



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 14, 2023 – 11:18 PM EDT

PDB ID : 8DV6
Title : Zika virus envelope protein structure in complex with a potent Human mAb
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Deposited on : 2022-07-28
Resolution : 3.38 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) : 1.13
EDS : 2.36
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) : 2.36

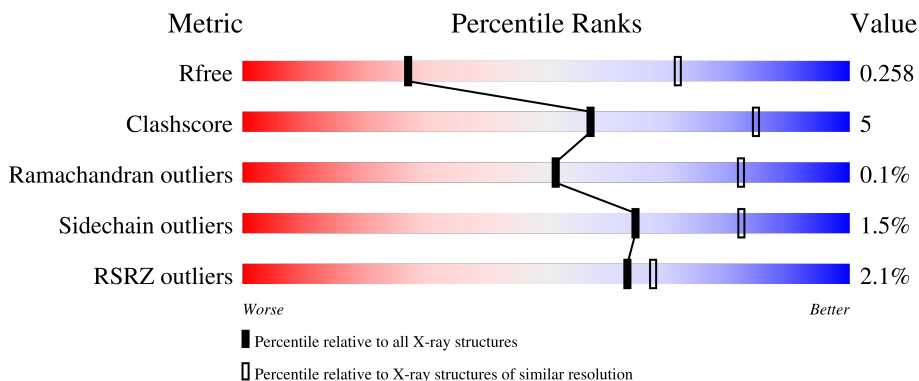
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.38 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.



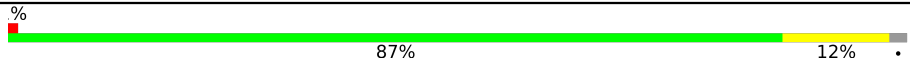
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1691 (3.46-3.30)
Clashscore	141614	1762 (3.46-3.30)
Ramachandran outliers	138981	1732 (3.46-3.30)
Sidechain outliers	138945	1731 (3.46-3.30)
RSRZ outliers	127900	1635 (3.46-3.30)

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	A	415	 84% 13% ..
1	B	415	 4% 82% 15% .
2	C	240	 4% 81% 15% .
2	H	240	 2% 85% 10% .
3	D	216	 92% 6% ..

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Mol	Chain	Length	Quality of chain
3	L	216	 <p>A horizontal bar chart representing the quality of chain. The bar is primarily green, indicating a high quality score of 87%. A small yellow segment at the end indicates a lower quality score of 12%. A small red square is visible at the very beginning of the bar. The percentage values '87%' and '12%' are printed below the bar. A '%' symbol is located at the top left of the bar area, and a small black dot is at the far right end.</p>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12838 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 Envelope protein E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	405	3095	1929	541	599	26	0	1	0
1	B	405	3095	1929	541	599	26	0	1	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	406	SER	-	expression tag	UNP A0A384KMW4
A	407	GLY	-	expression tag	UNP A0A384KMW4
A	408	GLY	-	expression tag	UNP A0A384KMW4
A	409	SER	-	expression tag	UNP A0A384KMW4
A	410	HIS	-	expression tag	UNP A0A384KMW4
A	411	HIS	-	expression tag	UNP A0A384KMW4
A	412	HIS	-	expression tag	UNP A0A384KMW4
A	413	HIS	-	expression tag	UNP A0A384KMW4
A	414	HIS	-	expression tag	UNP A0A384KMW4
A	415	HIS	-	expression tag	UNP A0A384KMW4
B	406	SER	-	expression tag	UNP A0A384KMW4
B	407	GLY	-	expression tag	UNP A0A384KMW4
B	408	GLY	-	expression tag	UNP A0A384KMW4
B	409	SER	-	expression tag	UNP A0A384KMW4
B	410	HIS	-	expression tag	UNP A0A384KMW4
B	411	HIS	-	expression tag	UNP A0A384KMW4
B	412	HIS	-	expression tag	UNP A0A384KMW4
B	413	HIS	-	expression tag	UNP A0A384KMW4
B	414	HIS	-	expression tag	UNP A0A384KMW4
B	415	HIS	-	expression tag	UNP A0A384KMW4

- Molecule 2 is a protein called mAb Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	231	Total 1737	C 1089	N 302	O 339	S 7	0	0	0
2	H	230	Total 1731	C 1086	N 301	O 338	S 6	0	0	0

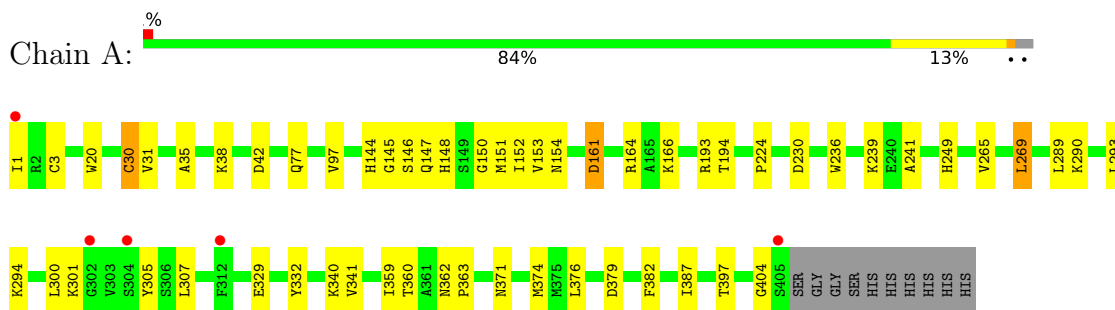
- Molecule 3 is a protein called mAb Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	212	Total 1590	C 997	N 266	O 323	S 4	0	0	0
3	L	212	Total 1590	C 997	N 266	O 323	S 4	0	0	0

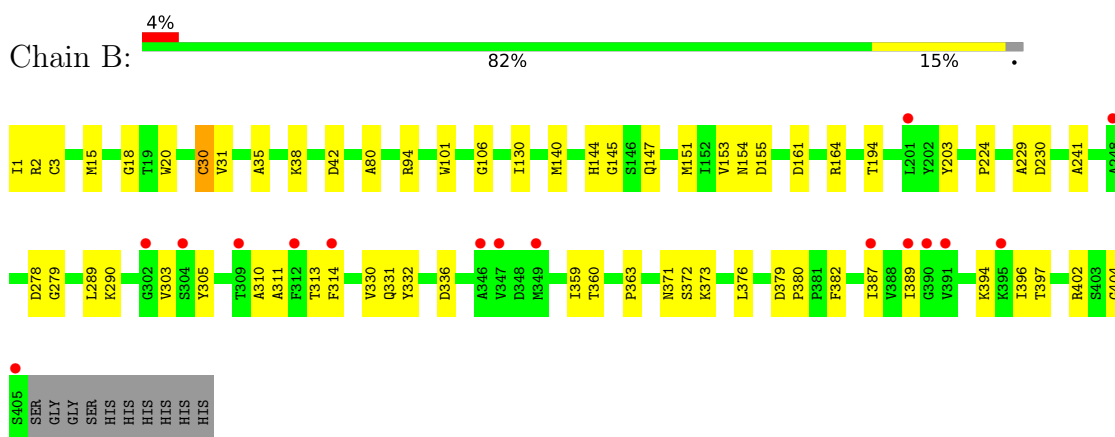
3 Residue-property plots [i](#)

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.

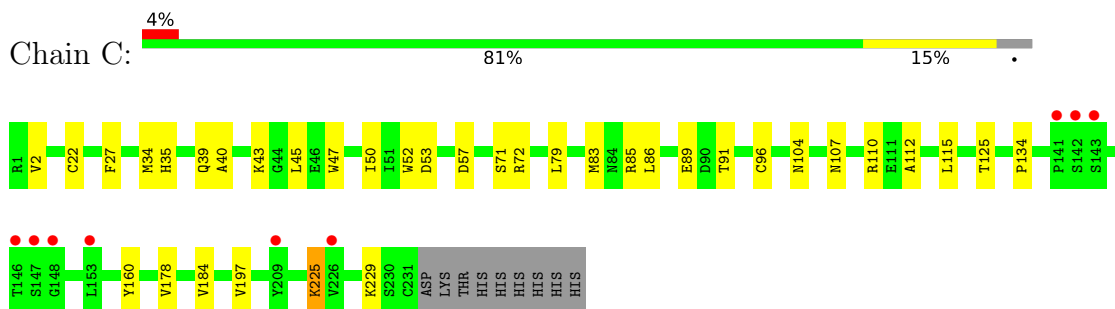
- Molecule 1: Envelope protein E



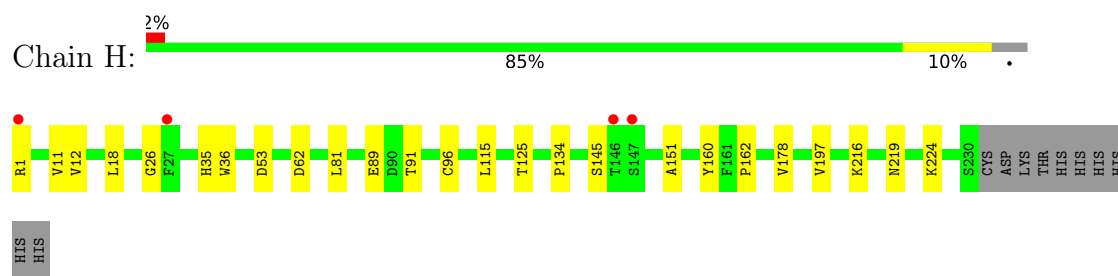
- Molecule 1: Envelope protein E



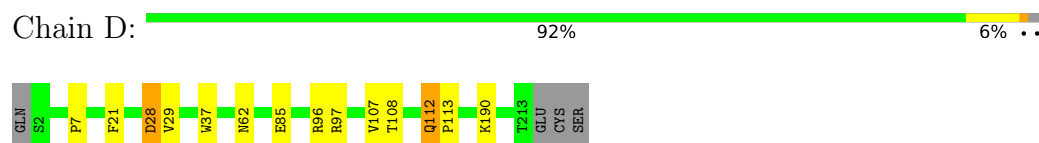
- Molecule 2: mAb Fab Heavy Chain



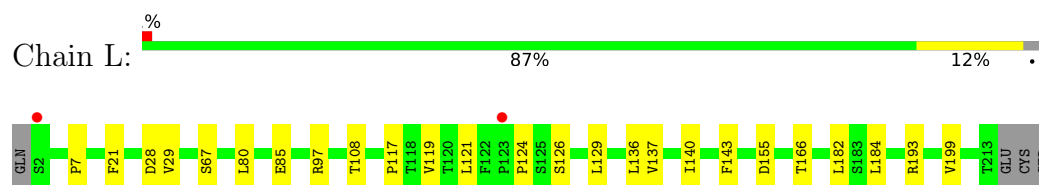
- Molecule 2: mAb Fab Heavy Chain



- Molecule 3: mAb Fab Light Chain



- Molecule 3: mAb Fab Light Chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.04Å 133.61Å 105.11Å 90.00° 106.49° 90.00°	Depositor
Resolution (Å)	45.57 – 3.38 45.57 – 3.38	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.57-3.38) 99.4 (45.57-3.38)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 3.40Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.232 , 0.259 0.232 , 0.258	Depositor DCC
R_{free} test set	1689 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	95.7	Xtrriage
Anisotropy	0.467	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12838	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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](#)

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	0.25	0/3160	0.49	0/4281
1	B	0.25	0/3160	0.47	0/4281
2	C	0.25	0/1780	0.47	0/2423
2	H	0.25	0/1774	0.48	0/2415
3	D	0.26	0/1630	0.47	0/2225
3	L	0.25	0/1630	0.46	0/2225
All	All	0.25	0/13134	0.48	0/17850

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	3095	0	3020	32	0
1	B	3095	0	3020	35	0
2	C	1737	0	1681	23	0
2	H	1731	0	1676	14	0
3	D	1590	0	1534	9	0
3	L	1590	0	1534	13	0
All	All	12838	0	12465	124	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 5.

The worst 5 of 124 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:L:7:PRO:HD3	3:L:21:PHE:HB2	1.39	1.02
3:D:7:PRO:HD3	3:D:21:PHE:HB2	1.40	1.01
2:H:216:LYS:NZ	2:H:219:ASN:OD1	2.20	0.74
1:B:332:TYR:O	1:B:371:ASN:N	2.20	0.74
1:B:30:CYS:SG	1:B:31:VAL:N	2.62	0.72

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	404/415 (97%)	359 (89%)	44 (11%)	1 (0%)	47	78
1	B	404/415 (97%)	362 (90%)	41 (10%)	1 (0%)	47	78
2	C	229/240 (95%)	213 (93%)	16 (7%)	0	100	100
2	H	228/240 (95%)	212 (93%)	16 (7%)	0	100	100
3	D	210/216 (97%)	196 (93%)	14 (7%)	0	100	100
3	L	210/216 (97%)	195 (93%)	15 (7%)	0	100	100
All	All	1685/1742 (97%)	1537 (91%)	146 (9%)	2 (0%)	51	82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	145	GLY
1	B	145	GLY

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	A	339/346 (98%)	331 (98%)	8 (2%)	49	74
1	B	339/346 (98%)	335 (99%)	4 (1%)	71	85
2	C	192/201 (96%)	189 (98%)	3 (2%)	62	81
2	H	191/201 (95%)	190 (100%)	1 (0%)	88	94
3	D	179/183 (98%)	176 (98%)	3 (2%)	60	80
3	L	179/183 (98%)	177 (99%)	2 (1%)	73	86
All	All	1419/1460 (97%)	1398 (98%)	21 (2%)	65	82

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	225	LYS
3	D	112	GLN
3	L	97	ARG
2	H	96	CYS
3	D	97	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	HIS
1	B	147	GLN

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, 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	A	405/415 (97%)	0.04	5 (1%) 79 83	57, 110, 172, 204	0
1	B	405/415 (97%)	0.24	16 (3%) 38 41	74, 140, 200, 237	0
2	C	231/240 (96%)	0.00	9 (3%) 39 43	84, 127, 201, 226	0
2	H	230/240 (95%)	-0.07	4 (1%) 70 74	29, 113, 158, 198	0
3	D	212/216 (98%)	-0.15	0 100 100	55, 93, 180, 216	0
3	L	212/216 (98%)	-0.09	2 (0%) 84 88	66, 96, 180, 205	0
All	All	1695/1742 (97%)	0.03	36 (2%) 63 67	29, 115, 189, 237	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	302	GLY	6.2
1	B	390	GLY	4.9
2	C	143	SER	4.0
2	C	147	SER	4.0
1	B	346	ALA	3.8

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.