

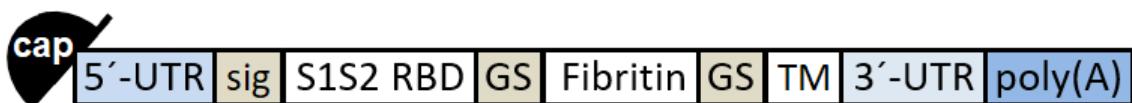


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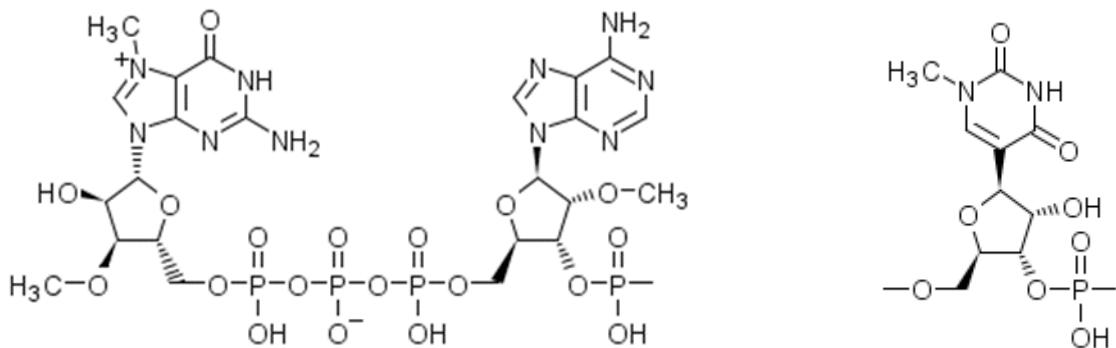
### Description

Messenger RNA encoding the receptor binding domain of the SARS-CoV-2 spike (S) glycoprotein connected to the T4 fibritin and the S glycoprotein transmembrane domain.

### Schematic



UTR = Untranslated region; sig = extended signal sequence of the S glycoprotein; S1S2 RBD = Receptor Binding Domain of the S glycoprotein; GS = glycine/serine-rich linker; Fibritin = trimerization domain of enterobacteria phage T4 fibritin; TM = transmembrane domain; poly(A) = polyadenylate signal tail.



#### 5'- capping structure

cap G<sup>1</sup>A<sup>2</sup> = m<sup>7</sup>G<sup>+</sup>m<sup>3'</sup>-5'-ppp-5'-Am<sup>2'</sup>-3'-p-  
[m<sup>7</sup> = 7-CH<sub>3</sub>; m<sup>3'</sup> = 3'-O-CH<sub>3</sub>; m<sup>2'</sup> = 2'-O-CH<sub>3</sub>;  
-ppp- = -PO<sub>2</sub>H-O-PO<sub>2</sub>H-O-PO<sub>2</sub>H)-; -p- = -PO<sub>2</sub>H-]

m<sup>1</sup>Ψ = 1-methyl-3'-pseudouridyl



### Table of features

<b>Element</b>	<b>Description</b>	<b>Position</b>
cap	A modified 5'-cap1 structure ( $m^7G^+m^3'-5'-ppp-5'-Am$ )	1-2
5'-UTR	5'-untranslated region derived from human alpha-globin RNA with an optimized Kozak sequence	3-54
sig	S glycoprotein signal peptide (extended leader sequence), which guides translocation of the nascent polypeptide chain into the endoplasmic reticulum.	55-111
S1S2 RBD	Codon-optimized sequence, encoding the Receptor Binding Domain (RBD) of the SARS-CoV-2 spike (S) glycoprotein.	112-717
GS	Sequences that code for short linker peptides consisting of the amino-acids glycine and serine.	718-744 and 826-843
Fibritin	Partial sequence of T4 fibritin (foldon), used as a trimerization domain.	745-825
TM	Transmembrane domain of the S glycoprotein.	844-993
3'-UTR	The 3'-untranslated region comprises two sequence elements derived from the amino-terminal enhancer of split (AES) mRNA and the mitochondrial encoded 12S ribosomal RNA to confer RNA stability and high total protein expression.	994-1288
poly(A)	A 110-nucleotide poly(A)-tail consisting of a stretch of 30 adenosine residues, followed by a 10-nucleotide linker sequence and another 70 adenosine residues.	1289-1398

### Sequence / Séquence / Secuencia

GAGAAΨAAAC ΨAGΨAΨΨCΨΨ CΨGGΨCCCCA CAGACΨCAGA GAGAACC CGC 50  
CACCAΨGΨΨΨ GΨGΨΨΨCΨΨG ΨGCΨGCΨGCC ΨCΨΨGΨGΨCΨ ΨCΨCAGΨGΨG 100  
ΨGAAΨΨΨGAC AGΨGAGAΨΨΨ CCAAΨAΨΨA CAAAΨCΨGΨG ΨCCAΨΨΨGGA 150  
GAAGΨGΨΨΨA AΨGCAACAAG AΨΨΨGCAΨCΨ GΨGΨAΨGCAΨ GGAAΨAGAAA 200  
AAGAAΨΨΨCΨ AΨΨΨGΨGΨGG CΨGAΨΨAΨΨC ΨGΨGCΨGΨAΨ AAΨAGΨGΨΨ 250  
CΨΨΨΨΨCCAC AΨΨΨAAAΨGΨ ΨAΨGGAGΨGΨ CΨCCAACAAA AΨΨAAAΨGΑΨ 300  
ΨΨAΨGΨΨΨΨA CAAAΨGΨGΨA ΨGCΨGAΨΨCΨ ΨΨΨGΨGΨAΨCA GAGGΨGΨAΨGA 350



**WHO**  
**International Nonproprietary Names Programme**

9/2020

АГΨГАГАСАГ	АΨΨГCCCCCG	ГАСАГАСАГГ	АААААΨΨГСΨ	ГАΨΨАСЛАΨΨ	400
АСАААСΨГСС	ΨГАΨГАΨΨΨΨ	АСАГГАΨГΨГ	ΨГАΨΨГСΨΨГ	ГАΑΨΨСΨΑΑΨ	450
АΑΨΨΨАГАΨΨ	СΨАААГΨГГГ	АГГАААΨΨАС	АΑΨΨАΨСΨГΨ	АСАГАСΨГΨΨ	500
ΨАГААААΨСА	АΑΨСΨГАААС	СΨΨΨГАААГ	АГАΨАΨΨΨСА	АСАГАААΨΨΨ	550
АΨСАГГСΨГГ	АΨСААСАССΨ	ΨГΨААΨГГАГ	ΨГГААГГАΨΨ	ΨΑΑΨΨГΨΨΑΨ	600
ΨΨΨССАΨΨАС	АГАГСΨАΨГГ	АΨΨΨСАГССА	АССААΨГГΨГ	ΨГГГАΨΑΨСА	650
ГССАΨАΨАГА	ГΨГГΨГГΨГС	ΨГΨСΨΨΨГА	АСΨГСΨГСАΨ	GCACCΨGCAA	700
САГΨГΨГΨГГ	АССΨАААГГС	ΨCCCCCCGСΨ	CCGGCΨCCGG	АΨСΨ <u>GGΨΨΑΨ</u>	750
АΨΨССΨГААГ	СΨССААГАГА	ΨГГГСААГСΨ	ΨАСГΨΨСГΨА	ААГАΨГГСГА	800
АΨГГГΨАΨΨΑ	СΨΨΨСΨАССΨ	ΨΨΨΨАГГААГ	CGGCAGCGGA	ΨСΨГААСАГΨ	850
АСАΨΨААААΨГ	GCCΨΨGGΨАС	АΨΨΨГГСΨΨГ	ГАΨΨΨАΨΨГС	AGGAΨΨААΨΨ	900
ГСААΨΨГΨГА	ΨГГΨГАСААΨ	ΨΑΨГΨΨАΨГΨ	ΨГΨАΨГАСАΨ	САΨГΨΨГΨΨС	950
ΨΨГΨΨΨАААА	ГГАΨГΨΨГΨΨ	СΨΨГΨГГААГ	СΨГΨΨГΨΨГА	ΨГАСΨCGAGC	1000
ΨГГΨАСΨГСА	ΨГСАСГСААΨ	GCΨАСГΨГСС	CCΨΨΨСССGΨ	ССΨГГГΨАСС	1050
ССГАГΨСΨСС	CCCCGАССΨCG	GGΨСССAGГΨ	АΨГСΨСССAC	СΨССАССΨGC	1100
СССАСΨСАСС	ACCΨСΨГСΨА	ГΨΨССАГАСА	CCΨСССAАGC	ACGCAGCAАΨ	1150
GCAGCΨСАА	ACGCΨΨАГСС	ΨАГССАСАСС	CCCACGGAA	ACAGCAGΨGA	1200
ΨΨAАССΨΨА	GСААΨАААСG	AAAGΨΨAАС	ΨААГСΨАΨАС	ΨAАСССАГГ	1250
ГΨΨGGΨСААΨ	ΨΨСGΨGCCAG	CCACАСССΨG	GAGCΨAGСАА	AAAAAAAAAAA	1300
AAAAAAAAAAAA	AAAAAAAAAGC	АΨАΨГАСΨАА	AAAAAAAAAAA	AAAAAAAAAAA	1350
AAAAAAAAAAAA	AAAAAAAAAAA	AAAAAAAAAAA	AAAAAAAAAAA	AAAAAAAAAAA	1398

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