**Supplementary Table S2.** X-ray data collection and refinement statistics for ORF68.

|  |  |
| --- | --- |
| **Parameter** | **ORF68 (PDB XXXX)** |
| **Data collection statistics** |  |
| Wavelength (Å) | 1.11589 |
| Resolution range (Å) | 49.54 - 2.22 (2.48 - 2.22) |
| Space group | C2221 |
| Unit cell dimensions |  |
| a, b, c (Å) | 135.0 224.0 192.3 |
| α=β=γ (°) [°](https://www.degreesymbol.net/)[°](https://www.degreesymbol.net/) | 90 |
| Total reflections | 1,213,852 (51,624) |
| Unique reflections | 91,387 (4,570) |
| Multiplicity | 13.3 (11.3) |
| Completeness (%) |  |
| spherical | 63.7 (11.3) |
| ellipsoidal | 95.3 (79.0) |
| Mean I/σ(I) | 19.4 (1.7) |
| Wilson B-factor | 54.8 |
| R-merge | 0.100 (1.715) |
| R-meas | 0.104 (1.796) |
| R-pim | 0.028 (0.525) |
| CC1/2 | 0.999 (0.565) |
|  |  |
| **Refinement statistics** |  |
| Rwork/Rfree | 0.22/0.25 (0.38/0.35) |
| Number of non-hydrogen atoms | 16,391 |
| macromolecules | 16,373 |
| ligands | 15 |
| solvent | 3 |
| Protein residues | 2124 |
| RMS (bonds) | 0.013 |
| RMS (angles) | 1.38 |
| Ramachandran favored (%) | 98.07 |
| Ramachandran allowed (%) | 1.93 |
| Ramachandran outliers (%) | 0.00 |
| Rotamer outliers (%) | 0.33 |
| Clashscore | 11.40 |
| Average B-factor | 62.79 |
| macromolecules | 62.81 |
| ligands | 48.61 |
| solvent | 40.49 |
| Number of TLS groups | 22 |

Statistics for the highest-resolution shell are shown in parentheses. The STARANISO server was used for ellipsoidal truncation (ref #). The worst diffraction limit after cut-off was 2.99 Å. The ellipsoidally truncated data set was deposited in the Protein Data Bank and is available as **Supplementary Data File 4**. Merged diffraction data that has not been ellipsoidally truncated is available as **Supplementary Data File 5**. The coordinate set deposited in the Protein Data Bank is available as **Supplementary Data File 6**. A summary PyMol session file is available as **Supplementary Data File 7**.