



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 12:50 AM EDT

PDB ID : 5L7O  
Title : X-ray structure of Triatoma virus empty capsid  
Authors : Sanchez-Eugenía, R.  
Deposited on : 2016-06-03  
Resolution : 3.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
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

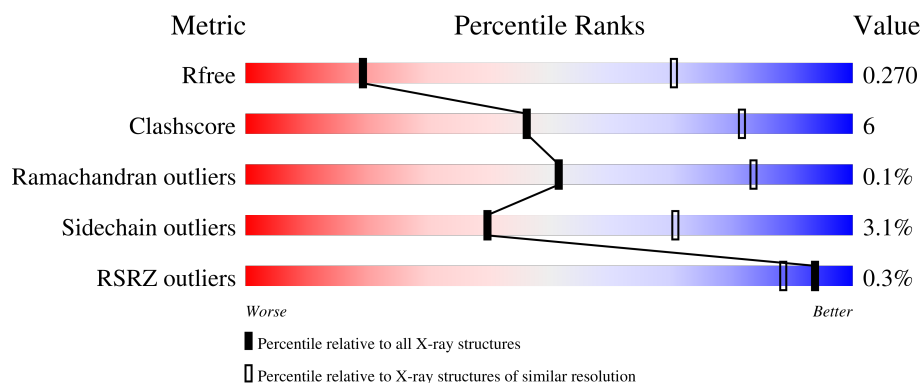
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.60 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))
$R_{free}$	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	271	
2	B	255	
3	C	285	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5398 atoms, of which 0 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 Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	0	0
			1785	1149	288	341	7			

- Molecule 2 is a protein called Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	179	Total	C	N	O	S	0	0	0
			1417	932	228	253	4			

- Molecule 3 is a protein called Capsid protein.

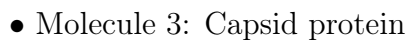
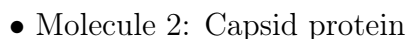
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	276	Total	C	N	O	S	0	0	0
			2196	1421	356	415	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	54	MET	VAL	conflict	UNP Q9QEY5



- Molecule 1: Capsid protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	305.59Å 305.59Å 796.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.91 – 3.60 49.91 – 3.60	Depositor EDS
% Data completeness (in resolution range)	98.3 (49.91-3.60) 98.3 (49.91-3.60)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.22 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.269 , 0.269 0.270 , 0.270	Depositor DCC
$R_{free}$ test set	6433 reflections (2.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	112.7	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 76.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.048 for -h-k,k,-l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	5398	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.97% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [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	A	0.38	0/1831	0.63	0/2497
2	B	0.39	0/1459	0.59	0/1994
3	C	0.40	0/2259	0.62	0/3095
All	All	0.39	0/5549	0.62	0/7586

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	A	1785	0	1753	29	0
2	B	1417	0	1425	21	0
3	C	2196	0	2165	26	0
All	All	5398	0	5343	68	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 6.

All (68) 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)
3:C:133:HIS:HB3	3:C:233:LEU:HD11	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:53:GLU:HA	3:C:58:TYR:CD2	2.31	0.66
1:A:81:MET:HE1	3:C:275:ARG:HA	1.80	0.63
1:A:198:SER:O	1:A:203:ASN:ND2	2.31	0.63
1:A:87:LYS:HG2	1:A:87:LYS:O	1.99	0.62
3:C:80:VAL:HG21	3:C:151:MET:HB3	1.83	0.59
1:A:68:LEU:HD11	1:A:147:ILE:HG23	1.88	0.56
3:C:96:THR:HG21	3:C:272:LEU:O	2.05	0.56
1:A:85:ALA:HB3	1:A:88:LEU:HD12	1.88	0.55
2:B:204:TYR:OH	2:B:209:LYS:HG2	2.07	0.54
1:A:133:VAL:HG22	1:A:165:PHE:CE1	2.43	0.54
1:A:105:SER:HA	3:C:268:PRO:HG3	1.92	0.49
3:C:129:LYS:HE3	3:C:170:LEU:O	2.12	0.49
3:C:236:SER:OG	3:C:238:ALA:HB3	2.12	0.49
2:B:183:LEU:C	2:B:183:LEU:HD23	2.32	0.49
1:A:92:THR:HA	1:A:253:VAL:CG2	2.42	0.49
3:C:182:PHE:CE2	3:C:184:SER:HB3	2.49	0.48
1:A:81:MET:CE	3:C:275:ARG:HA	2.43	0.47
1:A:108:ALA:HB1	1:A:234:PRO:HB3	1.95	0.47
2:B:154:VAL:HG22	2:B:155:PRO:HD2	1.96	0.47
2:B:202:VAL:HG23	2:B:203:GLN:HG3	1.97	0.47
1:A:81:MET:O	1:A:91:TRP:HA	2.15	0.47
2:B:158:ASP:HB2	2:B:211:THR:HG23	1.95	0.47
3:C:37:GLY:O	3:C:38:ASN:C	2.53	0.47
3:C:118:ARG:NH1	3:C:187:PRO:O	2.44	0.46
2:B:247:PHE:CD2	2:B:248:PRO:HD2	2.50	0.46
3:C:52:ASP:OD1	3:C:54:MET:N	2.49	0.46
2:B:100:ILE:HD12	2:B:101:GLU:O	2.14	0.46
1:A:56:ARG:HG3	3:C:21:ASN:HA	1.97	0.46
1:A:92:THR:HA	1:A:253:VAL:HG21	1.97	0.46
1:A:101:THR:HG21	1:A:219:HIS:CE1	2.51	0.46
1:A:118:ARG:HD3	3:C:27:ASP:CG	2.36	0.46
2:B:81:ILE:HG23	2:B:243:ILE:HD13	1.97	0.46
2:B:135:PHE:O	2:B:192:LEU:HA	2.15	0.46
2:B:211:THR:HG22	2:B:212:PRO:O	2.16	0.46
3:C:49:THR:HG22	3:C:51:SER:N	2.31	0.45
2:B:204:TYR:OH	2:B:209:LYS:CG	2.65	0.45
3:C:131:ASN:OD1	3:C:131:ASN:N	2.50	0.45
1:A:36:GLU:N	1:A:36:GLU:OE1	2.49	0.45
1:A:133:VAL:CG2	1:A:165:PHE:CE1	2.99	0.45
3:C:49:THR:HG22	3:C:51:SER:H	1.81	0.45
1:A:177:TYR:CE2	1:A:179:SER:HB3	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:ALA:HB2	3:C:106:LEU:HA	1.98	0.45
2:B:116:SER:O	2:B:120:ARG:HG3	2.17	0.44
1:A:121:ILE:HB	1:A:171:ALA:HB3	1.98	0.44
2:B:120:ARG:NH2	2:B:254:ALA:O	2.51	0.44
3:C:60:LEU:N	3:C:60:LEU:HD23	2.33	0.44
2:B:114:LEU:HD12	2:B:240:PHE:CZ	2.53	0.44
3:C:178:LEU:C	3:C:178:LEU:HD12	2.39	0.43
1:A:203:ASN:ND2	1:A:203:ASN:N	2.65	0.42
3:C:100:ALA:HB3	3:C:101:PRO:HD3	2.00	0.42
1:A:87:LYS:O	1:A:87:LYS:CG	2.67	0.42
1:A:176:PRO:HB2	1:A:178:TYR:CD2	2.55	0.42
2:B:87:PRO:HA	2:B:239:HIS:HB3	2.01	0.42
1:A:37:GLN:HB3	1:A:38:PRO:HD3	2.01	0.42
2:B:156:VAL:O	2:B:157:PRO:C	2.58	0.42
1:A:193:ASN:C	1:A:195:GLY:N	2.72	0.42
2:B:146:CYS:C	2:B:185:ILE:HD11	2.40	0.42
3:C:193:ASP:O	3:C:208:ARG:NH1	2.53	0.41
1:A:97:SER:HA	1:A:147:ILE:CD1	2.51	0.41
2:B:94:LEU:HD11	2:B:231:SER:HB2	2.02	0.41
2:B:138:GLN:HB2	2:B:235:ASN:HB2	2.03	0.41
2:B:222:ALA:HB2	3:C:247:LEU:HD11	2.02	0.41
1:A:146:ILE:CG2	1:A:147:ILE:N	2.84	0.41
2:B:183:LEU:HD23	2:B:184:ASP:N	2.35	0.41
3:C:158:VAL:O	3:C:158:VAL:HG23	2.21	0.41
1:A:161:ILE:HB	3:C:30:LEU:HD22	2.04	0.40
1:A:128:GLN:HB3	1:A:129:PRO:HD3	2.04	0.40

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 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	A	228/271 (84%)	211 (92%)	17 (8%)	0	100	100
2	B	177/255 (69%)	163 (92%)	13 (7%)	1 (1%)	25	64
3	C	274/285 (96%)	246 (90%)	28 (10%)	0	100	100
All	All	679/811 (84%)	620 (91%)	58 (8%)	1 (0%)	51	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	211	THR

### 5.3.2 Protein sidechains ⓘ

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	A	196/231 (85%)	189 (96%)	7 (4%)	35	67
2	B	161/231 (70%)	156 (97%)	5 (3%)	40	71
3	C	251/258 (97%)	244 (97%)	7 (3%)	43	72
All	All	608/720 (84%)	589 (97%)	19 (3%)	40	71

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	SER
1	A	64	ASP
1	A	92	THR
1	A	163	GLU
1	A	165	PHE
1	A	219	HIS
1	A	262	TYR
2	B	133	THR
2	B	199	SER
2	B	210	PHE
2	B	221	TYR
2	B	247	PHE

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Mol	Chain	Res	Type
3	C	51	SER
3	C	131	ASN
3	C	164	TYR
3	C	183	THR
3	C	226	CYS
3	C	228	SER
3	C	270	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	230/271 (84%)	-0.34	2 (0%) 84 73	87, 113, 146, 211	0
2	B	179/255 (70%)	-0.37	0 100 100	88, 111, 129, 170	0
3	C	276/285 (96%)	-0.43	0 100 100	89, 111, 133, 162	0
All	All	685/811 (84%)	-0.38	2 (0%) 94 88	87, 111, 139, 211	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	192	TYR	3.8
1	A	193	ASN	3.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.