



wwPDB EM Validation Summary Report ⓘ

Jun 2, 2026 – 04:15 PM JST

PDB ID : 9VG1 / pdb_00009vg1
EMDB ID : EMD-65043
Title : Structure of CVA6 empty capsid complexed with 3H7 Fab
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Deposited on : 2025-06-12
Resolution : 3.26 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : **FAILED**
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

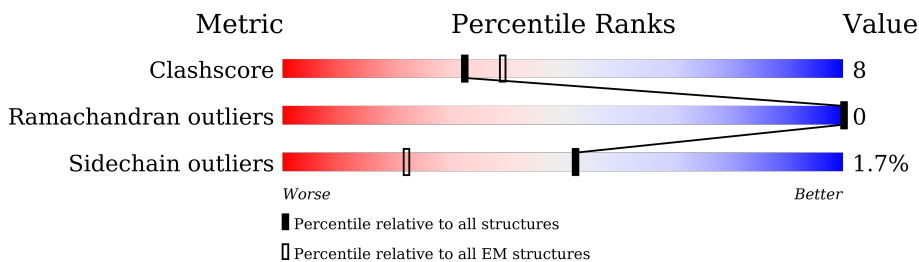
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	D	107	
2	E	124	
3	A	305	
4	C	240	
5	B	256	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6443 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called VL.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	106	Total	C	N	O	S	0	0
			750	470	131	147	2		

- Molecule 2 is a protein called VH.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	120	Total	C	N	O	S	0	0
			819	518	144	153	4		

- Molecule 3 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	214	Total	C	N	O	S	0	0
			1652	1056	286	301	9		

- Molecule 4 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	219	Total	C	N	O	S	1	0
			1639	1060	267	303	9		

- Molecule 5 is a protein called Genome polyprotein.

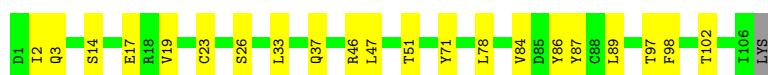
Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	207	Total	C	N	O	S	0	0
			1583	1026	264	287	6		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: VL

Chain D: 



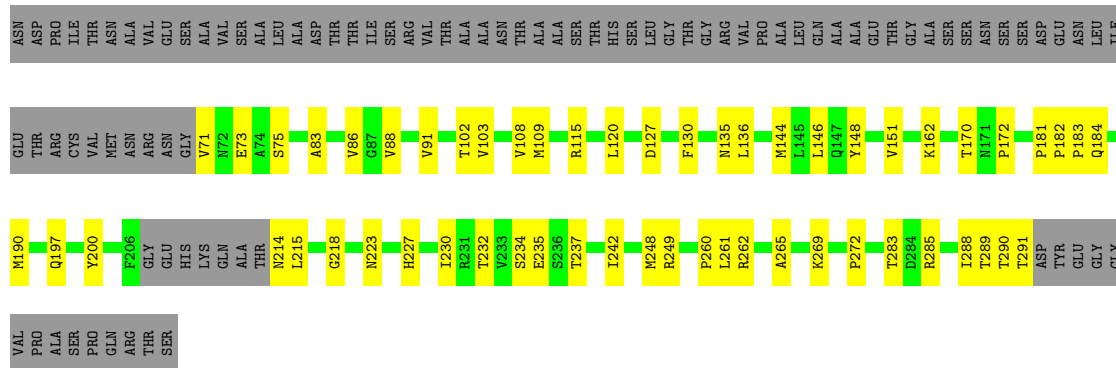
• Molecule 2: VH

Chain E: 



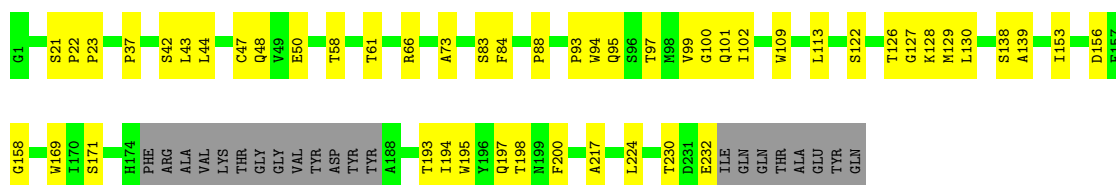
• Molecule 3: Genome polypeptide

Chain A: 



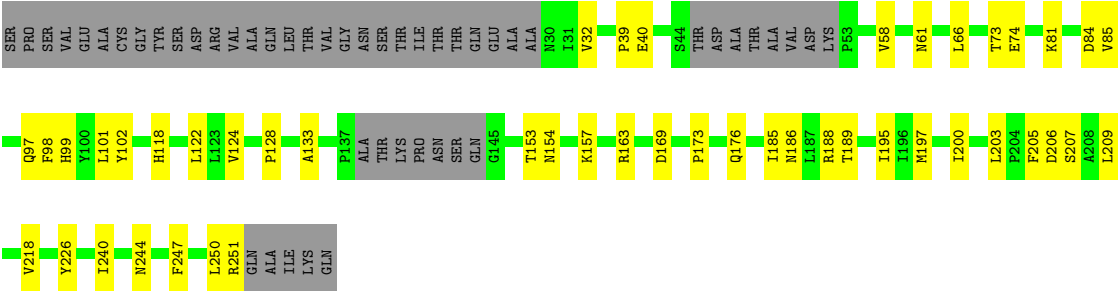
• Molecule 4: Genome polypeptide

Chain C: 



• Molecule 5: Genome polypeptide

Chain B: 62%18%19%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	810	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	D	0.11	0/766	0.32	0/1045
2	E	0.11	0/840	0.33	0/1147
3	A	0.18	0/1701	0.36	0/2327
4	C	0.16	0/1687	0.27	0/2318
5	B	0.15	0/1634	0.28	0/2241
All	All	0.15	0/6628	0.31	0/9078

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	750	0	649	13	0
2	E	819	0	662	11	0
3	A	1652	0	1573	34	0
4	C	1639	0	1607	28	0
5	B	1583	0	1499	30	0
All	All	6443	0	5990	105	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 105 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:53:SER:HG	5:B:73:THR:HG1	1.40	0.66
4:C:37:PRO:HG2	5:B:200:ILE:HG12	1.79	0.65
5:B:97:GLN:HG2	5:B:209:LEU:HD21	1.80	0.63
4:C:97:THR:HG22	4:C:99:VAL:H	1.64	0.63
1:D:37:GLN:HB2	1:D:47:LEU:HD11	1.80	0.63

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	104/107 (97%)	97 (93%)	7 (7%)	0	100	100
2	E	118/124 (95%)	106 (90%)	12 (10%)	0	100	100
3	A	210/305 (69%)	192 (91%)	18 (9%)	0	100	100
4	C	216/240 (90%)	201 (93%)	15 (7%)	0	100	100
5	B	201/256 (78%)	189 (94%)	12 (6%)	0	100	100
All	All	849/1032 (82%)	785 (92%)	64 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	67/93 (72%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	61/103 (59%)	59 (97%)	2 (3%)	33	57
3	A	175/260 (67%)	171 (98%)	4 (2%)	44	65
4	C	177/206 (86%)	175 (99%)	2 (1%)	65	75
5	B	167/218 (77%)	164 (98%)	3 (2%)	51	69
All	All	647/880 (74%)	636 (98%)	11 (2%)	52	69

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	C	153	ILE
5	B	102	TYR
5	B	203	LEU
5	B	169	ASP
3	A	237	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
5	B	210	ASN
5	B	244	ASN
5	B	30	ASN
5	B	119	GLN
5	B	154	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.