



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 11:34 PM EDT

PDB ID : 6FY0
Title : Crystal structure of a V2-directed, RV144 vaccine-like antibody from HIV-1 infection, CAP228-16H, bound to a heterologous V2 peptide
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Deposited on : 2018-03-10
Resolution : 2.57 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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
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

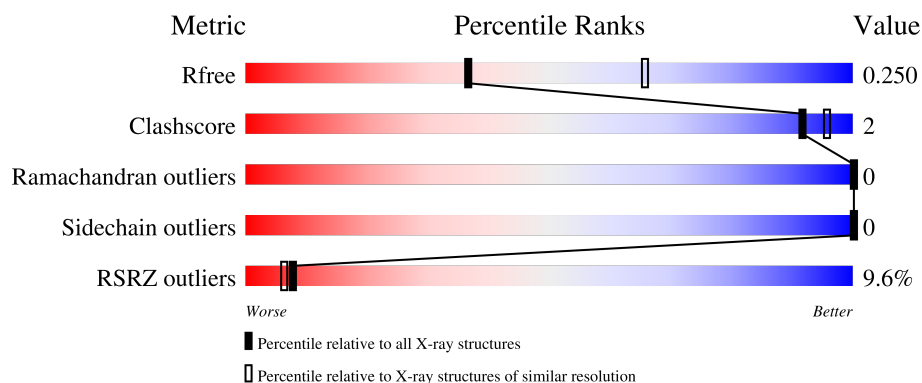
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 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	3676 (2.60-2.56)
Clashscore	141614	4049 (2.60-2.56)
Ramachandran outliers	138981	3979 (2.60-2.56)
Sidechain outliers	138945	3979 (2.60-2.56)
RSRZ outliers	127900	3614 (2.60-2.56)

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 $\leq 5\%$. 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	H	235	<div> <div>10%</div> <div>92%</div> <div>• •</div> </div>
1	I	235	<div> <div>6%</div> <div>89%</div> <div>• 8%</div> </div>
2	L	213	<div> <div>11%</div> <div>93%</div> <div>6% •</div> </div>
2	M	213	<div> <div>10%</div> <div>92%</div> <div>5% •</div> </div>
3	A	19	<div> <div>11%</div> <div>89%</div> <div>11%</div> </div>

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Mol	Chain	Length	Quality of chain
3	P	19	<div> <div style="width: 11%;"></div> <div style="width: 89%;"></div> <div style="width: 11%;"></div> </div> <div>11%89%11%</div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13501 atoms, of which 6616 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 CAP228-16H Heavy Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	226	Total	C	H	N	O	S	0	0	0
			3362	1068	1668	289	329	8			
1	I	216	Total	C	H	N	O	S	0	0	0
			3246	1036	1612	278	313	7			

- Molecule 2 is a protein called CAP228-16H Light Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	211	Total	C	H	N	O	S	0	0	0
			3102	989	1523	262	322	6			
2	M	208	Total	C	H	N	O	S	0	0	0
			3062	977	1505	259	316	5			

- Molecule 3 is a protein called CAP45 V2 peptide.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	A	17	Total	C	H	N	O		0	0	0
			302	97	154	27	24				
3	P	17	Total	C	H	N	O		0	0	0
			302	97	154	27	24				

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

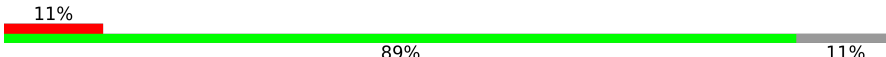


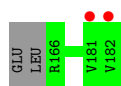
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	24	Total	O	0	0
			24	24		
5	L	35	Total	O	0	0
			35	35		
5	M	19	Total	O	0	0
			19	19		
5	I	33	Total	O	0	0
			33	33		
5	A	2	Total	O	0	0
			2	2		
5	P	2	Total	O	0	0
			2	2		

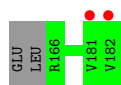
- Molecule 3: CAP45 V2 peptide

Chain A:  11% 89% 11%



- Molecule 3: CAP45 V2 peptide

Chain P:  11% 89% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	40.30Å 104.27Å 212.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.57 35.37 – 2.58	Depositor EDS
% Data completeness (in resolution range)	90.1 (50.00-2.57) 90.2 (35.37-2.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.13-2998	Depositor
R, R_{free}	0.210 , 0.250 0.213 , 0.250	Depositor DCC
R_{free} test set	1319 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	54.3	Xtriage
Anisotropy	1.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13501	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	H	0.26	0/1736	0.47	0/2360
1	I	0.26	0/1675	0.47	0/2278
2	L	0.26	0/1619	0.47	0/2218
2	M	0.26	0/1597	0.46	0/2188
3	A	0.25	0/151	0.46	0/201
3	P	0.25	0/151	0.47	0/201
All	All	0.26	0/6929	0.47	0/9446

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	H	1694	1668	1667	6	1
1	I	1634	1612	1611	4	0
2	L	1579	1523	1521	9	0
2	M	1557	1505	1504	6	1
3	A	148	154	153	0	0
3	P	148	154	153	0	0
4	H	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	5	0	0	0	0
5	A	2	0	0	0	0
5	H	24	0	0	1	0
5	I	33	0	0	0	0
5	L	35	0	0	0	0
5	M	19	0	0	0	0
5	P	2	0	0	0	0
All	All	6885	6616	6609	22	1

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 2.

The worst 5 of 22 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:I:159:LEU:HD21	1:I:182:VAL:HG21	1.66	0.78
1:H:28:ARG:NH1	5:H:401:HOH:O	2.29	0.65
1:H:181:VAL:HG21	2:L:135:LEU:HD13	1.85	0.58
2:L:48:ILE:HD12	2:L:73:LEU:CD1	2.34	0.58
2:M:32:LEU:HD13	2:M:50:ASP:OD1	2.07	0.54

All (1) 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:H:193:THR:OG1	2:M:201:THR:OG1[3_454]	2.18	0.02

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	H	224/235 (95%)	220 (98%)	4 (2%)	0	100	100
1	I	212/235 (90%)	209 (99%)	3 (1%)	0	100	100
2	L	209/213 (98%)	202 (97%)	7 (3%)	0	100	100
2	M	206/213 (97%)	200 (97%)	6 (3%)	0	100	100
3	A	15/19 (79%)	15 (100%)	0	0	100	100
3	P	15/19 (79%)	15 (100%)	0	0	100	100
All	All	881/934 (94%)	861 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	H	189/197 (96%)	189 (100%)	0	100	100
1	I	181/197 (92%)	181 (100%)	0	100	100
2	L	178/180 (99%)	178 (100%)	0	100	100
2	M	175/180 (97%)	175 (100%)	0	100	100
3	A	15/17 (88%)	15 (100%)	0	100	100
3	P	15/17 (88%)	15 (100%)	0	100	100
All	All	753/788 (96%)	753 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

5.3.3 RNA ⓘ

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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	I	301	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	H	301	-	4,4,4	0.14	0	6,6,6	0.07	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95th 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 ²)	Q<0.9
1	H	226/235 (96%)	0.68	23 (10%) 6 5	42, 73, 102, 181	0
1	I	216/235 (91%)	0.58	14 (6%) 18 16	47, 70, 111, 147	0
2	L	211/213 (99%)	0.75	24 (11%) 5 4	45, 68, 133, 175	0
2	M	208/213 (97%)	0.73	21 (10%) 7 5	48, 73, 130, 166	0
3	A	17/19 (89%)	1.15	2 (11%) 4 3	53, 65, 122, 143	0
3	P	17/19 (89%)	0.82	2 (11%) 4 3	55, 65, 102, 116	0
All	All	895/934 (95%)	0.70	86 (9%) 8 6	42, 71, 123, 181	0

The worst 5 of 86 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	204	ASN	7.9
2	M	206	VAL	6.7
3	A	182	VAL	6.5
3	A	181	VAL	6.1
2	L	189	ARG	5.7

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	H	301	5/5	0.82	0.25	107,108,109,109	0
4	SO4	I	301	5/5	0.83	0.15	134,134,135,135	0

6.5 Other polymers [i](#)

There are no such residues in this entry.