



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:01 PM UTC

PDB ID : 8ZXW / pdb_00008zxw
Title : Crystal structure of the anti-phosphorylated peptide C7 Fab antibody with peptide bound
Authors : Caaveiro, J.M.M.; Kasahara, K.; Tsumoto, K.
Deposited on : 2024-06-15
Resolution : 1.33 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

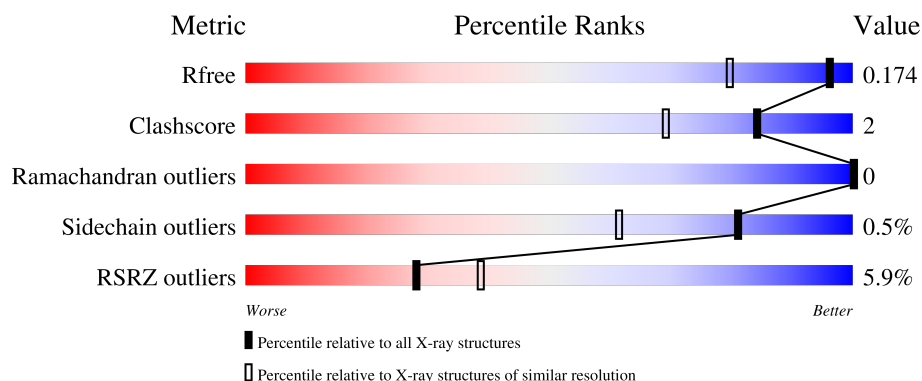
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.33 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	2194 (1.36-1.32)
Clashscore	190562	2222 (1.36-1.32)
Ramachandran outliers	187476	2197 (1.36-1.32)
Sidechain outliers	187428	2197 (1.36-1.32)
RSRZ outliers	180081	2193 (1.36-1.32)

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	228	5% 90% 6%
1	H	228	5% 88% 5% 7%
2	B	217	7% 95% 5%
2	L	217	3% 96% .
3	C	12	17% 67% 33%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	D	12	 A horizontal bar chart showing the quality of chain D. The bar is divided into four segments: red (33%), green (50%), yellow (17%), and grey (33%). The percentages are labeled above or below the segments.

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7553 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 Fab, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	213	Total	C	N	O	S	0	9	0
			1631	1032	271	321	7			
1	A	214	Total	C	N	O	S	0	6	0
			1616	1018	270	321	7			

- Molecule 2 is a protein called Fab, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	217	Total	C	N	O	S	0	13	0
			1649	1024	268	347	10			
2	B	217	Total	C	N	O	S	0	10	0
			1640	1017	268	346	9			

- Molecule 3 is a protein called RAC-gamma serine/threonine-protein kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	8	Total	C	N	O	P	0	0	0
			76	49	11	15	1			
3	D	8	Total	C	N	O	P	0	0	0
			76	49	11	15	1			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

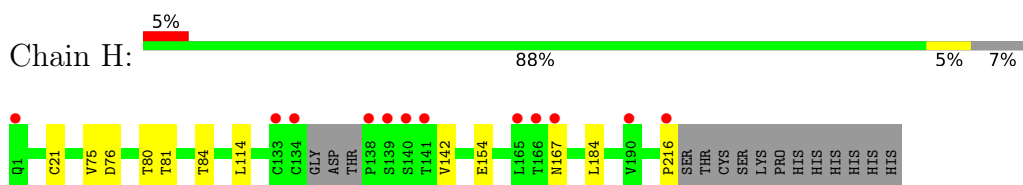
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	184	Total	O	0	4
			186	186		
6	L	234	Total	O	0	5
			237	237		
6	C	10	Total	O	0	2
			12	12		
6	A	225	Total	O	0	2
			226	226		
6	B	188	Total	O	0	3
			190	190		
6	D	7	Total	O	0	0
			7	7		

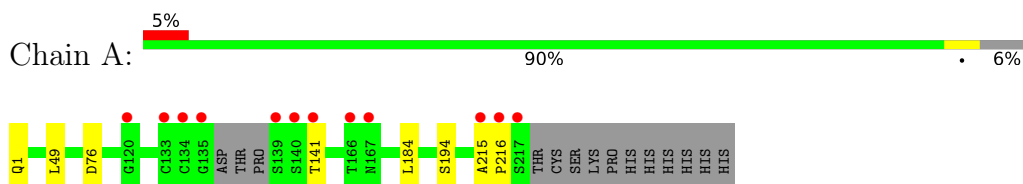
3 Residue-property plots [i](#)

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.

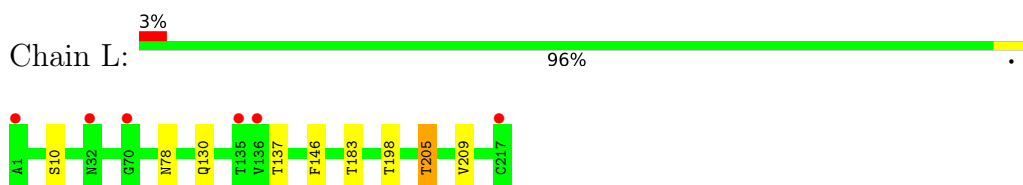
- Molecule 1: Fab, heavy chain



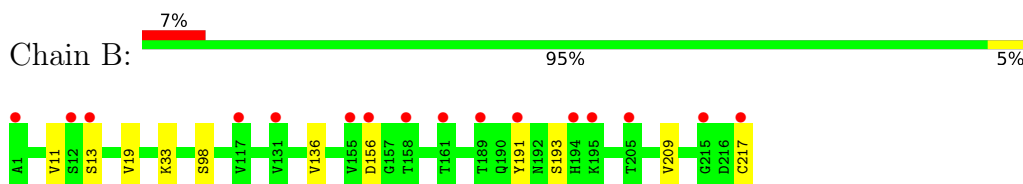
- Molecule 1: Fab, heavy chain



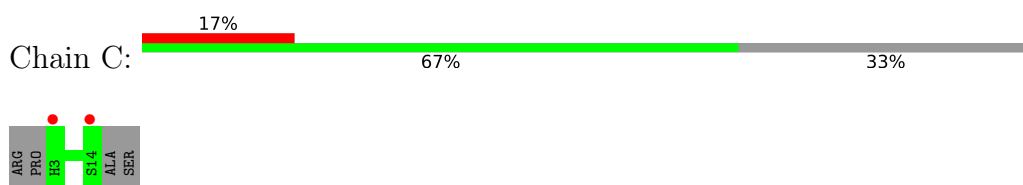
- Molecule 2: Fab, light chain



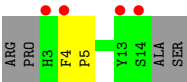
- Molecule 2: Fab, light chain



- Molecule 3: RAC-gamma serine/threonine-protein kinase



- Molecule 3: RAC-gamma serine/threonine-protein kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.35Å 67.84Å 71.34Å 112.54° 104.99° 98.31°	Depositor
Resolution (Å)	48.04 – 1.33 48.04 – 1.33	Depositor EDS
% Data completeness (in resolution range)	93.5 (48.04-1.33) 93.5 (48.04-1.33)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 1.33Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.137 , 0.165 0.146 , 0.174	Depositor DCC
R_{free} test set	9562 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	15.4	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.3	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	0.97	EDS
Total number of atoms	7553	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.04% 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: GOL, SEP, CL

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	0.58	0/1672	0.95	2/2292 (0.1%)
1	H	0.57	0/1697	0.90	2/2324 (0.1%)
2	B	0.67	2/1697 (0.1%)	0.91	0/2321
2	L	0.57	0/1715	0.89	2/2346 (0.1%)
3	C	0.55	0/69	0.97	0/91
3	D	0.54	0/69	0.84	0/91
All	All	0.60	2/6919 (0.0%)	0.91	6/9465 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	156	ASP	CG-OD2	14.24	1.52	1.25
2	B	156	ASP	CG-OD1	6.12	1.36	1.25

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	ASP	CA-CB-CG	6.65	119.25	112.60
2	L	205	THR	CA-CB-OG1	-5.92	100.72	109.60
1	A	141	THR	CA-CB-OG1	-5.72	101.02	109.60
1	H	76	ASP	CA-CB-CG	5.50	118.09	112.60
1	H	167	ASN	CB-CA-C	5.39	118.87	109.65
2	L	146	PHE	CA-CB-CG	-5.15	108.65	113.80

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	1616	0	1608	5	1
1	H	1631	0	1640	8	0
2	B	1640	0	1591	7	0
2	L	1649	0	1607	10	0
3	C	76	0	57	0	0
3	D	76	0	57	1	0
4	H	6	0	8	0	0
5	A	1	0	0	1	0
6	A	226	0	0	0	0
6	B	190	0	0	1	0
6	C	12	0	0	0	0
6	D	7	0	0	0	0
6	H	186	0	0	2	0
6	L	237	0	0	3	1
All	All	7553	0	6568	31	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 2.

All (31) 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:L:78[B]:ASN:ND2	6:L:301:HOH:O	2.32	0.62
2:L:130:GLN:HE22	2:L:137:THR:H	1.47	0.61
2:B:13:SER:HB2	2:B:19[A]:VAL:HG11	1.83	0.60
1:A:1:GLN:N	1:A:1:GLN:OE1	2.34	0.60
2:B:13:SER:HB2	2:B:19[A]:VAL:CG1	2.33	0.58
1:H:114:LEU:HD13	6:H:453:HOH:O	2.06	0.55
1:A:1:GLN:N	1:A:1:GLN:CD	2.64	0.55
2:L:137:THR:HG23	2:L:183[A]:THR:CG2	2.36	0.55
1:A:184:LEU:HD12	1:A:184:LEU:C	2.35	0.52
2:L:130:GLN:NE2	2:L:137:THR:H	2.08	0.50
2:L:137:THR:CG2	2:L:183[A]:THR:CG2	2.91	0.49
1:H:184:LEU:HD12	1:H:184:LEU:C	2.39	0.48
2:L:10[A]:SER:HB2	6:L:471[A]:HOH:O	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:84[B]:THR:HG23	5:A:301:CL:CL	2.53	0.46
1:A:215:ALA:O	1:A:216:PRO:C	2.58	0.45
3:D:4:PHE:HA	3:D:5:PRO:C	2.41	0.45
2:L:137:THR:CG2	2:L:183[A]:THR:HG23	2.47	0.45
2:L:183[B]:THR:HG23	6:L:402:HOH:O	2.17	0.44
1:H:114:LEU:CD1	6:H:453:HOH:O	2.62	0.44
2:L:198:THR:HG23	2:L:209[B]:VAL:HG13	2.01	0.43
1:A:49:LEU:C	1:A:49:LEU:HD12	2.43	0.42
2:B:136:VAL:HG21	2:B:191:TYR:CG	2.53	0.42
2:B:11:VAL:HG11	2:B:19[B]:VAL:HG21	2.01	0.42
2:B:191:TYR:C	2:B:193:SER:H	2.28	0.42
1:H:142:VAL:HG11	1:H:216:PRO:HG3	2.01	0.42
2:L:198:THR:HG23	2:L:209[A]:VAL:CG2	2.49	0.42
1:H:80:THR:HG22	1:H:81[B]:THR:HG23	2.01	0.41
1:H:114:LEU:CD2	1:H:154:GLU:HB2	2.50	0.41
2:B:33:LYS:HD2	6:B:396:HOH:O	2.19	0.41
1:H:21:CYS:HB3	1:H:75:VAL:HG13	2.03	0.41
2:B:136:VAL:HG21	2:B:191:TYR:HB2	2.03	0.40

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:194[B]:SER:OG	6:L:531:HOH:O[1_554]	1.97	0.23

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	216/228 (95%)	214 (99%)	2 (1%)	0	100	100
1	H	218/228 (96%)	215 (99%)	3 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	225/217 (104%)	217 (96%)	8 (4%)	0	100	100
2	L	228/217 (105%)	222 (97%)	6 (3%)	0	100	100
3	C	5/12 (42%)	5 (100%)	0	0	100	100
3	D	5/12 (42%)	5 (100%)	0	0	100	100
All	All	897/914 (98%)	878 (98%)	19 (2%)	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	A	190/198 (96%)	190 (100%)	0	100	100
1	H	193/198 (98%)	193 (100%)	0	100	100
2	B	192/182 (106%)	189 (98%)	3 (2%)	55	20
2	L	195/182 (107%)	194 (100%)	1 (0%)	81	61
3	C	7/10 (70%)	7 (100%)	0	100	100
3	D	7/10 (70%)	7 (100%)	0	100	100
All	All	784/780 (100%)	780 (100%)	4 (0%)	81	61

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	205	THR
2	B	98	SER
2	B	209	VAL
2	B	217	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	38	GLN
2	L	22	ASN
2	L	40	GLN
2	L	72	GLN
2	L	130	GLN
2	L	213	ASN
1	A	38	GLN
2	B	40	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
3	SEP	D	8	3	8,9,10	0.59	0	7,12,14	0.60	0
3	SEP	C	8	3	8,9,10	0.61	0	7,12,14	0.79	0

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	SEP	D	8	3	-	1/6/8/10	-
3	SEP	C	8	3	-	1/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	8	SEP	CA-CB-OG-P
3	D	8	SEP	CA-CB-OG-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
4	GOL	H	301	-	5,5,5	0.10	0	5,5,5	0.41	0

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
4	GOL	H	301	-	-	0/4/4/4	-

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	214/228 (93%)	0.12	12 (5%) 30 41	9, 18, 34, 69	6 (2%)
1	H	213/228 (93%)	0.11	12 (5%) 30 41	10, 18, 33, 55	9 (4%)
2	B	217/217 (100%)	0.42	16 (7%) 20 29	8, 21, 45, 74	10 (4%)
2	L	217/217 (100%)	0.16	6 (2%) 55 64	7, 18, 36, 57	13 (5%)
3	C	7/12 (58%)	0.97	2 (28%) 1 2	13, 15, 38, 44	0
3	D	7/12 (58%)	1.18	4 (57%) 0 0	15, 17, 39, 50	0
All	All	875/914 (95%)	0.22	52 (5%) 28 39	7, 19, 39, 74	38 (4%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	166	THR	6.1
2	L	1	ALA	5.9
1	H	166	THR	5.1
2	B	156	ASP	4.7
2	L	217	CYS	4.1
1	H	134	CYS	3.9
1	H	138	PRO	3.9
1	A	141	THR	3.8
2	B	194	HIS	3.8
1	A	135	GLY	3.6
1	H	141	THR	3.5
2	B	195	LYS	3.5
2	B	1	ALA	3.4
1	H	167	ASN	3.3
2	B	117	VAL	3.1
3	C	14	SER	3.1
2	B	217	CYS	3.1
1	A	140	SER	3.0
1	A	139	SER	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	189	THR	2.8
1	H	139	SER	2.8
1	H	140	SER	2.8
3	D	4	PHE	2.8
1	A	167	ASN	2.8
2	B	205	THR	2.8
3	C	3	HIS	2.7
2	B	191	TYR	2.7
1	A	215	ALA	2.7
1	A	217	SER	2.7
2	L	70	GLY	2.5
2	B	215	GLY	2.5
1	H	216	PRO	2.5
2	B	13	SER	2.5
2	B	155	VAL	2.5
1	A	120	GLY	2.4
1	A	216	PRO	2.4
2	L	136	VAL	2.4
3	D	3	HIS	2.4
2	B	131	VAL	2.4
2	B	158	THR	2.4
3	D	13	TYR	2.3
1	H	1	GLN	2.3
2	L	32	ASN	2.3
2	B	12	SER	2.2
1	H	133	CYS	2.2
1	H	190	VAL	2.2
1	A	133	CYS	2.2
1	A	134	CYS	2.2
3	D	14	SER	2.1
2	L	135	THR	2.1
2	B	161	THR	2.0
1	H	165	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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	SEP	C	8	10/11	0.99	0.03	12,13,15,17	0
3	SEP	D	8	10/11	0.99	0.04	12,14,19,21	0

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
4	GOL	H	301	6/6	0.92	0.10	26,27,29,31	0
5	CL	A	301	1/1	0.99	0.07	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.