Supplementary File 3: X-ray Crystallographic and Refinement statistics of MT polymerase:αβ-tubulin:DRP

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| --- | --- | --- | --- | --- |
| **Data collection** | **1:2:2 sk-Alp14-monomer:**  **αβ-Tubulin:DRP** | **1:2:2 sk-Alp14-monomer-SL:**  **αβ-Tubulin:DRP** | **1:2:2 sk-Alp14-monomer:**  **αβ-Tubulin:DRPΔN** | **1:2:2 sk-Alp14-dimer:**  **αβ-Tubulin:DRPΔN** |
| Resolution range (Å) | 96.59 - 4.40 (4.64- 4.40)*a* | 59.45 – 3.60 (3.79 – 3.60)*a* | 57.56 – 3.20 (3.37 – 3.20)*a* | 99.83 – 3.5 (3.69 – 3.50)*a* |
| Space group | *P* 21 | *P* 21 | *P* 21 | *P* 21 |
| Wavelength (Å) | 0.9792 | 0.9792 | 0.9792 | 0.9792 |
| Unit cell (Å): *a*, *b*, *c*  (°): β | 218.80, 107.65, 282.74  90.38 | 218.48, 106.15, 282.23  90.39 | 115.13, 194.99, 149.57  90.19 | 122.73 199.67, 162.70  90.09 |
| Total number of observed reflections | 229567 | 380856 | 298551 | 235576 |
| Unique reflections | 80099 {68039}*b* | 142673 {121943}*b* | 104265 {88337}*b* | 91368 |
| Average mosaicity | 0.57 | 0.38 | 0.64 | 0.50 |
| Multiplicity | 2.9 (2.9)*a* | 2.7 (2.7)*a* | 2.9 (2.9)*a* | 2.6 (2.4)*a* |
| Completeness (%) | 95.4 (94.8) {80.6}*b* | 95.0 (96.7) {79.0}*b* | 96.2 (97.9) {82.0}*b* | 92.9 (90.2)*a* |
| Wilson B-factor (Å2) | 82.7 | 81.4 | 46.6 | - |
| <*I*/*σ* (*I*)> | 4.9 (1.9)*a* | 4.8 (1.2)*a* | 5.8 (1.5)*a* | 4.8 (1.1)*a* |
| *R*merge*c* | 0.14 (0.48)*a* | 0.13(0.65)*a* | 0.13(0.65)*a* | 0.14 (0.63)*a* |
| **Structure refinement** |  |  |  |  |
| *R*work | 0.23 (0.26)*a* | 0.20 (0.24)*a* | 0.18 (0.23)*a* | - |
| *R*free | 0.26 (0.33)*a* | 0.24 (0.26)*a* | 0.24 (0.26)*a* | - |
| Complexes per asymmetric unit | 2 | 2 | 2 | - |
| Number of atoms | 78030 | 77878 | 36865 | - |
| Protein residues | 9989 | 9981 | 4661 | - |
| Ligand atoms | 496 | 496 | 248 | - |
| RMS bond lengths (Å) | 0.004 | 0.004 | 0.004 | - |
| RMS bond angles (°) | 0.94 | 0.98 | 0.93 | - |
| Ramachandran favored (%) | 94.0 | 94.0 | 95.0 | - |
| Ramachandran allowed (%) | 5.4 | 5.5 | 4.5 |  |
| Ramachandran outliers (%) | 0.3 | 0.3 | 0.2 | - |
| Clashscore | 4.5 | 4.8 | 5.6 | - |
| Mean *B* values (Å2) |  |  |  |  |
| Overall | 108.4 | 98.3 | 48.6 | - |
| Macromolecules | 108.6 | 98.4 | 48.6 | - |
| Ligands | 78.5 | 91.5 | 36.4 | - |

*a*Numbers represent the highest-resolution shell.

­­*b*Numbers represent the truncated data after treated with ellipsoidal truncation and anisotropic scaling

*cR*merge = Σ*hkl*Σ*i*|*Ii*(*hkl*)-*Iav*(*hkl*)|/Σ*hkl*Σ*iIi*(*hkl*).