THIRD PARTY OBSERVATIONS PURSUANT TO ARTICLE 115 EPC

BY MEDECINS DU MONDE

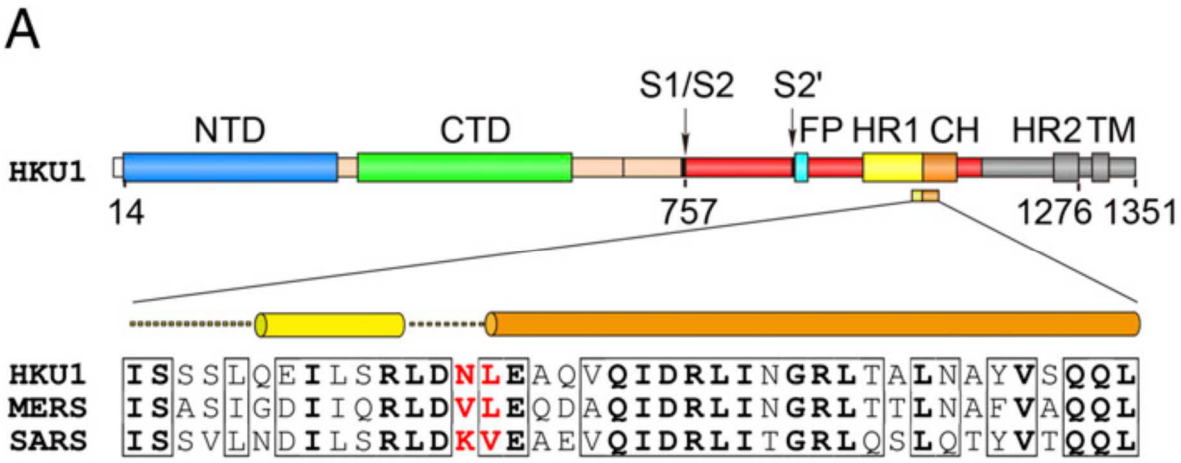
IN REGARD OF EP3901261 (EP21168950.0) IN THE NAME OF BIONTECH SE

The claimed composition lacks an inventive step, as the inventors **directly applied** the teachings of previous academic works of Pallesen *et al*. (2017) and Pardi *et al*. (2019) to the sequence of SARS-CoV-2 which was publicly released on 13 January 2020 (https://www.ncbi.nlm.nih.gov/nuccore/NC_045512.1).

More specifically, starting from Hodgson (2020) (D1 in the examination proceedings) it would have been obvious for the person of skill in the art to provide alternative anti-COVID-19 mRNA vaccines to those mentioned in Table 2 (*e.g.* BioNTech and Moderna), expressing a stabilized S protein of SARS-CoV-2 in the prefusion conformation, in particular represented by SEQ ID NO: 7 according to patent application EP21168938.5.

Indeed, Pallesen *et al*. (2017) teach that structure-based design was used to develop a generalizable strategy **for retaining coronavirus S proteins in the antigenically optimal prefusion conformation** and demonstrate that the engineered immunogen is able to elicit **high neutralizing antibody titers** against MERS-CoV.

The strategy involves replacing consecutive amino acids V1060 and L1061 of the S protein of MERS-CoV **by two prolines (2P)** (see page E7350, left column).



The position of the amino acids to be mutated to prolines is shown for MERS-CoV and SARS-CoV in the above Figure 1A.

Applying this strategy to the S protein of SARS-Cov-2 directly yields the modified stabilized SARS-CoV-2 S protein (SEQ ID NO: 7) of EP EP3901261.

We show below the alignments of the SARS-CoV-2 S protein from NC_045512.1 (Query) and SEQ ID NO: 7 (Sbjct) between amino acids 961 and 1020:

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Query  961   TLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRA  1020

             TLVKQLSSNFGAISSVLNDILSRLD  EAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRA

Sbjct  961   TLVKQLSSNFGAISSVLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRA  1020
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It can be readily seen that SEQ ID NO: 7 only differs from NC_045512.1 by the substitution of K986 and V987 by two prolines and that the position of the substituted amino acids corresponds exactly to that shown for SARS-CoV in the above-figure.

Accordingly, there was a clear incitation in the art to have a modified stabilized SARS-CoV-2 S protein of sequence SEQ ID NO: 7 expressed by the mRNA vaccine.

Besides, Pardi *et al*. (2019) teach that Intradermal anti-HIV vaccination with nucleoside-modified 1086C Env **mRNA-LNPs** elicited high levels of gp120-specific antibodies in rabbits and rhesus macaques.

As such, it would have been equally obvious to have SEQ ID NO: 7 expressed by a mRNA comprising N1-methyl-pseudouridine and formulated in LNPs comprising ionizable cationic lipid, phosphatidylcholine, cholesterol, and polyethylene glycol (PEG)-lipids as provided by Pardi *et al*. (2019) (see from page 42, right column, to page 43 left column) and initially described in WO2009127060 (see *e.g*. claims 14 and17).