



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:29 PM UTC

PDB ID : 1HM6 / pdb_00001hm6
Title : X-RAY STRUCTURE OF FULL-LENGTH ANNEXIN 1
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Deposited on : 2000-12-04
Resolution : 1.80 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

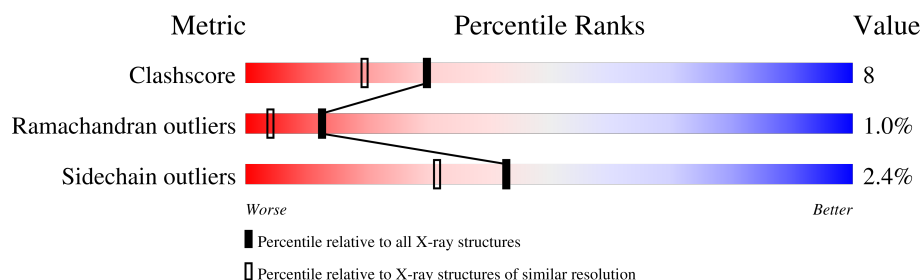
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	346	 79% 18% ..
1	B	346	 80% 18% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6191 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.

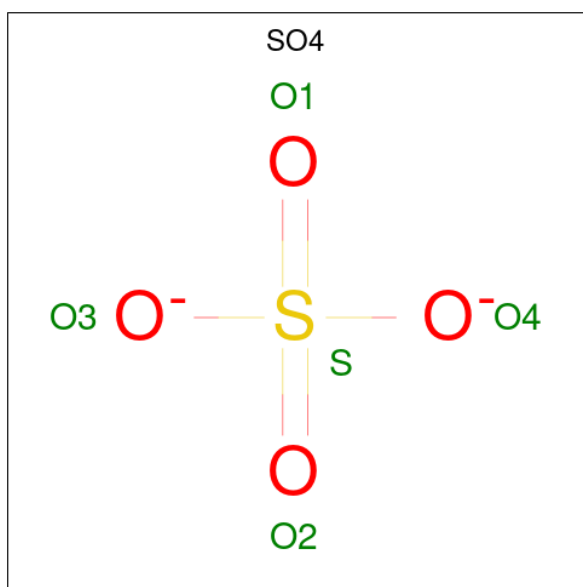
- Molecule 1 is a protein called ANNEXIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	0	0
			2696	1692	467	525	12			
1	B	343	Total	C	N	O	S	0	0	0
			2696	1692	467	525	12			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	SEE REMARK 999	UNP P19619
A	2	ALA	-	SEE REMARK 999	UNP P19619
A	3	MET	-	SEE REMARK 999	UNP P19619
A	4	VAL	-	SEE REMARK 999	UNP P19619
A	5	SER	-	SEE REMARK 999	UNP P19619
A	51	LEU	SER	SEE REMARK 999	UNP P19619
A	69	LEU	HIS	SEE REMARK 999	UNP P19619
A	231	PRO	LEU	SEE REMARK 999	UNP P19619
A	289	ILE	ASN	SEE REMARK 999	UNP P19619
B	1	MET	-	SEE REMARK 999	UNP P19619
B	2	ALA	-	SEE REMARK 999	UNP P19619
B	3	MET	-	SEE REMARK 999	UNP P19619
B	4	VAL	-	SEE REMARK 999	UNP P19619
B	5	SER	-	SEE REMARK 999	UNP P19619
B	51	LEU	SER	SEE REMARK 999	UNP P19619
B	69	LEU	HIS	SEE REMARK 999	UNP P19619
B	231	PRO	LEU	SEE REMARK 999	UNP P19619
B	289	ILE	ASN	SEE REMARK 999	UNP P19619

- 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	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	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

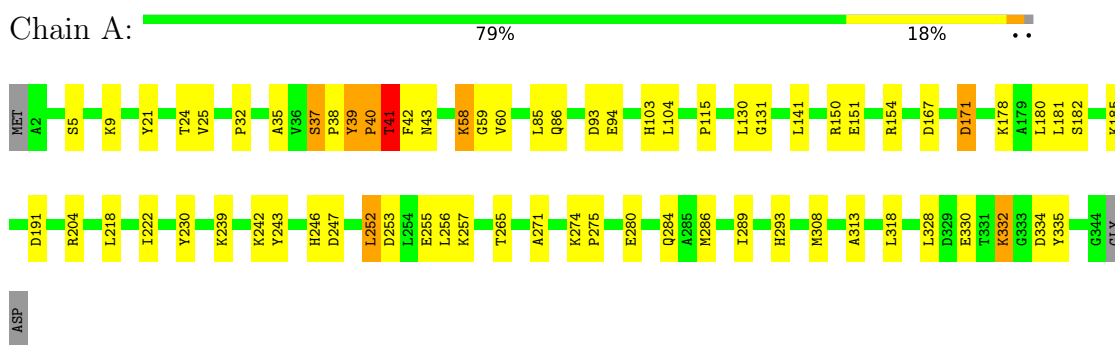
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	331	Total 331	O 331	0	0
3	B	408	Total 408	O 408	0	0

3 Residue-property plots

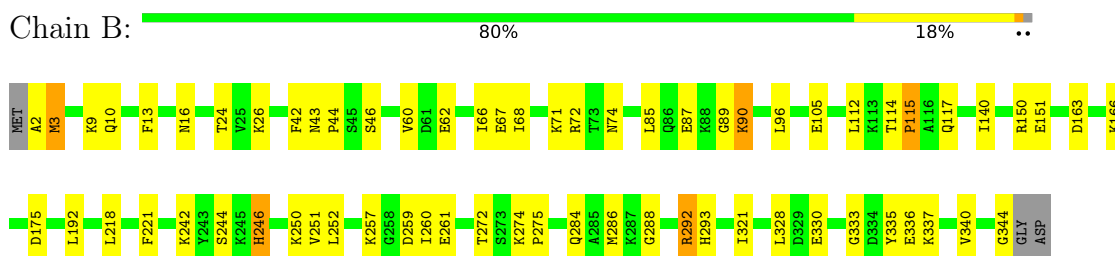
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: ANNEXIN 1



• Molecule 1: ANNEXIN 1



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.64Å 96.33Å 127.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.80	Depositor
% Data completeness (in resolution range)	93.0 (40.00-1.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.224 , 0.259	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6191	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

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	0.43	0/2731	1.01	10/3674 (0.3%)
1	B	0.39	0/2731	0.82	3/3674 (0.1%)
All	All	0.41	0/5462	0.92	13/7348 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	THR	CA-C-N	-17.91	95.59	122.09
1	A	41	THR	C-N-CA	-17.91	95.59	122.09
1	A	41	THR	CB-CA-C	-10.42	89.68	110.42
1	A	40	PRO	CB-CA-C	6.82	120.22	111.56
1	A	41	THR	O-C-N	-6.24	114.29	122.59
1	A	41	THR	CA-C-O	-6.14	111.73	120.51
1	A	42	PHE	CA-CB-CG	6.02	119.82	113.80
1	A	293	HIS	N-CA-C	5.81	117.29	111.07
1	A	43	ASN	CA-C-N	5.62	125.09	119.24
1	A	43	ASN	C-N-CA	5.62	125.09	119.24
1	B	16	ASN	N-CA-C	5.27	120.58	114.04
1	B	87	GLU	N-CA-C	5.18	116.73	111.14
1	B	140	ILE	N-CA-C	5.08	115.31	110.53

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	2696	0	2748	47	0
1	B	2696	0	2749	51	0
2	A	25	0	0	0	0
2	B	35	0	0	1	0
3	A	331	0	0	8	0
3	B	408	0	0	7	0
All	All	6191	0	5497	93	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 (93) 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:280:GLU:HG2	1:A:284:GLN:HE21	1.37	0.90
1:A:178:LYS:HE3	1:A:222:ILE:HD12	1.55	0.89
1:B:242:LYS:HA	1:B:242:LYS:HE2	1.57	0.85
1:A:182:SER:HA	1:A:185:LYS:HE2	1.70	0.74
1:A:280:GLU:HG2	1:A:284:GLN:NE2	2.06	0.70
1:A:239:LYS:O	1:A:242:LYS:HG2	1.95	0.66
1:B:175:ASP:OD1	1:B:218:LEU:HD12	1.96	0.66
1:A:39:TYR:N	1:A:40:PRO:CD	2.61	0.63
1:B:43:ASN:ND2	1:B:46:SER:H	1.98	0.61
1:B:96:LEU:HD12	1:B:112:LEU:HD11	1.83	0.61
1:A:58:LYS:HD3	1:A:59:GLY:N	2.16	0.61
1:B:292:ARG:HD2	1:B:292:ARG:N	2.14	0.61
1:B:43:ASN:HD22	1:B:46:SER:CB	2.15	0.60
1:B:3:MET:HE1	1:B:221:PHE:CD2	2.37	0.59
1:B:42:PHE:CZ	1:B:44:PRO:HG3	2.39	0.58
1:A:25:VAL:HG12	1:A:32:PRO:HG3	1.85	0.57
1:A:246:HIS:ND1	1:A:252:LEU:HD23	2.19	0.57
1:A:94:GLU:HG2	3:A:1003:HOH:O	2.05	0.57
1:B:246:HIS:ND1	1:B:251:VAL:HA	2.19	0.57
1:B:9:LYS:HG2	3:B:1213:HOH:O	2.05	0.57
1:A:191:ASP:HB3	3:A:1051:HOH:O	2.06	0.55
1:A:131:GLY:HA3	1:B:250:LYS:O	2.06	0.54
1:B:246:HIS:CE1	1:B:252:LEU:H	2.26	0.54
1:A:35:ALA:HB2	1:A:308:MET:HB3	1.91	0.53
1:B:328:LEU:HD23	1:B:328:LEU:C	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:TYR:N	1:A:40:PRO:HD2	2.24	0.52
1:A:289:ILE:HB	1:B:9:LYS:HD2	1.91	0.52
1:B:192:LEU:HD22	1:B:192:LEU:N	2.24	0.52
1:B:43:ASN:HD22	1:B:46:SER:H	1.56	0.52
1:B:3:MET:HG3	1:B:261:GLU:HG3	1.92	0.52
1:A:130:LEU:N	1:A:130:LEU:HD22	2.25	0.52
1:B:336:GLU:O	1:B:340:VAL:HG23	2.11	0.51
1:B:42:PHE:CE1	1:B:44:PRO:HG3	2.46	0.51
1:A:257:LYS:HD3	1:B:257:LYS:HD2	1.93	0.50
1:B:150:ARG:NH1	1:B:150:ARG:HB2	2.27	0.50
1:A:167:ASP:O	1:A:171:ASP:HB2	2.12	0.50
1:A:40:PRO:C	1:A:41:THR:HG23	2.38	0.49
1:A:37:SER:H	1:A:38:PRO:HD2	1.78	0.48
1:B:67:GLU:HG3	3:B:1115:HOH:O	2.14	0.48
1:B:244:SER:OG	1:B:246:HIS:NE2	2.46	0.48
1:B:328:LEU:HD23	1:B:328:LEU:O	2.13	0.48
1:A:24:THR:HG22	1:A:313:ALA:HB1	1.95	0.48
1:A:24:THR:HG21	3:A:882:HOH:O	2.14	0.48
1:A:328:LEU:HD12	3:A:1137:HOH:O	2.13	0.47
1:B:333:GLY:O	1:B:337:LYS:HD3	2.14	0.47
1:A:25:VAL:HG21	3:A:931:HOH:O	2.13	0.47
1:B:24:THR:HG21	3:B:1062:HOH:O	2.13	0.47
1:B:114:THR:OG1	1:B:117:GLN:HG3	2.13	0.47
3:A:1080:HOH:O	1:B:2:ALA:HB2	2.15	0.47
1:A:247:ASP:C	1:A:247:ASP:OD2	2.58	0.46
1:A:318:LEU:HD22	1:B:288:GLY:HA2	1.98	0.46
1:B:67:GLU:OE1	1:B:71:LYS:HG3	2.15	0.46
1:B:242:LYS:HA	1:B:242:LYS:CE	2.37	0.46
1:B:293:HIS:HB2	2:B:811:SO4:O1	2.16	0.46
1:A:150:ARG:HH11	1:A:150:ARG:HG3	1.81	0.45
1:A:246:HIS:CE1	1:A:252:LEU:HD23	2.52	0.45
1:B:293:HIS:HD2	1:B:335:TYR:OH	1.98	0.45
1:A:286:MET:HB3	1:A:330:GLU:HG3	1.98	0.45
1:B:344:GLY:HA2	3:B:1003:HOH:O	2.15	0.45
1:A:21:TYR:O	1:A:25:VAL:HG23	2.16	0.45
1:B:246:HIS:CE1	1:B:251:VAL:HA	2.52	0.44
1:B:284:GLN:NE2	3:B:905:HOH:O	2.49	0.44
1:B:286:MET:HB3	1:B:330:GLU:HG3	2.00	0.44
1:A:181:LEU:HD13	3:A:834:HOH:O	2.18	0.44
1:A:5:SER:O	1:A:9:LYS:HG3	2.17	0.43
1:A:218:LEU:HD21	1:A:256:LEU:HD21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:ASP:HB3	1:B:166:LYS:HB2	1.99	0.43
1:A:37:SER:HB3	1:A:38:PRO:HD3	2.01	0.43
1:B:43:ASN:HD22	1:B:46:SER:HB2	1.84	0.43
1:B:192:LEU:HD23	3:B:1173:HOH:O	2.17	0.43
1:B:321:ILE:HG21	3:B:903:HOH:O	2.18	0.43
1:A:104:LEU:HD22	1:A:334:ASP:HB3	2.00	0.42
1:B:89:GLY:O	1:B:90:LYS:HB3	2.19	0.42
1:B:10:GLN:OE1	1:B:272:THR:HG21	2.20	0.42
1:A:141:LEU:HD12	1:A:180:LEU:HD22	2.02	0.42
1:A:204:ARG:NE	1:A:243:TYR:OH	2.52	0.42
1:A:178:LYS:HE3	1:A:222:ILE:CD1	2.39	0.41
1:A:230:TYR:CG	1:A:271:ALA:HA	2.55	0.41
1:A:151:GLU:OE2	1:A:154:ARG:NH1	2.53	0.41
1:B:74:ASN:ND2	1:B:115:PRO:HD3	2.36	0.41
1:B:259:ASP:OD1	1:B:260:ILE:N	2.53	0.41
1:B:274:LYS:N	1:B:275:PRO:CD	2.83	0.41
1:B:68:ILE:O	1:B:72:ARG:HG2	2.21	0.41
1:B:71:LYS:HD3	1:B:71:LYS:HA	1.89	0.41
1:A:274:LYS:N	1:A:275:PRO:CD	2.84	0.40
1:A:103:HIS:HB3	1:A:335:TYR:CE1	2.56	0.40
1:A:253:ASP:C	1:A:255:GLU:H	2.28	0.40
1:A:289:ILE:HD13	1:B:13:PHE:HB2	2.02	0.40
1:A:93:ASP:OD2	1:A:94:GLU:N	2.54	0.40
1:A:332:LYS:HD3	1:A:332:LYS:N	2.36	0.40
1:B:62:GLU:O	1:B:66:ILE:HG13	2.21	0.40
1:B:151:GLU:OE1	1:B:151:GLU:HA	2.21	0.40
1:A:265:THR:HB	3:A:1084:HOH:O	2.20	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	341/346 (99%)	332 (97%)	5 (2%)	4 (1%)	10	3
1	B	341/346 (99%)	334 (98%)	4 (1%)	3 (1%)	14	5
All	All	682/692 (99%)	666 (98%)	9 (1%)	7 (1%)	12	4

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	VAL
1	B	60	VAL
1	B	246	HIS
1	A	41	THR
1	A	37	SER
1	B	90	LYS
1	A	39	TYR

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	292/294 (99%)	284 (97%)	8 (3%)	39	27
1	B	292/294 (99%)	286 (98%)	6 (2%)	47	36
All	All	584/588 (99%)	570 (98%)	14 (2%)	43	31

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	THR
1	A	58	LYS
1	A	85	LEU
1	A	86	GLN
1	A	115	PRO
1	A	171	ASP
1	A	252	LEU
1	A	332	LYS
1	B	3	MET

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Mol	Chain	Res	Type
1	B	26	LYS
1	B	85	LEU
1	B	105	GLU
1	B	115	PRO
1	B	292	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	19	GLN
1	A	86	GLN
1	A	284	GLN
1	A	309	ASN
1	B	16	ASN
1	B	43	ASN
1	B	79	GLN
1	B	86	GLN
1	B	177	GLN
1	B	284	GLN
1	B	293	HIS
1	B	309	ASN
1	B	316	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

12 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	803	-	4,4,4	0.40	0	6,6,6	0.05	0
2	SO4	B	812	-	4,4,4	0.37	0	6,6,6	0.08	0
2	SO4	B	807	-	4,4,4	0.38	0	6,6,6	0.12	0
2	SO4	A	804	-	4,4,4	0.38	0	6,6,6	0.07	0
2	SO4	B	800	-	4,4,4	0.38	0	6,6,6	0.09	0
2	SO4	B	811	-	4,4,4	0.38	0	6,6,6	0.08	0
2	SO4	B	802	-	4,4,4	0.37	0	6,6,6	0.10	0
2	SO4	A	806	-	4,4,4	0.38	0	6,6,6	0.06	0
2	SO4	B	808	-	4,4,4	0.38	0	6,6,6	0.07	0
2	SO4	A	805	-	4,4,4	0.37	0	6,6,6	0.15	0
2	SO4	A	801	-	4,4,4	0.38	0	6,6,6	0.06	0
2	SO4	B	809	-	4,4,4	0.38	0	6,6,6	0.09	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	811	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.