

# Full wwPDB X-ray Structure Validation Report (i)

#### Nov 20, 2023 – 07:19 PM JST

PDB ID	:	7D9Z
Title	:	Crystal structure of anti-basigin Fab fragment
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Deposited on	:	2020-10-14
Resolution	:	1.12  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* 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:

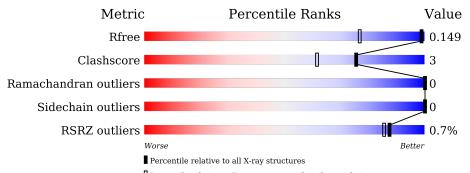
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 1.12 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.



Percentile relative to X-ray structures of similar resolution

Metric	Whole archive	Similar resolution
Metric	(# Entries)	$(\# { m Entries},  { m resolution}  { m range}({ m \AA}))$
$R_{free}$	130704	1168 (1.14-1.10)
Clashscore	141614	1205 (1.14-1.10)
Ramachandran outliers	138981	1168 (1.14-1.10)
Sidechain outliers	138945	1165 (1.14-1.10)
RSRZ outliers	127900	1146 (1.14-1.10)

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	L	218	94%	6%
2	Н	217	% • 92%	• •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	Н	305	-	-	Х	-



#### $7\mathrm{D9Z}$

## 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7544 atoms, of which 3391 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.

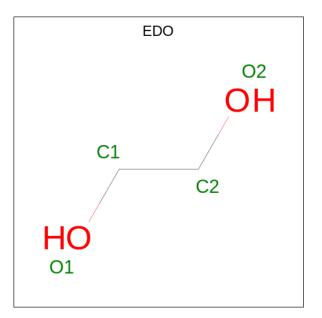
• Molecule 1 is a protein called Light chain of antibody Fab fragment.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	L	217	Total 3464	C 1094	Н 1710	N 286	O 364	S 10	0	29	0

• Molecule 2 is a protein called Heavy chain of antibody Fab fragment.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
2	Н	208	Total 3304	C 1054	Н 1640	N 266	O 336	S 8	0	30	0

• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	L	1	Total         C         H         O           10         2         6         2	0	0
3	Н	1	Total         C         H         O           10         2         6         2	0	0

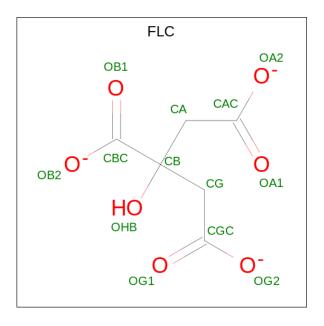
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	Ű	<b>D b b b b b b b b b b</b>	~	4			7	
Mol	Chain	Residues		ton	ns		ZeroUcc	AltConf
3	Н	1	Total	С	Η	0	0	0
0	11	I	10	2	6	2	0	0
3	Н	1	Total	С	Η	Ο	0	0
0	11	I	10	2	6	2	0	0
3	Н	1	Total	$\mathbf{C}$	Η	Ο	0	0
0	11	I	10	2	6	2	0	0
3	Н	1	Total	С	Η	0	0	0
5	11	1	10	2	6	2		0

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• Molecule 4 is CITRATE ANION (three-letter code: FLC) (formula:  $C_6H_5O_7$ ).



Mol	Chain	Residues	At	oms			ZeroOcc	AltConf
4	Н	1	Total 18	C H 6 5	-	O 7	0	0

• Molecule 5 is water.

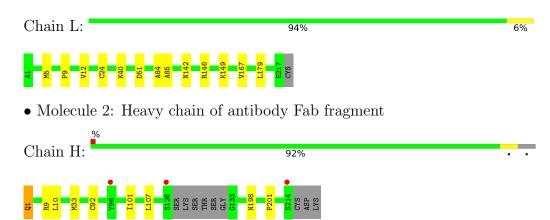
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	L	331	Total O 331 331	0	0
5	Н	367	Total O 367 367	0	0



# 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: Light chain of antibody Fab fragment





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	163.45Å 53.05Å 54.31Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $105.05^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	36.40 - 1.12	Depositor
Resolution (A)	78.92 - 1.12	EDS
% Data completeness	81.6 (36.40-1.12)	Depositor
(in resolution range)	81.6 (78.92-1.12)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.59 (at 1.12 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19rc1_4016	Depositor
D D	0.121 , $0.150$	Depositor
$R, R_{free}$	0.123 , $0.149$	DCC
$R_{free}$ test set	6811 reflections $(4.89%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	13.6	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.40 , $48.7$	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	7544	wwPDB-VP
Average B, all atoms $(Å^2)$	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.46% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: PCA, FLC, EDO

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	L	0.51	0/1861	0.69	1/2532~(0.0%)	
2	Н	0.51	0/1806	0.70	0/2475	
All	All	0.51	0/3667	0.70	1/5007~(0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	L	51	ASP	CB-CG-OD1	7.73	125.26	118.30

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	L	1754	1710	1631	10	0
2	Н	1664	1640	1530	11	0
3	Н	20	30	30	4	0
3	L	4	6	6	0	0
4	Н	13	5	5	0	0
5	Н	367	0	0	3	3
5	L	331	0	0	2	3
All	All	4153	3391	3202	21	3



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 3.

All $(21)$ close contacts	within the	e same	asymmetric	unit	are	listed	below,	sorted b	y their	$\operatorname{clash}$
magnitude.										

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:198[A]:ASN:OD1	5:H:401:HOH:O	1.69	1.10
2:H:107[B]:LEU:HD11	5:H:656:HOH:O	1.68	0.94
1:L:142[B]:ASN:ND2	5:L:401:HOH:O	1.94	0.89
1:L:40:LYS:HE3	1:L:84:ALA:O	1.89	0.73
2:H:9:ARG:NH2	5:H:402:HOH:O	2.24	0.68
1:L:167[B]:VAL:CG1	1:L:179:LEU:HD12	2.36	0.55
1:L:40:LYS:HD2	1:L:85:ALA:HB2	1.92	0.52
2:H:33:MET:CE	2:H:92[B]:CYS:SG	2.97	0.52
1:L:167[B]:VAL:HG12	1:L:179:LEU:HD12	1.91	0.51
2:H:1:PCA:HB2	2:H:101[B]:ILE:HD13	1.94	0.50
2:H:201:PRO:HG3	3:H:305:EDO:H22	1.97	0.47
2:H:1:PCA:HB2	2:H:101[B]:ILE:CD1	2.45	0.47
2:H:33:MET:HE3	2:H:92[B]:CYS:SG	2.56	0.46
1:L:9:PRO:HG2	1:L:12[B]:VAL:HG13	1.98	0.45
1:L:146:ARG:NH2	1:L:167[A]:VAL:HG21	2.31	0.45
1:L:5:MET:CE	1:L:24[B]:CYS:SG	3.05	0.44
2:H:10:LEU:H	3:H:305:EDO:H11	1.82	0.43
1:L:5:MET:HE2	1:L:24[B]:CYS:SG	2.59	0.42
2:H:9:ARG:HA	3:H:305:EDO:H11	2.01	0.42
1:L:149:LYS:NZ	5:L:403:HOH:O	2.35	0.42
2:H:10:LEU:N	3:H:305:EDO:H11	2.36	0.40

All (3) 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)	
5:L:729:HOH:O	5:H:717:HOH:O[4_556]	1.84	0.36	
5:L:729:HOH:O	5:H:693:HOH:O[4_556]	1.94	0.26	
5:L:726:HOH:O	5:H:709:HOH:O[4_556]	2.05	0.15	

### 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	Perce	ntiles
1	L	244/218~(112%)	236~(97%)	8(3%)	0	100	100
2	Н	234/217~(108%)	228~(97%)	6 (3%)	0	100	100
All	All	478/435 (110%)	464 (97%)	14 (3%)	0	100	100

There are no Ramachandran outliers to report.

#### 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	L	206/182~(113%)	206 (100%)	0	100 100		
2	Н	202/182~(111%)	202 (100%)	0	100 100		
All	All	408/364~(112%)	408 (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 (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	Turne	Chain	Res	Link	В	ond leng	gths	B	ond ang	gles
		туре				Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
	2	PCA	Н	1	2	7,8,9	1.43	1 (14%)	9,10,12	1.62	2 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PCA	Н	1	2	-	0/0/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	Н	1	PCA	CD-N	3.16	1.42	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	Н	1	PCA	CA-N-CD	-2.75	104.15	113.58
2	Н	1	PCA	CB-CA-N	2.40	110.19	103.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	Н	1	PCA	2	0

## 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



### 5.6 Ligand geometry (i)

7 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	Turne	Chain	Res	Link	Bond lengths			Bond angles		
10101	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2
3	EDO	Н	301	-	$3,\!3,\!3$	0.39	0	2,2,2	0.29	0
3	EDO	Н	304	-	$3,\!3,\!3$	0.40	0	2,2,2	0.58	0
3	EDO	Н	305	-	$3,\!3,\!3$	0.99	0	2,2,2	0.72	0
3	EDO	Н	302	-	$3,\!3,\!3$	0.48	0	2,2,2	0.16	0
3	EDO	L	301	-	3, 3, 3	0.42	0	$2,\!2,\!2$	0.03	0
4	FLC	Н	306	-	$12,\!12,\!12$	0.89	0	$17,\!17,\!17$	1.35	2 (11%)
3	EDO	Н	303	-	$3,\!3,\!3$	0.44	0	2,2,2	0.39	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	Н	301	-	-	0/1/1/1	-
3	EDO	Н	304	-	-	0/1/1/1	-
3	EDO	Н	305	-	-	1/1/1/1	-
3	EDO	Н	302	-	-	0/1/1/1	-
3	EDO	L	301	-	-	0/1/1/1	-
4	FLC	Н	306	-	-	0/16/16/16	-
3	EDO	Н	303	-	-	0/1/1/1	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^{o})$
4	Н	306	FLC	OB2-CBC-CB	3.42	118.99	113.05
4	Н	306	FLC	OB1-CBC-CB	-2.75	118.36	122.25

There are no chirality outliers.



All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	Н	305	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 4 short contacts:

M	bl	Chain	Res	Type	Clashes	Symm-Clashes
3		Н	305	EDO	4	0

## 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,  $95^{th}$  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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	Q < 0.9
1	L	217/218~(99%)	0.01	0 100 100	10, 16, 28, 45	0
2	Н	207/217~(95%)	-0.00	3 (1%) 75 72	9, 15, 24, 43	0
All	All	424/435~(97%)	0.00	3 (0%) 87 85	9, 15, 28, 45	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Н	96[A]	TYR	3.4
2	Н	214	SER	2.2
2	Н	126	SER	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains (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,  $95^{th}$  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
2	PCA	Н	1	8/9	0.96	0.08	17,22,26,27	0

### 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,



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	EDO	Н	305	4/4	0.84	0.32	$15,\!24,\!29,\!34$	0
3	EDO	Н	304	4/4	0.93	0.10	$16,\!21,\!23,\!25$	0
4	FLC	Н	306	13/13	0.93	0.15	$19,\!22,\!27,\!27$	0
3	EDO	Н	302	4/4	0.94	0.18	$26,\!31,\!35,\!35$	0
3	EDO	Н	301	4/4	0.96	0.09	18,22,24,29	0
3	EDO	Н	303	4/4	0.98	0.09	14,17,18,20	0
3	EDO	L	301	4/4	0.98	0.09	19,26,29,32	0

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.

## 6.5 Other polymers (i)

There are no such residues in this entry.

