



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:23 PM UTC

PDB ID : 5F2S / pdb\_00005f2s  
Title : Crystal structure of human KDM4A in complex with compound 15  
Authors : Le Bihan, Y.-V.; Dempster, S.; Westwood, I.M.; van Montfort, R.L.M.  
Deposited on : 2015-12-02  
Resolution : 2.08 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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)  
Xtrriage (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

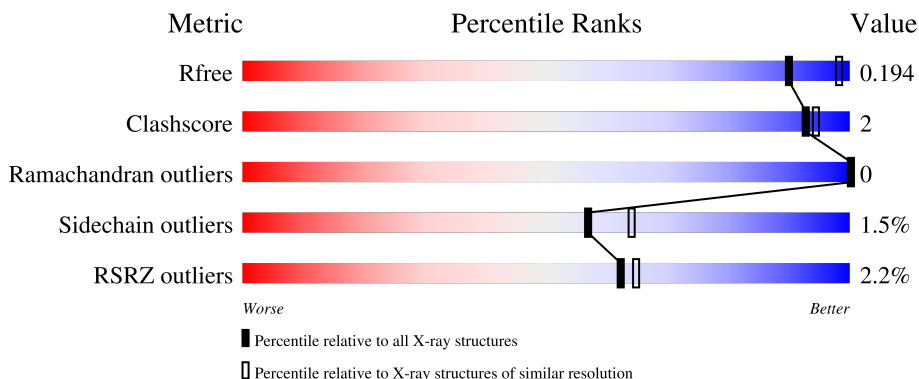
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.08 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	8172 (2.10-2.06)
Clashscore	190562	8714 (2.10-2.06)
Ramachandran outliers	187476	8641 (2.10-2.06)
Sidechain outliers	187428	8642 (2.10-2.06)
RSRZ outliers	180081	8177 (2.10-2.06)

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  $\geq 3$ , 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	360	 3% 88% 7% 5%
1	B	360	 0% 93% 5% .
1	C	360	 2% 92% 5% .
1	D	360	 2% 91% 6% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	D	406	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12312 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 4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	342	Total 2716	C 1769	N 442	O 491	S 14	0	3	0
1	B	352	Total 2819	C 1831	N 463	O 509	S 16	0	1	0
1	C	347	Total 2777	C 1809	N 451	O 501	S 16	0	4	0
1	D	349	Total 2828	C 1833	N 475	O 505	S 15	0	3	0

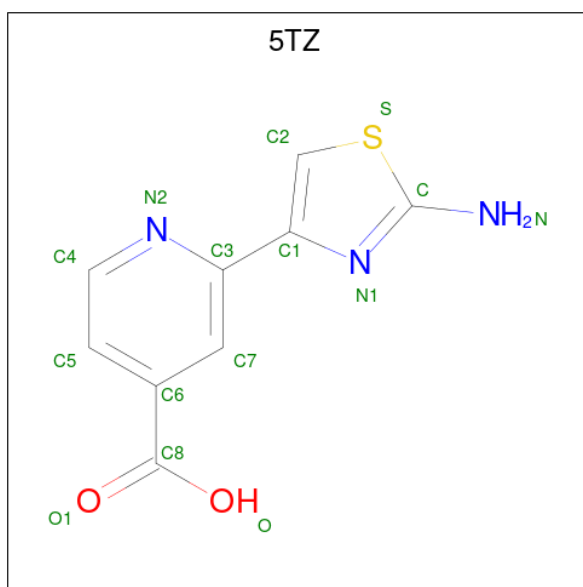
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O75164
B	0	SER	-	expression tag	UNP O75164
C	0	SER	-	expression tag	UNP O75164
D	0	SER	-	expression tag	UNP O75164

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total 2	Zn 2	0	0
2	B	2	Total 2	Zn 2	0	0
2	C	2	Total 2	Zn 2	0	0
2	D	2	Total 2	Zn 2	0	0

- Molecule 3 is 2-(2-azanyl-1,3-thiazol-4-yl)pyridine-4-carboxylic acid (CCD ID: 5TZ) (formula: C<sub>9</sub>H<sub>7</sub>N<sub>3</sub>O<sub>2</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	Total	C	N	O	S	0	0
			15	9	3	2	1		
3	B	1	Total	C	N	O	S	0	0
			15	9	3	2	1		
3	C	1	Total	C	N	O	S	0	0
			15	9	3	2	1		
3	D	1	Total	C	N	O	S	0	0
			15	9	3	2	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



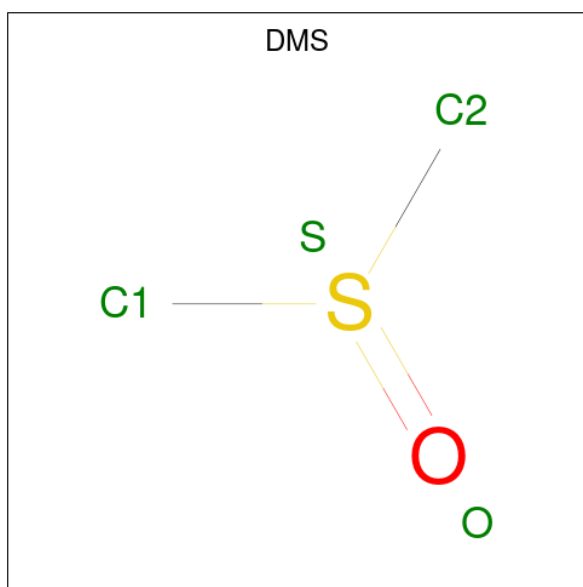
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0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

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

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	1	Total	Cl	0	0
			1	1		

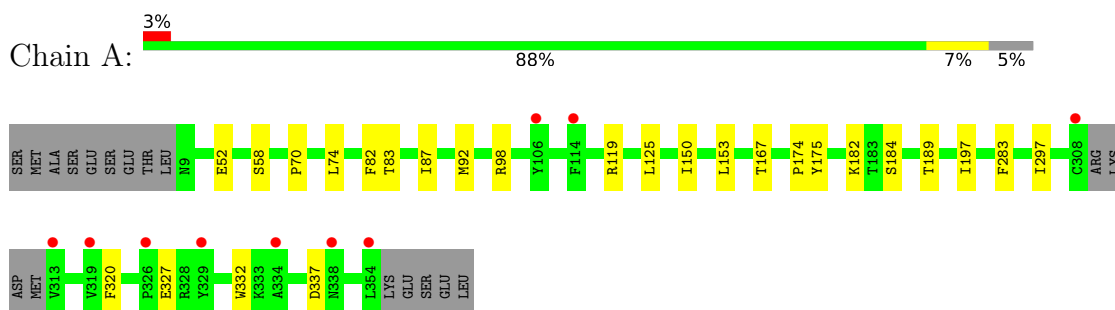
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	170	Total	O	0	0
			170	170		
7	B	253	Total	O	0	0
			253	253		
7	C	229	Total	O	0	0
			229	229		
7	D	287	Total	O	0	0
			287	287		

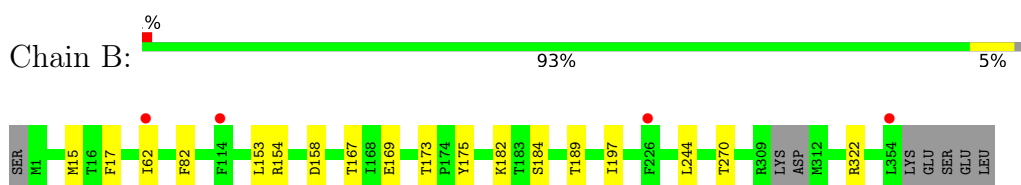
### 3 Residue-property plots [i](#)

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.

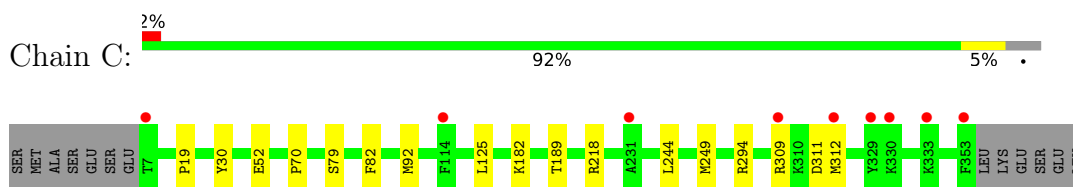
- Molecule 1: Lysine-specific demethylase 4A



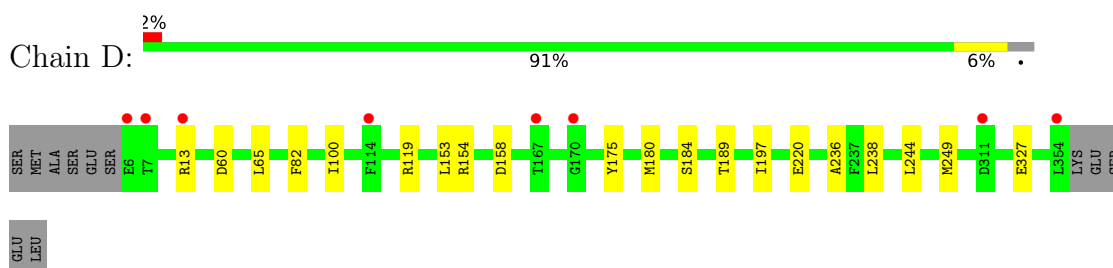
- Molecule 1: Lysine-specific demethylase 4A



- Molecule 1: Lysine-specific demethylase 4A



- Molecule 1: Lysine-specific demethylase 4A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.45Å 102.32Å 142.25Å 90.00° 99.82° 90.00°	Depositor
Resolution (Å)	56.61 – 2.08 56.61 – 2.08	Depositor EDS
% Data completeness (in resolution range)	98.4 (56.61-2.08) 98.4 (56.61-2.08)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 2.08Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, $R_{free}$	0.163 , 0.191 0.165 , 0.194	Depositor DCC
$R_{free}$ test set	4799 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.7	Xtrriage
Anisotropy	0.042	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 55.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.021 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12312	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.99 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.8620e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 5TZ, ZN, CL, DMS, EDO

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	0.82	0/2802	1.18	2/3818 (0.1%)
1	B	0.90	0/2906	1.14	2/3948 (0.1%)
1	C	0.85	0/2864	1.17	4/3895 (0.1%)
1	D	0.90	0/2916	1.13	4/3959 (0.1%)
All	All	0.87	0/11488	1.16	12/15620 (0.1%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	184	SER	N-CA-C	6.76	120.00	109.52
1	D	184	SER	N-CA-C	6.65	119.83	109.52
1	C	311	ASP	CA-CB-CG	6.46	119.06	112.60
1	A	184	SER	N-CA-C	6.41	118.92	109.24
1	B	189	THR	N-CA-C	-5.98	100.87	110.14

There are no chirality outliers.

There are no planarity outliers.

### 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	2716	0	2497	11	0
1	B	2819	0	2653	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2777	0	2581	6	0
1	D	2828	0	2660	12	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	15	0	6	0	0
3	B	15	0	6	0	0
3	C	15	0	6	0	0
3	D	15	0	6	0	0
4	A	28	0	42	2	0
4	B	44	0	66	0	0
4	C	36	0	54	0	0
4	D	40	0	60	6	0
5	A	8	0	12	2	0
5	C	4	0	6	0	0
5	D	4	0	6	0	0
6	D	1	0	0	0	0
7	A	170	0	0	0	0
7	B	253	0	0	0	0
7	C	229	0	0	0	0
7	D	287	0	0	0	0
All	All	12312	0	10661	34	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 2.

The worst 5 of 34 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:C:70:PRO:HG3	1:C:92:MET:HG2	1.82	0.62
1:A:297:ILE:HD12	1:A:320:PHE:HB3	1.84	0.59
1:A:119:ARG:HG2	4:A:406:EDO:H12	1.85	0.58
1:A:83:THR:HG23	4:A:405:EDO:H12	1.85	0.57
1:B:153:LEU:HD11	1:B:197:ILE:HG21	1.87	0.56

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	341/360 (95%)	336 (98%)	5 (2%)	0	100	100
1	B	349/360 (97%)	345 (99%)	4 (1%)	0	100	100
1	C	349/360 (97%)	346 (99%)	3 (1%)	0	100	100
1	D	350/360 (97%)	347 (99%)	3 (1%)	0	100	100
All	All	1389/1440 (96%)	1374 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

### 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	266/316 (84%)	260 (98%)	6 (2%)	44	49
1	B	286/316 (90%)	280 (98%)	6 (2%)	47	52
1	C	274/316 (87%)	271 (99%)	3 (1%)	65	73
1	D	284/316 (90%)	283 (100%)	1 (0%)	84	89
All	All	1110/1264 (88%)	1094 (99%)	16 (1%)	57	66

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	218	ARG
1	C	182	LYS
1	B	175	TYR

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Mol	Chain	Res	Type
1	C	52	GLU
1	B	167	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	128	ASN
1	C	215	HIS
1	C	128	ASN
1	C	84	GLN
1	C	137	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](#)

Of 54 ligands modelled in this entry, 9 are monoatomic - leaving 45 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	EDO	C	411	-	3,3,3	0.56	0	2,2,2	0.38	0
4	EDO	B	405	-	3,3,3	0.48	0	2,2,2	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	B	409	-	3,3,3	0.48	0	2,2,2	0.45	0
4	EDO	A	404	-	3,3,3	0.53	0	2,2,2	0.41	0
4	EDO	D	408	-	3,3,3	0.52	0	2,2,2	0.12	0
4	EDO	D	405	-	3,3,3	0.44	0	2,2,2	0.68	0
4	EDO	D	409	-	3,3,3	0.54	0	2,2,2	0.46	0
4	EDO	D	410	-	3,3,3	0.42	0	2,2,2	0.41	0
3	5TZ	D	403	2	16,16,16	0.99	2 (12%)	20,22,22	0.76	2 (10%)
4	EDO	A	409	-	3,3,3	0.48	0	2,2,2	0.45	0
4	EDO	D	413	-	3,3,3	0.43	0	2,2,2	0.40	0
5	DMS	A	411	-	3,3,3	0.26	0	3,3,3	0.24	0
3	5TZ	A	403	2	16,16,16	0.29	0	20,22,22	0.33	0
4	EDO	A	405	-	3,3,3	0.44	0	2,2,2	0.50	0
4	EDO	B	406	-	3,3,3	0.51	0	2,2,2	0.20	0
3	5TZ	B	403	2	16,16,16	0.79	2 (12%)	20,22,22	0.79	2 (10%)
4	EDO	C	412	-	3,3,3	0.44	0	2,2,2	0.47	0
5	DMS	A	412	-	3,3,3	0.32	0	3,3,3	0.39	0
4	EDO	A	407	-	3,3,3	0.52	0	2,2,2	0.27	0
4	EDO	C	406	-	3,3,3	0.53	0	2,2,2	0.42	0
4	EDO	B	407	-	3,3,3	0.57	0	2,2,2	0.38	0
4	EDO	B	411	-	3,3,3	0.46	0	2,2,2	0.48	0
5	DMS	C	413	-	3,3,3	0.33	0	3,3,3	0.30	0
4	EDO	D	414	-	3,3,3	0.50	0	2,2,2	0.38	0
4	EDO	B	413	-	3,3,3	0.62	0	2,2,2	0.25	0
4	EDO	C	410	-	3,3,3	0.46	0	2,2,2	0.49	0
4	EDO	C	408	-	3,3,3	0.55	0	2,2,2	0.27	0
4	EDO	C	409	-	3,3,3	0.45	0	2,2,2	0.49	0
4	EDO	D	406	-	3,3,3	0.24	0	2,2,2	0.80	0
4	EDO	D	411	-	3,3,3	0.46	0	2,2,2	0.39	0
4	EDO	B	408	-	3,3,3	0.51	0	2,2,2	0.42	0
3	5TZ	C	403	2	16,16,16	0.23	0	20,22,22	0.43	0
4	EDO	B	412	-	3,3,3	0.78	0	2,2,2	0.19	0
4	EDO	C	404	-	3,3,3	0.56	0	2,2,2	0.70	0
5	DMS	D	415	-	3,3,3	0.35	0	3,3,3	0.24	0
4	EDO	A	410	-	3,3,3	0.50	0	2,2,2	0.34	0
4	EDO	D	407	-	3,3,3	0.54	0	2,2,2	0.34	0
4	EDO	D	412	-	3,3,3	0.56	0	2,2,2	0.36	0
4	EDO	A	408	-	3,3,3	0.59	0	2,2,2	0.38	0
4	EDO	B	404	-	3,3,3	0.38	0	2,2,2	0.65	0
4	EDO	A	406	-	3,3,3	0.46	0	2,2,2	0.55	0
4	EDO	B	414	-	3,3,3	0.52	0	2,2,2	0.43	0
4	EDO	C	405	-	3,3,3	0.59	0	2,2,2	0.19	0
4	EDO	B	410	-	3,3,3	0.45	0	2,2,2	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	C	407	-	3,3,3	0.50	0	2,2,2	0.45	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	EDO	C	411	-	-	0/1/1/1	-
4	EDO	B	405	-	-	0/1/1/1	-
4	EDO	B	409	-	-	0/1/1/1	-
4	EDO	A	404	-	-	1/1/1/1	-
4	EDO	D	408	-	-	0/1/1/1	-
4	EDO	D	405	-	-	0/1/1/1	-
4	EDO	D	409	-	-	0/1/1/1	-
4	EDO	D	410	-	-	0/1/1/1	-
3	5TZ	D	403	2	-	6/8/8/8	0/2/2/2
4	EDO	A	409	-	-	1/1/1/1	-
4	EDO	D	413	-	-	0/1/1/1	-
3	5TZ	A	403	2	-	4/8/8/8	0/2/2/2
4	EDO	A	405	-	-	0/1/1/1	-
4	EDO	B	406	-	-	0/1/1/1	-
3	5TZ	B	403	2	-	6/8/8/8	0/2/2/2
4	EDO	C	412	-	-	0/1/1/1	-
4	EDO	A	407	-	-	0/1/1/1	-
4	EDO	C	406	-	-	0/1/1/1	-
4	EDO	B	407	-	-	0/1/1/1	-
4	EDO	B	411	-	-	0/1/1/1	-
4	EDO	D	414	-	-	0/1/1/1	-
4	EDO	B	413	-	-	1/1/1/1	-
4	EDO	C	410	-	-	1/1/1/1	-
4	EDO	C	408	-	-	0/1/1/1	-
4	EDO	C	409	-	-	0/1/1/1	-
4	EDO	D	406	-	-	0/1/1/1	-
4	EDO	D	411	-	-	1/1/1/1	-
4	EDO	B	408	-	-	0/1/1/1	-
3	5TZ	C	403	2	-	6/8/8/8	0/2/2/2
4	EDO	B	412	-	-	0/1/1/1	-
4	EDO	C	404	-	-	0/1/1/1	-
4	EDO	A	410	-	-	0/1/1/1	-
4	EDO	D	407	-	-	0/1/1/1	-
4	EDO	D	412	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	408	-	-	0/1/1/1	-
4	EDO	B	404	-	-	1/1/1/1	-
4	EDO	A	406	-	-	0/1/1/1	-
4	EDO	B	414	-	-	0/1/1/1	-
4	EDO	C	405	-	-	0/1/1/1	-
4	EDO	B	410	-	-	1/1/1/1	-
4	EDO	C	407	-	-	1/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	403	5TZ	O-C8	-3.00	1.21	1.30
3	B	403	5TZ	O-C8	-2.21	1.23	1.30
3	D	403	5TZ	O1-C8	2.14	1.29	1.22
3	B	403	5TZ	O1-C8	2.01	1.28	1.22

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	403	5TZ	O1-C8-C6	-2.32	115.37	121.46
3	B	403	5TZ	O1-C8-C6	-2.26	115.53	121.46
3	B	403	5TZ	O-C8-C6	2.26	120.63	114.84
3	D	403	5TZ	O-C8-C6	2.12	120.28	114.84

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	403	5TZ	N1-C1-C3-C7
3	A	403	5TZ	C2-C1-C3-C7
3	B	403	5TZ	N1-C1-C3-C7
3	B	403	5TZ	C2-C1-C3-C7
3	C	403	5TZ	N1-C1-C3-C7

There are no ring outliers.

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	409	EDO	1	0
4	D	413	EDO	1	0
5	A	411	DMS	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	405	EDO	1	0
4	D	406	EDO	4	0
4	A	406	EDO	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	342/360 (95%)	0.11	10 (2%) 53 56	20, 42, 72, 93	3 (0%)
1	B	352/360 (97%)	-0.30	4 (1%) 78 80	18, 33, 64, 81	1 (0%)
1	C	347/360 (96%)	-0.16	9 (2%) 57 60	21, 36, 67, 90	4 (1%)
1	D	349/360 (96%)	-0.34	8 (2%) 61 64	17, 30, 53, 83	3 (0%)
All	All	1390/1440 (96%)	-0.18	31 (2%) 62 65	17, 35, 66, 93	11 (0%)

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	114[A]	PHE	5.9
1	B	354	LEU	3.7
1	C	114[A]	PHE	3.6
1	A	308	CYS	3.5
1	D	311	ASP	3.5

### 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, 95<sup>th</sup> 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	EDO	B	404	4/4	0.77	0.19	31,35,39,40	0
4	EDO	A	410	4/4	0.78	0.16	68,68,68,69	0
4	EDO	A	406	4/4	0.78	0.17	55,55,59,61	0
4	EDO	B	411	4/4	0.78	0.17	52,52,53,57	0
5	DMS	D	415	4/4	0.78	0.31	94,95,96,96	0
4	EDO	D	405	4/4	0.80	0.15	39,40,41,43	0
5	DMS	A	412	4/4	0.80	0.23	114,114,115,115	0
4	EDO	B	410	4/4	0.80	0.18	52,53,53,56	0
4	EDO	D	414	4/4	0.81	0.17	56,59,61,63	0
4	EDO	C	406	4/4	0.83	0.15	53,55,55,55	0
4	EDO	C	404	4/4	0.83	0.20	44,45,46,48	0
4	EDO	D	413	4/4	0.83	0.19	68,68,68,68	0
4	EDO	C	409	4/4	0.84	0.19	66,66,66,66	0
4	EDO	B	409	4/4	0.84	0.15	59,60,63,65	0
4	EDO	A	404	4/4	0.85	0.17	43,46,46,49	0
4	EDO	C	410	4/4	0.85	0.13	55,60,63,66	0
4	EDO	C	412	4/4	0.85	0.17	61,63,65,66	0
4	EDO	A	405	4/4	0.85	0.15	56,58,59,61	0
4	EDO	C	405	4/4	0.86	0.16	60,63,65,67	0
4	EDO	B	412	4/4	0.86	0.14	33,34,40,41	0
4	EDO	A	409	4/4	0.86	0.16	50,52,56,59	0
4	EDO	D	411	4/4	0.86	0.14	62,63,63,63	0
5	DMS	A	411	4/4	0.87	0.23	82,83,84,84	0
4	EDO	D	409	4/4	0.87	0.12	31,35,41,46	0
4	EDO	B	407	4/4	0.87	0.15	34,38,41,43	0
4	EDO	D	407	4/4	0.88	0.14	60,62,62,63	0
4	EDO	B	414	4/4	0.88	0.15	62,63,63,64	0
4	EDO	D	410	4/4	0.88	0.15	35,37,42,47	0
4	EDO	C	407	4/4	0.88	0.14	52,53,56,60	0
5	DMS	C	413	4/4	0.88	0.20	62,67,67,69	0
4	EDO	D	412	4/4	0.88	0.17	39,47,52,57	0
4	EDO	D	408	4/4	0.89	0.15	47,51,54,55	0
4	EDO	A	408	4/4	0.90	0.13	53,54,55,55	0
4	EDO	A	407	4/4	0.90	0.10	58,59,59,59	0
4	EDO	C	408	4/4	0.91	0.14	44,48,51,55	0
4	EDO	B	406	4/4	0.92	0.10	50,52,53,53	0
4	EDO	B	413	4/4	0.92	0.15	38,40,41,42	0
4	EDO	D	406	4/4	0.92	0.11	41,45,45,50	0
6	CL	D	404	1/1	0.93	0.12	69,69,69,69	0
4	EDO	C	411	4/4	0.94	0.10	44,48,51,52	0
4	EDO	B	408	4/4	0.95	0.10	40,42,46,48	0
3	5TZ	A	403	15/15	0.96	0.09	28,30,32,33	15
3	5TZ	D	403	15/15	0.97	0.06	19,23,27,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	5TZ	C	403	15/15	0.97	0.06	21,23,30,32	15
4	EDO	B	405	4/4	0.98	0.04	26,26,29,31	0
3	5TZ	B	403	15/15	0.98	0.04	12,18,24,24	15
2	ZN	A	402	1/1	0.99	0.03	38,38,38,38	1
2	ZN	B	402	1/1	0.99	0.02	32,32,32,32	1
2	ZN	D	401	1/1	1.00	0.01	24,24,24,24	1
2	ZN	D	402	1/1	1.00	0.01	25,25,25,25	1
2	ZN	B	401	1/1	1.00	0.01	22,22,22,22	1
2	ZN	A	401	1/1	1.00	0.03	25,25,25,25	1
2	ZN	C	401	1/1	1.00	0.03	23,23,23,23	1
2	ZN	C	402	1/1	1.00	0.05	39,39,39,39	1

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.