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Cover Illustration: Structure of the Hendra henipavirus (HeV) nucleoprotein (N) protein-RNA double-ring assembly (PDB id: 8C4H; Passchier TC, White JB, Maskell DP, Byrne MJ, Ranson NA, Edwards TA, Barr JN. 2024. The cryoEM structure of the Hendra henipavirus nucleoprotein reveals insights into paramyxoviral nucleocapsid architectures. Sci Rep 14: 14099). The HeV N protein adopts a bi-lobed fold, where the N- and C-terminal globular domains are bisected by an RNA binding cleft. Neighboring N proteins assemble laterally and completely encapsidate the viral genomic and antigenomic RNAs. The two RNAs are depicted by green and red ribbons. The U bases of the poly(U) model are shown as cyan blocks. Proteins are represented as semitransparent gold ribbons. Cover image provided by X3DNA-DSSR, an NIGMS National Resource for structural bioinformatics of nucleic acids (R24GM153869; skmatics.x3dna.org). Image generated using DSSR and PyMOL (Lu XJ. 2020. Nucleic Acids Res 48: e74).

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^{OA}Open Access paper