

Weininger, A.; Weininger, S. (2016) “*Common Features in Picornaviruses, Alpha-bungarotoxin, Myelin P2, and CRABP Suggest Structural Bases for Multiple Sclerosis, Guillain-Barré Syndrome, and Paralysis Induction*”  
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## 5 Title

Common Features in Picornaviruses, Alpha-bungarotoxin, Myelin P2, and CRABP Suggest Structural Bases for Multiple Sclerosis, Guillain-Barré Syndrome, and Paralysis Induction

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## Abstract

We found the structural correlates of multiple sclerosis induction and paralysis induction in picornaviruses and  
15 proteins. We determined that myelin-P2/CRABP equivalent residues and alpha-bungarotoxin equivalent  
residues are threaded through the VP1, VP2, and VP3 sequences such that they are mutually exclusive and  
interrupted by internal and external inserts. We isolated specific proline residues that are sequence invariant in  
the VP1, VP2, and VP3 proteins and used their placement on the capsid icosahedron face to construct  
picornavirus capsid models. We present the basis for the hypothesis that picornavirus capsids evolved from  
20 cores of myelin P2 and toxin trimers. We have determined that picornaviruses that induce paralysis, such as  
EV-D68, EV-D70, and Mahoney poliovirus, have loops that are structurally and chemically similar to toxins, such  
as alpha-bungarotoxin, that induce paralysis. We have determined that specific viruses that induce or are  
associated with the induction of multiple sclerosis, present residues that are structurally and chemically similar to  
those presented by myelin P2 helices. In the picornaviruses, we identified what appears to be an ion channel  
25 gated by VP1 myelin P2 helices-like residues and also a diaphragm shutter-like pore formed by VP3 pentamers  
whose VP3 sequence invariant proline stays spatially fixed in the capsid. We identified the components of a  
sialic acid active site on the EV-D68 capsid.

## Introduction

We set as our goal the determination of the structural correlates in the picornaviruses of paralysis and multiple sclerosis induction. Picornaviruses are non-enveloped, positive strand viruses that cause significant disease in animals and humans. The *Picornaviradae* family includes: Foot and Mouth Disease Virus (“FMDV”) which is not known to induce either paralysis or multiple sclerosis; Theiler's murine encephalomyelitis virus (“TMEV”) which is known to cause multiple sclerosis; the *Enteroviruses*, which include EV-D68 which is associated with paralysis, Guillain-Barré Syndrome (“GBS”), and multiple sclerosis; and *Polioviruses* (PV1 or “Mahoney Strain”, PV2 or “Lansing Strain”, and PV3 or “Sabin Strain”) which are known to be associated with paralysis. EV-D68 is an emergent pathogenic picornavirus with expanded tissue preferences and new disease-inducing capability including the induction of irreversible flaccid paralysis in children [1], similar to that seen historically in poliovirus infections. Guillain-Barré Syndrome has been associated with EV-D68 infections, e.g., a cluster of atypical Guillain-Barré Syndrome in ten adults temporally related to a cluster of four children with acute flaccid paralysis from EV-D68 was observed over a 3-month period in Wales [2]. Simply put, EV-D68 and EV-D70 have apparently emerged with TMEV's capacity to induce multiple sclerosis and with the capacity of Mahoney poliovirus (PV1) to induce paralysis.

This study was started with the recognition that a multiple sclerosis-like condition, i.e. demyelination, in mice may be induced either with an infection of TMEV [3] or with an injection of myelin P2 (“MP2”) [4]. Because TMEV infection [3] and MP2 protein injection [4] can cause demyelination and because cellular retinoic acid binding protein (“CRABP”) (1CBS.PDB) [5], is in the same structural family as MP2 (2WUT.PDB) [6], we identified and analyzed the sequence and structural similarities among and the differences between MP2, CRABP, and picornavirus VP1, VP2, and VP3 proteins. Because acute flaccid paralysis can be individually caused by EV-D68, EV-D70, PV1, or specific toxins, we identified and analyzed the sequence and structural similarities among and the differences between a representative toxin that causes paralysis, alpha-bungarotoxin (“ABT”) (Krait snake venom, 2ABX.PDB) [7], and the VP1, VP2, and VP3 proteins of: the Mahoney strain poliovirus (“PV1”) (1HXS.PDB) [8], the Lansing strain poliovirus (“PV2”) (1EAH.PDB) [9], the Sabin strain poliovirus (“PV3”) [10], and an EV-D68 structure (“EV-D68-4WM7”) (4WM7.PDB) [11]. Because EV-D68 has expanded tissue preferences, we looked at whether EV-D68-4WM7 has residues that are spatially presented similarly to residues found in the active site of influenza neuraminidases, such as the influenza N6 neuraminidase (“N6 Neuraminidase”) (1WIX.PDB) [13], that are known to bind to and process sialic acid.

We aligned the sequences of picornavirus VP1, VP2, and VP3 proteins with each other and also with MP2, CRABP, ABT A chain (all residues), and ABT B chain (residues 1 – 48) using a unique alignment method that utilized: a co-grouping of methionine, cysteine, and tryptophan residues; use of glycines and prolines to bracket the sequences; and the use of the MP2, CRABP, and ABT sequences to parse the VP1, VP2, and VP3 sequences. This method of alignment was used to identify prolines that were both spatially conserved and sequence conserved in the VP1, VP2, and VP3 sequences. Atoms in these conserved prolines were used to map the picornavirus VP1234 structures onto an icosahedron in order to build and compare picornavirus capsid models. Atoms in sequence grouped conserved residues were also used to both create model MP2 trimers and CRABP trimers and to superpose these trimers onto all capsid tiling pieces. This allowed us to compare capsid tiling pieces, capsids, MP2 trimers, and CRABP trimers in the same spatial reference frame. We found that picornavirus capsids are comprised of residues in protein segments corresponding to the MP2, CRABP, and ABT sequences and that these segments are separated by well-defined inserts.

We determined that proteins that are associated with the induction of paralysis have common features with the capsids of viruses that are associated with the induction of paralysis and that these features are also common to toxins [12]. We determined that proteins that are associated with the induction of multiple sclerosis (i.e. MP2) have common features with the capsids of viruses that are associated with the induction of multiple sclerosis (i.e., TMEV-1, TMEV-2, and EV-D68) and that these features are located in the sections of sequence that align with the MP2 and CRABP helices. We determined that, for the picornaviruses in our representative set, Foot and Mouth Disease Virus (“FMDV”) (1BBT.PDB) [14] has the fewest residues outside of the MP2/CRABP-like and ABT-like sequence groupings, that FMDV VP1, VP2, and VP3 protein sequences are the least similar to other picornavirus VP1, VP2, and VP3 protein sequences, and that FMDV has no features consistent with the induction of either paralysis or multiple sclerosis.

Placement of atoms from the sequence conserved prolines in VP1, VP2, VP3, and VP4 protein assemblies (“VP1234”) onto specific points on the faces of a 135 Angstrom-on-a-side icosahedron produced capsid models for the twenty picornaviruses in the sample set. For each VP1234, there are nine points on an icosahedron face that can be used to position three VP1234 assemblies (“3xVP1234”) to complete a model capsid tiling piece. Three of these points representing VP3 atom positions are on the edges of the capsid icosahedron. Twenty model capsid tiling pieces in the shape of an icosahedron form the constructed capsid models. In each VP1234, the residues of the VP1, VP2, and VP3 protein assembly (“VP123”) are exposed to the outside of the capsid (“OUTER”). The VP4 residues are exposed to the inside of the capsid (“INNER”). The INNER VP4 proteins interact directly with the viral RNA on the inside of the capsid. It is known that mature

picornavirus particles bind to receptors, leading to the release of the N-terminus of VP1 [15] and VP4 [16] which forms a 135S intermediate called an “A particle”. The A particle is endocytosed [17] and delivers the RNA to the host cell. The VP1 protein has been shown to be partially extruded from the capsid during uncoating [18].

Examination of the spatial relationship between the conserved proline atoms in VP123 and the constructed capsid models showed that VP123 structures fall into two structural groups: common atomic structure occupancy group one (“CASOG-1”) and common atomic structure occupancy group two (“CASOG-2”). CASOG-1 and CASOG-2 differ in the relative positions of two of the conserved prolines in VP123, the VP1 and VP2 conserved prolines. The VP3 conserved proline is in the same position in CASOG-1 and CASOG-2. The VP3 protein positions are pivoted about the VP3 conserved proline. Since two different TMEV VP1234 structures were found with nearly identical sequence: “TMEV-1” (1TME.PDB) [19] in CASOG-1 and “TMEV-2” (1TMF.PDB) [20] in CASOG-2, we interpreted the difference in the VP1234 structure positions in the TMEV-1 and TMEV-2 constructed capsids as a permitted, relative motion of proteins within the capsids of picornaviruses as a class. In TMEV-1 and TMEV-2 capsid models, we identified diaphragm shutter-like pores at picornavirus capsid vertices, i.e., at the center of five VP3 proteins presented by a pentamer of five capsid tiling pieces. The five VP3 proteins lining the pore have positions that are rotated about the sequence and structurally invariant VP3 prolines. A comparison of the TMEV-1 and TMEV-2 structures suggests that the A particle can exit through a diaphragm shutter-like pore by a change in the position of VP3 relative to VP1 and VP2. The two positional endpoints are seen in the TMEV-1 and TMEV-2 constructed capsid models.

Atoms in MP2 monomers, CRABP monomers, and ABT dimers were superposed onto specific VP123 atoms in the model capsid tiling pieces to create model: MP2 trimers, CRABP trimers, and trimers of ABT dimers. The specific atoms used to create the model trimers of MP2, CRABP, and ABT are from structurally important sequence conserved residues in MP2, CRABP, and ABT. The constructed MP2 trimers, CRABP trimers, and trimers of ABT dimers are co-located with VP1234 trimers in the capsid tiling pieces. Co-location of the trimers (picornavirus VP1234, MP2, CRABP, and ABT dimer) allowed us to identify the existence of, and the basis for the function and gating of, an ion channel at the center of picornavirus capsid faces, i.e., at the center of tiling pieces. This co-location of the trimers allowed us to examine the relationship between this ion channel and VP4 proteins that anchor the viral RNA. From the comparative analysis of MP2 trimers, CRABP trimers, and picornavirus VP1 trimers, we suggest the structural basis for ion channel function and dysfunction.

The sequence alignment of ABT chains A (all residues) and B (residues 1 – 48 only) with VP1, VP2, and VP3 proteins was used to identify residues from picornavirus proteins that may historically have been derived from ABT and are still present in all picornaviruses. We also looked in picornaviruses for toxin loop residues that

are common to specific protein toxins (“TOX DOMAIN”, i.e., the residues listed in Table 9 of reference [12] and  
120 shown in Figure 12 of reference [12]), e.g., ABT, staphylococcal enterotoxin I, botulinum toxin, anthrax lethal  
factor, tetanus toxin, and an emergent influenza virus (H18N11) [12]. We found TOX DOMAIN loop residues in  
the structures of Mahoney poliovirus, PV1 [10], and in EV-D68 [11]. In PV1 and in EV-D68, these TOX DOMAIN  
loop residues are in ABT sequence aligned positions and separately are also in an insert (“INSERT LOOP”) that  
is not ABT sequence aligned (i.e., outside of the ABT threading). The spatial positions of the PV1 INSERT  
125 LOOP residues is similar to what would be expected if the PV1 INSERT LOOPS were derived from residues that  
were sequence aligned with ABT. If EV-D68-4WM7 had the same sequence as the pathogenic EV-D68 and if all  
of the positions of the EV-D68 INSERT LOOP residues were shown, then the spatial positions of the EV-D68  
INSERT LOOP residues would be similar to what would be expected if all ABT chain B residues, including  
residues 49 – 74, had been included historically in all picornavirus VP1, VP2, and VP3 sequences. The EV-D68  
130 TOX DOMAIN loops were derived from residues that were sequence aligned with ABT residues and from  
residues that have been added in non-Toxin Core segments of VP1 and VP2, including in the Insert sequences.  
The INSERT LOOP of EV-D68-4WM7 has flanking residues missing from the crystal structure, has critical  
residues (e.g., H87) different from other pathogenic EV-D68 sequences (e.g., D87), and presents groups in  
close contact with bound plecornaril (e.g., L220). Despite the difference in sequence between the EV-D68-  
135 4WM7 VP1 proteins and pathogenic EV-D68 proteins, and despite the absence of flanking residues in the  
EV-D68-4WM7 INSERT LOOP, the constructed capsid allowed us to isolate the position of pathogenic EV-D68-  
4WM7 INSERT LOOP residues, compare the EV-D68-4WM7 INSERT LOOP residues to PV1, and relate the  
EV-D68 TOX DOMAIN residues to the positions of bound plecornaril. In the EV-D68-4WM7 crystal structure, we  
also found a structural feature with the components of a sialic acid-binding site (“SIA SITE”, shown in Figure 2 of  
140 reference [12]) largely positioned adjacent to the TOX DOMAIN. The EV-D68 SIA SITE and the  
EV-D68 TOX DOMAIN overlap by sharing a residue.

From the co-located trimers, we identified structural features presented on EV-D68 and PV1 that are  
also present in MP2, CRABP, and ABT. From an analysis of these common structural features, we generated a  
hypothesis regarding the structural basis for the induction of acute flaccid paralysis. We hypothesize that viruses  
145 with TOX DOMAINS can bind to acetylcholine receptors. We hypothesize that acute flaccid paralysis is caused  
by specific picornavirus capsid engagement of acetylcholine receptors and that this is the event that causes  
permanent loss of ACH receptor patches in the junction between motor neurons and muscle.  
We hypothesize that mutations in EV-D68 or EV-D70 will be seen in residues at positions that either contact  
plecornaril (or similar molecules) and/or will be seen in residues that contact or impact TOX DOMAIN residues.

150 We suggest that the EV-D68 site with neuraminidase active site binding components binds sialic acid, and that the binding of small molecules to this site may compete with acetylcholine receptor binding by EV-D68.

We identified a common structural feature in MP2 helices, CRABP helices, and in specific picornavirus VP1 residues including TMEV, EV-D68, EV-D70, and EV-D94. We hypothesize that multiple sclerosis is induced when this common structural feature is presented to the immune system as an epitope (“MS Epitope”).

155 We hypothesize that induction of multiple sclerosis by emergent viruses (e.g., EV-D68 (including HRV-87), EV-D70, and EV-D94) and by historical viruses (e.g., TMEV) occurs when the MS Epitope on the picornavirus capsid is exposed due to defective viral uncoating. In EV-D68, EV-D70, and EV-D94, the exposure of this epitope may be related to the engagement of the acetylcholine receptors by these viruses using their toxin-like domains so that the epitope is exposed upon viral uncoating.

160 The combination of a parsed, comprehensive sequence alignment and complete capsid models provides the context for capsids to be searched for domains and functional structures, regardless of whether the structural domain exists within a single protein or spans multiple proteins. We have identified structures with functional implications that are ABT-like domains, ion channels, pores, MP2/CRABP helices-like domains, and sialic acid binding components. Examination of these characterized capsid components allowed us to specifically  
165 hypothesize: how the entire capsid is constructed and functions for picornaviruses as a class; the structural foundation of and the related functional basis for the induction of multiple sclerosis by Theiler's Viruses and EV-D68; the structural foundation of and the related functional basis for the induction of Guillain-Barré Syndrome and acute flaccid paralysis by EV-D68 and Mahoney strain polioviruses; the structural foundation of and the related functional basis for sialic acid binding by EV-D68; the structural foundation and related functional  
170 operation of MP2 as a gated ion channel; and the structural foundation and related functional operation of ABT and ABT-like toxins. This study provides an analytic procedure for understanding the structural context of expanded tissue preferences and pathology in historical and emergent viruses.

## Materials and Methods

### Sequences and Structures

175 Abbreviations, reference numbers, sequence sources, structure sources, and resolutions of the X-ray crystal structures used in the analysis are listed in Table 1. Sequences and structures of CRABP (1CBS.PDB) [5], myelin P2 protein (“MP2”) (2WUT.PDB) [6], and alpha-bungarotoxin dimer (“ABT”) (2ABX.PDB) [7] were aligned with representative picornavirus VP1, VP2, and VP3 proteins: *Aphthovirus* Foot and Mouth Disease Virus (“FMDV”) (1BBT.PDB) [14]; *Cardiovirus* Theiler's Murine Encephalomyelitis Virus (“TMEV-1”) (1TME.PDB)  
180 [19] and (“TMEV-2”) (1TMF.PDB) [20]; *Enterovirus A* species EV-A71-1 (3VBH.PDB) [21] and EV-A71-2

(4CEW.PDB) [22]; *Enterovirus B* species coxsackieviruses EV-B-CV-A9 (1D4M.PDB) [23] and EV-B-CV-B3M (1JEW.PDB) [24]; *Enterovirus B* species echovirus 7 EV-B-ECHOV-7 (1M11.PDB) [25]; *Enterovirus B* species Swine Vesicular Disease Virus, EV-B-B5-SVDV (1OOP.PDB) [26]; *Enterovirus C* species polioviruses EV-C-PV1-M (“Mahoney strain”) (1HXS.PDB) [8], EV-C-PV2-L (“Lansing strain”) (1EAH.PDB) [9], and EV-C-PV3-S (“Sabin strain”) (1PIV.PDB) [10]; *Enterovirus C* species coxsackieviruses EV-C-A21 (1Z7S.PDB) [27] and EV-C-A24 (4Q4Y.PDB) [28]; *Enterovirus D* species EV-D68-4WM7, (4WM7.PDB) [10]; *Enterovirus G* species bovine virus EV-G5-27 (1BEV.PDB) [29]; *Rhinovirus A* species HRV-A2 (1V9U.PDB) [30] and HRV-A16 (1AYM.PDB) [31]; and *Rhinovirus B* species HRV-B14 (1D3I.PDB) [32]. Also analyzed were sequences for *Enterovirus B* species coxsackieviruses EV-B-CV-B1-1 [33], EV-B-CV-B1-2 [34], EV-B-CV-B1-3 [35], EV-B-CV-B3 [36], EV-B-CV-B6 [37], *Enterovirus C* species coxsackievirus EV-C-CV-105 [38], *Enterovirus D* species EV-D68-CH14 [39], EV-D68-JP11 [40], EV-D68-NZ13 [41], EV-D68-SW07 [42], EV-D68-US14-1 [43], EV-D68-US14-2 [44], EV-D70-UK09 virus [45], EV-D94-FN07 [46] and a rhinovirus reclassified as an *Enterovirus D* species HRV-87-US04 [47]. The VP4 sequence for Echovirus 7 was obtained from GENBANK (AAK85711.1 [48]) as the 1M11.PDB structure did not contain a VP4 sequence.

## Sequence Alignment Method

### Bracketing Glycines and Prolines, Residue Grouping

In Figures 1 and 3, glycines (G) and prolines (P) in all sequences were placed on homogeneous columns filled with either glycines or prolines. These residues were used to “bracket” other residues in the sequences whether or not these residues were in any one sequence. The following sets of residues are grouped into columns, and residues within each set were considered identical for column positioning:

- (a) alanine (A), phenylalanine (F), isoleucine (I), leucine (L), valine (V), and tyrosine (Y);
- (b) cysteine (C), methionine (M), and tryptophan (W) residues;
- (c) aspartic acid (D) and glutamic acid (E);
- (d) histidine (H), lysine (K), and arginine (R);
- (e) asparagine (N) and glutamine (Q); and
- (f) serine (S) and threonine (T).

Residues bracketed between glycine (G) and proline (P) columns were brought into alignment to maximize the exact column alignment of identical residues in the column when possible. When there was not enough information to place a residue in one column versus another in an area between the glycines (G) and prolines (P), a column was selected to enhance exact residue alignment and visual grouping of residues. Examples of

possible alternate sequence alignments of residues were indicated with hyphens and greater-than/less-signs, e.g. "-->" and "<--".

### Using Reference Sequences MP2, CRABP, and ABT to Align Picornavirus Sequences

215 Figure 1 shows the picornavirus sequences of VP1, VP2, and VP3 aligned with each other and also with the reference sequences MP2, CRABP, and ABT. This alignment and isolated features are summarized in Figure 2 with a copy of Figure 2 embedded at the bottom right of Figure 1 for easy reference. Figure 3 shows picornavirus sequences of VP4 residues aligned with each other. Correspondence with the index sequences (MP2, CRABP, and ABT) was visually enhanced by coloring the entire column, and also positionally equivalent  
220 columns, with the background color of the index sequence residues as given in the Figure 1 legends. These sequences are divided into sections based on sequence correspondence with the reference sequences. In Figure 1, picornavirus sequences that have correspondence with: MP2/CRABP are found in or aligned with yellow and red Sections M1 – M16; ABT chain A are found in or aligned with magenta Sections A1 – A6; and ABT chain B are found in or aligned with cyan Sections B1 – B5. In Figure 1, sequences that have no  
225 sequential correspondence with either MP2/CRABP or the ABT chains A and B are found in sections marked as insertions. The insertions are grouped and colored as to whether they only occur in VP1 (dark blue Sections I1), only occur in VP2 (green Sections I2), only occur in VP3 (tan Sections I3), or if they occur in more than one or in all VP1, VP2, and VP3 sequence sections (purple Sections I13, I23, and I123). Figure 2 reflects these Figure 1 highlight colors as background colors for the lines representing the reference sequences, and as background  
230 colors for the insertion suffix numbers representing positions in the groupings that are not related to the reference sequences. Figure 1 sections that contain either toxin features or markers have subsection titles that include descriptive suffixes: "-T" for natural toxin residues that occur in ABT chain A or B; "-ST" for added toxin residues that are common to toxins but are either outside of the Toxin Cores or have been repurposed to a new toxin loop; "-SW" for sialic acid binding/sialidase binding pocket components; "-SP" for residues contacting the  
235 sialic acid in the 4Q4Y.PDB structure; and "-M" for residues used as markers for TMEV-1 and TMEV-2 to show their relative VP1234 internal positions of VP1, VP2, and VP3.

## Structural Alignment Method

### Structural Alignment Of A Representative Set Of VP1234 By Superposing Conserved VP1 Proline Atoms

240 In order to examine the structural variation in the relationship between the VP1, VP2, VP3, and VP4 proteins in the picornavirus VP1234 protein assemblies in our representative set, we first oriented the VP1234 for each picornavirus using residues internal to one protein, VP1. The atoms listed in Table 2 were superposed



to determine the structural variation in the VP1234 when the VP1 proteins are superposed. The positions of the conserved prolines whose main chain oxygens are listed in Table 2 are indicated in Figure 1 by the “@” symbol in the VP1 section header above the proline columns. These Figure 1 positions occur: between Sections M-11 and I13-2; between Subsections 3 and 4 of Section A-1; and between Subsections 8 and 9 of Section M-14. The positions of the conserved prolines whose main chain oxygens are listed in Table 2 are indicated in Figure 2 by the “@” symbol in the grey picornavirus protein threading line. The VP1234 structures that were superposed using VP1 internal prolines are shown in Figure 4 column 1. We determined that the VP1234 structures fell into two Common Atomic Spatial Occupancy Groups: CASOG-1 (18 structures) and CASOG-2 (2 structures). All but two structures, the two CASOG-2 structures FMDV (1BBT.PDB) and TMEV-2 (1TMF.PDB), have nearly identical VP1234 internal orientation. Because TMEV-1 and TMEV-2 have nearly the same sequence, they represent demonstrated VP1234 internal structural variation.

### Positioning Proteins Onto Icosahedron Faces

In order to examine the structural variation in the relationship between the VP1, VP2, VP3, and VP4 proteins in the picornavirus capsids in our representative set, we placed VP1234 assemblies onto specific locations on a model capsid face using atoms in conserved prolines. Three specific atoms were used for each VP1234 placement, one each from VP1, VP2, and VP3 proteins. Tables 3 and 4 lists these atoms, which are main chain oxygens from conserved prolines. These prolines are sequence invariant within each protein and structurally invariant within CASOG-1 and within CASOG-2. In Figure 1, the sequence positions of these conserved prolines are indicated by “\*” symbols shown both in the section headers on top of these conserved proline columns as well as in columns flanking these conserved proline columns. In Figure 1, these conserved prolines are between Sections M-11 and I13-2 for VP1 and VP2 and are between Sections B-3 and B-4 for VP3. In Figure 2, the positions of these conserved prolines are indicated by the “\*” symbol in the grey picornavirus protein threading line.

To facilitate construction of picornavirus model capsid tiling pieces, MP2 trimers, and CRABP trimers, we created sets of idealized points that represent specific atom destination positions located on the face of an icosahedron. A complete set of idealized points for creating picornavirus capsid tiling pieces, MP2 trimers, and CRABP trimers is provided as representative atoms in supporting information file **PICORNAVIRUS\_TILING\_POINTS.PDB** (“PICORNAVIRUS TILING POINTS”). Picornavirus, MP2, and CRABP proteins were placed in specific geometries on an icosahedron face by superposing three specific protein atoms with three specific points in PICORNAVIRUS TILING POINTS. These superpositions do not change the relative positions of the atoms within MP2 or CRABP, nor do they change the relative positions of the atoms within each

275 picornavirus VP1234 assembly. For visual reference, two sets of idealized points are provided as supporting  
information files: **ICOS135.PDB** (“ICOS135”) and **TRI78.PDB** (“TRI78”). ICOS135 contains points at the vertices  
of a 135 Angstrom-on-an-edge icosahedron, the icosahedron representing the picornavirus capsid face. TRI78  
contains points at the vertices of 78 Angstrom-on-a-side equilateral triangles that are positioned with their  
vertices on ICOS135 icosahedron edges and 45 (and 90) Angstroms away from the ICOS135 icosahedron  
vertices. PICORNAVIRUS TILING POINTS are all located on or within the first listed triangle in TRI78, which is  
280 within the first ICOS135 listed triangle (i.e., the first listed icosahedron face).

### Construction of Picornavirus Model Capsid Tiling Pieces

Models of picornavirus capsid tiling pieces (i.e., 3xVP1234 picornavirus capsid tiling pieces) were  
constructed by separately placing three VP1234 structures onto an icosahedron face. Individual VP1234  
structures were placed by superposing three specific VP1234 conserved proline atoms onto specific  
285 icosahedron face points. Models of CASOG-1 picornavirus VP1234 trimers (i.e., 3xVP1234 picornavirus capsid  
tiling pieces) were constructed by three superpositions of the atoms in the rows of Table 3 with consecutive  
PICORNAVIRUS TILING POINTS having the chain identifier “1” (e.g., the TMEV-1 (1TME.PDB) atoms listed in  
Table 3 were superposed onto consecutive PICORNAVIRUS TILING POINTS 1, 2, 3, then again onto 4, 5, 6,  
and lastly onto 7, 8, 9). Models of CASOG-2 picornavirus VP1234 trimers (i.e., 3xVP1234 picornavirus capsid  
290 tiling pieces) were constructed by three superpositions of the atoms in the rows of Table 4 with consecutive  
PICORNAVIRUS TILING POINTS having the chain identifier “2” (e.g., the TMEV-2 (1TMF.PDB) atoms listed in  
Table 4 were superposed onto consecutive PICORNAVIRUS TILING POINTS 11, 12, 13, then again onto  
14, 15, 16, and lastly onto 17, 18, 19).

The CASOG-1 and CASOG-2 model capsid tiling pieces constructed for our representative set of  
295 picornaviruses can be seen in Figure 4. Figure 4 columns 2 – 6 show trimers of VP1234, VP1, VP2, VP3, and  
VP4, respectively. A different picornavirus is shown in each row of Figure 4: 1AYM (B), 1BBT (C), 1BEV (D),  
1D4M (E), 1EAH (F), 1HXS (G), 1OOP (H), 1PIV (I), 1TME (J), 1TMF (K), 1V9U (L), 1Z7S (M), 3VBH (N),  
4CEW (O), 4Q4Y (P), and 4WM7 (Q). An examination of Figure 4 rows C and K show the two CASOG-2  
structures, FMDV (1BBT.PDB) and TMEV-2 (1TMF.PDB), which differ in the VP1234 orientation.

300 The process of creating the CASOG-1 and CASOG-2 model capsid tiling pieces and capsids is  
illustrated in Figure 5. Figure 5 Panel A shows both CASOG-1 and CASOG-2 tiling points on a single TRI78  
triangle. The vertices of the TRI78 triangles are points that represent positions of conserved VP3 proline atoms  
in both CASOG-1 and CASOG-2 picornavirus capsids. The VP3 atoms in Tables 2 – 4 are both sequence  
conserved and spatially conserved. In Figure 5, the VP1 CASOG tiling points are colored cyan, the VP2 CASOG

305 tiling points are colored green, and the VP3 CASOG tiling points are colored yellow. Figure 5 Panels B, D – F show CASOG-1 VP123 positions, i.e., the destination points for individual CASOG-1 VP1, VP2, and VP3 atoms listed in Table 3. Figure 5 Panels G – I show individually placed TMEV-1 VP1234 proteins. Figure 5 Panels P and S show the completed TMEV-1 capsid tiling pieces, i.e., placed CASOG-1 3xVP1234. Figure 5 Panels C, J – L show CASOG-2 VP123 positions, i.e., the destination points for individual CASOG-2 VP1, VP2, and  
310 VP3 atoms listed in Table 4. Figure 5 Panels M – O show individually placed TMEV-2 VP1234 proteins. Figure 5 Panels Q and T show the completed TMEV-2 capsid tiling pieces, i.e., placed CASOG-2 3xVP1234. Figure 5 Panels R and U show the completed TMEV-1 (CASOG-1) superposed with the nearly sequence identical TMEV-2 (CASOG-2) 3xVP1234 tiling pieces.

### Construction of Picornavirus Model Capsids

315 Models of picornavirus capsids were created with sixty separate placements of VP1234 structures onto an icosahedron. Each of these VP1234 placements was made with the superposition of three specific conserved proline atoms (listed in Tables 2 and 3) onto a set of three idealized points provided as one triplet of consecutive atoms (e.g., 1,2,3; or 4,5,6; etc. through 178,179,180) in either supporting information file  
CASOG\_ONE\_CAPSID\_POINTS.PDB for CASOG-1 structures or supporting information file  
320 CASOG\_TWO\_CAPSID\_POINTS.PDB for CASOG-2 structures. Each tiling piece of the resultant capsids has the appropriate CASOG-1 and CASOG-2 geometry illustrated in Figures 4 and 5. The overall structural features of CASOG-1 and CASOG-2 capsids are shown by representative tiling piece pentamers in Figure 6. Figure 6 column 1 Panels A, D, G, and J separately show INNER and OUTER views of the residue spheres and cartoons of a pentamer of TMEV-1 (CASOG-1) capsid tiling pieces. Figure 6 column 2 Panels B, E, H, and K separately  
325 show INNER and OUTER views of the residue spheres and cartoons of a pentamer of TMEV-2 (CASOG-2) capsid tiling pieces. Figure 6 column 3 Panels C, F, I, and L show the composite of structures and residues shown in columns 1 and 2.

### Construction of Model Myelin P2 Trimers and CRABP Trimers

330 Models of myelin P2 trimers and CRABP trimers were constructed by three superpositions of the atoms in the rows of Table 5 with consecutive PICORNAVIRUS TILING POINTS having the chain identifier “3”. Figure 7 Panel A shows the relationship between CASOG tiling points and myelin P2/CRABP trimer points. Three of these destination points map directly onto TMEV-1 atoms, three map onto TMEV-2 atoms, and three map onto idealized points on the face of the icosahedron such that the myelin P2/CRABP and TMEV-2  
Figure 1 Section M-2 Subsection 3 residues are in spatial alignment. Table 5 lists the three myelin P2 (2WUT)  
335 atoms and the three CRABP (1CBS) atoms that were separately used to construct myelin P2 and CRABP

trimers from three superpositions of their individual monomers. (e.g., the myelin P2 atoms listed in Table 5 were superposed onto consecutive PICORNAVIRUS TILING POINTS 21, 22, 23, then again onto 24, 25, 26, and lastly onto 27, 28, 29). The iterative superpositions of the Table 5 atoms onto the PICORNAVIRUS TILING POINTS are illustrated in Figure 7 Panel B. The resultant myelin P2 trimers are shown positioned on an icosahedron face as shown in Figure 7 Panels C and D. The resultant CRABP trimers, made by the same process as the myelin P2 trimers, are shown with the myelin P2 trimers in Figure 7 Panel D. This process co-locates constructed picornavirus trimers (3xVP1234), myelin trimers, and CRABP trimers so that a comparison of the molecular structural anatomy can be performed.

### Construction of Model Alpha-bungarotoxin (ABT) Trimers

Trimers of ABT dimers were created by superposing ABT chain A atoms in the ABT dimer (2ABX.PDB) onto EV-D68-4WM7 VP1 trimer atoms (4WM7.PDB), where both sets of atoms are specified in Table 6. The atoms in Table 6 are present in the ABT and EV-D68-4WM7 sequence aligned residues in Figure 1 Section A1 Subsections 3, 6, and 7. Using this method, trimers of ABT dimers (chains A and B) are created that will be co-located with the MP2 trimers, the CRABP trimers, and all picornavirus VP1234 trimers in the capsid tiling pieces. Figure 7 Panel E shows cartoons of a trimer of ABT in its superposed position and the ABT Table 6 atoms as spheres. Figure 7 Panel F shows cartoons of the EV-D68 VP1 trimer Toxin Section Residues and the EV-D68 VP1 Table 6 atoms as spheres. Figure 7 Panel G shows cartoons of a trimer of ABT in its superposed position, the EV-D68 VP1 trimer Toxin Section Residues overlapping the corresponding ABT A chain cartoon, and all of the Table 6 atoms as spheres. Figure 7 Panel H shows that the optimal alignment of all three ABT atoms with all three EV-D68 VP1 trimer atoms in Table 6 also produces a perfect overlap at the center of the trimers of ABT atom 91 with EV-D68 atom 1414; and ABT atom 96 with EV-D68 atom 1412; which can be used as an additional check on positioning the ABT trimer.

## Results

### 360 **Summary: Picornavirus VP1, VP2, and VP3 Proteins Are Comprised of Myelin P2/CRABP-like and Alpha-Bungarotoxin-like Cores Interrupted By and Separated By Inserts With Specific Viruses Containing The Components of Toxin Domains, Myelin P2 Epitopes, and Sialic Acid Binding Sites**

As can be seen from Figures 1 and 2, we have determined that picornavirus capsids are comprised largely of separate myelin P2/CRABP-like sequences (“MP2/CRABP Cores”- Figure 1 Sections M-1 to M-16 (i.e. M-1, M-2, ... , M-16)) and alpha-bungarotoxin-like sequences (“Toxin Cores” - Figure 1 Sections A-1 to A-6 (i.e., A-1, A-2, ... , A-6) and B-1 to B-5 (i.e., B-1, B-2, ... , B5)) interrupted by and separated by residues that are labelled as “Inserts.” Table 7 lists Figure 1 section locations for each of these inserts. The MP2/CRABP Cores, Toxin Cores, and Inserts are mutually exclusive and clustered into domains whose attributes are described below. The positions of the Inserts between the VP1, VP2, and VP3 proteins is not random. For example, it can be seen from an examination of Figure 2 that Inserts that are seen in VP1 only (VP1 ONLY INSERT I1-#) are embedded only in the ABT Cores. Figure 3 shows the VP4 proteins sequences that we aligned. The VP4 sequences are highly related to each other but unrelated to the MP2/CRABP Cores and Toxin Cores. The Figure 1 alignment allowed us to relate Insert sequences and associated structures with the functions that were added to the MP2/CRABP Cores and Toxin Cores to produce the functioning viral capsid. Understanding where the MP2/CRABP Cores, Toxin Cores, and Inserts are located in the sequence and located in the structure helped us to isolate the structural correlates of pathogenicity in specific picornaviruses, including TMEV, Mahoney poliovirus PV1, EV-D68, and EV-D70.

### **MP2/CRABP Cores and Central Channel Gating By Helix Two**

380 Myelin P2 and CRABP constructed trimers present residues that occupy a similar bulk volume to VP1 MP2/CRABP Cores. Figure 8 Rows A and B show OUTER and INNER views of trimers of: CRABP (Panels A0 and B0), myelin P2 (Panels A1 and B1); FMDV VP1 (Panels A2 and B2); TMEV-2 VP1 (Panels A3 and B3); TMEV-1 VP1 (Panels A4 and B4); PV1 VP1 (Panels A5 and B5); and EV-D68 VP1 (Panels A6 and B6). In Figure 8, the MP2/CRABP Core residues corresponding to Figure 1 Sections M-1 to M-16 are colored yellow with the exception that residues in Section M-2 and M-3 (MP2/CRABP “Helix One”) are colored red and M4 (MP2/CRABP “Helix Two”) are colored dark red in order to emphasize the variation in the position of these residues. TMEV-1 and TMEV-2 have nearly the same sequence but exhibit differences in the relative positions of their VP1, VP2, VP3, and VP4 MP2/CRABP Cores. We suggest that the TMEV-1 and TMEV-2 structural differences reflect endpoints of a structural reorientation of VP1, VP2, and VP3 residues within the VP1234 and

390 that these VP1234 configurations can be interpreted as permitted, relative motion in the capsid, including, but not limited to, the relative positions of Helix One and Helix Two.

It can be seen from an examination of Figure 8 Row B (Panels B1 – B7) that Helix Two residues can take up positions that vary from being radially distant to being concentrated at the center of the trimers (“Central Channel”). Rows C (Panels C2 – C6) and D (Panels D2 – D6) show the OUTER and INNER views of VP2 MP2/CRABP Cores and their residue positions varying from being radially distributed to being concentrated  
395 about the Central Channel. Rows E (Panels E2 – E6) and F (Panels F2 – F6) show the OUTER and INNER views of the VP3 MP2/CRABP Cores showing the positions of the VP3 MP2/CRABP Core residues pivot about the VP3 atoms in Tables 3 and 4. Rows G (Panels G2 – G6) and H (Panels H2 – H6) show the OUTER and INNER views of the VP1, VP2, and VP3 MP2/CRABP Cores showing that the VP123 MP2/CRABP Cores cover most of the capsid tiling piece and that the spatial relationship between the VP1, VP2, and VP3 Helix One and  
400 Helix Two residues can exist in completely radially distributed forms to radially concentrated forms in the constructed capsids.

## **Multiple Sclerosis Associated Domain Comprised of Helix One and Helix Two Residues in Specific Picornaviruses**

N-terminal residues in the VP1 sequences of specific picornaviruses, located in Figure 1 Sections  
405 M2 – M4 (Helix One and Helix Two), appear to be able to form a domain which is associated with the capacity to induce multiple sclerosis, i.e., the feature is present in viruses and other proteins known to induce or to be associated with multiple sclerosis. The MS-associated feature is found in myelin P2, TMEV, and pathogenic EV-D68 ET AL. The feature, the putative MS Epitope, includes the presentation of DD and EE residues in M-2 Subsection 1 or in M-2 Subsection 3 (whether presented side-by-side in the sequence or structurally  
410 side-by-side in the helix), a K or R residue in M-3, and NQ residues in M-4 Subsection 2.

## **Structural Compatibility Between Constructed Myelin P2 Trimers And Trimers Of Alpha-Bungarotoxin Dimers; Structural Compatibility Between Myelin P2/CRABP Cores And Toxin Cores**

The structural compatibility between: a) constructed Myelin P2 trimers and trimers of alpha-bungarotoxin  
415 dimers; and b) selected picornavirus VP1 Myelin P2/CRABP Cores and Toxin Cores can be seen in Figure 9. Panels A and B show that the constructed Myelin P2 trimers fit well with constructed trimers of alpha-bungarotoxin dimers. Figure 9 Panels C – L shows that this compatibility is maintained in the picornavirus VP1 Myelin P2/CRABP Cores and Toxin Cores of FMDV, TMEV-2, TMEV-1, PV1, and EV-D68. The variation in internal and external contacts within the Myelin P2/CRABP Cores and Toxin Cores can be utilized to understand

420 the structural variation internal to and external to (i.e., in relationship to the rest of the capsid) the VP1 Myelin P2/CRABP Cores and Toxin Core residues. It can also be used to determine whether features present on trimers of alpha-bungarotoxin dimers, largely missing in the picornaviruses due to the lack of threading of any ABT chain B residues 49 – 74 in the VP1 proteins, have been reconstituted and presented on emergent viruses that cause paralysis.

425 Although picornaviruses all have Toxin Cores (Figure 1 Sections A-1 to A-6 and B-1 to B-5), only the residues 1 – 48 of the ABT B chain are threaded in the VP1, VP2, and VP3 proteins. For this reason, only a subset of the loops that are presented by alpha-bungarotoxin dimers are presented by the Toxin Cores on the capsid surface. Because of the absence of the residues that would correspond to the C-terminal residues of ABT chain B, picornaviruses as a group have not maintained all the loop sequences necessary to form a toxin-like  
430 domain associated with a protein assembly's ability to engage acetylcholine receptors on their capsids.

## **Loops Common to Toxins Are Found on Mahoney Poliovirus and EV-D68 ET AL.**

We identified TOX DOMAINS formed from ABT-like loops from residues both within the Toxin Cores and outside of the Toxin Cores. Figure 1 shows the locations of distributed residues in the sequences of specific  
435 viruses that appear to be able to form a domain which is associated with the capacity to induce paralysis, i.e., the feature is present in toxins and viruses (and specific closely related viruses) known to induce paralysis. Loop residues in the ABT A chain and partial B chain present in the VP1 Toxin Cores are designated by “-T” in Figure 1 and are found in Figure 1 Sections: B4 Subsections 1 and 2; B5 Subsection 1, A-1 Subsections 6, 7, and 9; A-3 Subsections 1 and 2; and A-2 Subsections 1 and 2. These residues are shown in Figure 2 on the row  
440 labelled “ALPHA BUNGAROTOXIN LOOP RESIDUES.” Loop residues outside the Toxin Cores or outside of VP1 that present to spatial positions that are similar to positions of ABT common toxin residues in the complete superposed trimer of ABT dimers but that are missing from the VP1 Toxin Cores (“SPATIALLY RECONSTITUTED TOXIN LOOPS” ) are designated by “-ST” in Figure 1 and are found in Figure 1: PIV1, EV-D68 ET AL. VP1 Section I-1 Subsection 1 and Section I1-2 Subsections 3 and 4; PIV1 VP1 Sections M-12  
445 Subsections 1 and 2; and EV-D68 ET AL. VP2 Section A-3 Subsection 2.

## **Alpha-Bungarotoxin Cores, The Common Toxin Loops, and EV-D68**

The superposition of alpha-bungarotoxin residues on their corresponding EV-D68 VP1 residues allowed us to make construct a model trimer of ABT dimers. This produced several interesting results. We previously identified loop residues common to several toxins [12], including ABT, anthrax lethal factor, botulinum toxin,  
450 clostridium toxin, and staphylococcal enterotoxin I. It was not until we superposed the ABT atoms on the

corresponding EV-D68 atoms to make the ABT trimers that it became clear what role the residues in the conserved loops play in the toxin structure. Figure 10 Panel A shows the constructed ABT trimer and the residues in ABT that are relatively common to toxins. Figure 10 Panel B shows that two of the conserved ABT A chain loops (GENLC and TDKN) form an tight annulus of complimentary charge with the other two loops (YEE and DGF) taking up a position opposite one another such that the TYR and PHE residues can interact. This configuration would act to lock the trimer A chain annulus into position, presenting another set of toxin loops from the B chain. Since only the ABT chain B residues 1 – 48 are threaded in the VP1, VP2, and VP3 sequences, key loops engaged in the binding of acetylcholine receptors would be expected to be absent unless they were added to the sequence in places outside of the Toxin Core.

## 460 **Spatially Reconstituted Toxin Loops And The Paralysis Associated Domain**

Figure 2 shows the locations of the SPATIALLY RECONSTITUTED TOXIN LOOP residues in the rows marked “POLIO (PV-1 MAHONEY) CAPSID TOXIN-LIKE LOOP RESIDUES”. Figure 2 shows the locations of the Toxin Core loop residues in the rows marked “EV-D68 (PATHOGENIC) CAPSID TOXIN-LIKE LOOP RESIDUES”. Figure 10 Panels C and D show the toxin-like residues in the EV-D68-4WM7 constructed capsid. The EV-D68-4WM7 residues deviate from the other pathogenic sequences in that: the critical (A/T)TDK\_N SPATIALLY RECONSTITUTED TOXIN LOOP in the pathogens has been replaced by THKN in the crystal structure (4WM7.PDB); and the threonine and other residues N-terminal to the HNK (SSAGT) are missing from the structure. In the Figure 1 VP1 ONLY INSERTS I1-2 Section, residues in loops common to toxins [12] are found in two types of picornaviruses known to cause paralysis: pathogenic EV-D68 ET AL. and PV1 (Mahoney strain poliovirus). PV1 exhibits the KDK sequence (in the Figure 1 VP1 I1-2 Section) that is also found in clostridium tetanus toxin (Table 9 of reference [12]) while EV-D68 exhibits the VP1 I1-2 residues TDK\_N found in alpha bungarotoxin. A second set of loop residues (e.g., D or N in EV-D68 VP1 and DN in PV1 (and PV2 and PV3) VP1) are found in Figure 1 Section I1-1. An examination of VP1234 trimers, myelin P2 trimers, and trimers of ABT dimers shows that residues in the Figure 1 Insert Sections I1-1 and I1-2 present to the same spatial position as residues from ABT chain B if the entire ABT B chain (rather than only residues 1 – 48 of the ABT B chain) were threaded in the VP1, VP2 and VP3 proteins. The paralysis associated feature (designated by “-T” in the Figure 1 VP1 and VP2 header Section lines) is comprised of four loops which form a domain common to toxins [12] (see Figure 11 of Reference [12]) and is found in the poliovirus PV1 and in specific pathogenic enteroviruses (i.e., EV-D68 ET AL.). The toxin loops [12] in the picornaviruses are Figure 1: VP1 Section I1-2 Subsections 2 and 3 residues-(A/T) TDKN and KDK (“TOXLOOP1”); VP1 Section A1 residues DGF and DAF (“TOXLOOP2”); VP1 Section A2 residues GNLC and VP1 Section I1-1 residues DN (“TOXLOOP3”); and VP1



Section M-12 Subsections 1 and 2 residues DD (PV1 only) and VP2 Section A-3 Subsection 2 residues (pathogenic EV-D68 ET AL. VP2 only (“TOXLOOP4”). It can be seen that the appearance of one of these alternative sets of residues (see Figure 11 of reference [12]) in a position corresponding to Figure 1 Section I1-2 is coupled to the presence of a DD in VP2 in both EV-D68 sequence Section A3 Subsection 2 and in PV1 sequence Section M-12 Subsections 1 and 2. These two features (EV-D68 TOXLOOP1 TDKN in Figure 1 VP1 Section I1-2 and EV-D68 TOXLOOP4 DD in Figure 1 VP2 Section A-3 Subsection 3; and PV1 TOXLOOP1 KDK in Figure 1 VP1 Section I1-2 and PV1 TOXLOOP4 DD in Figure 1 VP1 Section M12 Subsections 1 and 2) are in the same spatial position and complete their respective TOX DOMAINS. We hypothesize that these TOX DOMAINS are responsible for the induction of paralysis by the virus.

TOXLOOP1 in the EV-D68 ET AL. TOX DOMAIN may act to enhance the binding of the EV-D68 capsid to acetylcholine receptors and/or the binding of plecornaril to EV-D68. Figure 10 panels C – J show VP1 residues H87-K88-N89 (Figure 1 Section I1-2 Subsections 3 and 4) as dots. Figure 10 panels I – J also show VP1 residues A80 (Figure 1 Section B2 Subsection 2), I211 (Figure 1 Section I1-4 Subsection 4), and T216-I217 (Figure 1 Section A2 Subsection 2) as dots. Figure 10 panels G – J show plecornaril, a proposed antiviral, as white spheres. An examination of Figure 1 VP1 Figure 1 Section I1-2 Subsections 3 and 4 shows that the 4WM7 EV-D68 (“EV-D68-4WM7”) sequence in the crystal structure deviates from other reported pathogenic EV-D68 sequences (e.g., AIS73051, BAK08580, AIS73057, ABL61317, AIZ48771, and AGC00381). The EV-D68-4WM7 sequence has T86/A86-**H87**-K88-N89 instead of the sequence T86-**D87**-K88-N89 found in AIS73051, BAK08580, AIS73057, ABL61317, AIZ48771, and AGC00381. This difference is easy to miss as the T86 residue and the preceding five residues (S81-S82-S83-A84-G85) are not reported in the EV-D68-4WM7 crystal structure. Also not reported in the EV-D68-4WM7 crystal structure are residues N212-P213-A214-D215 (found between Figure 1 Section I1-4 Subsection 4 and Figure 1 Section A2 Subsection 2). In Figure 10, residues A80 and H87 (shown by dots) represent the endpoints of the missing residues before the (T86/A86-**H87**-K88-N89)/(T86-**D87**-K88-N89) loop. Since the EV-D68-4WM7 crystal structure omits residues N212-P213-A214-D215 (Figure 1 Section, the residues just preceding the EV-D68-4WM7 G218-N219-L220-C221 toxin loop, in Figure 10 panels I and J, residues I211 and T216-I217 are shown by brown dots representing the endpoints of the missing residues N212-P213-A214-D215.

The residue difference at EV-D68 D87H and the absence of the S81-S82-S83-A84-G85 residues (Figure 1 Sections B-2, B-3 and A and I1-2) and N212-P213-A214-D215 residues (Figure 1 Sections I1-4 and A-2) are significant. The residues in the T86/A86-**H87**-K88-N89 loop would not be expected to engage an acetylcholine receptor but the T86-**D87**-K88-N89 is a key component of the toxin domain. The absence of the

S81-S82-S83-A84-G85 residues prevents an assessment of the mobility of the 86/A86-~~H87~~-K88-N89 loop by using the crystal structure. Given the endpoints of the missing residues N212-P213-A214-D215, it is clear that the N212-P213-A214-D215 residues are adjacent to the bound plecornaril, may contact the bound plecornaril, and may impact the binding of plecornaril. It cannot be determined whether the spatially adjacent EV-D68 VP1 loop residues G129-N130-N131-D132-S133-T134 (Figure 1 Section M-7) have any impact on the T86-~~D87H~~-K88-N89 loop as these residues are also absent from the 4WM7 structure. An examination of Figure 10 panels K and L show the location of the residues flanking the missing G129-N130-N131-D132-S133-T134 (Figure 1 Section M-7) in relationship to the residues flanking the missing S81-S82-S83-A84-G85, the residues flanking the missing N212-P213-A214-D215, and the bound plecornaril in the capsid tiling piece (i.e., in a single 3xVP1234). An examination of Figure 1 shows other differences between EV-D68-4WM7 and other pathogenic sequences, e.g. VP1 Sections M-6 Subsection 5 and M-7 shows that pathogenic EV-D68 VP1 proteins (AIS73051, BAK08580, AIS73057, ABL61317, AIZ48771, AGC00381) in Figure 1 have the sequence A-V-(N/S)-(G/\_)-S-(S/G/N)-(N/S)-(N/S)-T-Y. An examination of Figure 1 Sections E-6 to E-14 also shows that polio-associated VP1 sequences (EVC-PV1-M/1HXS, EVC-PV2-1EAH, and EVC-PV3-S-1PIV) have a sequence of (A/\_)-N-F-T-(E/D/N)-(A/T)-N-N. This is in contrast to VP1 EVD-94 FN07 (ABK88241) that has a sequence of L-Y-T-\_-S-T-G-A-S-Y and VP1 EV-D68 US14 (4WM7) that has a sequence of A-V-N-G-N-N-~~D~~-S-T-Y.

## Sialic Acid Binding Domain in EV-D68

Figure 1 identifies the sequence positions of residues that can form a binding pocket in EV-D68. This binding pocket is similar to that found in a functionally validated influenza sialidase. The components of a sialic acid binding site can be formed by residues found in Figure 1 Sections I13-1, I1-1, M-8, M-12, A-2, M-13, I1-5 and M-16. The putative sialic acid binding site residues in EV-D68 VP1 are identified in Figure 1 by a “-SW” and their positions are shown relative to other binding components that we have identified in Figure 2 in row marked “SIA BINDING SITE COMPONENT POSITION (WEININGER)”. The “SIA BINDING SITE COMPONENT POSITION (WEININGER)” residues can be compared to the VP1 residues contacting sialic acid in 4Q4Y.PDB. The 4Q4Y.PDB residues contacting sialic acid are identified in Figure 1 by a “-SP” and are identified in Figure 2 in the row marked “SIA BINDING SITE COMPONENT POSITION (4Q4Y.PDB)”.

Figure 11 shows that EV-D68 VP1 trimers contain and present the components of a sialic acid active site binding domain. Figure 11 also shows the spatial relationship between sialic acid binding site components and the toxin loop residues. Figure 11 Panels A and B show an influenza N6 neuraminidase [13] with key active site residues as spheres [12]. The common sialic acid active site residues in the N6 neuraminidase [12] are: Y412 (tan), D157 (red), R124 (cyan), G227 (red), R158 (cyan), R 299 (cyan), and W185 (orange). Panel B also

545 shows the sialic acid atom spheres (in green) in the functionally validated sialidase (N6 neuraminidase) binding pocket [13]. Figure 11 Panels C and D show EV-D68 VP1 trimer cartoons with the residues of the putative sialic acid binding site that we have identified shown as spheres. The Figure 1 sections containing putative sialic acid binding site residues are marked with subsection title suffix “-SW” in the Figure 1 row labeled “SUBSECTION DESCRIPTOR MARKER” (i.e., E75 (red, Figure 1 Section I13-1), Y76 (yellow, Figure 1 Section I13-1), D140 (red, Figure 1 Section M-8), W163 (orange, Figure 1 Section M-12), R223 (blue, Figure 1 Section A-2), 550 E227 (red, Figure 1 Section M-13), R270 (blue, Figure 1 Section I1-5) and R284 (blue, Figure 1 Section M-16). Figure 11 Panel D also shows, in only one VP1, the sialic acid atom spheres (in green) placed in the putative EV-D68 binding pocket. Panel E shows the same residues as in panel C for each VP1 in the EV-D68 3xVP1234 VP1 trimer. Panel F shows the same residues as in panel E but additionally shows the EV-D68 TOX DOMAIN residues (magenta spheres). The threading of the EV-D68 TOX DOMAIN residues is shown in Figure 2 in the 555 row labelled “EV-D68 (PATHOGENIC) CAPSID TOXIN-LIKE LOOP RESIDUES.” It can be seen from an examination of Figure 11 Panels C and E that the binding pocket can be constructed from residues in two separate VP1 chains, i.e., the two most C-terminal arginines are spatially best presented by adjacent chains. It can also be seen that the putative receptor binding sites for sialic acid and the acetylcholine receptor co-exist on the outer capsid tiling piece face and have a residue in common. The EV-D68 residues that we have 560 identified as a putative sialic acid binding site approximate many of the features of the N6 neuraminidase sialic acid binding site. Figure 1 shows that HRV-87 has the same sialic acid binding site as EV-D68. HRV-87 attachment and infection requires the presence of sialic acid on cellular receptors [47]. Although the presence of sialic acid binding components in EV-D68 is not sufficient to suggest that the components function as a sialidase, the presence of these components may indicate that EV-D68 is competent to engage sialic acid on 565 cellular receptors.

## **VP3 Protein Beta Sheets Circling The Pentamer Interface Form The Base Of A Diaphragm Shutter-like Pore**

570 Constructing the TMEV-1 and TMEV-2 capsid tiling pieces allowed us to explore the impact of residue positional variation in the constructed capsids. While the static coordinates of the X-ray crystal structures are dependent on the crystallization conditions, including solvents and co-crystallized molecules, they are examples of possible, stable, orientations of the crystallized VP1, VP2, VP3, and VP4 protein assemblies (VP1234). Figure 12 shows, in the context of constructed capsid proteins, how corresponding residues in the X-ray crystal structures of the VP1234 for TMEV-1 and TMEV-2 are in different positions. This structural variation between the TMEV-1 VP1234 and TMEV-2 VP1234 can be interpreted as permitted relative motion of capsid parts. Figure 12

575 Panels A and B show the VP1 proteins in the TMEV-1 and TMEV-2 capsid tiling pieces (3xVP1234) and Panel C shows their superposition; Panels D and E show the VP2 proteins in the TMEV-1 and TMEV-2 capsid tiling pieces and Panel F shows their superposition; Panels G and H show the VP3 proteins in the TMEV-1 and TMEV-2 capsid tiling pieces and Panel I shows their superposition; and Panels J and K show VP4 proteins and a portion of VP1 (i.e., the white and grey residue marker spheres) in the TMEV-1 and TMEV-2 capsid tiling  
580 pieces and Panel L shows their superposition. The position and identity of corresponding representative residue markers in TMEV-1 and TMEV-2 in Figure 12 are noted in the Figure 1 row labelled "SUBSECTION DESCRIPTOR MARKER" with the subsection title suffix "-M."

As can be seen in Figure 5, the sequence and spatially invariant VP3 prolines listed in Tables 3 and 4 are positioned at the yellow vertices of TRI-78. In Figure 12 Panels A– L, additional sequence equivalent  
585 residues ("markers") from TMEV-1 and TMEV-2 are shown and can be used to track relative positional differences in the TMEV-1 and TMEV-2 constructed capsids. In Figure 12 Panels M – O, the white (TMEV-1 VP1 S11-N12-D13-D14) and grey (TMEV-2 VP1 S11-N12-D13-D14) residue marker spheres indicate the small relative difference in position of these residues on the RNA side of the constructed capsid. The white and grey residue markers of Figure 12 Panels M – O correspond to residues in the myelin P2 helix residues in Figure 1  
590 Section M-2. The other residue markers (red, brown, orange, and purple) shown in Figure 12 Panels M – O have significantly different relative positions in the TMEV-1 and TMEV-2 capsid tiling pieces. Figure 12 Panels P and Q show the VP3 protein cartoons and the corresponding VP1, VP2, and VP3 residue marker spheres in pentamers of TMEV-1 and TMEV-2 capsid tiling pieces and Figure 12 Panel R shows their superposition. An examination of the similarities and differences in the position of these markers indicates that the VP3 proteins in  
595 the capsid appear to change position relative to one another in a way that resembles the opening and closing of an iris diaphragm shutter with the VP3 MP2/CRABP Cores acting as shutter components. The VP3 beta sheets are the shutter components lining the pore. The portion of the pore formed from the VP3 residues is set up to alternate between being a physical barrier and an opening for A-particle ejection.

Mapping of the relative positions of the VP3 atoms in the TMEV structures supports an interpretation  
600 that there may be a diaphragm shutter-like motion of VP3 proteins relative to VP1 and VP2 proteins. This motion would be sufficient to opens and shut the capsid pentamer pore. Figure 13 panels A, B, and C show TMEV-1 and/or TMEV-2 structure cartoons with their proline residue main chain oxygen atoms as spheres. Panel D shows lines between sequence equivalent proline main chain atoms in TMEV-1 and TMEV-2. The lines in Panel D show that there is an unhindered trajectory to move the TMEV-1 VP3 structure into the  
605 TMEV-2 VP3 structure position in a diaphragm shutter-like motion.

## Using Insert Residue Positions To Isolate Variations in Relative Position of Aligned Structures

Figure 14 shows the FMDV, TMEV-2, TMEV-1, PV1, and EV-D68 residues that are in the Insert sections of Figure 1, i.e., the residues that are not in the Myelin P2/CRABP Core or the Toxin Core sections. Figure 14 Panels A1 – A5 and Panels B1 – B5 show Insert residues for the VP1 trimers colored according to their Figure 1 Section color. These VP1 Insert residues: appear to be concentrated on the outer face of the capsid, include residues that we have identified as possible receptor binding residues, and may impact the state of the ion channel as they are positioned over the channel at the center of the capsid face. Figure 14 Panels C1 – C5 and Panels D1 – D5 show Insert residues for the VP2 trimers colored according to their Figure 1 Section color. Figure 14 panels C and D show that VP2 Inserts are found in extended and condensed structural forms. Whether the structures are extended or condensed may directly impact the positioning of residues at the capsid face interface and therefore the state of the assembled capsid. Figure 14 Panels E1 – E5 and Panels F1 – F5 show Insert residues for the VP3 trimers colored according to their Figure 1 Section color. Figure 14 panels E and F show the VP3 Inserts are positioned to impact the functioning of the capsid pore at the vertices of the capsid faces. If the structural positional variation between TMEV-1 and TMEV-2 can be interpreted as permitted relative motion, then the positional differences in the bulk distribution of the insert residues suggest that: a) VP1 inserts take up different radial positions on the outer capsid face over a channel at the center of the tiling piece; b) VP2 inserts can twist and interlock or be separated radially relative to a channel at the center of the tiling piece; and c) VP3 inserts can pivot about conserved VP3 proline atoms. Figure 14 Panels G1 – G5 and H1 – H5 are composites of VP1, VP2, and VP3 trimer Inserts that suggest that the capsid is capable of cooperatively and reversibly undergoing an extended to condensed structural change.

## Each Picornavirus Capsid Tiling Piece Has A Myelin-P2 Trimer-like Ion Channel At Its Center

Superposition of the myelin P2 trimers with the picornavirus capsid tiling pieces also reveals that each myelin trimer, CRABP trimer, and picornavirus capsid tiling piece presents an ion channel-like structure at their centers (“Ion Channel”). The Ion Channel is formed by residues in the Myelin P2/CRABP Core Figure 1 Sections M-5, M-6, M-7, M-8, M-9, M-10, M-13, and M-14 (“Channel Sections”). An examination and comparison of structures in Figure 8 indicates that the Ion Channels are gated by the residues found in Figure 1 Sections M2, M3, and M4 (“Helix Sections”). Figure 15 shows the Channel Section residues and Helix Section residues for the myelin P2 trimer and the FMDV, TMEV-2, TMEV-1, EV-D68, and PV1 VP1 trimers. Channel Section residues are shown as spheres. Helix Section residues are shown as dots. Figure 15 Panels in column one (A1, B1, C1,

D1, E1, and F1) and column two (A2, B2, C2, D2, E2, and F2) show the OUTER view. Figure 15 Panels in column three (A3, B3, C3, D3, E3, and F3) and column 4 (A4, B4, C4, D4, E4, and F4) show the INNER view. As can be seen in Figure 15 Panels A1 – A4, the myelin P2 Helix Section (Figure 1 Section B) residues are positioned such that they are not in the constructed myelin P2 Ion Channel. Similarly, the VP1 Helix Section residues in EV-D68, PV1, and TMEV-1 also take up a radial position that places these residues away from the Ion Channel. In contrast, FMDV and TMEV-2 have VP1 Helix Section residues placed in or about the Ion Channel. It can be seen from Figure 15 Panels B4 and C4 that FMDV and TMEV-2 have VP1 Helix Section residues (dots) in the Ion Channel. This is in extreme contrast to the TMEV-1 Helix Section residues shown in Figure 15 Panel D4. This suggests that the Helix Section residues can be moved into a position to gate the Ion Channels in the capsid when the Ion Channel is open. The fact that TMEV-1 and TMEV-2 have nearly identical sequences and that the Helices Section residues take up different radial positions (as shown in Figure 15 Panels C4 and D4) supports the assertion that the Helix Section residues are involved in “gating” the Ion Channel.

Any interaction that locks the Ion Channel, i.e., that prevents the transition of a closed channel to an open channel or prevents the Helix Section residues from taking up a position over the Ion Channel would be expected to impact the functioning of the Ion Channel and therefore impact viral uncoating. As shown in Figure 15 Panels E1 and F1, the ability to reposition VP1 residues between channel transition states may be altered in EV-D68 and PV1 as there are no negatively charged residues in the channel area lobes to attract positively charged potassium ions. For comparison, Figure 15 Panel G1 and G2 show residues (G53 to P83) from the functionally validated *Streptomyces lividans* potassium ion channel [49] holding potassium ions. As can be seen from Figure 15 Panels G1 and G2, the potassium ions (white spheres) are attracted to the channel by the negatively charged residues that ring the channel. Figure 15 Panels G3 and G4 show the same potassium atoms superposed in the TMEV-2 VP1 Ion Channel with the Helix Two residues not shown. As can be seen from an examination of Figure 15 Panels G3 and G4, the potassium atoms fit well within the Ion Channel with a set of valine (VP1 VAL41) residues poised to strip the waters from the potassium atoms as they transverse the Ion Channel. The VP1 Ion Channel appears to have many of the features of a potassium channel: negative residues to attract the potassium ion to the channel, residues in the channel that can strip the waters from the potassium ion as it transverses the channel, and residues that can “pull” the potassium atoms through the channel by changing position over the channel.

## 665 Discussion

Picornavirus capsids are formed largely from Myelin P2/CRABP Cores and Toxin Cores. We showed that myelin P2 and alpha-bungarotoxin sequences are threaded in specific regions of the picornavirus VP1, VP2,

and VP3 sequences, suggesting that the picornaviruses are evolutionarily related to myelin P2, CRABP, and toxins. Model myelin P2 and CRABP trimers can be formed by mapping atoms in myelin P2 and CRABP onto  
670 points used to tile the picornavirus VP1234. At the center of each picornavirus capsid face (seen in the center of the model capsid tiling piece) appears to be an ion channel gated by the MP2/CRABP-like helices. Each picornavirus capsid vertex (seen in the center of a pentamer of model capsid tiling pieces) presents a separate pore that has the features of a diaphragm shutter. An influx of ions entering through the gated ion channel may function to eject the A-particle through the pore.

675 EV-D68, EV-D70, and PV1 capsids present the components of TOX DOMAIN on their capsids and are associated with infection induced paralysis. This TOX DOMAIN has loops that are similar to those found on alpha-bungarotoxin, staphylococcal enterotoxin I, botulinum toxin, anthrax lethal factor, tetanus toxin, and the highly anomalous emergent influenza virus H18N11 (Table 9 of reference [12] and Figure 12 of reference [12]). The absence in specific picornaviruses of some of the residues in the alpha-bungarotoxin loops that are  
680 common to toxins suggests that the picornaviruses may not have had or may not have maintained all of the toxin binding components. However, we found that the complete TOX DOMAIN has been reacquired by specific emergent viruses such as EV-D68 and EV-D70. This TOX DOMAIN has previously been seen in Mahoney poliovirus PV1. A comparison of the presentation of alpha-bungarotoxin residues in alpha-bungarotoxin trimers superposed with the VP1 trimers of EV-D68 and PV1 suggests that residues from VP1 and VP2 trimers of EV-  
685 D68 and VP1 trimers of PV1 may have some capacity to engage acetylcholine receptors and that this is related to their ability to induce paralysis. We hypothesize that TOX DOMAINS found in ABT, PV1, EV-D68, and EV-D70 are the structures responsible for the binding of the capsids and the proteins toxins to the acetylcholine receptor and that this binding is the cause of paralysis. The PV1 TOX DOMAIN and pathogenic EV-D68, EV-D70, EV-D94, and HRV-87 TOX DOMAINS are comprised of residues on loops that are found in the same  
690 spatial position on the virus capsid as in the constructed alpha-bungarotoxin chain B trimer (all residues). There is no threading of alpha-bungarotoxin chain B residues 49 – 74 in VP1, instead, the loops that complete the TOX DOMAIN (“SPATIALLY RECONSTITUTED TOXIN LOOPS”) are seen in inserts and are in anomalous positions. SPATIALLY RECONSTITUTED TOXIN LOOPS are present both in Figure 1 VP1 ONLY Section I1-2 Inserts (as in the case of PV1, EV-D68, EV-D70, EV-D94, and HRV-87) and in positions in sequences not associated with  
695 the Toxin Cores (i.e., M-12, as in the case of PV1). Our findings suggest that the EV-D68, EV-D70, and PV1 virus can engage motor neurons by binding to the nicotinic acetylcholine receptor using the alpha-bungarotoxin-like residues. The presence of structures on the EV-D68 capsid necessary to engage the nicotinic acetylcholine receptor may be associated with the susceptibility, especially of young children, to limb paralysis due to EV-D68

infection. EV-D68 and EV-D70 may also be engaging cells using their ability to bind sialic acid. The ability to  
700 engage sialic acid broadens the cell entry options of the virus, broadens the cellular reservoirs of the virus, and  
creates a persistent threat of nervous system infection upon re-activation of the EV-D68 or EV-D70 virus.

That injected myelin P2 and infection by TMEV can each cause a multiple sclerosis-like disease, and  
that myelin P2-like helices are present on picornaviruses suggests that there is a viral origin to some human  
multiple sclerosis due to the presentation of the myelin P2-like helices by the virus to the immune system during  
705 infection. We suggest that any chemical that induces channel dysfunction may inhibit to some extent viral  
infection but could result in exposure of the MP2/CRABP-like helices to the immune system during viral  
uncoating. Molecules that bind to the alpha-bungarotoxin-like domains of EV-D68 may have the effect of  
inhibiting channel function but may also induce the exposure of the MP2/CRABP-like helices in viral particles  
that bind the acetylcholine receptor. Any chemical that induces the exposure of the MP2/CRABP-like helices  
710 during partial uncoating of the capsid would be expected to induce multiple sclerosis. We hypothesize that the  
binding of EV-D68/EV-D70 alpha-bungarotoxin components to acetylcholine receptors is the cause of Acute  
Flaccid Paralysis by EV-D68 and EV-D70, and that this binding produces incomplete capsids that expose the  
myelin P2/CRABP helices in the capsid tiling piece initiating multiple sclerosis. We hypothesize that it is the  
binding of the acetylcholine receptor and initiation of multiple sclerosis that results in episodic Guillain-Barré  
715 Syndrome.

The center of each picornavirus capsid face (seen in the center of the model capsid tiling piece) appears  
to be an ion channel gated by the MP2/CRABP-like helices. The fact that the constructed myelin P2 and CRABP  
trimers have internal channels lined with charged residues and that the same channel surfaces are presented in  
TMEV-2 argues that both myelin P2 trimers and picornavirus capsid tiling pieces may have ion channels. The  
720 fact that EV-D68-4WM7 does not have a balance of charge in the same structures that would form the channel  
in other picornaviruses suggests that EV-D68-4WM7 employs a different mechanism utilizing alpha-  
bungarotoxin-like or sialidase-like domains to enter cells. Each picornavirus capsid vertex (seen in the center of a  
pentamer of model capsid tiling pieces) presents a separate pore that has the features of a diaphragm shutter.  
An influx of ions entering through the gated ion channel may function to eject the A-particle through the pore.

725 Conserved proline atoms in the VP1, VP2, and VP3, when mapped onto the faces of an icosahedron,  
allow the construction of a complete model capsid for each picornavirus. The superposition of model  
picornavirus VP1-VP2-VP3-VP4 assemblies ("VP1234") onto an idealized structure using VP1, VP2, and VP3  
atoms that are internal to the VP1234 assembly shows that the tiling of the virus capsid and the overall capsid  
structure is inherent to the VP1-VP2-VP3 assembly structure. All picornavirus model structures thus created



730 share a common reference frame making it possible to perform a comparative structural analysis. The use of  
atoms with conserved geometry to superpose structures [12] is also a powerful tool and is essential for the  
comparative structural anatomy of molecules. The ability to identify and relate the structural and functional  
correlates of sequence variation in emergent viruses from previously unrelated molecules is especially critical in  
evaluating emerging pathogens and in identifying new features on emergent viruses. Alignment of sequences to  
735 reference sequences provides a means of isolating and relating common structural features in previously  
unassociated proteins. We have demonstrated the usefulness of using reference sequences, prolines and  
glycines, and unique residue groupings to bracket and align groups of residues. The previously unassociated  
proteins myelin P2, CRABP, and alpha-bungarotoxin were used to organize and parse the structures of the  
picornavirus VP1, VP2, and VP3 proteins. The use of reference structures, such as myelin P2, CRABP, and  
740 alpha-bungarotoxin, to define structural groupings within a functionally divergent class of proteins, such as the  
picornavirus VP1, VP2, and VP3 proteins, is a powerful, general tool. The identification of myelin P2-like,  
CRABP-like, and alpha-bungarotoxin-like sequences threaded through the picornavirus VP1, VP2, and VP3  
proteins illustrate the method of using reference sequences to align structural groups and isolate functional  
groups.

## 745 **Supporting Information**

### **ICOS135.PDB**

Ideal 135 Angstrom-on-an-edge icosahedron ("ICOS135").

### **TRI78.PDB**

750 Ideal 78 Angstrom-on-a-side equilateral triangles ("TRI78"), positioned with their vertices on ICOS135  
icosahedron edges, and 45 (and 90) Angstroms away from ICOS135 icosahedron vertices.

### **CASOG\_ONE\_CAPSID\_POINTS.PDB**

Points at the vertices of scalene equilateral triangles coplanar with, positioned within, and sharing one  
vertex with, TRI78 triangles.

### **CASOG\_TWO\_CAPSID\_POINTS.PDB**

755 Ideal 26 Angstrom-on-a-side equilateral triangles ("TRI26"), positioned at the corner of, and coplanar with,  
TRI78 equilateral triangles.

### **PICORNAVIRUS\_TILING\_POINTS.PDB**

760 Idealized superposition points ("PICORNAVIRUS TILING POINTS") for creating picornavirus capsid tiling  
pieces, myelin P2 trimers, and CRABP trimers. PICORNAVIRUS TILING POINTS are all located on or  
within the first listed triangle in TRI78, which is within the first ICOS135 listed triangle (i.e., the first  
icosahedron face). Chain 1 contains CASOG-1 tiling points. Chain 2 contains CASOG-2 tiling points.  
Chain 3 contains myelin P2/CRABP trimer tiling points.

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**Table 1.** Abbreviations, reference numbers, sequence and structure sources, description and structure resolutions.

Abbreviation.	Ref.	Source	Description	Res.
ABT	7	2ABX.pdb	Alpha-bungarotoxin	2.50°
CRABP	5	1CBS.pdb	CRABP I and II w/ all-trans-retinoic acid and a retinoid	1.80°
EVA-71-1	21	3VBH.pdb	Enterovirus 71 (FUYANG, ANHUI. P.R.C/17.08/1)	2.30°
EVA-71-2	22	4CEW.pdb	Human Enterovirus 71 with Uncoating Inhibitor ALD	2.75°
EV-B5-SVDV	26	1OOP.pdb	Swine Vesicular Disease Virus	3.00°
EV-B-CV-A9	23	1D4M.pdb	Coxsackievirus A9	2.90°
EV-B-CV-B1	33	AAO84300	Coxsackievirus B1	
EV-B-CV-B1	34	AET37232	Coxsackievirus B1	
EV-B-CV-B1	35	NP_040958	Coxsackievirus B1	
EV-B-CV-B3	36	P03313	Coxsackievirus B3 (strain Nancy)	
EV-B-CV-B3M	24	1JEW.pdb	Coxsackievirus B3 (M Strain) w/cellular receptor (CAR)	22.00°
EV-B-CV-B6	37	AAF12719	Coxsackievirus B6	
EV-B-ECHOV-7	25	1M11.pdb	Echovirus 7 w/bound Human Decay-Accelerating Factor	16.00°
EV-B-ECHOV-7+	45	AAK85711	Echovirus E7	
EV-C-CV-A21	27	1Z7S.pdb	Coxsackievirus A21	3.20°
EV-C-CV-A24	28	4Q4Y.pdb	Coxsackievirus A24V w/Disialyllacto-N-Tetraose (DSLNT)	1.88°
EV-C-CV-C105	38	JX514943	Human Enterovirus C105	
EV-C-PV1-M	8	1HXS.pdb	Poliovirus Type 1 (Mahoney)	2.20°
EV-C-PV2	9	1EAH.pdb	Poliovirus Type 2 (Lansing) with antiviral (SCH48973)	2.90°
EV-C-PV3-S	10	1PIV.pdb	Poliovirus Type 3 (P3/LEON) with antiviral (WIN51711)	2.90°
EV-D68-CH14	39	AIZ48771	Enterovirus D68	
EV-D68-JP11	40	BAK08580	Enterovirus D68	
EV-D68-NZ13	41	AGC00381	Enterovirus D68	
EV-D68-SW07	42	ABL61317	Enterovirus D68	
EV-D68-4WM7	11	4WM7.pdb	Enterovirus D68 complexed with PLECONARIL	2.32°
EV-D68-US14-1	43	AIS73051	Enterovirus D68	
EV-D68-US14-2	44	AIS73057	Enterovirus D68	
EV-D-HRV87-US4	47	AAQ19942	VP1 capsid protein, partial [BHuman rhinovirus 87]	
EV-D70-UK09	45	BAA18891	Enterovirus 70	
EV-D94-FN07	46	ABK88241	Enterovirus 94	
EV-G5-27	29	1BEV.pdb	Bovine Enterovirus VG-5-27	3.00°
FMDV	14	1BBT.pdb	Foot-And-Mouth Disease Virus (BFS, 1860)	2.60°

HRV-A16	31	1AYM.pdb	Rhinovirus 16	2.15°
HRV-A2	30	1V9U.pdb	Rhinovirus 2 with cellular receptor (VLDL receptor)	3.60°
HRV-B14	32	1D3I.pdb	Rhinovirus 14 with cellular receptor (D1D2-ICAM-1)	26.00°
MYELIN P2, MP2	6	2WUT.pdb	Human myelin protein P2 in complex with palmitate	1.85°
N6 NEURAMINIDASE	13	1WIX.pdb	N6 neuraminidase with sialic acid (NANA, NEU5AC)	2.00°
TMEV-1	19	1TME.pdb	Theiler's murine encephalomyelitis virus	2.80°
TMEV-2	20	1TMF.pdb	Theiler's murine encephalomyelitis virus (BeAn strain)	3.50°



**Table 2.** Spatially conserved atoms internal to the VP1 proteins of a representative set of picornaviruses.

		VP1 + VP2 + VP3 Internal							
		VP1-RES1		VP1-RES2		VP1-RES3			
PDB	Protein	Res.	Atom	Res.	Atom	Res.	Atom		
1AYM	HRV-A16	P 146	1162	P 182	1449	P 248	2047		
1BBT	FMDV	P 90	703	P 118	912	P 188	1293		
1BEV	EV-G5-27	P 147	1024	P 183	1287	P 248	1827		
1D4M	EV-B-CV-A9	P 148	1170	P 184	1443	P 250	1984		
1EAH	EV-C-PV2	P 161	1046	P 197	1325	P 271	1897		
1HXS	EV-C-PV1-M	P 161	1141	P 197	1425	P 271	2006		
1OOP	EV-B5-SVDV	P 147	1072	P 183	1343	P 249	1871		
1PIV	EV-C-PV3-S	P 161	1127	P 197	1406	P 272	2000		
1TME	TMEV-1	P 147	1147	P 188	1450	P 246	1912		
1TMF	TMEV-2	P 149	1164	P 190	1465	P 248	1927		
1V9U	HRV-A2	P 147	1047	P 183	1332	P 247	1857		
1Z7S	EV-C-CV-A21	P 156	1107	P 192	1393	P 266	1980		
3VBH	EVA-71-1	P 157	1188	P 193	1454	P 263	2032		
4CEW	EVA-71-2	P 157	1188	P 193	1454	P 263	2030		
4Q4Y	EV-C-CV-A24	P 163	1114	P 199	1396	P 273	1993		
4WM7	EV-D68-4WM7	P 149	1079	P 185	1357	P 251	1850		

935 Table 2 lists specific proline main chain oxygens in the VP1 proteins of a representative set of picornavirus VP1-VP2-VP3-VP4 structure assemblies (“VP1234”). For each structure, these atoms were superposed onto the listed 1BBT atoms. (1BBT was arbitrarily selected as a spatial reference frame.) The aligned picornavirus VP1234 structures are shown in Figure 4, Column 1. Proline residues listed are indicated by an “@” in the VP1 header in Figure 1 between sections: M-11 and I13-2; M14 Subsection 8 and Subsection 9; and A-1 Subsection 3 and Subsection 4.

940 **Table 3.** Common Spatial Occupancy Group One (CASOG-1) tiling atoms.

PDB	Protein	Orientation	VP1 + VP2 + VP3 External								
			VP1-PRO1			VP2-PRO1			VP3-PRO1		
			Res.	Atom		Res.	Atom		Res.	Atom	
1AYM	HRV-A16	CASOG ONE	P	146	1162	P	128	3305	P	135	5375
1BEV	EV-G5-27	CASOG ONE	P	147	1024	P	128	3048	P	135	5009
1D4M	EV-B-CV-A9	CASOG ONE	P	148	1170	P	128	3207	P	136	5266
1EAH	EV-C-PV2	CASOG ONE	P	161	1046	P	128	3077	P	136	5220
1HXS	EV-C-PV1-M	CASOG ONE	P	161	1141	P	128	3227	P	136	5376
1OOP	EV-B5-SVDV	CASOG ONE	P	147	1072	P	128	3081	P	136	5106
1PIV	EV-C-PV3-S	CASOG ONE	P	161	1127	P	128	3223	P	136	5378
1TME	TMEV-1	CASOG ONE	P	147	1147	P	132	2920	P	131	4997
1V9U	HRV-A2	CASOG ONE	P	147	1047	P	128	3077	P	135	5161
1Z7S	EV-C-CV-A21	CASOG ONE	P	156	1107	P	128	3204	P	135	5338
3VBH	EVA-71-1	CASOG ONE	P	157	1188	P	128	3240	P	137	5243
4CEW	EVA-71-2	CASOG ONE	P	157	1188	P	128	3238	P	137	5241
4Q4Y	EV-C-CV-A24	CASOG ONE	P	163	1114	P	128	3222	P	135	5372
4WM7	EV-D68-4WM7	CASOG ONE	P	149	1079	P	128	3154	P	135	5123

Table 3 lists specific proline main chain oxygens in the VP1, VP2, and VP3 proteins of CASOG-1 VP1234 crystal structures. These atoms were superposed onto consecutive PICORNAVIRUS TILING POINTS having a chain identifier of "1" (i.e., the VP1-PRO1, VP2-PRO1, and VP3-PRO1 atoms were first superposed onto PICORNAVIRUS TILING POINTS 1, 2, 3, then onto 4, 5, 6, and lastly onto 7, 8, 9).

945 Table 3 proline atoms are aligned in Figure 1 Sections F-1 and D-14. Figure 3 illustrates the three separate superpositions of VP1234 required to construct a CASOG-1 picornavirus capsid tiling piece (3xVP1234). The constructed CASOG-1 picornavirus capsid tiling pieces are shown in Figure 4. Proline residues listed are flanked by an "\*" in Figure 1.

**Table 4.** Common Spatial Occupancy Group Two (CASOG-2) tiling atoms.

PDB	Protein	Orientation	VP1 + VP2 + VP3 External					
			VP1-PRO1		VP2-PRO1		VP3-PRO1	
			Res.	Atom	Res.	Atom	Res.	Atom
1BBT	FMDV	CASOG TWO	P 90	703	P 127	2375	P 127	4083
1TMF	TMEV-2	CASOG TWO	P 149	1164	P 132	3160	P 131	5234

950 Table 4 lists specific proline main chain oxygens in the VP1, VP2, and VP3 proteins of CASOG-2 VP1234 crystal structures. These atoms were superposed onto consecutive PICORNAVIRUS TILING POINTS having a chain identifier of “2” (i.e., the VP1-PRO1, VP2-PRO1, and VP3-PRO1 atoms were first superposed onto PICORNAVIRUS TILING POINTS 11, 12, 13, then onto 14, 15, 16, and lastly onto 17, 18, 19). The residues containing the Table 4 proline atoms are aligned in Figure 1 Sections F-1 and D-14. Figure 3 illustrates the three  
 955 separate superpositions of VP1234 required to construct a CASOG-2 picornavirus capsid tiling piece (3xVP1234). The constructed CASOG-2 picornavirus capsid tiling pieces are shown in Figure 4. Proline residues listed are flanked by an “\*” in Figure 1.

**Table 5.** Myelin P2 trimer and CRABP trimer tiling atoms.

Point #	Source	Atom #	Atom Type	Residue	Chain	Figure 1 Section/Subsection
1	2WUT	877	C	K 105	A	M-14/1
1	1CBS	871	C	T 110	A	M-13/3
2	2WUT	330	CG2	I 41	A	M-5/2
2	1CBS	324	CD	E 42	A	M-5/1
3	2WUT	506	CG2	I 62	A	M-6/3
3	1CBS	495	CG2	I 63	A	M-6/3

960 Table 5 lists the three myelin P2 (2WUT) atoms and the three CRABP (1CBS) atoms that were separately used to construct trimers from three superpositions of individual monomers and their Figure 1 Section/Subsections. These atoms were superposed onto consecutive PICORNAVIRUS TILING POINTS having a chain identifier of “3” (i.e., points 1, 2, and 3 of 2WUT atoms, or separately of 1CBS atoms, were first superposed onto PICORNAVIRUS TILING POINTS 21, 22, 23, then onto 24, 25, 26, and lastly onto 27, 28, 29). The destination points are derived from TMEV-1 and TMEV-2 capsid tiling points. The iterative superpositions of the Table 5  
 965 atoms onto the PICORNAVIRUS TILING POINTS are illustrated in Figure 7 panels A and B. The resultant myelin P2 trimers are shown in Figure 7 panels C and D. The resultant CRABP trimers are shown with the myelin P2 trimers in Figure 7 panel D.

**Table 6.** Alpha-bungarotoxin and EV-D68 VP1 trimer tiling atoms.

Point #	Source	Atom	Atom Type	Residue	Chain
1	2ABX	91	CA	V 14	A
	4WM7	1412	CB	A 192	A
2	2ABX	94	CB	V 14	A
	4WM7	1415	C	Y 193	A
3	2ABX	69	O	P 10	A
	4WM7	1355	CA	P 185	A

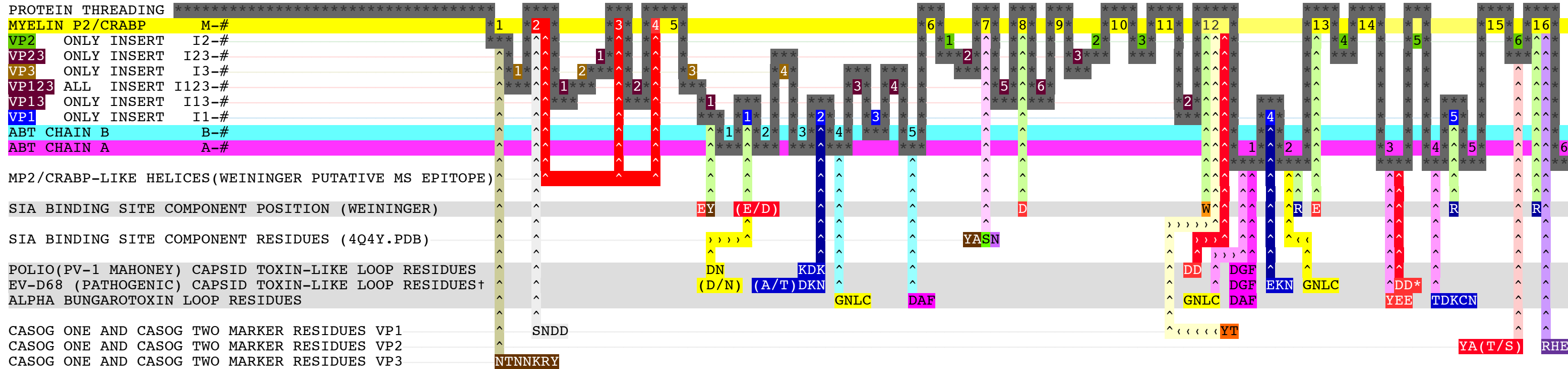
Table 6 lists the atoms in the alpha-bungarotoxin (2ABX) chain A that were directly superposed onto the listed atoms in the constructed EV-D68 (4WM7) VP1 trimers in the 3xVP1234 capsid tiling pieces. The alpha-bungarotoxin chain A and EV-D68 VP1 residues containing the atoms in Table 6 are found in Figure 1 Section A-1.

**Table 7.** Figure 1 Section locations for each picornavirus Insert.

Picornavirus Protein Location	Insert Reference	Figure 1 Section Location
Only VP1	“VP1 ONLY INSERTS”	Sections I1-1, I1-2, ... , I1-5
Only VP2	“VP2 ONLY INSERTS”	Sections I2-1, I2-2, ... , I2-6
Only VP3	“VP3 ONLY INSERTS”	Sections I3-1, I3-2, ... , I3-4
Both VP1 and VP3	“VP13 ONLY INSERTS”	Sections I13-1 and I13-2
Both VP2 and VP3	“VP23 ONLY INSERTS”	Sections I23-1, I23-2, and I23-3
Each of VP1, VP2, and VP3	“VP123 ALL INSERTS”	Sections I123-1, I123-2, ... , I123-6



**Figure 1 (previous page). Aligned sequences of myelin P2, CRABP, alpha-bungarotoxin, and picornavirus VP1, VP2, and VP3 proteins.** Figure 1 shows the aligned sequences of myelin P2, CRABP, alpha-bungarotoxin, and picornavirus VP1, VP2, and VP3 proteins. These aligned sequences are organized into sections and labeled by correspondence to the reference sequences of myelin P2/CRABP and alpha-bungarotoxin. Sections aligned with myelin P2 and CRABP sequences are yellow and red Sections M-1 to M-16 and include the red “MYELIN HELICES SECTIONS” M-2 to M-4. Sections aligned with an alpha-bungarotoxin chain A are magenta Sections A-1 to A-5. Sections aligned with residues 1 – 48 in alpha-bungarotoxin chain B are cyan Section B-1 to B-6. Insertions in or between Sections M-1 to M-16, Section A-1 to A-5, and Sections B-1 to B-6 are VP1 only inserts (blue I1 Sections), VP2 only inserts (green I2 Sections), VP3 only inserts (tan I3 Sections), and Inserts seen in more than one picornavirus protein (purple I13, I23, and I123 Sections). Residues are grouped into columns that are either identical or considered identical for column placement. Aligned residues have background colors as follows: A, F, I, L, V, and Y (brown); C, M, and W (orange); D and E (red); G (grey); H, K, and R (blue); N and Q (purple); P (black); and S and T (light green). All cells without residues are drawn without extra background color with the exception that all cells in any column containing a reference sequence residue (i.e., any myelin P2, CRABP, or alpha-bungarotoxin residue) is given the background color of the reference sequence. Columns that are both adjacent to a column containing a reference sequence residue and that share the same residue type as that reference sequence residue also have the background color drawn for the entire column. Columns in SUB-SECTION DESCRIPTOR-MARKER row number have added subsection title: “-T” when there are Toxin Core residues, “-ST” when there are toxin loop residues outside of the Toxin Cores, “-SW” when there are putative sialic acid binding residues found by us, “-SP” when there are sialic acid binding residues in 4Q4Y, and “-M” when there are marker residues in the SUB-SECTION. The VP1, VP2, and VP3 FEATURES row directly below each SUB-SECTION DESCRIPTOR-MARKER row have the residues marked when there are “-T”, “-SW”, “-SP”, and “-M” indicators in the SUB-SECTION DESCRIPTOR-MARKER row. Residues missing from the X-ray crystal structure, but present in the crystalized protein, are underlined. Additional row background color, not related to sequence, is used to aid in locating rows while scanning across Figure 1. At the bottom of the Figure 1 are rows that indicate whether a particular residue type is contained within groups specified, giving a visual representation of whether there are any residues in the column for any one or set of groups. A thumbnail sketch of Figure 2 is provided with Figure 1 for easy reference.



† All EV-D68 capsid toxin-like loop residues are in VP1 except 'DD\*', which are in VP2 in EV-D68, EV-D70, EV-D94, and HRV-87.

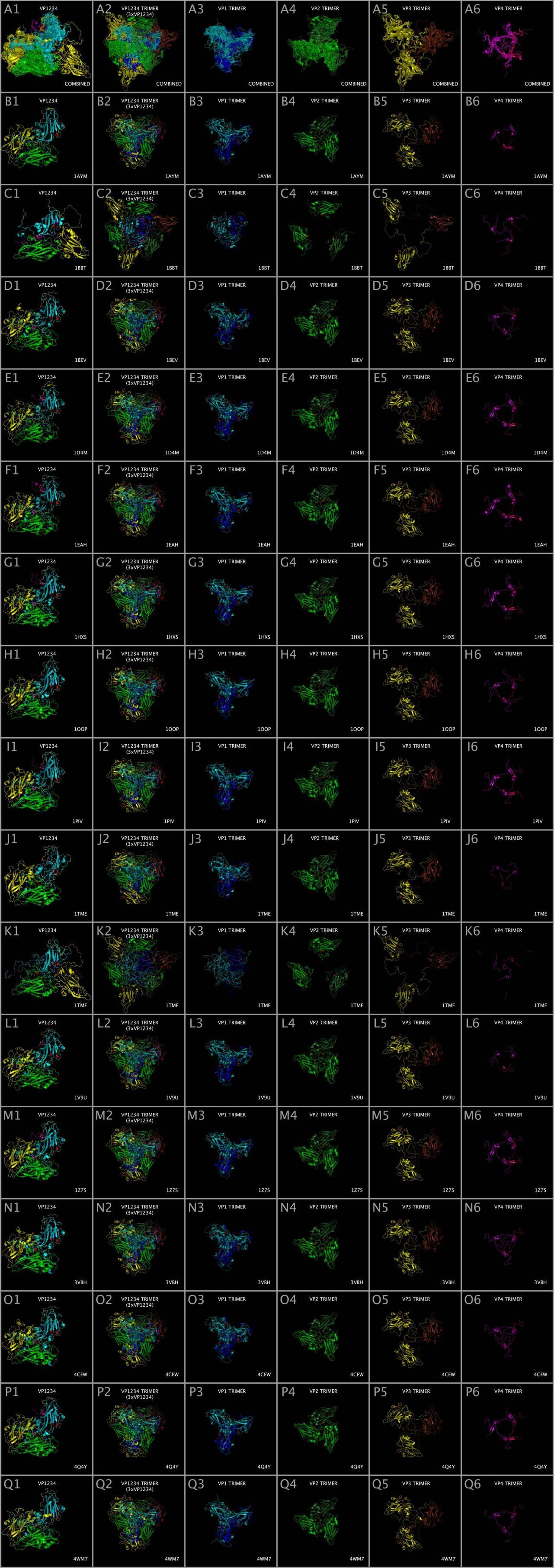
**Figure 2 (previous page). Summary graphic of the aligned sequences of myelin P2, CRABP, alpha-bungarotoxin, and picornavirus VP1, VP2, and VP3 proteins.** Figure 2 is a summary of how the sequences of myelin P2, CRABP, and alpha-bungarotoxin are threaded with inserts through the picornavirus VP1, VP2, and VP3 proteins. The aligned VP1, VP2, and VP3 sequences are represented by the winding grey line containing "\*". The grey line is threaded through rows marked MYELIN P2/CRABP, VP2 ONLY INSERT, VP23 ONLY INSERT, VP3 ONLY INSERT, VP123 ONLY INSERT, VP13 ONLY INSERT, VP1 ONLY INSERT, ABT CHAIN B, and ABT CHAIN A. The Figure 1 sections where the MP2/CRABP-LIKE HELICES ("WEININGER PUTATIVE MS EPITOPE") residues occur are shown in red. The putative WEININGER sialic acid binding site residues are shown on the line marked "SIA BINDING SITE COMPONENT POSITION (WEININGER)" with their Figure 1 section positions marked. Crystal structure based 4Q4Y.PDB contacting sialic acid are shown on the line "SIA BINDING SITE COMPONENT RESIDUES (4Q4Y.PDB)" with their Figure 1 section positions marked. The positions of loop residues making up the alpha-bungarotoxin domains in the Toxin Core Sections are shown on the line marked "ALPHA BUNGAROTOXIN LOOP RESIDUES." The positions of loop residues making up the PV1 domains (both in the Toxin Core Sections and outside of the Toxin Core Sections) are shown on the line marked "POLIO (PV-1 MAHONEY) CAPSID TOXIN-LIKE LOOP RESIDUES." The positions of loop residues making up the pathogenic (not including EV-D68-4WM7) domains (both in the Toxin Core Sections and outside of the Toxin Core Sections) are shown on the line marked "EV-D68 (PATHOGENIC) CAPSID TOXIN-LIKE LOOP RESIDUES." The positions of the VP1, VP2, and VP3 CASOG-1 and CASOG-2 marker residues shown in Figures 1 and Figure 12 are shown in the row marked "CASOG ONE AND CASOG TWO MARKER RESIDUES."



## VP4 SECTIONS

		1	2	3	4	5			
VP4 FMDV	1BBT.PDB	G AGC SS PATGS QNQC S G	N T G S I	INNNYY	M QQ Y	QN S MD T Q	L G N A G D AI SGG	SN EG S	
VP4 TMEV-1	1TME.PDB	G MASS	S LKS	SGNEG V	IINNYY	SNQ Y	QN SI D LS A	SG G N A G D A	F C NN GGISNLLGG
VP4 TMEV-2	1TMF.PDB		N E S	GNBEG V	IINNYY	SNQ Y	QN SI D LS A	SG G N A G D A	F C TN GGISNLL
VP4 EV-B-B5-SVDV	1OOP.PDB	MG A QVST	Q KT GA HE TS L SAA GN SVI	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	GKF T E P V KD IMV	K SM PA LN
VP4 EV-B-CV-B6	AAF12719	MG A QVST	Q KT GA HE T A LNA CGN SVI	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	S KF T E P V KD V MI	K S L PA LN S
VP4 EV-B-CV-B3	P03313.4	MG A QVST	Q KT GA HE T RLNAS GN SII	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	GKF T E P V KD IMI	K S L PA LN S
VP4 EV-B-CV-B3M	1JEW.PDB	G A QVST	Q KT GA HE T G LNAS GN SII	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	S KF T E P V KD IMI	K S L PA LN
VP4 EV-B-CV-B1-1	AAO84300	MG A QVST	Q KT GA HE T G LNAS GN SII	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	GKF T E P V KD IMI	K SM PA LN S
VP4 EV-B-CV-B1-2	AET37232	MG A QVST	Q KT GA HE T G LNAS GN SII	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	GKF T E P V KD IMI	K SM PA LN S
VP4 EV-B-CV-B1-3	NP040958	MG A QVST	Q KT GA HE T G LNAS GN SII	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	GKF T E P V KD IMI	K SM PA LN S
VP4 EV-B-CV-A9	1D4M.PDB	G A QVST	Q KT GA HE TS L SAA GN SII	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	S KF T E P V KD V MI	K S L PA LN
VP4 EVB-ECHOV-7+	AAK85711	MG A QVST	Q KT GA HE T G LNAS GN SII	H Y TN	IN YY KD AA SN S A	NRQ	D FT QDP	GKF T E P V KD IMI	K TM PA LN S
VP4 HRV-A16	1AYM.PDB	G A QVS	RQN VG TH ST	C N M V S N GSS	L N Y F N	IN YF KD AA S S	GAS R L D FS	QDF S KF T L F V KD VL	EK GIF TLO
VP4 HRV-A2	1V9U.PDB	G A QVS	RQN VG TH ST	C N SV S N GSS	L N Y F N	IN YF KD AA SN	GAS K L E FT	QDF S KF T L F V KD VL	EK GIF TLO
VP4 EV-C-CV-A24	4Q4Y.PDB	MG A QVSS	Q K VGA HE N T N VA TG GST	V N YT T	IN YY KDS A SN	A AS K L D FS	QDP S KF T E P V KD IMI	K T APA LN	
VP4 EV-C-CV-C105	JX514943	MG A QVS A	QNN G THE N S N S ASG GST	I N YT T	IN YY KDS A SN	A AT K MD FS	QDP S KF T E P V KD V MI	K T APA LN S	
VP4 EV-C-CV-A21	1Z7S.PDB	G A QVST	Q KT GA HE N Q N VAA N GST	I N YT T	IN YY KDS A SN S	A T RQ D LS	QDP S KF T E P V KD IML	K T APA LN	
VP4 EV-C-PV1-M	1HXS.PDB	G A QVSS	Q K VGA HE N S NR AY G GST	I N YT T	IN YY RDS A SN	A AS KQ D FS	QDP S KF T E P I KD VL I	K T AP M LN	
VP4 EV-C-PV2-L	1EAH.PDB	G A QVSS	Q K VGA HE N S NR AY G GST	I N YT T	IN YY RDS A SN	A AS KQ D F	QDP S KF T E P I KD VL I	K T AP TLN	
VP4 EV-C-PV3-S	1PIV.PDB	G A QVSS	Q K VGA HE N S NR AY G GST	I N YT T	IN YY KDS A SN	A AS KQ D YS	QDP S KF T E P L KD VL I	K T APA LN	
VP4 EV-G5-27	1BEV.PDB	G A GLS	R N TAG SH TT	C TYA TG GST	I N Y NN	IN YY SH AA S	A A ONKO D FT	QDP S KF TQ P IA D VI	KE T A VE L K
VP4 EV-A71-1	3VBH.PDB		SHE N S N S AT EGST	I N YT T	IN YY KDSYAA T	AG KOSL K	QDPD KFA N P V KD I FT	E MA AP L K	
VP4 HRV-B14	1D3I.PDB	G A QVST	Q KS G SHE N C N IL T N GS	NO T FT	VIN YY KD AA S	TSSAG Q SL SM	DP S KF T E P V KD IML	K GAPA LN	
VP4 EV-D94-FN07	ABK88241	MG A QVS	RQQ T G THE NA N IAT N GSSS	IT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VA D A L	K AGAPV L KS	
VP4 EV-D70-UK09	BAA18891	MG A QVS	RQQ T G THE NA N V ATG GSS	IT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VA E A L	K AGAPV L KS	
VP4 EV-D68-4WM7	4WM7.PDB	G A QVT	RQQ T G THE NA N IAT N GS	HIT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VV EG L	K AGAPV L K	
VP4 EV-D68-US14-1	AIS73051	MG A QVT	RQQ T G THE NA N IAT N GS	HIT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VV EG L	K AGAPV L KS	
VP4 EV-D68-JP11	BAK08580	MG A QVT	RQQ T G THE NA N IAT N GS	HIT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VV EG L	K AGAPV L KS	
VP4 EV-D68-SW07	ABL61317	MG A QVT	RQQ T G THE NA N IAT N GS	HIT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VV EG L	K AGAPV L KS	
VP4 EV-D68-CH14	AIZ48771	MG A QVT	RQQ T G THE NA N V AT N GS	HIT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VV EG L	K AGAPV L KS	
VP4 EV-D68-NZ13	AGC00381	MG A QVT	RQQ T G THE NA N IAT N GS	HIT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VV EG L	K AGAPV L KS	
VP4 EV-D68-US14-2	AIS73057	MG A QVT	RQQ T G THE NA N IAT N GS	HIT Y NO	IN FY KDSYAA S	A S KQ D FS	QDP S KF T E P VV EG L	K AGAPV L KS	

**Figure 3 (previous page). Aligned VP4 sequences.** Figure 3 shows the aligned sequences of picornavirus VP4 proteins. Residues are grouped into columns that are either identical or considered identical for column placement. Residues have background color as follows: A, F, I, L, V, and Y (brown); C, M, and W (orange); D and E (red); G (grey); H, K, and R (blue); N and Q (purple); P (black); and S and T (green). Section headers above the columns aid in location of referenced residues. Residues missing from the X-ray crystal structure, but present in the crystallized protein, are shown in italics and underlined. Sections where N-terminal residues are absent from the protein in the X-ray structure have a yellow background. The cyan section between isoleucines in the FMDV sequence shows where the ILE-ILE residues are consistent with being aligned on either side of the cyan strip. Additional row background color, not related to sequence, is used to aid in locating rows while scanning across the Figure 3.

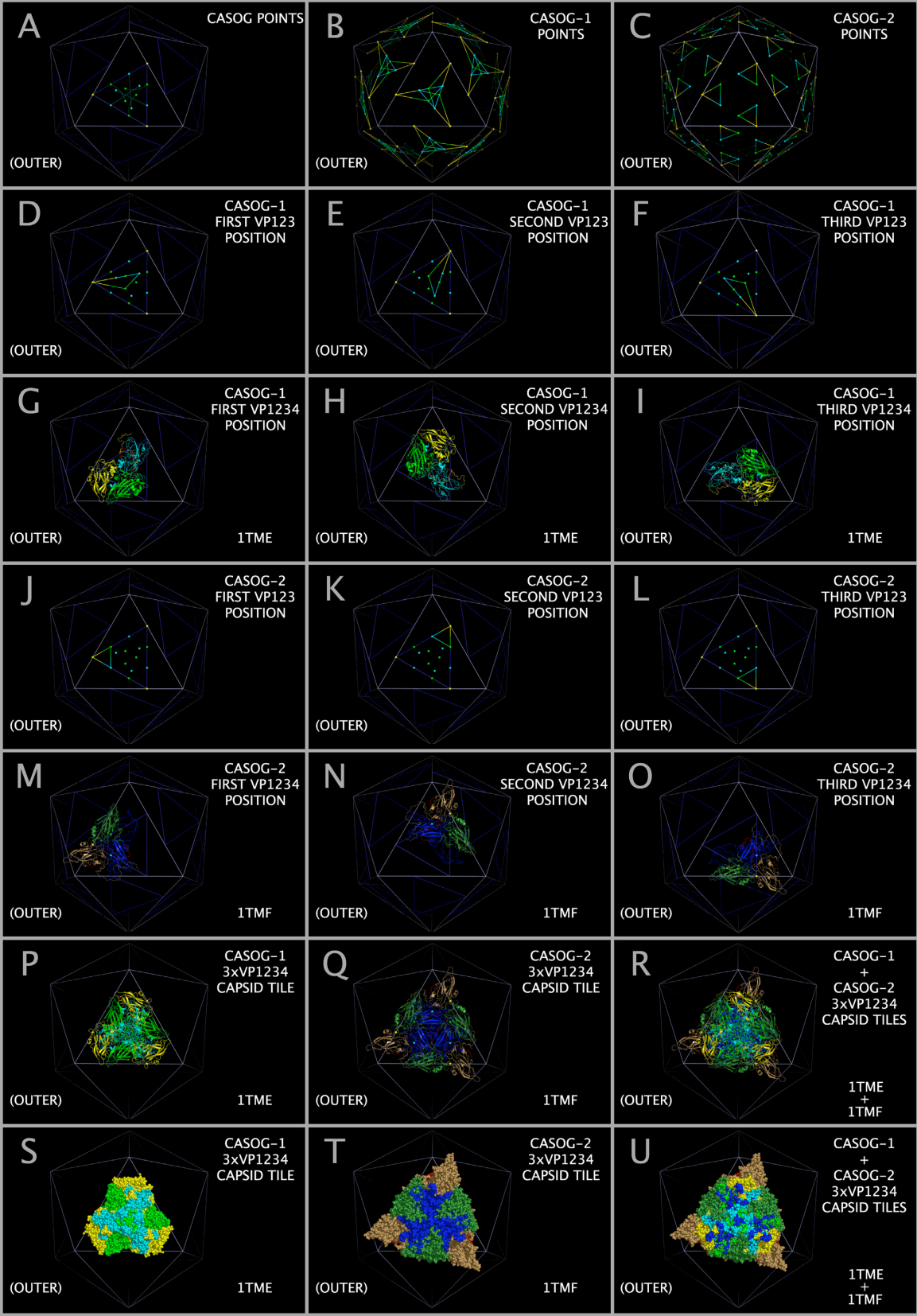


1040 **Figure 4 (previous page). Superposition of VP1-VP2-VP3 picornavirus protein assemblies showing CASOG-1 and CASOG-2 orientations.** Figure 4 shows, for a representative set of picornaviruses: picornavirus VP1234 orientations relative to one another, the tiling pieces (trimers) that are generated from composite superpositions of VP1 prolines, and the spatial relationship between VP1, VP2, VP3, and VP4 trimers. Column 1 VP1234 structures are oriented relative to one another by the superposition of atoms listed in Table 2.

1045 Columns 2 – 5 show trimers that are constructed using the method illustrated in Figure 5. VP1 structure ribbons are colored cyan, VP2 structure ribbons are colored green, VP3 structure ribbons are colored yellow, and VP4 structure ribbons are colored magenta. Columns 1 – 5 show individual VP1234 structures, VP1234 trimers, VP1 trimers, VP2 trimers, and VP3 trimers, and VP4 trimers respectively. These structures are oriented by superposition of the atoms listed in Table 2. The first row shows the superposition of

1050 all the rows in each column. Subsequent rows show one specific virus per row. The contents of the rows, indexed by letter, are: A=all superposed structures, B=1AYM, C=1BBT, D=1BEV, E=1D4M, F=1EAH, G=1HXS, H=1OOP, I=1PIV, J=1TME, K=1TMF, L=1V9U, M=1Z7S, N=3VBH, O=4CEW, P=4Q4Y, and Q=4WM7. A comparison of Figure 4 rows C (1BBT) and K (1TMF) with other individual virus rows (i.e., B, C – J, and L – Q) show a distinct difference in orientation. We classify these different orientations as “Common Atomic

1055 Structure Occupancy Groups”: CASOG-1 (seen in rows B, C – J, and L – Q) and CASOG-2 (seen in rows C and K). Row J (1TME, CASOG-1) and row K (1TMF, CASOG-2) have nearly identical sequences.



**Figure 5 (previous page). Model picornavirus capsid construction for the CASOG-1 and CASOG-2 proteins.**

Figure 5 illustrates the method of superposing the X-ray structures of picornavirus CASOG-1 and CASOG-2  
1060 VP1-VP2-VP3-VP4 protein assemblies (“VP1234”) onto an icosahedron to form model virus capsid tiling pieces.  
The VP1234 assemblies are placed on the icosahedral face using conserved prolines. The vertices of the TRI78  
triangles are points that represent positions of conserved VP3 proline atoms in both CASOG-1 and CASOG-2  
picornavirus capsids. The VP3 proline atom is both sequence and spatially invariant. The TRI78 triangles are  
colored dark blue. Capsid tiling points are colored cyan for VP1, green for VP2, yellow for VP3, and magenta for  
1065 VP4.

Panel A shows both CASOG-1 and CASOG-2 tiling points on and within a single TRI78 triangle. Dashed lines  
indicate the difference in the position of atoms (either from VP1 or VP2) between CASOG-1 and CASOG-2.

Panel B shows the destination points for the individual CASOG-1 VP1, VP2, and VP3 atoms listed in Table 3.

Panel C shows the destination points for the individual CASOG-2 VP1, VP2, and VP3 atoms listed in Table 4.

1070 Panels D – F show the three mapping positions for CASOG-1 VP1234.

Panels G – I show examples (TMEV-1 cartoons) of CASOG-1 VP1234 in these positions.

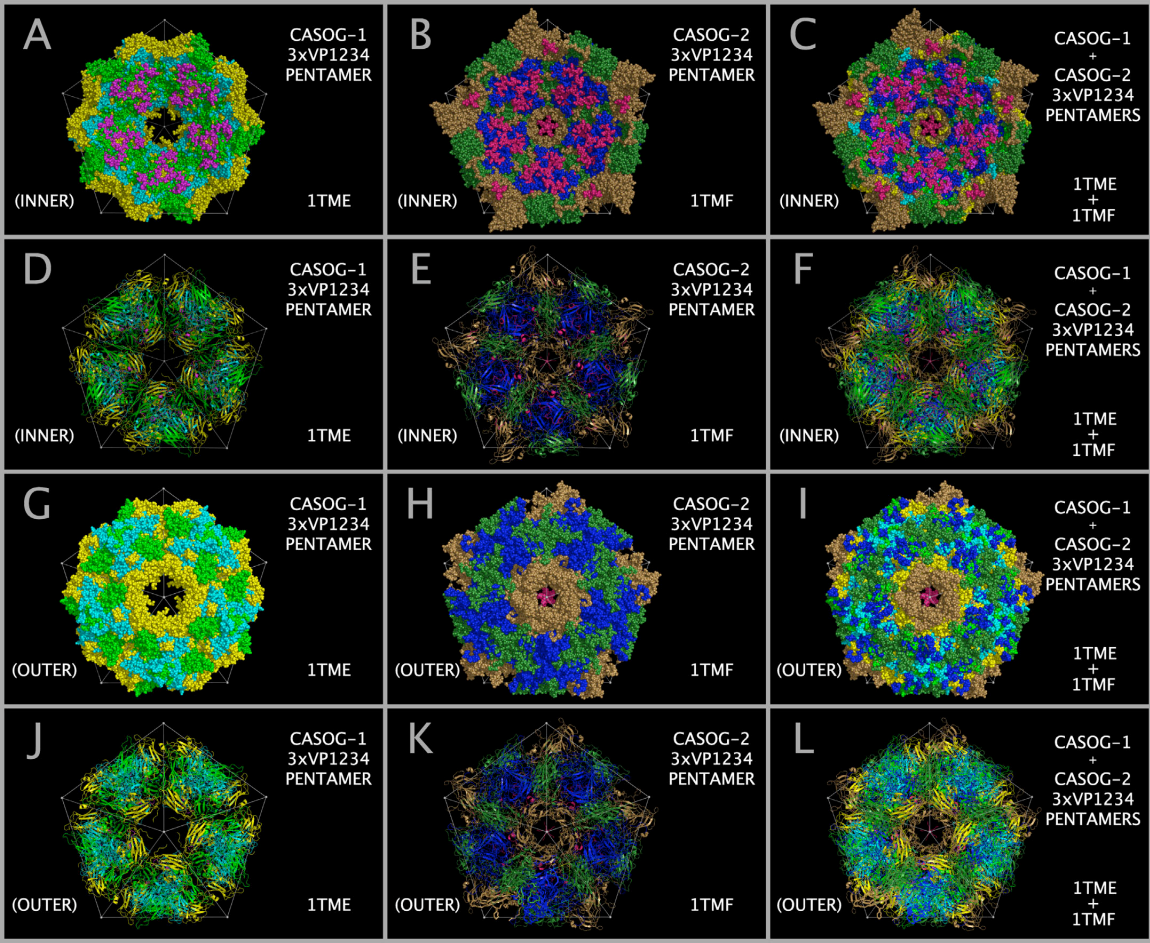
Panels J – L show the three mapping positions for CASOG-2 VP1234.

Panels M – O show examples (TMEV-2 cartoons) of CASOG-2 VP1234 in these positions.

Panel P shows these three VP1234 positioned together as a CASOG-1 capsid tiling piece (TMEV-1 cartoons)  
1075 and Panel S shows the same capsid tiling piece as spheres.

Panel Q shows these three VP1234 positioned together as a CASOG-2 capsid tiling piece (TMEV-2 cartoons)  
and Panel T shows the same capsid tiling piece as spheres.

Panel R shows the overlap of Panels P and Q. Panel U shows the overlap of Panels S and T.

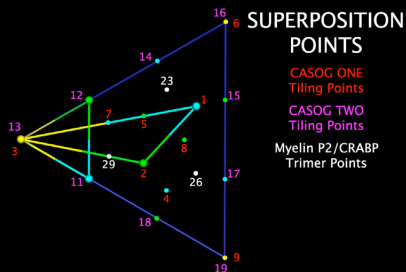


1080 **Figure 6 (previous page). Comparison of constructed CASOG-1 and CASOG-2 picornavirus capsid tiling piece pentamers.** Figure 6 shows the constructed capsid tiling piece pentamers for TMEV-1 (1TME.PDB) and TMEV-2 (1TMF.PDB), which are nearly identical in sequence. All Figure 6 Panels show ICOS135 points connected with white lines as a reference to the rest of the capsid. TMEV-1 VP1 proteins are shown in cyan, TMEV-1 VP2 proteins are shown in bright green, TMEV-1 VP3 proteins are shown in yellow, TMEV-2 VP1

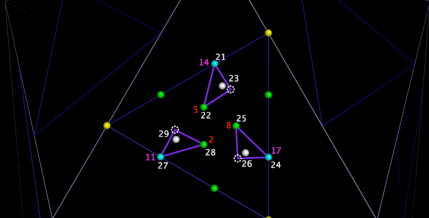
1085 proteins are shown in dark blue, TMEV-2 VP2 proteins are shown in dark green, TMEV-2 VP3 proteins are shown in tan. TMEV-1 and TMEV-2 VP4 proteins are shown in magenta. Pentamers of TMEV-1 3xVP1234 capsid tiling pieces are shown in the first column (Panels A, D, G, and J). Pentamers of TMEV-2 3xVP1234 capsid tiling pieces are shown in the second column (Panels B, E, H, and K). The last column (Panels C, F, I, and L) show the superposition of the first two columns. Panels A – F show the inner (RNA side)

1090 capsid face. Panels G – L show the outer (cellular side) capsid face. Panels D – F and J – L show structure cartoons. Panels A – C and G – I show protein residues as spheres.

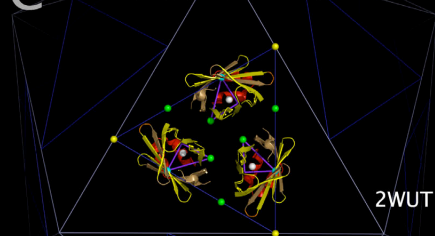


**A****B**

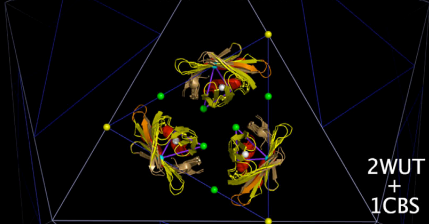
**MYELIN P2/CRABP  
SUPERPOSITION POINTS**

**C**

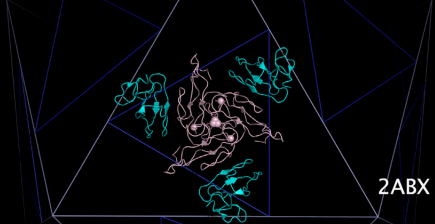
**MYELIN P2 TRIMER**

**D**

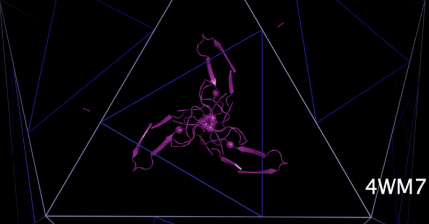
**MYELIN P2 TRIMER +  
CRABP TRIMER**

**E**

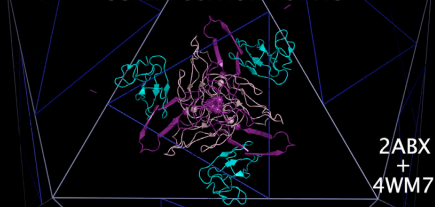
**ALPHA-BUNGAROTOXIN TRIMER +  
SUPERPOSITION POINTS**

**F**

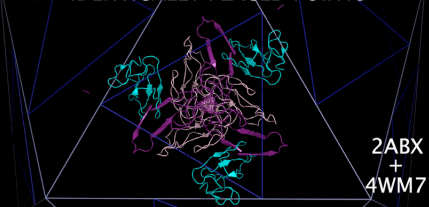
**EV-D68 VP1 TOXIN CORE +  
SUPERPOSITION POINTS**

**G**

**ALPHA-BUNGAROTOXIN TRIMER +  
EV-D68 VP1 TOXIN CORE +  
SUPERPOSITION POINTS**

**H**

**ALPHA-BUNGAROTOXIN TRIMER +  
EV-D68 VP1 TOXIN CORE +  
IDENTICALLY PLACED POINTS**

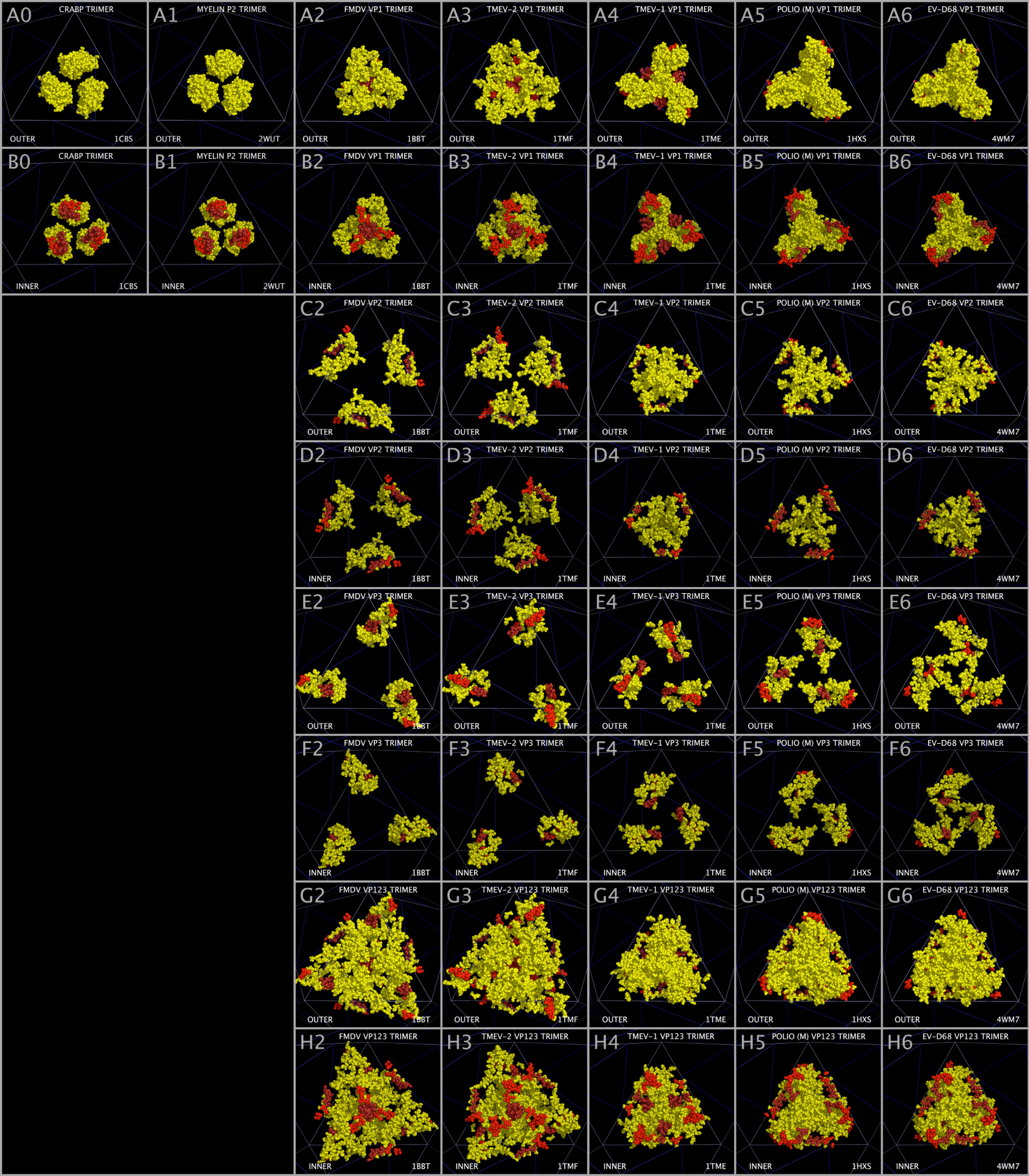


**Figure 7 (previous page). Construction of myelin P2 trimers, CRABP trimers, and Alpha-bungarotoxin Trimers.**

1095 Figure 7 illustrates the construction of myelin P2 trimers, CRABP trimers, and alpha-bungarotoxin trimers. Figure 7 Panel A shows the relationship between CASOG-1 and CASOG-2 tiling points and additional myelin P2 and CRABP tiling points. Figure 7 Panel B shows the superposition points for the myelin P2 and CRABP atoms: six of the superposition points are from the CASOG-1 and CASOG-2 tiling points and three points are added (white dashed circles) to create a complete set of nine destination points for three myelin P2 and three CRABP monomers. Figure 7 Panel C shows a Myelin P2 trimer positioned on an icosahedron face. Figure 7 Panel D shows co-located Myelin P2 and CRABP trimers positioned on an icosahedron face. Figure 7 Panel E shows cartoons of a trimer of ABT dimers in its superposed position on EV-D68-4WM7 VP1 trimer atoms with the ABT Table 6 atoms as spheres, the ABT chain A cartoon colored violet and the ABT chain B cartoons colored teal. Figure 7 Panel F shows cartoons of the purple EV-D68 VP1 trimer Toxin Section Residues and the EV-D68 VP1 Table 6 atoms as spheres. Figure 7 Panel G shows cartoons of a trimer of ABT in its superposed position, the EV-D68 VP1 trimer Toxin Section Residues overlapping the corresponding ABT A chain cartoon, and all of the Table 6 atoms as spheres. Figure 7 Panel H shows: the perfect overlap at the center of the trimers of ABT atom 91 with EV-D68 atom 1414; and ABT atom 96 with EV-D68 atom 1412 which can be used as an additional check on positioning the ABT trimer.

1100

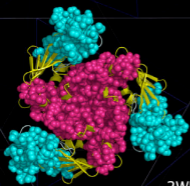
1105



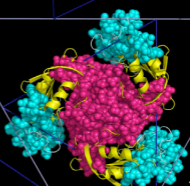
1110 **Figure 8 (previous page). Myelin P2, CRABP, and Picornavirus Myelin P2/CRABP Cores.** Figure 8 shows Myelin P2/CRABP Core residues in trimers of: CRABP (Panels A0 and B0); myelin P2 (Panels A1 and B1); FMDV VP1 (Panels A2 and B2); TMEV-2 VP1 (Panels A3 and B3); TMEV-1 VP1 (Panels A4 and B4); PV1 (POLIO) VP1 (Panels A5 and B5); EV-D68 VP1 (Panels A6 and B6); FMDV VP2 (Panels C2 and D2); TMEV-2 VP2 (Panels C3 and D3); TMEV-1 VP2 (Panels C4 and D4); PV1 (POLIO) VP2 (Panels C5 and D5);

1115 EV-D68 VP2 (Panels C6 and D6); FMDV VP3 (Panels E2 and F2); TMEV-2 VP3 (Panels E3 and F3); TMEV-1 VP3 (Panels E4 and F4); PV1 (POLIO) VP3 (Panels E5 and F5); EV-D68 VP3 (Panels E6 and F6); FMDV VP123 (Panels G2 and H2); TMEV-2 VP123 (Panels G3 and H3); TMEV-1 VP123 (Panels G4 and H4); PV1 (POLIO) VP123 (Panels G5 and H5); and EV-D68 VP123 (Panels G6 and H6). Myelin P2 Core residues in Figure 8 are colored yellow with the exception of Figure 1 Section M-2 to I123-2 which are colored red and

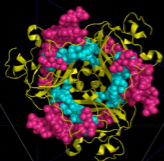
1120 Section M-4 residues which are colored dark red to highlight the positions of the individual helices relative to each other and to the rest of the Myelin P2/CRABP Core residues in each panel.

**A** Constructed Trimers of MP2 and ABT Dimers

(OUTER)

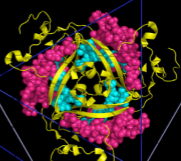
2WUT  
+  
2ABX**B** Constructed Trimers of MP2 and ABT Dimers

(INNER)

2WUT  
+  
2ABX**C** FMDV VP1 MP2/CRABP Cores and Toxin Cores

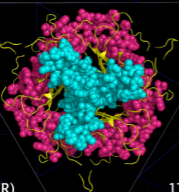
(OUTER)

1BBT

**D** FMDV VP1 MP2/CRABP Cores and Toxin Cores

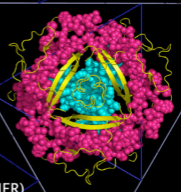
(INNER)

1BBT

**E** TMEV-2 VP1 MP2/CRABP Cores and Toxin Cores

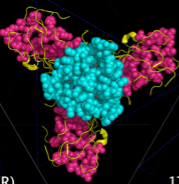
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1TMF

**F** TMEV-2 VP1 MP2/CRABP Cores and Toxin Cores

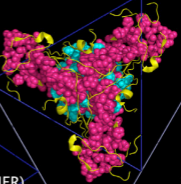
(INNER)

1TMF

**G** TMEV-1 VP1 MP2/CRABP Cores and Toxin Cores

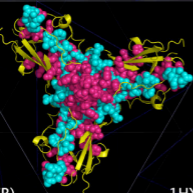
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1TME

**H** TMEV-1 VP1 MP2/CRABP Cores and Toxin Cores

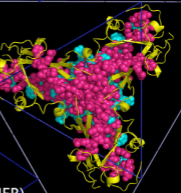
(INNER)

1TME

**I** PV1 VP1 MP2/CRABP Cores and Toxin Cores

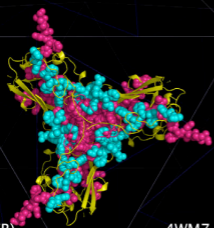
(OUTER)

1HXS

**J** PV1 VP1 MP2/CRABP Cores and Toxin Cores

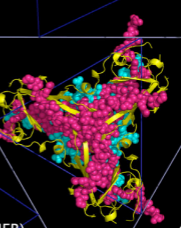
(INNER)

1HXS

**K** EV-D68 VP1 MP2/CRABP Cores and Toxin Cores

(OUTER)

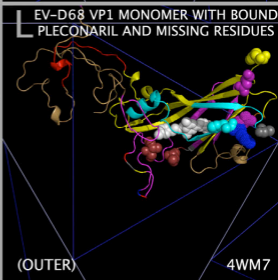
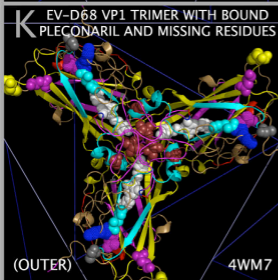
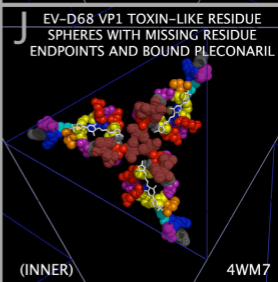
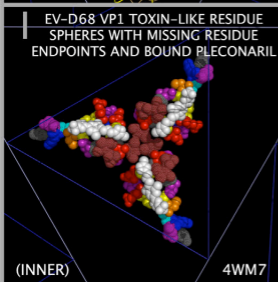
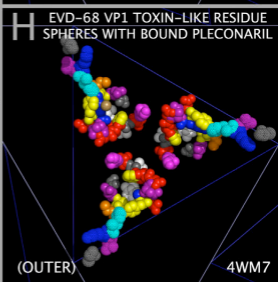
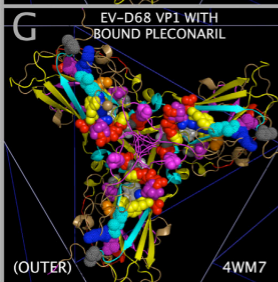
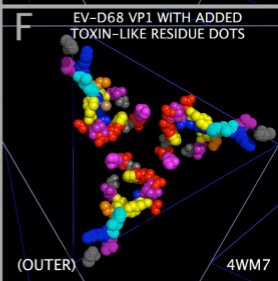
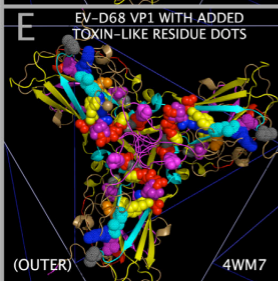
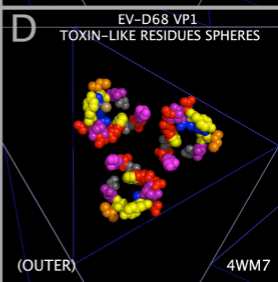
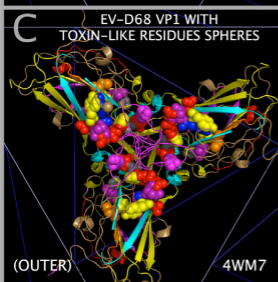
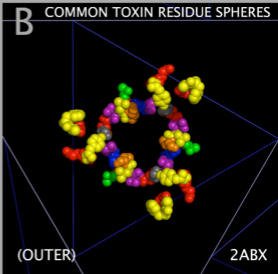
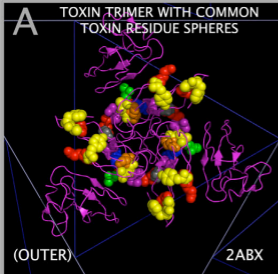
4WM7

**L** EV-D68 VP1 MP2/CRABP Cores and Toxin Cores

(INNER)

4WM7

**Figure 9 (previous page). Myelin P2 trimers, Alpha-bungarotoxin trimers, Picornavirus Myelin P2/CRABP Cores, and Picornavirus Toxin Cores.** Figure 9 shows the relationship between: a) constructed Myelin P2 trimers and trimers of alpha-bungarotoxin dimers; and b) selected picornavirus VP1 Myelin P2/CRABP Cores and Toxin Cores. Myelin P2 and VP1 Myelin P2/CRABP Cores cartoons are colored yellow. Alpha-bungarotoxin A chain trimer residue spheres are colored dark magenta. FMDV, TMEV-1, TMEV-2, PV1, and EV-D68 VP1 Toxin Core residue spheres for residues in Figure 1 Sections A-1 to A-6 (corresponding to ABT chain A) are colored dark magenta. Alpha-bungarotoxin B chain trimer residues 1 – 48 residue spheres are colored cyan. FMDV, TMEV-1, TMEV-2, PV1, and E-D68 VP1 Toxin Core residue spheres for residues in Figure 1 Sections B-1 to B-5 (corresponding to ABT chain B residues 1 – 48) are colored cyan. Alpha-bungarotoxin B chain trimer residues 49 – 74 are shown as a light cyan cartoon for reference. Panels A and B show cartoons of Myelin P2 trimers, cartoons of alpha-bungarotoxin B chain residues 49 – 74; and residue spheres of trimers of alpha-bungarotoxin A Chains and trimers of alpha-bungarotoxin B Chain residues 1 – 48. VP1 Myelin P2/CRABP Core (Figure 1 M-1 to M-16) cartoons and VP1 Toxin Core residue spheres (Figure 1 A-1 to A-6 and B-1 to B-5) for: FMDV are shown in Panels C and D; TMEV-2 are shown in Panels E and F; TMEV-1 are shown in Panels G and H; PV1 are shown in Panels I and J; and EV-D68 are shown in Panels K and L.



1140 **Figure 10 (previous page). Toxin Domain Structure in Alpha-bungarotoxin and EV-D68.** Figure 10 shows the TOX DOMAIN presentation in trimers of alpha-bungarotoxin dimers and EV-D68-4WM7 VP1 trimers with two VP2 residues shown. In Figure 10, residue spheres and dots are colored: D/E - red; R/K - blue; H – cyan; S/T - green; N/Q -purple; A light grey; G-grey; P – black; I/V/L/F – yellow; Y – tan; and C/W/M – orange. Plecornaril spheres and sticks are colored white. Figure 10 panel A shows purple cartoons of constructed trimers

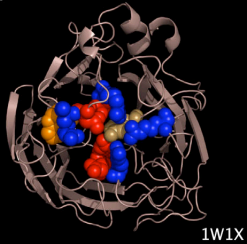
1145 of alpha-bungarotoxin (ABT) trimers. Figure 10 panels A and B show the toxin loop residue spheres for the A chain of ABT: G19-E20-N21-L22-C23 (Figure 1 Section A-1 ); T62-D63-K64-N66 (Figure 1 Section A-4); D30-A31-F32 (Figure 1 Section A-1); and Y54-E55-E56 (Figure 1 Section A-3). In Figure 10 Panels A and B, the ABT chain A residues E20-N21 and D63-K64-N66 form an annulus of complimentary charge and the Y54 and F32 rings are close enough to contact each other and add additional stability to the annulus structure. Figure 10

1150 panels C, E, G, K, and L show the EV-D68 VP1 trimer cartoon colored as in the Figure 1 Section header for spatial reference. Panels C, D, E, F, H, I, and J show EV-D68 residue spheres and dots specified in Figure 1: VP1 Section I1-2 Subsection 3 residues-HKN (non-pathogenic sequence in 4WM7.PDB where TOXLOOP1 would be present in pathogenic EV-D68 – shown as dots); VP1 Section A1 residues DGF (“TOXLOOP2” – shown as spheres); VP1 Section A2 residues GNLC (“TOXLOOP3” – shown as spheres); and VP2 Section A-3

1155 Subsection 2 residues (“TOXLOOP4” – shown as spheres). To demarcate the position of missing residues in the 4WM7.PDB structure, A80 (grey), H87 (cyan), K88 (blue), and N89 (purple) are represented by dots in Panels E, F, H, I, and J; residues G210, I211, T217, and I218 in Panels I and J are shown by brown dots; and residues I211 and T217 are represented by brown spheres in Panels K and L. In panels G, H, I , J, K, and L, plecornaril is represented by white spheres or sticks.

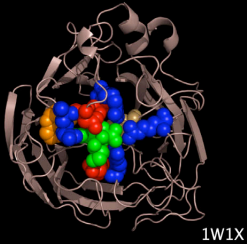


**A** N6 NEURAMINIDASE ACTIVE SITE RESIDUES



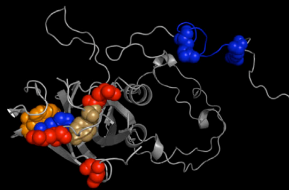
1W1X

**B** N6 NEURAMINIDASE ACTIVE SITE WITH BOUND SIALIC ACID



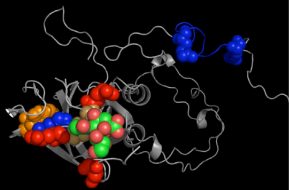
1W1X

**C** EV-D68 VP1 MONOMER WITH PUTATIVE SIALIC ACID BINDING SITE



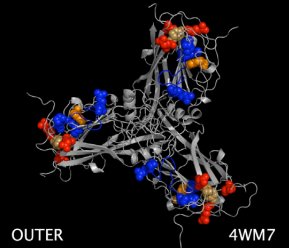
4WM7

**D** EV-D68 VP1 MONOMER WITH PUTATIVE SIALIC ACID BINDING SITE AND SIALIC ACID POSITION



4WM7

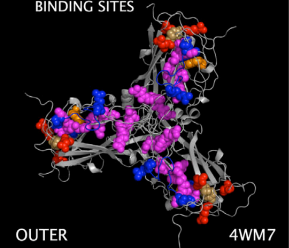
**E** EV-D68 VP1 TRIMER WITH PUTATIVE SIALIC ACID BINDING SITE



OUTER

4WM7

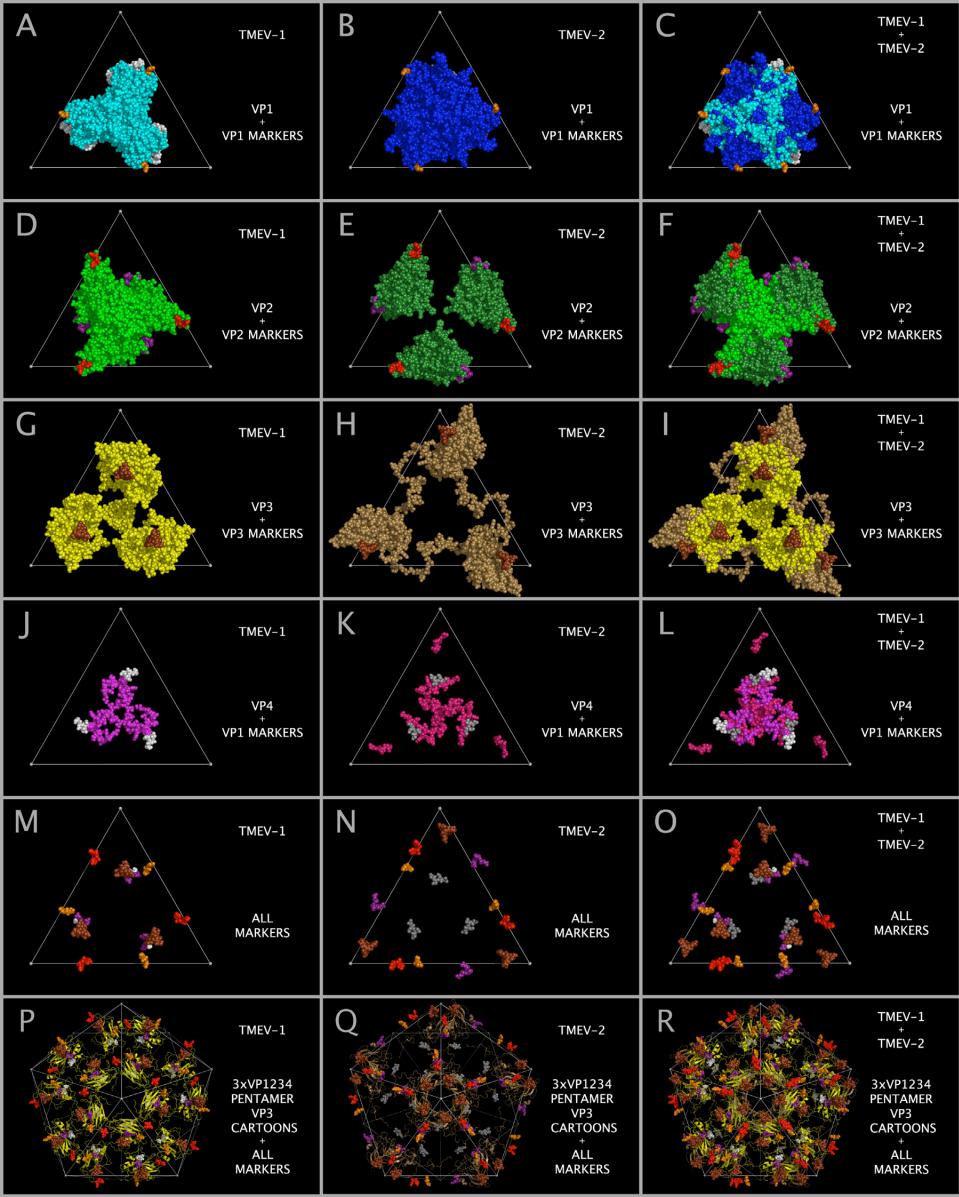
**F** EV-D68 VP1 TRIMER WITH PUTATIVE ACH RECEPTOR AND SIALIC ACID BINDING SITES



OUTER

4WM7

**Figure 11 (previous page). Sialic Acid Binding Domain Components on EV-D68 Capsid.** Figure 11 Panel A shows the influenza N6 neuraminidase [49] cartoon and residue spheres of: Y412 (tan), D157 (red), R124 (cyan), E227 (red), R158 (cyan), R 299 (cyan), and W185 (orange). Figure 11 Panel B adds green residue spheres of sialic acid to Panel A. Figure 11 Panel C shows a cartoon of EV-D68 VP1 and spheres for residues that we have identified in the Figure 1 row labelled “SUBSECTION DESCRIPTOR MARKER” with the subsection title suffix “-SW” (i.e., E75 (red, Figure 1 Section I13-1), Y76 (yellow, Figure 1 Section I13-1), D140 (red, Figure 1 Section M-8), W163 (orange, Figure 1 Section M-12), R223 (blue, Figure 1 Section A-2), E227 (red, Figure 1 Section M-13), R270 (blue, Figure 1 Section I1-5) and R284 (blue, Figure 1 Section M-16) residues. Panel C residues are also identified in Figure 2 in the row labelled “SIA BINDING SITE COMPONENT POSITION (WEININGER)”. Figure 11 Panel D adds a model built sialic acid (green carbons, red oxygens, and blue nitrogen atom spheres) to the partial, putative sialic acid binding site shown in Panel C. Figure 11 Panel E shows a trimer of putative sialic acid binding sites formed by a trimer of VP1 proteins shown as monomers in Panel C. Figure 11 Panel F adds to Panel E the residue spheres comprising the toxin domain in EV-D68, the residues of which are identified in Figure 2 in the row labelled “EV-D68 (PATHOGENIC) CAPSID TOXIN-LIKE LOOP RESIDUES”.



**Figure 12 (previous page). Differences in the spatial position of markers in constructed TMEV capsid tiling pieces and capsids.** Figure 12 shows the differences in the spatial position of corresponding residue markers in

the constructed TMEV-1 and TMEV-2 Capsids. All markers are shown in the Figure 1 headers under the

1180 Subsection title suffix “-M”.

Panel A shows TMEV-1 VP1 protein spheres (cyan) with orange Y161–T162 residue marker spheres.

Panel B shows TMEV-2 VP1 protein spheres (dark blue) with orange Y163–T164 residue marker spheres.

Panel C shows the superposition of Panels A and B.

1185 Panel D shows TMEV-1 VP2 protein spheres (bright green) with purple R260-H261-E262 and  
red Y235-A236-S237 residue marker spheres.

Panel E shows TMEV-2 VP2 protein spheres (dark green) with purple R260-H261-E262 and  
red Y235-A236-T237 residue marker spheres.

Panel F shows the superposition of Panels D and E.

1190 Panel G shows TMEV-1 VP3 protein spheres (yellow) with dark brown N58-S59-N60-N61-K62-R63-Y64 residue  
marker spheres.

Panel H shows TMEV-2 VP3 protein spheres (tan) with dark brown N58-T59-N60-N61-K62-R63-Y64 residue  
marker spheres.

Panel I shows the superposition of Panels G and H.

1195 Panel J shows TMEV-1 VP4 protein spheres (magenta) and TMEV-1 VP1 S11-N12-D13-D14 white marker  
spheres.

Panel K shows TMEV-2 VP4 protein spheres (dark pink) and TMEV-2 VP1 S11-N12-D13-D14: grey marker  
spheres.

Panel L shows the superposition of Panels J and K.

Panel M shows all of the TMEV-1 marker spheres.

1200 Panel N shows all of the TMEV-2 marker spheres.

Panel O shows the superposition of Panels M and N.

Panel P shows TMEV-1 3xVP1234 pentamer VP3 structure cartoons (in yellow) and the TMEV-1 marker  
spheres.

Panel Q shows TMEV-2 3xVP1234 pentamer VP3 structure cartoons (in tan) and the TMEV-2 marker spheres.

1205 Panel R shows the superposition between Panels P and Q.

**A**TMEV-1 VP3  
Cartoons with  
Markers

OUTER

1TME

**B**TMEV-2 VP3  
Cartoons with  
Markers

OUTER

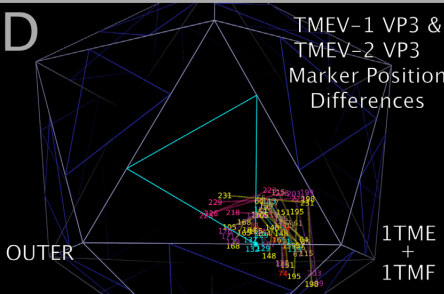
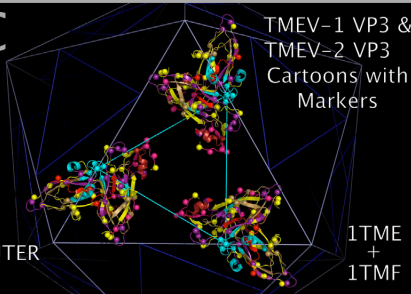
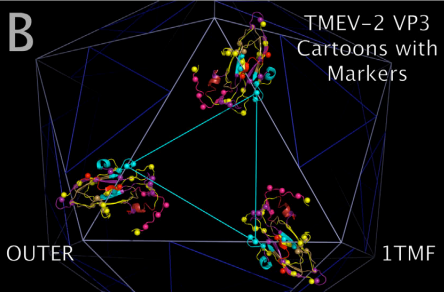
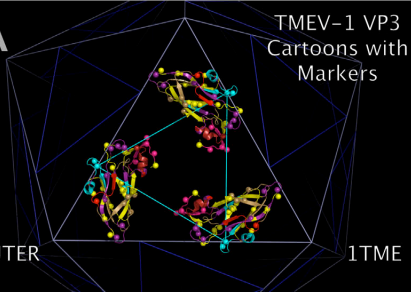
1TMF

**C**TMEV-1 VP3 &  
TMEV-2 VP3  
Cartoons with  
Markers

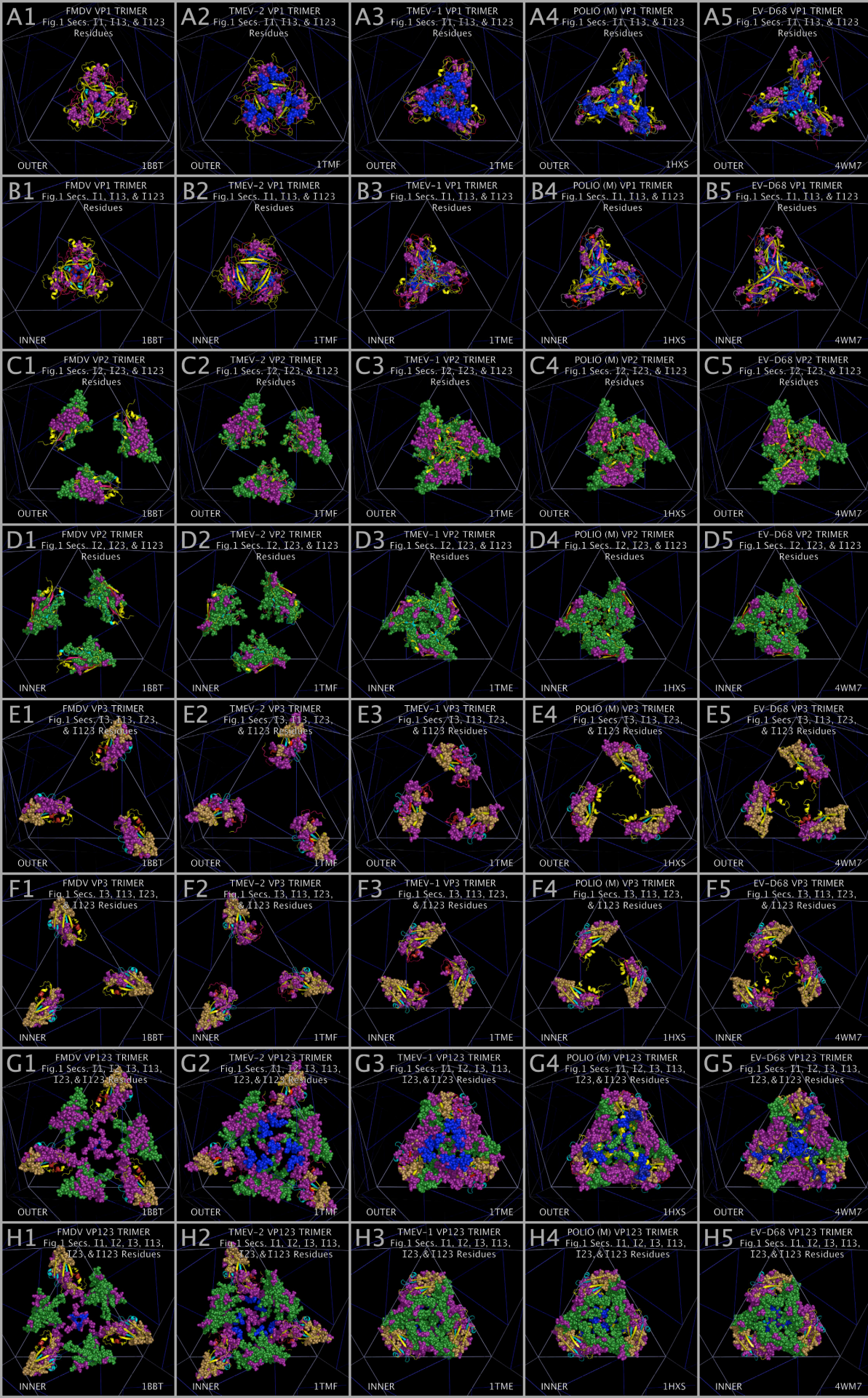
OUTER

1TME  
+  
1TMF**D**TMEV-1 VP3 &  
TMEV-2 VP3  
Marker Position  
Differences

OUTER

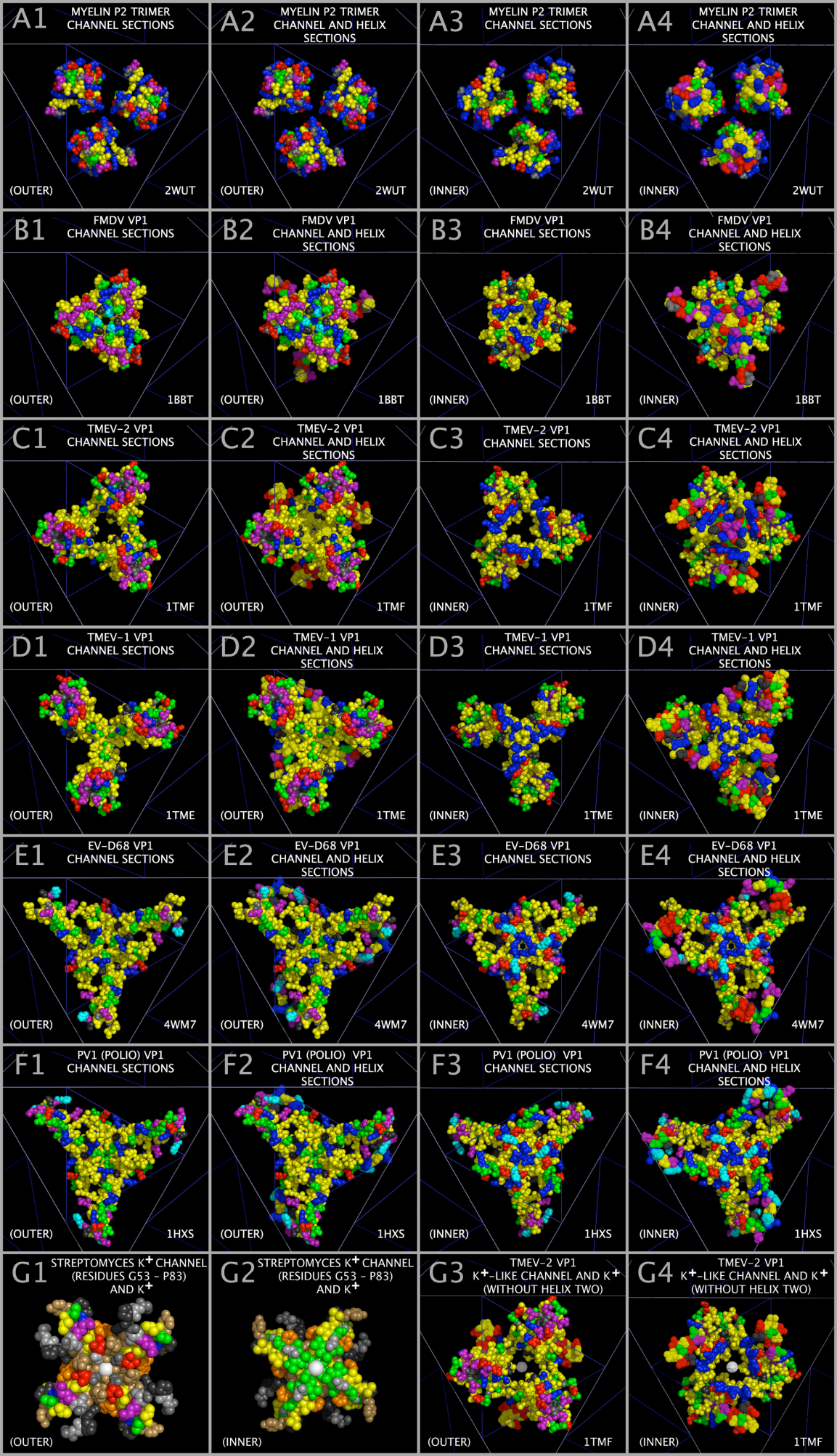
1TME  
+  
1TMF

1210 **Figure 13 (previous page). VP3 Protein Beta Sheets Circling The Pentamer Interface Form The Base Of A Diaphragm Shutter-like Pore.** Figure 13 panels A, B, and C show TMEV-1 and/or TMEV-2 structure cartoons with their proline residue main chain oxygen atoms as spheres. Panel D shows lines between sequence equivalent prolines in TMEV-1 and TMEV-2 along with the residue number of the matching prolines.



1215 **Figure 14 (previous page). Using Insert Residue Positions To Isolate Variations in Relative Position of Aligned Structures.** Figure 14 Panels A1 – A5 and Panels B1 – B5 show Insert residues for the VP1 trimers colored according to their Figure 1 Section color. Figure 1 Panels C1 – C5 and Panels D1 – D5 show Insert residues for the VP2 trimers colored according to their Figure 1 Section color. Figure 1 Panels E1 – E5 and Panels F1 – F5 show Insert residues for the VP3 trimers colored according to their Figure 1 Section color. Figure 14 Panels G1 – G5 and H1 – H5 show superposed composites of VP1, VP2, and VP3 trimer Inserts.





1220 **Figure 15 (previous page). Ion channel-like structure in the center of myelin P2 trimers and VP1 trimers.** Figure 15 shows the Figure 1 Sections M-2 to M-4 (“Helices”) residues and Sections M-5, M-6 to M-10, M-13, and M-14 (“Channel”) residues of myelin P2 trimer (Panels A1 – A4) and the VP1 trimers of FMDV (Panels B1 – B4), TMEV-2 (Panels C1 – C4, G3, and G4), TMEV-1 (Panels D1 – D4), EV-D68 (Panels E1 – E4), and PV1 (Panels F1 – F4). Panels A1, B1, C1, D1, E1, F1, A3, B3, C3, D3, E3, F3, and G3 contain Channel Residues (spheres)

1225 but no Helices residues. Panels A2, B2, C2, D2, E2, F2, A4, B4, C4, D4, E4, F4, and G4 contain Helices Residue (dots) and Channel Residues (spheres). Figure 15 Panels G1 and G2 show the residue spheres of a tetramer of *Streptomyces lividans* (“K-ION-CHANNEL”) for residues G53 to P83. Figure 15 Panels G1 – G4 also show a potassium ion as a white sphere. The position of the potassium ion in Panels G1 and G2 are from the X-ray crystal structure 1BL8.PDB and the position of the potassium ion in Panels G1 and G2 is model built.

1230 The residue dots and spheres in Figure 15 are colored yellow with the exceptions that the residues D, E, R, K, H, S, T, N, Q, G, and P are colored as in Figure 1 columns: D/E - red; R/K - blue; H - cyan; S/T - green; N/Q -purple; G-grey; P – black; and potassium ion – white. Panels in the first column of Figure 15 (A1, B1, C1, D1, E1, and F1) and Panels in the second column of Figure 15 (A2, B2, C2, D2, E2, and F2) show the Outer view. Panels in the third column of Figure 15 (A3, B3, C3, D3, E3, and F3) and Panels in the fourth column of

1235 Figure 15 (A4, B4, C4, D4, E4, and F4) show the Inner view. Figure 15 Panels G1 and G2 show a tetramer of *Streptomyces lividans* (“K-ION-CHANNEL”) for residues G53 to P83.

**Supporting Information File: ICOS135.PDB**

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      CONECT   1   6
      CONECT   2   3   6   7   11
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      CONECT   7   8  11  12
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1265 **Supporting Information File: TRI78.PDB**

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TITLE       3 THE 78-ANGSTROM TRIANGLE VERTICES ARE LOCATED ON THE ICOSAHEDRON EDGES
1270 TITLE   4 45 (AND 90) ANGSTROMS AWAY FROM THE ICOSAHEDRON VERTICES.
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HETATM     2 Zn TRI A 2 22.502 72.817 81.412 Zn
HETATM     3 Zn TRI A 3 22.502 0.000 109.225 Zn
HETATM     4 Zn TRI B 1 -22.502 0.000 109.225 Zn
1275 HETATM     5 Zn TRI B 2 45.003 -36.408 95.318 Zn
HETATM     6 Zn TRI B 3 -22.502 -72.816 81.412 Zn
HETATM     7 Zn TRI C 1 -45.003 -36.408 95.318 Zn
HETATM     8 Zn TRI C 2 -36.408 -95.318 45.003 Zn
HETATM     9 Zn TRI C 3 -95.318 -45.003 36.408 Zn
1280 HETATM    10 Zn TRI D 1 -81.412 -22.502 72.817 Zn
HETATM    11 Zn TRI D 2 -109.225 -22.502 0.000 Zn
HETATM    12 Zn TRI D 3 -95.318 45.003 36.408 Zn
HETATM    13 Zn TRI E 1 -81.412 22.502 72.817 Zn
HETATM    14 Zn TRI E 2 -72.817 81.412 22.502 Zn
1285 HETATM    15 Zn TRI E 3 -22.502 72.817 81.412 Zn
HETATM    16 Zn TRI F 1 45.003 36.408 95.318 Zn
HETATM    17 Zn TRI F 2 36.408 95.318 45.003 Zn
HETATM    18 Zn TRI F 3 95.318 45.003 36.408 Zn
HETATM    19 Zn TRI G 1 81.412 22.502 72.817 Zn
1290 HETATM    20 Zn TRI G 2 109.225 22.502 0.000 Zn
HETATM    21 Zn TRI G 3 95.318 -45.003 36.408 Zn
HETATM    22 Zn TRI H 1 81.412 -22.502 72.817 Zn
HETATM    23 Zn TRI H 2 72.817 -81.411 22.502 Zn
HETATM    24 Zn TRI H 3 22.502 -72.816 81.412 Zn
1295 HETATM    25 Zn TRI I 1 36.408 -95.318 45.003 Zn
HETATM    26 Zn TRI I 2 72.817 -81.411 -22.502 Zn
HETATM    27 Zn TRI I 3 0.000-109.224 -22.502 Zn
HETATM    28 Zn TRI J 1 0.000-109.224 22.502 Zn
HETATM    29 Zn TRI J 2 -36.408 -95.318 -45.003 Zn
1300 HETATM    30 Zn TRI J 3 -72.817 -81.411 22.502 Zn
HETATM    31 Zn TRI K 1 -81.412 -22.502 -72.817 Zn
HETATM    32 Zn TRI K 2 -72.817 -81.411 -22.502 Zn
HETATM    33 Zn TRI K 3 -22.502 -72.816 -81.412 Zn
HETATM    34 Zn TRI L 1 -81.412 22.502 -72.817 Zn
1305 HETATM    35 Zn TRI L 2 -109.225 22.502 0.000 Zn
HETATM    36 Zn TRI L 3 -95.318 -45.003 -36.408 Zn
HETATM    37 Zn TRI M 1 -45.003 36.408 -95.318 Zn
HETATM    38 Zn TRI M 2 -36.408 95.318 -45.003 Zn
HETATM    39 Zn TRI M 3 -95.318 45.003 -36.408 Zn
1310 HETATM    40 Zn TRI N 1 -36.408 95.318 45.003 Zn
HETATM    41 Zn TRI N 2 -72.817 81.412 -22.502 Zn
HETATM    42 Zn TRI N 3 0.000 109.225 -22.502 Zn
HETATM    43 Zn TRI O 1 0.000 109.225 22.502 Zn
HETATM    44 Zn TRI O 2 36.408 95.318 -45.003 Zn
1315 HETATM    45 Zn TRI O 3 72.817 81.412 22.502 Zn
HETATM    46 Zn TRI P 1 81.412 -22.502 -72.817 Zn
HETATM    47 Zn TRI P 2 109.225 -22.502 0.000 Zn
HETATM    48 Zn TRI P 3 95.318 45.003 -36.408 Zn
HETATM    49 Zn TRI Q 1 45.003 -36.408 -95.318 Zn
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HETATM    53 Zn TRI R 2 22.502 -72.816 -81.412 Zn
HETATM    54 Zn TRI R 3 22.502 0.000-109.225 Zn
1325 HETATM    55 Zn TRI S 1 -22.502 0.000-109.225 Zn
HETATM    56 Zn TRI S 2 45.003 36.408 -95.318 Zn
    
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Supporting Information File: CASOG\_ONE\_CAPSID\_POINTS.PDB

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TITLE       3 ARE POSITIONED WITHIN, AND SHARE ONE VERTEX POSITION WITH, VIRTUAL
TITLE       4 78-ANGSTROM-ON-AN-EDGE EQUILATERAL TRIANGLES. THESE 78-ANGSTROM
TITLE       5 TRIANGLES ARE POSITIONED ON A VIRTUAL 135 ANGSTROM-ON-AN-EDGE
1380 TITLE   6 ICOSAHEDRON SUCH THAT THE 78-ANGSTROM VERTICES ARE LOCATED ON THE
TITLE       7 ICOSAHEDRON EDGES 45 (AND 90) ANGSTROMS FROM THE ICOSAHEDRON VERTICES.
HETATM     1   Zn TRI a   1   12.943  46.826  91.339           Zn
HETATM     2   Zn TRI a   1   -4.498  29.130  98.098           Zn
HETATM     3   Zn TRI a   1  -45.003  36.408  95.318           Zn
HETATM     4   Zn TRI b   2    3.186  20.728 101.307           Zn
1385 HETATM     5   Zn TRI b   2   -4.498  43.687  92.538           Zn
HETATM     6   Zn TRI b   2   22.502  72.817  81.412           Zn
HETATM     7   Zn TRI c   3  -16.129  41.670  93.309           Zn
HETATM     8   Zn TRI c   3    8.997  36.408  95.318           Zn
HETATM     9   Zn TRI c   3   22.502    0.000 109.225           Zn
1390 HETATM    10   Zn TRI a   4   16.129 -41.670  93.309           Zn
HETATM    11   Zn TRI a   4   -8.997 -36.408  95.318           Zn
HETATM    12   Zn TRI a   4  -22.502    0.000 109.225           Zn
HETATM    13   Zn TRI b   5  -12.943 -46.826  91.339           Zn
HETATM    14   Zn TRI b   5    4.498 -29.130  98.098           Zn
1395 HETATM    15   Zn TRI b   5   45.003 -36.408  95.318           Zn
HETATM    16   Zn TRI c   6   -3.186 -20.728 101.307           Zn
HETATM    17   Zn TRI c   6    4.498 -43.686  92.538           Zn
HETATM    18   Zn TRI c   6  -22.502 -72.816  81.412           Zn
HETATM    19   Zn TRI a   7  -54.481 -72.579  49.668           Zn
1400 HETATM    20   Zn TRI a   7  -63.408 -51.631  61.690           Zn
HETATM    21   Zn TRI a   7  -45.003 -36.408  95.318           Zn
HETATM    22   Zn TRI b   8  -72.579 -49.668  54.481           Zn
HETATM    23   Zn TRI b   8  -51.631 -61.690  63.408           Zn
HETATM    24   Zn TRI b   8  -36.408 -95.318  45.003           Zn
1405 HETATM    25   Zn TRI c   9  -49.668 -54.481  72.579           Zn
HETATM    26   Zn TRI c   9  -61.690 -63.408  51.631           Zn
HETATM    27   Zn TRI c   9  -95.318 -45.003  36.408           Zn
HETATM    28   Zn TRI a  10 -101.307 -3.186  20.728           Zn
HETATM    29   Zn TRI a  10  -92.538  4.498  43.687           Zn
1410 HETATM    30   Zn TRI a  10  -81.412 -22.502  72.817           Zn
HETATM    31   Zn TRI b  11  -93.309  16.129  41.670           Zn
HETATM    32   Zn TRI b  11  -95.318  -8.997  36.408           Zn
HETATM    33   Zn TRI b  11 -109.225 -22.502    0.000           Zn
HETATM    34   Zn TRI c  12  -91.339 -12.943  46.826           Zn
1415 HETATM    35   Zn TRI c  12  -98.098  4.498  29.130           Zn
HETATM    36   Zn TRI c  12  -95.318  45.003  36.408           Zn
HETATM    37   Zn TRI a  13  -59.637  70.611  46.483           Zn
HETATM    38   Zn TRI a  13  -56.130  54.412  66.189           Zn
HETATM    39   Zn TRI a  13  -81.412  22.502  72.817           Zn
1420 HETATM    40   Zn TRI b  14  -46.483  59.637  70.611           Zn
HETATM    41   Zn TRI b  14  -66.189  56.130  54.412           Zn
HETATM    42   Zn TRI b  14  -72.817  81.412  22.502           Zn
HETATM    43   Zn TRI c  15  -70.611  46.483  59.637           Zn
HETATM    44   Zn TRI c  15  -54.412  66.189  56.130           Zn
1425 HETATM    45   Zn TRI c  15  -22.502  72.817  81.412           Zn
HETATM    46   Zn TRI a  16   54.481  72.579  49.668           Zn
HETATM    47   Zn TRI a  16   63.408  51.631  61.690           Zn
HETATM    48   Zn TRI a  16   45.003  36.408  95.318           Zn
HETATM    49   Zn TRI b  17   72.579  49.668  54.481           Zn
1430 HETATM    50   Zn TRI b  17   51.631  61.690  63.408           Zn
HETATM    51   Zn TRI b  17   36.408  95.318  45.003           Zn
HETATM    52   Zn TRI c  18   49.668  54.481  72.579           Zn
HETATM    53   Zn TRI c  18   61.690  63.408  51.631           Zn
    
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	HETATM	54	Zn	TRI	c	18	95.318	45.003	36.408	Zn
1435	HETATM	55	Zn	TRI	a	19	101.307	3.186	20.728	Zn
	HETATM	56	Zn	TRI	a	19	92.538	-4.498	43.687	Zn
	HETATM	57	Zn	TRI	a	19	81.412	22.502	72.817	Zn
	HETATM	58	Zn	TRI	b	20	93.309	-16.129	41.670	Zn
	HETATM	59	Zn	TRI	b	20	95.318	8.997	36.408	Zn
1440	HETATM	60	Zn	TRI	b	20	109.225	22.502	0.000	Zn
	HETATM	61	Zn	TRI	c	21	91.339	12.943	46.826	Zn
	HETATM	62	Zn	TRI	c	21	98.098	-4.498	29.130	Zn
	HETATM	63	Zn	TRI	c	21	95.318	-45.003	36.408	Zn
	HETATM	64	Zn	TRI	a	22	59.637	-70.610	46.483	Zn
1445	HETATM	65	Zn	TRI	a	22	56.130	-54.411	66.189	Zn
	HETATM	66	Zn	TRI	a	22	81.412	-22.502	72.817	Zn
	HETATM	67	Zn	TRI	b	23	46.483	-59.637	70.611	Zn
	HETATM	68	Zn	TRI	b	23	66.189	-56.130	54.412	Zn
	HETATM	69	Zn	TRI	b	23	72.817	-81.411	22.502	Zn
1450	HETATM	70	Zn	TRI	c	24	70.611	-46.482	59.637	Zn
	HETATM	71	Zn	TRI	c	24	54.412	-66.188	56.130	Zn
	HETATM	72	Zn	TRI	c	24	22.502	-72.816	81.412	Zn
	HETATM	73	Zn	TRI	a	25	46.826	-91.338	-12.943	Zn
	HETATM	74	Zn	TRI	a	25	29.130	-98.098	4.498	Zn
1455	HETATM	75	Zn	TRI	a	25	36.408	-95.318	45.003	Zn
	HETATM	76	Zn	TRI	b	26	20.728	-101.307	-3.186	Zn
	HETATM	77	Zn	TRI	b	26	43.687	-92.538	4.498	Zn
	HETATM	78	Zn	TRI	b	26	72.817	-81.411	-22.502	Zn
	HETATM	79	Zn	TRI	c	27	41.670	-93.308	16.129	Zn
1460	HETATM	80	Zn	TRI	c	27	36.408	-95.318	-8.997	Zn
	HETATM	81	Zn	TRI	c	27	0.000	-109.224	-22.502	Zn
	HETATM	82	Zn	TRI	a	28	-41.670	-93.308	-16.129	Zn
	HETATM	83	Zn	TRI	a	28	-36.408	-95.318	8.997	Zn
	HETATM	84	Zn	TRI	a	28	0.000	-109.224	22.502	Zn
1465	HETATM	85	Zn	TRI	b	39	-46.826	-91.338	12.943	Zn
	HETATM	86	Zn	TRI	b	39	-29.130	-98.098	-4.498	Zn
	HETATM	87	Zn	TRI	b	39	-36.408	-95.318	-45.003	Zn
	HETATM	88	Zn	TRI	c	30	-20.728	-101.307	3.186	Zn
	HETATM	89	Zn	TRI	c	30	-43.687	-92.538	-4.498	Zn
1470	HETATM	90	Zn	TRI	c	30	-72.817	-81.411	22.502	Zn
	HETATM	91	Zn	TRI	a	31	-59.637	-70.610	-46.483	Zn
	HETATM	92	Zn	TRI	a	31	-56.130	-54.411	-66.189	Zn
	HETATM	93	Zn	TRI	a	31	-81.412	-22.502	-72.817	Zn
	HETATM	94	Zn	TRI	b	32	-46.483	-59.637	-70.611	Zn
1475	HETATM	95	Zn	TRI	b	32	-66.189	-56.130	-54.412	Zn
	HETATM	96	Zn	TRI	b	32	-72.817	-81.411	-22.502	Zn
	HETATM	97	Zn	TRI	c	33	-70.611	-46.482	-59.637	Zn
	HETATM	98	Zn	TRI	c	33	-54.412	-66.188	-56.130	Zn
	HETATM	99	Zn	TRI	c	33	-22.502	-72.816	-81.412	Zn
1480	HETATM	100	Zn	TRI	a	34	-101.307	3.186	-20.728	Zn
	HETATM	101	Zn	TRI	a	34	-92.538	-4.498	-43.687	Zn
	HETATM	102	Zn	TRI	a	34	-81.412	22.502	-72.817	Zn
	HETATM	103	Zn	TRI	b	35	-93.309	-16.129	-41.670	Zn
	HETATM	104	Zn	TRI	b	35	-95.318	8.997	-36.408	Zn
1485	HETATM	105	Zn	TRI	b	35	-109.225	22.502	0.000	Zn
	HETATM	106	Zn	TRI	c	36	-91.339	12.943	-46.826	Zn
	HETATM	107	Zn	TRI	c	36	-98.098	-4.498	-29.130	Zn
	HETATM	108	Zn	TRI	c	36	-95.318	-45.003	-36.408	Zn
	HETATM	109	Zn	TRI	a	37	-54.481	72.579	-49.668	Zn
1490	HETATM	110	Zn	TRI	a	37	-63.408	51.631	-61.690	Zn
	HETATM	111	Zn	TRI	a	37	-45.003	36.408	-95.318	Zn
	HETATM	112	Zn	TRI	b	38	-72.579	49.668	-54.481	Zn
	HETATM	113	Zn	TRI	b	38	-51.631	61.690	-63.408	Zn
	HETATM	114	Zn	TRI	b	38	-36.408	95.318	-45.003	Zn
1495	HETATM	115	Zn	TRI	c	39	-49.668	54.481	-72.579	Zn
	HETATM	116	Zn	TRI	c	39	-61.690	63.408	-51.631	Zn

	HETATM	117	Zn	TRI	c	39	-95.318	45.003	-36.408	Zn
	HETATM	118	Zn	TRI	a	40	-46.826	91.339	-12.943	Zn
	HETATM	119	Zn	TRI	a	40	-29.130	98.098	4.498	Zn
1500	HETATM	120	Zn	TRI	a	40	-36.408	95.318	45.003	Zn
	HETATM	121	Zn	TRI	b	41	-20.728	101.307	-3.186	Zn
	HETATM	122	Zn	TRI	b	41	-43.687	92.538	4.498	Zn
	HETATM	123	Zn	TRI	b	41	-72.817	81.412	-22.502	Zn
	HETATM	124	Zn	TRI	c	42	-41.670	93.309	16.129	Zn
1505	HETATM	125	Zn	TRI	c	42	-36.408	95.318	-8.997	Zn
	HETATM	126	Zn	TRI	c	42	0.000	109.225	-22.502	Zn
	HETATM	127	Zn	TRI	a	43	41.670	93.309	-16.129	Zn
	HETATM	128	Zn	TRI	a	43	36.408	95.318	8.997	Zn
	HETATM	129	Zn	TRI	a	43	0.000	109.225	22.502	Zn
1510	HETATM	130	Zn	TRI	b	44	46.826	91.339	12.943	Zn
	HETATM	131	Zn	TRI	b	44	29.130	98.098	-4.498	Zn
	HETATM	132	Zn	TRI	b	44	36.408	95.318	-45.003	Zn
	HETATM	133	Zn	TRI	c	45	20.728	101.307	3.186	Zn
	HETATM	134	Zn	TRI	c	45	43.687	92.538	-4.498	Zn
1515	HETATM	135	Zn	TRI	c	45	72.817	81.412	22.502	Zn
	HETATM	136	Zn	TRI	a	46	101.307	-3.186	-20.728	Zn
	HETATM	137	Zn	TRI	a	46	92.538	4.498	-43.687	Zn
	HETATM	138	Zn	TRI	a	46	81.412	-22.502	-72.817	Zn
	HETATM	139	Zn	TRI	b	47	93.309	16.129	-41.670	Zn
1520	HETATM	140	Zn	TRI	b	47	95.318	-8.997	-36.408	Zn
	HETATM	141	Zn	TRI	b	47	109.225	-22.502	0.000	Zn
	HETATM	142	Zn	TRI	c	48	91.339	-12.943	-46.826	Zn
	HETATM	143	Zn	TRI	c	48	98.098	4.498	-29.130	Zn
	HETATM	144	Zn	TRI	c	48	95.318	45.003	-36.408	Zn
1525	HETATM	145	Zn	TRI	a	49	54.481	-72.579	-49.668	Zn
	HETATM	146	Zn	TRI	a	49	63.408	-51.631	-61.690	Zn
	HETATM	147	Zn	TRI	a	49	45.003	-36.408	-95.318	Zn
	HETATM	148	Zn	TRI	b	50	72.579	-49.668	-54.481	Zn
	HETATM	149	Zn	TRI	b	50	51.631	-61.690	-63.408	Zn
1530	HETATM	150	Zn	TRI	b	50	36.408	-95.318	-45.003	Zn
	HETATM	151	Zn	TRI	c	51	49.668	-54.481	-72.579	Zn
	HETATM	152	Zn	TRI	c	51	61.690	-63.408	-51.631	Zn
	HETATM	153	Zn	TRI	c	51	95.318	-45.003	-36.408	Zn
	HETATM	154	Zn	TRI	a	52	12.943	-46.826	-91.339	Zn
1535	HETATM	155	Zn	TRI	a	52	-4.498	-29.130	-98.098	Zn
	HETATM	156	Zn	TRI	a	52	-45.003	-36.408	-95.318	Zn
	HETATM	157	Zn	TRI	b	53	3.186	-20.728	-101.307	Zn
	HETATM	158	Zn	TRI	b	53	-4.498	-43.686	-92.538	Zn
	HETATM	159	Zn	TRI	b	53	22.502	-72.816	-81.412	Zn
1540	HETATM	160	Zn	TRI	c	54	-16.129	-41.670	-93.309	Zn
	HETATM	161	Zn	TRI	c	54	8.997	-36.408	-95.318	Zn
	HETATM	162	Zn	TRI	c	54	22.502	0.000	-109.225	Zn
	HETATM	163	Zn	TRI	a	55	16.129	41.670	-93.309	Zn
	HETATM	164	Zn	TRI	a	55	-8.997	36.408	-95.318	Zn
1545	HETATM	165	Zn	TRI	a	55	-22.502	0.000	-109.225	Zn
	HETATM	166	Zn	TRI	b	56	-12.943	46.826	-91.339	Zn
	HETATM	167	Zn	TRI	b	56	4.498	29.130	-98.098	Zn
	HETATM	168	Zn	TRI	b	56	45.003	36.408	-95.318	Zn
	HETATM	169	Zn	TRI	c	57	-3.186	20.728	-101.307	Zn
1550	HETATM	170	Zn	TRI	c	57	4.498	43.687	-92.538	Zn
	HETATM	171	Zn	TRI	c	57	-22.502	72.817	-81.412	Zn
	HETATM	172	Zn	TRI	a	58	59.637	70.611	-46.483	Zn
	HETATM	173	Zn	TRI	a	58	56.130	54.412	-66.189	Zn
	HETATM	174	Zn	TRI	a	58	81.412	22.502	-72.817	Zn
1555	HETATM	175	Zn	TRI	b	59	46.483	59.637	-70.611	Zn
	HETATM	176	Zn	TRI	b	59	66.189	56.130	-54.412	Zn
	HETATM	177	Zn	TRI	b	59	72.817	81.412	-22.502	Zn
	HETATM	178	Zn	TRI	c	60	70.611	46.483	-59.637	Zn
	HETATM	179	Zn	TRI	c	60	54.412	66.189	-56.130	Zn



1560	HETATM	180	Zn	TRI	c	60	22.502	72.817	-81.412	Zn
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	CONNECT	4	5	6						
	CONNECT	5	6							
1565	CONNECT	7	8	9						
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	CONNECT	13	14	15						
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	CONNECT	16	17	18						
	CONNECT	17	18							
	CONNECT	19	20	21						
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	CONNECT	25	26	27						
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	CONNECT	73	74	75						
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	CONNECT	88	89	90						
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	CONNECT	92	93							

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CONNECT 95 96
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CONNECT 178 179 180
1680 CONNECT 179 180
END
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Supporting Information File: CASOG\_TWO\_CAPSID\_POINTS.PDB

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HEADER      ICOSAHEDRON FACE POINTS: 26 A TRIANGLES
TITLE       26-ANGSTROM-ON-AN-EDGE EQUILATERAL TRIANGLES WITH ZN ATOM VERTICES ARE
1685 TITLE   2 POSITIONED ON VIRTUAL 78-ANGSTROM-ON-AN-EDGE EQUILATERAL TRIANGLES
TITLE       3 SUCH THAT EACH 26-ANGSTROM TRIANGLE IS LOCATED AT A CORNER OF, AND
TITLE       4 COPLANAR WITH, A 78-ANGSTROM TRIANGLE, AND FURTHERMORE THAT THE
TITLE       5 78-ANGSTROM TRIANGLES ARE POSITIONED ON A VIRTUAL 135 ANGSTROM-ON-AN-
1690 TITLE   6 EDGE ICOSAHEDRON SUCH THAT THE 78-ANGSTROM VERTICES ARE LOCATED ON THE
TITLE       7 ICOSAHEDRON EDGES 45 (AND 90) ANGSTROMS FROM THE ICOSAHEDRON VERTICES.
HETATM     1   Zn TRI a   1   -22.501  24.272  99.954           Zn
HETATM     2   Zn TRI a   1   -22.501  48.544  90.683           Zn
HETATM     3   Zn TRI a   1   -45.003  36.408  95.318           Zn
HETATM     4   Zn TRI b   2     0.000  60.681  86.047           Zn
1695 HETATM     5   Zn TRI b   2    22.502  48.545  90.683           Zn
HETATM     6   Zn TRI b   2    22.502  72.817  81.412           Zn
HETATM     7   Zn TRI c   3    22.502  24.272  99.954           Zn
HETATM     8   Zn TRI c   3     0.000  12.136 104.589           Zn
HETATM     9   Zn TRI c   3    22.502   0.000 109.225           Zn
1700 HETATM    10   Zn TRI a   4   -22.502 -24.272  99.954           Zn
HETATM    11   Zn TRI a   4    -0.000 -12.136 104.589           Zn
HETATM    12   Zn TRI a   4   -22.502   0.000 109.225           Zn
HETATM    13   Zn TRI b   5    22.501 -24.272  99.954           Zn
HETATM    14   Zn TRI b   5    22.501 -48.544  90.683           Zn
1705 HETATM    15   Zn TRI b   5    45.003 -36.408  95.318           Zn
HETATM    16   Zn TRI c   6    -0.000 -60.680  86.047           Zn
HETATM    17   Zn TRI c   6   -22.502 -48.544  90.683           Zn
HETATM    18   Zn TRI c   6   -22.502 -72.816  81.412           Zn
HETATM    19   Zn TRI a   7   -61.775 -39.273  75.681           Zn
1710 HETATM    20   Zn TRI a   7   -42.138 -56.045  78.546           Zn
HETATM    21   Zn TRI a   7   -45.003 -36.408  95.318           Zn
HETATM    22   Zn TRI b   8   -39.273 -75.681  61.775           Zn
HETATM    23   Zn TRI b   8   -56.045 -78.546  42.138           Zn
HETATM    24   Zn TRI b   8   -36.408 -95.318  45.003           Zn
1715 HETATM    25   Zn TRI c   9   -75.681 -61.775  39.273           Zn
HETATM    26   Zn TRI c   9   -78.546 -42.138  56.045           Zn
HETATM    27   Zn TRI c   9   -95.318 -45.003  36.408           Zn
HETATM    28   Zn TRI a  10   -86.047  -0.000  60.681           Zn
HETATM    29   Zn TRI a  10   -90.683 -22.502  48.545           Zn
1720 HETATM    30   Zn TRI a  10   -81.412 -22.502  72.817           Zn
HETATM    31   Zn TRI b  11   -99.954 -22.502  24.272           Zn
HETATM    32   Zn TRI b  11  -104.589  -0.000  12.136           Zn
HETATM    33   Zn TRI b  11  -109.225 -22.502   0.000           Zn
HETATM    34   Zn TRI c  12   -99.954  22.501  24.272           Zn
1725 HETATM    35   Zn TRI c  12   -90.683  22.501  48.544           Zn
HETATM    36   Zn TRI c  12   -95.318  45.003  36.408           Zn
HETATM    37   Zn TRI a  13   -61.775  39.274  75.682           Zn
HETATM    38   Zn TRI a  13   -78.547  42.139  56.045           Zn
HETATM    39   Zn TRI a  13   -81.412  22.502  72.817           Zn
1730 HETATM    40   Zn TRI b  14   -75.682  61.775  39.274           Zn
HETATM    41   Zn TRI b  14   -56.045  78.547  42.139           Zn
HETATM    42   Zn TRI b  14   -72.817  81.412  22.502           Zn
HETATM    43   Zn TRI c  15   -39.274  75.682  61.775           Zn
HETATM    44   Zn TRI c  15   -42.139  56.045  78.547           Zn
1735 HETATM    45   Zn TRI c  15   -22.502  72.817  81.412           Zn
HETATM    46   Zn TRI a  16    61.775  39.273  75.681           Zn
HETATM    47   Zn TRI a  16    42.138  56.045  78.546           Zn
HETATM    48   Zn TRI a  16    45.003  36.408  95.318           Zn
HETATM    49   Zn TRI b  17    39.273  75.681  61.775           Zn
1740 HETATM    50   Zn TRI b  17    56.045  78.546  42.138           Zn
HETATM    51   Zn TRI b  17    36.408  95.318  45.003           Zn
HETATM    52   Zn TRI c  18    75.681  61.775  39.273           Zn
HETATM    53   Zn TRI c  18    78.546  42.138  56.045           Zn
    
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	HETATM	54	Zn	TRI	c	18	95.318	45.003	36.408	Zn
1745	HETATM	55	Zn	TRI	a	19	86.047	0.000	60.681	Zn
	HETATM	56	Zn	TRI	a	19	90.683	22.502	48.545	Zn
	HETATM	57	Zn	TRI	a	19	81.412	22.502	72.817	Zn
	HETATM	58	Zn	TRI	b	20	99.954	22.502	24.272	Zn
	HETATM	59	Zn	TRI	b	20	104.589	0.000	12.136	Zn
1750	HETATM	60	Zn	TRI	b	20	109.225	22.502	0.000	Zn
	HETATM	61	Zn	TRI	c	21	99.954	-22.501	24.272	Zn
	HETATM	62	Zn	TRI	c	21	90.683	-22.501	48.544	Zn
	HETATM	63	Zn	TRI	c	21	95.318	-45.003	36.408	Zn
	HETATM	64	Zn	TRI	a	22	61.775	-39.273	75.682	Zn
1755	HETATM	65	Zn	TRI	a	22	78.547	-42.138	56.045	Zn
	HETATM	66	Zn	TRI	a	22	81.412	-22.502	72.817	Zn
	HETATM	67	Zn	TRI	b	23	75.682	-61.775	39.274	Zn
	HETATM	68	Zn	TRI	b	23	56.045	-78.546	42.139	Zn
	HETATM	69	Zn	TRI	b	23	72.817	-81.411	22.502	Zn
1760	HETATM	70	Zn	TRI	c	24	39.274	-75.681	61.775	Zn
	HETATM	71	Zn	TRI	c	24	42.139	-56.045	78.547	Zn
	HETATM	72	Zn	TRI	c	24	22.502	-72.816	81.412	Zn
	HETATM	73	Zn	TRI	a	25	24.272	-99.953	22.501	Zn
	HETATM	74	Zn	TRI	a	25	48.544	-90.682	22.501	Zn
1765	HETATM	75	Zn	TRI	a	25	36.408	-95.318	45.003	Zn
	HETATM	76	Zn	TRI	b	26	60.681	-86.047	-0.000	Zn
	HETATM	77	Zn	TRI	b	26	48.545	-90.682	-22.502	Zn
	HETATM	78	Zn	TRI	b	26	72.817	-81.411	-22.502	Zn
	HETATM	79	Zn	TRI	c	27	24.272	-99.953	-22.502	Zn
1770	HETATM	80	Zn	TRI	c	27	12.136	-104.589	-0.000	Zn
	HETATM	81	Zn	TRI	c	27	0.000	-109.224	-22.502	Zn
	HETATM	82	Zn	TRI	a	28	-24.272	-99.953	22.502	Zn
	HETATM	83	Zn	TRI	a	28	-12.136	-104.589	0.000	Zn
	HETATM	84	Zn	TRI	a	28	0.000	-109.224	22.502	Zn
1775	HETATM	85	Zn	TRI	b	39	-24.272	-99.953	-22.501	Zn
	HETATM	86	Zn	TRI	b	39	-48.544	-90.682	-22.501	Zn
	HETATM	87	Zn	TRI	b	39	-36.408	-95.318	-45.003	Zn
	HETATM	88	Zn	TRI	c	30	-60.681	-86.047	0.000	Zn
	HETATM	89	Zn	TRI	c	30	-48.545	-90.682	22.502	Zn
1780	HETATM	90	Zn	TRI	c	30	-72.817	-81.411	22.502	Zn
	HETATM	91	Zn	TRI	a	31	-61.775	-39.273	-75.682	Zn
	HETATM	92	Zn	TRI	a	31	-78.547	-42.138	-56.045	Zn
	HETATM	93	Zn	TRI	a	31	-81.412	-22.502	-72.817	Zn
	HETATM	94	Zn	TRI	b	32	-75.682	-61.775	-39.274	Zn
1785	HETATM	95	Zn	TRI	b	32	-56.045	-78.546	-42.139	Zn
	HETATM	96	Zn	TRI	b	32	-72.817	-81.411	-22.502	Zn
	HETATM	97	Zn	TRI	c	33	-39.274	-75.681	-61.775	Zn
	HETATM	98	Zn	TRI	c	33	-42.139	-56.045	-78.547	Zn
	HETATM	99	Zn	TRI	c	33	-22.502	-72.816	-81.412	Zn
1790	HETATM	100	Zn	TRI	a	34	-86.047	0.000	-60.681	Zn
	HETATM	101	Zn	TRI	a	34	-90.683	22.502	-48.545	Zn
	HETATM	102	Zn	TRI	a	34	-81.412	22.502	-72.817	Zn
	HETATM	103	Zn	TRI	b	35	-99.954	22.502	-24.272	Zn
	HETATM	104	Zn	TRI	b	35	-104.589	0.000	-12.136	Zn
1795	HETATM	105	Zn	TRI	b	35	-109.225	22.502	0.000	Zn
	HETATM	106	Zn	TRI	c	36	-99.954	-22.501	-24.272	Zn
	HETATM	107	Zn	TRI	c	36	-90.683	-22.501	-48.544	Zn
	HETATM	108	Zn	TRI	c	36	-95.318	-45.003	-36.408	Zn
	HETATM	109	Zn	TRI	a	37	-61.775	39.273	-75.681	Zn
1800	HETATM	110	Zn	TRI	a	37	-42.138	56.045	-78.546	Zn
	HETATM	111	Zn	TRI	a	37	-45.003	36.408	-95.318	Zn
	HETATM	112	Zn	TRI	b	38	-39.273	75.681	-61.775	Zn
	HETATM	113	Zn	TRI	b	38	-56.045	78.546	-42.138	Zn
	HETATM	114	Zn	TRI	b	38	-36.408	95.318	-45.003	Zn
1805	HETATM	115	Zn	TRI	c	39	-75.681	61.775	-39.273	Zn
	HETATM	116	Zn	TRI	c	39	-78.546	42.138	-56.045	Zn

	HETATM	117	Zn	TRI	c	39	-95.318	45.003	-36.408	Zn
	HETATM	118	Zn	TRI	a	40	-24.272	99.954	22.501	Zn
	HETATM	119	Zn	TRI	a	40	-48.544	90.683	22.501	Zn
1810	HETATM	120	Zn	TRI	a	40	-36.408	95.318	45.003	Zn
	HETATM	121	Zn	TRI	b	41	-60.681	86.047	-0.000	Zn
	HETATM	122	Zn	TRI	b	41	-48.545	90.683	-22.502	Zn
	HETATM	123	Zn	TRI	b	41	-72.817	81.412	-22.502	Zn
	HETATM	124	Zn	TRI	c	42	-24.272	99.954	-22.502	Zn
1815	HETATM	125	Zn	TRI	c	42	-12.136	104.589	-0.000	Zn
	HETATM	126	Zn	TRI	c	42	0.000	109.225	-22.502	Zn
	HETATM	127	Zn	TRI	a	43	24.272	99.954	22.502	Zn
	HETATM	128	Zn	TRI	a	43	12.136	104.589	0.000	Zn
	HETATM	129	Zn	TRI	a	43	0.000	109.225	22.502	Zn
1820	HETATM	130	Zn	TRI	b	44	24.272	99.954	-22.501	Zn
	HETATM	131	Zn	TRI	b	44	48.544	90.683	-22.501	Zn
	HETATM	132	Zn	TRI	b	44	36.408	95.318	-45.003	Zn
	HETATM	133	Zn	TRI	c	45	60.681	86.047	0.000	Zn
	HETATM	134	Zn	TRI	c	45	48.545	90.683	22.502	Zn
1825	HETATM	135	Zn	TRI	c	45	72.817	81.412	22.502	Zn
	HETATM	136	Zn	TRI	a	46	86.047	-0.000	-60.681	Zn
	HETATM	137	Zn	TRI	a	46	90.683	-22.502	-48.545	Zn
	HETATM	138	Zn	TRI	a	46	81.412	-22.502	-72.817	Zn
	HETATM	139	Zn	TRI	b	47	99.954	-22.502	-24.272	Zn
1830	HETATM	140	Zn	TRI	b	47	104.589	-0.000	-12.136	Zn
	HETATM	141	Zn	TRI	b	47	109.225	-22.502	0.000	Zn
	HETATM	142	Zn	TRI	c	48	99.954	22.501	-24.272	Zn
	HETATM	143	Zn	TRI	c	48	90.683	22.501	-48.544	Zn
	HETATM	144	Zn	TRI	c	48	95.318	45.003	-36.408	Zn
1835	HETATM	145	Zn	TRI	a	49	61.775	-39.273	-75.681	Zn
	HETATM	146	Zn	TRI	a	49	42.138	-56.045	-78.546	Zn
	HETATM	147	Zn	TRI	a	49	45.003	-36.408	-95.318	Zn
	HETATM	148	Zn	TRI	b	50	39.273	-75.681	-61.775	Zn
	HETATM	149	Zn	TRI	b	50	56.045	-78.546	-42.138	Zn
1840	HETATM	150	Zn	TRI	b	50	36.408	-95.318	-45.003	Zn
	HETATM	151	Zn	TRI	c	51	75.681	-61.775	-39.273	Zn
	HETATM	152	Zn	TRI	c	51	78.546	-42.138	-56.045	Zn
	HETATM	153	Zn	TRI	c	51	95.318	-45.003	-36.408	Zn
	HETATM	154	Zn	TRI	a	52	-22.501	-24.272	-99.954	Zn
1845	HETATM	155	Zn	TRI	a	52	-22.501	-48.544	-90.683	Zn
	HETATM	156	Zn	TRI	a	52	-45.003	-36.408	-95.318	Zn
	HETATM	157	Zn	TRI	b	53	0.000	-60.680	-86.047	Zn
	HETATM	158	Zn	TRI	b	53	22.502	-48.544	-90.683	Zn
	HETATM	159	Zn	TRI	b	53	22.502	-72.816	-81.412	Zn
1850	HETATM	160	Zn	TRI	c	54	22.502	-24.272	-99.954	Zn
	HETATM	161	Zn	TRI	c	54	0.000	-12.136	-104.589	Zn
	HETATM	162	Zn	TRI	c	54	22.502	0.000	-109.225	Zn
	HETATM	163	Zn	TRI	a	55	-22.502	24.272	-99.954	Zn
	HETATM	164	Zn	TRI	a	55	-0.000	12.136	-104.589	Zn
1855	HETATM	165	Zn	TRI	a	55	-22.502	0.000	-109.225	Zn
	HETATM	166	Zn	TRI	b	56	22.501	24.272	-99.954	Zn
	HETATM	167	Zn	TRI	b	56	22.501	48.544	-90.683	Zn
	HETATM	168	Zn	TRI	b	56	45.003	36.408	-95.318	Zn
	HETATM	169	Zn	TRI	c	57	-0.000	60.681	-86.047	Zn
1860	HETATM	170	Zn	TRI	c	57	-22.502	48.545	-90.683	Zn
	HETATM	171	Zn	TRI	c	57	-22.502	72.817	-81.412	Zn
	HETATM	172	Zn	TRI	a	58	61.775	39.274	-75.682	Zn
	HETATM	173	Zn	TRI	a	58	78.547	42.139	-56.045	Zn
	HETATM	174	Zn	TRI	a	58	81.412	22.502	-72.817	Zn
1865	HETATM	175	Zn	TRI	b	59	75.682	61.775	-39.274	Zn
	HETATM	176	Zn	TRI	b	59	56.045	78.547	-42.139	Zn
	HETATM	177	Zn	TRI	b	59	72.817	81.412	-22.502	Zn
	HETATM	178	Zn	TRI	c	60	39.274	75.682	-61.775	Zn
	HETATM	179	Zn	TRI	c	60	42.139	56.045	-78.547	Zn

1870	HETATM	180	Zn	TRI	c	60	22.502	72.817	-81.412	Zn
	CONNECT	1	2	3						
	CONNECT	2	3							
	CONNECT	4	5	6						
	CONNECT	5	6							
1875	CONNECT	7	8	9						
	CONNECT	8	9							
	CONNECT	10	11	12						
	CONNECT	11	12							
	CONNECT	13	14	15						
1880	CONNECT	14	15							
	CONNECT	16	17	18						
	CONNECT	17	18							
	CONNECT	19	20	21						
	CONNECT	20	21							
1885	CONNECT	22	23	24						
	CONNECT	23	24							
	CONNECT	25	26	27						
	CONNECT	26	27							
	CONNECT	28	29	30						
1890	CONNECT	29	30							
	CONNECT	31	32	33						
	CONNECT	32	33							
	CONNECT	34	35	36						
	CONNECT	35	36							
1895	CONNECT	37	38	39						
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	CONNECT	40	41	42						
	CONNECT	41	42							
	CONNECT	43	44	45						
1900	CONNECT	44	45							
	CONNECT	46	47	48						
	CONNECT	47	48							
	CONNECT	49	50	51						
	CONNECT	50	51							
1905	CONNECT	52	53	54						
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	CONNECT	56	57							
	CONNECT	58	59	60						
1910	CONNECT	59	60							
	CONNECT	61	62	63						
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	CONNECT	64	65	66						
	CONNECT	65	66							
1915	CONNECT	67	68	69						
	CONNECT	68	69							
	CONNECT	70	71	72						
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	CONNECT	73	74	75						
1920	CONNECT	74	75							
	CONNECT	76	77	78						
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	CONNECT	79	80	81						
	CONNECT	80	81							
1925	CONNECT	82	83	84						
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	CONNECT	85	86	87						
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	CONNECT	88	89	90						
1930	CONNECT	89	90							
	CONNECT	91	92	93						
	CONNECT	92	93							

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	CONNECT	95	96	
1935	CONNECT	97	98	99
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1945	CONNECT	112	113	114
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1950	CONNECT	119	120	
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1955	CONNECT	127	128	129
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1960	CONNECT	134	135	
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1965	CONNECT	142	143	144
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1975	CONNECT	157	158	159
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	CONNECT	160	161	162
	CONNECT	161	162	
	CONNECT	163	164	165
1980	CONNECT	164	165	
	CONNECT	166	167	168
	CONNECT	167	168	
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1985	CONNECT	172	173	174
	CONNECT	173	174	
	CONNECT	175	176	177
	CONNECT	176	177	
	CONNECT	178	179	180
1990	CONNECT	179	180	
	END			

**Supporting Information File: PICORNAVIRUS\_TILING\_POINTS.PDB**

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HEADER      PICORNAVIRUS CAPSID TARGET SUPERPOSITION POINTS
1995 TITLE    1 PICORNAVIRUS CAPSID TARGET SUPERPOSITION POINTS ALL MAP TO THE FIRST
TITLE       2 FACE OF A VIRTUAL 135 ANGSTROM-ON-AN-EDGE ICOSAHEDRON (ICOS-135).
TITLE       3 THESE SUPERPOSITION POINTS ARE GROUPED BY FUNCTION IN SEPARATE CHAINS.
TITLE       4 CASOG ONE TILING POINTS HAVE THE CHAIN IDENTIFIER "1".  CASOG TWO
TITLE       5 TILING POINTS HAVE THE CHAIN IDENTIFIER "2".  POINTS 3, 6, AND 9 ARE
2000 TITLE    6 IDENTICAL IN BOTH LISTED CASOG SETS.  TRIMER POINTS FOR BOTH MYELIN P2
TITLE       7 (2WUT) AND CELLULAR RETINOIC-ACID-BINDING PROTEIN (1CBS) ARE IDENTICAL
TITLE       8 AND INCLUDE THREE CASOG ONE POINTS (CHAIN 1), THREE CASOG TWO POINTS
TITLE       9 (CHAIN 2), AND THREE ADDITIONAL POINTS (POINTS 23, 26, AND 29).  THE
TITLE      10 CASOG POINTS USED FOR MYELIN P2/CRABP SUPERPOSITION ARE LISTED AGAIN
2005 TITLE    11 IN THE MYELIN P2/CRABP SUPERPOSITION POINTS.  THE SUPERPOSITION POINTS
TITLE      12 FOR MYELIN P2/CRABP HAVE THE CHAIN IDENTIFIER "3".
ATOM        1  O   PRO 1   1      12.943  46.826  91.339  1.00  0.00      O
ATOM        2  O   PRO 1   2      -4.498  29.130  98.098  1.00  0.00      O
ATOM        3  O   PRO 1   3     -45.003  36.408  95.318  1.00  0.00      O
ATOM        4  O   PRO 1   4       3.186  20.728 101.307  1.00  0.00      O
2010 ATOM        5  O   PRO 1   5      -4.498  43.687  92.538  1.00  0.00      O
ATOM        6  O   PRO 1   6      22.502  72.817  81.412  1.00  0.00      O
ATOM        7  O   PRO 1   7     -16.129  41.670  93.309  1.00  0.00      O
ATOM        8  O   PRO 1   8       8.997  36.408  95.318  1.00  0.00      O
ATOM        9  O   PRO 1   9      22.502   0.000 109.225  1.00  0.00      O
2015 TER      10
ATOM       11  O   PRO 2   1     -22.501  24.272  99.954  0.00  0.00      O
ATOM       12  O   PRO 2   2     -22.501  48.544  90.683  0.00  0.00      O
ATOM       13  O   PRO 2   3     -45.003  36.408  95.318  0.00  0.00      O
ATOM       14  O   PRO 2   4       0.000  60.681  86.047  0.00  0.00      O
2020 ATOM       15  O   PRO 2   5      22.502  48.545  90.683  0.00  0.00      O
ATOM       16  O   PRO 2   6      22.502  72.817  81.412  0.00  0.00      O
ATOM       17  O   PRO 2   7      22.502  24.272  99.954  0.00  0.00      O
ATOM       18  O   PRO 2   8       0.000  12.136 104.589  0.00  0.00      O
ATOM       19  O   PRO 2   9      22.502   0.000 109.225  0.00  0.00      O
2025 TER      20
ATOM       21  O   PRO 3   1       0.000  60.681  86.047  0.00  0.00      O
ATOM       22  O   PRO 3   2      -4.498  43.687  92.538  1.00  0.00      O
ATOM       23  O   PRO 3   3       3.088  52.039  89.291  1.00  0.00      O
ATOM       24  O   PRO 3   4      22.502  24.272  99.954  0.00  0.00      O
2030 ATOM       25  O   PRO 3   5       8.997  36.408  95.318  1.00  0.00      O
ATOM       26  O   PRO 3   6      12.847  26.009  99.248  1.00  0.00      O
ATOM       27  O   PRO 3   7     -22.501  24.272  99.954  0.00  0.00      O
ATOM       28  O   PRO 3   8      -4.498  29.130  98.098  1.00  0.00      O
ATOM       29  O   PRO 3   9     -16.162  31.180  97.331  1.00  0.00      O
2035 TER      30
END
    
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