Cryo-EM structure of rotavirus B NSP2 reveals its unique tertiary architecture

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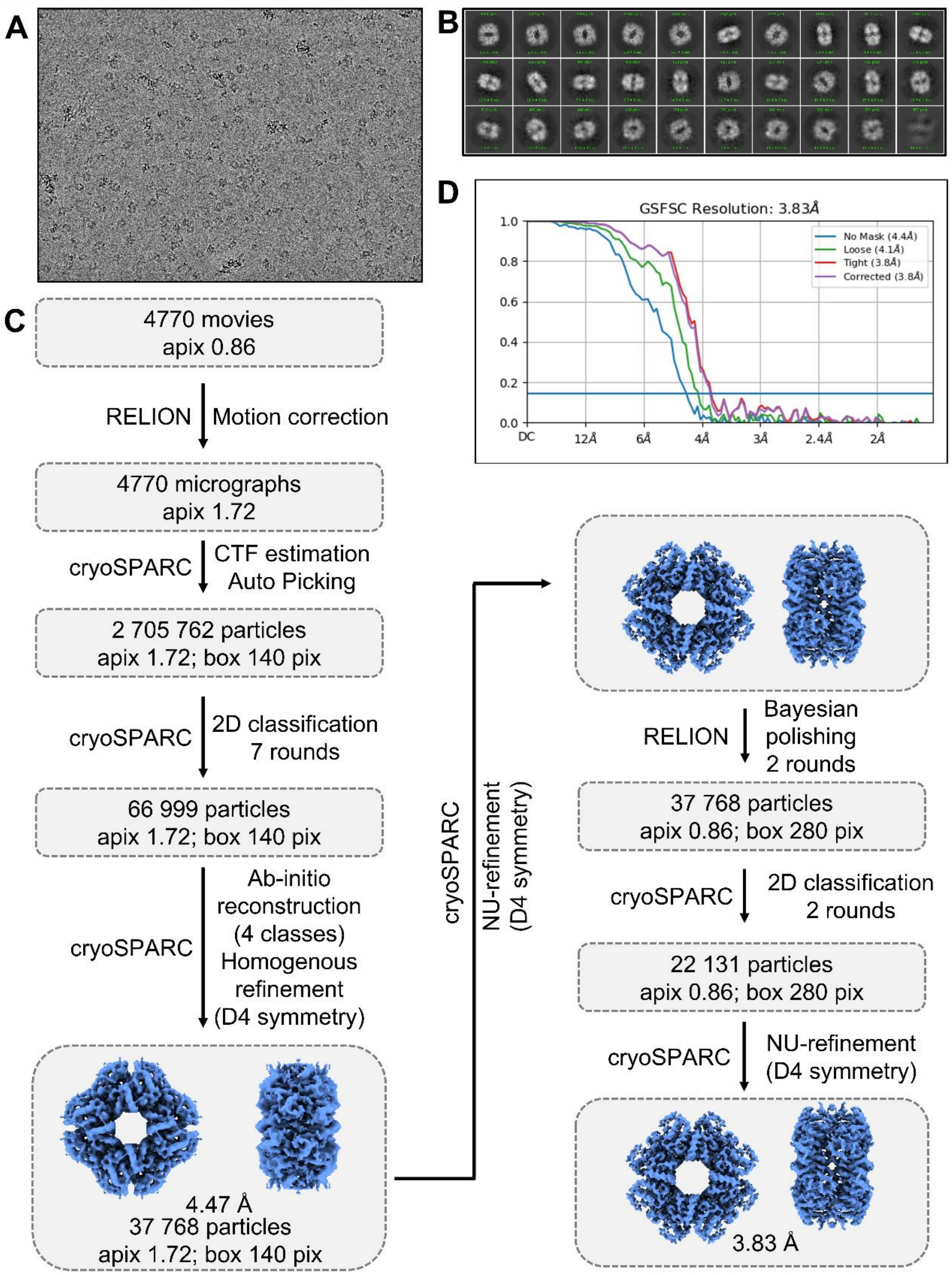
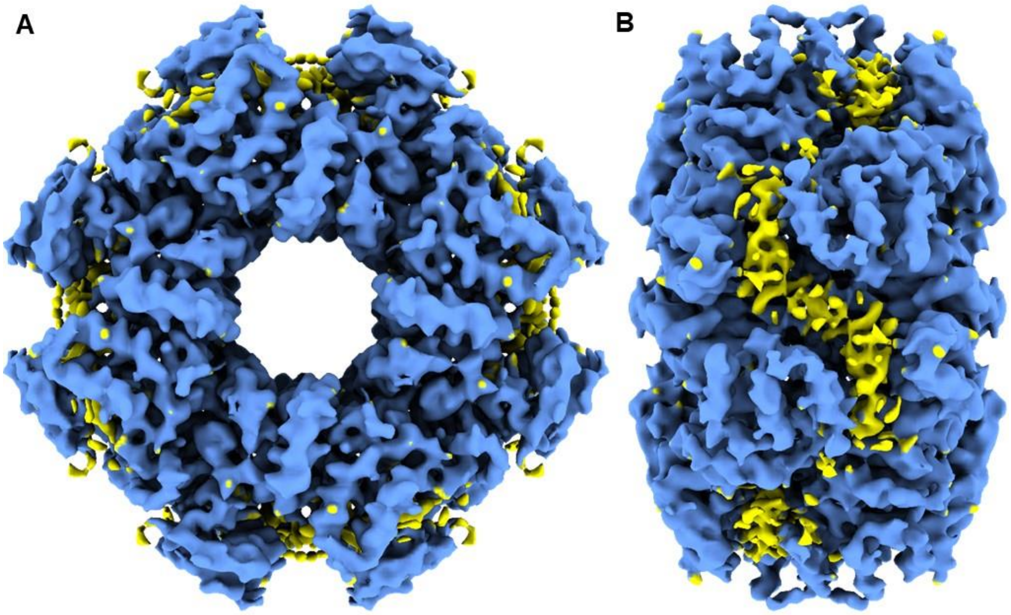
Supplemental information



Supplemental Figure S1. **RVB NSP2 cryo-EM data processing. (A)** Representative micrograph. **(B)** Representative two-dimensional classes after several rounds of two-dimensional classification. **(C)** Three-dimensional reconstruction pipeline.



Supplemental Figure S2. **NSP2 cryo-EM map. (A)** Four-fold symmetry and **(B)** two-fold symmetry views of RVB NSP2 (blue) with an additional density that may correspond to the RNA oligonucleotide (yellow).

Supplemental Table S1. **Data collection and processing**

Microscope	Titan Krios G3i
Camera	Gatan K3
Energy filter	Gatan BioQuantum with 20 eV slit
Voltage (kV)	300
Magnification	105 000x
Electron exposure (e/Å^2)	40
Defocus range (µm)	-2.5, -2.0, -1.5
Pixel size (Å)	0.86
Initial particle images (no.)	2 705 762
Final particle images (no.)	22 131
Symmetry imposed	D4
Resolution at 0.143 FSC (masked, Å)	3.83
Map sharpening B factor (Å^2)	-201.7
EMBD accession code	EMD-17323

Supplemental Table S2. **Refinement and validation statistics**

PDB accession code	8P00
Number of non-hydrogen atoms	16992
Protein residues	2376
Bonds (RMSD): Length (Å)	0.002
Bonds (RMSD): Angles (°)	0.581
Validation: Rotamer outliers (%)	0.06
Ramachandran plot: Outliers / Allowed / Favored (%)	0.00 / 4.58 / 95.42