

Moderna has five U.S. Patents containing the proprietary genetic sequence CTACGTGCCCGCCGAGGAG. These patents are **US9149506B2, US9216205B2, US9255129B2, US9301993B2 and US9587003B2**. The first four were filed for patent on 16-Dec-2013 and the last one on 4-Feb-2016. The reverse complement of this sequence is CTCCTCGGCGGGCACGTAG which can be found in the spike coding region of COVID-19 between bases 23501-23519(\*). This sequence codes for a Furin cleavage site. This match took some time to identify because it is the reverse complement that was patented. This is because their patent is listed as a DNA sequence and COVID-19 is the reverse complement mRNA of that DNA sequence. Also note that the patent sequence clearly indicates this sequence is an "Artificial Sequence" indicating it was generated in a laboratory.

The statistical chance that this sequence might occur randomly in SARS-CoV-2 is one in  $4^{19} / 30,000 = 9.1$  million where 4 is the number of nucleic acids (A,T,C,G), 19 is the length of the matching sequence above and 30,000 is the number of bases in the COVID-19 genome.

(\*) one sample has this at 23483-23501 due to a mutation in that sample.

Here is one example of that sequence in SEQ ID 11652 of US Patent 9587003 B2. The NIH Blast search results are attached.

**US Patent # US 9587003 B2 filed by Moderna and granted on Mar. 7, 2017.**

**SOURCE: <https://seqdata.uspto.gov/?pageRequest=viewSequence&DocID=9587003B2&seqID=11652>**

**Notice the 19 pair DNA sequence ctacgtgc cgcggagga g that is bolded and underlined below. Search for this DNA sequence using the NIH BLAST tool link below:**

**[https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE\\_TYPE=BlastSearch&LINK\\_LOC=blasthome](https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome)**

**The results are all SARS-CoV-2 entries! More specifically, these matches are to the "Furin Cleavage site" in the spike protein! Moderna has a total of 5 patents containing this DNA sequence dating back to patent applications made on Dec 16, 2013.**

SEQ ID NO 11652

LENGTH: 3387

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic coding sequence

SEQUENCE: 11652

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gagaccaga	ccagcctgct	gcactag				

## Alignments

Alignment view   CDS feature

Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/FRA/IHUCOVID-003247/2021, complete genome  
Sequence ID: **OP646598.1** Length: 29684 Number of Matches: 1  
Range 1: 23483 to 23501

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	5.9()	19/19(100%)	0/19(0%)	Plus/Minus	
Query 1	CTACGTGCCCCCGAGGAG	19			
Sbjct 23501	CTACGTGCCCCCGAGGAG	23483			

Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/FRA/IHUCOVID-002732/2020, complete genome  
Sequence ID: **OP646594.1** Length: 29698 Number of Matches: 1

Range 1: 23501 to 23519

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	5.9()	19/19(100%)	0/19(0%)	Plus/Minus	
Query 1	CTACGTGCCCCCGAGGAG	19			
Sbjct 23519	CTACGTGCCCCCGAGGAG	23501			

Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/FRA/IHUCOVID-002729/2020 ORF1ab polyprotein (ORF1ab), ORF1a polyprotein (ORF1ab), surface glycoprotein (S), ORF3a protein (ORF3a), envelope protein (E), membrane glycoprotein (M), ORF6 protein (ORF6), ORF7a protein (ORF7a), ORF7b (ORF7b), ORF8 protein (ORF8), nucleocapsid phosphoprotein (N), and ORF10 protein (ORF10) genes, complete cds  
Sequence ID: **OP646593.1** Length: 29648 Number of Matches: 1  
Range 1: 23501 to 23519

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	5.9()	19/19(100%)	0/19(0%)	Plus/Minus	
Query 1	CTACGTGCCCCCGAGGAG	19			
Sbjct 23519	CTACGTGCCCCCGAGGAG	23501			

Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/FRA/IHUCOVID-002725/2020, complete genome  
Sequence ID: **OP646592.1** Length: 29702 Number of Matches: 1  
Range 1: 23501 to 23519

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	5.9()	19/19(100%)	0/19(0%)	Plus/Minus	
Query 1	CTACGTGCCCCCGAGGAG	19			
Sbjct 23519	CTACGTGCCCCCGAGGAG	23501			

Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/human/FRA/IHUCOVID-002589/2020, complete genome  
Sequence ID: **OP646591.1** Length: 29702 Number of Matches: 1  
Range 1: 23501 to 23519

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	5.9()	19/19(100%)	0/19(0%)	Plus/Minus	
Query 1	CTACGTGCCCCCGAGGAG	19			
Sbjct 23519	CTACGTGCCCCCGAGGAG	23501			