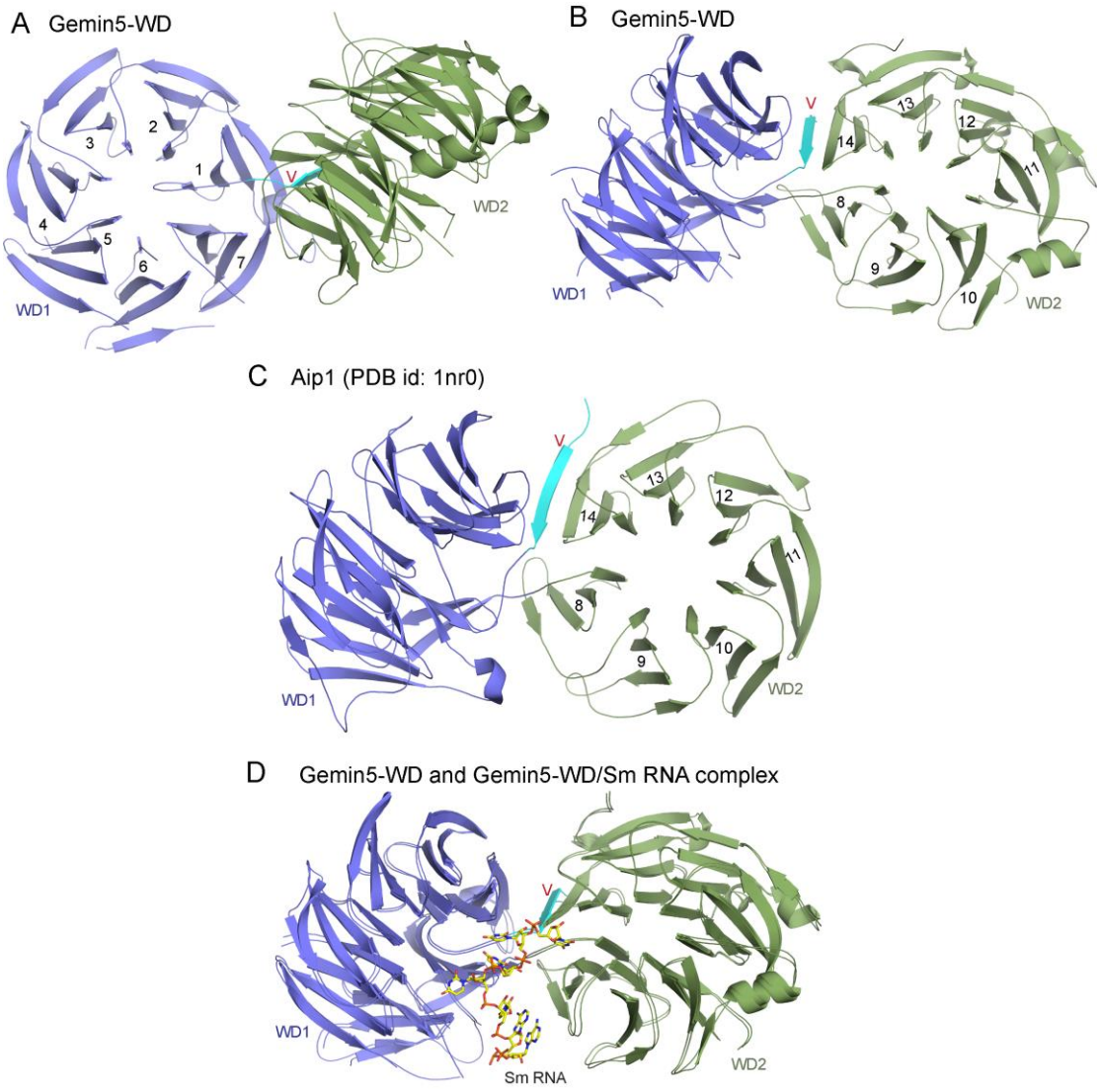
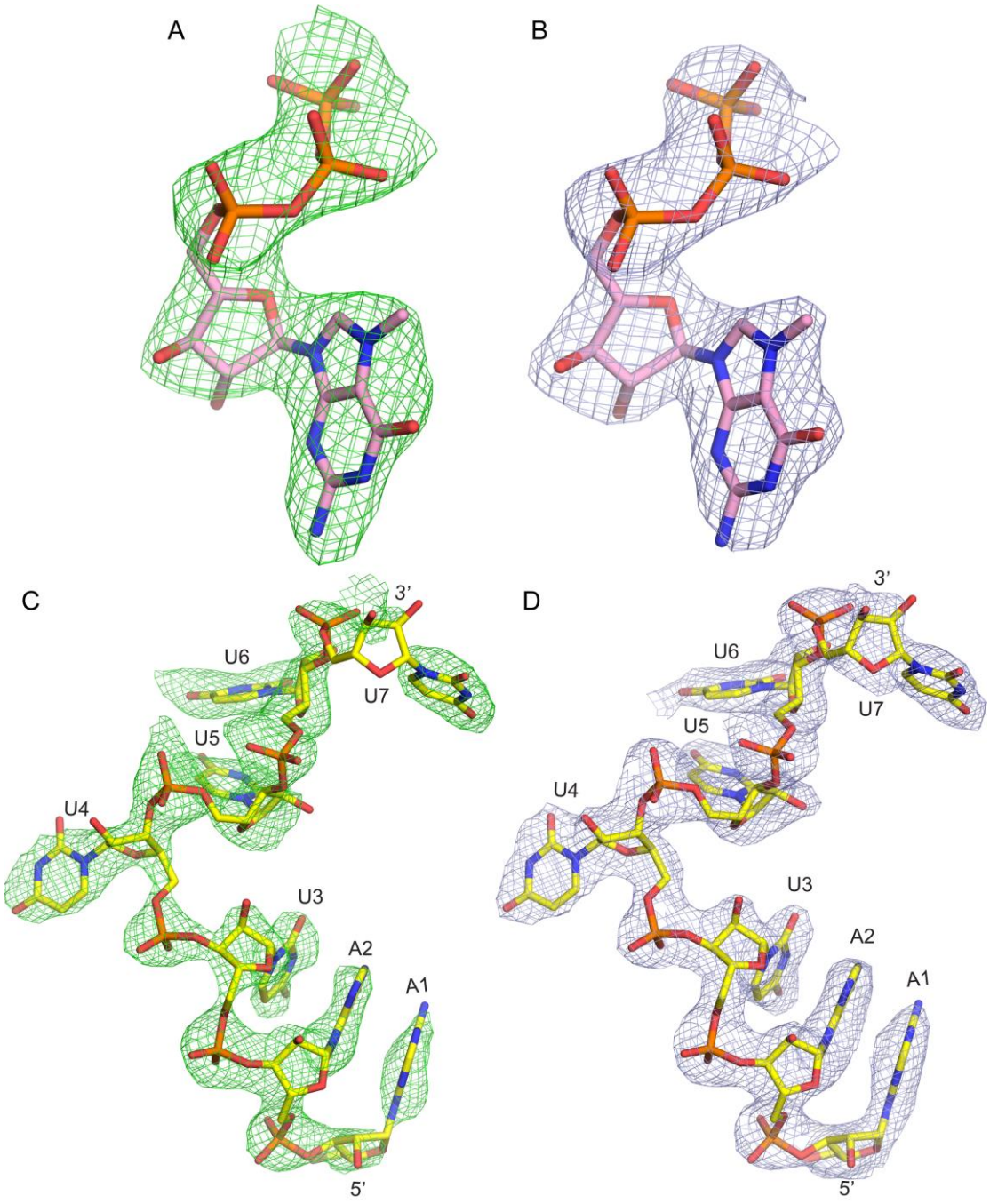
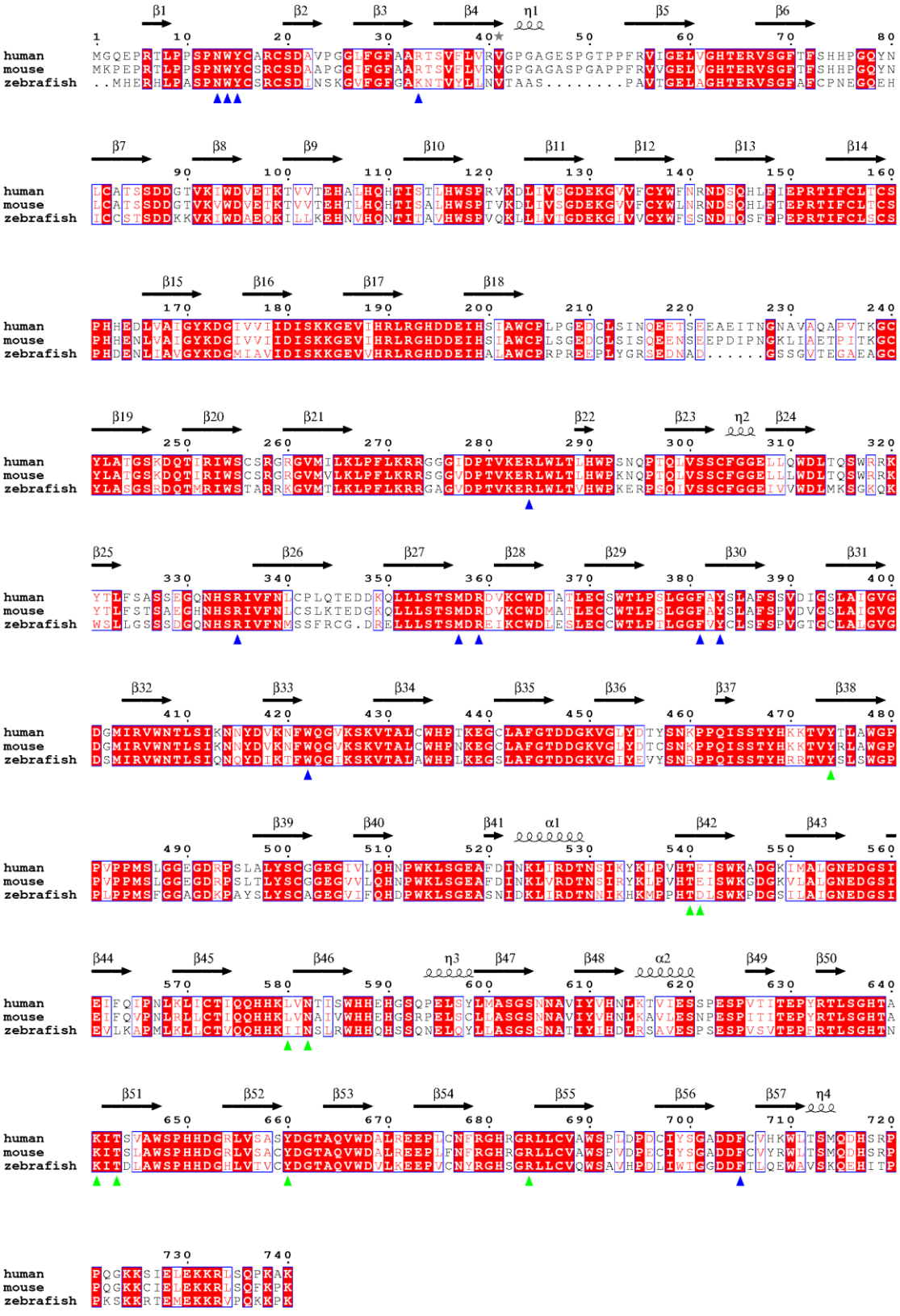


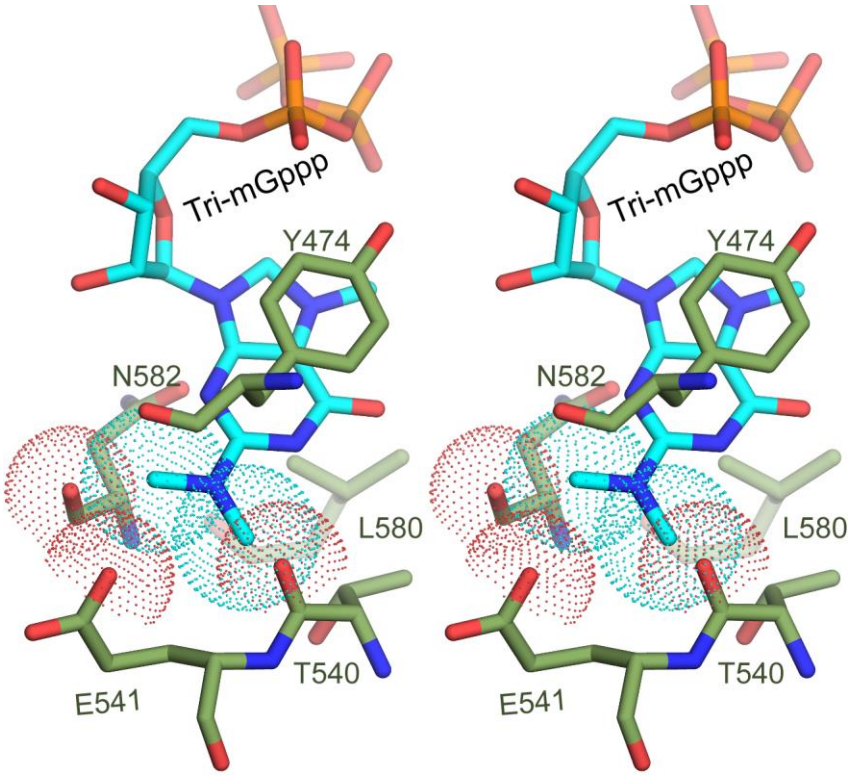

**Supplementary information, Figure S1A**: Gemin5-WD and actin interacting protein 1 (Aip1) share similar topology. Structure of Gemin5-WD consists of propeller domains. Blades 1-7 belonging to WD1 and 8-14 belonging to WD2 are marked in (A) and (B), respectively. The N-terminal β-strand is highlighted in cyan and is labeled V to denote its function as a molecular Velcro. (C) Structure of Aip1 (PDB id: 1nr0) showing the canonical architecture of interconnected β-propellers. (D) Apo Gemin5-WD and its complex with Sm RNA are identical in their orientations of the two propellers.



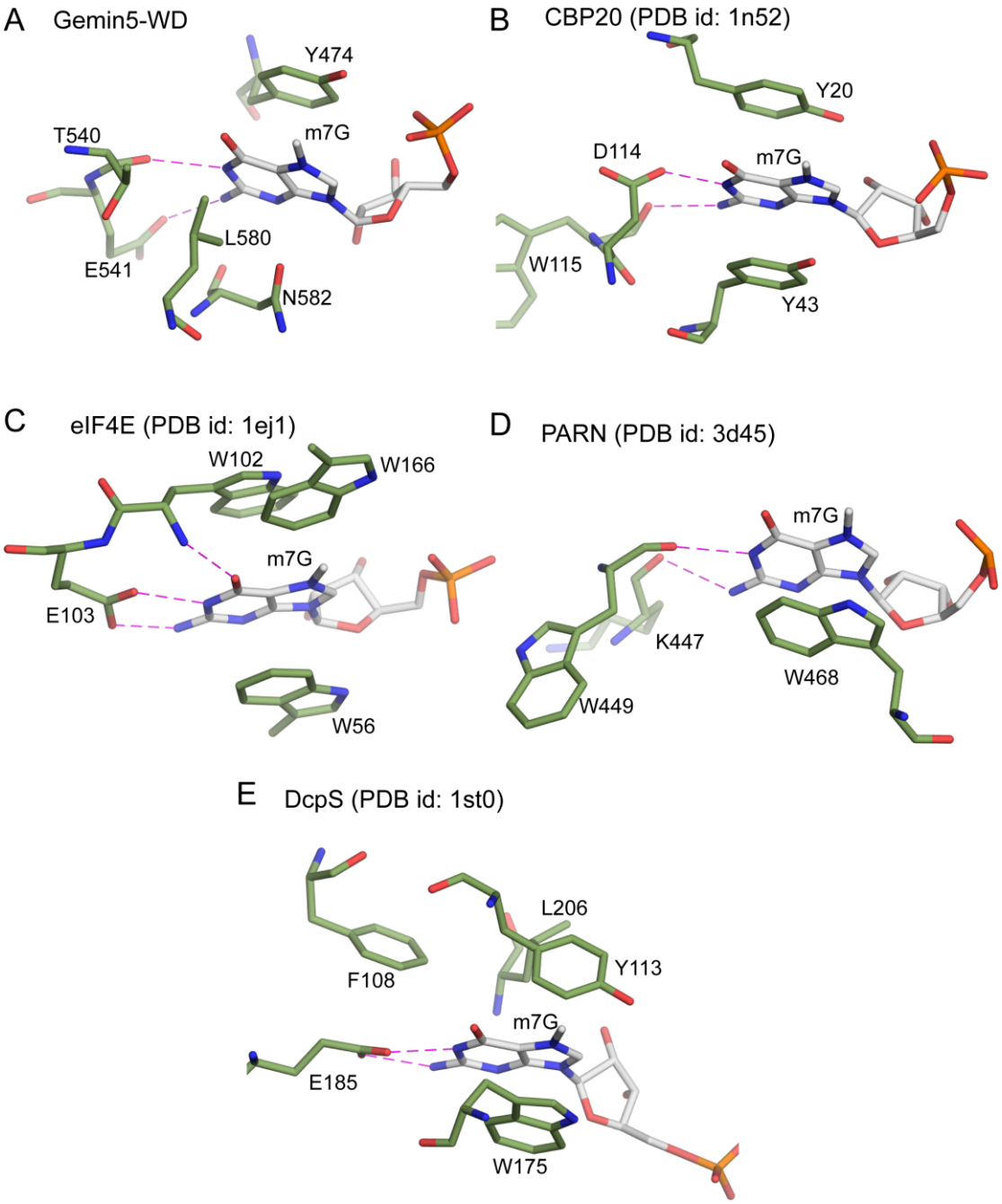

**Supplementary information, Figure S1B** Electron density map corresponding to the bound $m^7$Gppp and Sm RNA. Electron density around $m^7$GpppG binding site shows ordered density only for the methylated G and the three phosphates: Omit Fo-Fc map contoured at 2σ (A) and 2Fo-Fc map contoured at 1.5σ (B). Electron density observed around the nucleotide-binding surface allowed unambiguous detection of the polarity and identity of the bound RNA nucleotides: Omit Fo-Fc map contoured at 2σ (C) and 2Fo-Fc map contoured at 1.5σ (D).



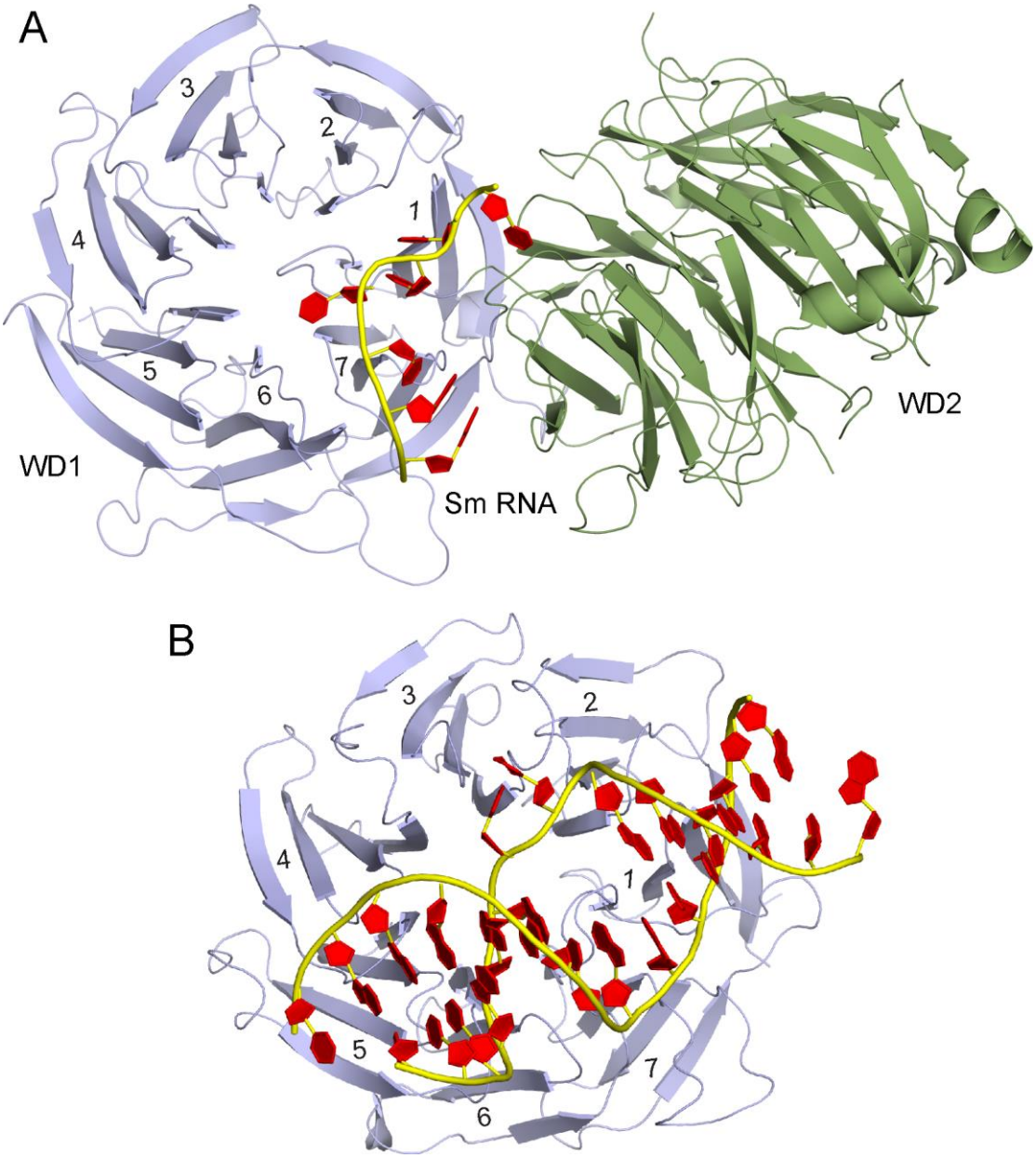

**Supplementary information, Figure S1C** Sequence alignment of human Gemin5-WD with its counterparts in mouse and zebrafish reveal conserved sequence motifs that recognize $m^7G$ (green triangles) and Sm RNA (blue triangles). The secondary structural elements of human Gemin5-WD are shown on top of the alignment.



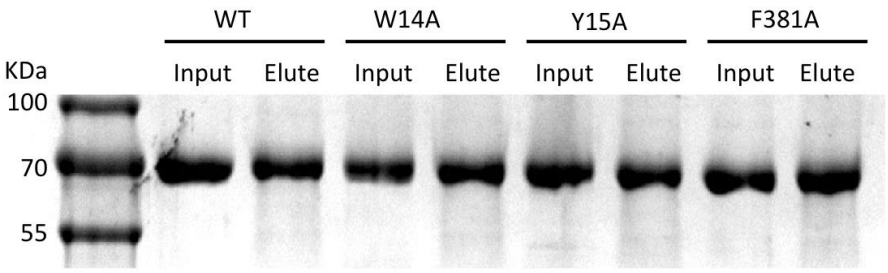

**Supplementary information, Figure S1D** Stereo-view of trimethylated Guanosine 5′ cap (Tri-mGppp) modeled in place of $m^7G$ in the structure of Gemin5-WD/$m^7$Gppp complex. Dimethyl group of Tri-mGppp has steric clashes with the neighboring residues such as the main chain carbonyls of Thr540 and Asn582 and side chain carboxyl of Glu541. Van der Waals' spheres around carbonyls of Thr540, Asn582 and carboxyl of Glu541 are shown as red dots while those around dimethyl groups of Tri-mGppp are shown in cyan.



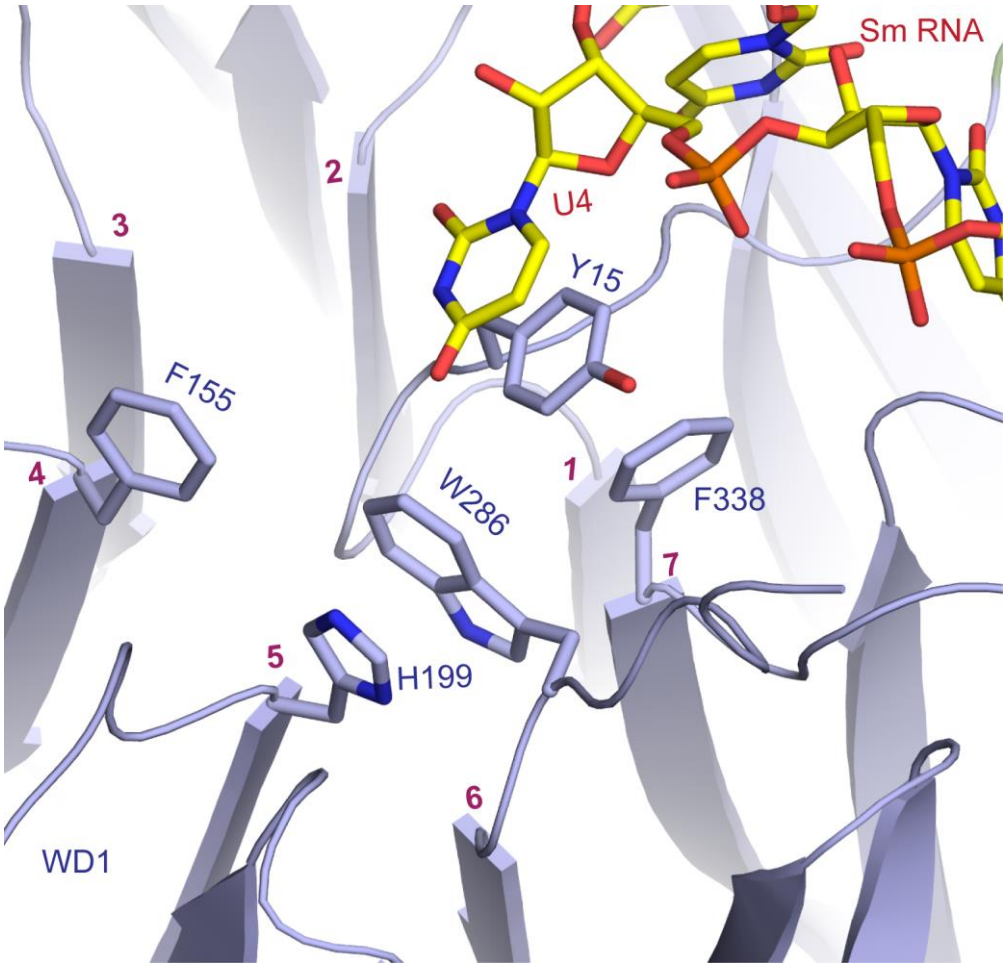

**Supplementary information, Figure S1E** 5′-m$^7$G cap is recognized by a variety of proteins using similar specificity determining features. Structural comparison of the m$^7$G binding sites in Gemin5-WD (A); cap binding protein, CBP20 (B); translation initiation factor, eIF4E (C); polyA specific ribonuclease, PARN (D) and the scavenger decapping enzyme, DcpS (E); show aromatic and hydrophobic residues packing against the nucleobase of m$^7$G.




**Supplementary information, Figure S1F** WD40 containing proteins recognize nucleic acids. Sm RNA bound to Gemin5-WD is represented in (A) while dsDNA bound to DDB2-WD40 β propeller (PDB id: 3ei1) is shown in (B). Blades of the propeller domains are labeled 1-7. The nucleobases and sugars are colored red and the phosphate backbone is shown in yellow.




**Supplementary information, Figure S1G** Cap-binding assays were performed with wild-type (WT) Gemin5-WD and Sm-RNA defective mutants.




**Supplementary information, Figure S1H** Conformation of Tyr15 is likely to be stabilized by its surrounding environment consisting of residues Trp286, Phe338, His199 and Phe155. Tyr15 stacks against the nucleobase U4 of Sm RNA. Innermost blades 1-7 of WD1 are also labeled.