**Supplementary Table 1**. Data collection and refinement statistics.

|  |  |
| --- | --- |
|  | **Structure** |
|  | GBAv | REPh(*P*1) merged | REPh(*P*3121) |
| **Data collection and unit cell dimensions*a*** |
| Wavelength (Å) | 1.0 | 1.0 | 1.0 |
| Synchrotron | SLS | SLS | Australian synchrotron |
| Space group | *P*212121 | *P*1 | *P*3121 |
| *a*, *b*, *c* (Å) | 94.28, 110.53, 122.07 | 105.74, 121.26, 129.55 | 119.10, 119.10, 351.40 |
| *α*, *β*, *γ* (°) | 90, 90, 90 | 61.85, 68.30, 74.16 | 90.00, 90.00, 120.00 |
| Resolution (Å) | 1.9 | 3.05 | 3.6 |
| No. of reflections | 1,027,690 | 517,157 | 186,010 |
| No. of unique reflections | 100,333 | 98,610 | 33,877 |
| *R*merge | 0.108 (1.432) | 0.111 (1.046) | 0.211 (0.936) |
| Rpim | 0.035 (0.488) | 0.053 (0.497) | 0.109 (0.488) |
| CC1/2 | 0.999 (0.706) | 0.998 (0.769) | 0.985 (0.504) |
| Mean I/σ (I) | 17 (1.8) | 14.5 (2.0) | 6.5 (2.0) |
| Completeness (%) | 100 (100) | 98.9 (98.9) | 99.1 (99.1) |
| Redundancy | 10.2 (9.4) | 5.2 (5.3) | 5.5 (5.4) |
| **Refinement** |
| Resolution (Å) | 28.08‒1.90 (2.00‒1.90) | 48.76‒3.05 (3.16‒3.05) | 19.85‒3.6 (3.78‒3.6) |
| *R*work/*R*free (%) | 19.2/21.9 | 24.5/28.5 | 20.6/28.1 |
| No. of atoms |  |  |  |
| Protein | 8,377 | 26,183 | 13,930 |
| Ligand (Glycerol) | 1 |  |  |
| Water | 783 |  |  |
| Protein residues | 1,075 | 3,343 | 1,834 |
| *B* factors (Å2) |  |  |  |
| Protein | 43.60 | 93.30 | 63.04 |
| Ligand (Glycerol) | 75.20 |  |  |
| Water | 44.50 |  |  |
| R.m.s deviations |  |  |  |
| Bond lengths (Å) | 0.003 | 0.012 | 0.012 |
| Bond angles (°) | 0.758 | 1.62 | 1.64 |
| Ramachandran favored (%) | 97 | 87 | 87 |
| Ramachandran outliers (%) | 0 | 4.3 | 4.5 |
| PDB accession code | 6AAA | 6ABH | 6AC3 |

*a*Values within parenthesis are for the highest resolution shell.