**Supplementary File 3. Cryo-EM data & model building statistics**

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|  | Cohesin Scc2 structure |
| Data collection and processing |  |
| Voltage (kV) | 300 |
| Electron exposure (e–/A2) | 40-45 |
| Defocus range (µm) | -0.5 to -0.9 |
| Pixel size (Å) | 1.16 |
| Symmetry imposed | C1 |
| Initial particle images (no.) | 450,000  |
| Final particle images (no.) | 32,491 |
| Map resolution (Å) | 16.7 (8.5) |
|  FSC threshold | 0.5 (0.143) |
|  | **Coiled-coil elbow structure** |
| Data collection and processing |  |
| Voltage (kV) | 300 |
| Electron exposure (e–/A2) | 40-45 |
| Defocus range (µm) | -0.5 to -0.9 |
| Pixel size (Å) | 1.16 |
| Symmetry imposed | C1 |
| Initial particle images (no.) | 4.5 million |
| Final particle images (no.) | 63,892 |
| Map resolution (Å) | 5.5 |
|  FSC thresholdRefinementInitial model used (PDB)Model resolution (Å) FSC thresholdModel resolution range (Å)Map sharpening B factor (Å2)Model composition Non-hydrogen atoms Protein residues*B* factors (Å2) ProteinR.m.s. deviations Bond lengths (Å) Bond angles (°)Validation MolProbity score Clashscore  Poor rotamers (%)Ramachandran plot  Favored (%) Allowed (%) Disallowed (%) | 0.143Ab initio, Homology model derived from 2WD55.5 Å0.1435.5-10-2007974139661.270.0060.5991.46 (96th Percentile)8.020.0097.92.10.00 |
|  | **ATP-engaged cohesin structure** |
| Data collection and processing |  |
| Voltage (kV) | 300 |
| Electron exposure (e–/A2) | 45 |
| Defocus range (µm) | -0.5 to -0.9 |
| Pixel size (Å) | 1.16 |
| Symmetry imposed | C1 |
| Initial particle images (no.) | 224,719 |
| Final particle images (no.) | 108,015 |
| Map resolution (Å) | 6 |
|  FSC threshold | 0.143 |
|  | **Cohesin-Pds5 structure** |
| Data collection and processing |  |
| Voltage (kV) | 300 |
| Electron exposure (e–/A2) | 42 |
| Defocus range (µm) | -0.5 to -0.9 |
| Pixel size (Å) | 1.16 |
| Symmetry imposed | C1 |
| Initial particle images (no.) | 455,705 |
| Final particle images (no.) | 6,259 |
| Map resolution (Å) | 14.8 |
|  FSC threshold | 0.143 |