



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2024 – 06:03 PM EDT

PDB ID : 2A9M
Title : Structural Analysis of a Tight-binding Fluorescein-scFv; apo form
Authors : Cambillau, C.; Spinelli, S.; Honegger, A.; Pluckthun, A.
Deposited on : 2005-07-12
Resolution : 2.10 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 ⓘ 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 : 2.36.1
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

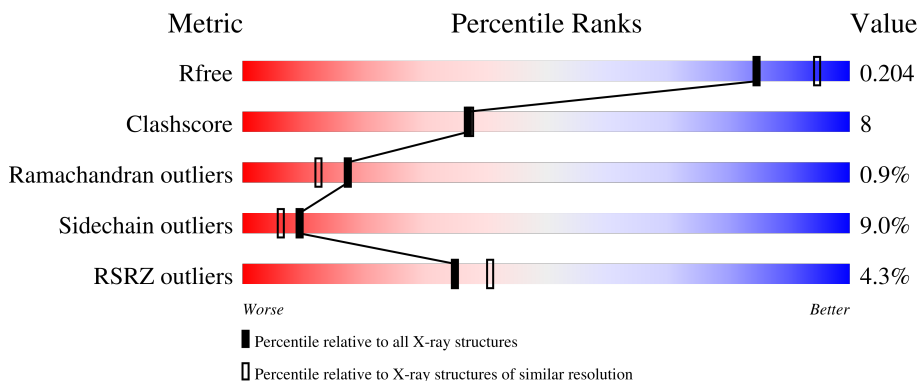
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 $\leq 5\%$. 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	264	 4% 72% 14% • 12%
1	B	264	 3% 70% 16% • 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3823 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 fluorescein-scfv.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	233	1744	1090	301	345	8	0	0	0
1	B	235	1764	1105	303	348	8	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	162	162	162	0	0
2	B	153	153	153	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.90Å 73.50Å 70.70Å 90.00° 97.11° 90.00°	Depositor
Resolution (Å)	15.00 – 2.10 19.73 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.4 (15.00-2.10) 94.1 (19.73-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.09Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.210 , 0.263 0.221 , 0.204	Depositor DCC
R_{free} test set	1152 reflections (4.02%)	wwPDB-VP
Wilson B-factor (Å ²)	15.9	Xtrriage
Anisotropy	0.131	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3823	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.44% 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	0.51	0/1784	0.71	2/2420 (0.1%)
1	B	0.54	0/1805	0.73	0/2449
All	All	0.53	0/3589	0.72	2/4869 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	ARG	NE-CZ-NH2	5.17	122.88	120.30
1	A	67	ARG	NE-CZ-NH1	-5.08	117.76	120.30

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	A	1744	0	1650	26	0
1	B	1764	0	1670	32	0
2	A	162	0	0	1	0
2	B	153	0	0	5	0
All	All	3823	0	3320	53	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 8.

All (53) 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:A:153:ASN:HD22	1:A:154:ILE:H	1.25	0.81
1:A:131:GLN:HE21	1:A:227:GLY:HA3	1.49	0.78
1:A:10:ASN:HD22	1:A:11:LEU:H	1.33	0.76
1:B:153:ASN:HD22	1:B:154:ILE:H	1.35	0.75
1:B:151:THR:HG22	2:B:308:HOH:O	1.87	0.73
1:B:127:SER:N	2:B:301:HOH:O	2.21	0.73
1:A:10:ASN:HD21	1:B:177:VAL:HG21	1.55	0.72
1:B:150:SER:O	1:B:154:ILE:O	2.11	0.69
1:A:204:LEU:HD11	1:A:232:LEU:HD21	1.77	0.67
1:B:131:GLN:HE21	1:B:227:GLY:HA3	1.60	0.67
1:A:110:PHE:HA	1:A:157:ASN:HD22	1.61	0.66
1:A:150:SER:H	1:A:153:ASN:HD21	1.43	0.64
1:B:59:HIS:CD2	2:B:368:HOH:O	2.50	0.64
1:B:149:GLY:HA3	1:B:153:ASN:HD21	1.63	0.64
1:A:119:GLN:NE2	1:B:156:ASN:ND2	2.46	0.63
1:B:10:ASN:HD22	1:B:11:LEU:H	1.44	0.63
1:A:67:ARG:NH1	1:A:90:ASP:OD1	2.31	0.63
1:A:119:GLN:HE22	1:B:156:ASN:ND2	1.99	0.59
1:B:40:ALA:HB1	1:B:41:PRO:CD	2.36	0.56
1:B:40:ALA:HB1	1:B:41:PRO:HD2	1.90	0.54
1:A:131:GLN:HE22	1:A:213:TYR:HA	1.73	0.54
1:B:131:GLN:HE22	1:B:213:TYR:HA	1.73	0.52
1:A:64:VAL:HG13	1:A:68:PHE:HB2	1.93	0.51
1:B:165:HIS:HE1	1:B:207:GLU:O	1.95	0.50
1:A:175:TYR:CE1	1:A:179:LYS:HD3	2.48	0.49
1:B:135:VAL:HG13	1:B:232:LEU:HD13	1.94	0.48
1:B:218:ASP:HB2	1:B:225:LEU:HD22	1.95	0.48
1:A:128:VAL:O	1:A:128:VAL:HG23	2.13	0.48
1:B:59:HIS:HD2	2:B:368:HOH:O	1.91	0.48
1:B:165:HIS:H	1:B:168:LYS:HE2	1.78	0.48
1:A:10:ASN:HD22	1:A:11:LEU:N	2.05	0.47
1:B:172:LEU:HD13	1:B:181:PRO:HG3	1.96	0.47
1:A:196:SER:HB2	2:A:306:HOH:O	2.15	0.46
1:B:180:ARG:HD3	1:B:188:PHE:O	2.15	0.46
1:A:129:LEU:HB2	1:A:227:GLY:HA2	1.96	0.46
1:B:69:THR:HG23	1:B:82:GLN:HB3	1.98	0.46
1:A:128:VAL:O	1:A:128:VAL:CG2	2.66	0.44
1:A:10:ASN:ND2	1:A:11:LEU:H	2.08	0.44
1:A:93:VAL:HG12	1:B:107:TRP:CZ2	2.52	0.44
1:B:149:GLY:HA3	1:B:153:ASN:ND2	2.31	0.44
1:A:19:ARG:NH2	1:A:82:GLN:HE21	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:SER:H	1:A:153:ASN:ND2	2.15	0.43
1:B:204:LEU:HD11	1:B:232:LEU:HD21	2.01	0.43
1:B:59:HIS:HD2	2:B:420:HOH:O	2.01	0.42
1:A:60:TYR:HB2	1:A:65:LYS:HG2	2.02	0.42
1:A:119:GLN:HE21	1:A:119:GLN:HB2	1.55	0.42
1:A:17:SER:HB2	1:A:84:ASN:HD22	1.85	0.41
1:A:10:ASN:HD21	1:B:177:VAL:CG2	2.28	0.41
1:B:10:ASN:ND2	1:B:11:LEU:H	2.15	0.41
1:B:9:GLY:H	1:B:121:THR:HG21	1.86	0.41
1:B:172:LEU:HD13	1:B:181:PRO:CG	2.50	0.41
1:B:174:ILE:HD12	1:B:199:LEU:CD1	2.51	0.40
1:B:150:SER:H	1:B:153:ASN:ND2	2.20	0.40

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	229/264 (87%)	220 (96%)	7 (3%)	2 (1%)	17	12
1	B	231/264 (88%)	223 (96%)	6 (3%)	2 (1%)	17	12
All	All	460/528 (87%)	443 (96%)	13 (3%)	4 (1%)	17	12

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	ALA
1	A	112	SER
1	B	112	SER
1	B	177	VAL

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	187/207 (90%)	171 (91%)	16 (9%)	10	7
1	B	189/207 (91%)	171 (90%)	18 (10%)	8	5
All	All	376/414 (91%)	342 (91%)	34 (9%)	9	6

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	18	LEU
1	A	29	PHE
1	A	38	ARG
1	A	45	LEU
1	A	93	VAL
1	A	98	ARG
1	A	114	MET
1	A	119	GLN
1	A	122	LEU
1	A	128	VAL
1	A	133	SER
1	A	153	ASN
1	A	172	LEU
1	A	191	SER
1	A	221	LEU
1	B	10	ASN
1	B	28	THR
1	B	29	PHE
1	B	38	ARG
1	B	41	PRO
1	B	45	LEU
1	B	48	VAL
1	B	51	LEU
1	B	64	VAL
1	B	119	GLN
1	B	121	THR

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Mol	Chain	Res	Type
1	B	122	LEU
1	B	129	LEU
1	B	136	SER
1	B	153	ASN
1	B	172	LEU
1	B	221	LEU
1	B	235	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	82	GLN
1	A	84	ASN
1	A	119	GLN
1	A	131	GLN
1	A	153	ASN
1	A	157	ASN
1	A	195	ASN
1	B	10	ASN
1	B	59	HIS
1	B	74	ASN
1	B	82	GLN
1	B	119	GLN
1	B	131	GLN
1	B	153	ASN
1	B	163	GLN
1	B	165	HIS
1	B	195	ASN

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

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	A	233/264 (88%)	0.15	11 (4%) 31 37	9, 16, 25, 38	0
1	B	235/264 (89%)	0.07	9 (3%) 40 46	8, 15, 23, 33	0
All	All	468/528 (88%)	0.11	20 (4%) 35 41	8, 16, 24, 38	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	54	ARG	4.4
1	A	128	VAL	4.4
1	A	56	SER	4.0
1	A	1	GLN	3.6
1	A	57	LEU	3.5
1	A	53	ALA	3.4
1	A	55	SER	3.2
1	A	182	SER	3.2
1	A	54	ARG	3.1
1	B	56	SER	2.7
1	A	42	GLY	2.6
1	B	182	SER	2.5
1	B	55	SER	2.3
1	B	183	GLY	2.2
1	B	42	GLY	2.2
1	A	59	HIS	2.1
1	B	106	TYR	2.1
1	A	105	GLY	2.1
1	B	57	LEU	2.0
1	B	154	ILE	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.