



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 05:48 am GMT

PDB ID : 2Z91
Title : Crystal structure of the Fab fragment of anti-ciguatoxin antibody 10C9
Authors : Ui, M.; Tanaka, Y.; Tsumoto, K.
Deposited on : 2007-09-14
Resolution : 2.60 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

<http://wwpdb.org/validation/2016/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)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

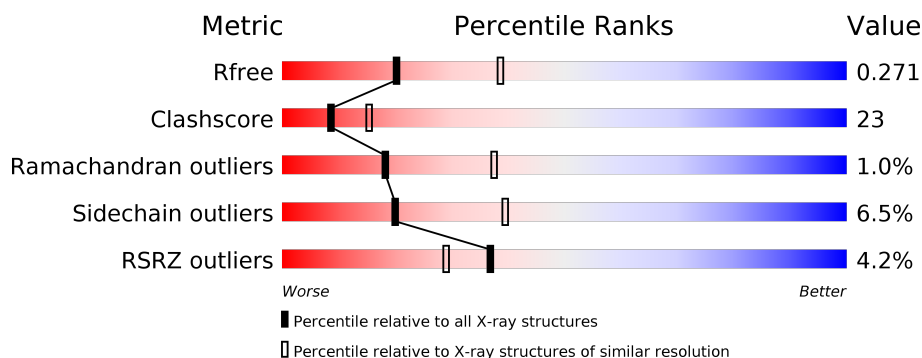
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	218	<div> <div>2%</div> <div> <div></div> <div>62%</div> <div>29%</div> <div>5%</div> </div> </div>
1	C	218	<div> <div>6%</div> <div> <div></div> <div>56%</div> <div>33%</div> <div>7%</div> </div> </div>
2	B	213	<div> <div>6%</div> <div> <div></div> <div>60%</div> <div>35%</div> <div></div> </div> </div>
2	D	213	<div> <div>3%</div> <div> <div></div> <div>58%</div> <div>36%</div> <div></div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6477 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 Anti-ciguatoxin antibody 10C9 FAB heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	0	0
			1598	1018	257	316	7			
1	C	203	Total	C	N	O	S	0	0	0
			1573	1005	253	308	7			

- Molecule 2 is a protein called Anti-ciguatoxin antibody 10C9 FAB light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	211	Total	C	N	O	S	0	0	0
			1611	998	270	334	9			
2	D	208	Total	C	N	O	S	0	0	0
			1592	988	267	328	9			

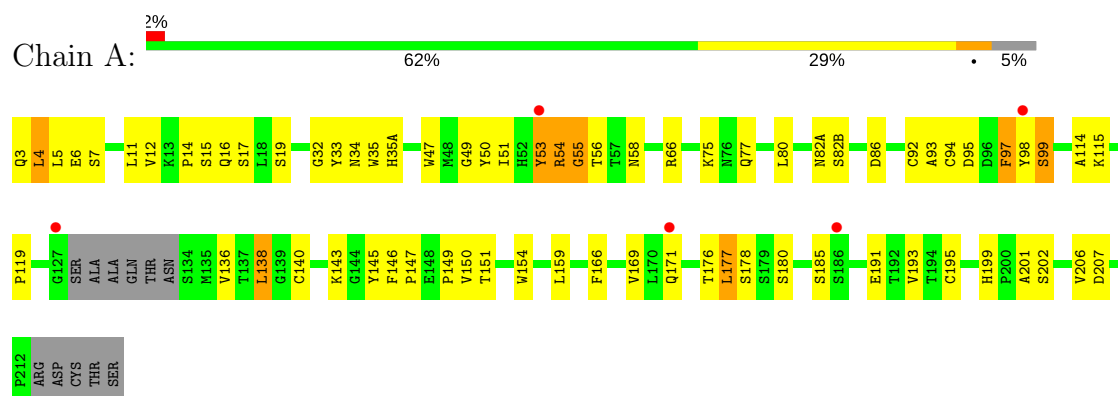
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total	O	0	0
			23	23		
3	B	27	Total	O	0	0
			27	27		
3	C	27	Total	O	0	0
			27	27		
3	D	26	Total	O	0	0
			26	26		

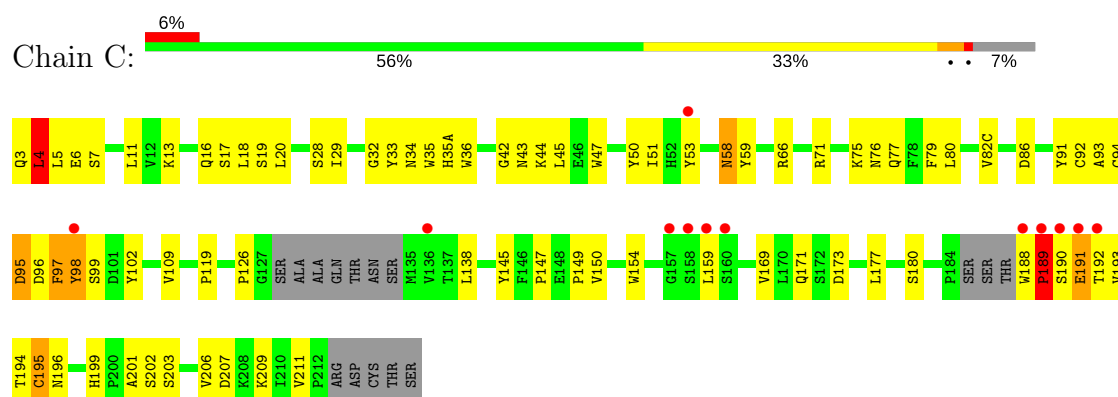
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

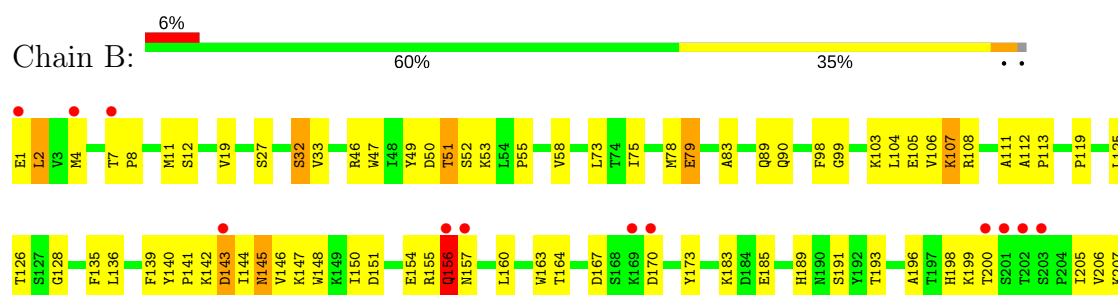
- Molecule 1: Anti-ciguatoxin antibody 10C9 FAB heavy chain



- Molecule 1: Anti-ciguatoxin antibody 10C9 FAB heavy chain



- Molecule 2: Anti-ciguatoxin antibody 10C9 FAB light chain



S208
F209
N210
R211
N212
GLU
CYS

● Molecule 2: Anti-ciguatoxin antibody 10C9 FAB light chain



E1	L2	V3	N4	P8	M11	P15	V19	A25	S26	S27	S32	V33	S43	R46	W47	I48	Y49	D50	T51	S52	K53	L54	P55	S56	S57	V58	F62	S67	I75	M78	E79	A80	D82	A83	Q89	Q90	N94	P95	V106	K107	D110
----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------

F118	P119	P120	E123	Q124	L125	T126	G129	V133	C134	F135	L136	N137	Y140	P141	K142	D143	I144	N145	V146	K147	W148	D151	G152	SER	K53	GLU	R155	Q156	N157	G158	V159	L160	N161	Y173	S174	M175	S176	L179	T182	K183	D184	E185	Y186	E187	R188	H189	N190	T193	C194	E195
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

H198	K199	THR	SER	T202	S203	P204	T206	V206	F209	N210	R211	N212	E213	CYS
------	------	-----	-----	------	------	------	------	------	------	------	------	------	------	-----

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.84Å 78.26Å 89.04Å 90.00° 99.25° 90.00°	Depositor
Resolution (Å)	10.00 – 2.60 38.32 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (10.00-2.60) 100.0 (38.32-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.61Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.220 , 0.270 0.220 , 0.271	Depositor DCC
R_{free} test set	2768 reflections (9.92%)	DCC
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.540	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6477	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% 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

5.1 Standard geometry

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	0.42	0/1644	0.73	1/2254 (0.0%)
1	C	0.40	0/1618	0.75	1/2217 (0.0%)
2	B	0.44	0/1650	0.70	1/2243 (0.0%)
2	D	0.40	0/1629	0.70	1/2211 (0.0%)
All	All	0.42	0/6541	0.72	4/8925 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	156	GLN	N-CA-C	7.69	131.77	111.00
2	B	156	GLN	N-CA-C	6.82	129.42	111.00
1	C	4	LEU	CA-CB-CG	5.78	128.59	115.30
1	A	140	CYS	CA-CB-SG	5.21	123.38	114.00

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	A	1598	0	1541	64	1
1	C	1573	0	1518	85	0
2	B	1611	0	1536	83	1
2	D	1592	0	1517	83	0
3	A	23	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	27	0	0	0	0
3	C	27	0	0	0	0
3	D	26	0	0	0	0
All	All	6477	0	6112	285	1

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 23.

The worst 5 of 285 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:C:18:LEU:HD21	1:C:109:VAL:HG11	1.32	1.10
1:C:188:TRP:CG	1:C:189:PRO:HD2	1.87	1.10
2:D:155:ARG:O	2:D:156:GLN:HB2	1.53	1.04
2:D:189:HIS:O	2:D:211:ARG:HD3	1.62	0.99
2:B:78:MET:HE3	2:B:104:LEU:HD21	1.49	0.94

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)
1:A:191:GLU:OE2	2:B:185:GLU:OE2[2_554]	2.08	0.12

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	203/218 (93%)	184 (91%)	17 (8%)	2 (1%)	18	37
1	C	197/218 (90%)	180 (91%)	16 (8%)	1 (0%)	32	58
2	B	209/213 (98%)	195 (93%)	12 (6%)	2 (1%)	18	37

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	202/213 (95%)	186 (92%)	13 (6%)	3 (2%)	12	24
All	All	811/862 (94%)	745 (92%)	58 (7%)	8 (1%)	18	37

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	GLY
1	A	99	SER
1	C	189	PRO
2	B	51	THR
2	B	156	GLN

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	A	187/196 (95%)	173 (92%)	14 (8%)	16	31
1	C	183/196 (93%)	167 (91%)	16 (9%)	12	23
2	B	186/188 (99%)	176 (95%)	10 (5%)	26	49
2	D	183/188 (97%)	175 (96%)	8 (4%)	33	60
All	All	739/768 (96%)	691 (94%)	48 (6%)	20	39

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	107	LYS
1	C	58	ASN
2	D	81	GLU
2	B	143	ASP
1	C	4	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	212	ASN
1	C	58	ASN
2	D	137	ASN
2	B	210	ASN
2	D	156	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 carbohydrates 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	207/218 (94%)	0.02	5 (2%) 59 52	14, 30, 49, 67	0
1	C	203/218 (93%)	0.27	12 (5%) 23 17	13, 31, 54, 79	0
2	B	211/213 (99%)	0.22	12 (5%) 24 18	17, 34, 51, 65	0
2	D	208/213 (97%)	0.16	6 (2%) 52 45	13, 36, 55, 76	0
All	All	829/862 (96%)	0.17	35 (4%) 37 29	13, 33, 53, 79	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	98	TYR	6.2
1	C	192	THR	4.7
1	A	98	TYR	4.4
2	B	202	THR	4.4
1	C	189	PRO	4.3

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 carbohydrates 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.