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| **Supplementary File 1.** Cryo-EM data collection, atomic models refinement and validation statistics. |
| Microscope model | FEI Titan Krios cryo-transmission electron microscope |
| Detector model | Gatan K2 summit direct electron detector |
| Number of datasets | 1 |
| Number of micrographs collected | 9,494 |
| Pixel size (Å) | 1.04 |
| Defocus range (μm) | 0.8 – 2.8 |
| Voltage (kV) | 300 |
| Electron dose (e-Å-2) | 29.88 |
| Name of 3D reconstruction/model | State A RIO1(kd)-StHA | State B RIO1(kd)-StHA | State A head | State A body | State A platform | State B head | State B body | State B platform |
| EMDB entry of map | EMD- 11440 | EMD-11441 | EMD-11446 | EMD-11445 | EMD-11447 | EMD-11443 | EMD-11442 | EMD-11444 |
| PDB entry of the full model | 6ZU0 | 6ZV6 |  |  |  |  |  |  |
| Final number of particles | 104,844 | 276,012 | 104,844 | 104,844 | 104,844 | 276,012 | 276,012 | 276,012 |
| Resolution (Å) (FSC threshold = 0.143) | 3.22 | 3.00 | 3.17 | 3.14 | 3.30 | 2.96 | 2.98 | 2.98 |
| Map sharpening B-factor (Å2) | -89 | -88 | -68 | -71 | -81 | -84 | -80 | -77 |
| **Refinement and model validation statistics(**a) |
| Model refinement resolution range ( Å)Model resolution (Å) (FSC threshold = 0.5)Clashscore (all atoms) | 40-2.73.617.53 | 40-2.63.526.72 |  |  |  |  |  |  |
| MolProbity ScoreProtein | 1.81 | 1.77 |  |  |  |  |  |  |
|  Rmsd (bonds lengths, Å) | 0.0084 | 0.01 |  |  |  |  |  |  |
|  Rmsd (angles, °) | 1.20 | 1.00 |  |  |  |  |  |  |
|  Ramachandran plot (%) favored | 94.19 | 94.15 |  |  |  |  |  |  |
|  allowed | 5.73 | 5.73 |  |  |  |  |  |  |
|  outliers | 0.08 | 0.12 |  |  |  |  |  |  |
| RNA |  |
|  Correct sugar puckers (%) | 97.2 | 97.8 |  |  |  |  |  |  |
|  Good backbone conformation (%) | 69.4 | 73.7 |  |  |  |  |  |  |
| (a)Models were validated using MolProbity implemented in PHENIX.REFINE (Adams et al., 2010) |