The Pfizer Vaccine CRISPR Experiment

Introduction

The CRISPR (**C**lustered **R**egularly **I**nterspaced **S**hort **P**alindromic **R**epeat) Technology is a genome-editing technique that has been used by Scientists to alterate the genome in a population. The synthetic alteration of a Wildtype population is called Gene Drive. A gene drive individual has an altered gene inserted into one of his chromosomes. After sexual reproduction with a Wildtype, each parent contributes one copy of each chromosome to their offspring. Thus, the offspring carries only in 50% the altered gene from the parent. The altered gene will persist in low frequency in the following generations or can even go distinct after several generations. It would take dozens of generations to recognize the characteristics of the altered gene within a substantial fraction of the population(1).

However, the new genome editing technique CRISPR CAS9 increases the odds that almost any altered gene will be inherited 100% to offspring, potentially allowing the altered gene to spread through even wild populations after only 12-15 generations for every thousand reproducing gene drive individuals(2).

The CRISPR CAS9 technology is a well-known genome editing mechanism that has been used by bacteria to defend itself from viral infections. CRISPR is a genetic sequence with short palindrome repeats interspaced with viral sequences called spacer RNA. The spacer RNA contains unique sequences of viral RNA collected from past infections. During a viral invasion, the bacterium transcribes a CRISPR RNA that contains the embedded memory of the past viral infections. If the invaded viral RNA sequence matches the transcribed CRISPR RNA with records from viral sequences, the bacterium produces an enzyme called CAS9 that cuts the viral RNA and destroys it.

This gene-editing mechanism of the bacteria has been used by researchers to insert and add altered gene sequences into the human DNA. Thus, an mRNA can be engineered that contains the genetic information for the altered gene, the information for the CAS9 enzyme and a guided RNA (gRNA) that tells the CAS9 enzyme, where to cut and paste the altered gene sequence into the human genome. After the mRNA has been injected into human cells, the information on the mRNA will be translated into a CRISPR CAS9 enzyme complex.

The CRISPR CAS 9 enzyme complex screens the human chromosomes for a specific DNA sequence that matches the sequence on the gRNA. A match activates the CAS 9 enzyme and induces a Double-Strand Break (DBS) by cutting the human DNA at a specific chromosome site. The gRNA guides the CAS9 to cut at this specific location. A short signal sequence of 2-6 nucleotides at the 3'end of the gRNA called PAM (protospacer adjacent motif), tells the CAS9 enzyme to cut the altered host RNA off the mRNA. The DNA cut stimulates the DNA repair system and inserts the free-floating altered gene sequence into the human genome(3).

In other words, the human cells copy and paste the altered gene into the Wild-type gene, when it repairs the DNA damage. Now, the gene-drive individual has two identical gene copies on each chromosome, which will be both transmitted to offspring. And the process repeats in subsequent generations causing the alteration and spread through the population(1). Because viruses are gene delivery systems, a virus is the perfect carrier for the CRISPR CAS9 technology.

Pfizer describes on his website, the Cominarty vaccine under section indication and usage as follows; COMIRNATY is a vaccine indicated for active immunization to prevent coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in individuals 16 years of age and older(4).

The increasing hospitalisation for Cominarty vaccines and reports of Covid infections despite vaccination required a detailed analyzes of the Cominarty mRNA code. The aim of this study was to analyze the mRNA code for CRISPR-CAS9 gene-editing technology, which would explain the failure in the SARS CoV-2 virus immunization and the increase in fatal side effects after vaccination.

Method

1. First, the full sequenced and published mRNA code of the Pfizer BNT-162b2, also known under the product name Cominarty was base by base compared with the SARS CoV-2 Wuhan Hu-1 spike protein RNA (Genbank Association MN908947.3) (6).

2. An online Palindrome sequence finder from the DNA sequencing company, Novo Pro Lab from China, was used to find Short Palindrome Repeats and DNA spacers(6).

3. An online DNA/RNA translation tool on the Website of the Swiss Institute of Bioinformatics, called Expasy, was used to detect Open Reading Frames(7). The results were confirmed and verified with the online NCBI ORF finder(8).

4. Two further online tools were used to search for gRNAs with cleavage sites for CAS enzymes. The gRNA search was mainly focused on the plus strand to keep the study as understandable as possible for every reader. The Giraldez Lab from Yale University offers an online CRISPR gRNA search tool. The search was customized for Human Genoms, without the occurrence of nucleotide mismatches and for cleavage sites for both CAS9 and CAS12a enzymes(9). The second online tool was the CRISPR Finder from the Sanger Institute for Genome Editing(10). The CRISPR Finder provides correspondent CRISPR ID for the gRNAs in the online Genome Database. Both CRISPR research tools gave the same results and confirmed the findings.

5. And last, the CRISPR ID of each gRNA was searched in the online BLAST Database for corresponding gene sequences in the human genome(11).

Results

1. Cominarty analogy with SARS CoV-2 Wuhan Hu-1 Spike protein

(Genbank Association MN908947.3)

The Cominarty mRNA matches in 24% with the SARS CoV-2 Wuhan Hu-1 Spike Protein. But 76% of the Cominarty genetic code is not related to the SARS CoV-2 spike protein. The inserted spike protein sequences are located mainly in the 3' end of the mRNA. Figure 1 shows highlighted in different colours gene sequences that match the SARS CoV-2 spike protein. As we can see from figure 1, fragmented spike protein sequences are added to new DNA sequences (not highlighted).

2. Short Palindrome Repeats

The palindrome sequencer found 12 short palindrome repeats in the mRNA. These are CAGCTG, CTGCAG, GCCGGC, CACGTG, TGTACA, AGATCT, GCATGC, GATATC, TGATCA, TGGCCA, GGCGCC, GCTAGC. The palindrome repeat CAGCTG appeared seven times and its reverse version CTGCAG occurred six times in the mRNA. The Short Palindrome repeats are highlighted in figure 2 in bright blue.

Between the short palindrome repeats are interspaced fragmented Spike protein sequences. The same in colour highlighted spike protein sequences from figure 1 are highlighted in figure 2 in gray. We can see in figure 2 that the mRNA exists of fragmented spike protein pieces. Not the full-length spike protein appears in the Cominarty mRNA as mentioned in the WHO Program paper from September 2020 but fragments of spike protein sequences that have been added to new gene sequences (12). Gene sequences from the spike protein were even used to create some of the Short Palindrome Repeats, which are presented in figure 3 as highlighted gray nucleotides within bright blue fields. Figure 3 shows an example of a DNA spacer. Fragmented virus spike protein sequences occur between short palindrome repeats.

3. Open Reading Frames in the mRNA

Both the WHO Program Paper for the Cominarty vaccine and the published Pfizer mRNA sequence show one large Open Reading Frame of over 3800 bp (12,5). This one open reading frame cannot possibly be translated into a full-length spike protein due to two features in the mRNA. First, the spike protein sequences express just fragmented amino acids and not complete proteins. Second, the mRNA has stop and start codons in the middle of the open reading frame, which triggers nonsense-mediated decay and degradation of the mRNA (13). Noticeable is that the Stop codon UGA was changed into UGAU.

But with the help of both, the expasy DNA/RNA translation tool and NCBI's ORF finder, 13 hidden open reading frames were found within the long open reading frame, which is translated into different fully functional proteins. Figure 2 shows highlighted in dark and bright pink several open reading frames.

Interestingly, the first protein nt 275-410 does not contain a single fragmented sequence from the spike protein (figure 4). The BLAST Protein search for this protein results in the human Coronavirus HKU1isolate N5 (figure 5). Another hidden open reading frame expresses into a hypothetical protein. A hypothetical protein is a computer-predicted protein that does not exist in nature. This hypothetical protein expresses from nt 2795-2822 including the start and stop codon (figure 6). The modified stop codon UGAU for the hypothetical protein matches in position with the spike protein sequence. Figure 7 shows the BLAST result.

The Cominarty mRNA expresses also two short proteins, both of which play a role in the human cell signalling pathway. The sequence CCCAGGCAC expresses the PRH protein, which has a role in cancer suppression. And the CCAGCGTCG expresses the PAS protein, which plays a role in cell signalling.

And we also find fully synthetic spike proteins that resemble either 96% or in another case 98% a measles mutant virus protein (figure 8 and 9). Right at the 3'end of the mRNA at nt 2254-3367 is a synthetic protein that shows in a FASTA search only analogy with the Human Homeobox Hox A-4. Interestingly, this synthetic protein is the only protein that contains mainly spike protein sequences (figure 3,10).

4. **CRISPR gRNA findings**

Three gRNAs including the PAM sequence were found for the plus strand by Yale's University CRISPR research tool and confirmed with the CRISPR sequence finder by the Sanger Institute. Each gRNA sequence ends with the PAM sequence GGG.

4.1. The first gRNA has the CRISPR ID1161208236. The 21 bp long sequence is AGCTGCCCCTTTCCCGTCCT GGG (figure 11).
4.2. The second gRNA has the CRISPR ID 992837047. The 21 bp long sequence is TTAGCCTAGCCACACCCCCAC GGG (figure 12).
4.3. The third gRNA has the CRISPR ID 1202628979. The 23 bp long sequence is AACTAAGCTATACTAACCCCA GGG (figure 13).

5. Corresponding gRNAs on human reference genome

All three gRNAs were searched in the BLAST Database for the human genome. The results show that all gRNA sequences correspond to the Human Reference Genome GRCh38.

The gRNA with CRISPR ID 1161208236 originates from Chromosome 5 (figure 14) of GRCh38. The gRNA with CRISPR ID 992837047 also originates from Chromosome 5 (figure 15). And gRNA with CRISPR ID 1202628979 originates from Chromosome 19 of the GRCH38 Human Reference Genome (figure 16).

6. In addition, this study found a protein sequence at nt 3879-4050 that translated into a synthetic novel gp130 protein. The novel gp130 protein was already engineered in 1998 by Y. Liu. The publication from 1998 has been completely removed from the web. The function of this protein, therefore, remains unclear.

Conclusion

The analysis clearly shows that the Cominarty vaccine cannot induce immunization because it translates not into the full Covid spike protein pathogen. Although all genome database searches result in fully synthetic spike protein production for the Cominarty mRNA, the complete spike protein, however, cannot possibly be translated due to the fragmented RNA sequences and induced translation discontinuation, which would lead to mRNA degradation. Thus, the inserted spike protein sequences mask the real intention behind the Cominarty vaccine. The manipulation of the human genome at Chromosome 5 and Chromosome 19 as part of a human gene drive experiment.

This human gene drive experiment consists of three parts. The first part hosts CRISPR RNA with typical features such as Short Palindrome Repeats interspaced with viral RNA spacer.

The second part has hidden open reading frames that are translated into 13 several synthetical proteins such as hypothetical protein, a measles virus mutant protein or even human coronavirus protein. The different fully synthetic proteins have nothing to do with the SARS Cov-2 virus pathogen and are designed to cause both, the collapse and breakdown of the immune system.

A vaccine designed to support the immune system would never contain a hypothetical protein, whose post-translational function in human cells remains unknown. Why would a vaccine manufacturer risk the overload of the immune system with such a protein? Also questionable is why the mRNA translates into a synthetic protein that is analogue to the human Coronavirus? The human Coronavirus is a completely different type of virus than the SARS CoV-2 (14). And finally, why should the vaccine manufacturer go through so much trouble hiding 13 protein sequences between Spacer DNAs instead of creating a simple mRNA that will be translated into 13 full functional spike proteins?

The third part of Pfizer's CRISPR experiment contains three gRNAs including the PAM sequence that cleavages for the CAS 9 and CAS 12a enzyme. The analyzed gRNAs relate only to the plus strand. Additional gRNAs emerged in the analysis for the reverse strand but hasn't been discussed in this study. A pharmaceutical company cannot market a new mRNA technology under the disguise of vaccines that actually contains a technology to manipulate the human genome, where the public has not been informed about.

The only individual, who could create such gRNAs in a stable mRNA environment is Feng Zhang from the MIT Zhang lab. And the research reveals that Pfizer announced back in 2016, a collaboration with MIT's Zhang lab for cloud-based storage and analysis of human gene regulation datasets(15). And in return, Pfizer, along with former Pfizer executive Devyn Smith, raised $215 million in funds for Arbor Technology, Feng Zhang's newly founded CRISPR company(16).

It comes as no surprise that MIT is the number one institution involved in the human genome project. The complete mapping of the human genome led to a database of stored reference genomes. The digital genome sequences of 13 volunteers were stored under the human reference genome GRCh38(17). Since the beginning of the Human Genome Project, the GRCh38 genome has been modified in the database (18). The aim is to create the desired human race using digital calculations and computer predictions. Such computer-predicted perfect gene sequences have now emerged in the Cominarty mRNA vaccine.

The individual, who was injected with a reference human genome from 13 different volunteers and the CRISPR CAS9 gene-editing tool was not informed before vaccination and did not give consent for his genome to be manipulated. Thus, this study also serves for criminal charges and legal disputes against the Pfizer company for conducting genome experiments on humans.

Reference

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Figures

Figure 1
Cominarty mRNA. Highlighted in colour are SARS CoV-2 spike protein sequences.

Figure 2
Highlighted in gray are fragmented spike protein interspaced with short palindrome repeats, which are highlighted in bright blue. Between the short palindrome repeats are open reading frames, which express full functional proteins, here high-lighted in dark and brigh pink. The open reading frames have in some cases

modified stop codons TGAT (UGAU), which are highlighted in bright green. Also visible in figure 2 are start codons in dark blue and stop codons in dark green that occure in the middle of the open reading frame, which cause nonsense decay and mRNA degradation. Gray highlighted nucleotides within open reading frames in pink or within short palindrome repeats in bright blue matches in position with the spike protein sequence.

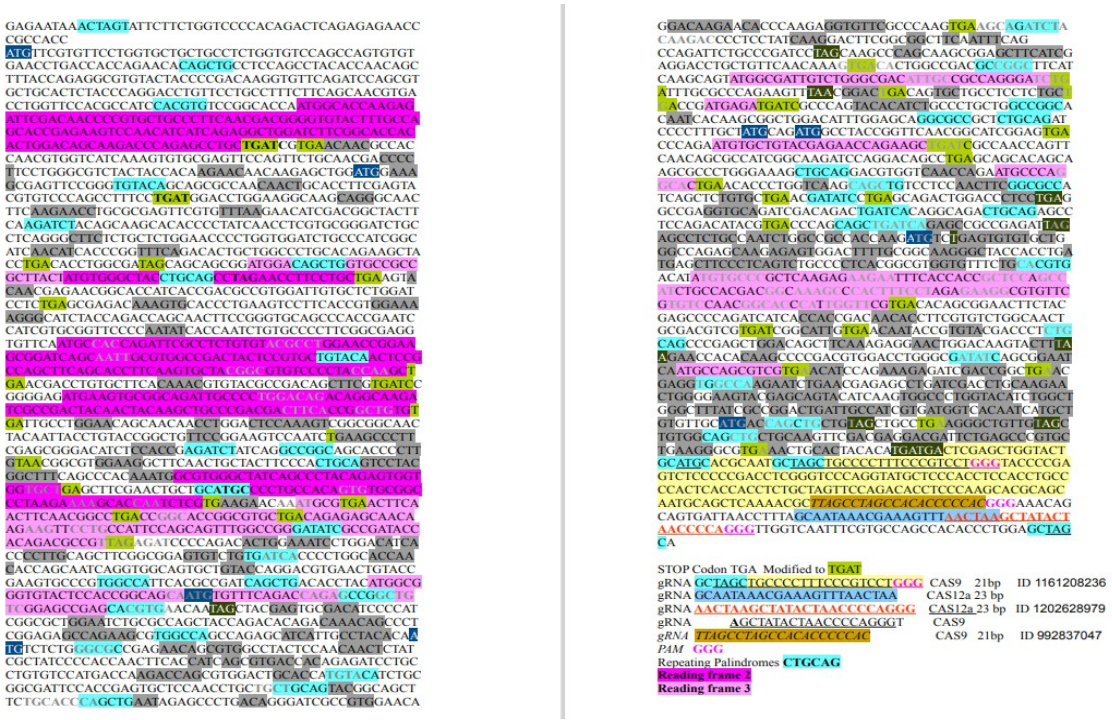


Figure 3.
Between two palindrome repeats in bright blue appear interspaced spike protein fragments as an example for a DNA spacer. Gray highlighted nucleotides within the palindromes in bright blue matches in position the spike protein sequence. The DNA spacer is followed by an open reading frame for a protein that has 58% analogy with the HoxA4 protein, here highlighted in pink. This fully synthetic protein contains mainly of spike protein amino acids.

Figure 4
Human Coronavirus protein without any analogy to the spike protein. The stop codon UGAU is modified.

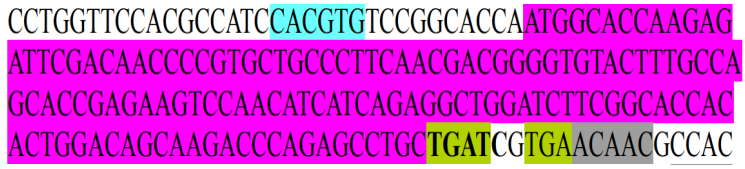


Figure 5
BLAST result for Human Coronavirus HKU1 isolate N5

RecName: Full=Replicase polyprotein 1a; Short=pp1a; AltName: Full=ORF1a polyprotein; Contains: RecName: Full=Non-structural protein 1; Short=nsp1; AltName: Full=p28; Contains: RecName: Full=Non-structural protein 2; Short=nsp2; AltName: Full=p65; Contains: RecName: Full=Non-structural protein 3; Short=nsp3; AltName: Full=PL1-PRO/PL2-PRO; AltName: Full=PL1/PL2; AltName: Full=Papain-like proteinases 1/2; AltName: Full=p210; Contains: RecName: Full=Non-structural protein 4; Short=nsp4; AltName: Full=Peptide HD2; AltName: Full=p44; Contains: RecName: Full=3C-like proteinase; Short=3CL-PRO; Short=3CLp; AltName: Full=M-PRO; AltName: Full=nsp5; AltName: Full=p27; Contains: RecName: Full=Non-structural protein 6; Short=nsp6; Contains: RecName: Full=Non-structural protein 7; Short=nsp7; AltName: Full=p10; Contains: RecName: Full=Non-structural protein 8; Short=nsp8; AltName: Full=p22; Contains: RecName: Full=Non-structural protein 9; Short=nsp9; AltName: Full=p12; Contains: RecName: Full=Non-structural protein 10; Short=nsp10; AltName: Full=Growth factor-like peptide; Short=GFL; AltName: Full=p15; Contains: RecName: Full=Non-structural protein 11; Short=nsp11 [Human coronavirus HKU1 (isolate N5)]

Sequence ID: **P0C6U5.1** Length: 4421 Number of Matches: 4

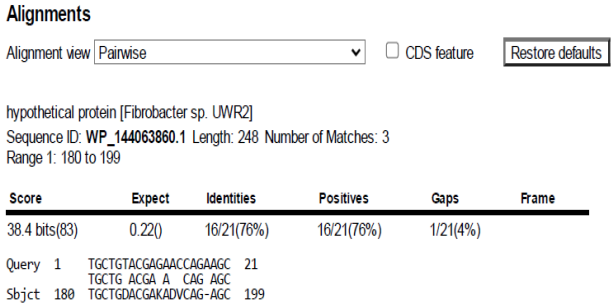
Range 1: 2781 to 2795

Score	Expect	Identities	Positives	Gaps	Frame
26.9 bits(56)	9.5()	11/15(73%)	11/15(73%)	1/15(6%)	

```
Query  12    TP-SLKGSTGLSNLL  25
             TP SLKG  LSNLL
Sbjct  2781  TPFSLKGGVVLSNLL  2795
```

Figure 6
Open Reading Frame that translates into a Hypothetical Protein. Stop codon has been modified and matches in nucleotide position with the spike protein.

Figure 7
BLAST result for the Hypothetical Protein



Alignments

Alignment view: Pairwise | CDS feature | Restore defaults

hypothetical protein [Fibrobacter sp. UWR2]
Sequence ID: **WP_144063860.1** Length: 248 Number of Matches: 3
Range 1: 180 to 199

Score	Expect	Identities	Positives	Gaps	Frame
38.4 bits(83)	0.22()	16/21(76%)	16/21(76%)	1/21(4%)	

```
Query  1    TGCTGTACGAGAACCAGAAGC  21
            TGCTG ACGA A  CAG AGC
Sbjct  180  TGCTGDACGAKADVCAG-AGC  199
```

Figure 8
BLAST result for fully synthetic protein with 96% analogy to a mutant measles virus strain.

Mutant Measles morbillivirus strain MeVvac2-SARS2-S(H), complete genome
Sequence ID: **MW090971.1** Length: 19800 Number of Matches: 1
Range 1: 10862 to 10975

Score	Expect	Identities	Gaps	Strand	Frame
183 bits(99)	2e-42()	109/114(96%)	0/114(0%)	Plus/Plus	

```
Query  1      CGTGAACTTCAACTTCAACGGCCTGACCGGCACCGGCGTGCTGACAGAGAGCAACAAGAA  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  10862  CGTGAACTTCAACTTCAACGGCCTGACCGGCACCGGCGTGCTGACAGAAAGCAACAAGAA  10921

Query  61     GTTCCTGCCATTCCAGCAGTTTGGCCGGGATATCGCCGATACCACAGACGCCGT  114
              ||||||||||||||||||||| ||| | |||||||||| ||||||||||||||
Sbjct  10922  GTTCCTGCCATTCCAGCAGTTCGGCAGAGATATCGCCGACACCACAGACGCCGT  10975
```

Figure 9
BLAST result for another fully synthetic spike potein with 98% analogy to a mutant measles virus strain.

Mutant Measles morbillivirus strain MeVvac2-SARS2-S(H), complete genome
Sequence ID: **MW090971.1** Length: 19800 Number of Matches: 1

s://blast.ncbi.nlm.nih.gov/Blast.cgi#alnShow_6

2/9/22, 9:52 AM NCBI Blast:Nucleotide Sequence

Range 1: 10465 to 10545

Score	Expect	Identities	Gaps	Strand	Frame
139 bits(75)	3e-29()	79/81(98%)	0/81(0%)	Plus/Plus	

```
Query  1      AAGTGCGGCAGATTGCCCCTGGACAGACAGGCAAGATCGCCGACTACAACTACAAGCTGC  60
              ||||||||||||  || ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10465  AAGTGCGGCAGATCGCTCCTGGACAGACAGGCAAGATCGCCGACTACAACTACAAGCTGC  10524

Query  61     CCGACGACTTCACCGGCTGTG  81
              |||||||||||||||||||||
Sbjct  10525  CCGACGACTTCACCGGCTGTG  10545
```

Figure 10
FASTA result for Hox A-4 protein

```
Statistics:  Expectation_n fit: rho(ln(x))= 3.9134+/-0.000885; mu= 10.9802+/- 0.050
 mean_var=42.5317+/- 8.173, 0's: 3 Z-trim(108.2): 8  B-trim: 134 in 1/60
 Lambda= 0.196661
 statistics sampled from 6390 (6391) to 6390 sequences
Algorithm: FASTA (3.8 Nov 2011) [optimized]
Parameters: BL50 matrix (15:-5), open/ext: -10/-2
 ktup: 2, E-join: 1 (0.873), E-opt: 0.2 (0.486), width:  16
 Scan time:  0.160
```

The best scores are:		opt	bits	E(13144)	%_id	%_sim	alen	
sp|Q00056|HXA4_HUMAN	Homeobox protein Hox-A4; Homeobox	(320)	78	28.0	0.57	0.412	0.588	34 align
sp|P08050|CXA1_RAT	Gap junction alpha-1 protein; Connex	(382)	73	26.6	1.8	0.423	0.692	26 align
sp|P23242|CXA1_MOUSE	Gap junction alpha-1 protein; Conn	(382)	73	26.6	1.8	0.423	0.692	26 align
sp|P18246|CXA1_BOVIN	Gap junction alpha-1 protein; Conn	(383)	73	26.6	1.8	0.423	0.692	26 align
sp|P06485|US02_HHV11	Protein US2	(291)	70	25.7	2.6	0.308	0.577	26 align
sp|P01425|NXS1_HEMHA	Short neurotoxin 1; Toxin II	(61)	62	22.9	3.7	0.412	0.824	17 align
sp|P01426|NXS1_NAJPA	Short neurotoxin 1; Neurotoxin alp	(61)	62	22.9	3.7	0.412	0.824	17 align
sp|P60775|NXSA_LATSE	Erabutoxin a; Short neurotoxin 1a;	(83)	62	23.0	4.7	0.412	0.824	17 align

Figure 11
CRISPR gRNA result for
ID1161208236

ID: 1161208236 View in Genome Browser (https://wge.stemcell.sanger.ac.uk/genoverse_browse?view_single=1&crispr_id=1161208236)

Species	Human (GRCh38)
Location	19:3053386-3053408 (https://www.ensembl.org/Homo_Sapiens/Location/View?r=19:3053386-3053408)
Sequence	AGCTGCCCCTTTCCCGTCCT GGG (reversed)
Strand	-
Crispr in exon?	Yes
Crispr in intron?	No

Figure 12
CRISPR gRNA result for ID
992837047

ID: 992837047 View in Genome Browser (https://wge.stemcell.sanger.ac.uk/genoverse_browse?crispr_id=992837047&view_single=1)

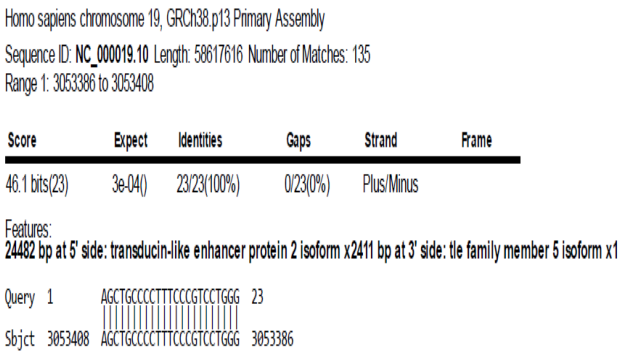
Species	Human (GRCh38)
Location	5:80651907-80651929 (https://www.ensembl.org/Homo_Sapiens/Location/View?r=5:80651907-80651929)
Sequence	TTAGCCTAGCCACACCCCCA CGG (reversed)
Strand	-
Crispr in exon?	No
Crispr in intron?	Yes

Figure 13
CRISPR gRNA result for ID
1202628979

ID: 1202628979 View in Genome Browser (https://wge.stemcell.sanger.ac.uk/genoverse_browse?view_single=1&crispr_id=1202628979)

Species	Human (GRCh38)
Location	M:851-873 (https://www.ensembl.org/Homo_Sapiens/Location/View?r=M:851-873)
Sequence	AACTAAGCTATACTAACCCC AGG
Strand	+
Crispr in exon?	No
Crispr in intron?	No

Figure 14
Corresponding BLAST result for CRISPR ID 1161208236 on Chromosome 19 of GRCH38



Homo sapiens chromosome 19, GRCh38.p13 Primary Assembly

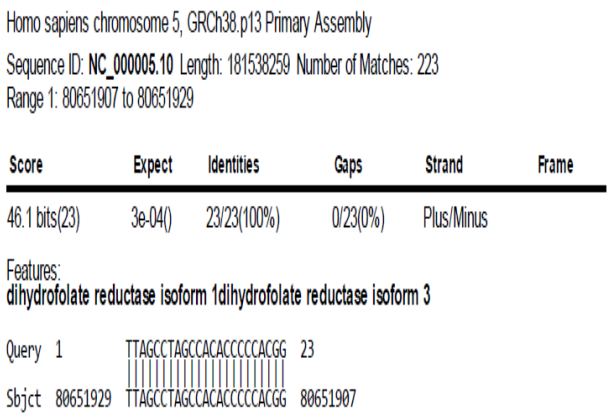
Sequence ID: **NC_000019.10** Length: 58617616 Number of Matches: 135
Range 1: 3053386 to 3053408

Score	Expect	Identities	Gaps	Strand	Frame
46.1 bits(23)	3e-04()	23/23(100%)	0/23(0%)	Plus/Minus	

Features:
24482 bp at 5' side: transducin-like enhancer protein 2 isoform x2411 bp at 3' side: tle family member 5 isoform x1

```
Query  1        AGCTGCCCCCTTTCCCGTCCTGGG  23
                ||||||||||||||||||||||||
Sbjct  3053408  AGCTGCCCCCTTTCCCGTCCTGGG  3053386
```

Figure 15
Corresponding BLAST result for CRISPR ID 992837047 on Chromosome 5 of GRCH38



Homo sapiens chromosome 5, GRCh38.p13 Primary Assembly

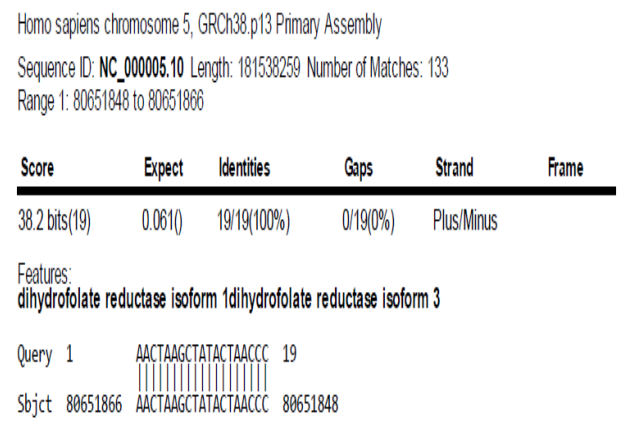
Sequence ID: **NC_000005.10** Length: 181538259 Number of Matches: 223
Range 1: 80651907 to 80651929

Score	Expect	Identities	Gaps	Strand	Frame
46.1 bits(23)	3e-04()	23/23(100%)	0/23(0%)	Plus/Minus	

Features:
dihydrofolate reductase isoform 1dihydrofolate reductase isoform 3

```
Query  1        TTAGCCTAGCCACACCCCCACGG  23
                |||||||||||||||||||||||
Sbjct  80651929 TTAGCCTAGCCACACCCCCACGG  80651907
```

Figure 16
Corresponding BLAST result for CRISPR ID 1202628979 on Chromosome 5 of GRCH38



Homo sapiens chromosome 5, GRCh38.p13 Primary Assembly

Sequence ID: **NC_000005.10** Length: 181538259 Number of Matches: 133
Range 1: 80651848 to 80651866

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	0.061()	19/19(100%)	0/19(0%)	Plus/Minus	

Features:
dihydrofolate reductase isoform 1dihydrofolate reductase isoform 3

```
Query  1        AACTAAGCTATACTAACCC  19
                |||||||||||||||||||
Sbjct  80651866 AACTAAGCTATACTAACCC  80651848
```