



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 12:26 am BST

PDB ID : 5FXV
Title : Crystal structure of JmjC domain of human histone demethylase UTY in complex with N05859b
Authors : Nowak, R.; Krojer, T.; Johansson, C.; Gileadi, C.; Kupinska, K.; Srikanthathan, V.; Oerum, S.; Pearce, N.M.; von Delft, F.; Arrowsmith, C.H.; Bountra, C.; Edwards, A.; Oppermann, U.
Deposited on : 2016-03-03
Resolution : 1.91 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

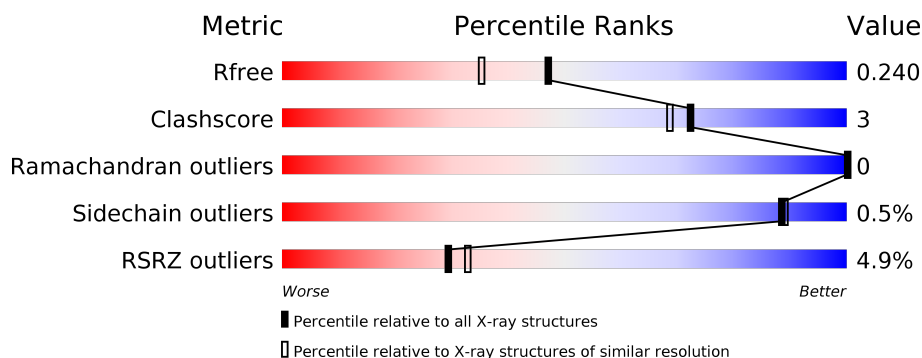
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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}	130704	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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 on 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	478	<div> <div>3%</div> <div> <div></div> <div>86%</div> <div>6%</div> <div>8%</div> </div> </div>
1	B	478	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>7%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7885 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 HISTONE DEMETHYLASE UTY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	442	Total	C	N	O	S	0	2	0
			3535	2267	604	644	20			
1	B	439	Total	C	N	O	S	0	3	0
			3519	2256	598	645	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	877	MET	-	expression tag	UNP O14607
A	1348	ALA	-	expression tag	UNP O14607
A	1349	GLU	-	expression tag	UNP O14607
A	1350	ASN	-	expression tag	UNP O14607
A	1351	LEU	-	expression tag	UNP O14607
A	1352	TYR	-	expression tag	UNP O14607
A	1353	PHE	-	expression tag	UNP O14607
A	1354	GLN	-	expression tag	UNP O14607
B	877	MET	-	expression tag	UNP O14607
B	1348	ALA	-	expression tag	UNP O14607
B	1349	GLU	-	expression tag	UNP O14607
B	1350	ASN	-	expression tag	UNP O14607
B	1351	LEU	-	expression tag	UNP O14607
B	1352	TYR	-	expression tag	UNP O14607
B	1353	PHE	-	expression tag	UNP O14607
B	1354	GLN	-	expression tag	UNP O14607

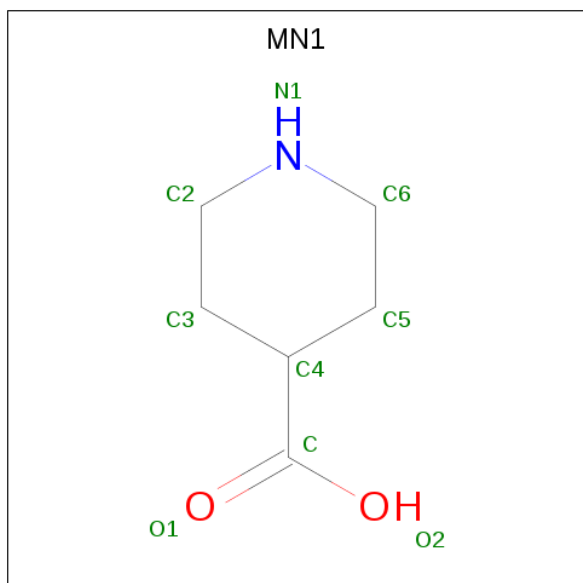
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 4 is 4-CARBOXYPIPERIDINE (three-letter code: MN1) (formula: C₆H₁₁NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			9	6	1	2		
4	B	1	Total	C	N	O	0	0
			9	6	1	2		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: 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		
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	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

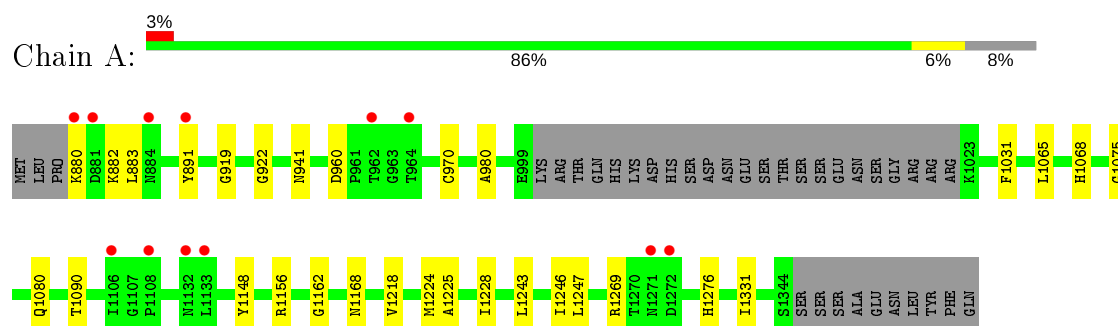
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	413	Total	O	0	0
			413	413		
6	B	356	Total	O	0	0
			356	356		

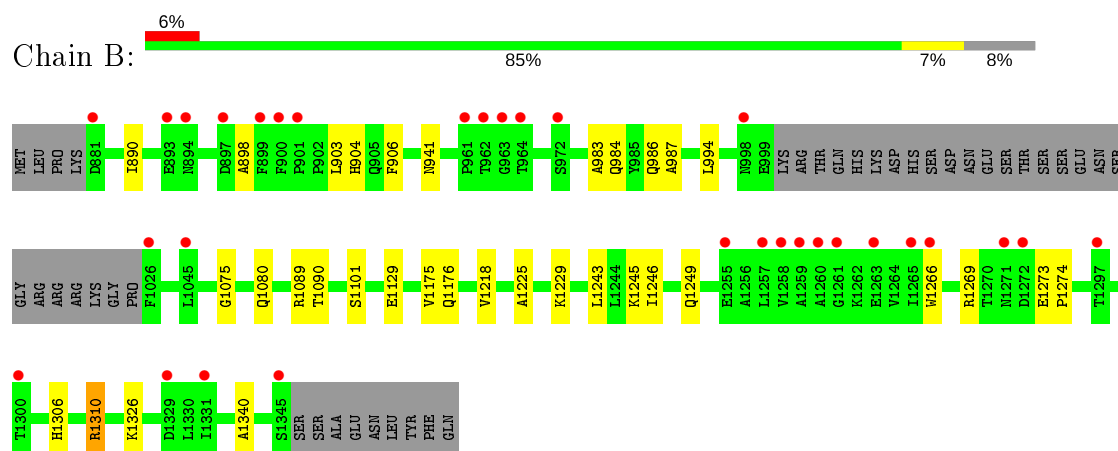
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: HISTONE DEMETHYLASE UTY



• Molecule 1: HISTONE DEMETHYLASE UTY



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.65Å 109.91Å 117.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.90 – 1.91 41.90 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.9 (41.90-1.91) 99.9 (41.90-1.91)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 1.91Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.199 , 0.240 0.200 , 0.240	Depositor DCC
R_{free} test set	4544 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	32.6	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7885	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% 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: MN1, ZN, MN, 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	0.42	1/3630 (0.0%)	0.54	0/4951
1	B	0.42	0/3612	0.51	0/4928
All	All	0.42	1/7242 (0.0%)	0.53	0/9879

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	970	CYS	CB-SG	-7.01	1.70	1.82

There are no bond angle outliers.

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	3535	0	3413	22	0
1	B	3519	0	3397	23	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	9	0	8	2	0
4	B	9	0	8	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	24	0	36	6	0
5	B	16	0	24	0	0
6	A	413	0	0	5	0
6	B	356	0	0	7	0
All	All	7885	0	6886	47	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 3.

All (47) 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:B:983:ALA:O	6:B:2088:HOH:O	1.80	0.99
1:A:1162:GLY:HA3	5:A:2352:EDO:H21	1.60	0.83
1:B:1229:LYS:HE3	1:B:1340:ALA:HB2	1.71	0.73
1:B:941:ASN:ND2	6:B:2045:HOH:O	2.28	0.63
1:B:1075:GLY:HA2	1:B:1080:GLN:HG3	1.83	0.61
1:B:1245:LYS:O	1:B:1249[B]:GLN:HG2	2.01	0.60
1:A:1247:LEU:HD21	1:A:1331:ILE:HD13	1.86	0.58
1:A:1090:THR:HG21	4:A:2347:MN1:H21	1.85	0.57
1:A:1168:ASN:HB3	5:A:2353:EDO:C2	2.37	0.55
1:A:1269:ARG:NH1	6:A:2319:HOH:O	2.26	0.55
1:B:1269:ARG:NH2	1:B:1273:GLU:O	2.40	0.54
1:A:1075:GLY:HA2	1:A:1080:GLN:HG3	1.92	0.52
1:B:1175:VAL:HG21	4:B:2348:MN1:H51	1.91	0.50
1:A:891:TYR:OH	6:A:2016:HOH:O	2.18	0.50
1:B:1266:TRP:CZ3	1:B:1326:LYS:HD3	2.48	0.49
1:B:987:ALA:N	6:B:2088:HOH:O	1.91	0.49
1:A:919:GLY:HA2	5:A:2352:EDO:H22	1.94	0.49
1:A:1276:HIS:ND1	6:A:2330:HOH:O	2.35	0.49
1:A:1168:ASN:HB3	5:A:2353:EDO:H22	1.95	0.49
1:B:1306:HIS:CE1	1:B:1310:ARG:HH11	2.31	0.49
1:B:1218:VAL:HG13	1:B:1246:ILE:HD13	1.96	0.48
1:A:880:LYS:N	1:A:1148:TYR:HH	2.12	0.47
1:B:984:GLN:C	6:B:2088:HOH:O	2.52	0.47
1:B:1225:ALA:HB2	1:B:1243:LEU:HD11	1.98	0.46
1:B:1090:THR:HG21	4:B:2348:MN1:H21	1.97	0.46
1:A:880:LYS:HE3	1:A:880:LYS:HB2	1.84	0.46
1:A:1068:HIS:CG	1:A:1228:ILE:HD11	2.51	0.46
1:B:898:ALA:O	1:B:903:LEU:HD23	2.17	0.45
1:A:1218:VAL:HG13	1:A:1246:ILE:HD13	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1225:ALA:HB2	1:A:1243:LEU:HD11	1.99	0.44
1:B:1089:ARG:HG2	1:B:1176:GLN:HB3	1.98	0.44
1:A:1090:THR:HG21	4:A:2347:MN1:H31	2.00	0.44
1:B:1273:GLU:HA	1:B:1274:PRO:HD3	1.82	0.44
6:A:2149:HOH:O	1:B:1129:GLU:OE1	2.20	0.43
1:A:1065:LEU:HD21	1:A:1224:MET:HE3	2.01	0.43
1:A:880:LYS:HG2	1:A:882:LYS:H	1.83	0.43
1:A:880:LYS:HB3	1:A:883:LEU:HG	2.01	0.42
1:A:941:ASN:HB2	1:A:980:ALA:HB2	2.02	0.42
1:A:922:GLY:N	5:A:2352:EDO:O2	2.51	0.41
1:B:994:LEU:HD23	1:B:994:LEU:HA	1.91	0.41
1:B:890:ILE:HD11	1:B:906:PHE:CD1	2.55	0.41
1:B:1306:HIS:HE1	1:B:1310:ARG:HH11	1.68	0.41
1:B:986:GLN:N	6:B:2088:HOH:O	2.54	0.41
1:A:1156:ARG:HG2	6:A:2200:HOH:O	2.20	0.41
1:B:904:HIS:CE1	6:B:2021:HOH:O	2.73	0.40
4:B:2348:MN1:H22	6:B:2145:HOH:O	2.20	0.40
5:A:2348:EDO:O1	5:A:2349:EDO:H21	2.21	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	440/478 (92%)	434 (99%)	6 (1%)	0	100	100
1	B	438/478 (92%)	431 (98%)	7 (2%)	0	100	100
All	All	878/956 (92%)	865 (98%)	13 (2%)	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	383/432 (89%)	381 (100%)	2 (0%)	88	89
1	B	382/432 (88%)	380 (100%)	2 (0%)	88	89
All	All	765/864 (88%)	761 (100%)	4 (0%)	88	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	960	ASP
1	A	1031	PHE
1	B	1101	SER
1	B	1310	ARG

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

Mol	Chain	Res	Type
1	A	1336	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 4 are monoatomic - leaving 12 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	2352	-	3,3,3	0.36	0	2,2,2	0.52	0
5	EDO	B	2352	-	3,3,3	0.34	0	2,2,2	0.55	0
5	EDO	A	2353	-	3,3,3	0.36	0	2,2,2	0.77	0
4	MN1	B	2348	3	6,9,9	4.42	6 (100%)	6,11,11	4.43	6 (100%)
5	EDO	B	2351	-	3,3,3	0.46	0	2,2,2	0.25	0
4	MN1	A	2347	3	6,9,9	4.54	6 (100%)	6,11,11	4.40	6 (100%)
5	EDO	B	2350	-	3,3,3	0.49	0	2,2,2	0.42	0
5	EDO	A	2350	-	3,3,3	0.50	0	2,2,2	0.41	0
5	EDO	A	2349	-	3,3,3	0.51	0	2,2,2	0.16	0
5	EDO	B	2349	-	3,3,3	0.53	0	2,2,2	0.31	0
5	EDO	A	2348	-	3,3,3	0.41	0	2,2,2	0.52	0
5	EDO	A	2351	-	3,3,3	0.42	0	2,2,2	0.47	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	2352	-	-	0/1/1/1	-
5	EDO	B	2352	-	-	1/1/1/1	-
5	EDO	A	2353	-	-	1/1/1/1	-
4	MN1	B	2348	3	-	0/0/12/12	0/1/1/1
5	EDO	B	2351	-	-	0/1/1/1	-
4	MN1	A	2347	3	-	0/0/12/12	0/1/1/1
5	EDO	B	2350	-	-	0/1/1/1	-
5	EDO	A	2350	-	-	0/1/1/1	-
5	EDO	A	2349	-	-	0/1/1/1	-
5	EDO	B	2349	-	-	0/1/1/1	-
5	EDO	A	2348	-	-	0/1/1/1	-
5	EDO	A	2351	-	-	1/1/1/1	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2348	MN1	C5-C4	-5.73	1.37	1.53
4	A	2347	MN1	C5-C4	-5.70	1.37	1.53
4	A	2347	MN1	C3-C4	-5.44	1.38	1.53
4	B	2348	MN1	C3-C4	-5.28	1.38	1.53
4	A	2347	MN1	C2-N1	-4.30	1.31	1.47
4	A	2347	MN1	C5-C6	-4.19	1.39	1.52
4	B	2348	MN1	C5-C6	-4.15	1.39	1.52
4	A	2347	MN1	C3-C2	-3.91	1.39	1.52
4	B	2348	MN1	C2-N1	-3.86	1.32	1.47
4	B	2348	MN1	C3-C2	-3.71	1.40	1.52
4	A	2347	MN1	C6-N1	-3.25	1.34	1.47
4	B	2348	MN1	C6-N1	-3.22	1.35	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	2348	MN1	C5-C4-C3	5.33	120.67	109.56
4	A	2347	MN1	C5-C4-C3	5.18	120.35	109.56
4	A	2347	MN1	C5-C6-N1	5.04	120.84	110.64
4	B	2348	MN1	C5-C6-N1	5.03	120.83	110.64
4	B	2348	MN1	C3-C2-N1	4.56	119.87	110.64
4	A	2347	MN1	C6-N1-C2	4.26	122.58	110.34
4	A	2347	MN1	C3-C2-N1	4.21	119.16	110.64
4	B	2348	MN1	C3-C4-C	4.04	120.46	111.88
4	B	2348	MN1	C6-N1-C2	4.01	121.86	110.34
4	A	2347	MN1	C5-C4-C	3.81	119.97	111.88
4	A	2347	MN1	C3-C4-C	3.68	119.68	111.88
4	B	2348	MN1	C5-C4-C	3.29	118.87	111.88

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	2352	EDO	O1-C1-C2-O2
5	A	2353	EDO	O1-C1-C2-O2
5	A	2351	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2352	EDO	3	0
5	A	2353	EDO	2	0
4	B	2348	MN1	3	0
4	A	2347	MN1	2	0
5	A	2349	EDO	1	0
5	A	2348	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 ⓘ

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	442/478 (92%)	0.27	12 (2%) 54 57	23, 33, 50, 72	0
1	B	439/478 (91%)	0.39	31 (7%) 16 18	22, 35, 56, 78	0
All	All	881/956 (92%)	0.33	43 (4%) 29 33	22, 34, 53, 78	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1345	SER	6.5
1	B	1258	VAL	5.0
1	B	1261	GLY	4.8
1	A	880	LYS	4.1
1	B	893	GLU	3.7
1	B	964	THR	3.6
1	B	1272	ASP	3.5
1	B	901	PRO	3.5
1	B	1255	GLU	3.4
1	B	900	PHE	3.3
1	B	899	PHE	3.2
1	B	961	PRO	3.2
1	B	1329	ASP	2.9
1	B	1265	ILE	2.9
1	A	884	ASN	2.8
1	B	1266	TRP	2.8
1	B	1260	ALA	2.8
1	B	1045	LEU	2.8
1	A	881	ASP	2.7
1	B	1257	LEU	2.7
1	A	962	THR	2.7
1	A	964	THR	2.7
1	B	894	ASN	2.6
1	B	963	GLY	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	881	ASP	2.6
1	B	962	THR	2.5
1	B	1297	THR	2.5
1	A	1106	ILE	2.5
1	A	1132	ASN	2.4
1	B	998	ASN	2.3
1	B	972	SER	2.3
1	B	1259	ALA	2.3
1	B	897	ASP	2.3
1	A	1133	LEU	2.2
1	B	1026	PHE	2.2
1	B	1271	ASN	2.2
1	A	891	TYR	2.1
1	A	1272	ASP	2.1
1	B	1331	ILE	2.1
1	B	1263	GLU	2.0
1	A	1271	ASN	2.0
1	A	1108	PRO	2.0
1	B	1300	THR	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 carbohydrates 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(\AA^2)	Q<0.9
5	EDO	A	2353	4/4	0.77	0.24	35,37,41,42	0
5	EDO	A	2349	4/4	0.83	0.17	39,41,43,48	0
5	EDO	A	2351	4/4	0.89	0.17	42,44,44,57	0
5	EDO	A	2352	4/4	0.90	0.28	33,33,34,36	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	A	2350	4/4	0.90	0.10	43,48,50,55	0
5	EDO	B	2352	4/4	0.90	0.17	37,38,41,42	0
5	EDO	B	2351	4/4	0.90	0.14	36,41,47,52	0
5	EDO	B	2350	4/4	0.90	0.13	40,43,44,52	0
4	MN1	A	2347	9/9	0.91	0.20	20,21,25,27	9
5	EDO	A	2348	4/4	0.93	0.12	30,36,37,45	0
4	MN1	B	2348	9/9	0.94	0.15	22,24,28,29	9
5	EDO	B	2349	4/4	0.96	0.15	34,37,38,40	0
2	ZN	B	2346	1/1	0.98	0.09	31,31,31,31	0
3	MN	A	2346	1/1	0.98	0.07	30,30,30,30	0
2	ZN	A	2345	1/1	0.98	0.08	32,32,32,32	0
3	MN	B	2347	1/1	0.99	0.08	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.