



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:40 AM UTC

PDB ID : 6ETV / pdb_00006etv
Title : Crystal structure of KDM4D with tetrazolhydrazide compound 2
Authors : Malecki, P.H.; Link, A.; Weiss, M.S.; Heinemann, U.
Deposited on : 2017-10-27
Resolution : 1.18 Å(reported)

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

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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

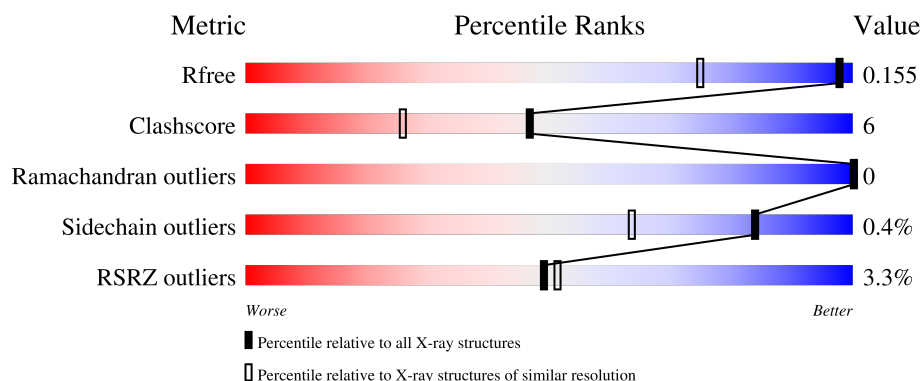
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.18 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	1789 (1.20-1.16)
Clashscore	190562	1845 (1.20-1.16)
Ramachandran outliers	187476	1789 (1.20-1.16)
Sidechain outliers	187428	1789 (1.20-1.16)
RSRZ outliers	180081	1787 (1.20-1.16)

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	342	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 6865 atoms, of which 3219 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 4D.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	330	Total	C	H	N	O	S	0	75	0
			6203	1996	3130	521	537	19			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

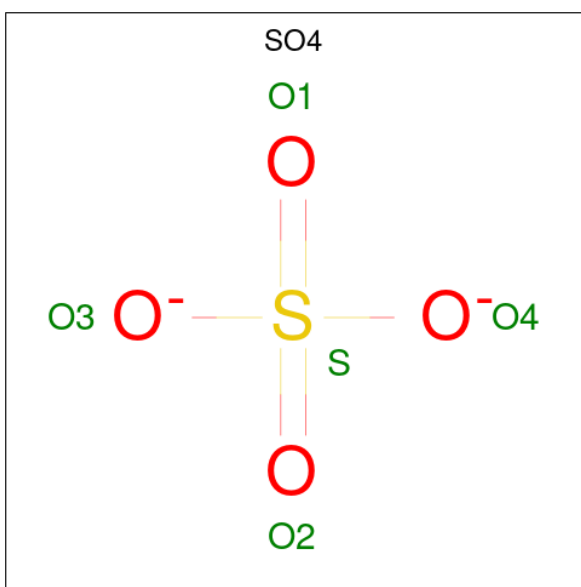
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	0
			10	2	6	2		
5	A	1	Total	C	H	O	0	1
			10	2	6	2		
5	A	1	Total	C	H	O	0	1
			20	4	12	4		
5	A	1	Total	C	H	O	0	1
			10	2	6	2		

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

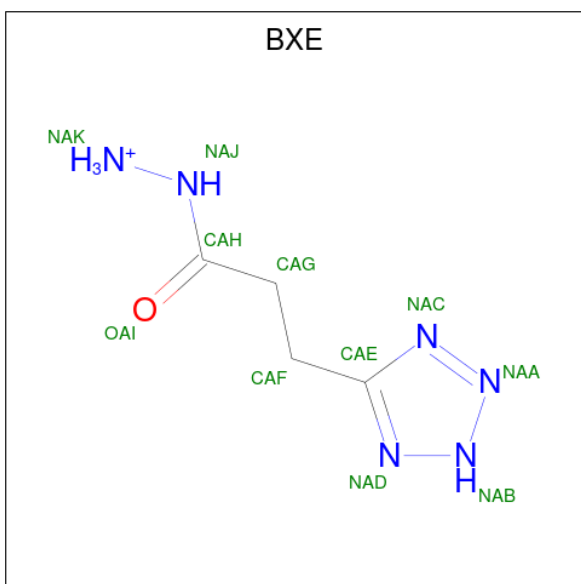


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	1
			5	4	1		

- Molecule 7 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

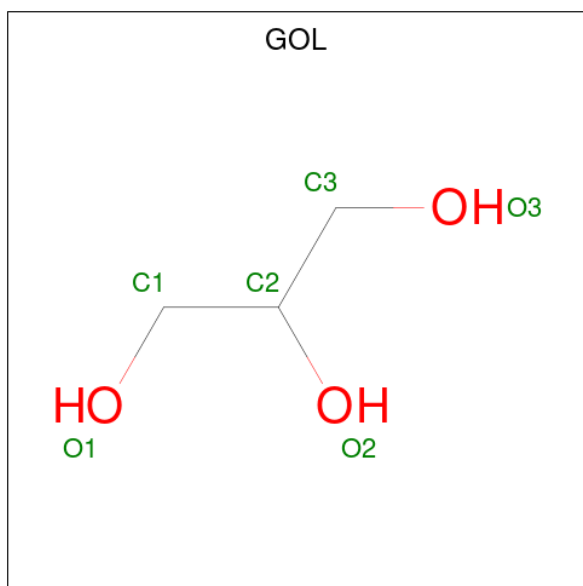
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ni	0	0
			1	1		

- Molecule 8 is [3-(2 {H}-1,2,3,4-tetrazol-5-yl)propanoylamino]azanium (CCD ID: BXE) (formula: C₄H₉N₆O).



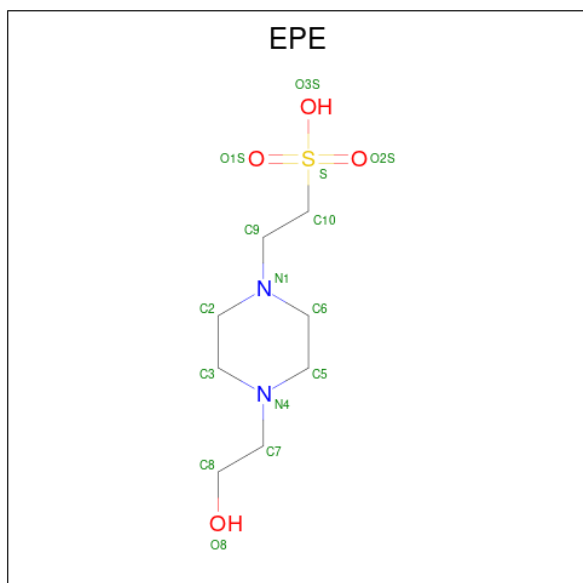
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	0	0
			20	4	9	6	1		

- Molecule 9 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	H	O	0	1
			27	6	15	6		

- Molecule 10 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
10	A	1	Total	C	H	N	O	S	0	1
			32	8	17	2	4	1		

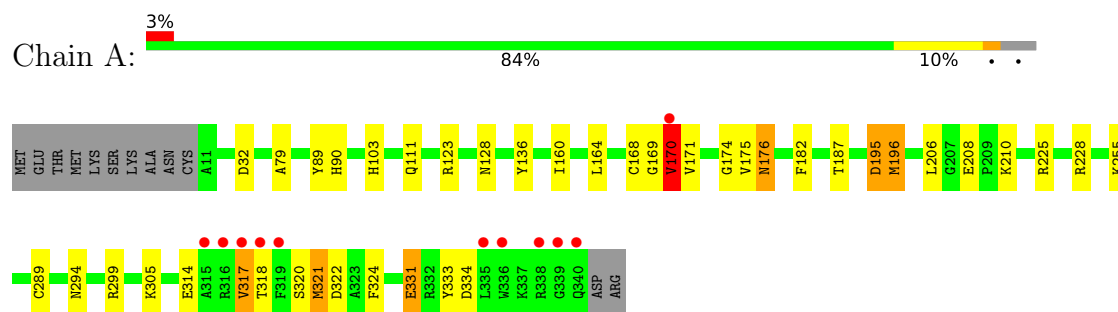
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	474	Total	O	0	63
			494	494		

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 4D



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	71.49Å 71.49Å 150.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.92 – 1.18 47.92 – 1.18	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.92-1.18) 100.0 (47.92-1.18)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 1.18Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.121 , 0.150 0.123 , 0.155	Depositor DCC
R_{free} test set	1360 reflections (1.05%)	wwPDB-VP
Wilson B-factor (Å ²)	11.1	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 54.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	6865	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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: GOL, EPE, BXE, CL, SO4, NI, EDO, ZN, NA

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	1.30	31/3385 (0.9%)	1.07	15/4574 (0.3%)

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	210[A]	LYS	CA-C	8.83	1.62	1.52
1	A	210[B]	LYS	CA-C	8.83	1.62	1.52
1	A	123[A]	ARG	CA-C	8.63	1.64	1.52
1	A	123[B]	ARG	CA-C	8.63	1.64	1.52
1	A	170	VAL	C-O	-7.81	1.14	1.24
1	A	334[A]	ASP	CA-C	7.74	1.63	1.52
1	A	334[B]	ASP	CA-C	7.74	1.63	1.52
1	A	195	ASP	C-O	-6.88	1.15	1.23
1	A	334[A]	ASP	N-CA	6.85	1.54	1.46
1	A	334[B]	ASP	N-CA	6.85	1.54	1.46
1	A	314	GLU	C-O	-6.64	1.16	1.24
1	A	294[A]	ASN	N-CA	6.51	1.54	1.45
1	A	294[B]	ASN	N-CA	6.51	1.54	1.45
1	A	321[A]	MET	CA-C	6.51	1.61	1.52
1	A	321[B]	MET	CA-C	6.51	1.61	1.52
1	A	324[A]	PHE	CA-C	5.90	1.60	1.52
1	A	324[B]	PHE	CA-C	5.90	1.60	1.52
1	A	331[A]	GLU	C-O	-5.84	1.17	1.24
1	A	331[B]	GLU	C-O	-5.84	1.17	1.24
1	A	318	THR	C-O	-5.67	1.17	1.23
1	A	89	TYR	CA-C	-5.62	1.46	1.52
1	A	322	ASP	C-O	-5.59	1.17	1.24
1	A	169[A]	GLY	C-O	-5.59	1.16	1.24
1	A	169[B]	GLY	C-O	-5.59	1.16	1.24
1	A	176[A]	ASN	C-N	5.49	1.40	1.33
1	A	176[B]	ASN	C-N	5.49	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	79	ALA	CA-C	5.46	1.60	1.52
1	A	164[A]	LEU	CA-C	5.17	1.59	1.52
1	A	164[B]	LEU	CA-C	5.17	1.59	1.52
1	A	171	VAL	C-O	-5.13	1.18	1.24
1	A	208	GLU	C-O	-5.11	1.17	1.23

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	TYR	CA-C-O	7.09	129.12	121.11
1	A	321[A]	MET	CA-C-O	6.54	127.49	120.10
1	A	321[B]	MET	CA-C-O	6.54	127.49	120.10
1	A	128	ASN	N-CA-C	6.51	122.02	113.30
1	A	164[A]	LEU	CA-C-O	6.33	127.26	120.55
1	A	164[B]	LEU	CA-C-O	6.33	127.26	120.55
1	A	324[A]	PHE	CA-C-O	5.87	126.77	120.55
1	A	324[B]	PHE	CA-C-O	5.87	126.77	120.55
1	A	176[A]	ASN	CA-C-O	5.82	126.99	120.70
1	A	176[B]	ASN	CA-C-O	5.82	126.99	120.70
1	A	321[A]	MET	N-CA-C	5.81	118.39	111.71
1	A	321[B]	MET	N-CA-C	5.81	118.39	111.71
1	A	196	MET	CG-SD-CE	5.54	113.08	100.90
1	A	333	TYR	N-CA-C	5.42	116.87	111.07
1	A	317	VAL	N-CA-C	5.26	114.95	108.53

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	3073	3130	3042	35	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	32	48	48	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	5	0	0	0	0
7	A	1	0	0	0	0
8	A	11	9	0	0	0
9	A	12	15	15	1	0
10	A	15	17	18	0	0
11	A	494	0	0	15	0
All	All	3646	3219	3123	36	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 6.

All (36) 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:196:MET:HG2	1:A:321[B]:MET:HE1	1.59	0.84
1:A:225[A]:ARG:HG2	1:A:228[A]:ARG:HH22	1.48	0.77
1:A:170:VAL:HB	11:A:557[A]:HOH:O	1.85	0.77
1:A:176[B]:ASN:HB3	11:A:601:HOH:O	1.86	0.76
1:A:195:ASP:HB3	1:A:321[B]:MET:CE	2.17	0.74
1:A:90[B]:HIS:HE1	11:A:513:HOH:O	1.70	0.73
1:A:225[A]:ARG:HG2	1:A:228[A]:ARG:NH2	2.06	0.71
1:A:206[B]:LEU:HD11	1:A:289[B]:CYS:SG	2.31	0.70
1:A:255:LYS:HD3	11:A:510[A]:HOH:O	1.96	0.65
1:A:195:ASP:HB3	1:A:321[B]:MET:HE3	1.77	0.65
1:A:160[B]:ILE:HG12	11:A:512[B]:HOH:O	1.97	0.64
1:A:196:MET:HG2	1:A:321[B]:MET:CE	2.27	0.64
1:A:317:VAL:HG21	1:A:321[A]:MET:SD	2.39	0.63
1:A:136[B]:TYR:HB3	1:A:187[B]:THR:HG21	1.81	0.63
1:A:225[B]:ARG:HH21	1:A:225[B]:ARG:HG2	1.66	0.61
1:A:320[A]:SER:HB2	11:A:818:HOH:O	2.01	0.60
1:A:168[A]:CYS:SG	11:A:557[A]:HOH:O	2.58	0.55
1:A:225[B]:ARG:HG2	1:A:225[B]:ARG:NH2	2.22	0.54
1:A:174:GLY:C	1:A:175[B]:VAL:CG1	2.81	0.53
1:A:170:VAL:CB	11:A:557[A]:HOH:O	2.52	0.52
1:A:90[B]:HIS:CE1	11:A:513:HOH:O	2.50	0.51
1:A:103:HIS:ND1	9:A:414[B]:GOL:H12	2.24	0.51
1:A:206[B]:LEU:HD21	1:A:289[B]:CYS:SG	2.52	0.49
1:A:174:GLY:C	1:A:175[B]:VAL:HG13	2.36	0.49
1:A:305[A]:LYS:HD2	11:A:739:HOH:O	2.13	0.48
1:A:196:MET:CG	1:A:321[B]:MET:HE1	2.39	0.48
1:A:160[B]:ILE:HD11	1:A:176[B]:ASN:OD1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320[B]:SER:HB3	11:A:818:HOH:O	2.16	0.46
1:A:111[B]:GLN:HG2	11:A:580:HOH:O	2.19	0.42
1:A:136[B]:TYR:HB2	1:A:182:PHE:O	2.20	0.42
1:A:195:ASP:CB	1:A:321[B]:MET:HE3	2.48	0.42
5:A:410[A]:EDO:H22	11:A:860:HOH:O	2.18	0.42
1:A:299[B]:ARG:HD3	1:A:299[B]:ARG:H	1.85	0.42
1:A:299[B]:ARG:HD2	11:A:881:HOH:O	2.19	0.41
1:A:32[B]:ASP:HB2	11:A:525[B]:HOH:O	2.21	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	403/342 (118%)	399 (99%)	4 (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	349/292 (120%)	348 (100%)	1 (0%)	86	66

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	VAL

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	77	GLN

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 17 ligands modelled in this entry, 4 are monoatomic - leaving 13 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	404	-	3,3,3	0.42	0	2,2,2	0.34	0
5	EDO	A	409[B]	-	3,3,3	0.21	0	2,2,2	0.99	0
8	BXE	A	413	7	11,11,11	1.63	3 (27%)	10,13,13	1.37	1 (10%)
9	GOL	A	414[A]	-	5,5,5	0.98	0	5,5,5	2.79	4 (80%)
9	GOL	A	414[B]	-	5,5,5	1.41	1 (20%)	5,5,5	1.40	1 (20%)
5	EDO	A	405	-	3,3,3	0.54	0	2,2,2	0.32	0
5	EDO	A	406	-	3,3,3	0.30	0	2,2,2	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	A	410[A]	-	3,3,3	0.45	0	2,2,2	0.27	0
5	EDO	A	407	-	3,3,3	0.41	0	2,2,2	0.61	0
6	SO4	A	411[A]	-	4,4,4	0.46	0	6,6,6	0.58	0
5	EDO	A	408[A]	-	3,3,3	0.29	0	2,2,2	0.36	0
10	EPE	A	415[A]	-	15,15,15	1.42	1 (6%)	19,20,20	3.80	9 (47%)
5	EDO	A	409[A]	-	3,3,3	0.23	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
5	EDO	A	404	-	-	1/1/1/1	-
5	EDO	A	409[B]	-	-	1/1/1/1	-
8	BXE	A	413	7	-	0/7/7/7	0/1/1/1
9	GOL	A	414[A]	-	-	0/4/4/4	-
9	GOL	A	414[B]	-	-	2/4/4/4	-
5	EDO	A	405	-	-	0/1/1/1	-
5	EDO	A	406	-	-	0/1/1/1	-
5	EDO	A	410[A]	-	-	0/1/1/1	-
5	EDO	A	407	-	-	0/1/1/1	-
5	EDO	A	408[A]	-	-	0/1/1/1	-
10	EPE	A	415[A]	-	-	5/9/19/19	0/1/1/1
5	EDO	A	409[A]	-	-	1/1/1/1	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	415[A]	EPE	C10-S	-4.83	1.70	1.77
8	A	413	BXE	NAK-NAJ	-3.49	1.36	1.41
9	A	414[B]	GOL	O2-C2	-2.70	1.35	1.43
8	A	413	BXE	NAB-NAA	-2.69	1.27	1.31
8	A	413	BXE	CAF-CAE	2.15	1.52	1.49

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	415[A]	EPE	O1S-S-C10	-10.10	91.47	106.73
10	A	415[A]	EPE	O2S-S-C10	8.09	118.95	106.73
10	A	415[A]	EPE	O3S-S-C10	5.76	117.27	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	415[A]	EPE	C5-N4-C3	4.33	118.18	108.84
10	A	415[A]	EPE	C6-N1-C2	4.26	118.03	108.84
9	A	414[A]	GOL	O2-C2-C3	-4.17	91.90	109.18
10	A	415[A]	EPE	C7-N4-C5	3.47	120.48	111.24
10	A	415[A]	EPE	C9-N1-C6	3.39	120.28	111.24
9	A	414[A]	GOL	O2-C2-C1	3.03	121.74	109.18
8	A	413	BXE	CAH-NAJ-NAK	-2.67	116.73	122.12
9	A	414[A]	GOL	C3-C2-C1	-2.54	102.48	111.80
10	A	415[A]	EPE	O3S-S-O2S	-2.41	105.36	111.40
9	A	414[A]	GOL	O1-C1-C2	2.33	120.85	110.38
9	A	414[B]	GOL	O2-C2-C3	-2.23	99.93	109.18
10	A	415[A]	EPE	C6-C5-N4	-2.16	106.30	110.65

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	415[A]	EPE	C10-C9-N1-C6
10	A	415[A]	EPE	C9-C10-S-O1S
10	A	415[A]	EPE	C9-C10-S-O3S
10	A	415[A]	EPE	C8-C7-N4-C5
9	A	414[B]	GOL	C1-C2-C3-O3
10	A	415[A]	EPE	C9-C10-S-O2S
9	A	414[B]	GOL	O2-C2-C3-O3
5	A	409[A]	EDO	O1-C1-C2-O2
5	A	404	EDO	O1-C1-C2-O2
5	A	409[B]	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	414[B]	GOL	1	0
5	A	410[A]	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 [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, 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	330/342 (96%)	-0.37	11 (3%)	49 51	5, 12, 28, 80	64 (19%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	315	ALA	6.9
1	A	317	VAL	5.4
1	A	318	THR	5.2
1	A	319[A]	PHE	5.0
1	A	316	ARG	3.4
1	A	336	TRP	2.8
1	A	170	VAL	2.7
1	A	339	GLY	2.7
1	A	338	ARG	2.5
1	A	335	LEU	2.4
1	A	340	GLN	2.3

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(Å ²)	Q<0.9
5	EDO	A	404	4/4	0.74	0.19	39,47,48,49	0
9	GOL	A	414[A]	6/6	0.80	0.17	41,49,50,51	14
9	GOL	A	414[B]	6/6	0.80	0.17	40,41,48,49	13
5	EDO	A	410[A]	4/4	0.86	0.14	43,52,52,52	0
5	EDO	A	406	4/4	0.88	0.12	33,40,44,44	0
5	EDO	A	409[B]	4/4	0.90	0.11	29,35,35,35	10
5	EDO	A	409[A]	4/4	0.90	0.11	19,23,26,29	10
6	SO4	A	411[A]	5/5	0.91	0.10	25,26,26,27	5
5	EDO	A	405	4/4	0.93	0.10	17,21,26,26	0
5	EDO	A	408[A]	4/4	0.93	0.10	19,22,26,27	10
10	EPE	A	415[A]	15/15	0.93	0.14	13,23,29,30	32
5	EDO	A	407	4/4	0.94	0.10	27,35,41,42	0
8	BXE	A	413	11/11	0.96	0.07	9,11,14,14	20
3	CL	A	402	1/1	0.98	0.06	32,32,32,32	0
4	NA	A	403	1/1	0.99	0.03	11,11,11,11	1
2	ZN	A	401	1/1	1.00	0.01	17,17,17,17	0
7	NI	A	412	1/1	1.00	0.03	10,10,10,10	0

6.5 Other polymers [i](#)

There are no such residues in this entry.