



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 06:15 am BST

PDB ID : 4RLV
Title : Crystal Structure of AnkB 24 Ankyrin Repeats in Complex with AnkR Autoinhibition Segment
Authors : Wei, Z.; Wang, C.; Zhang, M.
Deposited on : 2014-10-18
Resolution : 3.49 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

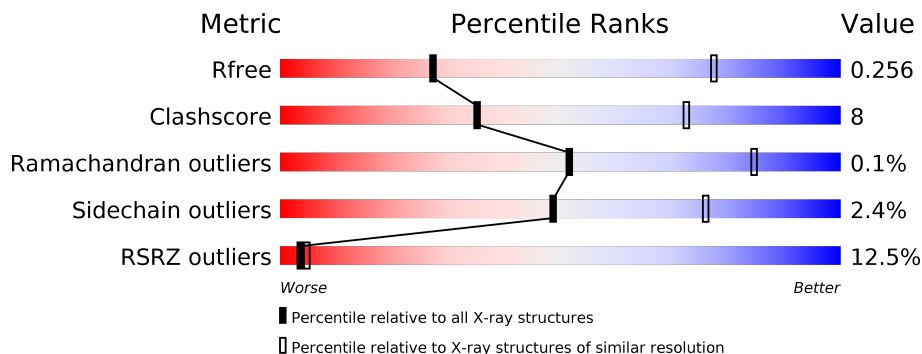
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.49 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 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	910	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6305 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 Ankyrin-1, Ankyrin-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	838	6260	3905	1156	1176	7	16	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1571	GLY	-	EXPRESSION TAG	UNP D3YTV8
A	1572	PRO	-	EXPRESSION TAG	UNP D3YTV8
A	1573	GLY	-	EXPRESSION TAG	UNP D3YTV8
A	1574	SER	-	EXPRESSION TAG	UNP D3YTV8
A	1575	GLU	-	EXPRESSION TAG	UNP D3YTV8
A	1576	PHE	-	EXPRESSION TAG	UNP D3YTV8
A	1625	GLY	-	LINKER	UNP D3YTV8
A	1626	SER	-	LINKER	UNP D3YTV8
A	1627	LEU	-	LINKER	UNP D3YTV8
A	1628	VAL	-	LINKER	UNP D3YTV8
A	1629	PRO	-	LINKER	UNP D3YTV8
A	1630	ARG	-	LINKER	UNP D3YTV8
A	2024	GLY	-	LINKER	UNP Q01484
A	2025	SER	-	LINKER	UNP Q01484
A	2026	GLY	-	LINKER	UNP Q01484
A	2027	SER	-	LINKER	UNP Q01484

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	179.69Å 179.69Å 304.86Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.59 – 3.49 42.73 – 3.49	Depositor EDS
% Data completeness (in resolution range)	94.5 (38.59-3.49) 74.4 (42.73-3.49)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 3.48Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.220 , 0.253 0.221 , 0.256	Depositor DCC
R_{free} test set	1394 reflections (6.01%)	wwPDB-VP
Wilson B-factor (Å ²)	100.4	Xtrriage
Anisotropy	0.613	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 65.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6305	wwPDB-VP
Average B, all atoms (Å ²)	113.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% 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](#)

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	0.56	0/6341	0.78	8/8585 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	2252	LEU	CB-CG-CD2	-8.97	95.75	111.00
1	A	2394	ARG	NE-CZ-NH1	-6.94	116.83	120.30
1	A	2182	LEU	CB-CG-CD2	-6.28	100.33	111.00
1	A	2116	LEU	CB-CG-CD2	-6.05	100.72	111.00
1	A	2333	LEU	CB-CG-CD2	-5.63	101.42	111.00
1	A	2183	LEU	CB-CG-CD2	-5.60	101.48	111.00
1	A	2300	LEU	CB-CG-CD2	-5.58	101.52	111.00
1	A	1609	VAL	CB-CA-C	-5.20	101.52	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1607	MSE	Peptide

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	6260	0	6385	104	0
2	A	45	0	0	3	0
All	All	6305	0	6385	104	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 (104) 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:2583:LEU:HD13	1:A:2618:LYS:HG3	1.66	0.78
1:A:2649:LEU:HD13	1:A:2684:LYS:HG3	1.67	0.76
1:A:2048:VAL:HG13	1:A:2086:ARG:HH21	1.57	0.70
1:A:2757:LYS:HG2	1:A:2763:THR:HG22	1.76	0.67
1:A:2721:GLN:O	1:A:2730:THR:OG1	2.07	0.67
1:A:2369:LEU:HD11	1:A:2381:THR:HG23	1.78	0.66
1:A:2046:LYS:HE2	1:A:2050:TYR:HE2	1.62	0.64
1:A:2798:LEU:HD21	1:A:2814:LYS:HE2	1.81	0.63
1:A:2035:PHE:HE1	1:A:2047:VAL:HG13	1.64	0.63
1:A:2253:LEU:HA	1:A:2257:ALA:HB3	1.81	0.62
1:A:2637:ALA:HA	1:A:2677:MSE:HE2	1.81	0.62
1:A:2050:TYR:HD1	1:A:2055:ILE:HG13	1.66	0.61
1:A:2800:ILE:HG23	1:A:2803:ARG:HH21	1.66	0.61
1:A:2253:LEU:HD23	1:A:2257:ALA:HB3	1.83	0.60
1:A:2507:LEU:HB3	1:A:2509:LYS:HE2	1.85	0.57
1:A:2241:ALA:O	1:A:2278:ASN:ND2	2.37	0.57
1:A:2791:THR:H	1:A:2795:ASN:H	1.50	0.57
1:A:2601:HIS:HD2	1:A:2635:ILE:HD11	1.69	0.56
1:A:2050:TYR:CD1	1:A:2055:ILE:HG13	2.40	0.56
1:A:2138:ALA:HB1	1:A:2170:ALA:HB2	1.87	0.55
1:A:2481:ARG:NH2	2:A:2907:SO4:O4	2.35	0.55
1:A:2189:GLY:HA2	1:A:2192:ARG:HB2	1.90	0.54
1:A:2427:ILE:HD12	1:A:2431:GLY:HA2	1.88	0.54
1:A:2330:LYS:HG2	1:A:2331:ASN:N	2.23	0.53
1:A:2270:LEU:HD11	1:A:2282:VAL:HG13	1.91	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2703:ALA:HB2	1:A:2743:MSE:HE2	1.90	0.53
1:A:1607:MSE:HE2	1:A:2267:ILE:HD12	1.91	0.52
1:A:2682:LEU:HD23	1:A:2686:ALA:HB3	1.93	0.51
1:A:2723:ALA:O	1:A:2730:THR:OG1	2.28	0.50
1:A:2567:LEU:HD23	1:A:2599:PRO:HG2	1.93	0.50
1:A:2724:HIS:HB3	1:A:2728:GLY:HA2	1.93	0.50
1:A:2465:GLU:OE2	1:A:2473:ARG:NH2	2.45	0.50
1:A:2061:ASN:HD21	1:A:2065:LEU:HD12	1.76	0.50
1:A:2328:ARG:HB3	1:A:2332:GLY:HA2	1.94	0.50
1:A:2329:THR:HG21	1:A:2338:MSE:CE	2.42	0.49
1:A:2193:LEU:HB3	1:A:2194:PRO:HD3	1.94	0.49
1:A:2640:ASN:HB2	1:A:2674:HIS:CE1	2.48	0.48
1:A:2141:ASN:HB2	1:A:2175:HIS:CD2	2.48	0.48
1:A:2769:ALA:HA	1:A:2777:ILE:HD11	1.94	0.48
1:A:1585:VAL:HG21	1:A:2470:MSE:HE1	1.95	0.48
1:A:2144:ASP:OD1	1:A:2144:ASP:N	2.45	0.48
1:A:2514:GLN:HG2	1:A:2548:VAL:HG11	1.95	0.48
1:A:1596:THR:O	1:A:1600:THR:HG23	2.14	0.48
1:A:2212:LEU:HD23	1:A:2225:MSE:HE2	1.96	0.48
1:A:2329:THR:HG21	1:A:2338:MSE:HE2	1.95	0.48
1:A:2343:ASP:OD2	1:A:2377:HIS:HB3	2.14	0.47
1:A:2508:GLY:HA2	1:A:2545:VAL:HG21	1.96	0.47
1:A:1599:ASP:OD2	1:A:2330:LYS:NZ	2.48	0.47
1:A:2232:SER:HB2	1:A:2264:ARG:HH21	1.78	0.47
1:A:1625:GLY:O	1:A:1627:LEU:HG	2.14	0.46
1:A:2766:HIS:NE2	1:A:2795:ASN:O	2.47	0.46
1:A:2691:SER:HB2	1:A:2695:GLY:HA2	1.97	0.46
1:A:2084:LEU:HD13	1:A:2119:GLU:HG2	1.97	0.46
1:A:2787:PRO:HG3	1:A:2816:VAL:O	2.15	0.46
1:A:1597:GLU:O	1:A:1600:THR:OG1	2.32	0.46
1:A:2303:LEU:HD11	1:A:2315:VAL:HG13	1.97	0.46
1:A:2798:LEU:HD11	1:A:2814:LYS:HE3	1.98	0.46
1:A:1588:ILE:HD11	1:A:2437:VAL:HG13	1.96	0.45
1:A:2295:LYS:HE2	1:A:2295:LYS:HB3	1.73	0.45
1:A:2385:LEU:HD13	1:A:2420:TYR:CG	2.51	0.45
1:A:2572:LYS:HG3	1:A:2606:TYR:CE2	2.51	0.45
1:A:2167:LEU:HD23	1:A:2191:VAL:HG12	1.99	0.45
1:A:2079:LEU:O	1:A:2083:LEU:HG	2.17	0.45
1:A:2202:LYS:HE3	2:A:2909:SO4:O3	2.17	0.44
1:A:2411:ILE:HG12	1:A:2446:ILE:HD11	1.99	0.44
1:A:2336:LEU:HD11	1:A:2348:VAL:HG13	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2550:LEU:HD13	1:A:2585:ARG:HG3	2.00	0.44
1:A:2316:GLU:HB2	1:A:2350:HIS:CD2	2.52	0.44
1:A:2697:THR:O	1:A:2700:HIS:HB2	2.18	0.43
1:A:2690:MSE:HB3	1:A:2690:MSE:HE2	1.96	0.43
1:A:2262:THR:HG22	1:A:2268:THR:HG22	2.00	0.43
1:A:2770:GLN:HG2	1:A:2771:GLN:NE2	2.33	0.43
1:A:2134:LEU:HD21	1:A:2156:GLN:HB3	2.00	0.43
1:A:2427:ILE:HG22	1:A:2433:THR:HG22	2.00	0.43
1:A:2507:LEU:HB2	1:A:2509:LYS:HG2	2.00	0.43
1:A:1601:MSE:O	1:A:1605:SER:N	2.52	0.43
1:A:2162:ASP:N	1:A:2162:ASP:OD2	2.49	0.43
1:A:2083:LEU:HA	1:A:2083:LEU:HD23	1.74	0.42
1:A:2277:GLY:HA2	1:A:2314:VAL:HG21	2.01	0.42
1:A:2343:ASP:HB2	1:A:2377:HIS:CD2	2.55	0.42
1:A:2495:ARG:O	1:A:2498:GLN:HG2	2.20	0.42
1:A:2676:ASP:OD1	1:A:2676:ASP:N	2.51	0.42
1:A:2732:LEU:HD22	1:A:2752:ALA:HB1	2.01	0.42
1:A:2188:LYS:O	1:A:2192:ARG:HG3	2.20	0.41
1:A:2357:PRO:HB2	1:A:2360:ASP:HB2	2.03	0.41
1:A:2145:VAL:O	1:A:2149:LEU:HG	2.20	0.41
1:A:2754:VAL:HA	1:A:2764:PRO:HG2	2.02	0.41
1:A:2300:LEU:HA	1:A:2300:LEU:HD23	1.76	0.41
1:A:1597:GLU:HG3	1:A:1598:HIS:N	2.30	0.41
1:A:2310:GLY:HA2	1:A:2347:CYS:SG	2.60	0.41
1:A:2343:ASP:HA	1:A:2380:VAL:HG21	2.02	0.41
1:A:2129:ASN:HB2	1:A:2131:PHE:CE2	2.55	0.41
1:A:2402:LEU:HA	1:A:2402:LEU:HD12	1.73	0.41
1:A:2692:THR:HG23	1:A:2696:LEU:O	2.21	0.41
1:A:2746:PHE:HA	1:A:2749:LYS:HD2	2.02	0.41
1:A:2227:ASN:HB3	1:A:2261:PHE:CE1	2.56	0.41
1:A:2673:GLY:HA2	1:A:2710:VAL:HG21	2.03	0.41
1:A:2601:HIS:CD2	1:A:2635:ILE:HD11	2.53	0.41
1:A:2688:ILE:H	1:A:2688:ILE:HG13	1.62	0.41
1:A:2244:GLY:HA2	1:A:2281:MSE:HG3	2.03	0.40
1:A:2436:HIS:HD2	1:A:2470:MSE:HG3	1.86	0.40
1:A:2529:ASN:OD1	1:A:2529:ASN:N	2.51	0.40
1:A:1594:ALA:HB2	2:A:2908:SO4:O1	2.21	0.40
1:A:2378:TYR:CE1	1:A:2416:LEU:HD22	2.56	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	834/910 (92%)	791 (95%)	42 (5%)	1 (0%)	51 84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1610	TRP

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	660/706 (94%)	644 (98%)	16 (2%)	49 76

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1597	GLU
1	A	1601	MSE
1	A	1611	SER
1	A	1614	LEU
1	A	1616	PRO
1	A	1622	GLU
1	A	1628	VAL
1	A	2162	ASP
1	A	2172	GLN
1	A	2261	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2330	LYS
1	A	2470	MSE
1	A	2595	ASN
1	A	2641	GLN
1	A	2684	LYS
1	A	2730	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

9 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	A	2906	-	4,4,4	0.18	0	6,6,6	0.35	0
2	SO4	A	2902	-	4,4,4	0.25	0	6,6,6	0.24	0
2	SO4	A	2905	-	4,4,4	0.16	0	6,6,6	0.39	0
2	SO4	A	2907	-	4,4,4	0.19	0	6,6,6	0.19	0
2	SO4	A	2908	-	4,4,4	0.18	0	6,6,6	0.20	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	2903	-	4,4,4	0.11	0	6,6,6	0.28	0
2	SO4	A	2909	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	A	2904	-	4,4,4	0.13	0	6,6,6	0.26	0
2	SO4	A	2901	-	4,4,4	0.08	0	6,6,6	0.54	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.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2907	SO4	1	0
2	A	2908	SO4	1	0
2	A	2909	SO4	1	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	A	822/910 (90%)	0.85	103 (12%) 3 5	28, 108, 225, 265	0

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2769	ALA	19.6
1	A	2816	VAL	14.3
1	A	2812	THR	13.2
1	A	2770	GLN	12.0
1	A	2755	ASN	10.6
1	A	2784	GLY	10.0
1	A	2776	ILE	7.9
1	A	2768	ALA	7.7
1	A	2802	LYS	7.4
1	A	2736	CYS	6.9
1	A	2783	HIS	6.9
1	A	2790	THR	6.7
1	A	2788	ASN	6.0
1	A	2792	ALA	6.0
1	A	2815	VAL	5.7
1	A	2813	LEU	5.5
1	A	2761	GLY	5.2
1	A	2775	HIS	4.8
1	A	2785	ALA	4.7
1	A	2781	LEU	4.6
1	A	2757	LYS	4.6
1	A	2773	HIS	4.5
1	A	2791	THR	4.5
1	A	2786	LYS	4.2
1	A	2782	GLN	4.1
1	A	2751	GLY	3.9
1	A	2075	GLY	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	2779	VAL	3.9
1	A	2710	VAL	3.8
1	A	2767	GLN	3.8
1	A	2794	GLY	3.7
1	A	2516	LEU	3.7
1	A	2072	ALA	3.7
1	A	2065	LEU	3.7
1	A	2766	HIS	3.5
1	A	2073	LYS	3.3
1	A	2765	LEU	3.3
1	A	2597	LEU	3.2
1	A	2086	ARG	3.2
1	A	2759	LYS	3.1
1	A	2711	ALA	3.1
1	A	2512	ILE	3.1
1	A	2595	ASN	3.1
1	A	2793	ASN	3.1
1	A	2569	VAL	3.1
1	A	2811	ASP	3.1
1	A	2582	LEU	3.0
1	A	2727	LEU	3.0
1	A	2054	GLY	3.0
1	A	2578	VAL	3.0
1	A	2809	VAL	3.0
1	A	2189	GLY	3.0
1	A	2717	HIS	3.0
1	A	2660	LYS	2.9
1	A	2600	LEU	2.9
1	A	2798	LEU	2.9
1	A	2040	ARG	2.9
1	A	2806	TYR	2.9
1	A	1589	ASP	2.8
1	A	2789	ALA	2.7
1	A	2100	ALA	2.7
1	A	2587	ALA	2.7
1	A	2714	LEU	2.6
1	A	2699	LEU	2.6
1	A	2797	ALA	2.6
1	A	2704	GLN	2.6
1	A	2615	LEU	2.6
1	A	2055	ILE	2.6
1	A	2611	VAL	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	2105	SER	2.5
1	A	2090	VAL	2.5
1	A	2635	ILE	2.5
1	A	2800	ILE	2.5
1	A	2044	LEU	2.5
1	A	2117	VAL	2.4
1	A	2624	ALA	2.4
1	A	2152	ASN	2.4
1	A	1627	LEU	2.4
1	A	2772	GLY	2.3
1	A	2778	ASN	2.3
1	A	2068	LEU	2.3
1	A	2063	ASN	2.3
1	A	2630	TYR	2.3
1	A	2612	ALA	2.3
1	A	2726	LYS	2.3
1	A	1624	SER	2.2
1	A	2780	LEU	2.2
1	A	1586	ALA	2.2
1	A	1588	ILE	2.2
1	A	2545	VAL	2.1
1	A	2762	TYR	2.1
1	A	2505	SER	2.1
1	A	2801	ALA	2.1
1	A	2734	VAL	2.1
1	A	2531	TYR	2.1
1	A	2670	SER	2.1
1	A	2123	ILE	2.1
1	A	2668	LEU	2.1
1	A	2805	GLY	2.1
1	A	2671	GLN	2.0
1	A	2567	LEU	2.0
1	A	2735	ALA	2.0
1	A	2057	ILE	2.0

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

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](#)

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(\AA^2)	Q<0.9
2	SO4	A	2904	5/5	0.64	0.26	108,112,114,116	5
2	SO4	A	2907	5/5	0.69	0.17	142,143,145,148	0
2	SO4	A	2908	5/5	0.74	0.38	140,143,146,150	0
2	SO4	A	2905	5/5	0.81	0.18	121,125,128,130	0
2	SO4	A	2901	5/5	0.85	0.12	92,112,116,116	0
2	SO4	A	2903	5/5	0.90	0.19	100,101,110,113	0
2	SO4	A	2909	5/5	0.91	0.13	137,138,140,142	0
2	SO4	A	2902	5/5	0.93	0.12	93,100,102,104	0
2	SO4	A	2906	5/5	0.96	0.09	116,117,126,133	0

6.5 Other polymers [i](#)

There are no such residues in this entry.