**Cryo-EM data processing, refinement and validation statistics**

**Supplementary table 1**

|  |  |
| --- | --- |
| **LMB Krios G2** | **2c**(EMDB-14023)(PDB 7QJV) |
| **Data processing** |  |
| Initial particle images (no.) | 314921 |
| Final particle images (no.) | 37499 |
| Helical twist (º) | -0.797 |
| Helical rise (Å) | 4.75 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 3.29 |
| **Refinement** |  |
| Initial model used (PDB code) | 6HRE |
| Model resolution FSC 0.5 (Å) | 3.6 |
| Map sharpening *B* factor (Å2) | -22.2 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 69369120 |
| *B* factors (Å2) Protein Ligand | 49.38na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0122.254 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.230.650 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 90.549.470 |

**Supplementary table 2**

|  |  |
| --- | --- |
| **LMB Krios G1** | **4a**(EMDB-14063)(PDB 7QL4) |
| **Data processing** |  |
| Initial particle images (no.) | 114 023 |
| Final particle images (no.) | 40521 |
| Helical twist (º) | 179.47 |
| Helical rise (Å) | 2.358 |
| Symmetry imposed | 21 |
| Map resolution FSC 0.143 (Å)  | 3.20 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.2 |
| Map sharpening *B* factor (Å2) | -62.41 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 3468456 |
| *B* factors (Å2) Protein Ligand | 50.01NA |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0111.993 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.10.280 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 91.678.330 |

**Supplementary table 3**

|  |  |  |
| --- | --- | --- |
| **LMB Krios G2** | **8a**(EMDB-14024)(PDB 7QJW) | **8b**(EMDB-14062)(PDB 7QL3) |
| **Data processing** |  |  |
| Initial particle images (no.) | 677401 | 677401 |
| Final particle images (no.) | 56911 | 36253 |
| Helical twist (º) | 179.44 | -1.26 |
| Helical rise (Å) | 2.43 | 4.844 |
| Symmetry imposed | 21 | 1 |
| Map resolution FSC 0.143 (Å)  | 2.81 | 3.31 |
| **Refinement** |  |  |
| Initial model used (PDB code) | 6NWP | na |
| Model resolution FSC 0.5 (Å) | 2.8 | 3.3 |
| Map sharpening *B* factor (Å2) | -108.66 | -95.72 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 345645012 | 32464260 |
| *B* factors (Å2) Protein Ligand | 11569.52 | 39.48na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0112.059 | 0.0112.067 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.7400 | 0.9800 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 93.154.111.37 | 92.277.730 |

**Supplementary table 4**

|  |  |  |
| --- | --- | --- |
| **TFS Krios G4** | **9a**(EMDB-14026)(PDB 7QJY) | **9b**(EMDB-14027)(PDB 7QJZ) |
| **Data processing** |  |  |
| Initial particle images (no.) | 91908 | 91908 |
| Final particle images (no.) | 24754 | 8701 |
| Helical twist (º) | -1.26 | -1.02 |
| Helical rise (Å) | 4.74 | 4.74 |
| Symmetry imposed | 2 | 1 |
| Map resolution FSC 0.143 (Å)  | 3.14 | 3.4 |
| **Refinement** |  |  |
| Initial model used (PDB code) | na | na |
| Model resolution FSC 0.5 (Å) | 3.10 | 3.8 |
| Map sharpening *B* factor (Å2) | -32.69 | -14.56 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 34444500 | 33784440 |
| *B* factors (Å2) Protein Ligand | 38.93na | 39.11na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0101.965 | 0.0112.13 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.8900.25 | 0.990.240 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 94.295.710 | 94.445.320.23 |

**Supplementary table 5**

|  |  |  |
| --- | --- | --- |
| **LMB Krios G2** | **10a**(EMDB-14038)(PDB 7QK5) | **10b**(EMD-14320)(PDB 7R5H) |
| **Data processing** |  |  |
| Initial particle images (no.) | 2087042 | 189313 |
| Final particle images (no.) | 108932 | 114483 |
| Helical twist (º) | -1.129 | -0.885 |
| Helical rise (Å) | 4.75 | 4.77 |
| Symmetry imposed | 3 | 1 |
| Map resolution FSC 0.143 (Å)  | 1.92 | 2.59 |
| **Refinement** |  |  |
| Initial model used (PDB code) | na | na |
| Model resolution FSC 0.5 (Å) | 1.90 | 2.80 |
| Map sharpening *B* factor (Å2) | -13.20 | -37.09 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 51126660 | 36544770 |
| *B* factors (Å2) Protein Ligand | 49.46na | 51.37na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0111.977 | 0.011.953 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.8100 | 0.920.670 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 95.524.480 | 96.773.230 |

**Supplementary table 6**

|  |  |
| --- | --- |
| **LMB Krios G2** | **11a**(EMDB-14046)(PDB 7QKL) |
| **Data processing** |  |
| Initial particle images (no.) | 98287 |
| Final particle images (no.) | 74337 |
| Helical twist (º) | 179.402 |
| Helical rise (Å) | 2.378 |
| Symmetry imposed | 21 |
| Map resolution FSC 0.143 (Å)  | 2.07 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.1 |
| Map sharpening *B* factor (Å2) | -52.98 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 34564560 |
| *B* factors (Å2) Protein Ligand | 40.42na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0112.47 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.80.140 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 96.43.60 |

**Supplementary table 7**

|  |  |
| --- | --- |
| **LMB Krios G2** | **12a**(EMDB-14040)(PDB 7QKF) |
| **Data processing** |  |
| Initial particle images (no.) | 51533 |
| Final particle images (no.) | 17783 |
| Helical twist (º) | -1.69 |
| Helical rise (Å) | 4.8 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 2.83 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.2 |
| Map sharpening *B* factor (Å2) | -35.91 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 18572490 |
| *B* factors (Å2) Protein Ligand | 52.51na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0112.336 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.10.260 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 91.568.440 |

**Supplementary table 8**

|  |  |  |
| --- | --- | --- |
| **TFS Krios G4** | **14a**(EMDB-14053)(PDB 7QKU) | **14b**(EMDB-14044)(PDB 7QKJ) |
| **Data processing** |  |  |
| Initial particle images (no.) | 224815 | 224815 |
| Final particle images (no.) | 18013 | 28075 |
| Helical twist (º) | -1.25 | -0.99 |
| Helical rise (Å) | 4.75 | 4.78 |
| Symmetry imposed | 1 | 1 |
| Map resolution FSC 0.143 (Å)  | 2.57 | 3.26 |
| **Refinement** |  |  |
| Initial model used (PDB code) | na | na |
| Model resolution FSC 0.5 (Å) | 2.6 | 3.4 |
| Map sharpening *B* factor (Å2) | -29.2 | -66.5 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 34564530 | 68889000 |
| *B* factors (Å2) Protein Ligand | 44.56na | 38.93Na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.011.926 | 0.0122.087 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.970.280 | 1.130.210 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 94.785.220 | 90.079.930 |

**Supplementary table 9**

|  |  |  |  |
| --- | --- | --- | --- |
| **LMB Krios G2** | **15a**(EMDB-14054)(PDB 7QKV) | **15b**(EMDB-14056)(PDB 7QKX) | **15c**(EMDB-14059)(PDB 7QL0) |
| **Data processing** |  |  |  |
| Initial particle images (no.) | 122945 | 122945 | 122945 |
| Final particle images (no.) | 7127 | 19606 | 14590 |
| Helical twist (º) | -1.3 | 179.426 | -1.33 |
| Helical rise (Å) | 4.75 | 2.37 | 4.75 |
| Symmetry imposed | 3 | 21 | 1 |
| Map resolution FSC 0.143 (Å)  | 3.23 | 3.16 | 3.13 |
| **Refinement** |  |  |  |
| Initial model used (PDB code) | na | na | na |
| Model resolution FSC 0.5 (Å) | 3.3 | 3.0 | 3.1 |
| Map sharpening *B* factor (Å2) | -54.72 | -45.01 | -46.55 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 46986210 | 33424380 | 31324140 |
| *B* factors (Å2) Protein Ligand | 101.29na | 110.93na | 101.29na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0111.97 | 0.011.88 | 0.011.948 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.930.630 | 0.7100 | 0.7700 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 96.523.480 | 96.713.290 | 96.023.980 |

**Supplementary table 10**

|  |  |
| --- | --- |
| **LMB Krios G2** | **16a**(EMDB-14316)(PDB 7R4T) |
| **Data processing** |  |
| Initial particle images (no.) | 103382 |
| Final particle images (no.) | 32386 |
| Helical twist (º) | 179.483 |
| Helical rise (Å) | 2.39 |
| Symmetry imposed | 21 |
| Map resolution FSC 0.143 (Å)  | 2.75 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.7 |
| Map sharpening *B* factor (Å2) | -40.94 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 34684560 |
| *B* factors (Å2) Protein Ligand | 40.39na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.011.867 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.7600 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 96.173.830 |

**Supplementary table 11**

|  |  |
| --- | --- |
| **LMB Krios G2** | **20a**(EMDB-14061)(PDB 7QL2) |
| **Data processing** |  |
| Initial particle images (no.) | 87428 |
| Final particle images (no.) | 55338 |
| Helical twist (º) | -1.62 |
| Helical rise (Å) | 4.78 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 2.95 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.3 |
| Map sharpening *B* factor (Å2) | -84.83 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 11071500 |
| *B* factors (Å2) Protein Ligand | 45.17na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.012.173 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.9700 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 92.367.640 |

**Supplementary table 12**

|  |  |
| --- | --- |
| **TFS Krios G4** | **23a**(EMDB-14060)(PDB 7QL1) |
| **Data processing** |  |
| Initial particle images (no.) | 147647 |
| Final particle images (no.) | 23243 |
| Helical twist (º) | -1.25 |
| Helical rise (Å) | 4.75 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 3.34 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.2 |
| Map sharpening *B* factor (Å2) | -55.26 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 11071500 |
| *B* factors (Å2) Protein Ligand | 46.71na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.012.061 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.080.290 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 92.497.510 |

**Supplementary table 13**

|  |  |
| --- | --- |
| **TFS Glacios** | **27a**(EMDB-14058)(PDB 7QKZ) |
| **Data processing** |  |
| Initial particle images (no.) | 1005768 |
| Final particle images (no.) | 54983 |
| Helical twist (º) | -0.75 |
| Helical rise (Å) | 4.70 |
| Symmetry imposed | 3 |
| Map resolution FSC 0.143 (Å)  | 2.65 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.44 |
| Map sharpening *B* factor (Å2) | -44.56 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 810990 |
| *B* factors (Å2) Protein Ligand | 52.47na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0122.833 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.240.590 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 90.129.880 |

**Supplementary table 14**

|  |  |
| --- | --- |
| **LMB Krios G2** | **34b**(EMDB-14025)(PDB 7QJX) |
| **Data processing** |  |
| Initial particle images (no.) | 618020 |
| Final particle images (no.) | 34209 |
| Helical twist (º) | -0.978 |
| Helical rise (Å) | 4.90 |
| Symmetry imposed | 2 |
| Map resolution FSC 0.143 (Å)  | 2.99 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.3 |
| Map sharpening *B* factor (Å2) | -63.18 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 69129120 |
| *B* factors (Å2) Protein Ligand | 40.42na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0132.517 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.560.140 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 98.21.690.11 |

**Supplementary table 15**

|  |  |
| --- | --- |
| **TFS Krios G4** | **35d**(EMDB-14028)(PDB 7QK1) |
| **Data processing** |  |
| Initial particle images (no.) | 214567 |
| Final particle images (no.) | 7045 |
| Helical twist (º) | -1.25 |
| Helical rise (Å) | 4.77 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 3.03 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.1 |
| Map sharpening *B* factor (Å2) | -11.08 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 34444500 |
| *B* factors (Å2) Protein Ligand | 38.93na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.012.033 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.8700 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 94.525.480 |

**Supplementary table 16**

|  |  |
| --- | --- |
| **TFS Krios G4** | **36a**(EMDB-14029)(PDB 7QK2) |
| **Data processing** |  |
| Initial particle images (no.) | 564821 |
| Final particle images (no.) | 31627 |
| Helical twist (º) | -1.37 |
| Helical rise (Å) | 4.74 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 2.61 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.53 |
| Map sharpening *B* factor (Å2) | -31.51 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 32464260 |
| *B* factors (Å2) Protein Ligand | 39.48na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.011.969 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.840.150 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 95.894.110.11 |

**Supplementary table 17**

|  |  |
| --- | --- |
| **TFS Krios G4** | **38a**(EMDB-14030)(PDB 7QK3) |
| **Data processing** |  |
| Initial particle images (no.) | 677859 |
| Final particle images (no.) | 37574 |
| Helical twist (º) | -1.49 |
| Helical rise (Å) | 4.74 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 2.44 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.61 |
| Map sharpening *B* factor (Å2) | -24.7 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 13351830 |
| *B* factors (Å2) Protein Ligand | 42.58na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.012.172 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.7200 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 96.613.390 |

**Supplementary table 18**

|  |  |
| --- | --- |
| **LMB Krios G2** | **39a**(EMDB-14041)(PDB 7QKG) |
| **Data processing** |  |
| Initial particle images (no.) | 678451 |
| Final particle images (no.) | 165084 |
| Helical twist (º) | -1.18 |
| Helical rise (Å) | 4.79 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 3.36 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.54 |
| Map sharpening *B* factor (Å2) | -81 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 11911620 |
| *B* factors (Å2) Protein Ligand | 44.1na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.012.054 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.9200 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 93.596.410 |

**Supplementary table 19**

|  |  |
| --- | --- |
| **TFS Krios G4** | **40a**(EMDB-14039)(PDB 7QK6) |
| **Data processing** |  |
| Initial particle images (no.) | 135479 |
| Final particle images (no.) | 81220 |
| Helical twist (º) | -1.07 |
| Helical rise (Å) | 4.77 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 2.27 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.6 |
| Map sharpening *B* factor (Å2) | -27.12 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 11911620 |
| *B* factors (Å2) Protein Ligand | 44.1na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.011.958 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.8500 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 94.875.130 |

**Supplementary table 20**

|  |  |
| --- | --- |
| **TFS Krios G4** | **41a**(EMDB-14042)(PDB 7QKH) |
| **Data processing** |  |
| Initial particle images (no.) | 116487 |
| Final particle images (no.) | 26532 |
| Helical twist (º) | -0.807 |
| Helical rise (Å) | 4.77 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 3.17 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.36 |
| Map sharpening *B* factor (Å2) | -9.73 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 15122040 |
| *B* factors (Å2) Protein Ligand | 33.26na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0112.473 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.511.290 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 85.4214.580 |

**Supplementary table 21**

|  |  |
| --- | --- |
| **LMB Krios G2** | **42a**(EMDB-14043)(PDB 7QKI) |
| **Data processing** |  |
| Initial particle images (no.) | 181285 |
| Final particle images (no.) | 82803 |
| Helical twist (º) | 179.59 |
| Helical rise (Å) | 2.38 |
| Symmetry imposed | 21 |
| Map resolution FSC 0.143 (Å)  | 3.13 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.24 |
| Map sharpening *B* factor (Å2) | -63.04 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 34684560 |
| *B* factors (Å2) Protein Ligand | 50.07na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0112.093 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.0500 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 89.8610.140 |

 **Supplementary table 22**

|  |  |
| --- | --- |
| **LMB Krios G2** | **43a**(EMDB-14045)(PDB 7QKK) |
| **Data processing** |  |
| Initial particle images (no.) | 180999 |
| Final particle images (no.) | 84513 |
| Helical twist (º) | -1.29 |
| Helical rise (Å) | 4.77 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 2.8 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 3.24 |
| Map sharpening *B* factor (Å2) | -41.5 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 17342880 |
| *B* factors (Å2) Protein Ligand | 71.71na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0112.261 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.0800 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 88.7411.260 |

**Supplementary table 23**

|  |  |
| --- | --- |
| **LMB Krios G2** | **44a**(EMDB-14055)(PDB 7QKW) |
| **Data processing** |  |
| Initial particle images (no.) | 156521 |
| Final particle images (no.) | 9794 |
| Helical twist (º) | -1.01 |
| Helical rise (Å) | 4.78 |
| Symmetry imposed | 1 |
| Map resolution FSC 0.143 (Å)  | 2.32 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.5 |
| Map sharpening *B* factor (Å2) | -10.12 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 22683060 |
| *B* factors (Å2) Protein Ligand | 71.71na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.012.038 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.8700 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 94.565.440 |

**Supplementary table 24**

|  |  |
| --- | --- |
| **LMB Krios G2** | **45a**(EMDB-14047)(PDB 7QKM) |
| **Data processing** |  |
| Initial particle images (no.) | 88226 |
| Final particle images (no.) | 29079 |
| Helical twist (º) | 179.59 |
| Helical rise (Å) | 2.4 |
| Symmetry imposed | 21 |
| Map resolution FSC 0.143 (Å)  | 2.66 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.5 |
| Map sharpening *B* factor (Å2) | -33.12 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 24363300 |
| *B* factors (Å2) Protein Ligand | 30.84na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.011.994 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 0.9600 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 92.777.230 |

**Supplementary table 25**

|  |  |
| --- | --- |
| **TFS Krios G4** | **47a**(EMDB-14057)(PDB 7QKY) |
| **Data processing** |  |
| Initial particle images (no.) | 11158705 |
| Final particle images (no.) | 41080 |
| Helical twist (º) | 179.597 |
| Helical rise (Å) | 2.368 |
| Symmetry imposed | 21 |
| Map resolution FSC 0.143 (Å)  | 1.86 |
| **Refinement** |  |
| Initial model used (PDB code) | na |
| Model resolution FSC 0.5 (Å) | 2.0 |
| Map sharpening *B* factor (Å2) | -21.05 |
| Model composition Non-hydrogen atoms Protein residues Ligands | 30004020 |
| *B* factors (Å2) Protein Ligand | 30.44na |
| R.m.s. deviations Bond lengths (Å) Bond angles (°) | 0.0111.967 |
|  Validation MolProbity score Clashscore Poor rotamers (%)  | 1.020.340.88 |
|  Ramachandran plot Favored (%) Allowed (%) Disallowed (%) | 94.15.90 |