



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 08:51 PM EDT

PDB ID : 3ZL4 / pdb_00003zl4
Title : Antibody structural organization: Role of kappa - lambda chain constant domain switch in catalytic functionality
Authors : Chatziefthimiou, S.D.; Ponomarenko, N.A.; Kurkova, I.N.; Smirnov, A.V.; Smirnov, I.V.; Lamzin, V.S.; Gabibov, A.G.; Wilmanns, M.
Deposited on : 2013-01-28
Resolution : 1.95 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

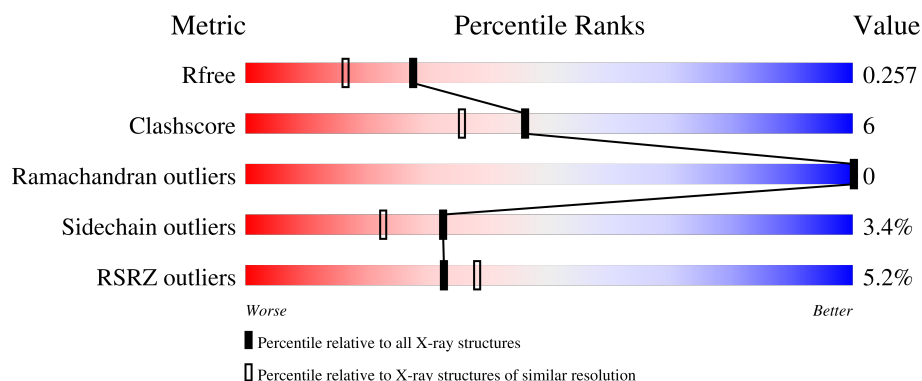
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

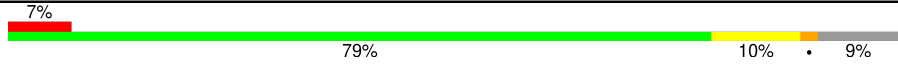
The reported resolution of this entry is 1.95 Å.

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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	H	255	
2	L	247	

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	MES	L	1217	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3648 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.

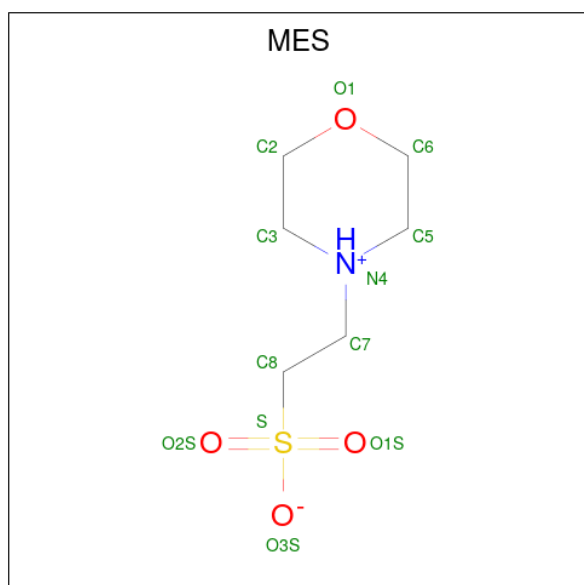
- Molecule 1 is a protein called A17 ANTIBODY FAB FRAGMENT HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	231	Total	C	N	O	S	0	2	0
			1734	1092	286	350	6			

- Molecule 2 is a protein called A17 ANTIBODY FAB FRAGMENT LAMBDA LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	2	0
			1592	994	265	328	5			

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	L	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

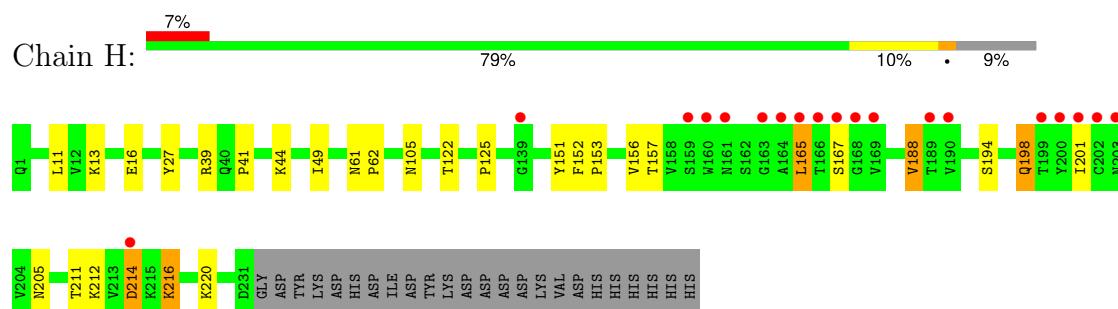
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	173	Total 173	O 173	0	0
4	L	137	Total 137	O 137	0	0

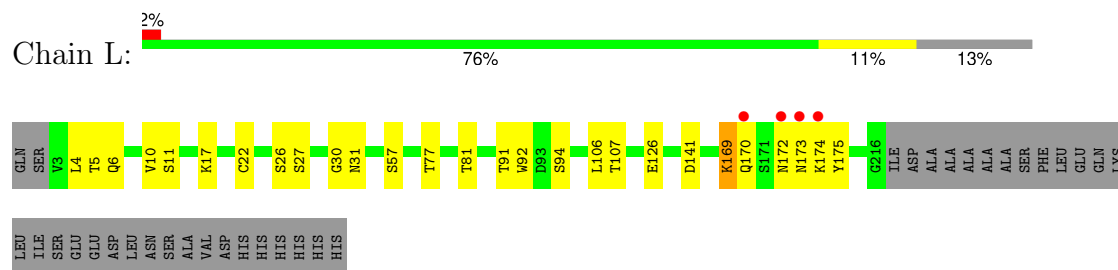
3 Residue-property plots [i](#)

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: A17 ANTIBODY FAB FRAGMENT HEAVY CHAIN



- Molecule 2: A17 ANTIBODY FAB FRAGMENT LAMBDA LIGHT CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	60.63Å 60.63Å 279.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.40 – 1.95 24.40 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.8 (24.40-1.95) 99.8 (24.40-1.95)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 1.95Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8.1_1168)	Depositor
R, R_{free}	0.205 , 0.255 0.206 , 0.257	Depositor DCC
R_{free} test set	1975 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.704	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 36.8	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	0.95	EDS
Total number of atoms	3648	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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: MES

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	H	0.44	0/1778	0.77	0/2429
2	L	0.46	0/1631	0.77	0/2230
All	All	0.45	0/3409	0.77	0/4659

There are no bond length outliers.

There are no bond angle outliers.

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	H	1734	0	1690	20	0
2	L	1592	0	1542	16	0
3	L	12	0	12	9	0
4	H	173	0	0	3	0
4	L	137	0	0	1	0
All	All	3648	0	3244	38	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 6.

All (38) 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:H:105:ASN:HD22	3:L:1217:MES:H61	1.34	0.90
2:L:92:TRP:CD2	3:L:1217:MES:H22	2.14	0.83
1:H:216:LYS:HE3	1:H:216:LYS:H	1.46	0.80
2:L:141:ASP:HA	2:L:174:LYS:HB3	1.64	0.80
1:H:13:LYS:HB2	1:H:16:GLU:HG3	1.71	0.71
2:L:81:THR:O	2:L:173:ASN:ND2	2.26	0.69
2:L:17:LYS:HD3	2:L:77:THR:HG22	1.75	0.68
1:H:157:THR:HG22	1:H:205:ASN:HB3	1.74	0.68
1:H:125:PRO:HD2	1:H:211:THR:HG21	1.74	0.68
4:H:2127:HOH:O	3:L:1217:MES:H51	1.96	0.65
2:L:91:THR:C	3:L:1217:MES:H21	2.24	0.62
2:L:10:VAL:HG13	2:L:106:LEU:HD13	1.84	0.59
1:H:105:ASN:ND2	3:L:1217:MES:H61	2.14	0.57
2:L:92:TRP:CG	3:L:1217:MES:H22	2.40	0.57
2:L:169:LYS:HD2	2:L:175:TYR:CZ	2.40	0.57
1:H:39:ARG:HB3	1:H:49:ILE:HD11	1.87	0.57
1:H:201:ILE:HG12	1:H:216:LYS:HA	1.88	0.55
1:H:11:LEU:HD23	1:H:122[B]:THR:HG22	1.92	0.51
2:L:27:SER:HB3	2:L:94:SER:HB3	1.92	0.51
1:H:165:LEU:HD13	1:H:188:VAL:HG21	1.93	0.50
2:L:26:SER:HA	2:L:30:GLY:HA3	1.92	0.49
1:H:125:PRO:HB3	1:H:151:TYR:HB3	1.93	0.49
1:H:157:THR:CG2	1:H:205:ASN:HB3	2.43	0.48
2:L:4:LEU:HD11	2:L:91:THR:HG22	1.97	0.47
1:H:214:ASP:OD1	1:H:214:ASP:N	2.48	0.47
2:L:92:TRP:CE2	3:L:1217:MES:H22	2.51	0.46
2:L:172:ASN:C	2:L:174:LYS:H	2.25	0.45
1:H:41:PRO:HB2	1:H:44:LYS:HD3	1.98	0.44
1:H:105:ASN:HB2	3:L:1217:MES:C5	2.48	0.44
1:H:220:LYS:NZ	4:H:2166:HOH:O	2.32	0.43
1:H:61:ASN:HA	1:H:62:PRO:HD2	1.87	0.43
1:H:27:TYR:OH	4:H:2047:HOH:O	2.20	0.42
2:L:11:SER:HB3	2:L:107:THR:HB	2.03	0.41
2:L:126:GLU:HB2	4:L:2086:HOH:O	2.19	0.41
3:L:1217:MES:H31	3:L:1217:MES:H82	1.52	0.41
1:H:194:SER:O	1:H:198:GLN:HB2	2.21	0.40
2:L:5:THR:O	2:L:22:CYS:HA	2.21	0.40
1:H:152:PHE:HA	1:H:153:PRO:HA	1.85	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	H	231/255 (91%)	225 (97%)	6 (3%)	0	100	100
2	L	214/247 (87%)	206 (96%)	8 (4%)	0	100	100
All	All	445/502 (89%)	431 (97%)	14 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	H	200/221 (90%)	192 (96%)	8 (4%)	28	17
2	L	181/206 (88%)	176 (97%)	5 (3%)	38	30
All	All	381/427 (89%)	368 (97%)	13 (3%)	32	23

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	156	VAL
1	H	165	LEU
1	H	167	SER
1	H	188	VAL
1	H	198	GLN
1	H	212	LYS
1	H	214	ASP
1	H	216	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	L	6	GLN
2	L	31	ASN
2	L	57	SER
2	L	169	LYS
2	L	170	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	3	GLN
1	H	40	GLN
1	H	161	ASN
2	L	39	GLN
2	L	131	ASN
2	L	170	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](#)

1 ligand 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	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MES	L	1217	-	12,12,12	2.57	2 (16%)	15,16,16	3.10	9 (60%)

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	MES	L	1217	-	-	2/6/14/14	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	1217	MES	C8-S	-8.34	1.65	1.77
3	L	1217	MES	O1S-S	2.01	1.50	1.45

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	1217	MES	C6-C5-N4	-6.76	99.84	110.12
3	L	1217	MES	C2-C3-N4	-4.29	103.60	110.12
3	L	1217	MES	C5-N4-C3	4.28	118.06	108.84
3	L	1217	MES	C7-N4-C3	3.61	120.86	111.24
3	L	1217	MES	C7-N4-C5	3.51	120.58	111.24
3	L	1217	MES	O1-C6-C5	-3.16	104.97	111.77
3	L	1217	MES	O3S-S-C8	3.04	111.96	106.00
3	L	1217	MES	O1-C2-C3	2.65	117.48	111.77
3	L	1217	MES	C8-C7-N4	-2.40	103.28	112.36

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L	1217	MES	C8-C7-N4-C3
3	L	1217	MES	N4-C7-C8-S

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	1217	MES	9	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 ⓘ

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	H	231/255 (90%)	0.25	19 (8%)	17 20	9, 22, 52, 63	2 (0%)
2	L	214/247 (86%)	-0.04	4 (1%)	66 74	11, 22, 37, 54	2 (0%)
All	All	445/502 (88%)	0.11	23 (5%)	33 38	9, 22, 49, 63	4 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	173	ASN	6.1
1	H	164	ALA	4.1
1	H	201	ILE	3.9
1	H	163	GLY	3.3
1	H	160	TRP	3.1
2	L	174	LYS	2.9
1	H	169	VAL	2.9
1	H	165	LEU	2.7
1	H	139	GLY	2.6
1	H	202	CYS	2.6
1	H	167	SER	2.6
2	L	170	GLN	2.6
1	H	161	ASN	2.5
1	H	200	TYR	2.3
1	H	190	VAL	2.3
1	H	168	GLY	2.3
1	H	199	THR	2.3
1	H	166	THR	2.2
2	L	172	ASN	2.1
1	H	189	THR	2.1
1	H	214	ASP	2.1
1	H	159	SER	2.1
1	H	203	ASN	2.1

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($\text{\AA}^2$)	Q<0.9
3	MES	L	1217	12/12	0.86	0.12	9,18,25,34	12

6.5 Other polymers [i](#)

There are no such residues in this entry.