

wwPDB X-ray Structure Validation Summary Report (i)

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8DS7
Tumor-activated antibody derivatives targeting CTLA4
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2022-07-21
1.88 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:

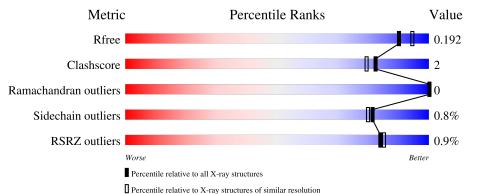
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.88 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	219	95%	5%
2	Н	216	2% 91%	8% •
3	М	10	90%	10%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7338 atoms, of which 3346 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 IgG light chain Fab.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	L	219	Total 3443	C 1093	Н 1684	N 296	O 360	S 10	0	10	0

• Molecule 2 is a protein called IgG heavy chain Fab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	Н	214	Total 3233	C 1044	Н 1594	N 260	O 326	S 9	0	3	0

• Molecule 3 is a protein called ACNLIVEGHC peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
3	М	10	Total 139	C 43	Н 68	N 13	O 13	${ m S} { m 2}$	0	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	L	234	Total O 234 234	0	0
4	Н	276	Total O 276 276	0	0
4	М	13	Total O 13 13	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.

Chain L:	95%	5%
D1 S14 S14 S14 S12 S12 S127 S17 S17 S17 S17 S17 S17 S17 S17 S17 S1		
• Molecule 2: IgG heavy chain Fab		
Chain H:	91%	8% •
E1 V10 V10 V12 V12 E3 E46 E46 E46 V12 E89 W100 V100 V125 G132 G132 G132 G132 G132 G132 G132 G132	S164 S165 1186 1187 9188 S207 V210 P216	
• Molecule 3: ACNLIVEGHC peptide)	
Chain M:	90%	10%

• Molecule 1: IgG light chain Fab





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants	37.01Å 88.49Å 128.70Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.00 - 1.88	Depositor
Resolution (A)	33.00 - 1.88	EDS
% Data completeness	98.7 (33.00-1.88)	Depositor
(in resolution range)	98.7 (33.00-1.88)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.93 (at 1.88 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
D D.	0.156 , 0.191	Depositor
R, R_{free}	0.156 , 0.192	DCC
R_{free} test set	1746 reflections $(5.01%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	15.6	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.37, 45.5	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7338	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 5.69% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
1	L	0.31	0/1804	0.55	0/2444
2	Н	0.29	0/1684	0.52	0/2301
3	М	0.34	0/71	0.40	0/95
All	All	0.30	0/3559	0.53	0/4840

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	24	ARG	Sidechain

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	1759	1684	1671	8	0
2	Н	1639	1594	1591	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes	
3	М	71	68	68	1	0	
4	Н	276	0	0	1	1	
4	L	234	0	0	1	1	
4	М	13	0	0	1	0	
All	All	3992	3346	3330	17	1	

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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 17 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)
2:H:1:GLU:HG2	2:H:1:GLU:O	1.94	0.67
3:M:1:ALA:N	4:M:101:HOH:O	2.28	0.66
2:H:23[B]:LYS:HZ3	2:H:77:SER:HB2	1.66	0.61
1:L:29:ILE:O	1:L:29:ILE:HG22	2.02	0.59
1:L:200:GLU:HG3	1:L:211:VAL:HG22	1.85	0.59

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)
4:L:411:HOH:O	4:H:472:HOH:O[3_557]	2.19	0.01

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	227/219~(104%)	225~(99%)	2(1%)	0	100	100
2	Н	213/216~(99%)	210 (99%)	3 (1%)	0	100	100

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	3	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
3	М	8/10 (80%)	8 (100%)	0	0	100	100
All	All	448/445 (101%)	443 (99%)	5 (1%)	0	100	100

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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	206/196~(105%)	206 (100%)	0	100 100
2	Η	188/186 (101%)	185~(98%)	3(2%)	62 56
3	М	8/8 (100%)	8 (100%)	0	100 100
All	All	402/390~(103%)	399~(99%)	3 (1%)	81 83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Н	100	TYR
2	Н	103	TRP
2	Н	207	SER

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such side chains are listed below:

Mol	Chain	Res	Type
3	М	9	HIS

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, 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	$OWAB(Å^2)$	$\mathbf{Q}{<}0.9$
1	L	219/219~(100%)	-0.51	0 100 100	9, 16, 29, 48	0
2	Н	214/216~(99%)	-0.41	4 (1%) 66 68	8, 16, 39, 60	0
3	М	10/10 (100%)	-0.24	0 100 100	15, 20, 34, 38	0
All	All	443/445~(99%)	-0.45	4 (0%) 84 85	8, 16, 33, 60	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Н	132	CYS	3.0
2	Н	135	ALA	2.9
2	Н	163	LEU	2.7
2	Н	1	GLU	2.0

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.

