



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 03:30 AM UTC

PDB ID : 5FYT / pdb_00005fyt
Title : Crystal structure of the catalytic domain of human JARID1B in complex with 3D fragment (5-fluoro-2-oxo-2,3-dihydro-1H-indol-3-yl)acetic acid (N09996a)
Authors : Nowak, R.; Krojer, T.; Johansson, C.; Pearce, N.; Gileadi, C.; Kupinska, K.; Strain-Damerell, C.; Szykowska, A.; Burgess-Brown, N.A.; Arrowsmith, C.H.; Bountra, C.; Edwards, A.M.; von Delft, F.; Brennan, P.E.; Oppermann, U.
Deposited on : 2016-03-09
Resolution : 1.87 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

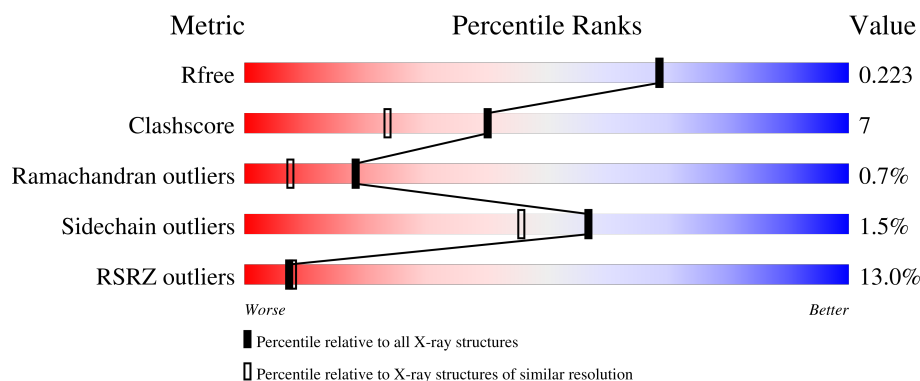
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.87 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	1220 (1.88-1.88)
Clashscore	190562	1234 (1.88-1.88)
Ramachandran outliers	187476	1222 (1.88-1.88)
Sidechain outliers	187428	1222 (1.88-1.88)
RSRZ outliers	180081	1220 (1.88-1.88)

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	479	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 4207 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 LYSINE-SPECIFIC DEMETHYLASE 5B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	455	Total	C	N	O	S	0	8	0
			3739	2405	622	673	39			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP Q9UGL1
A	0	MET	-	expression tag	UNP Q9UGL1
A	102	GLY	-	linker	UNP Q9UGL1
A	103	GLY	-	linker	UNP Q9UGL1
A	104	GLY	-	linker	UNP Q9UGL1
A	105	GLY	-	linker	UNP Q9UGL1

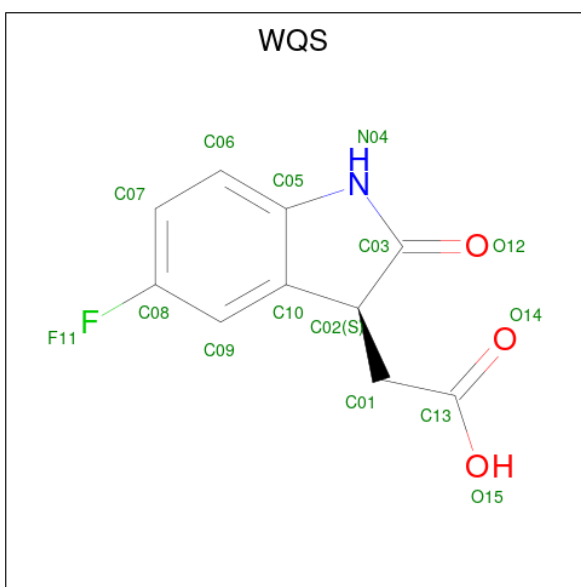
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

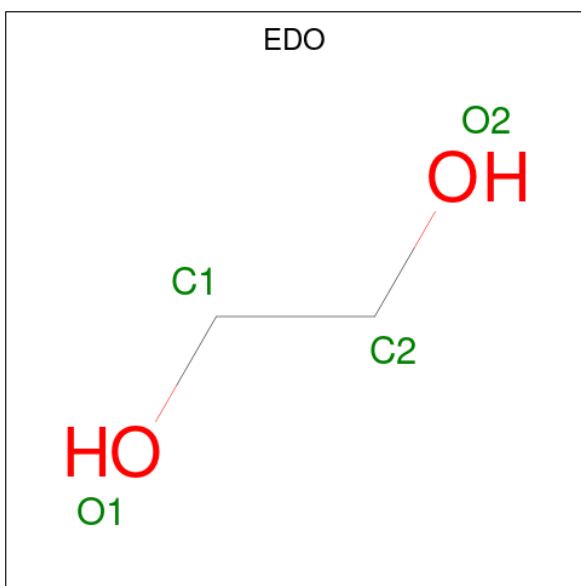
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mn	0	0
			1	1		

- Molecule 4 is 2-[(3S)-5-fluoranyl-2-oxidanylidene-1,3-dihydroindol-3-yl]ethanoic acid (CCD ID: WQS) (formula: C₁₀H₈FNO₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	0	0
			15	10	1	1	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



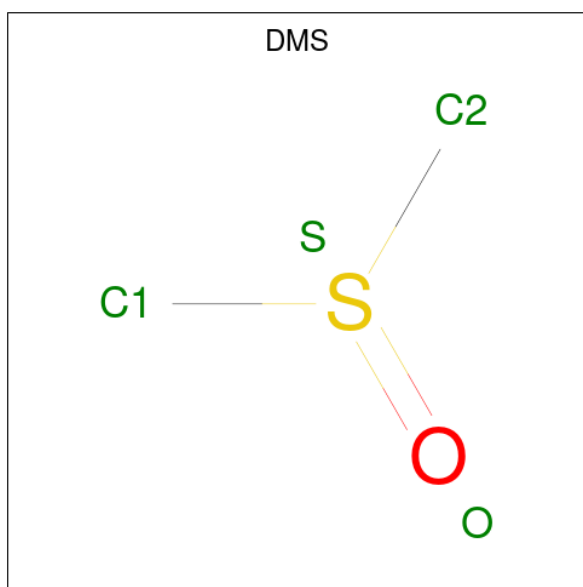
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		

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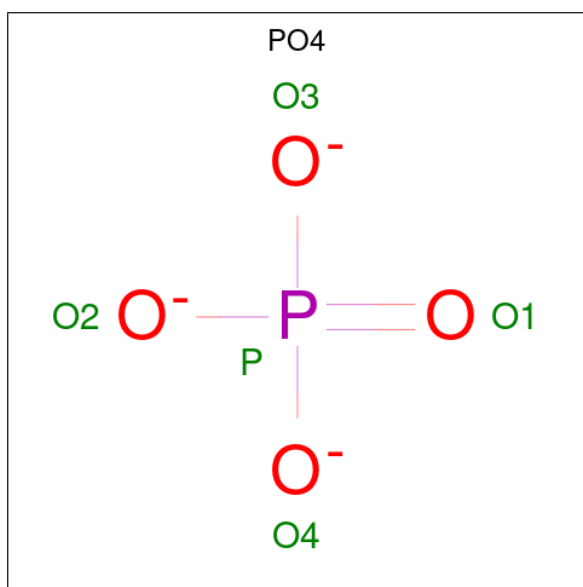
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total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

- Molecule 6 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



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

- Molecule 7 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

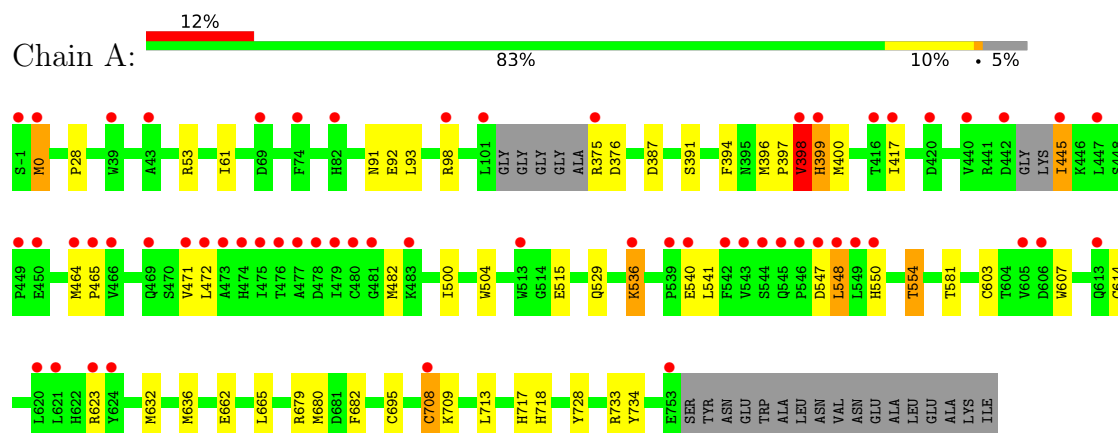
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	360	Total 360	O 360	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 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: LYSINE-SPECIFIC DEMETHYLASE 5B



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	141.81Å 141.81Å 151.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	70.91 – 1.87 70.91 – 1.87	Depositor EDS
% Data completeness (in resolution range)	100.0 (70.91-1.87) 92.5 (70.91-1.87)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 1.87Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.188 , 0.222 0.194 , 0.223	Depositor DCC
R_{free} test set	3808 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4207	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: ZN, DMS, WQS, CL, MN, EDO, PO4

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	0.47	0/3852	0.75	1/5235 (0.0%)

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 (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	554	THR	N-CA-C	5.07	116.78	109.07

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	398	VAL	Peptide

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	3739	0	3594	47	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	15	0	0	1	0
5	A	72	0	108	10	0
6	A	12	0	18	0	0
7	A	5	0	0	0	0
8	A	1	0	0	1	0
9	A	360	0	0	16	1
All	All	4207	0	3720	50	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 7.

All (50) 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)
4:A:1757:WQS:N04	9:A:2216:HOH:O	1.94	0.99
1:A:662:GLU:OE1	5:A:1769:EDO:O2	2.04	0.76
1:A:733:ARG:HH22	5:A:1767:EDO:H11	1.58	0.68
1:A:376:ASP:OD1	9:A:2062:HOH:O	2.13	0.67
1:A:417:ILE:O	9:A:2144:HOH:O	2.15	0.65
1:A:387:ASP:HB3	5:A:1765:EDO:H11	1.82	0.62
1:A:504:TRP:CD1	1:A:614:CYS:HG	2.19	0.60
1:A:398:VAL:HG13	1:A:399:HIS:ND1	2.18	0.58
1:A:0:MET:O	9:A:2001:HOH:O	2.18	0.57
1:A:665:LEU:HD13	5:A:1769:EDO:H11	1.86	0.56
1:A:717:HIS:HE1	9:A:2258:HOH:O	1.89	0.55
1:A:417:ILE:H	1:A:417:ILE:HD12	1.73	0.54
1:A:680:MET:HE2	1:A:682:PHE:CE2	2.43	0.54
1:A:98[B]:ARG:NH1	9:A:2089:HOH:O	2.40	0.53
1:A:397:PRO:O	1:A:399:HIS:N	2.38	0.53
5:A:1769:EDO:H21	9:A:2355:HOH:O	2.07	0.53
1:A:53:ARG:NH1	9:A:2030:HOH:O	2.41	0.52
1:A:391:SER:HB2	1:A:398:VAL:HB	1.93	0.50
1:A:540:GLU:CD	1:A:540:GLU:H	2.20	0.50
1:A:547:ASP:HB2	1:A:550:HIS:ND1	2.27	0.49
5:A:1774:EDO:O1	9:A:2358:HOH:O	2.19	0.49
1:A:679:ARG:HE	5:A:1772:EDO:H12	1.77	0.49
1:A:397:PRO:HB2	1:A:400:MET:HE3	1.94	0.49
1:A:515:GLU:HG3	9:A:2134:HOH:O	2.14	0.48
1:A:394:PHE:HB3	1:A:396:MET:HE3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:728:TYR:HB3	9:A:2300:HOH:O	2.15	0.47
1:A:0:MET:HE1	9:A:2141:HOH:O	2.15	0.46
1:A:92:GLU:HG2	1:A:93:LEU:HG	1.98	0.46
1:A:708:CYS:SG	1:A:709:LYS:HG2	2.56	0.46
1:A:464:MET:HE2	1:A:464:MET:HB2	1.90	0.46
1:A:541:LEU:HD11	1:A:554:THR:HB	1.97	0.45
1:A:398:VAL:HG22	1:A:398:VAL:O	2.17	0.45
1:A:399:HIS:CE1	9:A:2115:HOH:O	2.69	0.45
1:A:713:LEU:HD21	5:A:1780:EDO:H22	1.99	0.45
1:A:28:PRO:O	5:A:1768:EDO:O2	2.35	0.44
1:A:695:CYS:HB3	1:A:718:HIS:CE1	2.52	0.44
1:A:536:LYS:HD2	1:A:536:LYS:HA	1.77	0.44
1:A:632[B]:MET:SD	1:A:636:MET:HE2	2.57	0.44
1:A:98[A]:ARG:NH2	1:A:500:ILE:O	2.48	0.44
1:A:529:GLN:HG3	9:A:2220:HOH:O	2.17	0.44
1:A:465:PRO:HA	9:A:2174:HOH:O	2.17	0.43
1:A:375:ARG:N	9:A:2098:HOH:O	2.51	0.43
1:A:445:ILE:HD13	1:A:445:ILE:HA	1.91	0.42
1:A:91:ASN:OD1	8:A:1779:CL:CL	2.74	0.42
1:A:61:ILE:HG22	1:A:581:THR:HG22	2.02	0.42
1:A:603:CYS:HB3	1:A:607:TRP:CE3	2.54	0.41
1:A:464:MET:N	1:A:465:PRO:HD2	2.36	0.41
1:A:734:TYR:CE1	5:A:1759:EDO:H21	2.56	0.40
1:A:548:LEU:HD23	1:A:623:ARG:HH12	1.86	0.40
1:A:472:LEU:HD11	1:A:482:MET:HE2	2.02	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)
9:A:2159:HOH:O	9:A:2209:HOH:O[9_765]	2.19	0.01

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	457/479 (95%)	444 (97%)	10 (2%)	3 (1%)	18 7

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	398	VAL
1	A	0	MET
1	A	399	HIS

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	411/427 (96%)	405 (98%)	6 (2%)	57 46

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

Mol	Chain	Res	Type
1	A	398	VAL
1	A	445	ILE
1	A	471	VAL
1	A	536	LYS
1	A	548	LEU
1	A	708	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	462	ASN

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 ⓘ

Of 27 ligands modelled in this entry, 4 are monoatomic - leaving 23 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	$\# Z > 2$
5	EDO	A	1771	-	3,3,3	0.41	0	2,2,2	0.46	0
5	EDO	A	1768	-	3,3,3	0.44	0	2,2,2	0.47	0
5	EDO	A	1773	-	3,3,3	0.45	0	2,2,2	0.58	0
5	EDO	A	1763	-	3,3,3	0.44	0	2,2,2	0.35	0
5	EDO	A	1762	-	3,3,3	0.54	0	2,2,2	0.18	0
5	EDO	A	1767	-	3,3,3	0.48	0	2,2,2	0.33	0
5	EDO	A	1769	-	3,3,3	0.26	0	2,2,2	0.78	0
4	WQS	A	1757	3	16,16,16	3.84	6 (37%)	20,23,23	4.92	9 (45%)
5	EDO	A	1759	-	3,3,3	0.36	0	2,2,2	0.73	0
6	DMS	A	1776	-	3,3,3	0.67	0	3,3,3	0.37	0
5	EDO	A	1774	-	3,3,3	0.48	0	2,2,2	0.47	0
5	EDO	A	1761	-	3,3,3	0.50	0	2,2,2	0.18	0
5	EDO	A	1765	-	3,3,3	0.43	0	2,2,2	0.36	0
7	PO4	A	1778	-	4,4,4	0.90	0	6,6,6	0.48	0
5	EDO	A	1772	-	3,3,3	0.46	0	2,2,2	0.40	0
5	EDO	A	1760	-	3,3,3	0.43	0	2,2,2	0.76	0
5	EDO	A	1770	-	3,3,3	0.43	0	2,2,2	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	A	1780	-	3,3,3	0.48	0	2,2,2	0.23	0
5	EDO	A	1758	-	3,3,3	0.44	0	2,2,2	0.44	0
6	DMS	A	1775	-	3,3,3	0.67	0	3,3,3	0.22	0
5	EDO	A	1766	-	3,3,3	0.45	0	2,2,2	0.36	0
6	DMS	A	1777	-	3,3,3	0.68	0	3,3,3	0.26	0
5	EDO	A	1764	-	3,3,3	0.47	0	2,2,2	0.28	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
5	EDO	A	1771	-	-	0/1/1/1	-
5	EDO	A	1768	-	-	0/1/1/1	-
5	EDO	A	1773	-	-	0/1/1/1	-
5	EDO	A	1763	-	-	0/1/1/1	-
5	EDO	A	1762	-	-	1/1/1/1	-
5	EDO	A	1767	-	-	0/1/1/1	-
5	EDO	A	1769	-	-	1/1/1/1	-
4	WQS	A	1757	3	-	2/4/16/16	0/2/2/2
5	EDO	A	1759	-	-	1/1/1/1	-
5	EDO	A	1774	-	-	0/1/1/1	-
5	EDO	A	1761	-	-	0/1/1/1	-
5	EDO	A	1765	-	-	1/1/1/1	-
5	EDO	A	1772	-	-	0/1/1/1	-
5	EDO	A	1760	-	-	1/1/1/1	-
5	EDO	A	1770	-	-	0/1/1/1	-
5	EDO	A	1780	-	-	0/1/1/1	-
5	EDO	A	1758	-	-	0/1/1/1	-
5	EDO	A	1766	-	-	0/1/1/1	-
5	EDO	A	1764	-	-	0/1/1/1	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1757	WQS	C05-C10	9.15	1.48	1.39
4	A	1757	WQS	C02-C03	-7.96	1.37	1.52
4	A	1757	WQS	C05-N04	7.35	1.52	1.38
4	A	1757	WQS	C07-C08	3.30	1.43	1.37
4	A	1757	WQS	C03-N04	-2.98	1.33	1.35
4	A	1757	WQS	C09-C08	2.41	1.41	1.37

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1757	WQS	C02-C03-N04	15.41	117.89	108.02
4	A	1757	WQS	C05-N04-C03	-9.43	106.01	111.81
4	A	1757	WQS	C10-C05-N04	-6.05	105.66	109.37
4	A	1757	WQS	C10-C02-C03	5.82	104.30	102.40
4	A	1757	WQS	O12-C03-N04	-5.62	121.09	125.96
4	A	1757	WQS	O12-C03-C02	-5.23	120.96	126.72
4	A	1757	WQS	O15-C13-C01	2.21	120.87	114.00
4	A	1757	WQS	C07-C08-C09	-2.17	120.37	123.23
4	A	1757	WQS	C06-C07-C08	2.03	120.46	118.38

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1765	EDO	O1-C1-C2-O2
4	A	1757	WQS	C02-C01-C13-O15
5	A	1759	EDO	O1-C1-C2-O2
5	A	1762	EDO	O1-C1-C2-O2
4	A	1757	WQS	C02-C01-C13-O14
5	A	1760	EDO	O1-C1-C2-O2
5	A	1769	EDO	O1-C1-C2-O2

There are no ring outliers.

9 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1768	EDO	1	0
5	A	1767	EDO	1	0
5	A	1769	EDO	3	0
4	A	1757	WQS	1	0
5	A	1759	EDO	1	0
5	A	1774	EDO	1	0
5	A	1765	EDO	1	0
5	A	1772	EDO	1	0
5	A	1780	EDO	1	0

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	455/479 (94%)	0.65	59 (12%) 7 8	15, 37, 65, 96	8 (1%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	399	HIS	8.3
1	A	39[A]	TRP	7.4
1	A	543	VAL	6.6
1	A	445	ILE	6.5
1	A	398	VAL	6.1
1	A	101	LEU	5.7
1	A	74	PHE	5.7
1	A	546	PRO	5.6
1	A	417	ILE	5.3
1	A	480	CYS	5.3
1	A	548	LEU	5.2
1	A	466	VAL	5.1
1	A	478	ASP	4.9
1	A	474	HIS	4.8
1	A	549	LEU	4.8
1	A	-1	SER	4.8
1	A	476	THR	4.7
1	A	545	GLN	4.5
1	A	513	TRP	4.3
1	A	544	SER	4.2
1	A	465	PRO	4.1
1	A	547	ASP	4.0
1	A	98[A]	ARG	3.9
1	A	82[A]	HIS	3.7
1	A	464	MET	3.5
1	A	477	ALA	3.5
1	A	447	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	442	ASP	3.3
1	A	472	LEU	3.3
1	A	623	ARG	3.2
1	A	0	MET	3.2
1	A	475	ILE	3.1
1	A	416	THR	3.1
1	A	542	PHE	3.1
1	A	479	ILE	2.9
1	A	708	CYS	2.8
1	A	620	LEU	2.8
1	A	375	ARG	2.8
1	A	536	LYS	2.8
1	A	539	PRO	2.7
1	A	624	TYR	2.6
1	A	450	GLU	2.6
1	A	471	VAL	2.5
1	A	550	HIS	2.5
1	A	420	ASP	2.4
1	A	449	PRO	2.4
1	A	613[A]	GLN	2.3
1	A	606	ASP	2.3
1	A	473	ALA	2.3
1	A	481	GLY	2.2
1	A	605	VAL	2.2
1	A	69	ASP	2.2
1	A	753	GLU	2.1
1	A	469	GLN	2.1
1	A	43	ALA	2.1
1	A	621	LEU	2.1
1	A	540	GLU	2.0
1	A	483	LYS	2.0
1	A	440	VAL	2.0

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
5	EDO	A	1772	4/4	0.77	0.22	54,58,64,64	0
5	EDO	A	1767	4/4	0.78	0.20	66,66,68,68	0
8	CL	A	1779	1/1	0.78	0.19	56,56,56,56	0
5	EDO	A	1774	4/4	0.79	0.25	43,56,57,66	0
7	PO4	A	1778	5/5	0.80	0.12	55,63,80,83	0
5	EDO	A	1770	4/4	0.86	0.17	49,56,56,62	0
5	EDO	A	1765	4/4	0.87	0.16	42,52,58,66	0
5	EDO	A	1763	4/4	0.88	0.14	51,54,57,60	0
5	EDO	A	1771	4/4	0.88	0.21	65,68,69,73	0
5	EDO	A	1769	4/4	0.88	0.31	33,38,46,47	0
5	EDO	A	1768	4/4	0.89	0.15	53,56,58,58	0
5	EDO	A	1761	4/4	0.89	0.16	45,52,58,69	0
5	EDO	A	1780	4/4	0.91	0.14	45,49,57,60	0
5	EDO	A	1773	4/4	0.91	0.16	29,30,51,70	0
5	EDO	A	1766	4/4	0.91	0.14	53,55,56,67	0
5	EDO	A	1759	4/4	0.92	0.15	42,43,48,57	0
6	DMS	A	1775	4/4	0.92	0.18	52,57,62,71	0
5	EDO	A	1760	4/4	0.94	0.16	39,47,48,56	0
5	EDO	A	1758	4/4	0.94	0.12	34,38,40,49	0
5	EDO	A	1762	4/4	0.94	0.14	35,40,43,44	0
4	WQS	A	1757	15/15	0.96	0.08	25,28,37,44	15
5	EDO	A	1764	4/4	0.97	0.09	32,34,37,40	0
6	DMS	A	1776	4/4	0.98	0.11	34,38,39,40	0
6	DMS	A	1777	4/4	0.98	0.07	25,32,35,35	0
2	ZN	A	1754	1/1	0.99	0.03	29,29,29,29	0
2	ZN	A	1755	1/1	0.99	0.06	47,47,47,47	1
3	MN	A	1756	1/1	1.00	0.02	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.