3.2.S.1.2 STRUCTURE

The molecular sequence of CX-024414, including the 5' cap, the 5' untranslated region (UTR), the Open Reading Frame (ORF), the 3' UTR, and the 3' polyA tail, is provided in Figure 1. CX-024414 is the mRNA that encodes for the pre-fusion stabilized Spike protein of 2019-novel Coronavirus (SARS-CoV-2).

Figure 1: Molecular Sequence of CX-024414

GGUGAGCAGCCAGUGCGUGAACCUGACCACCCGGACCCAGCUGCCACCAGCCUACACCAACAGCUUCACCCGGGGCGUCUACUACUACCCCGACAAGGU GUUCCGGAGCAGCGUCCUGCACAGCACCCAGGACCUGUUCCUGCCCUUCUUCAGCAACGUGACCUGGUUCCACGCCAUCCACGUGAGCGGCACCAA CGGCACCAAGCGGUUCGACAACCCCGUGCUGCCCUUCAACGACGGCGUGUACUUCGCCAGCACCAGAAGAGCAACAUCAUCCGGGGCUGGAUCUU CGGCACCACCUGGACAGCAGAGCCCAGAGCCUGCUGAUCGUGAAUAACGCCACCAACGUGGUGAUCAAGGUGUGCGAGUUCCAGUUCUGCAACGA CGUGAGCCAGCCCUUCCUGAUGGACCUGGAGGGCAAGCAGGGCAACUUCAAGAACCUGCGGGGAGUUCGUGUUCAAGAACAUCGACGGCUACUUCAA GAUCUACAGCAAGCACCCCAAUCAACCUGGUGCGGGAUCUGCCCCAGGGCUUCUCAGCCCUGGAGCCCCUGGUGACCUGCCCAUCGGCAUCAA CAUCACCGGUUCCAGACCCUGCUGGCCCUGCACCGGAGCUACCUGACCCCAGGCGACAGCAGCAGCGGGUGGACAGCAGCGGCUGCUUACUA CGUGGGCUACCUGCAGCCCCGGACCUUCCUGCUGAAGUACAACGAGAACGGCACCAUCACCGACGCCGUGGACUGCGCCCUGGACCCUCUGAGCGA GACCAAGUGCACCCUGAAGAGCUUCACCGUGGAGAAGGGCAUCUACCAGACCAGCAACUUCCGGGUGCAGCCCACCGAGAGCAUCGUGCGGUUCCC CAACAUCACCAACCUGUGCCCCUUCGGCGAGGUGUUCAACGCCACCCGGUUCGCCAGCGUGUACGCCUGGAACCGGAAGCGGAUCAGCAACUGCGU GGCCGACUACAGCGUGCUGUACAACAGCGCCAGCUUCAGCACCUUCAAGUGCUACGGCGUGAGCCCACCAAGCUGAACGACCUGUGCUUCACCAA CGUGUACGCCGACAGCUUCGUGAUCCGUGGCGACGAGGUGCGGCAGAUCGCACCCGGCCAGACAGGCAAGAUCGCCGACUACAACUACAAGCUGCC CGACGACUUCACCGGCUGCGUGAUCGCCUGGAACAGCAACAACCUCGACAGCAGGUGGGCGGCAACUACAACUACCUGUACCGGCUGUUCCGGAA GAGCAACCUGAAGCCCUUCGAGCGGGACAUCAGCACCGAGAUCUACCAAGCCGGCUCCACCCCUUGCAACGGCGUGGAGGGCUUCAACUGCUACUU CCCUCUGCAGAGCUACGGCUUCCAGCCCACCAACGGCGUGGGCUACCAGCCCUACCGGGUGGUGCUGAGCUUCGAGCUGCACGCCCCAGC CACCGUGUGUGGCCCCAAGAAGAGCACCAACCUGGUGAAGAACAAGUGCGUGAACUUCAACUUCAACGGCCUUACCGGCACCGGCGUGCUGACCGA GAGCAACAAGAAAUUCCUGCCCUUUCAGCAGUUCGGCCGGGACAUCGCCGACACCACCGACGCUGUGCGGGAUCCCCAGACCCUGGAGAUCCUGGA CAUCACCCCUUGCAGCUUCGGCGGCGUGAGCGUGAUCACCCCAGGCACCAACACCAGCAACCAGGUGGCCGUGCUGUACCAGGACGUGAACUGCAC GAGGGCAAGGAGCGUGGCCAGCCAGAGCAUCAUCGCCUACACCAUGAGCCUGGGCGCCGAGAACAGCGUGGCCUACAGCAACAACAGCAUCGCCAU CCCCACCACUUCACCAUCAGCGUGACCACCGAGAUUCUGCCCGUGAGCAUGACCAAGACCAGCGUGGACUGCACCAUGUACAUCUGCGGCGACAG CACCGAGUGCAGCAACCUGCUGCUGCAGUACGGCAGCUUCUGCACCCAGCUGAACCGGGCCCUGACCGGCAUCGCCGUGGAGCAGGACAAGAACAC CCAGGAGGUGUUCGCCCAGGUGAAGCAGAUCUACAAGACCCCUCCCAUCAAGGACUUCGGCGGCUUCAACUUCAGCCAGAUCCUGCCCGACCCCAG CAAGCCCAGCAAGCGGAGCUUCAUCGAGGACCUGCUGUUCAACAAGGUGACCCUAGCCGACGCCGGCUUCAUCAAGCAGUACGGCGACUGCCUCGG CGACAUAGCCGCCCGGGACCUGAUCUGCGCCCAGAAGUUCAACGGCCUGACCGUGCUGCCCCCCUGCUGACCGACGAGAUGAUCGCCCAGUACAC CAGCGCCCUGUUAGCCGGAACCAUCACCAGCGGCUGGACUUUCGGCGCUGGAGCCGCUCUGCAGAUCCCCUUCGCCAUGCAGAUGGCCUACCGGUU CAACGGCAUCGGCGUGACCCAGAACGUGCUGUACGAGAACCAGAAGCUGAUCGCCAACCAGUUCAACAGCGCCAUCGGCAAGAUCCAGGACAGCCU GAGCAGCACCGCUAGCGCCCUGGGCAAGCUGCAGGACGUGGUGAACCAGAACGCCCAGGCCCUGAACACCCUGGUGAAGCAGCUGAGCAGCAACUU CGGCGCCAUCAGCAGCGUGCUGAACGACAUCCUGAGCCGGCUGGACCCUCCCGAGGCCGAGGUGCAGAUCGACCGGCUGAUCACUGGCCGGCUGCA CUACGUGCCGGCCAGGAGAAGAACUUCACCACCGCCCAGCCAUCUGCCACGACGGCAAGGCCCACUUUCCCCGGGAGGGCGUGUUCGUGAGCAA CGGCACCCACUGGUUCGUGACCCAGCGGAACUUCUACGAGCCCCAGAUCAUCACCACCGACAACACCUUCGUGAGCGGCAACUGCGACGUGGUGAU CGGCAUCGUGAACAACACCGUGUACGAUCCCCUGCAGCCCGAGCUGGACAGCUUCAAGGAGGAGCUGGACAAGUACUUCAAGAAUCACCAGCCC CAUCGUGAUGGUGACCAUCAUGCUGUGCAUGACCAGCUGCUGCAGCUGCCUGAAGGGCUGUUGCAGCUGCGGCAGCUGCUGCAAGUUCGACGA GGACGACAGCGAGCCCGUGCUGAAGGGCGUGAAGCUGCACUACACCUGAUAAUAGGCUGGAGCCUCGGUGGCCUAGCUUCUUGCCCCUUGGGCCUC

Where: A, C, G and U = AMP, CMP, GMP and N1-Me- Ψ MP, respectively; Me = methyl: p = inorganic phosphate.

mRNA Sequence Molecular Weight (free acid)	1,329,683 Daltons	
mRNA Sequence Molecule Length	4,101 nucleotides	
mRNA Sequence Elements	ORF:	3819 nucleotides
	5'UTR:	Cap + 57 nucleotides
	3'UTR:	119 nucleotides
	PolyA tail:	105 nucleotides

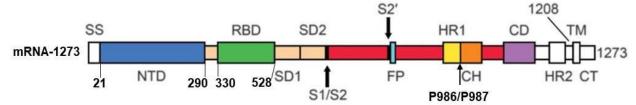
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The protein sequence encoded by CX-024414 was designed by the Applicant and is consistent with a Coronavirus spike protein. The Open Reading Frame (ORF design) is consistent with all current guidelines as provided by WHO on based on the genomic sequence of the SARS-CoV-2 that was made public by China on January 11, 2020. The UTRs are consistent with current recommendations within the Applicant's proprietary mRNA platform.

mRNA platform and S1S2 protein sequence.

The single mRNA that encodes the full-length SARS-CoV-2 spike (S) protein modified with 2 proline substitutions within the heptad repeat 1 domain (S 2P) to stabilize the S protein into the prefusion conformation. The S protein is stabilized in the so-called pre-fusion conformation by two amino acid mutations, K986P and V987P.

Figure 2: Protein Sequence of CX-024414



3.2.S.1.2.1 Open Reading Frame (ORF) and Incorporation of Pseudouridine

Table 1 presents in more detail each part of CX-024414. The codons used to encode the engineered prefusion S1/S2 protein were generated using Moderna's proprietary software, which makes the codon usage utilized unique (See Figure 3).

Table 1: Table of Features

Element	Description	Position	
Cap	5'-cap1 structure (m7G-5'-ppp-5'-Gm) (additional information in Figure 4)	1 - 2	
5' UTR	The 5'UTR sequence in mRNA-1273 is based on the 5' UTR from Warren et	3 - 58	
	al., 2010 that confers robust protein expression. It has been further optimized		
	with a GC-rich sequence near the start codon to increase the fidelity of		
	translation initiation at the designated start codon.		
ORF	Codon-optimized sequence encoding full-length SARS-CoV-2 spike (S)		
	glycoprotein containing mutations K986P and V987P (nucleosides 2956-2961)	59 - 3880	
	to stabilize pre-fusion conformation; stop codons: 3888-3896 (underlined)		
3' UTR	The 3 UTR is derived from the human HBA1 gene, which has been associated	3881 - 3996	
	with prolonged mRNA half-life (Waggoner 2003). It has been further		
	optimized by additional of two further stop codons to ensure complete		
	translation termination and removal of an AUG in the 3 UTR to eliminate the		
	risk of any aberrant translation.		
polyA tail	A 100-nucleotide poly(A)-tail followed by a 5-nucleotide XbaI scar.	3997 - 4101	

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Figure 3: Schematic Map - Detailed Graphic of the Composition of the Full mRNA Sequence



Nucleotides 2956-2961 in the ORF are corresponding to 2 Proline mutations in prefusion stabilized construct. All uridines in the mRNA are replaced by 1-methylpseudouridine.

N1-methyl-pseudouridine modified mRNA has been incorporated into mRNA-1273, as it has been in previous Moderna vaccines tested in clinical trials. Recent reports have demonstrated that use of N1-methyl-pseudouridine modified mRNA results in robust protein translation (Corbett et al., 2020a; Corbett et al., 2020b; Jackson et al., 2020; John et al., 2018). mRNA with this nucleoside-modification was found to circumvent TLR7/8 activation, thus decreasing innate immune activation (Espeseth et al., 2020; Kariko et al., 2005), while still eliciting strong immune responses both preclinically and clinically (Corbett et al., 2020a; Corbett et al., 2020b; Espeseth et al., 2020; Jackson et al., 2020; John et al., 2018)

Figure 4: Cap Structure of CX-024414

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