SARS-CoV-2 neutralizing antibody structures inform therapeutic strategies

In the format provided by the authors and unedited
Supplementary Table 1. X-ray crystallography data collection and refinement statistics

<table>
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<td>Resolution (Å)</td>
<td>48.85-3.2 (3.31-3.2)</td>
<td>37.93-1.65 (1.71-1.65)</td>
<td>34.1-1.92 (1.99-1.92)</td>
<td>38.7 - 1.80 (1.86-1.80)</td>
<td>39.1-2.0 (2.05-2.0)</td>
<td>45.7-2.0 (2.07-2.0)</td>
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<td>R_merge (%)</td>
<td>16.0 (49.2)</td>
<td>9.58 (148)</td>
<td>7.21 (203)</td>
<td>8.7 (107)</td>
<td>58.1 (136)</td>
<td>8.5 (213)</td>
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<tr>
<td>R_pim (%)</td>
<td>6.8 (23.2)</td>
<td>2.27 (33.4)</td>
<td>2.38 (71.4)</td>
<td>4.1 (81.9)</td>
<td>11.4 (81)</td>
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<tr>
<td>CC_1/2 (%)</td>
<td>98.7 (97.4)</td>
<td>99.8 (80.7)</td>
<td>99.9 (80.7)</td>
<td>99.6 (78.2)</td>
<td>99.5 (24.8)</td>
<td>99.8 (30.5)</td>
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<td>Completeness (%)</td>
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<td>99.97 (99.95)</td>
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<td>99.4 (98.4)</td>
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<td>Redundancy</td>
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<td>4.7 (2.0)</td>
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<td>6.8 (6.6)</td>
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<td>Wilson B-factor</td>
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<td>28.5</td>
<td>32.1</td>
<td>23.8</td>
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<td><strong>Refinement and Validation</strong></td>
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<td>Resolution (Å)</td>
<td>48.5 - 3.2</td>
<td>37.9 - 1.65</td>
<td>34.1-1.92</td>
<td>38.9 - 1.80</td>
<td>36.4 - 2.0</td>
<td>45.7 - 2.0</td>
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<td>Unique Reflections</td>
<td>14,722 (1413)</td>
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<td>Rwork/Rfree (%)</td>
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<td>19.7/22.7</td>
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<td>R.m.s. deviations</td>
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<td>Bond lengths (Å)</td>
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<td>Bond angles (°)</td>
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<td>Poor rotamers (%)</td>
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<td>Ramachandran plot</td>
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<td>Average B-factor (Å)</td>
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1For each structure reported, data were derived from a single crystal.
2Numbers in parentheses correspond to the highest resolution shell
**Data collection conditions**

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<td>Defocus range (µm)</td>
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