Electron breakthrough for COVID-19 omicron variant

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On 26-Nov-2021 the World Health Organization named a new variant of the SARS-CoV-2 virus that causes COVID-19 disease. The variant was named omicron (the Greek letter O). It was reported to have many mutations some of which might increase the spread of the virus.

Here a structure is presented for the omicron spike protein variant based on a recently deposited sequence in the PubMed protein database[1]. Like the delta variant[2] it is based on an electron-gated ion channel model similar to the L-type calcium channel oscillator model described in Sect. 8-7 (Figs. 8-4.,8-5.,8-6.) of my book[3].

The omicron spike protein structure presented here reveals two important differences with the delta variant. **1)** The model has a smaller time constant in Domain 2, allowing omicron to replicate faster, and likely making it more contagious. **2)** Omicron has 20 more amino acid residues than delta on S1 in Domain 2. This reduces the deep binding cavities for S1 and S2 helices, thus providing less area for contact with host receptor molecules and reduced potential binding force in the Domain 2 region. This likely makes omicron less deadly than delta.

The deadly nature of COVID-19 and its variants is determined by the amino acid sequence of the spike protein, how it contacts the host molecule it infects, how strong it binds with receptor molecules and how fast it replicates.

About 30–100 spike proteins protrude from the surface of each virus particle. The particle has a reported diameter of about 0.1 microns in the dry state. The diameter can be up to 0.3 microns or more when it picks-up water and other substances. It needs water and ions in the ion channel to replicate.

A 3-D electron-gated structure for the omicron spike protein ion channel was developed and is presented in Fig. 23A and Fig. 23B.

It reveals why omicron is less deadly than the delta variant; it has 20 extra amino acid residues on S1 in Domain 2 (shown in Red in Fig. 23A). This reduces the contact distance for binding to a host molecule and potential binding force.

Replication of the virus particle is controlled by the electron tunneling time constants for inactivation (Table 23-1. Domain 2 and 4). This can only occur when the particle picks up water and other substances. In the dry state replication stops. The fast 60 ms time constant in Domain 1 might be for replicating the 30-100 spike proteins that surround the virus particle - or it might be charged.

Finally, all the models need Arg/Lys NH3 energy amplification to function[4]. This is a fundamental breakthrough that reduces the noise by 23-24 fold. The Noise temperature is reduced to 13K. This amplification mechanism is nature's supreme trick to make life possible. It violates the 2nd law of thermodynamics by reducing entropy[4].

References:

1. NCBI Accession 7T9L_A., release Dec 29, 2021; deposition: Dec 19, 2021
SARS-CoV-2 Omicron variant: ACE2 Binding, Cryo-EM Structure of Spike Protein-ACE2 Complex and Antibody Evasion. Journal: unpublished. Authors: Mannar, D., Saville, J.W., Zhu, X., Srivastava, S.S., Berezuk,A.M., Tuttle, K.S., Marquez, C., Sekirov, I., and Suoramaniam, S.

2. Ralston, W.P., (Aug-2021). Electron breakthrough for COVID-19 delta variant. www.biokinetix.org/covid-19-delta-electron.html

3. Ralston, W.P., (2005) *Electron-gated ion channels* : *with amplification by NH3 inversion resonance.* SciTech Publishing, Inc. Raleigh, NC

4. Ralston, W.P., (1-27-2022). The Arg/Lys NH3 energy amplifier. www.biokinetix.org/nh3-energy-amplifier.html

Fig. 23A. Omicron spike protein, Electron-gated ion channel structure & reported mutations

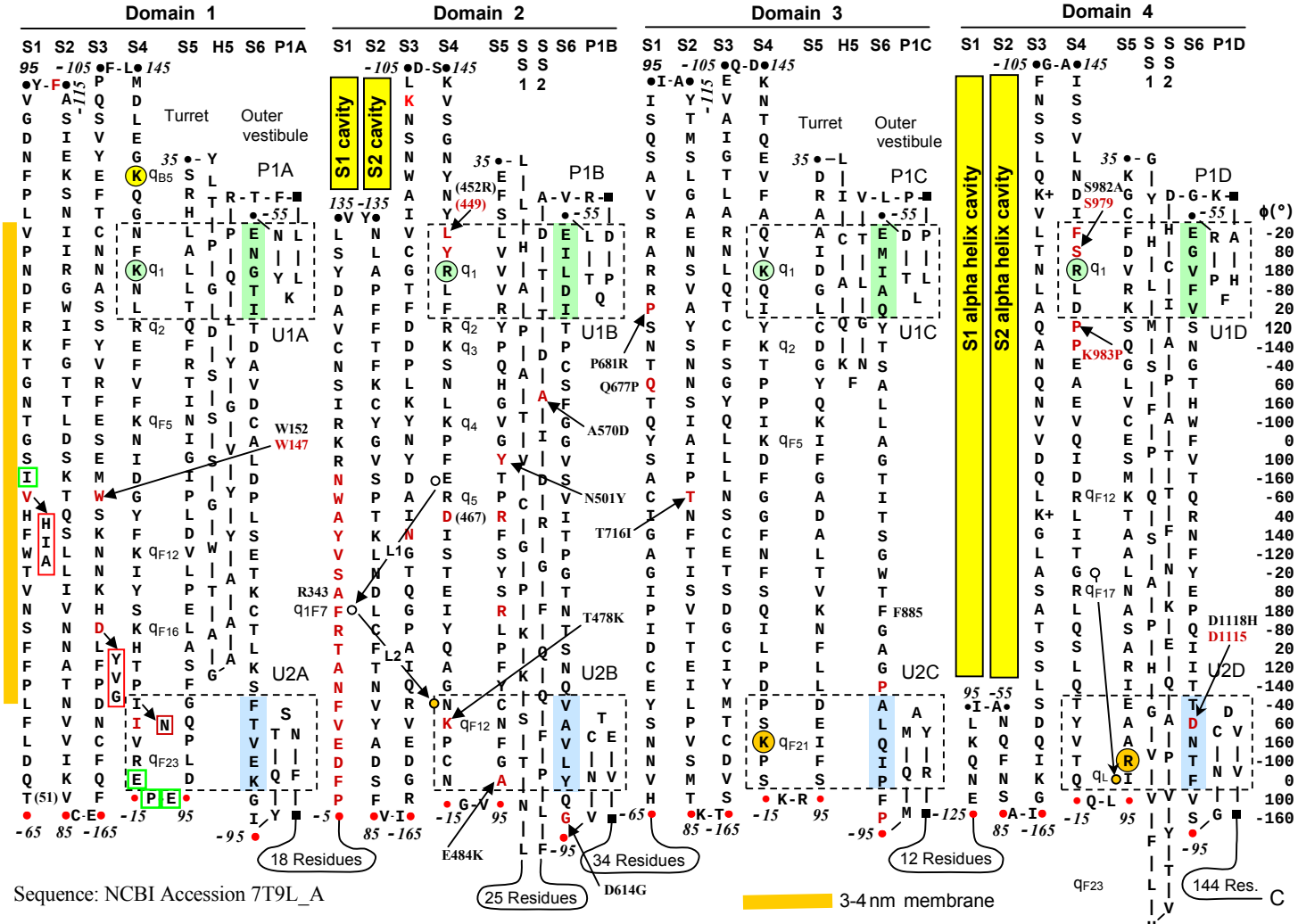
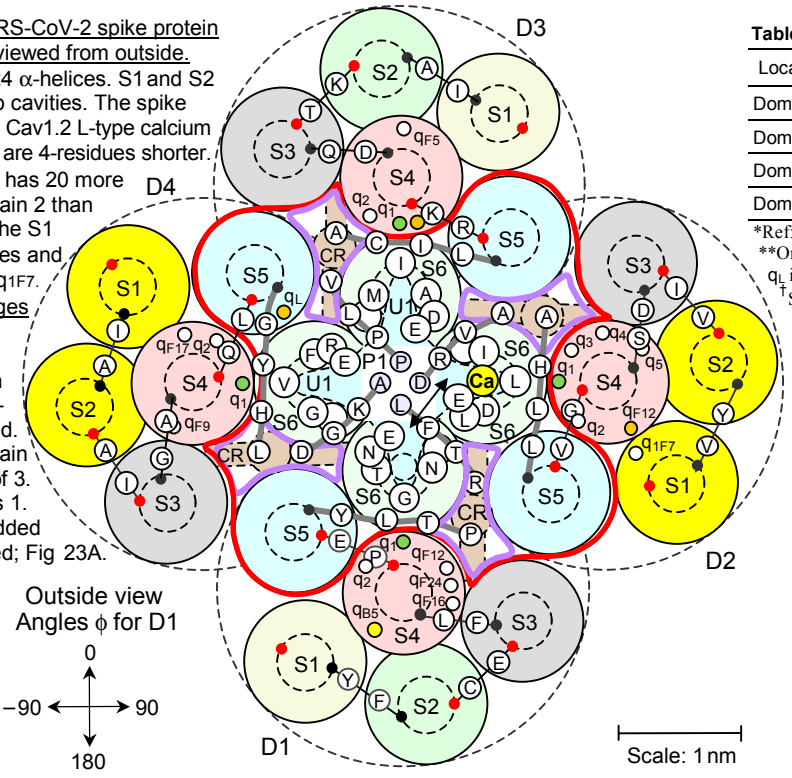


Fig. 23B.



Cross section of SARS-CoV-2 spike protein for Omicron variant viewed from outside.
Large circles show 24 α-helices. S1 and S2 on D4 are 5 nm-deep cavities. The spike structure is similar to Cav1.2 L-type calcium channels; S6 helices are 4-residues shorter. The Omicron variant has 20 more residues on S1 Domain 2 than delta. This reduces the S1 and S2 α-helix cavities and adds R342 with site q_{1F7}.
Omicron spike changes compared to delta:
Added residues are surrounded by green band. Removed residues have a red band.
On D1: S1 has net gain of 2. S3 has a gain of 3. S4 gains 3 and loses 1.
On D2: S1 has 20 added residues shown in red; Fig 23A.

Table 23-1. Omicron Electron tunneling time constants

Location	Sites	Residues	Distance*	Time*
Domain 1	q_{F16} -q_{F23} †	7	10.6 Å	60 ms
Domain 2	q_5 -q_{F12} **	12&L1+L2	13 Å	1 s
Domain 3	q_{F5} -q_{F21}	16	25.2 Å	hrs-days
Domain 4	q_{F17} - q_L	11	16.5 Å	1 min

*Ref: Ch. 8 and Table 8-1, Electron-gated ion channels (2005).
**Omicron variant mutation T478K increases replication rate.
q_L is lateral tunneling site not on S4, but on D2-S1 and D4-S5.
† Site q_{F23} may be charged and not an electron tunneling site.

H5 residue chain
Periphery of outer vestibule
Intra-helix crevices (IHC)
NH_3 Arg/Lys tunneling site
Arg/Lys charged or neutral
Glu/Asp charged or neutral
Activation control site
Inactivation control site
α-helix end residue terminal
(CR) Crevice Residues

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