



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:19 AM UTC

PDB ID : 7SMD / pdb_00007smd
Title : p107 pocket domain complexed with EID1 peptide
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Deposited on : 2021-10-25
Resolution : 2.15 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

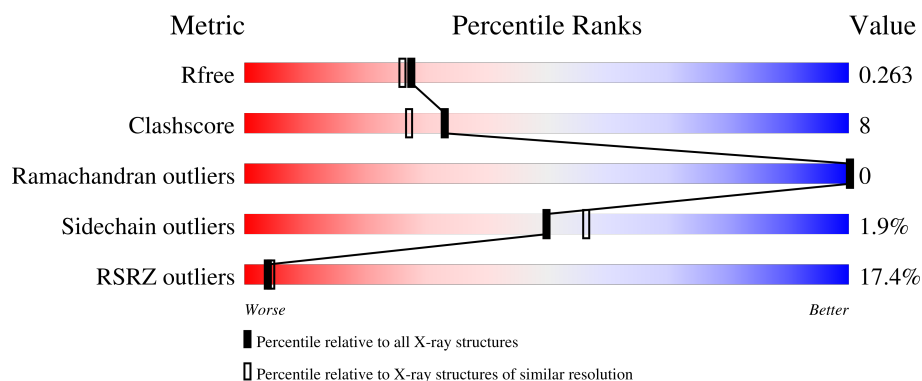
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	371	15% 74% 17% • 8%
2	B	14	57% 79% 21%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2950 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 Retinoblastoma-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	342	2774	1785	466	505	18	0	0	0

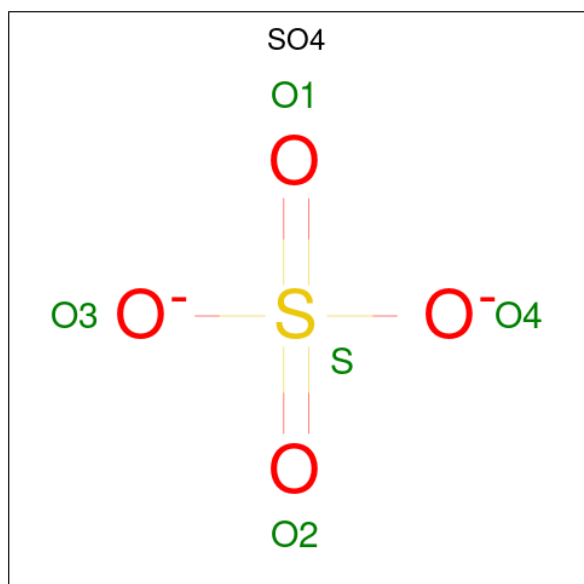
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	388	GLY	-	expression tag	UNP P28749
A	389	GLU	-	expression tag	UNP P28749
A	390	PHE	-	expression tag	UNP P28749

- Molecule 2 is a protein called EP300-interacting inhibitor of differentiation 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	14	108	65	17	25	1	0	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

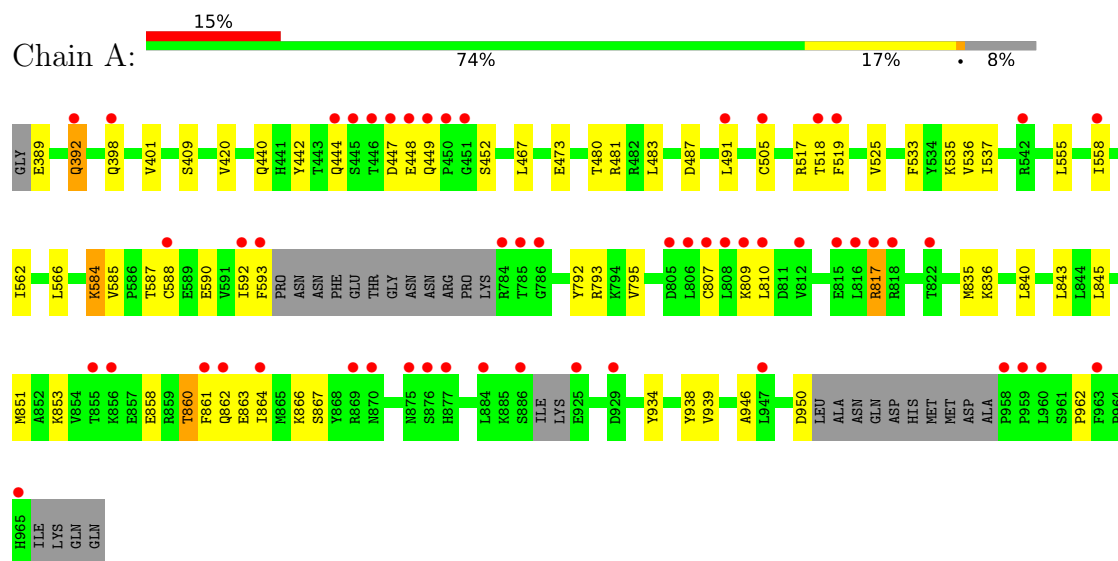
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total	O	0	0
			58	58		

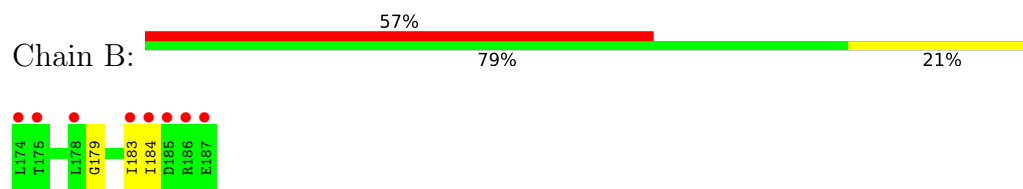
3 Residue-property plots [i](#)

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: Retinoblastoma-like protein 1



• Molecule 2: EP300-interacting inhibitor of differentiation 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	98.74Å 75.87Å 71.97Å 90.00° 108.48° 90.00°	Depositor
Resolution (Å)	33.92 – 2.15 33.92 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.92-2.15) 99.8 (33.92-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.227 , 0.259 0.230 , 0.263	Depositor DCC
R_{free} test set	1313 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.7	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	0.94	EDS
Total number of atoms	2950	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.54% 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	0.99	0/2834	1.43	11/3837 (0.3%)
2	B	0.98	0/107	1.35	0/143
All	All	0.98	0/2941	1.43	11/3980 (0.3%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	860	THR	CA-C-N	-7.40	110.36	120.28
1	A	860	THR	C-N-CA	-7.40	110.36	120.28
1	A	517	ARG	CA-C-N	6.97	130.71	120.95
1	A	517	ARG	C-N-CA	6.97	130.71	120.95
1	A	392	GLN	CA-C-N	6.16	129.04	120.29
1	A	392	GLN	C-N-CA	6.16	129.04	120.29
1	A	836	LYS	O-C-N	5.72	130.05	123.02
1	A	535	LYS	CA-C-N	5.64	129.56	120.30
1	A	535	LYS	C-N-CA	5.64	129.56	120.30
1	A	584	LYS	O-C-N	5.46	129.49	122.93
1	A	525	VAL	O-C-N	5.34	127.05	121.87

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	2774	0	2747	45	0
2	B	108	0	99	3	0
3	A	10	0	0	0	0
4	A	58	0	0	0	0
All	All	2950	0	2846	45	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 (45) 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:440:GLN:O	1:A:444:GLN:HG2	1.49	1.13
1:A:587:THR:OG1	1:A:590:GLU:HG3	1.71	0.90
1:A:440:GLN:O	1:A:444:GLN:CG	2.20	0.89
1:A:420:VAL:HG23	1:A:487:ASP:OD1	1.94	0.68
1:A:793:ARG:HH11	1:A:793:ARG:HG2	1.68	0.58
1:A:862:GLN:NE2	2:B:183:ILE:O	2.37	0.58
1:A:518:THR:HG22	1:A:519:PHE:O	2.05	0.56
1:A:555:LEU:O	1:A:558:ILE:HG12	2.06	0.56
1:A:585:VAL:HG13	1:A:792:TYR:CZ	2.40	0.56
1:A:592:ILE:HD11	1:A:593:PHE:CE2	2.41	0.56
1:A:793:ARG:HG2	1:A:793:ARG:NH1	2.21	0.55
1:A:835:MET:SD	1:A:843:LEU:HD22	2.47	0.55
1:A:442:TYR:CE1	1:A:452:SER:HB3	2.42	0.54
1:A:533:PHE:O	1:A:536:VAL:HG12	2.07	0.54
1:A:481:ARG:HD3	1:A:491:LEU:HD11	1.91	0.53
1:A:480:THR:HA	1:A:483:LEU:HD12	1.89	0.53
1:A:592:ILE:HD11	1:A:962:PRO:HB2	1.91	0.53
1:A:934:TYR:O	1:A:939:VAL:HG23	2.08	0.52
1:A:853:LYS:HA	1:A:858:GLU:HG3	1.93	0.51
1:A:389:GLU:HA	1:A:389:GLU:OE1	2.11	0.50
1:A:392:GLN:H	1:A:392:GLN:CD	2.19	0.50
1:A:809:LYS:O	1:A:810:LEU:HD23	2.12	0.50
1:A:420:VAL:HG23	1:A:487:ASP:CG	2.37	0.50
1:A:409:SER:OG	1:A:473:GLU:OE1	2.29	0.48
1:A:934:TYR:HA	1:A:938:TYR:HB3	1.95	0.48
1:A:861:PHE:O	1:A:862:GLN:C	2.57	0.46
1:A:934:TYR:CZ	1:A:939:VAL:HG22	2.51	0.45
1:A:851:MET:SD	1:A:946:ALA:HB1	2.57	0.44
1:A:398:GLN:HA	1:A:401:VAL:HG22	1.99	0.44
1:A:845:LEU:HD22	1:A:864:ILE:CG2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:588:CYS:SG	1:A:592:ILE:HG21	2.59	0.43
1:A:584:LYS:HD2	1:A:584:LYS:HA	1.85	0.43
1:A:537:ILE:HG23	1:A:555:LEU:HB3	2.00	0.42
1:A:950:ASP:OD1	1:A:950:ASP:C	2.62	0.42
1:A:795:VAL:HG13	1:A:840:LEU:HD21	2.01	0.42
1:A:862:GLN:NE2	2:B:184:ILE:HB	2.35	0.42
1:A:807:CYS:SG	1:A:817:ARG:HB2	2.60	0.42
1:A:592:ILE:HG13	1:A:593:PHE:CD2	2.55	0.42
1:A:562:ILE:HA	1:A:566:LEU:HB2	2.01	0.41
1:A:845:LEU:HD22	1:A:864:ILE:HG22	2.01	0.41
1:A:853:LYS:NZ	2:B:179:GLY:O	2.53	0.41
1:A:440:GLN:O	1:A:444:GLN:HG3	2.15	0.41
1:A:467:LEU:HB3	1:A:505:CYS:SG	2.60	0.41
1:A:860:THR:OG1	1:A:863:GLU:HG3	2.21	0.41
1:A:587:THR:HG1	1:A:590:GLU:HG3	1.80	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	334/371 (90%)	326 (98%)	8 (2%)	0	100	100
2	B	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
All	All	346/385 (90%)	337 (97%)	9 (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	A	309/342 (90%)	303 (98%)	6 (2%)	50	56
2	B	12/13 (92%)	12 (100%)	0	100	100
All	All	321/355 (90%)	315 (98%)	6 (2%)	50	56

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	447	ASP
1	A	448	GLU
1	A	449	GLN
1	A	817	ARG
1	A	866	LYS
1	A	867	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	411	GLN
1	A	440	GLN
1	A	814	ASN

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](#)

2 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	$\# Z > 2$
3	SO4	A	1001	-	4,4,4	0.39	0	6,6,6	0.09	0
3	SO4	A	1002	-	4,4,4	0.51	0	6,6,6	0.13	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

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	342/371 (92%)	0.91	54 (15%) 5 5	31, 50, 79, 104	0
2	B	14/14 (100%)	2.54	8 (57%) 0 0	67, 73, 101, 104	0
All	All	356/385 (92%)	0.97	62 (17%) 4 4	31, 51, 80, 104	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	184	ILE	6.7
1	A	886	SER	5.5
1	A	593	PHE	5.2
2	B	187	GLU	5.1
1	A	450	PRO	4.8
1	A	808	LEU	4.5
1	A	861	PHE	4.3
1	A	959	PRO	4.3
1	A	784	ARG	3.9
2	B	183	ILE	3.8
1	A	815	GLU	3.6
1	A	805	ASP	3.6
1	A	518	THR	3.5
1	A	958	PRO	3.5
1	A	875	ASN	3.5
1	A	446	THR	3.5
1	A	965	HIS	3.3
2	B	174	LEU	3.2
1	A	588	CYS	3.2
1	A	877	HIS	3.1
1	A	448	GLU	3.0
1	A	392	GLN	3.0
1	A	806	LEU	3.0
1	A	960	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	869	ARG	2.9
1	A	542	ARG	2.9
1	A	449	GLN	2.8
2	B	175	THR	2.8
1	A	862	GLN	2.8
1	A	818	ARG	2.7
1	A	785	THR	2.7
1	A	592	ILE	2.7
1	A	444	GLN	2.6
2	B	178	LEU	2.6
1	A	925	GLU	2.6
2	B	185	ASP	2.5
1	A	876	SER	2.5
1	A	817	ARG	2.5
1	A	558	ILE	2.5
1	A	447	ASP	2.4
1	A	807	CYS	2.4
1	A	963	PHE	2.3
1	A	809	LYS	2.3
1	A	398	GLN	2.3
1	A	870	ASN	2.3
1	A	929	ASP	2.3
1	A	812	VAL	2.3
1	A	855	THR	2.2
1	A	856	LYS	2.2
1	A	810	LEU	2.2
1	A	519	PHE	2.2
1	A	451	GLY	2.2
2	B	186	ARG	2.2
1	A	864	ILE	2.1
1	A	786	GLY	2.1
1	A	491	LEU	2.1
1	A	884	LEU	2.1
1	A	947	LEU	2.1
1	A	505	CYS	2.1
1	A	816	LEU	2.0
1	A	822	THR	2.0
1	A	445	SER	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 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	SO4	A	1001	5/5	0.79	0.11	64,69,84,86	0
3	SO4	A	1002	5/5	0.95	0.12	47,48,57,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.