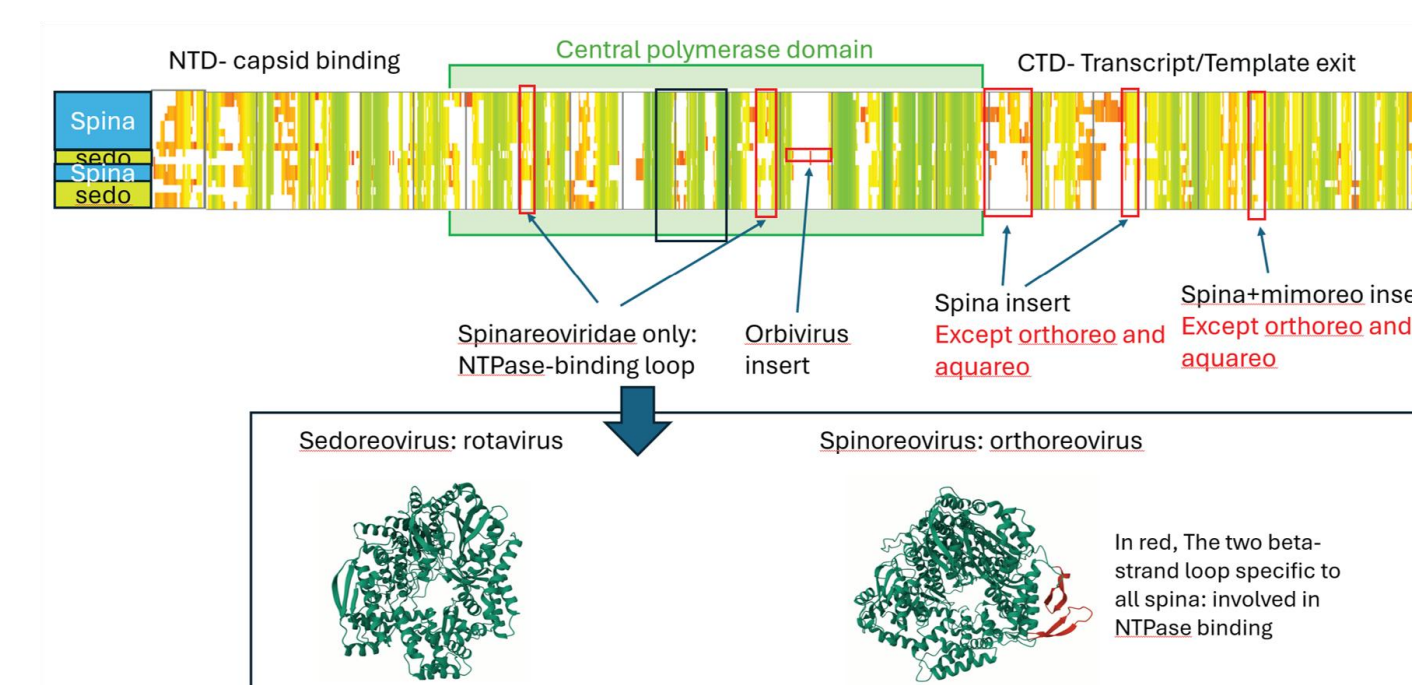
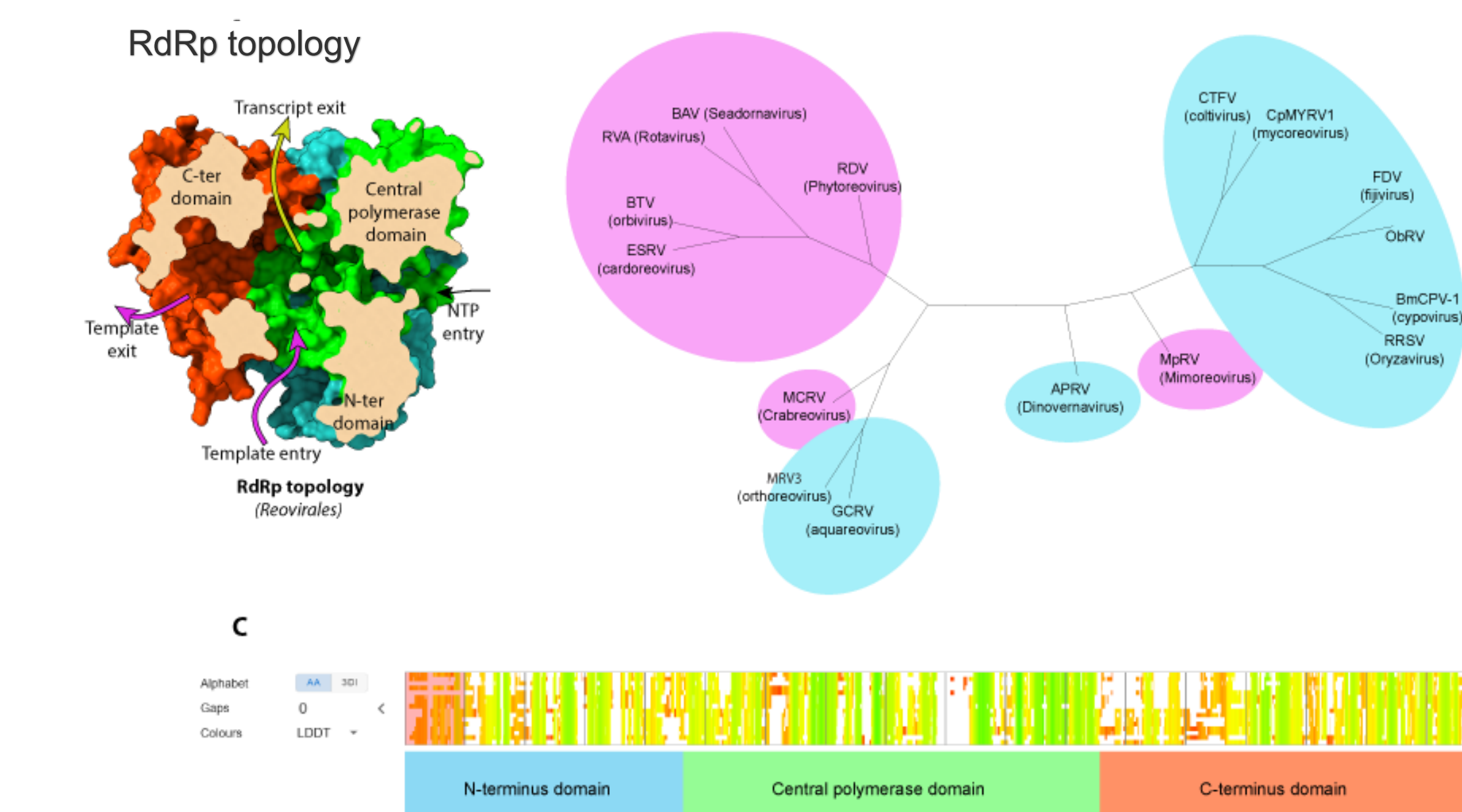
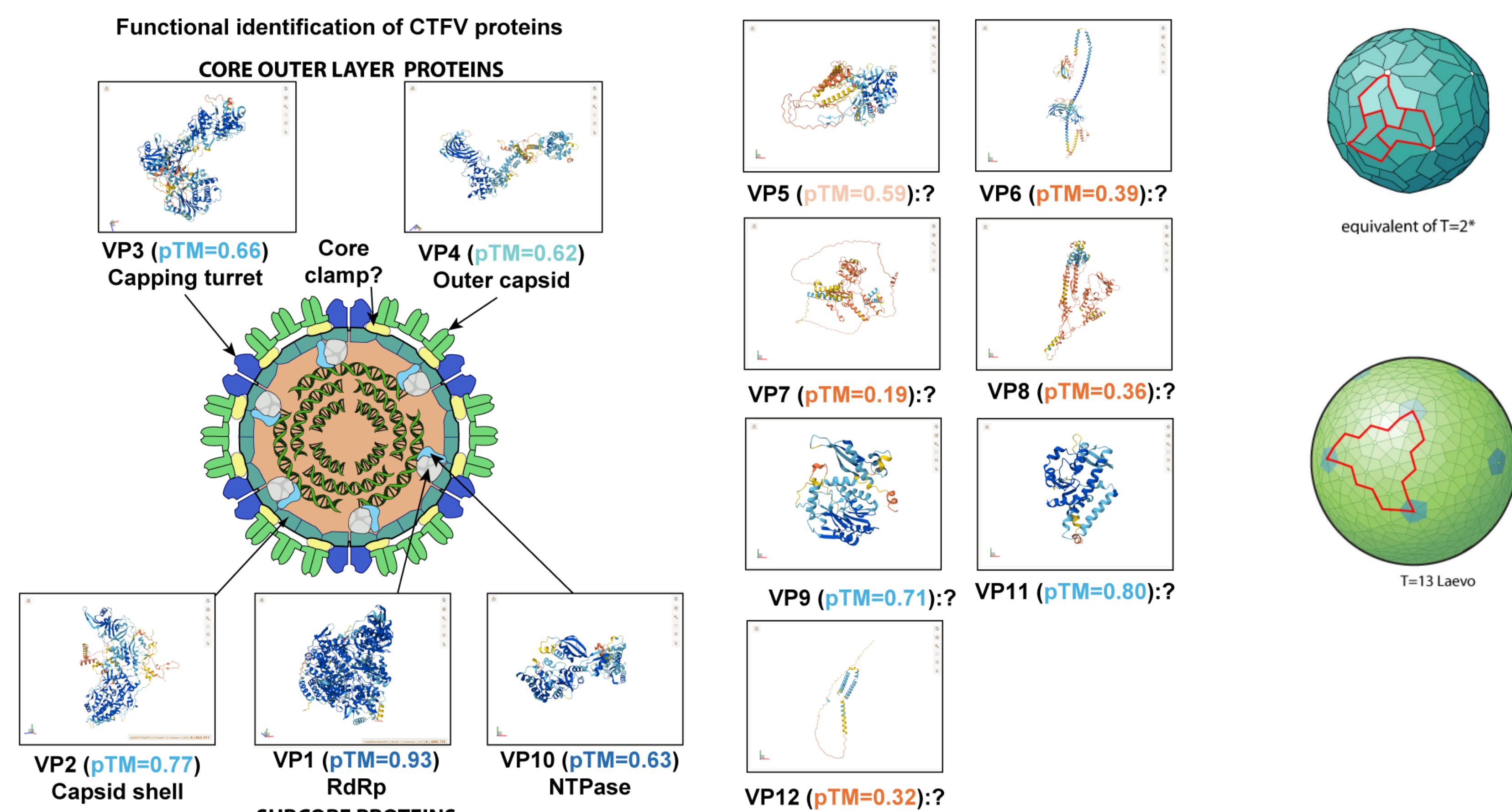


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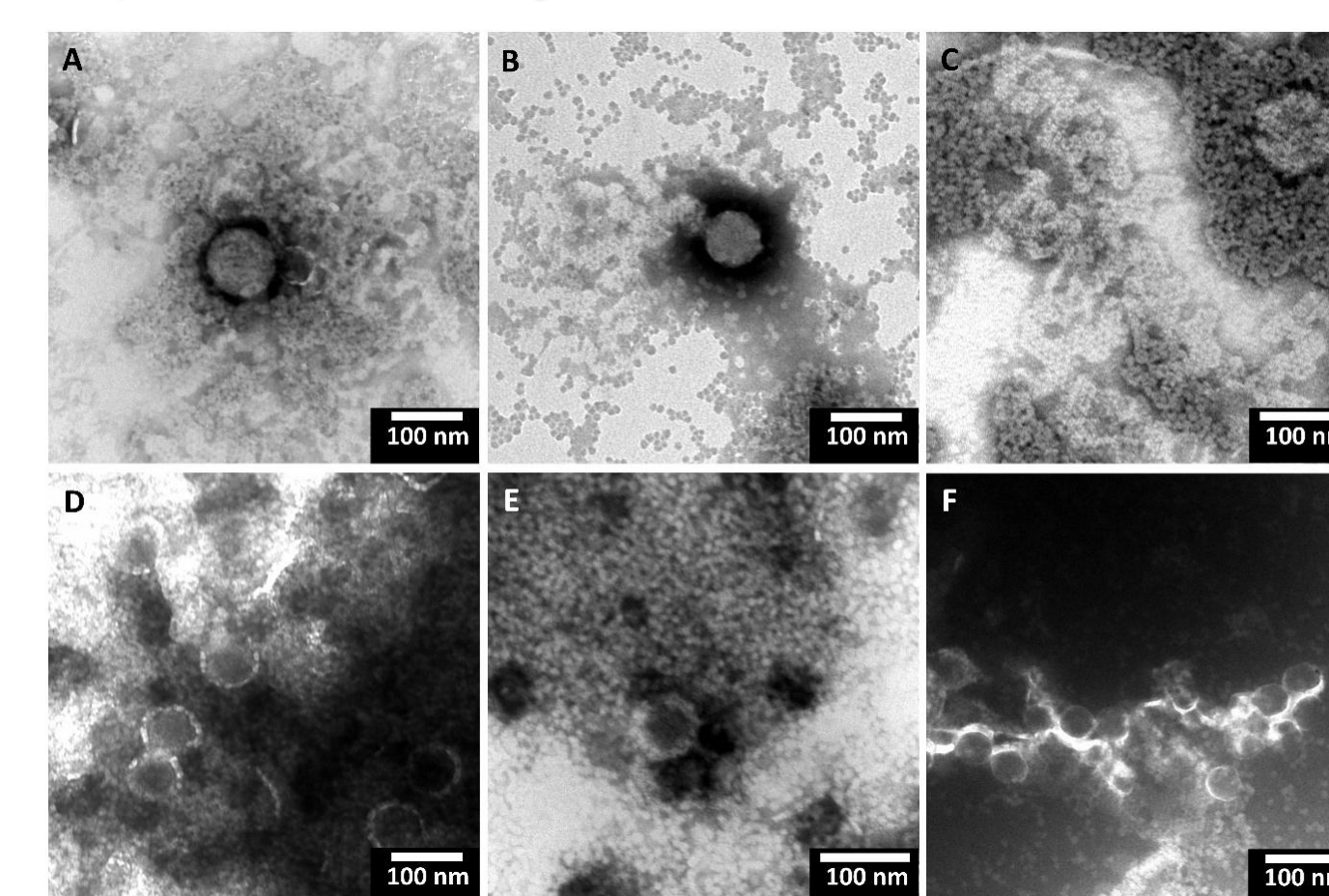
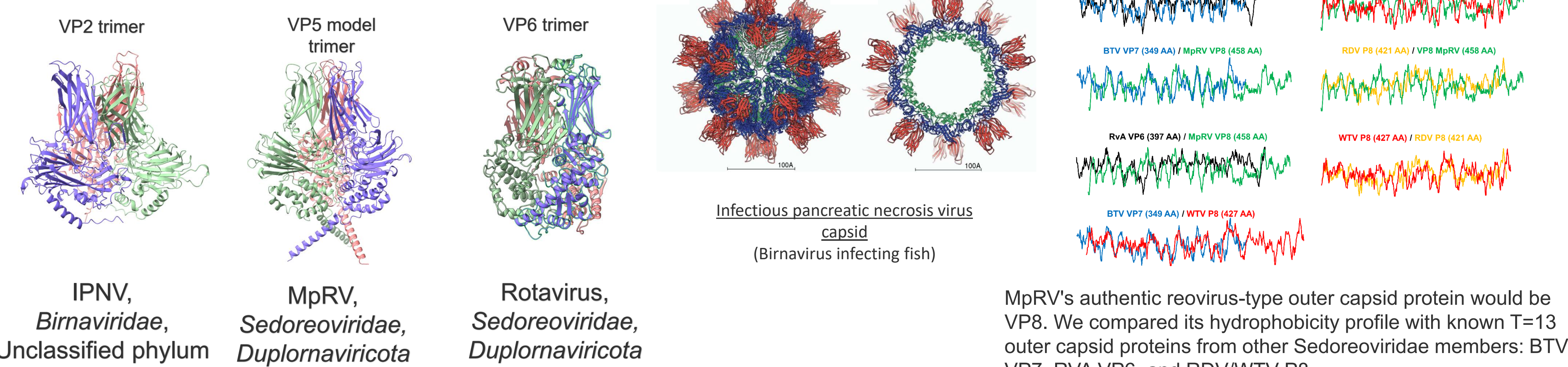
Using AlphaFold3 combined with Foldseek structural similarity searches, we predicted three-dimensional structures of proteins from representative *Reovirales* members. Structure-based analyses identified multiple previously uncharacterized virion components—inner capsid, outer capsid, and capping enzymes (turret proteins)—providing a near-complete structural map despite negligible sequence similarity to known homologs.

Experimental structure (PDB)		Confirmed by structural modelling			Newly identified by structural modelling			Not applicable / absent			
Genus	Virus (abbrev.)	Subcore T ₂	Capping enzyme	RdRp	NTase	Core outer layer	Outer capsid 1	Outer capsid 2	Seg.	Assembly	
Orthoreovirus	Mammalian orthoreovirus 3 (MRV3)	Lambda3 6XF7	Lambda2 7ELL	Lambda1 2CSE	Mu2 7ELH	Sigma2 2CSE	Mu1 2CSE	Sigma1, Sig ma3 2CSE	10	GCA_0862983	
Aquareovirus	Grass carp reovirus (GCRV)	VP3 31YL	VP1 31YL	VP2 31YL	VP4 31YL	VP6 31YL	VP5 31YL	VP7 pTM = 0.4 paxis-model 6.70	11	GCA_0036263	
Coltivirus	Colorado Tick Fever virus (CTFV)	VP2	VP3	VP1	VP10	?	VP4	?	12	GCF_00089585	
		pTM = 0.96	pTM = 0.80	pTM = 0.92	pTM = 0.63	?	pTM = 0.64	?			
Cypovirus	Bombyx mori cypovirus1 (BmCPV-1)	VP1(s1) 3J81	VP3(s4) 3J81	VP2(s2) 6T2Z	VP4(s6) 6T2Z	VP5 (s8) 31ZX	no	no	10	GCA_0231513	
Fijivirus	Fiji disease virus (FIV)	VP3 pTM = 0.66 BFDV 79	VP2 pTM = 0.42 BFDV 79	VP1 pTM = 0.91	VP8 pTM = 0.64	VP7 pTM = 0.79	?	?	10	GCF_00089665	
Mycoreovirus	Cyphophthia parasitica mycoreovirus-1 (CgMYRV1)	VP2 pTM = 0.82	VP3 pTM = 0.37	VP1 pTM = 0.93	VP6 pTM = 0.53	?	?	?	11	GCF_00089795	
Dinovornovirus	Aedes pseudoscutellaris s reovirus (APRV)	VP3 pTM = 0.83	VP5 pTM = 0.85	VP2 pTM = 0.93	VP6 pTM = 0.71	VP7 pTM = 0.77	no	no	9	GCF_00089685	
Oryzavirus	Rice ragged stunt virus (RRSV)	P3 pTM = 0.83	P2 pTM = 0.70	P4A pTM = 0.94	P7 pTM = 0.73	P8B7 pTM = 0.43	P97 pTM = 0.62	no	10	GCF_00089585	
Idnoreovirus	Diadromus pulchellus idnoreovirus1 (DpnRV1)	VP2? pTM = 0.34 BFDV 67	?	?	?	?	?	?	10	GCF_00082385	
Idnoreovirus	Oporophthora brumata reovirus 1 (OBRV)	VP2 pTM = 0.77 BFDV 83	VP3 pTM = 0.43 BFDV 83	VP1 pTM = 0.92	?	?	?	?	10	GCF_00089665	
Genus	Virus (abbrev.)	Subcore T ₂	Capping enzyme	RdRp	Core outer layer T ₂ L	Outer capsid 1	Outer capsid 2	Seg.	Assembly		
Cardoreovirus	Eriocher shensis reovirus 1 (ESRV)	VP2 pTM = 0.64	VP3 pTM = 0.87	VP1 pTM = 0.92	?	?	?	12	09019212 (+12)		
Crabreovirus	Mud crab reovirus (MCRV)	VP3 7X83	VP2 pTM = 0.32	VP1 7X83	VP12 7X82	VP11	?	12	GCA_03133890		
Minoreovirus	Micromonas putellus reovirus (MPRV)	VP3 pTM = 0.2	?	VP2 pTM = 0.94	VP8? pTM = 0.16	VP7 pTM = 0.32	VP5* pTM = 0.81	11	GCF_00089518		
Orbivirus	Bluetongue virus (BTV)	VP3 2BTV	VP4 2JHC	VP1 6PNS	VP7 2BTV	VP2 3J9D	VP5 3J9E	10	GCF_00085454		
Phytoreovirus	Rice dwarf virus (RDV)	P3 10FZ	P3HC 5X71	P1 pTM = 0.91	P8 10FZ	P2 pTM = 0.37	?	12	GCF_00081072		
Rotavirus	Rotavirus A (RAV)	VP2 047D	VP3 54Z	VP1 2B7D	VP6 047D	VP4 547D	VP7 047D	11	GCF_00089873		
Sednareovirus	Bama virus (BAV)	VP2 pTM = 0.64	VP1 pTM = 0.92	VP3 pTM = 0.92	VP4 pTM = 0.84	VP5 pTM = 0.83	VP4 pTM = 0.64	12	GCF_00085618		



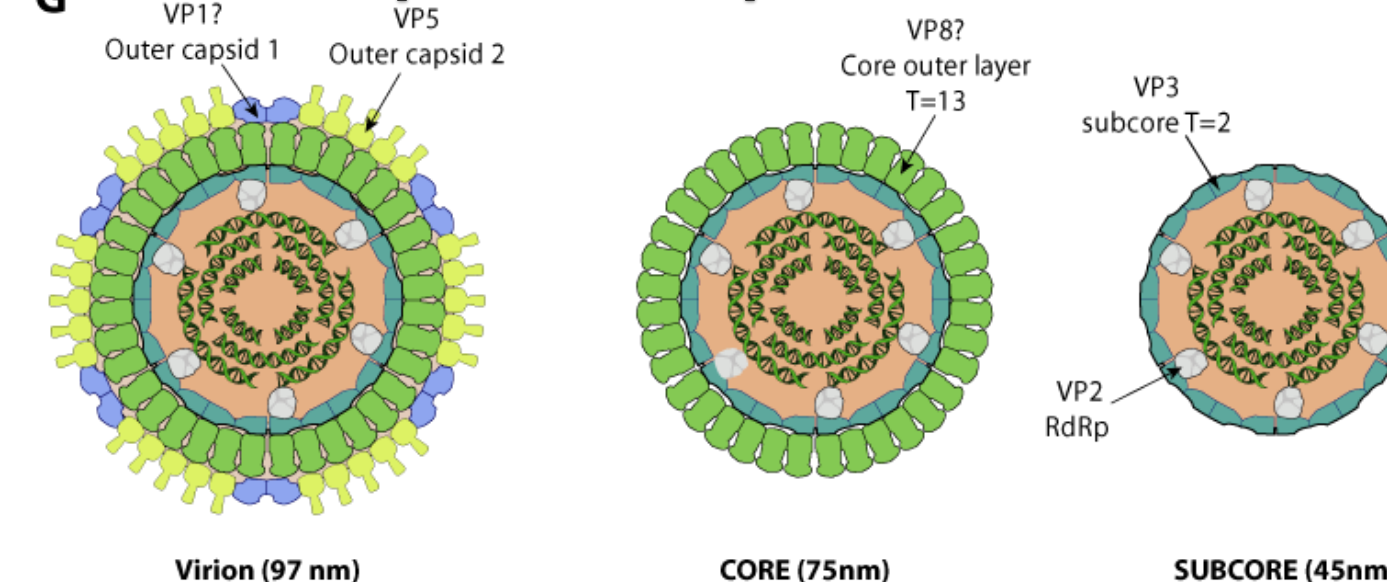
Identification of regions of interest in the FoldMaso similarity map, showing the structural alignment of sequences heat-colored by LDDT score. Two β -strand loops at the surface of the spinareovirus RdRp correspond to the binding interface with the NTPase, a spinareovirus-specific enzyme.

T=13 capsid proteins



electron micrographs of purified MpRV particles with various treatments. **[A]:** Whole MpRV particles purified on Percoll gradient. The mean diameter of these particles is ~97 nm. **[B, C]:** Whole MpRV particles purified on Percoll gradient followed by further purification on a discontinuous caesium chloride gradient. The mean diameter of these particles is ~75 nm. Note the layer of the ring shaped capsomers visible in the micrographs. **[D, E]:** Whole MpRV particles purified on Percoll gradient followed by a short treatment (3 min) treatment with CaCl₂ 1.5 M. The mean diameter of the particles is ~75 nm. **[F]:** Whole MpRV particles purified on Percoll gradient followed by a treatment with CaCl₂ 1.5 M for 30 min at 37°C. The mean diameter of these particles is ~45 nm. **[G]** MpRV structural models: the complete viral particle (~97 nm, as in A), the core (~75 nm, as in B–E), and the subcore (~45 nm, as in F).

MpRV capsid model



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