



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:39 AM UTC

PDB ID : 6K3E / pdb_00006k3e
Title : LSD1/Co-Rest structure with an inhibitor
Authors : Wang, J.
Deposited on : 2019-05-17
Resolution : 2.87 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

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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

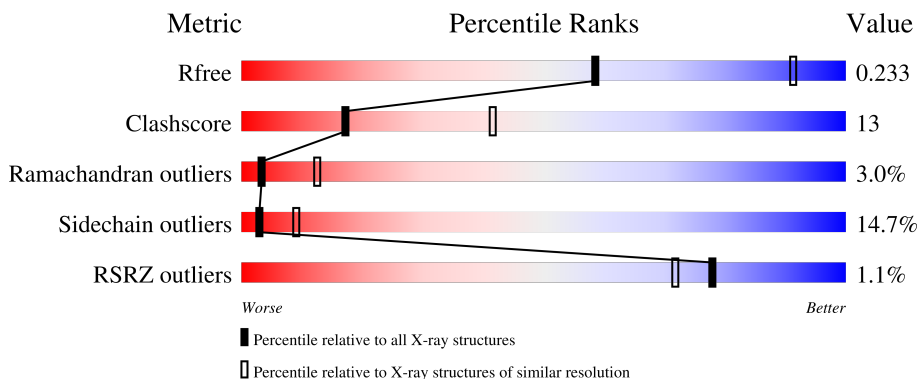
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.87 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	3557 (2.90-2.86)
Clashscore	190562	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)
RSRZ outliers	180081	3558 (2.90-2.86)

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	662	% 66% 29% 5%
2	B	140	% 44% 35% 15% • 5%

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 6483 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 histone demethylase 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	661	Total	C	N	O	S	0	0	0
			5177	3297	901	959	20			

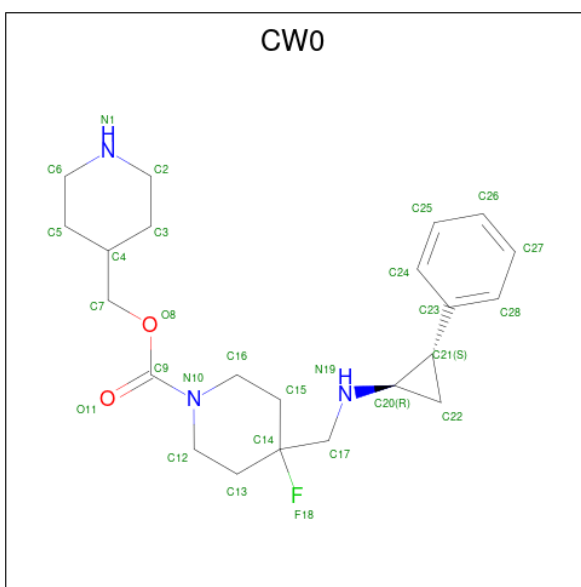
- Molecule 2 is a protein called REST corepressor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	133	Total	C	N	O	S	0	0	0
			1076	676	194	203	3			

There are 7 discrepancies between the modelled and reference sequences:

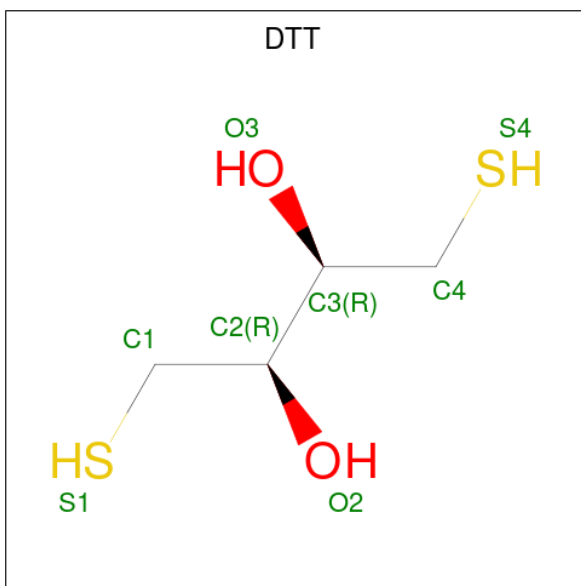
Chain	Residue	Modelled	Actual	Comment	Reference
B	301	GLY	-	expression tag	UNP Q9UKL0
B	302	SER	-	expression tag	UNP Q9UKL0
B	303	SER	-	expression tag	UNP Q9UKL0
B	304	GLY	-	expression tag	UNP Q9UKL0
B	305	SER	-	expression tag	UNP Q9UKL0
B	306	ALA	-	expression tag	UNP Q9UKL0
B	307	SER	-	expression tag	UNP Q9UKL0

- Molecule 3 is piperidin-4-ylmethyl 4-fluoranyl-4-[[[(1 {R},2 {S})-2-phenylcyclopropyl]amino]methyl]piperidine-1-carboxylate (CCD ID: CW0) (formula: C₂₂H₃₂FN₃O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	1
			28	22	1	3	2		

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (CCD ID: DTT) (formula: $C_4H_{10}O_2S_2$).



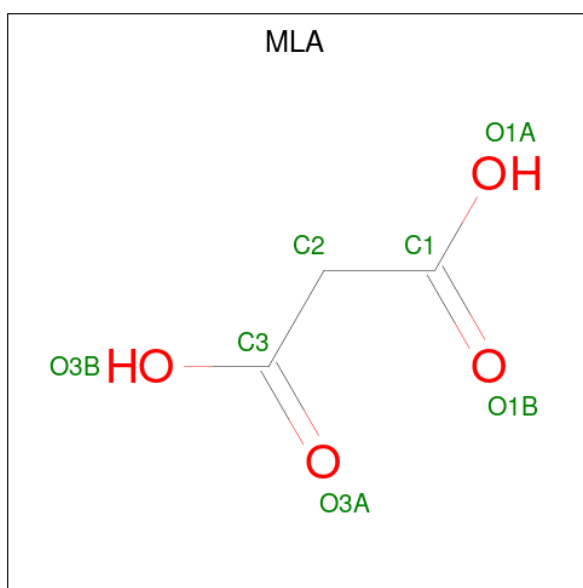
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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		

- Molecule 6 is MALONIC ACID (CCD ID: MLA) (formula: C₃H₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	3	4		
6	A	1	Total	C	O	0	0
			7	3	4		

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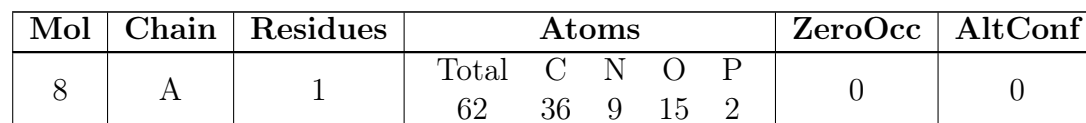
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	3	4		

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is 2-PCPA derivative (CCD ID: D3U) (formula: $C_{36}H_{41}N_9O_{15}P_2$).



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- EDO
- Chemical structure of EDO (Ethane-1,2-diol) showing a zigzag conformation. The carbon atoms are labeled C1 and C2 in green. The hydroxyl groups are labeled HO and OH in red, with their respective oxygen atoms labeled O1 and O2 in green.

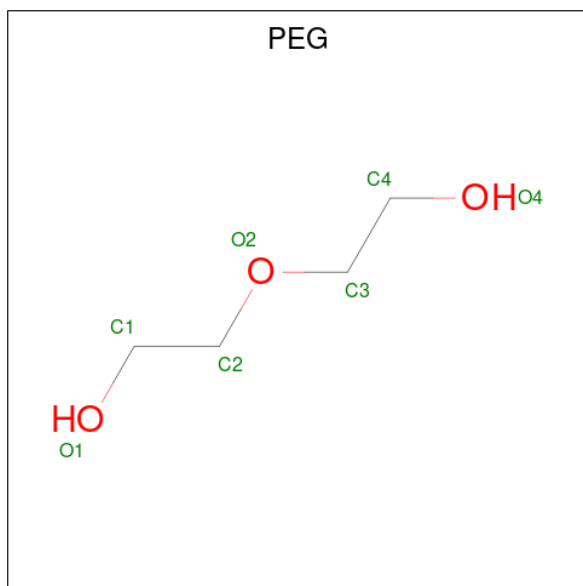
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C O 4 2 2	0	0
9	A	1	Total C O 4 2 2	0	0
9	A	1	Total C O 4 2 2	0	0



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

- Molecule 10 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			7	4	3		
10	A	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 11 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	2	Total	Cl	0	0
			2	2		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	8	Total	O	0	0
			8	8		

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	121.51Å 179.44Å 234.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.46 – 2.87 76.46 – 2.87	Depositor EDS
% Data completeness (in resolution range)	98.7 (76.46-2.87) 98.7 (76.46-2.87)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.189 , 0.223 (Not available) , 0.233	Depositor DCC
R_{free} test set	2828 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	93.3	Xtriage
Anisotropy	0.621	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 89.3	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	0.97	EDS
Total number of atoms	6483	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% 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: EDO, CW0, D3U, ACT, CL, MLA, DTT, GOL, PEG

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	1.12	8/5289 (0.2%)	1.56	25/7174 (0.3%)
2	B	1.10	0/1091	1.61	3/1471 (0.2%)
All	All	1.12	8/6380 (0.1%)	1.57	28/8645 (0.3%)

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	2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	777	ALA	C-O	7.70	1.34	1.24
1	A	618	CYS	C-O	7.06	1.32	1.23
1	A	635	PRO	C-O	-6.37	1.16	1.23
1	A	756	TRP	C-O	5.88	1.31	1.24
1	A	592	GLN	C-O	5.42	1.29	1.23

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	626	PRO	CB-CA-C	-6.57	102.98	111.39
1	A	473	ASP	CA-CB-CG	6.03	118.63	112.60
1	A	712	ALA	O-C-N	5.99	128.24	122.07
1	A	373	GLU	CA-C-N	5.96	128.74	120.63
1	A	373	GLU	C-N-CA	5.96	128.74	120.63

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	336	GLY	Peptide
1	A	792	PRO	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	5177	0	5212	122	0
2	B	1076	0	1091	55	0
3	A	28	0	0	1	0
4	A	8	0	10	1	0
5	A	8	0	6	1	0
6	A	21	0	6	2	0
7	A	24	0	32	1	0
8	A	62	0	0	1	0
9	A	48	0	72	0	0
10	A	21	0	30	0	0
11	A	2	0	0	0	0
12	A	8	0	0	0	0
All	All	6483	0	6459	163	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 13.

The worst 5 of 163 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:566:THR:HG21	1:A:697:LEU:HD12	1.56	0.88
1:A:693:LEU:HD12	1:A:694:PHE:N	1.96	0.81
1:A:308:GLU:OE2	8:A:912:D3U:O3'	1.99	0.80
2:B:381:ALA:HA	2:B:416:GLN:HE22	1.45	0.79
2:B:309:LYS:HE3	2:B:309:LYS:HA	1.67	0.76

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	659/662 (100%)	560 (85%)	85 (13%)	14 (2%)	5	19
2	B	131/140 (94%)	100 (76%)	21 (16%)	10 (8%)	1	2
All	All	790/802 (98%)	660 (84%)	106 (13%)	24 (3%)	3	12

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	ALA
1	A	468	VAL
2	B	379	CYS
2	B	425	ARG
1	A	244	SER

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	561/562 (100%)	489 (87%)	72 (13%)	4	12
2	B	117/121 (97%)	89 (76%)	28 (24%)	1	2
All	All	678/683 (99%)	578 (85%)	100 (15%)	3	9

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	696	ASN

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Mol	Chain	Res	Type
1	A	821	GLU
2	B	438	GLU
1	A	702	ILE
1	A	745	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	806	ASN
2	B	411	ASN
2	B	416	GLN
2	B	348	GLN
1	A	484	HIS

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 29 ligands modelled in this entry, 2 are monoatomic - leaving 27 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
9	EDO	A	914	-	3,3,3	0.35	0	2,2,2	0.53	0
4	DTT	A	902	-	7,7,7	0.52	0	4,8,8	1.21	1 (25%)
9	EDO	A	918	-	3,3,3	0.06	0	2,2,2	0.15	0
10	PEG	A	927	-	6,6,6	0.30	0	5,5,5	0.17	0
7	GOL	A	909	-	5,5,5	0.27	0	5,5,5	0.56	0
7	GOL	A	908	-	5,5,5	0.26	0	5,5,5	0.48	0
9	EDO	A	913	-	3,3,3	0.25	0	2,2,2	0.49	0
10	PEG	A	925	-	6,6,6	0.13	0	5,5,5	0.17	0
5	ACT	A	904	-	3,3,3	1.38	0	3,3,3	0.65	0
9	EDO	A	916	-	3,3,3	0.22	0	2,2,2	0.29	0
9	EDO	A	923	-	3,3,3	0.43	0	2,2,2	0.75	0
10	PEG	A	926	-	6,6,6	0.30	0	5,5,5	0.17	0
9	EDO	A	920	-	3,3,3	0.22	0	2,2,2	0.14	0
5	ACT	A	903	-	3,3,3	1.12	0	3,3,3	1.52	0
3	CW0	A	901[A]	-	30,31,31	1.82	9 (30%)	33,43,43	2.78	15 (45%)
6	MLA	A	907	-	6,6,6	1.27	0	7,7,7	0.90	0
9	EDO	A	919	-	3,3,3	0.23	0	2,2,2	0.23	0
6	MLA	A	906	-	6,6,6	1.45	1 (16%)	7,7,7	0.99	0
9	EDO	A	915	-	3,3,3	0.07	0	2,2,2	0.17	0
6	MLA	A	905	-	6,6,6	1.54	0	7,7,7	0.86	0
8	D3U	A	912	-	65,69,69	3.36	27 (41%)	88,107,107	2.03	29 (32%)
7	GOL	A	910	-	5,5,5	0.12	0	5,5,5	0.35	0
9	EDO	A	921	-	3,3,3	0.14	0	2,2,2	0.27	0
7	GOL	A	911	-	5,5,5	0.19	0	5,5,5	0.47	0
9	EDO	A	922	-	3,3,3	0.13	0	2,2,2	0.11	0
9	EDO	A	924	-	3,3,3	0.18	0	2,2,2	0.15	0
9	EDO	A	917	-	3,3,3	0.16	0	2,2,2	0.27	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
9	EDO	A	914	-	-	1/1/1/1	-
4	DTT	A	902	-	-	4/8/8/8	-
9	EDO	A	918	-	-	0/1/1/1	-
10	PEG	A	927	-	-	2/4/4/4	-
7	GOL	A	909	-	-	3/4/4/4	-
7	GOL	A	908	-	-	0/4/4/4	-
9	EDO	A	913	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	PEG	A	925	-	-	2/4/4/4	-
9	EDO	A	916	-	-	0/1/1/1	-
9	EDO	A	923	-	-	1/1/1/1	-
10	PEG	A	926	-	-	2/4/4/4	-
9	EDO	A	920	-	-	1/1/1/1	-
3	CW0	A	901[A]	-	-	7/18/44/44	0/4/4/4
6	MLA	A	907	-	-	2/4/4/4	-
9	EDO	A	919	-	-	0/1/1/1	-
6	MLA	A	906	-	-	2/4/4/4	-
9	EDO	A	915	-	-	1/1/1/1	-
6	MLA	A	905	-	-	2/4/4/4	-
8	D3U	A	912	-	-	2/38/103/103	0/8/8/8
7	GOL	A	910	-	-	4/4/4/4	-
9	EDO	A	921	-	-	1/1/1/1	-
7	GOL	A	911	-	-	3/4/4/4	-
9	EDO	A	922	-	-	1/1/1/1	-
9	EDO	A	924	-	-	1/1/1/1	-
9	EDO	A	917	-	-	0/1/1/1	-

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	912	D3U	PBB-OBE	10.42	1.70	1.59
8	A	912	D3U	CCB-CCD	-10.11	1.39	1.52
8	A	912	D3U	C2-N1	8.73	1.49	1.33
8	A	912	D3U	CCE-CCB	-8.25	1.44	1.52
8	A	912	D3U	CAK-NAM	6.75	1.48	1.37

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	901[A]	CW0	C12-C13-C14	5.86	116.77	112.38
3	A	901[A]	CW0	O8-C9-O11	-5.69	114.86	124.76
8	A	912	D3U	CAH-NAI-CCC	-5.61	115.30	123.64
3	A	901[A]	CW0	C16-C15-C14	-5.50	108.26	112.38
3	A	901[A]	CW0	O8-C9-N10	5.35	121.11	111.77

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	901[A]	CW0	C5-C4-C7-O8
3	A	901[A]	CW0	C13-C14-C17-N19
3	A	901[A]	CW0	C15-C14-C17-N19
3	A	901[A]	CW0	C22-C20-N19-C17
3	A	901[A]	CW0	N10-C9-O8-C7

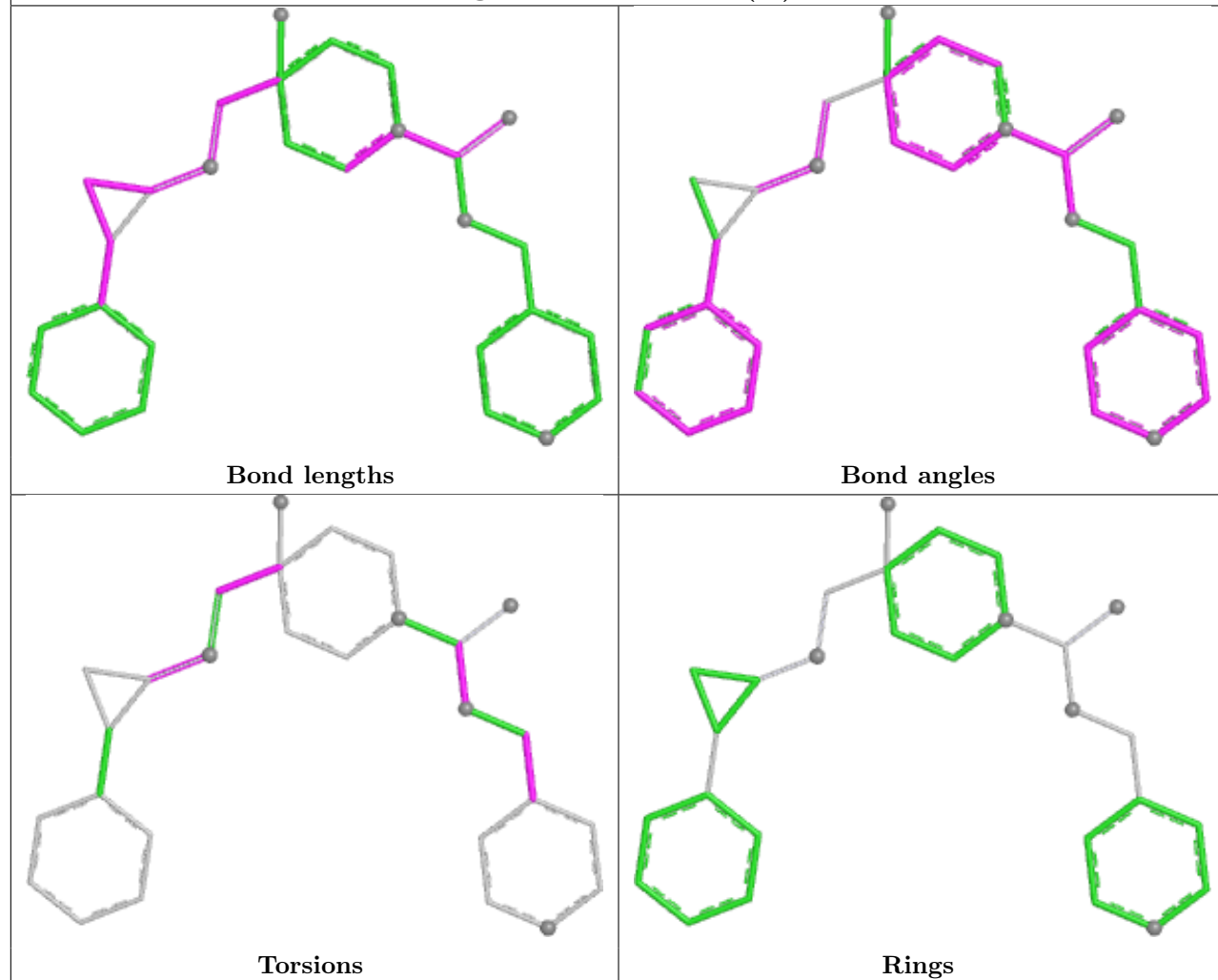
There are no ring outliers.

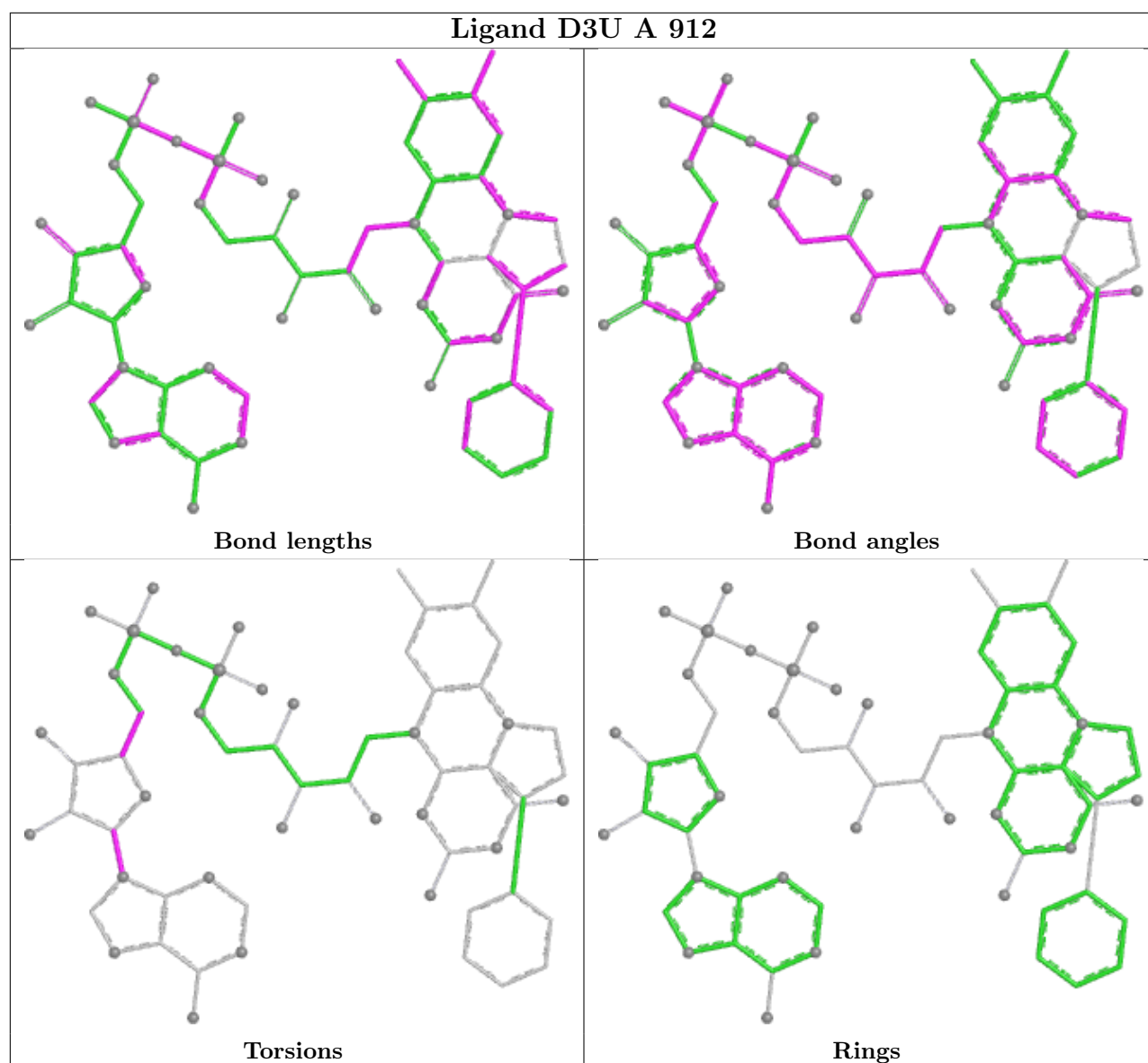
7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	902	DTT	1	0
5	A	903	ACT	1	0
3	A	901[A]	CW0	1	0
6	A	906	MLA	2	0
8	A	912	D3U	1	0
7	A	910	GOL	1	0
7	A	911	GOL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand CW0 A 901 (A)





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, 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	661/662 (99%)	-0.16	8 (1%)	76 70	68, 105, 150, 199	0
2	B	133/140 (95%)	0.19	1 (0%)	82 77	96, 140, 170, 208	0
All	All	794/802 (99%)	-0.10	9 (1%)	78 72	68, 112, 158, 208	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	833	MET	4.7
1	A	744	LYS	4.7
1	A	832	ALA	3.9
1	A	173	GLY	3.5
1	A	271	LYS	2.6

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](#)

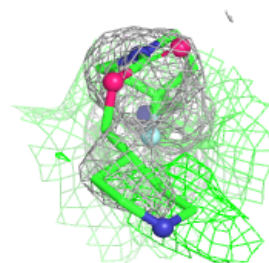
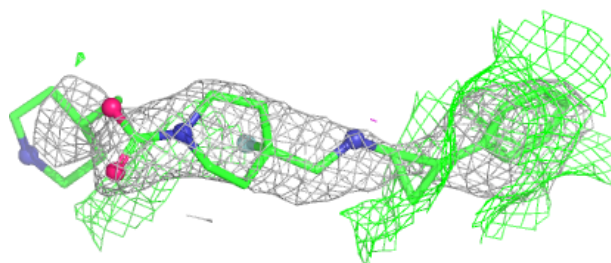
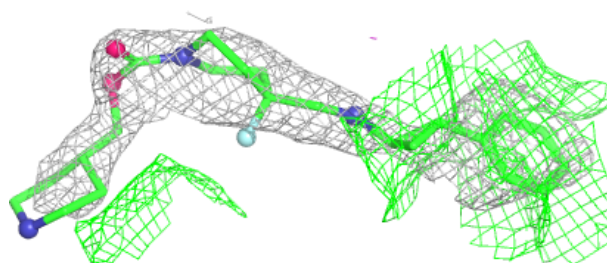
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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
7	GOL	A	911	6/6	0.73	0.19	145,176,184,189	0
6	MLA	A	907	7/7	0.74	0.11	149,174,180,180	0
10	PEG	A	926	7/7	0.78	0.19	146,167,179,182	0
9	EDO	A	913	4/4	0.79	0.29	117,120,129,137	0
10	PEG	A	927	7/7	0.79	0.32	146,164,179,195	0
5	ACT	A	904	4/4	0.82	0.19	129,140,148,152	0
9	EDO	A	919	4/4	0.82	0.27	138,141,151,151	0
9	EDO	A	924	4/4	0.83	0.27	133,135,137,140	0
9	EDO	A	915	4/4	0.83	0.17	147,151,152,155	0
4	DTT	A	902	8/8	0.83	0.23	159,196,217,226	0
9	EDO	A	922	4/4	0.84	0.15	141,147,150,151	0
9	EDO	A	916	4/4	0.85	0.24	135,135,139,140	0
10	PEG	A	925	7/7	0.85	0.22	146,155,166,166	0
11	CL	A	928	1/1	0.85	0.24	143,143,143,143	0
9	EDO	A	917	4/4	0.87	0.17	113,139,140,145	0
3	CW0	A	901[A]	28/28	0.88	0.33	132,168,191,195	0
9	EDO	A	923	4/4	0.89	0.26	122,128,134,138	0
9	EDO	A	920	4/4	0.89	0.27	118,128,141,147	0
6	MLA	A	906	7/7	0.91	0.14	96,109,127,139	0
6	MLA	A	905	7/7	0.91	0.14	120,124,131,133	0
9	EDO	A	914	4/4	0.91	0.29	112,128,132,147	0
11	CL	A	929	1/1	0.91	0.16	140,140,140,140	0
9	EDO	A	918	4/4	0.92	0.24	146,148,157,163	0
9	EDO	A	921	4/4	0.92	0.32	131,133,137,139	0
5	ACT	A	903	4/4	0.93	0.19	85,88,94,104	0
7	GOL	A	909	6/6	0.93	0.18	118,139,153,162	0
7	GOL	A	908	6/6	0.94	0.18	104,118,144,145	0
7	GOL	A	910	6/6	0.94	0.22	115,139,150,158	6
8	D3U	A	912	62/62	0.98	0.08	53,88,111,114	0

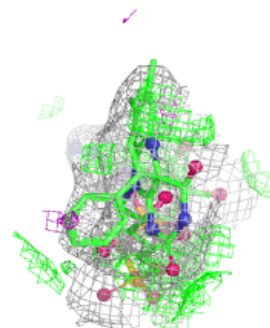
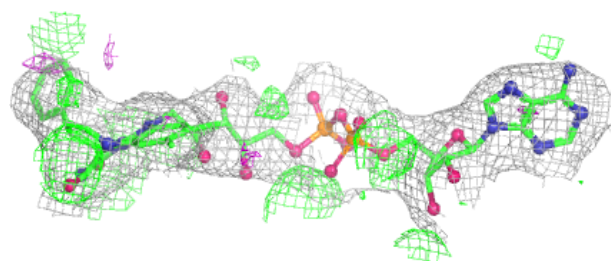
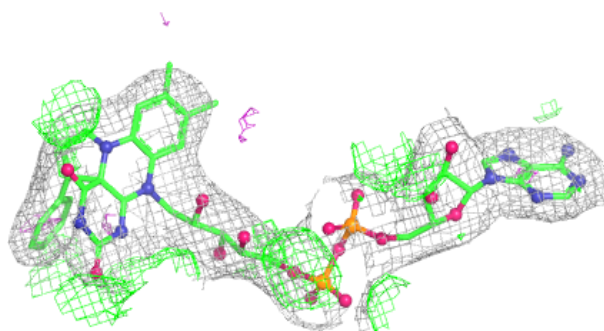
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around CW0 A 901 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around D3U A 912:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.