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# 3.2.S.1.2. STRUCTURE, OMICRON (BA.4/BA.5)

The active principle in the BNT162b2 Omicron BA.4/BA.5 (herein referred to as Omicron) drug substance (DS) is a single-stranded, 5'-capped mRNA that is translated into the respective protein (the encoded antigen). Figure 3.2.S.1.2-1 illustrates the general structure of the antigen-encoding RNA, which is determined by the respective nucleotide sequence of the DNA used as template for *in vitro* RNA transcription. In addition to the codon-optimized sequence encoding the antigen, the RNA contains common structural elements optimized for mediating high RNA stability and translational efficiency (5'-cap, 5'UTR, 3'-UTR, poly(A) - tail; see below). Furthermore, an intrinsic signal peptide (sec) is part of the antigen-encoding regions and is translated as N-terminal tag.

#### Figure 3.2.S.1.2-1. General structure of the Omicron BA.4/BA.5 mRNA



Schematic illustration of the general structure of the BNT162b2 Omicron BA.4/BA.5 mRNA drug substance with 5'-cap, 5'- and 3'untranslated regions (hAg-Kozak and FI element, respectively), coding sequence for variant of concern and intrinsic signal peptide (sec) as well as poly(A)-tail (A30L70). Individual elements are not drawn to scale compared to their respective sequence lengths.

### mRNA cap

A cap1 structure  $m_2^{7,3'-O}Gppp(m_1^{2'-O})ApG$  is utilized as specific capping structure at the 5'end of the RNA drug substance (Figure 3.2.S.1.2-2).

# Figure 3.2.S.1.2-2. 5'-cap analog (m<sub>2</sub><sup>7,3'-O</sup>Gppp(m<sub>1</sub><sup>2'-O</sup>)ApG) for production of RNA containing a cap1 structure



The cap1 structure (i.e., containing a 2'-O-methyl group on the penultimate nucleoside of the 5'-end of the RNA chain) is incorporated into the RNA drug substance by using a respective cap analog during *in vitro* transcription. For RNAs with modified uridine nucleotides, the cap1 structure is superior to other cap structures, since cap1 is not recognized by cellular factors such as IFIT1<sup>1</sup> and, thus, cap1-dependent translation is not inhibited by competition with eukaryotic translation initiation factor  $4E^2$ . In the context of IFIT1 expression, mRNAs with a cap1 structure give higher protein expression.

In addition, use of the cap1 structure leads to low amounts of uncapped transcripts<sup>3</sup>. In general, the T7 Polymerase prefers a guanosine as priming nucleoside with the highest transcription efficiencies as compared to other starting nucleosides<sup>4</sup>. Capping structures with a guanosine moiety compete with GTP for incorporation in the mRNA resulting in uncapped transcripts. The m<sub>2</sub><sup>7,3'-O</sup>Gppp(m<sub>1</sub><sup>2'-O</sup>)ApG cap analog rescues transcription efficiency from templates starting with adenosines, because the ApG moiety of cap1 allows transcription initiation at the second position, a guanosine, thereby giving mainly capped mRNAs.

### **Modified** Uridine

The RNA does not contain any uridines; instead of uridine the modified N1-methylpseudouridine is used in RNA synthesis. Several reports have demonstrated that such a substitution often strongly enhances translation of *in vitro* transcribed mRNA sequences by reducing its immunogenicity<sup>5,6,7</sup>. Accordingly, the drug substance is synthesized in the presence of N1-methylpseudouridine triphosphate ( $^{m1}\Psi$ TP) instead of uridine triphosphate (UTP).

<sup>3</sup> Trilink Patent auf CC413 cap. Accessed at https://patentimages.storage.googleapis.com/4c/83/15/99418d175a3be2/WO2017053297A1.pdf

<sup>4</sup> Kuzmine I, Gottlieb PA, Martin CT. Binding of the priming nucleotide in the initiation of transcription by T7 RNA polymerase. 2003. J Biol Chem;278(5):2819-23.

<sup>5</sup> Kariko K, Muramatsu H, Welsh FA, et al. Incorporation of pseudouridine into mRNA yields superior nonimmunogenic vector with increased translational capacity and biological stability. 2008. Mol Ther;16(11):1833-40.

<sup>6</sup> Andries O, Mc Cafferty S, De Smedt SC, et al. N(1)-methylpseudouridine-incorporated mRNA outperforms pseudouridine-incorporated mRNA by providing enhanced protein expression and reduced immunogenicity in mammalian cell lines and mice. 2015. J Control Release; 217:337-44.

<sup>7</sup> Richner JM, Himansu S, Dowd KA, et al. Modified mRNA Vaccines Protect against Zika Virus Infection. 2017. Cell;168(6):1114-25.e10

<sup>&</sup>lt;sup>1</sup> Habjan M, Hubel P, Lacerda L, et al. Sequestration by IFIT1 Impairs Translation of 2'O-unmethylated Capped RNA. 2013. PLOS Pathog;9(10):e1003663

<sup>&</sup>lt;sup>2</sup> Diamond MS. IFIT1: A dual sensor and effector molecule that detects non-2'-O methylated viral RNA and inhibits its translation. 2014. Cytokine Growth Factor Rev;25(5):543-50.

#### **RNA** sequence

The general sequence elements of the BNT162b2 Omicron BA.4/BA.5 mRNA drug substance, as depicted in Figure 3.2.S.1.2-1, are given below. The full sequence is given in Figure 3.2.S.1.2-3.

**hAg-Kozak (nucleotides 1 to 53):** 5'-UTR sequence of the human alpha-globin mRNA with an optimized 'Kozak sequence' to increase translational efficiency<sup>8</sup>.

Sec (nucleotides 54 to 101, intrinsic to S protein): Sec corresponds to the intrinsic S1S2 protein signal peptide (sec), which guides translocation of the nascent polypeptide chain into the endoplasmic reticulum.

S protein omicron (nucleotides 54 to 3863; including sec 54 to 101 and stop codons 3858 to 3863): Codon-optimized sequences encoding the respective antigen of SARS-CoV-2 protein has following point mutations/deletions (reference for numbering Genbank ID QHD43416.1): T19I,  $\Delta$ LPP24-26, A27S,  $\Delta$ HV69-70, G142D, V213G, G339D, S371L, S373P, S375F, T376A, D405N, K417N, N440K, L452R, S477N, T478K, E484A, F486V, Q498R, N501Y, Y505H, D614G, H655Y, N679K, P681H, N764K, D796Y, Q954H, N969K, KV986-987PP.

**FI element (nucleotides 3864 to 4158):** The 3'-UTR is a combination of two sequence elements derived from the "amino terminal enhancer of split" (AES) mRNA (called F) and the mitochondrial encoded 12S ribosomal RNA (called I). These were identified by an *ex vivo* selection process for sequences that confer RNA stability and augment total protein expression<sup>9</sup>.

A30L70 (nucleotides 4159 to 4268): The circular plasmid, described in Section 3.2.S.2.3 Control of Materials – Source, History and Generation of Plasmids BNT162b2 [Omicron (BA.4/BA.5) Variant], provides a template for an mRNA transcript that contains two poly(A) tracts of 30 and approximately 70 adenosine residues joined by a linker <sup>10</sup>.

<sup>&</sup>lt;sup>8</sup> Kozak M. An analysis of 5'-noncoding sequences from 699 vertebrate messenger RNAs. 1987. Nucleic Acids Res;15(20):8125-48.

<sup>&</sup>lt;sup>9</sup> Orlandini von Niessen AG, Poleganov MA, Rechner C, et al. Improving mRNA-Based Therapeutic Gene Delivery by Expression-Augmenting 3' UTRs Identified by Cellular Library Screening. 2019. Mol Ther;27(4):1-13.

<sup>&</sup>lt;sup>10</sup> BioNTech Patent auf STABILISIERUNG VON DNA-SEQUENZEN ZUR POLY(A)SEQUENZ-CODIERUNG. Accessed at https://data.epo.org/publication-server/pdf-document?pn=3167059&ki=B1&cc=EP&pd=20190626

# Figure 3.2.S.1.2-3. RNA nucleotide Sequence of the BNT162b2 (Omicron (BA.4/BA.5) Variant) drug substance

# The nucleotide sequence $5' \rightarrow 3'$ :

#### Cap-

AGAAUAAACU	AGUAUUCUUC	UGGUCCCCAC	AGACUCAGAG	AGAACCCGCC	ACCAUGUUCG	60
UGUUCCUGGU	GCUGCUGCCU	CUGGUGUCCA	GCCAGUGUGU	GAACCUGAUC	ACCAGAACAC	120
AGUCAUACAC	CAACAGCUUU	ACCAGAGGCG	UGUACUACCC	CGACAAGGUG	UUCAGAUCCA	180
GCGUGCUGCA	CUCUACCCAG	GACCUGUUCC	UGCCUUUCUU	CAGCAACGUG	ACCUGGUUCC	240
ACGCCAUCUC	CGGCACCAAU	GGCACCAAGA	GAUUCGACAA	CCCCGUGCUG	CCCUUCAACG	300
ACGGGGUGUA	CUUUGCCAGC	ACCGAGAAGU	CCAACAUCAU	CAGAGGCUGG	AUCUUCGGCA	360
CCACACUGGA	CAGCAAGACC	CAGAGCCUGC	UGAUCGUGAA	CAACGCCACC	AACGUGGUCA	420
UCAAAGUGUG	CGAGUUCCAG	UUCUGCAACG	ACCCCUUCCU	GGACGUCUAC	UACCACAAGA	480
ACAACAAGAG	CUGGAUGGAA	AGCGAGUUCC	GGGUGUACAG	CAGCGCCAAC	AACUGCACCU	540
UCGAGUACGU	GUCCCAGCCU	UUCCUGAUGG	ACCUGGAAGG	CAAGCAGGGC	AACUUCAAGA	600
ACCUGCGCGA	GUUCGUGUUU	AAGAACAUCG	ACGGCUACUU	CAAGAUCUAC	AGCAAGCACA	660
CCCCUAUCAA	CCUCGGCCGG	GAUCUGCCUC	AGGGCUUCUC	UGCUCUGGAA	CCCCUGGUGG	720
AUCUGCCCAU	CGGCAUCAAC	AUCACCCGGU	UUCAGACACU	GCUGGCCCUG	CACAGAAGCU	780
ACCUGACACC	UGGCGAUAGC	AGCAGCGGAU	GGACAGCUGG	UGCCGCCGCU	UACUAUGUGG	840
GCUACCUGCA	GCCUAGAACC	UUCCUGCUGA	AGUACAACGA	GAACGGCACC	AUCACCGACG	900
CCGUGGAUUG	UGCUCUGGAU	CCUCUGAGCG	AGACAAAGUG	CACCCUGAAG	UCCUUCACCG	960
UGGAAAAGGG	CAUCUACCAG	ACCAGCAACU	UCCGGGUGCA	GCCCACCGAA	UCCAUCGUGC	1020
GGUUCCCCAA	UAUCACCAAU	CUGUGCCCCU	UCGACGAGGU	GUUCAAUGCC	ACCAGAUUCG	1080
CCUCUGUGUA	CGCCUGGAAC	CGGAAGCGGA	UCAGCAAUUG	CGUGGCCGAC	UACUCCGUGC	1140
UGUACAACUU	CGCCCCUUC	UUCGCAUUCA	AGUGCUACGG	CGUGUCCCCU	ACCAAGCUGA	1200
ACGACCUGUG	CUUCACAAAC	GUGUACGCCG	ACAGCUUCGU	GAUCCGGGGA	AACGAAGUGC	1260
GGCAGAUUGC	CCCUGGACAG	ACAGGCAACA	UCGCCGACUA	CAACUACAAG	CUGCCCGACG	1320
ACUUCACCGG	CUGUGUGAUU	GCCUGGAACA	GCAACAAGCU	GGACUCCAAA	GUCGGCGGCA	1380
ACUACAAUUA	CAGGUACCGG	CUGUUCCGGA	AGUCCAAUCU	GAAGCCCUUC	GAGCGGGACA	1440
UCUCCACCGA	GAUCUAUCAG	GCCGGCAACA	AGCCUUGUAA	CGGCGUGGCA	GGCGUGAACU	1500
GCUACUUCCC	ACUGCAGUCC	UACGGCUUUA	GGCCCACAUA	CGGCGUGGGC	CACCAGCCCU	1560
ACAGAGUGGU	GGUGCUGAGC	UUCGAACUGC	UGCAUGCCCC	UGCCACAGUG	UGCGGCCCUA	1620
AGAAAAGCAC	CAAUCUCGUG	AAGAACAAAU	GCGUGAACUU	CAACUUCAAC	GGCCUGACCG	1680
GCACCGGCGU	GCUGACAGAG	AGCAACAAGA	AGUUCCUGCC	AUUCCAGCAG	UUUGGCCGGG	1740
AUAUCGCCGA	UACCACAGAC	GCCGUUAGAG	AUCCCCAGAC	ACUGGAAAUC	CUGGACAUCA	1800
CCCCUUGCAG	CUUCGGCGGA	GUGUCUGUGA	UCACCCCUGG	CACCAACACC	AGCAAUCAGG	1860

BNT162b2 3.2.S.1.2 Structure [Omicron (BA.4/BA.5) Variant]

UGGCAGUGCU	GUACCAGGGC	GUGAACUGUA	CCGAAGUGCC	CGUGGCCAUU	CACGCCGAUC	1920
AGCUGACACC	UACAUGGCGG	GUGUACUCCA	CCGGCAGCAA	UGUGUUUCAG	ACCAGAGCCG	1980
GCUGUCUGAU	CGGAGCCGAG	UACGUGAACA	AUAGCUACGA	GUGCGACAUC	CCCAUCGGCG	2040
CUGGAAUCUG	CGCCAGCUAC	CAGACACAGA	CAAAGAGCCA	CCGGAGAGCC	AGAAGCGUGG	2100
CCAGCCAGAG	CAUCAUUGCC	UACACAAUGU	CUCUGGGCGC	CGAGAACAGC	GUGGCCUACU	2160
CCAACAACUC	UAUCGCUAUC	CCCACCAACU	UCACCAUCAG	CGUGACCACA	GAGAUCCUGC	2220
CUGUGUCCAU	GACCAAGACC	AGCGUGGACU	GCACCAUGUA	CAUCUGCGGC	GAUUCCACCG	2280
AGUGCUCCAA	CCUGCUGCUG	CAGUACGGCA	GCUUCUGCAC	CCAGCUGAAA	AGAGCCCUGA	2340
CAGGGAUCGC	CGUGGAACAG	GACAAGAACA	CCCAAGAGGU	GUUCGCCCAA	GUGAAGCAGA	2400
UCUACAAGAC	CCCUCCUAUC	AAGUACUUCG	GCGGCUUCAA	UUUCAGCCAG	AUUCUGCCCG	2460
AUCCUAGCAA	GCCCAGCAAG	CGGAGCUUCA	UCGAGGACCU	GCUGUUCAAC	AAAGUGACAC	2520
UGGCCGACGC	CGGCUUCAUC	AAGCAGUAUG	GCGAUUGUCU	GGGCGACAUU	GCCGCCAGGG	2580
AUCUGAUUUG	CGCCCAGAAG	UUUAACGGAC	UGACAGUGCU	GCCUCCUCUG	CUGACCGAUG	2640
AGAUGAUCGC	CCAGUACACA	UCUGCCCUGC	UGGCCGGCAC	AAUCACAAGC	GGCUGGACAU	2700
UUGGAGCAGG	CGCCGCUCUG	CAGAUCCCCU	UUGCUAUGCA	GAUGGCCUAC	CGGUUCAACG	2760
GCAUCGGAGU	GACCCAGAAU	GUGCUGUACG	AGAACCAGAA	GCUGAUCGCC	AACCAGUUCA	2820
ACAGCGCCAU	CGGCAAGAUC	CAGGACAGCC	UGAGCAGCAC	AGCAAGCGCC	CUGGGAAAGC	2880
UGCAGGACGU	GGUCAACCAC	AAUGCCCAGG	CACUGAACAC	CCUGGUCAAG	CAGCUGUCCU	2940
CCAAGUUCGG	CGCCAUCAGC	UCUGUGCUGA	ACGAUAUCCU	GAGCAGACUG	GACCCUCCUG	3000
AGGCCGAGGU	GCAGAUCGAC	AGACUGAUCA	CAGGCAGACU	GCAGAGCCUC	CAGACAUACG	3060
UGACCCAGCA	GCUGAUCAGA	GCCGCCGAGA	UUAGAGCCUC	UGCCAAUCUG	GCCGCCACCA	3120
AGAUGUCUGA	GUGUGUGCUG	GGCCAGAGCA	AGAGAGUGGA	CUUUUGCGGC	AAGGGCUACC	3180
ACCUGAUGAG	CUUCCCUCAG	UCUGCCCCUC	ACGGCGUGGU	GUUUCUGCAC	GUGACAUAUG	3240
UGCCCGCUCA	AGAGAAGAAU	UUCACCACCG	CUCCAGCCAU	CUGCCACGAC	GGCAAAGCCC	3300
ACUUUCCUAG	AGAAGGCGUG	UUCGUGUCCA	ACGGCACCCA	UUGGUUCGUG	ACACAGCGGA	3360
ACUUCUACGA	GCCCCAGAUC	AUCACCACCG	ACAACACCUU	CGUGUCUGGC	AACUGCGACG	3420
UCGUGAUCGG	CAUUGUGAAC	AAUACCGUGU	ACGACCCUCU	GCAGCCCGAG	CUGGACAGCU	3480
UCAAAGAGGA	ACUGGACAAG	UACUUUAAGA	ACCACACAAG	CCCCGACGUG	GACCUGGGCG	3540
AUAUCAGCGG	AAUCAAUGCC	AGCGUCGUGA	ACAUCCAGAA	AGAGAUCGAC	CGGCUGAACG	3600
AGGUGGCCAA	GAAUCUGAAC	GAGAGCCUGA	UCGACCUGCA	AGAACUGGGG	AAGUACGAGC	3660
AGUACAUCAA	GUGGCCCUGG	UACAUCUGGC	UGGGCUUUAU	CGCCGGACUG	AUUGCCAUCG	3720
UGAUGGUCAC	AAUCAUGCUG	UGUUGCAUGA	CCAGCUGCUG	UAGCUGCCUG	AAGGGCUGUU	3780
GUAGCUGUGG	CAGCUGCUGC	AAGUUCGACG	AGGACGAUUC	UGAGCCCGUG	CUGAAGGGCG	3840
UGAAACUGCA	CUACACAUGA	UGACUCGAGC	UGGUACUGCA	UGCACGCAAU	GCUAGCUGCC	3900
CCUUUCCCGU	CCUGGGUACC	CCGAGUCUCC	CCCGACCUCG	GGUCCCAGGU	AUGCUCCCAC	3960
CUCCACCUGC	CCCACUCACC	ACCUCUGCUA	GUUCCAGACA	CCUCCCAAGC	ACGCAGCAAU	4020
GCAGCUCAAA	ACGCUUAGCC	UAGCCACACC	CCCACGGGAA	ACAGCAGUGA	UUAACCUUUA	4080
GCAAUAAACG	AAAGUUUAAC	UAAGCUAUAC	UAACCCCAGG	GUUGGUCAAU	UUCGUGCCAG	4140
CCACACCCUG	GAGCUAGCAA	АААААААААА	АААААААААА	AAAAAAAAGC	AUAUGACUAA	4200
ААААААААА	ААААААААА	АААААААААА	АААААААААА	АААААААААА	ААААААААА	4260
ААААААА						4268

Sequence length: 4269, which includes "Cap-" to denote the presence of the 5'-cap analog G: 1058; C: 1305; A: 1108; U: 797

A = Adenine; C = Cytosine; G = Guanine; U = N1-methylpseudouridine