



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 7, 2021 – 12:03 PM EDT

PDB ID : 7MF9
Title : Crystal structure of antibody 10E8v4-P100fA Fab in space group C2
Authors : Kwon, Y.D.; Kwong, P.D.
Deposited on : 2021-04-08
Resolution : 3.70 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 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	:	2.22
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)	:	2.22

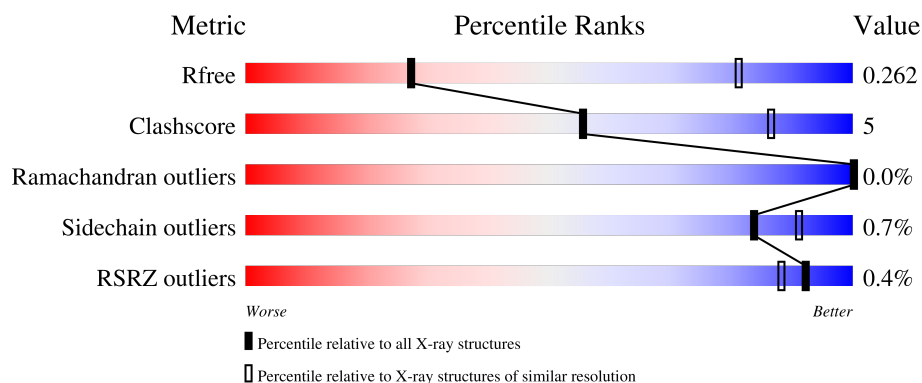
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)

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 ≥ 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	C	233	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>17%</div> <div>• 5%</div> </div> </div>
1	G	233	<div> <div>76%</div> <div>18%</div> <div>5%</div> </div>
1	H	233	<div> <div>79%</div> <div>16%</div> <div>•</div> </div>
1	M	233	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>18%</div> <div>•</div> </div> </div>
1	Q	233	<div> <div>%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>5%</div> </div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	215	 87% 11% .
2	I	215	 87% 10% .
2	L	215	 88% 10% .
2	N	215	 92% 6% .
2	R	215	 91% 7% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16398 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 Antibody 10E8v4 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	223	Total	C	N	O	S	0	0	0
			1709	1089	284	330	6			
1	C	221	Total	C	N	O	S	0	0	0
			1699	1083	282	328	6			
1	G	221	Total	C	N	O	S	0	0	0
			1699	1083	282	328	6			
1	M	224	Total	C	N	O	S	0	0	0
			1716	1093	285	332	6			
1	Q	222	Total	C	N	O	S	0	0	0
			1704	1086	283	329	6			

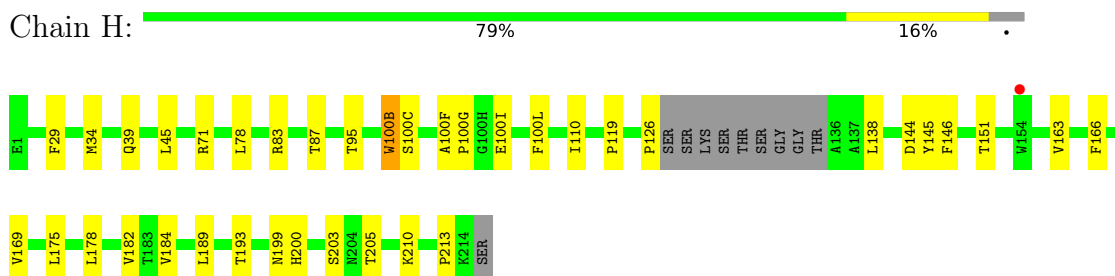
- Molecule 2 is a protein called Antibody 10E8v4 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	210	Total	C	N	O	S	0	0	0
			1579	984	273	318	4			
2	D	209	Total	C	N	O	S	0	0	0
			1573	981	272	316	4			
2	I	209	Total	C	N	O	S	0	0	0
			1573	981	272	316	4			
2	N	209	Total	C	N	O	S	0	0	0
			1573	981	272	316	4			
2	R	209	Total	C	N	O	S	0	0	0
			1573	981	272	316	4			

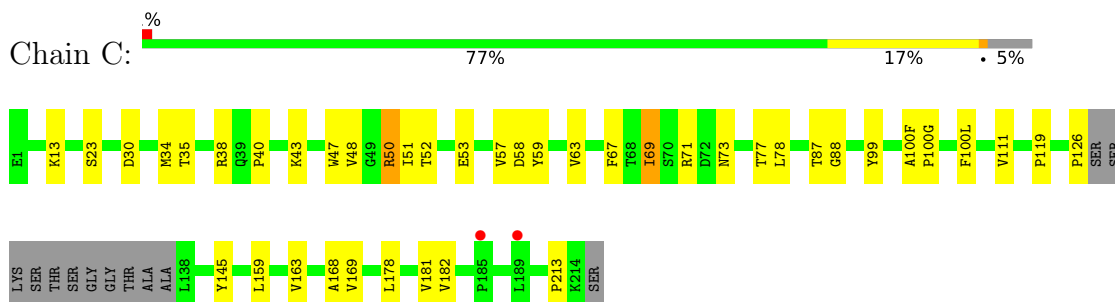
3 Residue-property plots [i](#)

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.

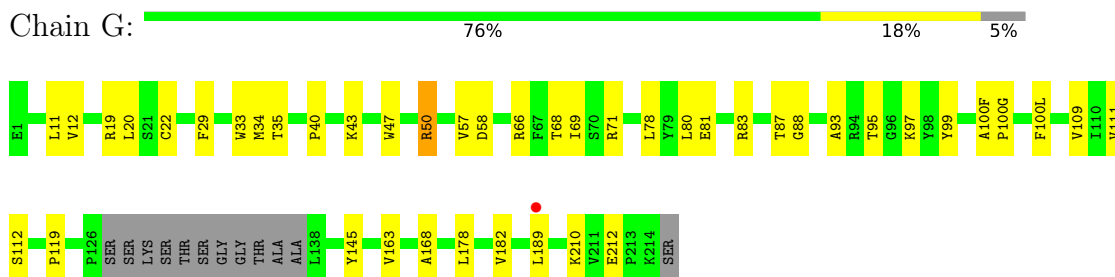
- Molecule 1: Antibody 10E8v4 Fab heavy chain



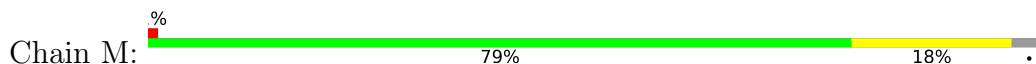
- Molecule 1: Antibody 10E8v4 Fab heavy chain



- Molecule 1: Antibody 10E8v4 Fab heavy chain



- Molecule 1: Antibody 10E8v4 Fab heavy chain



ALA	SER	E3	A14	Q17	R24	Q37	K38	P44	L47	R70	E83	V106	V116	I137	V196	K205	P209	THR	GLU	CYS	SER
-----	-----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.97Å 141.30Å 137.41Å 90.00° 109.17° 90.00°	Depositor
Resolution (Å)	40.21 – 3.70 40.21 – 3.69	Depositor EDS
% Data completeness (in resolution range)	76.7 (40.21-3.70) 76.7 (40.21-3.69)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 3.66Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.240 , 0.269 0.242 , 0.262	Depositor DCC
R_{free} test set	1205 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	87.5	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 26.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	16398	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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	C	0.42	0/1747	0.62	0/2379
1	G	0.28	0/1747	0.48	0/2379
1	H	0.32	0/1757	0.54	0/2393
1	M	0.46	0/1764	0.60	0/2403
1	Q	0.46	0/1752	0.59	0/2386
2	D	0.24	0/1609	0.48	0/2190
2	I	0.24	0/1609	0.48	0/2190
2	L	0.26	0/1615	0.48	0/2198
2	N	0.27	0/1609	0.49	0/2190
2	R	0.24	0/1609	0.48	0/2190
All	All	0.34	0/16818	0.53	0/22898

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	C	1699	0	1635	27	1
1	G	1699	0	1635	27	6
1	H	1709	0	1645	29	0
1	M	1716	0	1652	24	10
1	Q	1704	0	1640	21	0
2	D	1573	0	1540	16	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	1573	0	1540	14	0
2	L	1579	0	1545	13	4
2	N	1573	0	1540	10	0
2	R	1573	0	1540	7	0
All	All	16398	0	15912	165	11

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 165 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:Q:193:THR:HG23	1:Q:210:LYS:HE2	1.66	0.78
1:M:100(G):PRO:HG2	2:N:31:HIS:HE1	1.50	0.77
1:Q:87:THR:HG22	1:Q:111:VAL:H	1.50	0.76
1:Q:33:TRP:HE3	1:Q:50:ARG:HD2	1.52	0.74
1:C:63:VAL:HG13	1:C:67:PHE:HB2	1.69	0.73

The worst 5 of 11 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:C:99:TYR:OH	1:C:100(F):ALA:O[2_555]	1.61	0.59
2:L:189:HIS:CE1	1:M:100(B):TRP:CZ2[3_445]	1.63	0.57
2:L:189:HIS:ND1	1:M:100(B):TRP:CH2[3_445]	1.72	0.48
1:G:97:LYS:CG	1:M:100(A):PHE:CE2[3_445]	1.72	0.48
1:G:97:LYS:CB	1:M:100(A):PHE:CE2[3_445]	1.85	0.35

5.3 Torsion angles

5.3.1 Protein backbone

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	C	217/233 (93%)	209 (96%)	7 (3%)	1 (0%)	29	66
1	G	217/233 (93%)	210 (97%)	7 (3%)	0	100	100
1	H	219/233 (94%)	217 (99%)	2 (1%)	0	100	100
1	M	220/233 (94%)	216 (98%)	4 (2%)	0	100	100
1	Q	218/233 (94%)	214 (98%)	4 (2%)	0	100	100
2	D	207/215 (96%)	201 (97%)	6 (3%)	0	100	100
2	I	207/215 (96%)	199 (96%)	8 (4%)	0	100	100
2	L	208/215 (97%)	203 (98%)	5 (2%)	0	100	100
2	N	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
2	R	207/215 (96%)	202 (98%)	5 (2%)	0	100	100
All	All	2127/2240 (95%)	2074 (98%)	52 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	88	GLY

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	C	187/195 (96%)	182 (97%)	5 (3%)	44	68
1	G	187/195 (96%)	186 (100%)	1 (0%)	88	94
1	H	187/195 (96%)	185 (99%)	2 (1%)	73	85
1	M	188/195 (96%)	187 (100%)	1 (0%)	88	94
1	Q	187/195 (96%)	184 (98%)	3 (2%)	62	80
2	D	175/180 (97%)	175 (100%)	0	100	100
2	I	175/180 (97%)	175 (100%)	0	100	100
2	L	176/180 (98%)	176 (100%)	0	100	100
2	N	175/180 (97%)	175 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	R	175/180 (97%)	175 (100%)	0	100	100
All	All	1812/1875 (97%)	1800 (99%)	12 (1%)	84	91

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	50	ARG
1	M	101	GLN
1	Q	101	GLN
1	Q	89	TYR
1	C	38	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	M	101	GLN
1	Q	101	GLN

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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, 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	C	221/233 (94%)	-0.01	2 (0%) 84 76	68, 92, 140, 183	0
1	G	221/233 (94%)	0.08	1 (0%) 91 85	73, 92, 129, 173	0
1	H	223/233 (95%)	-0.03	1 (0%) 92 88	67, 87, 118, 132	0
1	M	224/233 (96%)	-0.02	2 (0%) 84 76	77, 98, 136, 155	0
1	Q	222/233 (95%)	0.00	2 (0%) 84 76	80, 101, 128, 161	0
2	D	209/215 (97%)	-0.16	0 100 100	68, 90, 109, 115	0
2	I	209/215 (97%)	-0.14	0 100 100	78, 93, 110, 122	0
2	L	210/215 (97%)	-0.15	0 100 100	70, 88, 104, 115	0
2	N	209/215 (97%)	-0.10	0 100 100	75, 93, 122, 131	0
2	R	209/215 (97%)	-0.16	0 100 100	75, 92, 114, 126	0
All	All	2157/2240 (96%)	-0.07	8 (0%) 92 88	67, 93, 124, 183	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	185	PRO	4.9
1	G	189	LEU	4.2
1	Q	189	LEU	3.4
1	C	189	LEU	2.6
1	M	189	LEU	2.4

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 [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.