



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:49 AM UTC

PDB ID : 6PK8 / pdb_00006pk8
Title : Antibody scFv-M204 dimeric state
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Deposited on : 2019-06-28
Resolution : 2.91 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

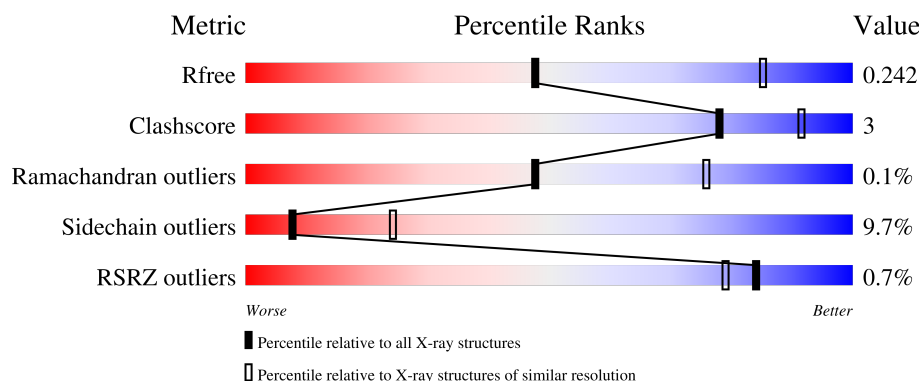
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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}	180053	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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	257	
1	B	257	
1	C	257	
1	D	257	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6841 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 scFv-M204 antibody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1701	1080	274	340	7			
1	B	225	Total	C	N	O	S	0	0	0
			1701	1080	274	340	7			
1	C	225	Total	C	N	O	S	0	0	0
			1701	1080	274	340	7			
1	D	224	Total	C	N	O	S	0	0	0
			1686	1070	273	336	7			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

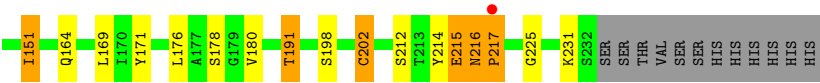
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		
3	B	9	Total	O	0	0
			9	9		
3	C	6	Total	O	0	0
			6	6		
3	D	8	Total	O	0	0
			8	8		



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.60Å 105.26Å 176.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.41 – 2.91 90.41 – 2.91	Depositor EDS
% Data completeness (in resolution range)	98.0 (90.41-2.91) 98.0 (90.41-2.91)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.186 , 0.238 0.194 , 0.242	Depositor DCC
R_{free} test set	2504 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	57.1	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6841	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.11% 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

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	1.04	0/1742	1.28	2/2375 (0.1%)
1	B	1.03	1/1742 (0.1%)	1.32	6/2375 (0.3%)
1	C	1.03	0/1742	1.30	5/2375 (0.2%)
1	D	1.06	0/1727	1.35	10/2355 (0.4%)
All	All	1.04	1/6953 (0.0%)	1.31	23/9480 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	45	GLY	C-O	5.47	1.29	1.23

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	24	THR	CB-CA-C	9.02	125.32	109.72
1	B	82	THR	CA-CB-OG1	-7.59	98.22	109.60
1	B	24	THR	CA-CB-OG1	-7.41	98.49	109.60
1	D	217	PRO	N-CA-C	-6.70	98.68	112.47
1	C	105	ASP	CA-CB-CG	5.89	118.49	112.60
1	C	24	THR	CA-CB-OG1	-5.75	100.98	109.60
1	B	105	ASP	CA-CB-CG	5.71	118.31	112.60
1	D	110	GLY	CA-C-O	-5.66	117.71	122.29
1	D	215	GLU	CA-C-O	-5.61	113.17	119.79
1	B	147	ALA	CA-C-N	5.54	127.97	120.38
1	B	147	ALA	C-N-CA	5.54	127.97	120.38
1	C	110	GLY	CA-C-O	-5.54	117.80	122.29
1	A	105	ASP	CA-CB-CG	5.47	118.07	112.60
1	D	125	ASP	CA-CB-CG	5.41	118.01	112.60
1	C	147	ALA	CA-C-N	5.39	127.76	120.38
1	C	147	ALA	C-N-CA	5.39	127.76	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	129	THR	CB-CA-C	-5.38	101.95	110.02
1	A	110	GLY	CA-C-O	-5.36	117.58	122.24
1	D	105	ASP	CA-CB-CG	5.33	117.93	112.60
1	D	225	GLY	CA-C-O	-5.29	118.58	122.23
1	D	10	GLY	CA-C-O	-5.11	116.98	121.58
1	D	103	GLY	CA-C-O	-5.10	116.69	121.18
1	D	214	TYR	CB-CA-C	5.07	118.11	109.80

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	1701	0	1649	10	0
1	B	1701	0	1649	13	0
1	C	1701	0	1649	6	0
1	D	1686	0	1633	12	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	9	0	0	0	0
3	B	9	0	0	0	0
3	C	6	0	0	0	0
3	D	8	0	0	1	0
All	All	6841	0	6580	37	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 3.

All (37) 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:D:216:ASN:HB3	1:D:217:PRO:HD3	1.51	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:MET:HE3	1:B:145:CYS:SG	2.22	0.80
1:D:216:ASN:HB3	1:D:217:PRO:CD	2.18	0.72
1:A:202:CYS:HB3	1:B:202:CYS:SG	2.30	0.71
1:A:44:LYS:HG2	1:A:45:GLY:N	2.06	0.70
1:B:53:SER:OG	1:B:57:VAL:HG22	2.01	0.60
1:A:41:ALA:HB3	1:A:44:LYS:HD3	1.86	0.58
1:B:13:VAL:HG22	1:B:17:THR:HB	1.87	0.57
1:D:33:TYR:CD1	1:D:96:ARG:HD3	2.40	0.56
1:D:151:ILE:HG22	1:D:191:THR:HG23	1.89	0.55
1:B:11:ARG:HD2	1:C:142:THR:HG21	1.87	0.55
1:A:44:LYS:HE2	1:A:45:GLY:O	2.07	0.54
1:C:13:VAL:HG22	1:C:17:THR:HB	1.88	0.54
1:C:202:CYS:HB3	1:D:202:CYS:SG	2.52	0.50
1:B:230:VAL:O	1:B:231:LYS:C	2.56	0.48
1:B:102:TRP:CD1	1:B:215:GLU:HG2	2.49	0.48
1:B:67:ARG:NH1	1:B:88:ASP:OD1	2.47	0.48
1:C:102:TRP:CD1	1:C:215:GLU:HG2	2.50	0.47
1:A:102:TRP:CD1	1:A:215:GLU:HG2	2.50	0.46
1:A:13:VAL:HG22	1:A:17:THR:HB	1.96	0.46
1:C:202:CYS:SG	1:D:202:CYS:HB3	2.56	0.46
1:D:169:LEU:HA	1:D:180:VAL:HG21	1.98	0.45
1:B:53:SER:OG	1:B:57:VAL:CG2	2.64	0.44
1:B:169:LEU:HA	1:B:180:VAL:HG21	2.00	0.44
1:D:164:GLN:HB2	3:D:405:HOH:O	2.18	0.43
1:D:5:VAL:HG13	1:D:94:CYS:SG	2.59	0.43
1:D:126:MET:HE2	1:D:212:SER:OG	2.19	0.42
1:A:169:LEU:HA	1:A:180:VAL:HG21	2.02	0.42
1:A:97:LYS:HG2	1:A:98:TYR:O	2.20	0.41
1:B:170:ILE:HG12	1:B:176:LEU:HD12	2.03	0.41
1:C:97:LYS:HG2	1:C:98:TYR:O	2.21	0.41
1:B:126:MET:CE	1:B:145:CYS:SG	3.03	0.41
1:A:44:LYS:HG2	1:A:45:GLY:H	1.81	0.40
1:A:44:LYS:CG	1:A:45:GLY:N	2.80	0.40
1:B:125:ASP:H	1:B:148:SER:HB3	1.85	0.40
1:D:97:LYS:HE3	1:D:98:TYR:CZ	2.57	0.40
1:D:103:GLY:HA3	1:D:171:TYR:CE2	2.56	0.40

There are no symmetry-related clashes.

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	A	221/257 (86%)	215 (97%)	6 (3%)	0	100	100
1	B	221/257 (86%)	213 (96%)	8 (4%)	0	100	100
1	C	221/257 (86%)	215 (97%)	6 (3%)	0	100	100
1	D	220/257 (86%)	212 (96%)	7 (3%)	1 (0%)	24	53
All	All	883/1028 (86%)	855 (97%)	27 (3%)	1 (0%)	48	76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	216	ASN

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	187/207 (90%)	167 (89%)	20 (11%)	6	21
1	B	187/207 (90%)	168 (90%)	19 (10%)	7	22
1	C	187/207 (90%)	171 (91%)	16 (9%)	10	29
1	D	185/207 (89%)	168 (91%)	17 (9%)	8	26
All	All	746/828 (90%)	674 (90%)	72 (10%)	8	24

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	13	VAL
1	A	14	THR
1	A	24	THR
1	A	26	SER
1	A	34	SER
1	A	44	LYS
1	A	62	THR
1	A	72	LYS
1	A	74	SER
1	A	76	THR
1	A	96	ARG
1	A	106	LEU
1	A	124	LEU
1	A	125	ASP
1	A	144	LYS
1	A	176	LEU
1	A	198	SER
1	A	200	LEU
1	A	221	SER
1	B	5	VAL
1	B	13	VAL
1	B	24	THR
1	B	26	SER
1	B	34	SER
1	B	62	THR
1	B	72	LYS
1	B	74	SER
1	B	76	THR
1	B	83	SER
1	B	106	LEU
1	B	127	THR
1	B	143	ILE
1	B	161	LYS
1	B	191	THR
1	B	194	THR
1	B	200	LEU
1	B	202	CYS
1	B	221	SER
1	C	5	VAL
1	C	13	VAL
1	C	26	SER
1	C	72	LYS

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Mol	Chain	Res	Type
1	C	74	SER
1	C	96	ARG
1	C	106	LEU
1	C	123	GLU
1	C	124	LEU
1	C	129	THR
1	C	144	LYS
1	C	148	SER
1	C	176	LEU
1	C	198	SER
1	C	202	CYS
1	C	221	SER
1	D	5	VAL
1	D	24	THR
1	D	26	SER
1	D	62	THR
1	D	72	LYS
1	D	74	SER
1	D	76	THR
1	D	82	THR
1	D	127	THR
1	D	151	ILE
1	D	176	LEU
1	D	178	SER
1	D	191	THR
1	D	198	SER
1	D	202	CYS
1	D	215	GLU
1	D	231	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	40	GLN
1	A	160	GLN
1	A	164	GLN
1	C	40	GLN
1	C	149	GLN
1	C	160	GLN
1	C	164	GLN
1	D	40	GLN
1	D	159	GLN

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Mol	Chain	Res	Type
1	D	160	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	C	301	-	4,4,4	0.32	0	6,6,6	0.19	0
2	SO4	D	301	-	4,4,4	0.30	0	6,6,6	0.09	0
2	SO4	A	301	-	4,4,4	0.40	0	6,6,6	0.12	0
2	SO4	B	301	-	4,4,4	0.36	0	6,6,6	0.06	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	225/257 (87%)	-0.31	1 (0%) 88 85	38, 53, 73, 90	0
1	B	225/257 (87%)	-0.22	2 (0%) 81 74	35, 55, 77, 116	0
1	C	225/257 (87%)	-0.18	1 (0%) 88 85	38, 59, 86, 99	0
1	D	224/257 (87%)	-0.14	2 (0%) 81 74	36, 56, 83, 109	0
All	All	899/1028 (87%)	-0.21	6 (0%) 84 79	35, 55, 82, 116	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	232	SER	2.8
1	B	2	ALA	2.6
1	C	232	SER	2.5
1	D	102	TRP	2.3
1	D	217	PRO	2.3
1	B	117	SER	2.3

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 oligosaccharides 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,

median, 95th 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	SO4	C	301	5/5	0.87	0.10	38,44,49,53	5
2	SO4	D	301	5/5	0.87	0.18	41,48,56,58	5
2	SO4	A	301	5/5	0.92	0.10	33,33,42,53	5
2	SO4	B	301	5/5	0.94	0.08	37,38,44,47	5

6.5 Other polymers [i](#)

There are no such residues in this entry.