**Table S5. Cryo-EM data collection, processing, and validation statistics**

| | S6P in complex with the Fabs of BD-368-2, BD-604, and N12-9 (PDB:7E8C; EMDB: EMD-31014) | The local structure of NTD-RBD together with the Fabs of BD-368-2, BD-604, and N12-9 (PDB: 7E8F; EMDB: EMD-31017) |
|---|---|---|
| **Data collection and processing** | | |
| Voltage (kV) | 300 | |
| Microscope | FEI Titan Krios G3 | |
| Camera | K2 Summit (Gatan) | |
| Magnification (calibrated) | 130,000X | |
| Electron exposure ($e^-/Å^2$) | 63.27 | |
| Exposure rate ($e^-/Å^2/s$) | 7.6046 | |
| Number of frames collected per micrograph | 32 | |
| Energy filter slit width | 20 eV | |
| Automation software | SerialEM | |
| Defocus range (μm) | –0.6 to –1.2 | |
| Pixel size (Å) | 1.052 | |
| Micrographs used | 3,957 | |
| Symmetry imposed | C1 | C1 |
| Initial particle images | 858,315 | 535,671 |
| Final particle images | 178,557 | 304,696 |
| Resolution at 0.5 FSC of masked reconstruction (Å) | 3.79 | 3.66 |
| Resolution at 0.143 FSC of masked reconstruction (Å) | 3.16 | 3.18 |
| Map sharpening B factor ($Å^2$) | –70.48 | –113.22 |
| **Refinement** | | |
| Initial model used (PDB code) | 7CHH, 7CHF | 7CHH, 7CHF |
| Refinement package | Phenix v1.18 (Real-space refinement at 3.16 Å) | Phenix v1.18 (Real-space refinement at 3.18 Å) |
| Map-model CC | | |
|   CC_mask | 0.70 | 0.81 |
|   CC_box | 0.71 | 0.68 |
|   CC_peaks | 0.57 | 0.62 |
|   CC_volume | 0.69 | 0.79 |
| Model composition | | |
|   Non-hydrogen atoms | 40,225 | 8,768 |
|   Protein residues | 5,218 | 1,134 |
|   Ligands | 0 | 0 |
| R.m.s. deviations | | |
|   Bond lengths (Å) | 0.009 | 0.005 |
|   Bond angles (°) | 0.872 | 0.674 |
| $B$ factors ($Å^2$) | | |
|   Protein | 73.71 | 64.92 |
| Validation | | |
|   MolProbity score | 2.71 | 1.95 |
|   Clashscore | 14.31 | 8.89 |
|   Poor rotamers (%) | 6.48 | 0 |

| | | |
|---|---|---|
| Ramachandran plot | | |
| Favored (%) | 93.37 | 92.45 |
| Allowed (%) | 6.61 | 5.24 |
| Disallowed (%) | 0.02 | 0 |
| Cβ outliers (%) | 0.00 | 0.00 |
| CaBLAM outliers (%) | 3.34 | 3.21 |