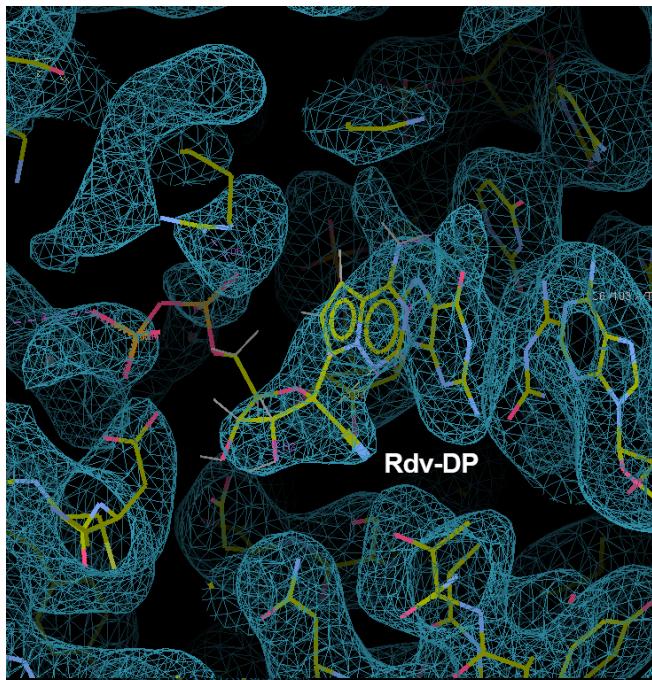
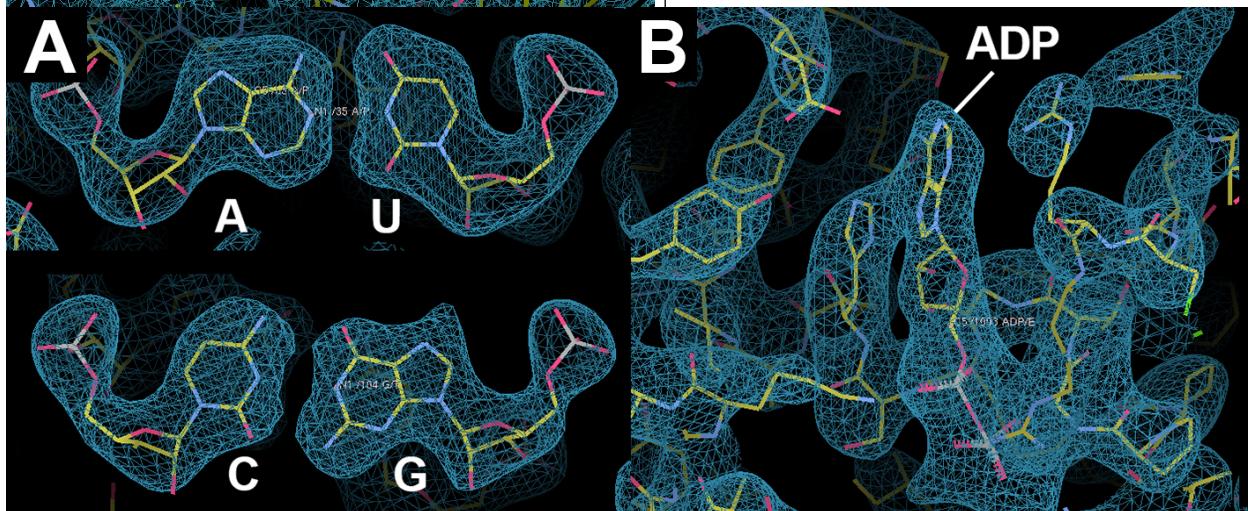


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**Fig. 1.** Cryo-EM density (blue mesh) of structure 1 (Table 1; 3.1 Å nominal resolution). A preliminary structural model is superimposed. Rdv-DP is bound in a pre-insertion conformation.



**Fig. 2.** Cryo-EM map and models for high-resolution nsp13<sub>2</sub>-RTC (2.8 Å nominal resolution). **A.** RNA base pair identity clearly seen. **B.** Nucleotide binding site of nsp13 (ADP modeled, AlF<sub>3</sub> and Mg<sup>2+</sup> not yet modeled).

Table 1: Proposed Rdv structures

Priority	structure	RNA sequence	ligand
	1	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCUAAGAACUG <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGAUUCUUCGACUCGGCGAGUGUACCCUAUC	Rdv-DP
	2	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCUAAGAACUGC <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGAUUCUUCGACUCGGCGAGUGUACCCUAUC	Rdv-TP
	3	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCUAAGAACUGC <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGAUUCUUCGACUCGGCGAGUGUACCCUAUC	ATP
4	4	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCUAAGAACUGC <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGAUUCUUCGACUCGGCGAGUGUACCCUAUC	-
5	5	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCUAAGAACUGA <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGAUUCUUCGACUCGGCGAGUGUACCCUAUC	-
2	6	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCacgcgaagc <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGUGcgcuucgu <u>R</u> cuguuguuuUACCCUAUC	-
3	7	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCacgcgaagc <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGUGcgcuucgu <u>A</u> cuguuguuuUACCCUAUC	-
	8	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCacgcgaagc <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGUGcgcuucgu <u>R</u> cuguuguuuUACCCUAUC	-
1	10	<sup>5'</sup> cgcguagcaugcuacGUCAUUCUCCacgcgaagc <sup>3'</sup> <sup>3'</sup> gcgcaucguacgaugCAGUAAGAGGUGcgcuucgu <u>A</u> cuguuguuuUACCCUAUC	-

Color key

Cryo-EM data already collected (structure not refined)