

Keine Verschwörungstheorie mehr!! Die Pfizer Dokumente über die Corona Giftspritze sprechen eindeutig von Graphen-Oxid in der Todesimpfung!! Das Dokument ist von der FDA (amerikanische Gesundheitsbehörde) Hast du dich schon einmal gefragt, wie die Welt wirklich funktioniert?

PF-07302048: Structural and Biophysical Characterization of SARS-CoV-2 Spike Glycoprotein (P2 S) as a Vaccine Antigen
VR-VTR-10741, Ver. 2.0

a P2 S concentration series, after initial baseline equilibration of 120 seconds, the sensors were dipped in a 10 $\mu\text{g/mL}$ solution of Avi-tagged ACE2-PD or B38 mAb for 300 seconds to achieve capture levels of 1 nM using the threshold function. Then, after another 120 seconds of baseline, binding data were collected for 300 seconds of association and 600 seconds of dissociation.

Biolayer interferometry data were collected with Octet Data Acquisition software version 10.0.0.87 and processed using FortéBio Data Analysis software version 10.0. Data were reference subtracted and fit to a 1:1 binding model with R^2 value greater than 0.95 to determine kinetics and affinity of binding using Octet Data Analysis Software v10.0 (FortéBio).

3.4. Cryo-EM of P2 S

For TwinStrep-tagged P2 S, 4 μL purified protein at 0.5 mg/mL were applied to gold Quantifoil R1.2/1.3 300 mesh grids freshly overlaid with graphene oxide. The sample was blotted using a Vitrobot Mark IV for 4 seconds with a force of 2 before being plunged into liquid ethane cooled by liquid nitrogen. 27,701 micrographs were collected from two identically prepared grids. Data were collected from each grid over a defocus range of -1.2 to -3.4 μm with a total electron dose of 50.32 and 50.12 $\text{e}/\text{\AA}^2$, respectively, fractionated into 40 frames over a 6-second exposure for 1.26 and 1.25 $\text{e}/\text{\AA}^2/\text{frame}$. On-the-fly motion correction, CTF estimation, and particle picking and extraction with a box size of 450 pixels were performed in Warp (Tegunov & Cramer, 2019), during which super-resolution data were binned to give a pixel size of 0.87 \AA . A total of 1,119,906 particles were extracted. All subsequent processing was performed in RELION 3.1-beta (Zivanov et al, 2018). Particle heterogeneity was filtered out with 2D and 3D classification, yielding a set of 73,393 particles, which refined to 3.6 \AA with C3 symmetry. 3D classification of this dataset without particle alignment separated out one class with a single RBD up, representing 15,098 particles. The remaining 58,295 particles, in the three RBD 'down' conformation, were refined to give a final model at 3.29 \AA . The atomic model from PDB ID 6XR8 (Cai et al, 2020) was rigid-body fitted into the map density, then flexibly fitted to the density using real-space refinement in Phenix (Adams et al, 2010) alternating with manual building in Coot (Emsley et al, 2010). Data collection, 3D reconstruction and model refinement statistics are listed in Table 1.

