wwPDB X-ray Structure Validation Summary Report (i)

Nov 10, 2026 – 06:06 PM EST

PDB ID	:	9ZXZ / pdb_00009zxz
Title	:	Anti-HCV Fab RM1-38 in complex with E2 HVR1 peptide
Authors	:	Stanfield, R.L.; Wilson, I.A.
Deposited on	:	2026-01-05
Resolution	:	2.83 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 (i) 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 (1)) were used in the production of this report:

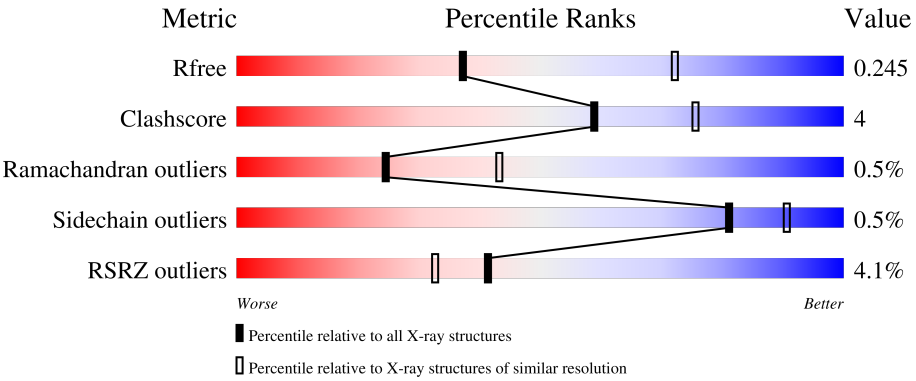
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.83 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}	180053	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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 <=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	AAAA	224	4% 98%
2	AAAB	214	4% 98%
3	AAAC	14	14% 79% 21%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3411 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 Fab RM1-38 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAAA	221	1669	1062	273	327	7	0	0	0

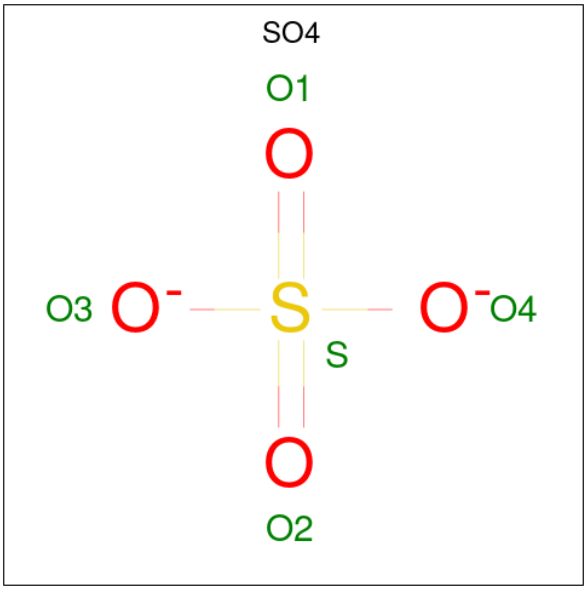
- Molecule 2 is a protein called Fab RM1-38 lambda light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	AAAB	212	1601	1005	265	327	4	0	1	0

- Molecule 3 is a protein called Envelope glycoprotein E2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	AAAC	11	79	53	13	13	0	0	0

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAAA	1	Total O S 5 4 1	0	0
4	AAAA	1	Total O S 5 4 1	0	0
4	AAAA	1	Total O S 5 4 1	0	0
4	AAAB	1	Total O S 5 4 1	0	0
4	AAAB	1	Total O S 5 4 1	0	0
4	AAAB	1	Total O S 5 4 1	0	0
4	AAAB	1	Total O S 5 4 1	0	0
4	AAAB	1	Total O S 5 4 1	0	0

- Molecule 5 is water.

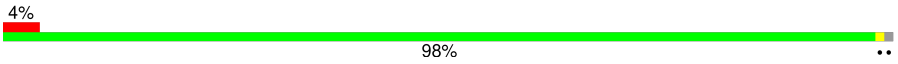
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAAA	8	Total O 8 8	0	0
5	AAAB	13	Total O 13 13	0	0
5	AAAC	1	Total O 1 1	0	0

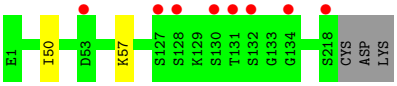
3 Residue-property plots (i)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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: Fab RM1-38 heavy chain

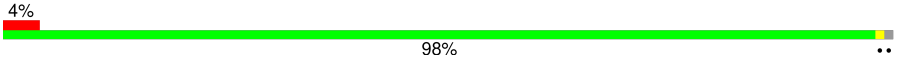
Chain AAAA:

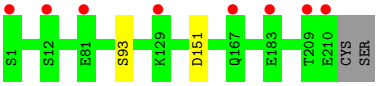




- Molecule 2: Fab RM1-38 lambda light chain

Chain AAAB:

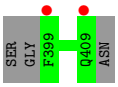




- Molecule 3: Envelope glycoprotein E2

Chain AAAC:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α, β, γ	192.88Å 192.88Å 117.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.83 – 2.83 37.83 – 2.83	Depositor EDS
% Data completeness (in resolution range)	98.0 (37.83-2.83) 98.1 (37.83-2.83)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.11 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.21rc1_5127	Depositor
R, R_{free}	0.221 , 0.246 0.221 , 0.245	Depositor DCC
R_{free} test set	1280 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å^2)	62.1	Xtriage
Anisotropy	0.506	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 52.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	3411	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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

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	AAAA	0.09	0/1710	0.30	0/2323
2	AAAB	0.08	0/1646	0.27	0/2249
3	AAAC	0.12	0/80	0.29	0/107
All	All	0.08	0/3436	0.29	0/4679

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

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	AAAA	1669	0	0	0	0
2	AAAB	1601	0	0	0	0
3	AAAC	79	0	0	0	0
4	AAAA	15	0	0	0	0
4	AAAB	25	0	0	0	0
5	AAAA	8	0	0	0	0
5	AAAB	13	0	0	0	0
5	AAAC	1	0	0	0	0
All	All	3411	0	0	0	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 4.

There are no clashes within the asymmetric unit.

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	AAAA	219/224 (98%)	208 (95%)	11 (5%)	0	100 100
2	AAAB	211/214 (99%)	199 (94%)	10 (5%)	2 (1%)	14 27
3	AAAC	9/14 (64%)	9 (100%)	0	0	100 100
All	All	439/452 (97%)	416 (95%)	21 (5%)	2 (0%)	24 43

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AAAB	151	ASP
2	AAAB	93	SER

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	AAAA	187/190 (98%)	185 (99%)	2 (1%)	65 81
2	AAAB	180/181 (99%)	180 (100%)	0	100 100
3	AAAC	8/10 (80%)	8 (100%)	0	100 100
All	All	375/381 (98%)	373 (100%)	2 (0%)	81 90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAAA	50	ILE
1	AAAA	57	LYS

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	AAAB	304	-	4,4,4	0.67	0	6,6,6	0.08	0
4	SO4	AAAA	301	-	4,4,4	0.67	0	6,6,6	0.08	0
4	SO4	AAAB	302	-	4,4,4	0.67	0	6,6,6	0.07	0
4	SO4	AAAB	301	-	4,4,4	0.67	0	6,6,6	0.07	0
4	SO4	AAAB	305	-	4,4,4	0.67	0	6,6,6	0.08	0
4	SO4	AAAA	303	-	4,4,4	0.67	0	6,6,6	0.09	0
4	SO4	AAAA	302	-	4,4,4	0.67	0	6,6,6	0.07	0
4	SO4	AAAB	303	-	4,4,4	0.67	0	6,6,6	0.09	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

6.1 Protein, DNA and RNA chains

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^{th} 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	AAAA	221/224 (98%)	0.43	8 (3%) 46 37	44, 67, 93, 131	0
2	AAAB	212/214 (99%)	0.35	8 (3%) 44 35	46, 66, 91, 138	1 (0%)
3	AAAC	11/14 (78%)	0.84	2 (18%) 3 3	66, 73, 100, 101	0
All	All	444/452 (98%)	0.40	18 (4%) 41 33	44, 66, 94, 138	1 (0%)

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAAA	130	SER	5.5
1	AAAA	131	THR	5.2
2	AAAB	1	SER	4.3
1	AAAA	218	SER	3.2
1	AAAA	53	ASP	3.0

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

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

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, 95^{th} 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(Å^2)	Q<0.9
4	SO4	AAAA	301	5/5	0.56	0.14	112,116,148,153	0
4	SO4	AAAB	305	5/5	0.72	0.12	114,118,135,159	0
4	SO4	AAAB	304	5/5	0.75	0.11	86,127,144,161	0
4	SO4	AAAA	302	5/5	0.76	0.16	113,113,137,145	0
4	SO4	AAAA	303	5/5	0.76	0.22	106,119,126,129	0
4	SO4	AAAB	302	5/5	0.80	0.15	86,104,110,127	0
4	SO4	AAAB	303	5/5	0.80	0.19	94,98,128,140	0
4	SO4	AAAB	301	5/5	0.93	0.07	66,67,82,88	0

6.5 Other polymers (i)

There are no such residues in this entry.