGCCAGAAAGTTTAAACGGACTGACAGT 2579
 Query 2634 GCTGCCTCCTCTGCTGACCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGG 2693
 Sbjct 2580 GCTGCCTCCTCTGCTGACCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGG 2639
 Query 2694 CACAATCACAAGCGGCTGGACATTTGGAGCAGGCGCCGCTCTGCAGATCCCCCTTGTCTAT 2753
 Sbjct 2640 CACAATCACAAGCGGCTGGACATTTGGAGCAGGCGCCGCTCTGCAGATCCCCCTTGTCTAT 2699
 Query 2754 GCAGATGGCCTACCGGTTCAACGGCATCGGAGTGACCCAGAATGTGCTGTACGAGAACCA 2813
 Sbjct 2700 GCAGATGGCCTACCGGTTCAACGGCATCGGAGTGACCCAGAATGTGCTGTACGAGAACCA 2759
 Query 2814 GAAGCTGATCGCCAAACAGTTCAACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGCAG 2873
 Sbjct 2760 GAAGCTGATCGCCAAACAGTTCAACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGCAG 2819
 Query 2874 CACAGCAAGCGCCCTGGGAAAGCTGCAGGACGTGGTCAACAGAAATGCCAGGCACTGAA 2933
 Sbjct 2820 CACAGCAAGCGCCCTGGGAAAGCTGCAGGACGTGGTCAACAGAAATGCCAGGCACTGAA 2879
 Query 2934 CACCCTGGTCAAGCAGCTGTCTCCAACCTCGGCGCCATCAGCTCTGTGCTGAACGATAT 2993
 Sbjct 2880 CACCCTGGTCAAGCAGCTGTCTCCAACCTCGGCGCCATCAGCTCTGTGCTGAACGATAT 2939
 Query 2994 CCTGAGCAGACTGGACCTCTGAGGCGGAGTGACAGTGCAGAGACTGATCACAGGCAG 3053
 Sbjct 2940 CCTGAGCAGACTGGACAAGGTGGAAGCGAGTGACAGTGCAGAGACTGATCACAGGCAG 2999
 Query 3054 ACTGCAGAGCCTCCAGACATACGTGACCCAGCAGTGCAGAGCCGCGAGATTAGAGC 3113
 Sbjct 3000 GCTGCAGTCCCTGCAGACCTACGTTACCCAGCAGTGCAGAGCCGCGAGATTAGAGC 3059
 Query 3114 CTCTGCCAATCTGGCCGCCACCAAGATGTCTGAGTGTGCTGGGCCAGAGCAAGAGAGT 3173
 Sbjct 3060 CTCTGCCAATCTGGCCGCCACCAAGATGTCTGAGTGTGCTGGGCCAGAGCAAGAGAGT 3119
 Query 3174 GGACTTTTGGGGCAAGGGCTACACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGT 3233
 Sbjct 3120 GGACTTTTGGGGCAAGGGCTACACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGT 3179
 Query 3234 GGTGTTTCTGCACGTGACATATGTGCCCGCTCAAGAGAAGAATTTACCACCGCTCCAGC 3293
 Sbjct 3180 GGTGTTTCTGCACGTGACATACGTTGCCCGCTCAAGAGAAGAATTTACCACCGCTCCAGC 3239
 Query 3294 CATCTGCCACGACGGCAAAGCCACTTCTTAGAGAAGGCGTGTCTGTGTTCAACGGCAC 3353
 Sbjct 3240 CATCTGCCACGACGGCAAAGCCACTTCTTAGAGAAGGCGTGTCTGTGTTCAACGGCAC 3299
 Query 3354 CCATTGGTTCGTGACACAGCGGAATTTACGAGCCAGATCATCACCACCGACAACAC 3413
 Sbjct 3300 CCATTGGTTCGTGACCCAGCGGAATTTACGAGCCAGATCATCACCACCGACAACAC 3359
 Query 3414 CTTCTGTCTGGCAACTGCGACGTCGTGATCGGCATTGTGAACAATACCGTGTACGACCC 3473
 Sbjct 3360 CTTCTGTCTGGCAACTGCGACGTCGTGATCGGCATTGTGAACAATACCGTGTACGACCC 3419
 Query 3474 TCTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGACAAGTACTTTAAGAACACAC 3533
 Sbjct 3420 TCTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGATAAGTACTTTAAGAACACAC 3479
 Query 3534 AAGCCCGACGTGGACCTGGGCGATATCAGCGGAATCAATGCCAGCGTCGTGAACATCCA 3593
 Sbjct 3480 AAGCCCGACGTGGACCTGGGCGATATCAGCGGAATCAATGCCAGCGTCGTGAACATCCA 3539
 Query 3594 GAAAGAGATCGACCGGCTGAACGAGGTGGCCAAAGAACTGAACGAGAGCCTGATCGACCT 3653
 Sbjct 3540 GAAAGAGATCGACCGGCTGAACGAGGTGGCCAAAGAACTGAACGAGAGCCTGATCGACCT 3599
 Query 3654 GCAAGAACTGGGGAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTT 3713
 Sbjct 3600 GCAAGAACTGGGGAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTT 3659
 Query 3714 TATCGCCGGACTGATTGCCATCGTGATGGTCAACATCATGCTGTGTTGCATGACCAAGCTG 3773
 Sbjct 3660 TATCGCCGGACTGATTGCCATCGTGATGGTCAACATCATGCTGTGTTGCATGACCAAGCTG 3719
 Query 3774 CTGTAGCTGCCTGAAGGGCTGTTGTAGCTGTGGCAGCTG 3812
 Sbjct 3720 CTGTAGCTGCCTGAAGGGCTGTTGTAGCTGTGGCAGCTG 3758

Synthetic construct clone rcVSV-CoV2-S surface glycoprotein gene, complete cds
 Sequence ID: **MZ771336.1** Length: 3759 Number of Matches: 1
 Range 1: 1 to 3758

Score	Expect	Identities	Gaps	Strand	Frame
6735 bits(3647)	0.0()	3722/3759(99%)	2/3759(0%)	Plus/Plus	
Query 55	ATGTTTCGTGTTCTTGGTGTGCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACC				114
Sbjct 1	ATGTTTCGTGTTCTTGGTGTGCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACA				60
Query 115	AGAACACAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTGTACTACCCCGAC				174
Sbjct 61	AGAACCAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTGTACTACCCCGAC				120
Query 175	AAGGTGTTTCAGATCCAGCGTGTGCACTCTACCCAGGACCTGTTCTGCTCTTCTTCAGC				234
Sbjct 121	AAGGTGTTTCAGATCCAGCGTGTGCACTCTACCCAGGACCTGTTCTGCTCTTCTTCAGC				180

Query 235 AACGTGACCTGGTTCCACGCCATCCACGTGTCGGGCACCAATGGCACCAGAGATTTCGAC 294
Sbjct 181 AACGTGACCTGGTTCCACGCCATCCACGTGTCGGGCACCAATGGCACCAGAGATTTCGAC 240

Query 295 AACCCCGTGTGCTCCCTTCAACGACGGGGTGTACTTTGCCAGCACCAGAAAGTCCAACATC 354
Sbjct 241 AACCCCGTGTGCTCCCTTCAACGACGGGGTGTACTTTGCCAGCACCAGAAAGTCCAACATC 300

Query 355 ATCAGAGGCTGGATCTTCGGCACCACACTGGACAGCAAGACCAGAGCCTGCTGATCGTG 414
Sbjct 301 ATCAGAGGCTGGATCTTCGGCACCACACTGGACAGCAAGACCAGAGCCTGCTGATCGTG 360

Query 415 AACAAACGCCACCAACGTGGTTCATCAAAGTGTGCGAGTTCCAGTTCTGCAACGACCCCTTC 474
Sbjct 361 AACAAACGCCACCAACGTGGTTCATCAAAGTGTGCGAGTTCCAGTTCTGCAACGACCCCTTC 420

Query 475 CTGGGCGTCTACTACCACAAGAAACAACAAGAGCTGGATGGAAAGCGAGTTCCGGGTGTAC 534
Sbjct 421 CTGGGCGTCTACTATACAAGAAACAACAAGAGCTGGATGGAAAGCGAGTTCCGGGTGTAC 480

Query 535 AGCAGCGCCACAACCTGCACCTTCGAGTACGTGCCAGCCTTCTCTGATGGACCTGGAA 594
Sbjct 481 AGCAGCGCCACAACCTGCACCTTCGAGTACGTGCCAGCCTTCTCTGATGGACCTGGAA 540

Query 595 GGC AAGCAGGGCAACTTCAAGAACTGCGCGAGTTCTGTGTTAAGAACTCGACGGCTAC 654
Sbjct 541 GGC AAGCAGGGCAACTTCAAGAACTGCGCGAGTTCTGTGTTAAGAACTCGACGGCTAC 600

Query 655 TTC AAGATCTACAGCAAGCACACCCCTATCAACCTCGTCCGGGATCTGCCTCAGGGCTTC 714
Sbjct 601 TTC AAGATCTACAGCAAGCACACCCCTATCAACCTCGTCCGGGATCTGCCTCAGGGCTTC 660

Query 715 TCTGCTCTGGAACCCCTGGTGGATCTGCCCATCGGCATCAACATCACC CGGTTTCAGACA 774
Sbjct 661 TCTGCTCTGGAACCCCTGGTGGATCTGCCCATCGGCATCAACATCACC CGGTTTCAGACA 720

Query 775 CTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT 834
Sbjct 721 CTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT 780

Query 835 GGTGCCCGCCGCTTACTATGTGGGTACCTGCAGCCTAGAACCTTCTGCTGAAGTACAAC 894
Sbjct 781 GGTGCCCGCCGCTTACTATGTGGGTACCTGCAGCCTAGAACCTTCTGCTGAAGTACAAC 840

Query 895 GAGAAACGGCACCATCACCAGCGCCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAAG 954
Sbjct 841 GAGAAACGGCACCATCACCAGCGCCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAAG 900

Query 955 TGCACCTGAAGTCCCTCACCCTGGAAAAGGGCATCTACAGACCAGCAACTTCCGGGTG 1014
Sbjct 901 TGCACCTGAAGTCCCTCACCCTGGAAAAGGGCATCTACAGACCAGCAACTTCCGGGTG 960

Query 1015 CAGCCACCGAATCCATCGTGCCTTCCCAATATCACC AATCTGTGCCCTTCGGCGAG 1074
Sbjct 961 CAGCCACCGAATCCATCGTGCCTTCCCAATATCACC AATCTGTGCCCTTCGGCGAG 1020

Query 1075 GTGTTCAATGCCACCAGATTGCGCTCTGTGTACGCC TGGAAACCGGAAGCGGATCAGCAAT 1134
Sbjct 1021 GTGTTCAATGCCACCAGATTGCGCTCTGTGTACGCC TGGAAACCGGAAGCGGATCAGCAAT 1080

Query 1135 TGCCTGGCCGACTACTCCGTGCTGTACAACCTCCGC CAGCTTTCAGCACCTTCAAGTGTAC 1194
Sbjct 1081 TGCCTGGCCGACTACTCCGTGCTGTACAACCTCCGC CAGCTTTCAGCACCTTCAAGTGTAC 1140

Query 1195 GGC GTGTCCTTACCAAGCTGAACGACCTGTGCTTCA CAAACGTGTACGCCGACAGCTTC 1254
Sbjct 1141 GGC GTGTCCTTACCAAGCTGAACGACCTGTGCTTCA CAAACGTGTACGCCGACAGCTTC 1200

Query 1255 GTGATCCGGGGAGATGAAGTGC CGCAGATTGCCCC TGGACAGACAGGCAAGATCGCCGAC 1314
Sbjct 1201 GTGATCCGGGGAGATGAAGTGC CGCAGATTGCCCC TGGACAGACAGGCAAGATCGCCGAC 1260

Query 1315 TACAATACAAGCTGCCCGACGACTTACC CGGTGTGTGATTGCC TGGAAACAGCAACAAC 1374
Sbjct 1261 TACAATACAAGCTGCCCGACGACTTACC CGGTGTGTGATTGCC TGGAAACAGCAACAAC 1320

Query 1375 CTGGACTCCAAGTGGCGGCAACTACAATTACCTGTG TACC CGGTGTTCGGAAAGTCCAAT 1434
Sbjct 1321 CTGGACTCCAAGTGGCGGCAACTACAATTACCTGTG TACC CGGTGTTCGGAAAGTCCAAT 1380

Query 1435 CTGAAGCCCTTCGAGCGGGACATCTCC ACCGAGATCTATCAGGCCGGCAGCACCCCTTGT 1494
Sbjct 1381 CTGAAGCCCTTCGAGCGGGACATCTCC ACCGAGATCTATCAGGCCGGGAGCACCCCTTGT 1440

Query 1495 AACGGCGTGGAAAGGCTTCAACTGCTACTTCCCACT GCAAGTCTACGGCTTTCAGCCACA 1554
Sbjct 1441 AACGGCGTGGAAAGGCTTCAACTGCTACTTCCCACT GCAAGTCTACGGCTTTCAGCCACA 1500

Query 1555 AATGGCGTGGGTATCAGCCCTACAGAGTGGTGGTGT GCTGAGCTTCAAGTGTGATGCC 1614
Sbjct 1501 AATGGCGTGGGTATCAGCCCTACAGAGTGGTGGTGT GCTGAGCTTCAAGTGTGATGCC 1560

Query 1615 CCTGCCACAGTGTGCGGCCCTAAGAAAAGCACCAAT CCGTGAAGAAACAAATGCGTGAAC 1674
Sbjct 1561 CCTGCCACAGTGTGCGGCCCTAAGAAAAGCACCAAT CCGTGAAGAAACAAATGCGTGAAC 1620

Query 1675 TTC AACTTCAACGGCCTGACCGGCACCGCGTGTGAC AGAGAGCAACAAGAAGTTCCTG 1734
Sbjct 1621 TTC AACTTCAACGGCCTGACCGGCACCGCGTGTGAC AGAGAGCAACAAGAAGTTCCTG 1680

Query 1735 CCATTCAGCAGTTTGGCCGGGATATCGCCGATACC CACAGACCGCTTAGAGATCCCAG 1794
Sbjct 1681 CCATTCAGCAGTTTGGCCGGGATATCGCCGATACC CACAGACCGCTTAGAGATCCCAG 1740

Query 1795 ACACCTGGAATTCCTGGACATCACCCCTTGCAGCT TCGCGGAGTGTCTGTGATCACCCCT 1854
Sbjct 1741 ACACCTGGAATTCCTGGACATCACCCCTTGCAGCT TCGCGGAGTGTCTGTGATCACCCCT 1800

Query 1855 GGCACCAACACCAGCAATCAGGTGGCAGTGTGTACC GAGACGTGAACGTACCGAAGTG 1914
Sbjct 1801 GGCACCAACACCAGCAATCAGGTGGCAGTGTGTACC GAGACGTGAACGTACCGAAGTG 1860

Query 1915 CCCGTGGCCATTACGCGGATCAGCTGACACCTACAT GGC GGGTACTCCACCGGCAGC 1974
Sbjct 1861 CCCGTGGCCATTACGCGGATCAGCTGACACCTACAT GGC GGGTACTCCACCGGCAGC 1920

Query 1975 AATGTGTTTTCAGACCAGAGCCGGCTGTCTGATCG GAGCCGAGACGTGAACAATAGCTAC 2034
Sbjct 1921 AATGTGTTTTCAGACCAGAGCCGGCTGTCTGATCG GAGCCGAGACGTGAACAATAGCTAC 1980

Query 2035 GAGTGCAGACATCCCCATCGCGCTGGAATCTGCGC CAGTACCAGACACAGACAAACGC 2094

Sbjct	1981	GAGTGCACATCCCCATCGGCGCTGGCATCTGTGCCAGCTACCAGACACAGACAAACAGC	2040
Query	2095	CCTCGGA-GAGCCAGAAGCGTGGCCAGCCAGAGCATATTGCCACACAATGTCTCTGGG	2153
Sbjct	2041	CC-CAGACGGGCCAGATCTGTGGCCAGCCAGAGCATATTGCCACACAATGTCTCTGGG	2099
Query	2154	CGCCGAGAACAGCGTGGCCACTCCAACAACCTTATCGCTATCCCCACCAACTTACCAT	2213
Sbjct	2100	CGCCGAGAACAGCGTGGCCACTCCAACAACCTTATCGCTATCCCCACCAACTTACCAT	2159
Query	2214	CAGCGTGACCACAGAGATCCTGCCTGTGTCCATGACCAAGACCAGCGTGGACTGCACCAT	2273
Sbjct	2160	CAGCGTGACCACAGAGATCCTGCCTGTGTCCATGACCAAGACCAGCGTGGACTGCACCAT	2219
Query	2274	GTACATCTCGGGCGATTCCACCAGTGCTCCAACCTGCTGCTGCAGTACGGCAGCTTCTG	2333
Sbjct	2220	GTACATCTCGGGCGATTCCACCAGTGCTCCAACCTGCTGCTGCAGTACGGCAGCTTCTG	2279
Query	2334	CACCCAGCTGAATAGAGCCCTGACAGGGATCGCCGTGGAACAGGACAAGAACACCCAAGA	2393
Sbjct	2280	CACCCAGCTGAATAGAGCCCTGACAGGGATCGCCGTGGAACAGGACAAGAACACCCAAGA	2339
Query	2394	GGTGTTCGCCCAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTT	2453
Sbjct	2340	GGTGTTCGCCCAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTT	2399
Query	2454	CAATTTTCAGCCAGATTCTGCCCGATCTTAGCAAGCCAGCAAGCGGAGCTTCATCGAGGA	2513
Sbjct	2400	CAATTTTCAGCCAGATTCTGCCCGATCTTAGCAAGCCAGCAAGCGGAGCTTCATCGAGGA	2459
Query	2514	CCTGCTGTTCAACAAGTGACACTGGCCGACGCCGGCTTCATCAAGCAGTATGGCGATTG	2573
Sbjct	2460	CCTGCTGTTCAACAAGTGACACTGGCCGACGCCGGCTTCATCAAGCAGTATGGCGATTG	2519
Query	2574	TCTGGGCGACATTGCCCGCAGGGATCTGATTTGCGCCAGAAAGTTAACGGACTGACAGT	2633
Sbjct	2520	TCTGGGCGACATTGCCCGCAGGGATCTGATTTGCGCCAGAAAGTTAACGGACTGACAGT	2579
Query	2634	GCTGCCTCCTCTGCTGACCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGG	2693
Sbjct	2580	GCTGCCTCCTCTGCTGACCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGG	2639
Query	2694	CACAAATCACAAAGCGCTGGACATTTGGAGCAGCGCCGCTTGCAGATCCCCTTTGTAT	2753
Sbjct	2640	CACAAATCACAAAGCGCTGGACATTTGGAGCAGCGCCGCTTGCAGATCCCCTTTGTAT	2699
Query	2754	GCAGATGGCCTACCGGTTCAACGGCATCGGAGTGACCCAGAATGTGCTGTACGAGAACCA	2813
Sbjct	2700	GCAGATGGCCTACCGGTTCAACGGCATCGGAGTGACCCAGAATGTGCTGTACGAGAACCA	2759
Query	2814	GAAGCTGATCGCCAAACAGTTCAACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGCAG	2873
Sbjct	2760	GAAGCTGATCGCCAAACAGTTCAACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGCAG	2819
Query	2874	CACAGCAAGCGCCCTGGGAAAGCTGACAGGACGTGGTCAACCAGAATGCCAGGCACTGAA	2933
Sbjct	2820	CACAGCAAGCGCCCTGGGAAAGCTGACAGGACGTGGTCAACCAGAATGCCAGGCACTGAA	2879
Query	2934	CACCCTGGTCAAGCAGCTGCTCCAACCTCGGCGCCATCAGCTCTGTGCTGAACGATAT	2993
Sbjct	2880	CACCCTGGTCAAGCAGCTGCTCCAACCTCGGCGCCATCAGCTCTGTGCTGAACGATAT	2939
Query	2994	CCTGAGCAGACTGGACCCTCTGAGGCGGAGGTGCAGATCGACAGACTGATCACAGGCAG	3053
Sbjct	2940	CCTGAGCAGACTGGACAAGGTGGAAGCCGAGGTGCAGATCGACAGACTGATCACGGAAAG	2999
Query	3054	ACTGCAGAGCCTCCAGACATACGTGACCCAGCAGCTGATCAGAGCCGCGAGATTAGAGC	3113
Sbjct	3000	GCTGCAGTCCCTGCAGACCTACGTTACCCAGCAGCTGATCAGAGCCGCGAGATTAGAGC	3059
Query	3114	CTCTGCCAATCTGGCCGCCACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGAGT	3173
Sbjct	3060	CTCTGCCAATCTGGCCGCCACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGAGT	3119
Query	3174	GGACTTTTGGGCAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGT	3233
Sbjct	3120	GGACTTTTGGGCAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGT	3179
Query	3234	GGTGTTCCTGCACGTGACATATGTGCCCGCTCAAGAGAAGAATTTACCACCCTCCAGC	3293
Sbjct	3180	GGTGTTCCTGCACGTGACATACGTGCCCGCTCAAGAGAAGAATTTACCACCCTCCAGC	3239
Query	3294	CATCTGCCACGACGGCAAAGCCACTTTCTTAGAGAAGGCGTTCGTGTCCAACGGCAC	3353
Sbjct	3240	CATCTGCCACGACGGCAAAGCCACTTTCTTAGAGAAGGCGTTCGTGTCCAACGGCAC	3299
Query	3354	CCATTGGTTCTGTGACACAGCGGAACCTTACGAGCCCGAGATCATCACCACCGACAACAC	3413
Sbjct	3300	CCATTGGTTCTGTGACCCAGCGGAACCTTACGAGCCCGAGATCATCACCACCGACAACAC	3359
Query	3414	CTTCGTGTCTGGCAACTGCGACGTCGTGATCGGCATTGTGAACAATACCGTGTACGACCC	3473
Sbjct	3360	CTTCGTGTCTGGCAACTGCGACGTCGTGATCGGCATTGTGAACAATACCGTGTACGACCC	3419
Query	3474	TCTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGACAAGTACTTTAAGAACACAC	3533
Sbjct	3420	TCTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGACAAGTACTTTAAGAACACAC	3479
Query	3534	AAGCCCCGACGTGGACCTGGGCGATATCAGCGGAATCAATGCCAGCGTCGTGAACATCCA	3593
Sbjct	3480	AAGCCCCGACGTGGACCTGGGCGATATCAGCGGAATCAATGCCAGCGTCGTGAACATCCA	3539
Query	3594	GAAAGAGATCGACCGCTGAACGAGGTGGCCAAAGAACTGAACGAGAGCCTGATCGACCT	3653
Sbjct	3540	GAAAGAGATCGACCGCTGAACGAGGTGGCCAAAGAACTGAACGAGAGCCTGATCGACCT	3599
Query	3654	GCAAGAATCGGGGAAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTT	3713
Sbjct	3600	GCAAGAATCGGGGAAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTT	3659
Query	3714	TATCGCCGGACTGATTGCCATCGTGATGGTCACAATCATGCTGTGTTGCATGACCAGCTG	3773
Sbjct	3660	TATCGCCGGACTGATTGCCATCGTGATGGTCACAATCATGCTGTGTTGCATGACCAGCTG	3719
Query	3774	CTGTAGCTGCCTGAAGGGCTGTTGTAGCTGTGGCAGCTG	3812
Sbjct	3720	CTGTAGCTGCCTGAAGGGCTGTTGTAGCTGTGGCAGCTG	3758

Synthetic construct SARS_CoV_2_ectoCSPP gene, complete cds

Sequence ID: **MT380725.1** Length: 3771 Number of Matches: 1

Range 1: 1 to 3630

Score	Expect	Identities	Gaps	Strand	Frame
6529 bits(3535)	0.0()	3606/3639(99%)	9/3639(0%)	Plus/Plus	
Query 55	ATGTTTCGTGTTCTCTGGTGTGCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACC				114
Sbjct 1	ATGTTTCGTGTTCTCTGGTGTGCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACA				60
Query 115	AGAACACAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTGTACTACCCCGAC				174
Sbjct 61	AGAACCAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTGTACTACCCCGAC				120
Query 175	AAGGTGTTTCAGATCCAGCGTGTGCACTCTACCCAGGACCTGTTCTGCCTTTCTTCAGC				234
Sbjct 121	AAGGTGTTTCAGATCCAGCGTGTGCACTCTACCCAGGACCTGTTCTGCCTTTCTTCAGC				180
Query 235	AACGTGACCTGGTTCACGCCATCCACGTGTCCGGCACC AATGGCACC AAGAGATTGAC				294
Sbjct 181	AACGTGACCTGGTTCACGCCATCCACGTGTCCGGCACC AATGGCACC AAGAGATTGAC				240
Query 295	AACCCCGTGTGCCCTTCAACGACGGGGTGTACTTTGCCAGCACGAGAGTCCAACATC				354
Sbjct 241	AACCCCGTGTGCCCTTCAACGACGGGGTGTACTTTGCCAGCACGAGAGTCCAACATC				300
Query 355	ATCAGAGGCTGGATCTTCGGCACCACACTGGACAGCAAGACCCAGAGCTGCTGATCGTG				414
Sbjct 301	ATCAGAGGCTGGATCTTCGGCACCACACTGGACAGCAAGACCCAGAGCTGCTGATCGTG				360
Query 415	AACAACGCCACCAACGTGGTCAAAAGTGTGCGAGTTCAGTTCGCAACGACCCCTTC				474
Sbjct 361	AACAACGCCACCAACGTGGTCAAAAGTGTGCGAGTTCAGTTCGCAACGACCCCTTC				420
Query 475	CTGGGCGTCTACTACCAAGAACCAAGAGCTGGATGGAAAGCGAGTTCCGGGTGTAC				534
Sbjct 421	CTGGGCGTCTACTATACAAGAACCAAGAGCTGGATGGAAAGCGAGTTCCGGGTGTAC				480
Query 535	AGCAGCGCCCAACACTGCACCTTCGAGTACGTGTCCAGCCTTCTCTGATGGACCTGGAA				594
Sbjct 481	AGCAGCGCCCAACACTGCACCTTCGAGTACGTGTCCAGCCTTCTCTGATGGACCTGGAA				540
Query 595	GGCAAGCAGGGCAACTTCAAGAACCTGCGCGAGTTCGTGTTTAAAGAACATCGACGGCTAC				654
Sbjct 541	GGCAAGCAGGGCAACTTCAAGAACCTGCGCGAGTTCGTGTTTAAAGAACATCGACGGCTAC				600
Query 655	TTCAGATCTACAGCAAGCACACCCCTATCAACCTCGTGCGGGATCTGCCTCAGGGCTTC				714
Sbjct 601	TTCAGATCTACAGCAAGCACACCCCTATCAACCTCGTGCGGGATCTGCCTCAGGGCTTC				660
Query 715	TCTGCTCTGGAACCCCTGGTGGATCTGCCATCGGCATCAACATCACCCGGTTTCAGACA				774
Sbjct 661	TCTGCTCTGGAACCCCTGGTGGATCTGCCATCGGCATCAACATCACCCGGTTTCAGACA				720
Query 775	CTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT				834
Sbjct 721	CTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT				780
Query 835	GGTGCCCGCTTACTATGTGGGTACCTGCAGCTAGAACCTTCTGCTGAAGTACAAC				894
Sbjct 781	GGTGCCCGCTTACTATGTGGGTACCTGCAGCTAGAACCTTCTGCTGAAGTACAAC				840
Query 895	GAGAACGGCACCATCACCGACCCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAAG				954
Sbjct 841	GAGAACGGCACCATCACCGACCCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAAG				900
Query 955	TGCACCTGAAGTCTTACCCTGGAAAAGGGCATCTACCAGACCAGCAACTTCCGGGTG				1014
Sbjct 901	TGCACCTGAAGTCTTACCCTGGAAAAGGGCATCTACCAGACCAGCAACTTCCGGGTG				960
Query 1015	CAGCCACCGAATCCATCGTGCGGTCCCAATATCACCAATCTGTGCCCTTCCGGCGAG				1074
Sbjct 961	CAGCCACCGAATCCATCGTGCGGTCCCAATATCACCAATCTGTGCCCTTCCGGCGAG				1020
Query 1075	GTGTTCAATGCCACCAGATTGCTCTGTGTACGCTGGAAACCGAAGCGGATCAGCAAT				1134
Sbjct 1021	GTGTTCAATGCCACCAGATTGCTCTGTGTACGCTGGAAACCGAAGCGGATCAGCAAT				1080
Query 1135	TGCGTGGCCGACTACTCCGTGCTACAACCTCCGCCAGCTTCAGCACCTTCAAGTGTACT				1194
Sbjct 1081	TGCGTGGCCGACTACTCCGTGCTACAACCTCCGCCAGCTTCAGCACCTTCAAGTGTACT				1140
Query 1195	GGCGTGTCCCTACCAAGCTGAACGACCTGTGCTTACAAACGTGTACGCCGACAGCTTC				1254
Sbjct 1141	GGCGTGTCCCTACCAAGCTGAACGACCTGTGCTTACAAACGTGTACGCCGACAGCTTC				1200
Query 1255	GTGATCCGGGGAGATGAAGTGCGGCAGATTGCCCTGGACAGACAGGCAAGATCGCCGAC				1314
Sbjct 1201	GTGATCCGGGGAGATGAAGTGCGGCAGATTGCCCTGGACAGACAGGCAAGATCGCCGAC				1260
Query 1315	TACAACTACAAGCTGCCCGACGACTTACCAGGCTGTGTGATTGCCTGGAACAGCAACAAC				1374
Sbjct 1261	TACAACTACAAGCTGCCCGACGACTTACCAGGCTGTGTGATTGCCTGGAACAGCAACAAC				1320
Query 1375	CTGGACTCCAAGTCCGGCGCAACTACAATTACCTGTACCAGCTGTTCCGGAAAGTCCAAT				1434
Sbjct 1321	CTGGACTCCAAGTCCGGCGCAACTACAATTACCTGTACCAGCTGTTCCGGAAAGTCCAAT				1380
Query 1435	CTGAAGCCCTTCGAGCGGGACATCTCCACCGAGATCTATCAGGCCGGCAGCACCCCTTGT				1494
Sbjct 1381	CTGAAGCCCTTCGAGCGGGACATCTCCACCGAGATCTATCAGGCCGGCAGCACCCCTTGT				1440
Query 1495	AACGGCGTGGAAAGCTTCAACTGCTACTTCCACTGCACTTACGGCTTTCAGCCACA				1554
Sbjct 1441	AACGGCGTGGAAAGCTTCAACTGCTACTTCCACTGCACTTACGGCTTTCAGCCACA				1500
Query 1555	AATGGCGTGGGCTATCAGCCCTACAGAGTGGTGGTGTGAGCTTCAACTGCTGATGCC				1614
Sbjct 1501	AATGGCGTGGGCTATCAGCCCTACAGAGTGGTGGTGTGAGCTTCAACTGCTGATGCC				1560
Query 1615	CCTGCCACAGTGTGCGGCCCTAAGAAAAGCACC AATCTCGTGAAGAACAAATGCGTGAAC				1674
Sbjct 1561	CCTGCCACAGTGTGCGGCCCTAAGAAAAGCACC AATCTCGTGAAGAACAAATGCGTGAAC				1620
Query 1675	TTCAACTTCAACGGCCTGACCGGCACCGCGTGTGACAGAGAGCAACAAGAAGTTCCTG				1734
Sbjct 1621	TTCAACTTCAACGGCCTGACCGGCACCGCGTGTGACAGAGAGCAACAAGAAGTTCCTG				1680

Query	1735	CCATTCCAGCAGTTTGGCCGGGATATCGCCGATACACAGACGCCGTTAGAGATCCCCAG	1794
Sbjct	1681	CCATTCCAGCAGTTTGGCCGGGATATCGCCGATACACAGACGCCGTTAGAGATCCCCAG	1740
Query	1795	ACACTGGAATTCCTGGACATCACCCCTTGCAGCTTCGGCGGAGTGTCTGTGATCACCCCT	1854
Sbjct	1741	ACACTGGAATTCCTGGACATCACCCCTTGCAGCTTCGGCGGAGTGTCTGTGATCACCCCT	1800
Query	1855	GGCACCAACACCAGCAATCAGGTGGCAGTGTGTACCAGGACGTGAACTGTACCGAAGTG	1914
Sbjct	1801	GGCACCAACACCAGCAATCAGGTGGCAGTGTGTACCAGGACGTGAACTGTACCGAAGTG	1860
Query	1915	CCCGTGGCCATTACGCGGATCAGCTGACACCTACATGGCGGGTGTACTCCACCGGCAGC	1974
Sbjct	1861	CCCGTGGCCATTACGCGGATCAGCTGACACCTACATGGCGGGTGTACTCCACCGGCAGC	1920
Query	1975	AATGTGTTTTCAGACCAGAGCCGGCTGTCTGATCGGAGCCGAGCACGTGAACAATAGCTAC	2034
Sbjct	1921	AATGTGTTTTCAGACCAGAGCCGGCTGTCTGATCGGAGCCGAGCACGTGAACAATAGCTAC	1980
Query	2035	GAGTGGCAGATCCCCATCGCGCTGGCACTGTGTCAGCTACCAGACACAGACAAACAGC	2094
Sbjct	1981	GAGTGGCAGATCCCCATCGCGCTGGCACTGTGTCAGCTACCAGACACAGACAAACAGC	2040
Query	2095	CCTCGGAGAGCCAGAAGCGTGGCCAGCCAGAGCATCATTGCCTACACAATGTCTCTGGGC	2154
Sbjct	2041	CC-CG-----CCTCT---GTGGCCAGCCAGAGCATCATTGCCTACACAATGTCTCTGGGC	2091
Query	2155	GCCGAGAACAGCGTGGCCCTACTCCAACAACCTCTATCGCTATCCCACCAACTTCACCATC	2214
Sbjct	2092	GCCGAGAACAGCGTGGCCCTACTCCAACAACCTCTATCGCTATCCCACCAACTTCACCATC	2151
Query	2215	AGCGTGACCACAGAGATCTGCCTGTGTCCATGACCAAGACCAGCGTGGACTGCACCATG	2274
Sbjct	2152	AGCGTGACCACAGAGATCTGCCTGTGTCCATGACCAAGACCAGCGTGGACTGCACCATG	2211
Query	2275	TACATCTGCGCGGATTCACCGAGTGTCTCAACCTGTCTGCTGTCAGTACGGCAGCTTCTGC	2334
Sbjct	2212	TACATCTGCGCGGATTCACCGAGTGTCTCAACCTGTCTGCTGTCAGTACGGCAGCTTCTGC	2271
Query	2335	ACCCAGCTGAATAGAGCCCTGACAGGGATCGCCGTGGAAACAGGACAAGAACACCCAAAGAG	2394
Sbjct	2272	ACCCAGCTGAATAGAGCCCTGACAGGGATCGCCGTGGAAACAGGACAAGAACACCCAAAGAG	2331
Query	2395	GTGTTCCGCCAAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTTC	2454
Sbjct	2332	GTGTTCCGCCAAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTTC	2391
Query	2455	AATTTTCAGCCAGATTCGCGGATCTAGCAAGCCAGCAAGCGGAGCTTCATCGAGGAC	2514
Sbjct	2392	AATTTTCAGCCAGATTCGCGGATCTAGCAAGCCAGCAAGCGGAGCTTCATCGAGGAC	2451
Query	2515	CTGCTGTTCAACAAGTGACACTGGCCGACGCGCGCTTCATCAAGCAGTATGGCGATTGT	2574
Sbjct	2452	CTGCTGTTCAACAAGTGACACTGGCCGACGCGCGCTTCATCAAGCAGTATGGCGATTGT	2511
Query	2575	CTGGGCGACATTGCGCCAGGGATCTGATTTGCGCCAGAAAGTTAACGGACTGACAGTG	2634
Sbjct	2512	CTGGGCGACATTGCGCCAGGGATCTGATTTGCGCCAGAAAGTTAACGGACTGACAGTG	2571
Query	2635	CTGCCTCTCTGCTGACCCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGGC	2694
Sbjct	2572	CTGCCTCTCTGCTGACCCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGGC	2631
Query	2695	ACAATCACAAAGCGCTGGACATTTGGAGCAGGCGCCGCTCTGCAGATCCCCTTTGCTATG	2754
Sbjct	2632	ACAATCACAAAGCGCTGGACATTTGGAGCAGGCGCCGCTCTGCAGATCCCCTTTGCTATG	2691
Query	2755	CAGATGGCTACCGGTTCAACGGCATCGGAGTGACCCAGAAATGTGCTGTACGAGAACCAG	2814
Sbjct	2692	CAGATGGCTACCGGTTCAACGGCATCGGAGTGACCCAGAAATGTGCTGTACGAGAACCAG	2751
Query	2815	AAGCTGATCGCAACCAAGTTCAACAGCGCCATCGGCAAGATCCAGGACGCTGAGCAGC	2874
Sbjct	2752	AAGCTGATCGCAACCAAGTTCAACAGCGCCATCGGCAAGATCCAGGACGCTGAGCAGC	2811
Query	2875	ACAGCAAGCGCCCTGGGAAAGCTGCAGGACGTGGTCAACAGAAATGCCAGGCACTGAAC	2934
Sbjct	2812	ACAGCAAGCGCCCTGGGAAAGCTGCAGGACGTGGTCAACAGAAATGCCAGGCACTGAAC	2871
Query	2935	ACCCTGGTCAAGCAGCTGTCTCCAACCTTCGGCGCCATCAGCTCTGTGCTGAACGATATC	2994
Sbjct	2872	ACCCTGGTCAAGCAGCTGTCTCCAACCTTCGGCGCCATCAGCTCTGTGCTGAACGATATC	2931
Query	2995	CTGAGCAGACTGGACCCTCTGAGGCCGAGGTGCAGATCGACAGACTGATCACAGGCAGA	3054
Sbjct	2932	CTGAGCAGACTGGACCCTCTGAGGCCGAGGTGCAGATCGACAGACTGATCACAGGCAGA	2991
Query	3055	CTGCAGAGCCTCAGACATACGTGACCCAGCAGCTGATCAGAGCCGCGAGATTAGAGCC	3114
Sbjct	2992	CTGCAGAGCCTCAGAGACTACGTTACCCAGCAGCTGATCAGAGCCGCGAGATTAGAGCC	3051
Query	3115	TCTGCCAATCTGGCCGCCAACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGAGTG	3174
Sbjct	3052	TCTGCCAATCTGGCCGCCAACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGAGTG	3111
Query	3175	GACTTTTGGCGCAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGTG	3234
Sbjct	3112	GACTTTTGGCGCAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGTG	3171
Query	3235	GTGTTTCTGCAGTGCACATATGTGCCCGCTCAAGAGAAGAAATTCACCACCGCTCCAGCC	3294
Sbjct	3172	GTGTTTCTGCAGTGCACATACGTGCCCGCTCAAGAGAAGAAATTCACCACCGCTCCAGCC	3231
Query	3295	ATCTGCCACGACGGCAAGCCCACTTTCTAGAGAAGGCGTGTTCGTGTCCAACGGCACC	3354
Sbjct	3232	ATCTGCCACGACGGCAAGCCCACTTTCTAGAGAAGGCGTGTTCGTGTCCAACGGCACC	3291
Query	3355	CATTGGTTCTGTGACACAGCGGAACCTTCTACGAGCCCGATCATCACCACCGACAACACC	3414
Sbjct	3292	CATTGGTTCTGTGACACAGCGGAACCTTCTACGAGCCCGATCATCACCACCGACAACACC	3351
Query	3415	TTCTGTCTGGCAACTGCGACGTCTGTGATCGGCATTGTGAACAATACCGTGTACGACCCT	3474
Sbjct	3352	TTCTGTCTGGCAACTGCGACGTCTGTGATCGGCATTGTGAACAATACCGTGTACGACCCT	3411
Query	3475	CTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGACAAGTACTTTAAGAACCACACA	3534
Sbjct	3412	CTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGACAAGTACTTTAAGAACCACACA	3471
Query	3535	AGCCCCGACGTGGACCTGGCGGATATCAGCGGAATCAATGCCAGCGCTGTGAACATCCAG	3594

```

Sbjct 3472 |AGCCCCGACGTGGACCTGGGCGATATCAGCGGAATCAATGCCAGCGCTGTGAACATCCAG| 3531
Query 3595 |AAAGAGATCGACCGGCTGAACGAGGTGGCCAAGAATCTGAACGAGAGCCTGATCGACCTG| 3654
Sbjct 3532 |AAAGAGATCGACCGGCTGAACGAGGTGGCCAAGAATCTGAACGAGAGCCTGATCGACCTG| 3591
Query 3655 |CAAGAACTGGGAAGTACGAGCAGTACATCAAGTGGCCC| 3693
Sbjct 3592 |CAAGAACTGGGAAGTACGAGCAGTACATCAAGTGGCCC| 3630
    
```

Mutant Measles morbillivirus strain MeVvac2-SARS2-S(H), complete genome

Sequence ID: **MW090971.1** Length: 19800 Number of Matches: 1

Range 1: 9249 to 13066

Score	Expect	Identities	Gaps	Strand	Frame
6037 bits(3269)	0.0()	3635/3818(95%)	0/3818(0%)	Plus/Plus	
Query 55	ATGTTCTGTGTTCTGGTGTCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACC	114			
Sbjct 9249	ATGTTCTGTGTTCTGGTGTCTGCCTCTGGTGTCCAGCCAGTGTGTGAACCTGACCACC	9308			
Query 115	AGAAACACAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTGTACTACCCCGAC	174			
Sbjct 9309	AGAAACACAGCTGCCTCCAGCCTACACCAACAGCTTTACCAGAGGCGTGTACTACCCCGAC	9368			
Query 175	AAGGTGTTTCAGATCCAGCGTGTGCACTTACCAGGACCTGTTCTGCCTTTCTTCAGC	234			
Sbjct 9369	AAGGTGTTTCAGATCCAGCGTGTGCACTTACCAGGACCTGTTCTGCCTTTCTTCAGC	9428			
Query 235	AACGTGACCTGGTTCACGCCATCCACGTGTCCGGCACCAATGGCACCAAGAGATTCGAC	294			
Sbjct 9429	AACGTGACCTGGTTCACGCCATCCACGTGTCCGGCACCAAGAGATTCGAC	9488			
Query 295	AACCCCGTGTGCCTTTCAACGACGGGGTGTACTTTGCCAGCACCGAGAAGTCCAACATC	354			
Sbjct 9489	AACCCCGTGTGCCTTTCAACGACGGGGTGTACTTTGCCAGCACCGAGAAGTCCAACATC	9548			
Query 355	ATCAGAGGCTGGATCTTCGGCACCACTGGACAGCAAGACCCAGAGCCTGCTGATCGTG	414			
Sbjct 9549	ATCAGAGGCTGGATCTTCGGCACCACTGGACAGCAAGACCCAGAGCCTGCTGATCGTG	9608			
Query 415	AACAACGCCACCAACGTGGTCAAAAGTGTGCGAGTTCAGTTCTGCAACGACCCCTTC	474			
Sbjct 9609	AACAACGCCACCAACGTGGTCAAAAGTGTGCGAGTTCAGTTCTGCAACGACCCCTTC	9668			
Query 475	CTGGCGTCTACTACCACAAGAACAACAGAGCTGGATGGAAAGCGAGTTCGGGGTGTAC	534			
Sbjct 9669	CTGGCGTCTACTACCACAAGAACAACAGAGCTGGATGGAAAGCGAGTTCAGGGTGTAC	9728			
Query 535	AGCAGCGCCAAACAATGCACCTTCGAGTACGTGTCCAGCCTTTCTGATGGACCTGGAA	594			
Sbjct 9729	AGCAGCGCCAAACAATGCACCTTCGAGTACGTGTCCAGCCTTTCTGATGGACCTGGAA	9788			
Query 595	GGCAAGCAGGGCAACTTCAAGAACCTGCGCGAGTTCGTGTTAAGAACATCGACGGCTAC	654			
Sbjct 9789	GGCAAGCAGGGCAACTTCAAGAACCTGCGCGAGTTCGTGTTAAGAACATCGACGGCTAC	9848			
Query 655	TTCAAGATCTACAGCAAGCACACCCCTATCAACCTCGTGCGGGATCTGCCTCAGGGCTTC	714			
Sbjct 9849	TTCAAGATCTACAGCAAGCACACCCCTATCAACCTCGTGCGGGATCTGCCTCAGGGCTTC	9908			
Query 715	TCTGCTCTGGAAACCCCTGGTGGATCTGCCCATCGGCATCAACATCACCCGGTTTCAGACA	774			
Sbjct 9909	TCTGCTCTGGAAACCCCTGGTGGATCTGCCCATCGGCATCAACATCACCCAGATTCAGACA	9968			
Query 775	CTGCTGGCCCTGCACAGAAGTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT	834			
Sbjct 9969	CTGCTGGCCCTGCACAGAAGTACCTGACACCTGGCGATAGCAGCTGTGGATGGACAGCT	10028			
Query 835	GGTGCAGCCGCTTACTATGTGGGCTACCTGCAGCCTAGAACCCTTCTGCTGAAGTACAAC	894			
Sbjct 10029	GGCGTGCCTTACTACGTGGGATACCTGCAGCCTAGAACCCTTCTGCTGAAGTACAAC	10088			
Query 895	GAGAAGCGCACCATCACCGACCGCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAG	954			
Sbjct 10089	GAGAAGCGCACCATCACCGACCGCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAG	10148			
Query 955	TGCACCTGAAGTCTTACCCTGGAAAAGGGCATCTACCAGACCAGCAACTCCGGGGT	1014			
Sbjct 10149	TGCACCTGAAGTCTTACCCTGGAAAAGGGCATCTACCAGACCAGCAACTCCGGGGT	10208			
Query 1015	CAGCCACCAAGTCAATCGTGCGGTTCCTCAATACCAATCTGTGCCCTTCGGCGAG	1074			
Sbjct 10209	CAGCCACCAAGTCAATCGTGCGGTTCCTCAATACCAATCTGTGCCCTTCGGCGAG	10268			
Query 1075	GTGTTCAATGCCACAGATTGCCTCTGTGTACGCTGGAAACGGAAGCGGATCAGCAAT	1134			
Sbjct 10269	GTGTTCAATGCCACAGATTGCCTCTGTGTACGCTGGAAACGGAAGCGGATCAGCAAC	10328			
Query 1135	TGCGTGGCCGACTACTCCGTGTGTACAACCTCCGCCAGCTTACGACCTTCAAGTGTAC	1194			
Sbjct 10329	TGCGTGGCCGACTACTCCGTGTGTACAACCTCCGCCAGCTTACGACCTTCAAGTGTAC	10388			
Query 1195	GGCGTGTCCCTACCAAGCTGAACGACCTGTGCTTCAAAACGTGTACGCCGACAGCTTC	1254			
Sbjct 10389	GGCGTGTCCCTACCAAGCTGAACGACCTGTGCTTCAAAACGTGTACGCCGACAGCTTC	10448			
Query 1255	GTGATCGGGGAGATGAAGTGCAGGAGATTGCCCTGGACAGACAGGCAAGATCGCCGAC	1314			
Sbjct 10449	GTGATCAGAGGCGACGAAGTGCAGGAGATCGCTCCTGGACAGACAGGCAAGATCGCCGAC	10508			
Query 1315	TACAACCTACAAGTGCCTGACGACTTACCAGGCTGTGATTGCCTGGAAACAGCAACAAC	1374			
Sbjct 10509	TACAACCTACAAGTGCCTGACGACTTACCAGGCTGTGATTGCCTGGAAACAGCAACAAC	10568			
Query 1375	CTGGACTCCAAGTGCAGGCAACTACAATTACCTGTACCGGCTGTTCCGGAAGTCCAAT	1434			
Sbjct 10569	CTGGACTCCAAGTGCAGGCAACTACAATTACCTGTACCGGCTGTTCCGGAAGTCCAAT	10628			
Query 1435	CTGAAGCCCTTCGAGCGGACATCTCCACCGAGATCTACAGGCCGGCAGCACCCCTTGT	1494			
Sbjct 10629	CTGAAGCCCTTCGAGCGGACATCTCCACCGAGATCTACAGGCCGGCAGCACCCCTTGT	10688			
Query 1495	AACGGCGTGAAGGCTTCAACTGCTACTTCCCACTGCAGTCTACGGCTTTCAGCCCA	1554			

Sbjct	10689	AACGGCGTGAAGGCTTCAACTGCTACTTCCCACTGCAGTCTACGGCTTTCAGCCACA	10748
Query	1555	AATGGCGTGGGCTATCAGCCCTACAGAGTGGTGGTGTGAGCTTGAAGTCTGCATGCC	1614
Sbjct	10749	AATGGCGTGGGCTACCAGCCTTACAGAGTGGTGGTGTGAGCTTGCAGTCTGCACGCT	10808
Query	1615	CCTGCCACAGTGTGGCCCTAAGAAAAGCACAATCTCGTGAAGAACAAATGCGTGAAC	1674
Sbjct	10809	CCTGCTACAGTGTGGCCCTAAGAAAAGCACAACCTCGTGAAGAACAAATGCGTGAAC	10868
Query	1675	TTCAACTTCAACGGCTGACCGCACCGCGTGTGACAGAGAGAACAAAGATTCCTG	1734
Sbjct	10869	TTCAACTTCAACGGCTGACCGCACCGCGTGTGACAGAAAGAACAAAGATTCCTG	10928
Query	1735	CCATTCCAGCAGTTTGGCCGGATATCGCCGATACCAGAGACGCCGTTAGAGATCCCCAG	1794
Sbjct	10929	CCATTCCAGCAGTTTGGCCGGATATCGCCGATACCAGAGACGCCGTTAGAGATCCCCAG	10988
Query	1795	ACACTGGAATCTGGACATCACCCTTGCAGCTTCGGCGGAGTGTCTGTGATCACCCT	1854
Sbjct	10989	ACACTGGAATCTGGACATCACCCTTGCAGCTTCGGCGGAGTGTCTGTGATCACCCT	11048
Query	1855	GGCACCACACAGCAATCAGGTGGCAGTGTGTACCAGGACGTGAACGTACCGAAGTG	1914
Sbjct	11049	GGCACCACACCTTAACAGGTGGCAGTGTGTACCAGGACGTGAACGTACCGAAGTG	11108
Query	1915	CCCGTGGCCATTACGCCGATCAGCTGACACCTACATGGCGGGTGTACTCCACCGGCAGC	1974
Sbjct	11109	CCAGTGGCTATCCACGCCGATCAGCTGACCCCTACTTGGAGAGTGTACTCCACCGGCTCC	11168
Query	1975	AATGTGTTTTCAGACCAGAGCCGGTGTGTGATCGGAGCCGAGCACGTGAACAATAGCTAC	2034
Sbjct	11169	AACGTGTTTTCAGACAAGAGCCGGTGTGTGATCGGAGCCGAGCACGTGAACAATAGCTAC	11228
Query	2035	GAGTGCAGACATCCCATCGGCCTGGAACTGCGCCAGTACCAGACACAGACAAACAGC	2094
Sbjct	11229	GAGTGCAGACATCCCATCGGCCTGGAACTGCGCCAGTACCAGACACAGACAAACAGC	11288
Query	2095	CCTCGGAGGCCAGAAGCGTGGCCAGCCAGAGCATATTGCTTACACAATGTCTTGGGC	2154
Sbjct	11289	CCTAGAAGGCCAGAAGCGTGGCCAGCCAGAGCATATTGCTTACACAATGAGCTTGGGC	11348
Query	2155	GCCGAGAAGCGTGGCCACTCCAACAACCTTATCGCTATCCCAACCACTTACCATC	2214
Sbjct	11349	GCTGAGAAGCGTGGCCACTCCAACAACCTTATCGCTATCCCAACCACTTACCATC	11408
Query	2215	AGCGTGACCACAGAGATCCTGCCTGTGTCCATGACCAAGACAGCGTGGACTGCACCATG	2274
Sbjct	11409	AGCGTGACCACAGAGATCCTGCCTGTGTCCATGACCAAGACAGCGTGGACTGCACCATG	11468
Query	2275	TACATCTGCGGCATTCCACCGAGTGTCCAACTGCTGCTGACGTACGGCAGCTTCTGC	2334
Sbjct	11469	TACATCTGCGGCATTCCACCGAGTGTCCAACTGCTGCTGACGTACGGCAGCTTCTGC	11528
Query	2335	ACCCAGCTGAATAGAGCCCTGACAGGGATCGCCGTGGAACAGGACAAGAACACCCAAAGAG	2394
Sbjct	11529	ACCCAGCTGAACAGAGCCCTGACAGGGATCGCCGTGGAACAGGACAAGAACACCCAAAGAG	11588
Query	2395	GTGTTTCGCCCAAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTT	2454
Sbjct	11589	GTGTTTCGCCCAAGTGAAGCAGATCTACAAGACCCCTCTATCAAGGACTTCGGCGGCTT	11648
Query	2455	AATTTTCAGCCAGATCTGCCCGATCCTAGCAAGCCAGCAAGCGGAGCTTATCGAGGAC	2514
Sbjct	11649	AATTTTCAGCCAGATCTGCCCGATCCTAGCAAGCCAGCAAGCGGAGCTTATCGAGGAC	11708
Query	2515	CTGCTGTTTCAACAAAGTACACTGGCCGACGCCGGCTTTCATCAAGCAGTATGGCGATTGT	2574
Sbjct	11709	CTGCTGTTTCAACAAAGTACACTGGCCGACGCCGGCTTTCATCAAGCAGTATGGCGATTGT	11768
Query	2575	CTGGCGACATTGCCGCCAGGGATCTGATTTGCGCCAGAAGTTTAAAGGACTGACAGTG	2634
Sbjct	11769	CTGGCGACATTGCCGCCAGGGATCTGATTTGCGCCAGAAGTTTAAAGGACTGACAGTG	11828
Query	2635	CTGCCTCCTCTGCTGACCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGGC	2694
Sbjct	11829	CTGCCTCCTCTGCTGACCGATGAGATGATCGCCAGTACACATCTGCCCTGCTGGCCGGC	11888
Query	2695	ACAATCACAAAGCGCTGGACATTTGGAGCAGGCGCCGCTTGCAGATCCCCCTTGCCTATG	2754
Sbjct	11889	ACAATCACAAAGCGCTGGACATTTGGAGCAGGCGCCGCTTGCAGATCCCCCTTGCCTATG	11948
Query	2755	CAGATGGCCTACCGGTTCAACGGCATCGGAGTACCCAGAATGTGCTGTACGAGAACCAG	2814
Sbjct	11949	CAGATGGCCTACCGGTTCAACGGCATCGGAGTACCCAGAATGTGCTGTACGAGAACCAG	12008
Query	2815	AAGCTGATCGCCAAACAGTTCAACAGCGCCATCGGCAAGATCCAGGACGCTGAGCAGC	2874
Sbjct	12009	AAGCTGATCGCCAAACAGTTCAACAGCGCCATCGGCAAGATCCAGGACGCTGAGCAGC	12068
Query	2875	ACAGCAAGCGCCCTGGGAAAGCTGACAGGAGTGGTCAACCAGAATGCCAGGCACTGAAC	2934
Sbjct	12069	ACCGTTCCTGCCCTGGGAAAGCTGACAGGAGTGGTCAACCAGAATGCCAGGCACTGAAC	12128
Query	2935	ACCCTGGTCAAGCAGCTGTCTCCAACCTCGGCGCCATCAGCTCTGTGCTGAACGATATC	2994
Sbjct	12129	ACCCTGGTCAAGCAGCTGTCTCCAACCTCGGCGCCATCAGCTCTGTGCTGAACGATATC	12188
Query	2995	CTGAGCAGACTGGACCTCCTGAGGCCGAGGTGCAGATCGACAGACTGATCACAGGCAGA	3054
Sbjct	12189	CTGAGCAGACTGGACAAGGTGAAGCCGAGGTGCAGATCGACAGACTGATCACAGGCAGA	12248
Query	3055	CTGCAGAGCTCCAGACATACGTGACCCAGCAGCTGATCAGAGCCGCGAGATTAGAGCC	3114
Sbjct	12249	CTGCAGTCCCTGCAGACCTACGTTACCCAGCAGCTGATTAGAGCCGCGAGATTAGAGCC	12308
Query	3115	TCTGCCAATCTGGCCGCCACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGAGTG	3174
Sbjct	12309	TCTGCTAACCTGGCCGCCACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGAGTG	12368
Query	3175	GACTTTTTCGGCAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGTG	3234
Sbjct	12369	GACTTTTTCGGCAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGCGTG	12428
Query	3235	GTGTTTCTGCACGTGACATATGTGCCCGCTCAAGAGAAGAATTTACCACCGCTCCAGCC	3294
Sbjct	12429	GTGTTTCTGCACGTGACATACGTGCCCGCTCAAGAGAAGAATTTACCACCGCTCCAGCC	12488
Query	3295	ATCTGCCACGACGGCAAAGCCACTTCTTAGAGAAGGCGTGTCTGTGCTCAACGGCACC	3354
Sbjct	12489	ATCTGCCACGACGGCAAAGGCTCACTTCTTAGAGAAGGCGTGTCTGTGCTCAACGGCACC	12548

```

Query 3355  CATTGGTTCGTGACACAGCGGAACCTTCTACGAGCCCAGATCATCACCACCGACAACACC 3414
Sbjct 12549  CATTGGTTCGTGACACAGAGAACTTCTACGAGCCCAGATCATCACCACCGACAACACC 12608

Query 3415  TTCGTGTCTGGCAACTGCGACGCTGTGATCGGCATTGTGAACAATACCGGTACGACCCCT 3474
Sbjct 12609  TTCGTGTCTGGCAACTGCGACGCTGTGATCGGCATTGTGAACAATACCGGTACGACCCCT 12668

Query 3475  CTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGACAAGTACTTTAAGAACACACACA 3534
Sbjct 12669  CTGCAGCCCGAGCTGGACAGCTTCAAAGAGGAACTGGATAAGTACTTTAAGAACACACACA 12728

Query 3535  AGCCCCGACGTGGACCTGGGCGATATCAGCGGAATCAATGCCAGCGTCGTGAACATCCAG 3594
Sbjct 12729  AGCCCCGACGTGGACCTGGGCGATATCAGCGGAATCAACGCCAGCGTGGTCAACATCCAG 12788

Query 3595  AAAGAGATCGACCCGCTGAACGAGGTGGCCAAGAACTGAACGAGAGCCTGATCGACCTG 3654
Sbjct 12789  AAAGAGATCGACCCGCTGAACGAGGTGGCCAAGAACTGAACGAGAGCCTGATCGACCTG 12848

Query 3655  CAAGAACTGGGGAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTTT 3714
Sbjct 12849  CAAGAACTGGGGAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGCTTT 12908

Query 3715  ATCGCCGGACTGATTGCCATCGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 3774
Sbjct 12909  ATCGCTGGCCTGATCGTATCGTATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 12968

Query 3775  TGTAGCTGCCTGAAGGGCTGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 3834
Sbjct 12969  TGTAGCTGCCTGAAGGGCTGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 13028

Query 3835  TCTGAGCCCGTGTGAAGGGCGTGAAGTGCCTACAC 3872
Sbjct 13029  TCTGAGCCAGTGTGAAGGGCGTGAAGTGCCTACAC 13066
    
```

Synthetic construct HCV1146 Moderna (mRNA-1273) SARS-CoV-2 vaccine sequence

Sequence ID: **OK120841.1** Length: 3828 Number of Matches: 1

Range 1: 1 to 3823

Score	Expect	Identities	Gaps	Strand	Frame
5060 bits(2740)	0.0()	3465/3826(91%)	6/3826(0%)	Plus/Plus	
Query 55	ATGTTTCGTGTTTCCTGGTGTGCTGCCCTTGGTGTCCAGCCAGTGTGTGAACCTGACCACC	114			
Sbjct 1	ATGTTTCGTGTTTCCTGGTGTGCTGCCCTTGGTGTCCAGCCAGTGTGTGAACCTGACCACC	60			
Query 115	AGAACACAGCTGCCCTCCAGCCTACACCAACAGCTTTACAGAGGCGTGTACTACCCCGAC	174			
Sbjct 61	CGGACCCAGCTGCCCACCAGCCTACACCAACAGCTTTACCCGGGGCGTCTACTACCCCGAC	120			
Query 175	AAGGTGTTTTCAGATCCAGCGTGTGCACTCTACCCAGGACCTGTTCTGCCTTCTTTCAGC	234			
Sbjct 121	AAGGTGTTCCGGAGCAGCGTCTTGCACAGCACCAGGACCTGTTCTGCCTTCTTTCAGC	180			
Query 235	AACGTGACCTGGTTCACGCCATCCACGTGCCGGCACCAGTGGCACCAGAGATTTCGAC	294			
Sbjct 181	AACGTGACCTGGTTCACGCCATCCACGTGAGCGGCACCAGTGGCACCAGAGCGTTTCGAC	240			
Query 295	AACCCCGTGTGCCCTTCAACGACGGGGTGTACTTTGCCAGCACCAGAGAGTCCAACATC	354			
Sbjct 241	AACCCCGTGTGCCCTTCAACGACGGGGTGTACTTTCGCCAGCACCAGAGAGAGCAACATC	300			
Query 355	ATCAGAGGCTGGATCTTCGGCACCACACTGGACAGCAAGACCCAGAGCCTGCTGATCGTG	414			
Sbjct 301	ATCCGGGGCTGGATCTTCGGCACCACCTGGACAGCAAGACCCAGAGCCTGCTGATCGTG	360			
Query 415	AACAACGCCACCAACGTGGTTCATCAAAGTGTGCGAGTTCAGTTCGCAACGACCCCTTC	474			
Sbjct 361	AATAACGCCACCAACGTGGTTCATCAAAGTGTGCGAGTTCAGTTCGCAACGACCCCTTC	420			
Query 475	CTGGGCGTCTACTACCACAAGAAACAAGAGCTGGATGGAAAGCGAGTTCCGGGTGTAC	534			
Sbjct 421	CTGGGCGTGTACTACCACAAGAAACAAGAGCTGGATGGAGAGCGAGTTCCGGGTGTAC	480			
Query 535	AGCAGCGCCAACTGACACCTTCGAGTACGTGCCAGCCTTCTGATGGACCTGGAA	594			
Sbjct 481	AGCAGCGCCAACTGACACCTTCGAGTACGTGAGCAGCCTTCTGATGGACCTGGAG	540			
Query 595	GGCAAGCAGGGCAACTTCAAGAACTGCGCGAGTTCGTGTTTAAAGAACATCGACGGCTAC	654			
Sbjct 541	GGCAAGCAGGGCAACTTCAAGAACTGCGGGAGTTCGTGTTCAAGAACATCGACGGCTAC	600			
Query 655	TTCAAGATCTACAGCAAGCACACCCCTATCAACCTCGTGCAGGATCTGCCTCAGGGCTTC	714			
Sbjct 601	TTCAAGATCTACAGCAAGCACACCCCAATCAACCTGGTGCAGGATCTGCCACAGGGCTTC	660			
Query 715	TCTGCTTGGAAACCCCTGGTGGATCTGCCATCGGCATCAACATCACCAGGTTCCAGACA	774			
Sbjct 661	TCAGCCCTGGAGCCCTGGTGGACTGCCATCGGCATCAACATCACCAGGTTCCAGACC	720			
Query 775	CTGCTGGCCCTGCACAGAAGCTACCTGACACCTGGCGATAGCAGCAGCGGATGGACAGCT	834			
Sbjct 721	CTGCTGGCCCTGCACCGAGCTACCTGACCCAGGCGACAGCAGCAGCGGATGGACAGCA	780			
Query 835	GGTGCCGCCCTTACTATGTGGGTACCTGACGCTAGAACCTTCTGCTGAAGTACAAC	894			
Sbjct 781	GGCGGGCTGCTTACTACGTGGGTACCTGACGCCCCGACCTTCTGCTGAAGTACAAC	840			
Query 895	GAGAACGGCACCATCACCGACGCCGTGGATTGTGCTCTGGATCCTCTGAGCGAGACAAAG	954			
Sbjct 841	GAGAACGGCACCATCACCGACGCCGTGGACTGCGCCTTGGACCTCTGAGCGAGACAAAG	900			
Query 955	TGCACCTGAAGTCTTACCCTGGAAAAGGGCATCTACCAGACCAGCAACTTCCGGGTG	1014			
Sbjct 901	TGCACCTGAAGAGCTTACCCTGGAGAAGGGCATCTACCAGACCAGCAACTTCCGGGTG	960			
Query 1015	CAGCCACCGAATCCATCGTGCAGTTCCCAATATCACAATCTGTGCCCTTCCGGCGAG	1074			
Sbjct 961	CAGCCACCGAGAGCATCGTGCAGTTCCCAATATCACAATCTGTGCCCTTCCGGCGAG	1020			
Query 1075	GTGTTCAATGCCACCAAGATTGCCTCTGTGTACGCTGGAAACCGAAGCGGATCAGCAAT	1134			
Sbjct 1021	GTGTTCAATGCCACCAAGATTGCCTCTGTGTACGCTGGAAACCGAAGCGGATCAGCAAC	1080			
Query 1135	TGCGTGGCCGACTACTCCGTGCTGTAACAACCTCCGCGAGCTTACGACCTTCAAGTGTAC	1194			

Sbjct	1081	TGCGTGGCCGACTACAGCGTGTACACAGCGCCAGCTTCAGCACCTTCAAGTGCTAC	1140
Query	1195	GGCGTGTCCCTTACCAAGCTGAACGACCTGTGCTTCAACAACTGTACGCCGACAGCTTC	1254
Sbjct	1141	GGCGTGAAGCCACCAAGCTGAACGACCTGTGCTTCAACAACTGTACGCCGACAGCTTC	1200
Query	1255	GTGATCCGGGGAGATGAAGTGGCGGAGATTGCCCTGGACAGACAGGCAAGATCGCCGAC	1314
Sbjct	1201	GTGATCCGTGGCGACAGGATGGCGGAGATCGACCCGGCCAGACAGGCAAGATCGCCGAC	1260
Query	1315	TACAACTACAAGCTGCCGACGACTTACCAGGCTGTGATTGCCGGAACAGCAACAAC	1374
Sbjct	1261	TACAACTACAAGCTGCCGACGACTTACCAGGCTGCGTATCGCTGGAACAGCAACAAC	1320
Query	1375	CTGGACTCCAAGTGGCGGCAACTACAATTACCTGTACCAGGCTTCCGGAAAGTCCAAT	1434
Sbjct	1321	CTGACAGCAAGTGGCGGCAACTACAATTACCTGTACCAGGCTTCCGGAAAGAGCAAC	1380
Query	1435	CTGAAGCCCTTCGAGCGGGACATCTCCACCGAGATCTATCAGGCCGGCAGCACCCCTTGT	1494
Sbjct	1381	CTGAAGCCCTTCGAGCGGGACATCAGCACCGAGATCTACCAGCCGGCTCCACCCCTTGC	1440
Query	1495	AACGGCGTGGAAAGGCTTCAACTGTACTTCCCACTGCAGTCTACGGCTTTCAGCCACA	1554
Sbjct	1441	AACGGCGTGGAAAGGCTTCAACTGTACTTCCCTCTGACAGACTACGGCTTTCAGCCACC	1500
Query	1555	AATGGCGTGGGCTATCAGCCCTACAGAGTGGTGGTGTGAGCTTCAACTGCTGCATGCC	1614
Sbjct	1501	AACGGCGTGGGCTACCAGCCCTACCAGGTTGGTGGTGTGAGCTTCAACTGCTGCATGCC	1560
Query	1615	CCTGCCACAGTGTGGCCCTAAGAAAAGCACCAATCTCGTGAAGAAACAATGCGTGAAC	1674
Sbjct	1561	CCAGCCACCGTGTGGCCCTAAGAAAGACCAACCTGGTGAAGAAACAATGCGTGAAC	1620
Query	1675	TTCAACTTCAACGGCTGACCGCCACCGCGTGTGACAGAGAGCAACAAGAAAGTTCCTG	1734
Sbjct	1621	TTCAACTTCAACGGCTTACCAGCCACCGCGTGTGACCGAGAGCAACAAGAAATTCCTG	1680
Query	1735	CCATTCAGCAGTTCGGCCGGGATATCGCCGATACCAGACGCGTTAGAGATCCCAG	1794
Sbjct	1681	CCCTTTCAGCAGTTCGGCCGGGACATCGCCGACACCAGCAGCTGTGCGGGATCCCAG	1740
Query	1795	ACACTGGAAATCCTGGACATCACCCCTTGCAGCTTCCGGGGAGTGTCTGTGATCACCCCT	1854
Sbjct	1741	ACCTGGAGATCCTGGACATCACCCCTTGCAGCTTCCGGGGAGTGTGATCACCCCA	1800
Query	1855	GGCACCAACACAGCAATCAGTGGCAGTGTACCAGGACGTGAAGTGTACCGAAGTG	1914
Sbjct	1801	GGCACCAACACAGCAATCAGTGGCAGTGTACCAGGACGTGAAGTGTACCGAAGTG	1860
Query	1915	CCCCTGGCCATTACGCGGATCAGTGCACCTACATGGCGGGTGTACTCCACCGGCAGC	1974
Sbjct	1861	CCCCTGGCCATTCACGCGGATCAGTGCACCTACATGGCGGGTGTACTCCACCGGCAGC	1920
Query	1975	AATGTGTTTCAGACAGCCGGCTGTCTGATCGGACGAGACGTGAACAATAGCTAC	2034
Sbjct	1921	AAGTGTTCAGACAGCCGGCGGTTGCTGATCGGCGCCGAGACGTGAACAACAGCTAC	1980
Query	2035	GAGTGCACATCCCCATCGGCGTGGAACTGCGCCAGCTACCAGACACAGAC-AA-ACA	2092
Sbjct	1981	GAGTGCACATCCCCATCGGCGCGGCACTGTGTCAGCTACCAGACCCAGACCAATTC	2040
Query	2093	GCCCTCGGAGAGCCAGAAAGCGTGGCCAGCCAGAGCATATTGCCACCAATGTCTCTGG	2152
Sbjct	2041	-CCC-CGGAGGGCAAGGAGCGTGGCCAGCCAGAGCATATCGCTACACCATGAGCTTGG	2098
Query	2153	GCGCCGAGAAACAGCGTGGCTACTCCAACAACCTATCGCTATCCCACCACTTACCA	2212
Sbjct	2099	GCGCCGAGAAACAGCGTGGCTTACAGCAACAACAGCATCGCCATCCCACCACTTACCA	2158
Query	2213	TCAGCGTGACCACAGAGATCTGCTGTGTCATGACCAAGACCAGCGTGGACTGCACCA	2272
Sbjct	2159	TCAGCGTGACCACAGAGATCTGCTGTGTCATGACCAAGACCAGCGTGGACTGCACCA	2218
Query	2273	TGTACATCTGCGGGCATTCACCGAGTGTCCAACCTGTGCTGTCAGTACGGCAGCTTCT	2332
Sbjct	2219	TGTACATCTGCGGGCAGCAGCAGGATGTCAGCAACCTGTGCTGTCAGTACGGCAGCTTCT	2278
Query	2333	GCACCCAGCTGAATAGAGCCCTGACAGGGATCGCCGTGGAACAGGACAAGAACCCCAAG	2392
Sbjct	2279	GCACCCAGCTGAACCGGGCCCTGACCGGCATCGCCGTGGAGCAGGACAAGAACCCCAAG	2338
Query	2393	AGGTGTTTCGCCCAAGTGAAGCAGATCTACAAGACCCCTCCTATCAAGGACTTCGGCGGCT	2452
Sbjct	2339	AGGTGTTTCGCCCAAGTGAAGCAGATCTACAAGACCCCTCCTATCAAGGACTTCGGCGGCT	2398
Query	2453	TCAATTTACAGCAGATTCTGCCGATCCTAGCAAGCCAGCAAGCGGAGCTTCATCGAGG	2512
Sbjct	2399	TCAATTTACAGCAGATTCTGCCGACCCAGCAAGCCAGCAAGCGGAGCTTCATCGAGG	2458
Query	2513	ACCTGTGTTCAACAAGTGAACACTGGCCGACCGCGCTTTCATCAAGCAGTATGGCGATT	2572
Sbjct	2459	ACCTGTGTTCAACAAGTGAACACTAGCCGACCGCGCTTTCATCAAGCAGTACGGCGACT	2518
Query	2573	GTCTGGCGACATGGCCGACGGGATCTGATTTGCGCCAGAAAGTTTAAACGGACTGACAG	2632
Sbjct	2519	GCCTCGGCGACATAGCCGCGCGGACCTGATCTGCGCCAGAAAGTTTAAACGGCTGACCG	2578
Query	2633	TGCTGCTCCTCTGCTGACCGATGAGATGATCGCCAGTACAC-ATCTGCCCTGTGGCC	2691
Sbjct	2579	TGCTGCTCCTCTGCTGACCGAGATGATCGCCAGTACACAGC-GCCCTGTTAGCC	2637
Query	2692	GGCACAATCACAAGCGGCTGGACATTTGGAGCAGGCGCGCTCTGCAGATCCCCTTTGCT	2751
Sbjct	2638	GGAAACCATCACAGCGGCTGGACTTTTCGGCGCTGGAGCGCTCTGCAGATCCCCTTCGCC	2697
Query	2752	ATGCAGATGGCTACCGGTTCAACGGCATCGGAGTGACCCAGAATGTGCTGTACGAGAAC	2811
Sbjct	2698	ATGCAGATGGCTACCGGTTCAACGGCATCGGCGTGACCCAGAAGCTGTGTACGAGAAC	2757
Query	2812	CAGAAGCTGATCGCAACAGTTCACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGC	2871
Sbjct	2758	CAGAAGCTGATCGCAACAGTTCACAGCGCCATCGGCAAGATCCAGGACAGCCTGAGC	2817
Query	2872	AGCACAGCAAGCGCCCTGGGAAAGCTGACAGGACGTGGTCAACAGAATGCCAGGCACTG	2931
Sbjct	2818	AGCACAGCTAGCGCCCTGGGCAAGCTGACAGGACGTGGTCAACAGAAGCGCCAGGCACTG	2877
Query	2932	AACACCTGGTCAAGCAGCTGTCTCCAACCTTCGGCGCCATCAGCTCTGTGCTGAACGAT	2991
Sbjct	2878	AACACCTGGTGAAGCAGCTGACAGCAACTTCGGCGCCATCAGCAGCGTGTGAACGAC	2937

```

Query 2992 ATCCTGAGCAGACTGGACCTCCTGAGGCCGAGGTGCAGATCGACAGACTGATCACAGGC 3051
Sbjct 2938 ATCCTGAGCCGGCTGGACCTCCCGAGGCCGAGGTGCAGATCGACCGGCTGATCACTGGC 2997
Query 3052 AGACTGCAGAGCCTCCAGACATACGTGACCCAGCAGCTGATCAGAGCCGCCGAGATTAGA 3111
Sbjct 2998 CGGCTGCAGAGCCTGCAGACCTACGTGACCCAGCAGCTGATCCGGGCCGCCGAGATTCCGG 3057
Query 3112 GCCTCTGCCAATCTGGCCGCCACCAAGATGTCTGAGTGTGTGCTGGGCCAGAGCAAGAGA 3171
Sbjct 3058 GCCAGCGCCAACTGGCCGCCACCAAGATGAGCGAGTGCCTGCTGGGCCAGAGCAAGCGG 3117
Query 3172 GTGGACTTTTGGCGCAAGGGCTACCACCTGATGAGCTTCCCTCAGTCTGCCCTCACGGC 3231
Sbjct 3118 GTGGACTTCTCGCGCAAGGGCTACCACCTGATGAGCTTCCCGAGCGCACCCACCGGA 3177
Query 3232 GTGGTGTTCCTGCACGTGACATATGTGCCCGCTCAAGAGAAGAAATTTACCACCGCTCCA 3291
Sbjct 3178 GTGGTGTTCCTGCACGTGACCTACGTGCCCGCCAGGAGAAGAACTTACCACCGCCCA 3237
Query 3292 GCCATCTGCCACGACGGCAAGGCCACTTTCCCTAGAGAAGGGCTGTTCTGTCTCAACGGC 3351
Sbjct 3238 GCCATCTGCCACGACGGCAAGGCCACTTTCCCGGGAGGGCGTGTTCGTGAGCAACGGC 3297
Query 3352 ACCATTGGTTCGTGACACAGCGGAACCTTCTACGAGCCCAGATCATACCACCGACAAC 3411
Sbjct 3298 ACCACTGGTTCGTGACCCAGCGGAACCTTCTACGAGCCCAGATCATACCACCGACAAC 3357
Query 3412 ACCTTCGTGTCTGGCAACTGCGACGTGATCGGCATTGTGAACAATACCGTGTACGAC 3471
Sbjct 3358 ACCTTCGTGAGCGCAACTGCGACGTGATCGGCATTGTGAACAACACCGTGTACGAT 3417
Query 3472 CCTCTGCAGCCGAGCTGGACAGCTTCAAGAGGAACCTGGACAAGTACTTTAAGAACCAC 3531
Sbjct 3418 CCCCTGCAGCCGAGCTGGACAGCTTCAAGAGGAGCTGGACAAGTACTTCAAGAATCAC 3477
Query 3532 ACAAGCCCCGACGTGGACCTGGGCGATATCAGCGGAATCAATGCCAGCGCTGTGAACATC 3591
Sbjct 3478 ACCAGCCCCGACGTGGACCTGGGCGACATCAGCGGCATCAACGCCAGCGTGGTGAACATC 3537
Query 3592 CAGAAAGAGATCGACCCGGCTGAACGAGGTGGCCAAAGAACTGAACGAGAGCCTGATCGAC 3651
Sbjct 3538 CAGAAGGAGATCGATCGGCTGAACGAGGTGGCCAAAGAACTGAACGAGAGCCTGATCGAC 3597
Query 3652 CTGCAAGAACTGGGGAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGC 3711
Sbjct 3598 CTGCAAGGAGTGGGCAAGTACGAGCAGTACATCAAGTGGCCCTGGTACATCTGGCTGGGC 3657
Query 3712 TTTATCGCCGGACTGATTGCCATCGTGTGTTGACCAATCATGCTGTTGATGACACAGC 3771
Sbjct 3658 TTTATCGCCGGCTGATCGCCATCGTGTGTTGACCAATCATGCTGTTGATGACACAGC 3717
Query 3772 TGCTGTAGCTGCCGTAAGGGCTGTTGTAGCTGTGGCAGCTGCTGCAAGTTCGACGAGGAC 3831
Sbjct 3718 TGCTGTAGCTGCCGTAAGGGCTGTTGTAGCTGTGGCAGCTGCTGCAAGTTCGACGAGGAC 3777
Query 3832 GATTCTGAGCCCGTCTGAAGGGCGTGAAGTGCACCTACACATGAT 3877
Sbjct 3778 GACAGCGAGCCGTCTGAAGGGCGTGAAGTGCACCTACACATGAT 3823
    
```

Taxonomie

Reports

◦ **Lineage**

Organism	Blast Name	Score	Number of Hits	Description
root			100	
.artificial sequences	other sequences		30	
..synthetic construct	other sequences	6746	16	synthetic construct hits
..Recombinant vector AAVCOVID19-1	other sequences	4215	1	Recombinant vector AAVCOVID19-1 hits
..Cloning vector pCDNA3.1.2S	other sequences	4185	1	Cloning vector pCDNA3.1.2S hits
..Expression vector SARSCoV2SGFP	other sequences	4120	1	Expression vector SARSCoV2SGFP hits
..Expression vector SARSCoV2S&SmBit	other sequences	4120	1	Expression vector SARSCoV2S&SmBit hits
..Expression vector SARSCoV2SP681H	other sequences	4120	1	Expression vector SARSCoV2SP681H hits
..Expression vector SARSCoV2S	other sequences	4120	1	Expression vector SARSCoV2S hits
..Expression vector SARSCoV2SD614G	other sequences	4115	1	Expression vector SARSCoV2SD614G hits
..Expression vector SARSCoV2SN501Y	other sequences	4115	1	Expression vector SARSCoV2SN501Y hits
..Expression vector SARSCoV2SY453F	other sequences	4115	1	Expression vector SARSCoV2SY453F hits
..Expression vector SARS-CoV-2-S-E484K	other sequences	4115	1	Expression vector SARS-CoV-2-S-E484K hits
..Expression vector SARS-CoV-2-S-N439K	other sequences	4115	1	Expression vector SARS-CoV-2-S-N439K hits
..Recombinant vector AAV-COVID19-06	other sequences	2217	1	Recombinant vector AAV-COVID19-06 hits
..Recombinant vector AAV-COVID19-05	other sequences	2217	1	Recombinant vector AAV-COVID19-05 hits
..Recombinant vector AAVCOVID19-3	other sequences	2176	1	Recombinant vector AAVCOVID19-3 hits
.Measles morbillivirus	viruses	6037	1	Measles morbillivirus hits
.Homo sapiens	primates	257	69	Homo sapiens hits

◦ **Organism**

Description	Score	E value	Accession
synthetic construct [other sequences]			
Synthetic construct clone E484K Spike del21aa spike gene, complete cds	6746	0.0	MW816500
Synthetic construct clone rcVSV-CoV2-S surface glycoprotein gene, complete cds	6735	0.0	MZ771336
Synthetic construct SARS CoV 2 ectoCSPP gene, complete cds	6529	0.0	MT380725
Synthetic construct HCV1146 Moderna (mRNA-1273) SARS-CoV-2 vaccine sequence	5060	0.0	OK120841
Synthetic construct chimeric spike vaccine construct sequence	4289	0.0	MZ393690
Synthetic construct chimeric spike vaccine construct sequence	4228	0.0	MZ393689
Synthetic construct HCV1147 Pfizer-BioNTech (BTN162b2) SARS-CoV-2 vaccine sequence	3472	0.0	OK120842
Synthetic construct chimeric spike vaccine construct sequence	3201	0.0	MZ393687
Synthetic construct chimeric spike vaccine construct sequence	2918	0.0	MZ393688
Synthetic construct HCV1101 Moderna (mRNA-1273) SARS-CoV-2 vaccine sequence	1694	0.0	OK120840
Synthetic construct SARS CoV 2RBD his gene, complete cds	1236	0.0	MT380724
Synthetic construct p1.1-Tr2-RBDv1, complete sequence	1236	0.0	MW187858
Synthetic construct pTM-RBDv2, complete sequence	1208	0.0	MW187856
Synthetic construct SARS CoV-2 spike protein receptor binding domain gene, complete cds	929	0.0	MT649401
Synthetic construct SpyTag/RBD fusion protein gene, complete cds	652	0.0	MT945427
Synthetic construct SARS CoV-1 spike protein receptor binding domain gene, complete cds	472	2e-127	MT649402
Measles morbillivirus [viruses]			
Mutant Measles morbillivirus strain MeVvac2-SARS2-S(H), complete genome	6037	0.0	MW090971
Recombinant vector AAVCOVID19-1 [other sequences]			
Recombinant vector AAVCOVID19-1, complete sequence	4215	0.0	MW408785
Cloning vector pCDNA3.1.2S [other sequences]			
Cloning vector pCDNA3.1.2S, complete sequence	4185	0.0	MT613044
Expression vector SARSCoV2SGFP [other sequences]			
Expression vector SARSCoV2SGFP, complete sequence	4120	0.0	MW560963
Expression vector SARSCoV2S&SmBit [other sequences]			
Expression vector SARSCoV2S&SmBit, complete sequence	4120	0.0	MW560962
Expression vector SARSCoV2SP681H [other sequences]			
Expression vector SARSCoV2SP681H, complete sequence	4120	0.0	MW560961
Expression vector SARSCoV2S [other sequences]			
Expression vector SARSCoV2S, complete sequence	4120	0.0	MW560957
Expression vector SARSCoV2SD614G [other sequences]			
Expression vector SARSCoV2SD614G, complete sequence	4115	0.0	MW560960
Expression vector SARSCoV2SN501Y [other sequences]			
Expression vector SARSCoV2SN501Y, complete sequence	4115	0.0	MW560959
Expression vector SARSCoV2SY453F [other sequences]			
Expression vector SARSCoV2SY453F, complete sequence	4115	0.0	MW560958
Expression vector SARS-CoV-2-S-E484K [other sequences]			
Expression vector SARS-CoV-2-S-E484K, complete sequence	4115	0.0	MW598454
Expression vector SARS-CoV-2-S-N439K [other sequences]			
Expression vector SARS-CoV-2-S-N439K, complete sequence	4115	0.0	MW598453
Recombinant vector AAV-COVID19-06 [other sequences]			
Recombinant vector AAV-COVID19-06, complete sequence	2217	0.0	OK272511
Recombinant vector AAV-COVID19-05 [other sequences]			
Recombinant vector AAV-COVID19-05, complete sequence	2217	0.0	OK272510
Recombinant vector AAVCOVID19-3 [other sequences]			
Recombinant vector AAVCOVID19-3, complete sequence	2176	0.0	MW408786
Homo sapiens (human) [primates]			
Homo sapiens isolate CO41 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397878
Homo sapiens isolate CO39 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397877
Homo sapiens isolate CO35 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397876
Homo sapiens isolate CO22 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397875
Homo sapiens isolate CO14 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397874
Homo sapiens isolate CO1 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397873
Homo sapiens isolate CHI92 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397872
Homo sapiens isolate CHI91 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397871
Homo sapiens isolate CHI35 haplogroup D1f mitochondrion, complete genome	257	6e-63	MZ397870
Homo sapiens isolate CHI29 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397869
Homo sapiens isolate CHI25 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397868
Homo sapiens isolate CHI24 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397867

Description	Score	E value	Accession
Homo sapiens isolate CHI23 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397866
Homo sapiens isolate CHI20 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397865
Homo sapiens isolate CHI14 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397864
Homo sapiens isolate CHI13 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397863
Homo sapiens isolate CHI12 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397862
Homo sapiens isolate CHI11 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397861
Homo sapiens isolate CHI9 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397860
Homo sapiens isolate CHI4 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397859
Homo sapiens isolate CHI3 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397858
Homo sapiens isolate CHI2 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397857
Homo sapiens isolate CHI1 haplogroup D1 mitochondrion, complete genome	257	6e-63	MZ397856
Homo sapiens isolate CO44 haplogroup C1b mitochondrion, complete genome	257	6e-63	MZ397855
Homo sapiens isolate CO34 haplogroup C1b mitochondrion, complete genome	257	6e-63	MZ397854
Homo sapiens isolate CO29 haplogroup C1b mitochondrion, complete genome	257	6e-63	MZ397853
Homo sapiens isolate CHI10 haplogroup C1b12 mitochondrion, complete genome	257	6e-63	MZ397852
Homo sapiens isolate CHI7 haplogroup C1b12 mitochondrion, complete genome	257	6e-63	MZ397851
Homo sapiens isolate CO40 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397827
Homo sapiens isolate CO38 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397826
Homo sapiens isolate CO37 mitochondrion, complete genome	257	6e-63	MZ397825
Homo sapiens isolate CO36 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397824
Homo sapiens isolate CO33 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397823
Homo sapiens isolate CO32 haplogroup A2w mitochondrion, complete genome	257	6e-63	MZ397822
Homo sapiens isolate CO31 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397821
Homo sapiens isolate CO30 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397820
Homo sapiens isolate CO13 haplogroup A2w mitochondrion, complete genome	257	6e-63	MZ397819
Homo sapiens isolate CO7 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397818
Homo sapiens isolate CHI96 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397816
Homo sapiens isolate CHI93 haplogroup A2 mitochondrion, complete genome	257	6e-63	MZ397815
Homo sapiens isolate CHI34 mitochondrion, complete genome	257	6e-63	MZ397814
Homo sapiens isolate CHI18 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397813
Homo sapiens isolate CHI15 haplogroup A2ac mitochondrion, complete genome	257	6e-63	MZ397812
Homo sapiens isolate CHI8 haplogroup A2k mitochondrion, complete genome	257	6e-63	MZ397811
Homo sapiens isolate CHI6 haplogroup A2k mitochondrion, complete genome	257	6e-63	MZ397810
Homo sapiens isolate CHI5 haplogroup A2k mitochondrion, complete genome	257	6e-63	MZ397809
Homo sapiens isolate 1113002343 S91 mitochondrion, complete genome	257	6e-63	MZ921390
Homo sapiens isolate 1113001817 S2 mitochondrion, complete genome	257	6e-63	MZ921389
Homo sapiens isolate 1113001079 S53 mitochondrion, complete genome	257	6e-63	MZ921388
Homo sapiens isolate ALP266 mitochondrion, complete genome	257	6e-63	MZ921386
Homo sapiens isolate ALP129 mitochondrion, complete genome	257	6e-63	MZ921385
Homo sapiens isolate ALP029 mitochondrion, complete genome	257	6e-63	MZ921384
Homo sapiens isolate LBZ00057 mitochondrion, complete genome	257	6e-63	MZ921383
Homo sapiens isolate LBZ00056 mitochondrion, complete genome	257	6e-63	MZ921382
Homo sapiens isolate LBZ00055 mitochondrion, complete genome	257	6e-63	MZ921381
Homo sapiens isolate LBN00097 mitochondrion, complete genome	257	6e-63	MZ921380
Homo sapiens isolate LBG00337 mitochondrion, complete genome	257	6e-63	MZ921379
Homo sapiens isolate LBG00336 mitochondrion, complete genome	257	6e-63	MZ921378
Homo sapiens isolate LBG00335 mitochondrion, complete genome	257	6e-63	MZ921377
Homo sapiens isolate LBG00334 mitochondrion, complete genome	257	6e-63	MZ921376
Homo sapiens isolate LBG00333 mitochondrion, complete genome	257	6e-63	MZ921375
Homo sapiens isolate PT-351-314 mitochondrion, complete genome	257	6e-63	MZ921374
Homo sapiens isolate PT-351-283 mitochondrion, complete genome	257	6e-63	MZ921373
Homo sapiens isolate PT-351-218 mitochondrion, complete genome	257	6e-63	MZ921372
Homo sapiens isolate PT-351-160 mitochondrion, complete genome	257	6e-63	MZ921371
Homo sapiens isolate PT-351-132 mitochondrion, complete genome	257	6e-63	MZ921370
Homo sapiens isolate PT-351-124 mitochondrion, complete genome	257	6e-63	MZ921369
Homo sapiens isolate PT-351-088 mitochondrion, complete genome	257	6e-63	MZ921368
Homo sapiens isolate PT-351-083 mitochondrion, complete genome	257	6e-63	MZ921367

- **Taxonomy**

Taxonomy	Number of hits	Number of Organisms	Description
root	100	17	
. artificial sequences	30	15	
.. synthetic construct	16	1	synthetic construct hits
... vectors	14	14	
... Recombinant vector AAVCOVID19-1	1	1	Recombinant vector AAVCOVID19-1 hits
... Cloning vector pCDNA3.1.2S	1	1	Cloning vector pCDNA3.1.2S hits
... Expression vector SARSCoV2SGFP	1	1	Expression vector SARSCoV2SGFP hits
... Expression vector SARSCoV2S&SmBit	1	1	Expression vector SARSCoV2S&SmBit hits
... Expression vector SARSCoV2SP681H	1	1	Expression vector SARSCoV2SP681H hits
... Expression vector SARSCoV2S	1	1	Expression vector SARSCoV2S hits
... Expression vector SARSCoV2SD614G	1	1	Expression vector SARSCoV2SD614G hits
... Expression vector SARSCoV2SN501Y	1	1	Expression vector SARSCoV2SN501Y hits
... Expression vector SARSCoV2SY453F	1	1	Expression vector SARSCoV2SY453F hits
... Expression vector SARS-CoV-2-S-E484K	1	1	Expression vector SARS-CoV-2-S-E484K hits
... Expression vector SARS-CoV-2-S-N439K	1	1	Expression vector SARS-CoV-2-S-N439K hits
... Recombinant vector AAV-COVID19-06	1	1	Recombinant vector AAV-COVID19-06 hits
... Recombinant vector AAV-COVID19-05	1	1	Recombinant vector AAV-COVID19-05 hits
... Recombinant vector AAVCOVID19-3	1	1	Recombinant vector AAVCOVID19-3 hits
. Measles morbillivirus	1	1	Measles morbillivirus hits
. Homo sapiens	69	1	Homo sapiens hits

Culme