



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 15, 2024 – 09:52 AM EDT

PDB ID : 2BFU
Title : X-ray structure of CPMV top component
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Deposited on : 2004-12-13
Resolution : 4.00 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

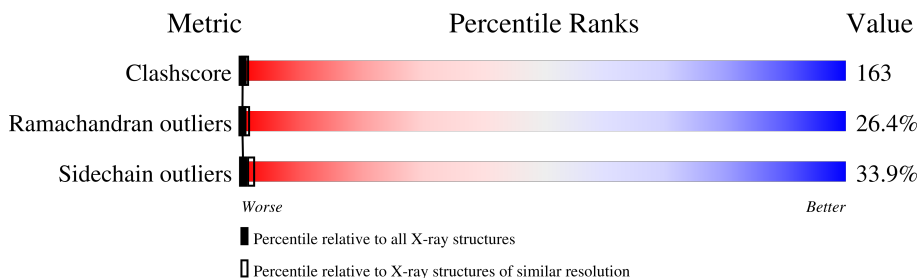
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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	L	369	
2	S	189	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5282 atoms, of which 939 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 COWPEA MOSAIC VIRUS, LARGE (L) SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	L	369	Total	C	H	N	O	S	0	0	0
			3500	1822	634	480	542	22			

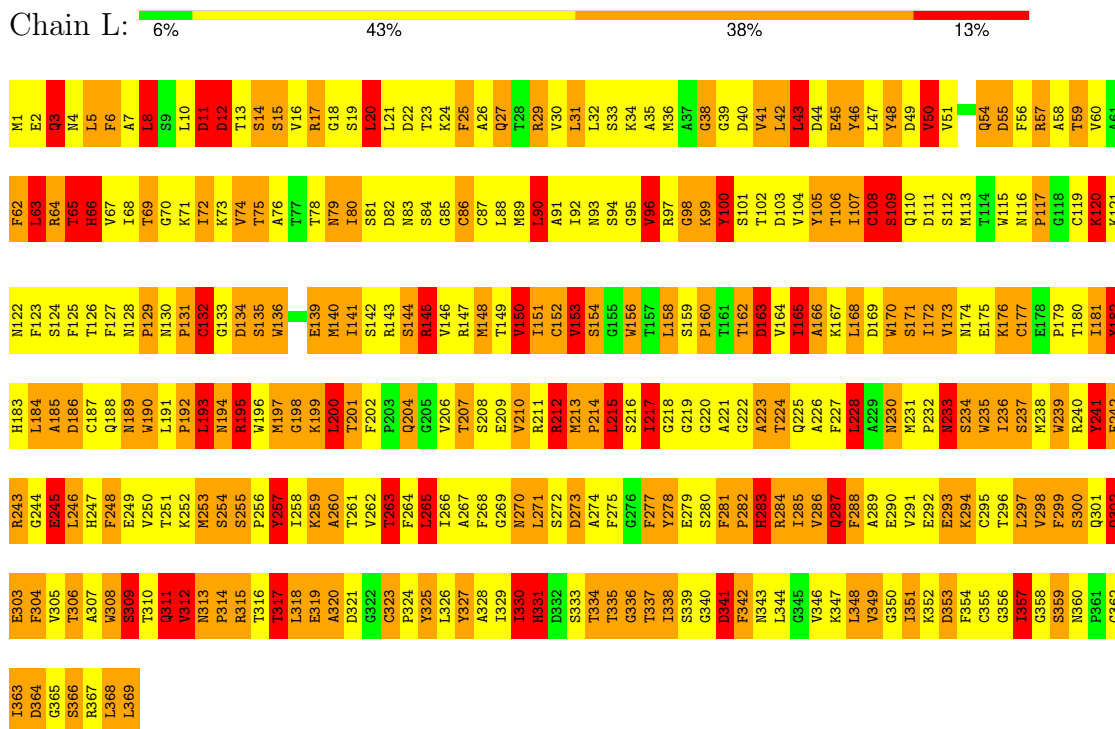
- Molecule 2 is a protein called COWPEA MOSAIC VIRUS, SMALL (S) SUBUNIT.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	S	189	Total	C	H	N	O	S	0	0	0
			1782	944	305	247	277	9			

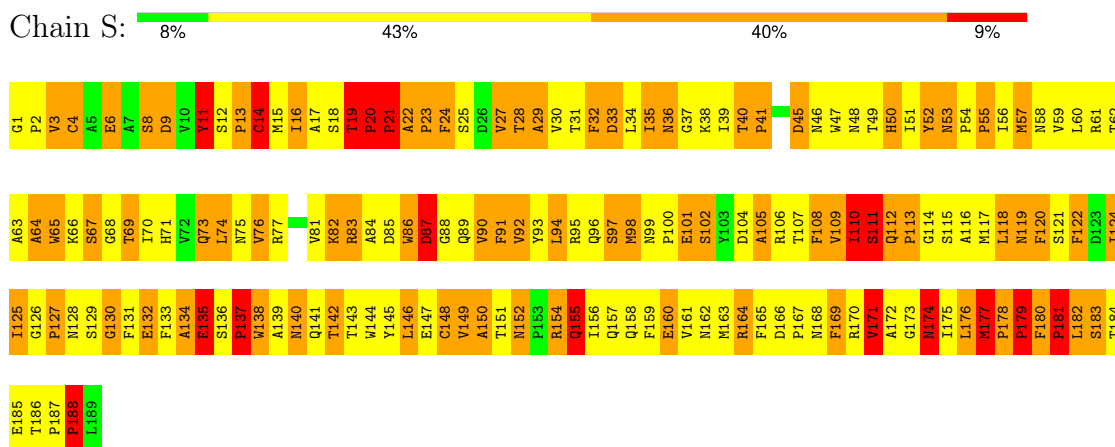
3 Residue-property plots

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: COWPEA MOSAIC VIRUS, LARGE (L) SUBUNIT



- Molecule 2: COWPEA MOSAIC VIRUS, SMALL (S) SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	311.41Å 311.41Å 311.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 4.00 56.85 – 4.00	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.00-4.00) 92.8 (56.85-4.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.45 (at 4.01Å)	Xtriage
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.230 , (Not available) 0.497 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	100.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.12 , -2.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.51	EDS
Total number of atoms	5282	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	L	1.23	7/2933 (0.2%)	1.50	36/3983 (0.9%)
2	S	1.21	6/1524 (0.4%)	1.46	16/2089 (0.8%)
All	All	1.22	13/4457 (0.3%)	1.49	52/6072 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	6
2	S	0	1
All	All	0	7

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	245	GLU	CB-CG	7.86	1.67	1.52
1	L	108	CYS	CB-SG	7.32	1.94	1.82
1	L	235	TRP	CB-CG	7.30	1.63	1.50
1	L	132	CYS	CB-SG	7.29	1.94	1.82
2	S	132	GLU	CB-CG	6.83	1.65	1.52

The worst 5 of 52 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	20	PRO	N-CA-C	9.67	137.23	112.10
2	S	177	MET	N-CA-C	8.96	135.18	111.00
2	S	19	THR	C-N-CD	-8.24	102.47	120.60
1	L	168	LEU	CA-CB-CG	-8.15	96.55	115.30
1	L	153	VAL	N-CA-C	-7.82	89.89	111.00

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	105	TYR	Sidechain
1	L	182	TYR	Sidechain
1	L	241	TYR	Sidechain
1	L	257	TYR	Sidechain
1	L	48	TYR	Sidechain

5.2 Too-close contacts ⓘ

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	L	2866	634	2813	956	29
2	S	1477	305	1413	488	0
All	All	4343	939	4226	1394	29

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 163.

The worst 5 of 1394 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)
1:L:308:TRP:HB3	1:L:323:CYS:SG	1.61	1.39
2:S:89:GLN:HA	2:S:111:SER:HA	1.19	1.16
2:S:54:PRO:HB2	2:S:57:MET:HB3	1.27	1.15
2:S:36:ASN:HB2	2:S:61:ARG:HA	1.16	1.13
1:L:73:LYS:HB2	1:L:126:THR:HG22	1.30	1.13

The worst 5 of 29 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:56:PHE:O	1:L:60:VAL:CG1[2_555]	1.34	0.86
1:L:59:THR:CG2	1:L:59:THR:CG2[2_555]	1.38	0.82
1:L:1:MET:N	1:L:124:SER:OG[2_555]	1.42	0.78
1:L:1:MET:O	1:L:122:ASN:ND2[2_555]	1.50	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:1:MET:H2	1:L:124:SER:CA[2_555]	0.94	0.66

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 X-ray entries followed by that with respect to entries of similar resolution.

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	L	367/369 (100%)	174 (47%)	94 (26%)	99 (27%)	0	0
2	S	187/189 (99%)	87 (46%)	53 (28%)	47 (25%)	0	1
All	All	554/558 (99%)	261 (47%)	147 (26%)	146 (26%)	0	1

5 of 146 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	8	LEU
1	L	14	SER
1	L	50	VAL
1	L	55	ASP
1	L	66	HIS

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 X-ray entries followed by that with respect to entries of similar resolution.

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	L	318/318 (100%)	209 (66%)	109 (34%)	0	1
2	S	163/163 (100%)	109 (67%)	54 (33%)	0	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	481/481 (100%)	318 (66%)	163 (34%)	0 1

5 of 163 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	S	28	THR
2	S	135	GLU
2	S	40	THR
2	S	87	ASP
2	S	160	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	S	119	ASN
2	S	158	GLN
2	S	174	ASN
2	S	155	GLN
1	L	247	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.