



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 22, 2023 – 08:34 PM JST

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

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
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) : 2.36

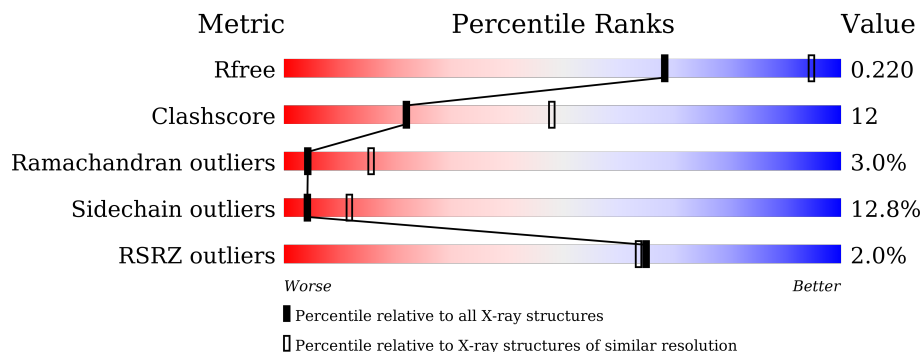
1 Overall quality at a glance

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}	130704	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (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	 2% 71% 26%
2	B	140	 4% 46% 36% 11% 5%

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
10	PEG	A	925	-	-	-	X
10	PEG	A	926	-	-	-	X
10	PEG	A	927	-	-	-	X
3	CW0	A	901[A]	-	-	-	X
5	ACT	A	904	-	-	-	X
6	MLA	A	907	-	-	-	X
7	GOL	A	911	-	-	-	X
9	EDO	A	913	-	-	-	X
9	EDO	A	914	-	-	-	X
9	EDO	A	915	-	-	-	X
9	EDO	A	917	-	-	-	X
9	EDO	A	918	-	-	-	X
9	EDO	A	919	-	-	-	X
9	EDO	A	920	-	-	-	X
9	EDO	A	921	-	-	-	X
9	EDO	A	923	-	-	-	X

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
			Total	C	N	O	S			
1	A	661	5177	3297	901	959	20	0	0	0

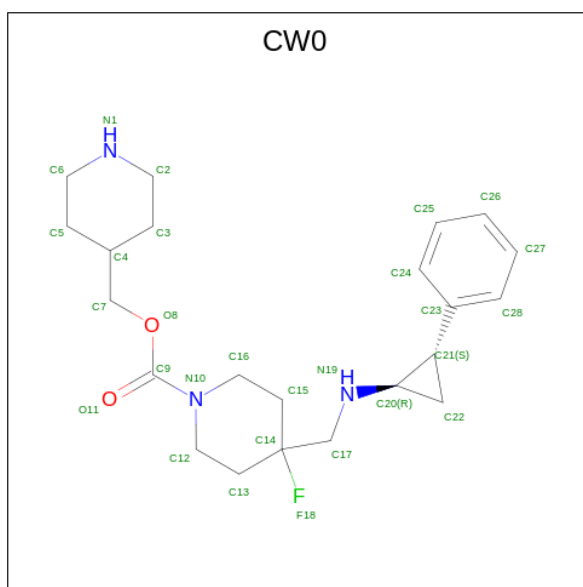
- Molecule 2 is a protein called REST corepressor 1.

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

There are 7 discrepancies between the modelled and reference sequences:

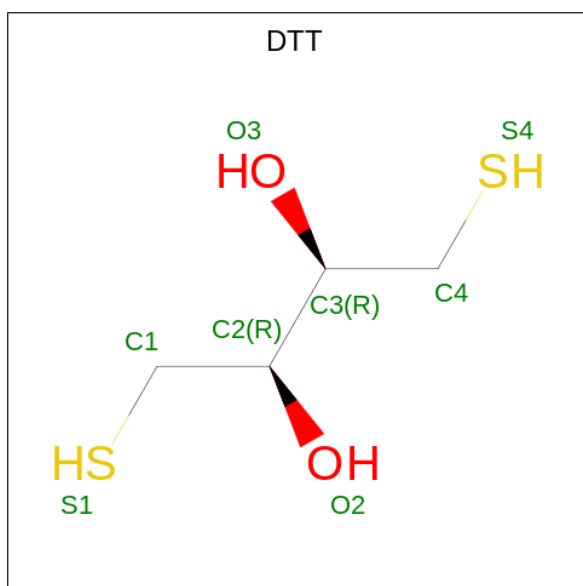
Chain	Residue	Modelled	Actual	Comment	Reference
B	301	GLY	-	expression tag	UNP Q9UKL0
B	302	SER	-	expression tag	UNP Q9UKL0
B	303	SER	-	expression tag	UNP Q9UKL0
B	304	GLY	-	expression tag	UNP Q9UKL0
B	305	SER	-	expression tag	UNP Q9UKL0
B	306	ALA	-	expression tag	UNP Q9UKL0
B	307	SER	-	expression tag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

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



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

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



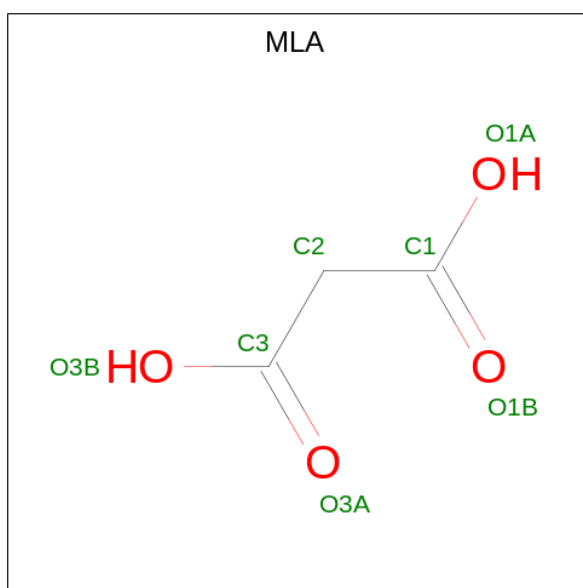
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
4	A	1	8	4	2	2	0	0

- Molecule 5 is ACETATE ION (three-letter code: 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 (three-letter code: MLA) (formula: C₃H₄O₄).



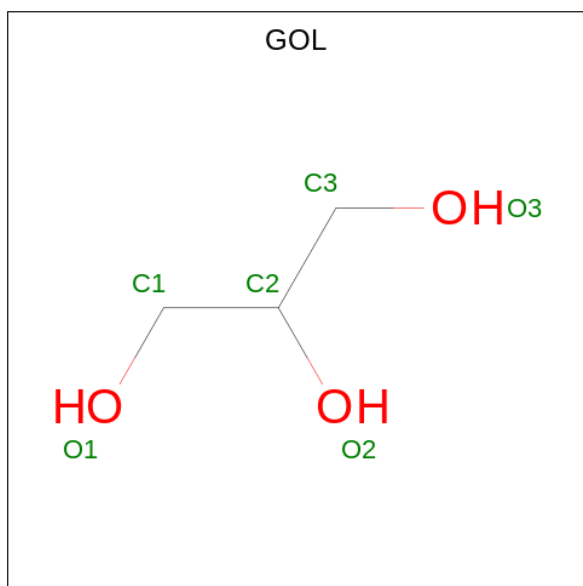
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	3	4		
6	A	1	Total	C	O	0	0
			7	3	4		

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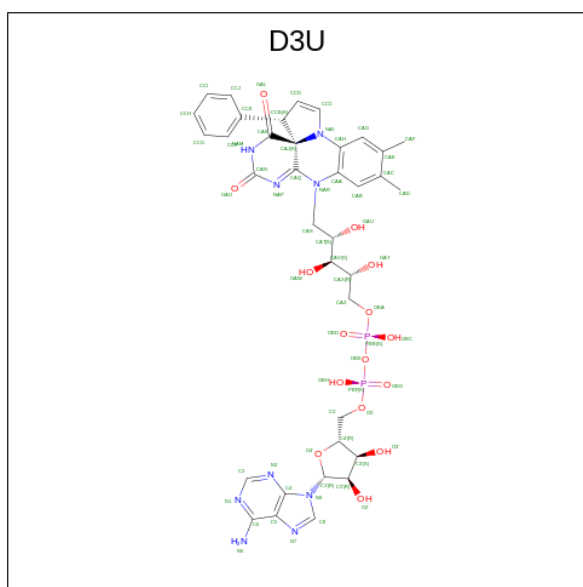
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	3	4		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



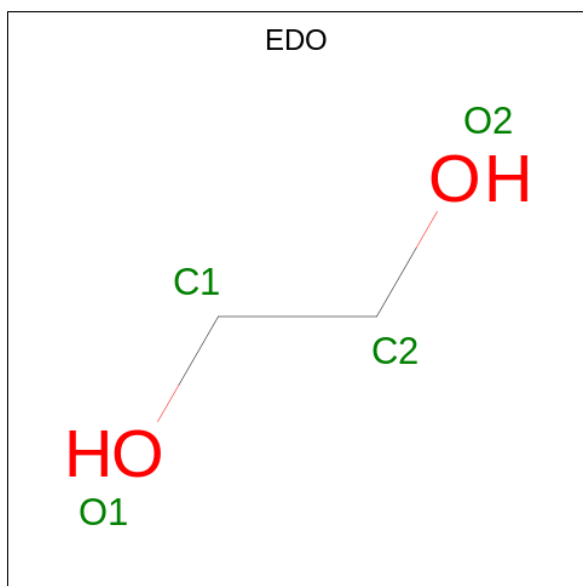
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
8	A	1	62	36	9	15	2	0	0

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



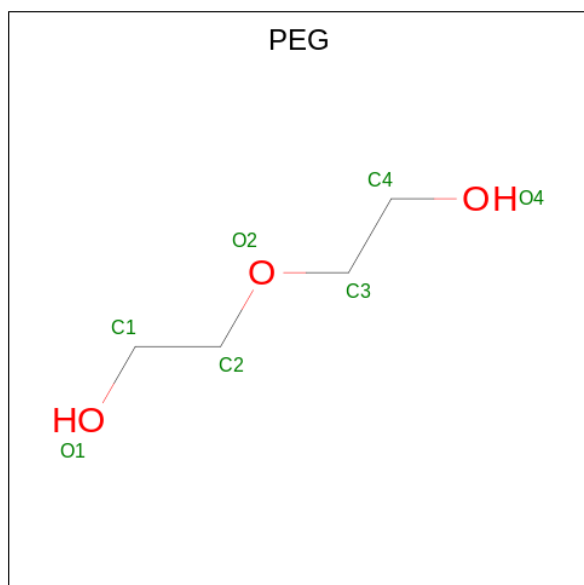
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	C O		
9	A	1	4	2 2	0	0
9	A	1	4	2 2	0	0
9	A	1	4	2 2	0	0

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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 (three-letter code: PEG) (formula: C₄H₁₀O₃).



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 (three-letter code: CL) (formula: Cl).

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

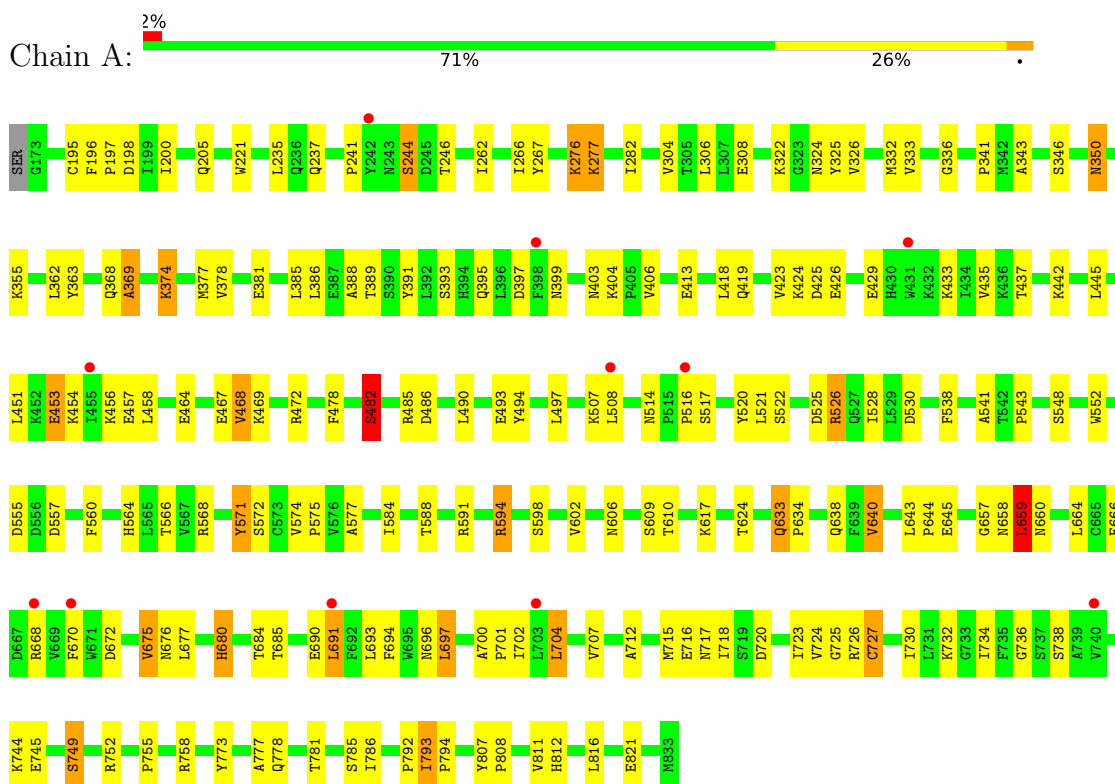
- Molecule 12 is water.

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

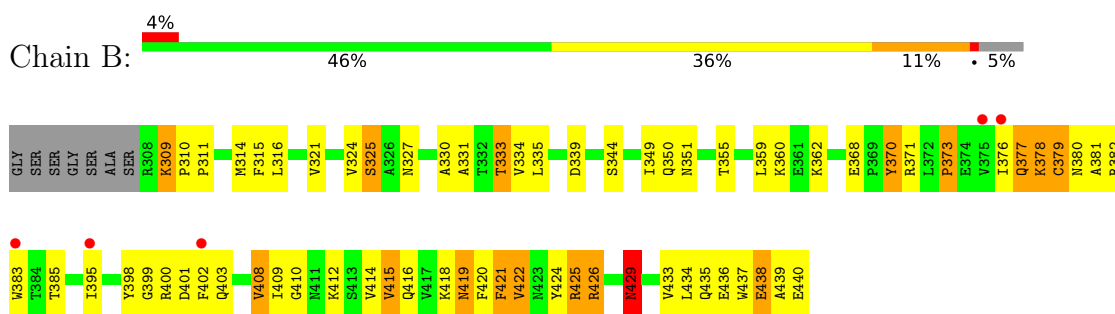
3 Residue-property plots [i](#)

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 histone demethylase 1A



• Molecule 2: REST corepressor 1



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 76.34 – 2.87	Depositor EDS
% Data completeness (in resolution range)	98.7 (76.46-2.87) 98.7 (76.34-2.87)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.86Å)	Xtrriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.189 , 0.223 0.194 , 0.220	Depositor DCC
R_{free} test set	2828 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	93.3	Xtrriage
Anisotropy	0.621	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 85.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
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

Xtrriage'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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, D3U, DTT, PEG, MLA, CL, EDO, ACT, CW0

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	0.76	2/5289 (0.0%)	0.98	1/7174 (0.0%)
2	B	0.74	0/1091	0.95	0/1471
All	All	0.76	2/6380 (0.0%)	0.98	1/8645 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	777	ALA	C-O	5.74	1.34	1.23
1	A	690	GLU	CD-OE1	5.02	1.31	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	571	TYR	CB-CG-CD1	5.71	124.43	121.00

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	111	0
2	B	1076	0	1091	52	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	152	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 12.

All (152) 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
2:B:381:ALA:HA	2:B:416:GLN:NE2	2.03	0.74
1:A:282:ILE:HG21	1:A:602:VAL:HG21	1.71	0.71
2:B:422:VAL:O	2:B:425:ARG:HB2	1.90	0.71
1:A:385:LEU:O	1:A:388:ALA:HB3	1.91	0.71
1:A:693:LEU:HD12	1:A:694:PHE:H	1.58	0.68
1:A:672:ASP:O	1:A:675:VAL:HG12	1.93	0.68
1:A:350:ASN:O	1:A:350:ASN:ND2	2.28	0.66
1:A:363:TYR:CD2	1:A:734:ILE:HG23	2.32	0.64
1:A:418:LEU:CD1	2:B:324:VAL:HG21	2.27	0.64
1:A:660:ASN:HA	1:A:749:SER:OG	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:453:GLU:HA	1:A:453:GLU:OE1	1.97	0.64
2:B:368:GLU:OE2	2:B:371:ARG:NH1	2.28	0.63
1:A:451:LEU:HD23	1:A:494:TYR:HB2	1.79	0.63
1:A:363:TYR:CE2	1:A:734:ILE:HG23	2.33	0.62
1:A:548:SER:O	1:A:552:TRP:HB3	1.98	0.62
1:A:666:PHE:O	1:A:701:PRO:HG2	2.00	0.62
1:A:807:TYR:N	1:A:808:PRO:HD3	2.14	0.62
1:A:691:LEU:HD22	1:A:727:CYS:SG	2.41	0.61
2:B:424:TYR:O	2:B:426:ARG:N	2.35	0.60
1:A:700:ALA:HB1	1:A:701:PRO:HD2	1.82	0.59
1:A:235:LEU:HD21	1:A:246:THR:CG2	2.33	0.58
1:A:793:ILE:N	1:A:793:ILE:HD13	2.19	0.58
1:A:196:PHE:N	1:A:197:PRO:CD	2.67	0.57
1:A:594:ARG:HA	1:A:640:VAL:O	2.04	0.57
1:A:658:ASN:ND2	1:A:752:ARG:HB2	2.20	0.56
1:A:566:THR:HG21	1:A:697:LEU:CD1	2.33	0.56
2:B:381:ALA:CA	2:B:416:GLN:HE22	2.17	0.56
1:A:520:TYR:CE2	1:A:521:LEU:HD12	2.41	0.55
1:A:720:ASP:O	1:A:724:VAL:HG23	2.06	0.55
2:B:309:LYS:HG3	2:B:310:PRO:HD2	1.88	0.55
1:A:677:LEU:HD23	1:A:677:LEU:N	2.22	0.55
1:A:195:CYS:SG	4:A:902:DTT:S4	3.05	0.55
7:A:910:GOL:H32	7:A:911:GOL:C3	2.38	0.54
1:A:442:LYS:HE3	2:B:355:THR:HG21	1.88	0.54
2:B:403:GLN:OE1	2:B:403:GLN:HA	2.06	0.54
1:A:437:THR:HG22	1:A:508:LEU:HD21	1.88	0.53
2:B:414:VAL:O	2:B:418:LYS:HG3	2.08	0.53
1:A:725:GLY:O	1:A:727:CYS:N	2.42	0.53
1:A:266:ILE:HD12	1:A:577:ALA:HB1	1.89	0.52
1:A:468:VAL:O	1:A:472:ARG:NH1	2.41	0.52
2:B:416:GLN:O	2:B:419:ASN:HB2	2.09	0.52
2:B:359:LEU:HD23	2:B:359:LEU:N	2.25	0.52
2:B:310:PRO:O	2:B:311:PRO:C	2.48	0.52
1:A:391:TYR:CD1	1:A:395:GLN:HG3	2.45	0.51
1:A:418:LEU:HD12	2:B:324:VAL:HG21	1.93	0.51
1:A:445:LEU:CD1	2:B:360:LYS:HG3	2.41	0.51
1:A:241:PRO:O	1:A:244:SER:HB3	2.11	0.50
1:A:391:TYR:CE1	2:B:310:PRO:HD3	2.45	0.50
1:A:419:GLN:HE22	2:B:315:PHE:H	1.59	0.50
1:A:343:ALA:O	1:A:346:SER:OG	2.30	0.50
1:A:564:HIS:ND1	3:A:901[A]:CW0:C12	2.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:812:HIS:O	1:A:816:LEU:HG	2.12	0.50
1:A:725:GLY:C	1:A:727:CYS:H	2.14	0.50
1:A:413:GLU:HG3	5:A:903:ACT:H2	1.92	0.50
1:A:332:MET:CE	1:A:704:LEU:HD13	2.42	0.50
1:A:325:TYR:O	1:A:326:VAL:HG23	2.12	0.49
2:B:378:LYS:O	2:B:380:ASN:N	2.45	0.49
1:A:464:GLU:O	1:A:467:GLU:HB2	2.12	0.49
2:B:421:PHE:HE1	2:B:434:LEU:HD11	1.77	0.49
2:B:324:VAL:HG12	2:B:324:VAL:O	2.13	0.49
2:B:395:ILE:HG22	2:B:433:VAL:CG1	2.42	0.49
1:A:725:GLY:C	1:A:727:CYS:N	2.66	0.49
2:B:350:GLN:HA	2:B:350:GLN:OE1	2.13	0.49
1:A:235:LEU:HD21	1:A:246:THR:HG22	1.95	0.48
1:A:437:THR:HG22	1:A:508:LEU:CD2	2.43	0.48
1:A:723:ILE:O	1:A:727:CYS:HB2	2.12	0.48
2:B:395:ILE:HG22	2:B:433:VAL:HG12	1.95	0.48
2:B:399:GLY:HA3	2:B:437:TRP:CE3	2.49	0.48
1:A:781:THR:OG1	1:A:794:PRO:HB3	2.12	0.48
1:A:332:MET:HG2	1:A:333:VAL:HG23	1.95	0.47
2:B:370:TYR:N	2:B:370:TYR:CD1	2.82	0.47
2:B:400:ARG:O	2:B:402:PHE:N	2.46	0.47
1:A:341:PRO:CG	1:A:816:LEU:HD21	2.44	0.47
1:A:418:LEU:HD11	2:B:324:VAL:HG21	1.97	0.47
1:A:541:ALA:O	1:A:657:GLY:HA3	2.15	0.47
2:B:309:LYS:CG	2:B:310:PRO:HD2	2.44	0.47
1:A:807:TYR:N	1:A:808:PRO:CD	2.78	0.47
1:A:707:VAL:HG11	1:A:715:MET:HG3	1.97	0.47
2:B:383:TRP:CZ2	2:B:420:PHE:HB2	2.50	0.47
2:B:383:TRP:CE3	2:B:412:LYS:HE2	2.49	0.46
1:A:235:LEU:HD21	1:A:246:THR:HG21	1.97	0.46
1:A:276:LYS:HE2	1:A:277:LYS:N	2.30	0.46
2:B:309:LYS:HD3	2:B:310:PRO:CD	2.45	0.46
1:A:793:ILE:N	1:A:793:ILE:CD1	2.78	0.46
2:B:370:TYR:N	2:B:370:TYR:HD1	2.13	0.46
1:A:606:ASN:HD22	1:A:609:SER:H	1.63	0.46
1:A:374:LYS:O	1:A:377:MET:N	2.43	0.46
1:A:755:PRO:HA	1:A:758:ARG:NH1	2.31	0.45
2:B:321:VAL:O	2:B:325:SER:OG	2.35	0.45
1:A:266:ILE:CD1	1:A:577:ALA:HB1	2.46	0.45
1:A:660:ASN:HD21	1:A:716:GLU:CG	2.29	0.45
1:A:693:LEU:HD12	1:A:693:LEU:C	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:GLU:O	1:A:497:LEU:HD13	2.17	0.45
1:A:660:ASN:HD21	1:A:716:GLU:HG3	1.81	0.45
1:A:694:PHE:HA	1:A:704:LEU:O	2.17	0.44
1:A:707:VAL:HG12	1:A:712:ALA:HA	1.99	0.44
1:A:486:ASP:OD1	2:B:398:TYR:OH	2.30	0.44
1:A:530:ASP:OD2	1:A:685:THR:HA	2.18	0.44
1:A:697:LEU:N	1:A:697:LEU:CD2	2.81	0.44
1:A:456:LYS:HA	2:B:370:TYR:CE2	2.53	0.43
1:A:391:TYR:HE1	2:B:309:LYS:HE3	1.83	0.43
2:B:309:LYS:HA	2:B:309:LYS:CE	2.39	0.43
1:A:478:PHE:O	1:A:482:SER:HB3	2.17	0.43
1:A:664:LEU:HD11	1:A:727:CYS:SG	2.58	0.43
2:B:429:ASN:N	2:B:429:ASN:OD1	2.52	0.43
1:A:442:LYS:CE	2:B:355:THR:HG21	2.49	0.43
1:A:386:LEU:O	1:A:389:THR:N	2.48	0.43
1:A:435:VAL:CG1	2:B:349:ILE:HG13	2.49	0.43
1:A:306:LEU:HD13	1:A:584:ILE:HG12	2.00	0.42
1:A:778:GLN:HG2	6:A:906:MLA:C3	2.48	0.42
2:B:408:VAL:HG12	2:B:409:ILE:N	2.34	0.42
1:A:391:TYR:CE1	1:A:395:GLN:HG3	2.55	0.42
2:B:438:GLU:O	2:B:440:GLU:N	2.53	0.42
1:A:332:MET:HE1	1:A:704:LEU:HD13	2.00	0.42
1:A:341:PRO:HG3	1:A:816:LEU:HD21	2.01	0.42
2:B:415:VAL:CG2	2:B:416:GLN:N	2.83	0.42
1:A:221:TRP:CD1	1:A:262:ILE:HA	2.55	0.42
1:A:362:LEU:C	1:A:363:TYR:CD1	2.93	0.42
1:A:525:ASP:O	1:A:528:ILE:N	2.53	0.42
1:A:680:HIS:CD2	1:A:730:ILE:HG23	2.55	0.42
2:B:377:GLN:HB2	2:B:410:GLY:O	2.20	0.42
1:A:670:PHE:CD1	1:A:670:PHE:O	2.73	0.41
1:A:378:VAL:O	1:A:381:GLU:N	2.53	0.41
1:A:560:PHE:CE1	1:A:807:TYR:HE2	2.39	0.41
1:A:574:VAL:HB	1:A:575:PRO:HD3	2.02	0.41
2:B:433:VAL:O	2:B:436:GLU:HB2	2.20	0.41
1:A:658:ASN:OD1	1:A:659:LEU:N	2.51	0.41
1:A:732:LYS:O	1:A:736:GLY:N	2.51	0.41
1:A:467:GLU:O	1:A:469:LYS:N	2.53	0.41
1:A:643:LEU:HA	1:A:644:PRO:HD2	1.86	0.41
1:A:660:ASN:CA	1:A:749:SER:OG	2.65	0.41
1:A:368:GLN:O	1:A:369:ALA:O	2.38	0.41
1:A:393:SER:O	1:A:397:ASP:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:380:ASN:OD1	2:B:381:ALA:N	2.54	0.41
2:B:309:LYS:HD3	2:B:310:PRO:HD2	2.03	0.41
2:B:378:LYS:H	2:B:378:LYS:CD	2.33	0.41
1:A:811:VAL:O	1:A:812:HIS:C	2.60	0.41
2:B:333:THR:HG22	2:B:334:VAL:N	2.37	0.41
1:A:368:GLN:C	1:A:369:ALA:O	2.59	0.40
1:A:424:LYS:O	1:A:426:GLU:N	2.54	0.40
1:A:522:SER:O	1:A:525:ASP:N	2.51	0.40
1:A:633:GLN:HA	1:A:634:PRO:HA	1.90	0.40
2:B:327:ASN:ND2	2:B:330:ALA:HB2	2.36	0.40
1:A:399:ASN:C	1:A:406:VAL:HG23	2.41	0.40
1:A:490:LEU:HD23	1:A:490:LEU:N	2.36	0.40
1:A:773:TYR:CE2	1:A:808:PRO:HB3	2.57	0.40
1:A:778:GLN:HG2	6:A:906:MLA:O3A	2.22	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	659/662 (100%)	560 (85%)	85 (13%)	14 (2%)	7	24
2	B	131/140 (94%)	100 (76%)	21 (16%)	10 (8%)	1	2
All	All	790/802 (98%)	660 (84%)	106 (13%)	24 (3%)	4	15

All (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

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Mol	Chain	Res	Type
1	A	244	SER
1	A	425	ASP
2	B	429	ASN
2	B	439	ALA
1	A	403	ASN
1	A	726	ARG
2	B	331	ALA
2	B	373	PRO
1	A	507	LYS
1	A	659	LEU
2	B	351	ASN
2	B	401	ASP
2	B	419	ASN
1	A	482	SER
1	A	526	ARG
1	A	322	LYS
1	A	423	VAL
1	A	457	GLU
1	A	516	PRO
2	B	333	THR

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	561/562 (100%)	498 (89%)	63 (11%)	6 16
2	B	117/121 (97%)	93 (80%)	24 (20%)	1 3
All	All	678/683 (99%)	591 (87%)	87 (13%)	4 12

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	198	ASP
1	A	200	ILE
1	A	205	GLN

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Mol	Chain	Res	Type
1	A	237	GLN
1	A	267	TYR
1	A	276	LYS
1	A	277	LYS
1	A	304	VAL
1	A	324	ASN
1	A	350	ASN
1	A	355	LYS
1	A	374	LYS
1	A	404	LYS
1	A	429	GLU
1	A	433	LYS
1	A	453	GLU
1	A	454	LYS
1	A	458	LEU
1	A	482	SER
1	A	485	ARG
1	A	514	ASN
1	A	517	SER
1	A	526	ARG
1	A	538	PHE
1	A	543	PRO
1	A	555	ASP
1	A	557	ASP
1	A	568	ARG
1	A	571	TYR
1	A	572	SER
1	A	588	THR
1	A	591	ARG
1	A	594	ARG
1	A	598	SER
1	A	610	THR
1	A	617	LYS
1	A	624	THR
1	A	633	GLN
1	A	638	GLN
1	A	640	VAL
1	A	645	GLU
1	A	659	LEU
1	A	668	ARG
1	A	675	VAL
1	A	676	ASN

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Mol	Chain	Res	Type
1	A	680	HIS
1	A	684	THR
1	A	691	LEU
1	A	696	ASN
1	A	697	LEU
1	A	702	ILE
1	A	704	LEU
1	A	717	ASN
1	A	718	ILE
1	A	727	CYS
1	A	738	SER
1	A	744	LYS
1	A	745	GLU
1	A	749	SER
1	A	785	SER
1	A	786	ILE
1	A	793	ILE
1	A	821	GLU
2	B	309	LYS
2	B	314	MET
2	B	316	LEU
2	B	325	SER
2	B	335	LEU
2	B	339	ASP
2	B	344	SER
2	B	362	LYS
2	B	370	TYR
2	B	373	PRO
2	B	376	ILE
2	B	377	GLN
2	B	378	LYS
2	B	379	CYS
2	B	382	ARG
2	B	385	THR
2	B	408	VAL
2	B	415	VAL
2	B	421	PHE
2	B	422	VAL
2	B	426	ARG
2	B	429	ASN
2	B	435	GLN
2	B	438	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	237	GLN
1	A	395	GLN
1	A	422	HIS
1	A	438	GLN
1	A	633	GLN
1	A	717	ASN
2	B	337	GLN
2	B	348	GLN
2	B	377	GLN
2	B	416	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 monosaccharides 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	$\# Z > 2$
6	MLA	A	905	-	6,6,6	1.51	0	7,7,7	0.85	0
7	GOL	A	908	-	5,5,5	0.26	0	5,5,5	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	EDO	A	919	-	3,3,3	0.24	0	2,2,2	0.30	0
9	EDO	A	913	-	3,3,3	0.26	0	2,2,2	0.57	0
7	GOL	A	909	-	5,5,5	0.27	0	5,5,5	0.55	0
9	EDO	A	923	-	3,3,3	0.46	0	2,2,2	0.86	0
3	CW0	A	901[A]	-	28,31,31	1.78	9 (32%)	35,43,43	3.25	15 (42%)
6	MLA	A	907	-	6,6,6	1.24	0	7,7,7	0.87	0
9	EDO	A	916	-	3,3,3	0.23	0	2,2,2	0.37	0
6	MLA	A	906	-	6,6,6	1.41	1 (16%)	7,7,7	0.97	0
9	EDO	A	915	-	3,3,3	0.07	0	2,2,2	0.20	0
9	EDO	A	922	-	3,3,3	0.12	0	2,2,2	0.07	0
9	EDO	A	918	-	3,3,3	0.06	0	2,2,2	0.17	0
5	ACT	A	904	-	3,3,3	1.29	0	3,3,3	0.63	0
8	D3U	A	912	-	62,69,69	3.91	24 (38%)	70,107,107	2.08	22 (31%)
9	EDO	A	921	-	3,3,3	0.14	0	2,2,2	0.28	0
9	EDO	A	920	-	3,3,3	0.23	0	2,2,2	0.21	0
7	GOL	A	911	-	5,5,5	0.19	0	5,5,5	0.47	0
9	EDO	A	924	-	3,3,3	0.18	0	2,2,2	0.09	0
4	DTT	A	902	-	7,7,7	0.50	0	4,8,8	1.16	0
9	EDO	A	917	-	3,3,3	0.17	0	2,2,2	0.35	0
9	EDO	A	914	-	3,3,3	0.36	0	2,2,2	0.63	0
10	PEG	A	926	-	6,6,6	0.29	0	5,5,5	0.18	0
7	GOL	A	910	-	5,5,5	0.12	0	5,5,5	0.36	0
10	PEG	A	925	-	6,6,6	0.14	0	5,5,5	0.16	0
5	ACT	A	903	-	3,3,3	1.05	0	3,3,3	1.54	1 (33%)
10	PEG	A	927	-	6,6,6	0.30	0	5,5,5	0.18	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
6	MLA	A	905	-	-	2/4/4/4	-
7	GOL	A	908	-	-	0/4/4/4	-
9	EDO	A	919	-	-	0/1/1/1	-
9	EDO	A	913	-	-	1/1/1/1	-
7	GOL	A	909	-	-	3/4/4/4	-
9	EDO	A	923	-	-	1/1/1/1	-
3	CW0	A	901[A]	-	-	6/16/44/44	0/4/4/4
6	MLA	A	907	-	-	2/4/4/4	-
9	EDO	A	916	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MLA	A	906	-	-	2/4/4/4	-
9	EDO	A	915	-	-	1/1/1/1	-
9	EDO	A	922	-	-	1/1/1/1	-
9	EDO	A	918	-	-	0/1/1/1	-
8	D3U	A	912	-	-	1/34/103/103	0/8/8/8
9	EDO	A	921	-	-	1/1/1/1	-
9	EDO	A	920	-	-	1/1/1/1	-
7	GOL	A	911	-	-	4/4/4/4	-
9	EDO	A	924	-	-	1/1/1/1	-
4	DTT	A	902	-	-	4/8/8/8	-
9	EDO	A	917	-	-	0/1/1/1	-
9	EDO	A	914	-	-	1/1/1/1	-
10	PEG	A	926	-	-	2/4/4/4	-
7	GOL	A	910	-	-	4/4/4/4	-
10	PEG	A	925	-	-	2/4/4/4	-
10	PEG	A	927	-	-	2/4/4/4	-

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	912	D3U	CAJ-CAK	-18.28	1.34	1.54
8	A	912	D3U	CCB-CCD	-9.76	1.39	1.52
8	A	912	D3U	C2-N1	8.35	1.49	1.33
8	A	912	D3U	CCE-CCB	-8.31	1.44	1.52
8	A	912	D3U	CAK-NAM	6.74	1.48	1.37
8	A	912	D3U	C2-N3	5.81	1.41	1.32
8	A	912	D3U	CAF-CAE	-5.78	1.39	1.51
8	A	912	D3U	CAJ-CCB	5.52	1.66	1.58
8	A	912	D3U	CAH-NAI	-5.38	1.28	1.40
8	A	912	D3U	CAS-CAT	5.13	1.59	1.52
8	A	912	D3U	PBF-OBH	5.12	1.79	1.55
8	A	912	D3U	CAD-CAC	-4.78	1.41	1.51
3	A	901[A]	CW0	C9-N10	3.88	1.41	1.35
3	A	901[A]	CW0	C22-C20	3.87	1.54	1.49
8	A	912	D3U	CAN-NAM	3.55	1.47	1.39
8	A	912	D3U	PBB-OBA	3.38	1.73	1.59
8	A	912	D3U	O3'-C3'	3.34	1.50	1.43
8	A	912	D3U	PBB-OBD	3.20	1.62	1.50
3	A	901[A]	CW0	O11-C9	2.98	1.25	1.21
8	A	912	D3U	CAJ-NAI	2.87	1.50	1.47
8	A	912	D3U	CAS-NAR	2.81	1.55	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	912	D3U	CCJ-CCE	2.80	1.43	1.39
8	A	912	D3U	CCC-NAI	-2.76	1.35	1.39
3	A	901[A]	CW0	C20-N19	2.67	1.53	1.47
3	A	901[A]	CW0	C22-C21	2.47	1.54	1.50
3	A	901[A]	CW0	C23-C21	2.36	1.55	1.51
3	A	901[A]	CW0	C16-N10	2.20	1.50	1.47
8	A	912	D3U	OAL-CAK	2.20	1.26	1.22
8	A	912	D3U	CAQ-NAP	2.18	1.37	1.31
8	A	912	D3U	O4'-C4'	2.18	1.49	1.45
3	A	901[A]	CW0	C17-N19	2.13	1.49	1.46
3	A	901[A]	CW0	C15-C16	2.07	1.57	1.52
8	A	912	D3U	CAG-CAE	-2.04	1.36	1.39
6	A	906	MLA	O3A-C3	2.03	1.28	1.22

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	901[A]	CW0	C15-C14-C13	-7.92	104.99	110.75
3	A	901[A]	CW0	O8-C9-N10	7.69	121.11	111.66
8	A	912	D3U	O4'-C1'-C2'	-6.90	96.85	106.93
3	A	901[A]	CW0	C15-C14-C17	6.13	121.84	109.39
3	A	901[A]	CW0	O8-C9-O11	-5.82	114.86	124.78
3	A	901[A]	CW0	C12-C13-C14	5.57	116.77	112.38
8	A	912	D3U	CAH-NAI-CCC	-5.38	115.30	123.82
3	A	901[A]	CW0	C16-C15-C14	-5.22	108.26	112.38
3	A	901[A]	CW0	C17-N19-C20	5.16	122.29	115.04
8	A	912	D3U	PBF-OBE-PBB	-4.19	118.43	132.83
8	A	912	D3U	N3-C2-N1	-4.14	122.21	128.68
3	A	901[A]	CW0	C22-C20-N19	3.93	125.17	117.50
8	A	912	D3U	CAB-CAA-CAH	-3.79	114.35	120.11
8	A	912	D3U	CAH-CAA-NAR	3.41	123.36	118.92
8	A	912	D3U	CCI-CCJ-CCE	3.26	124.68	120.65
3	A	901[A]	CW0	C6-C5-C4	-3.26	107.11	112.14
8	A	912	D3U	OAL-CAK-NAM	3.10	125.44	120.50
3	A	901[A]	CW0	C2-N1-C6	2.98	118.90	110.34
3	A	901[A]	CW0	C2-C3-C4	-2.88	107.69	112.14
8	A	912	D3U	N6-C6-N1	2.87	124.53	118.57
8	A	912	D3U	CAJ-CAK-NAM	-2.73	113.34	116.97
8	A	912	D3U	PBB-OBA-CAZ	-2.70	105.84	121.68
3	A	901[A]	CW0	C16-N10-C9	2.68	129.43	121.77
8	A	912	D3U	OBA-CAZ-CAX	2.65	116.43	109.36
8	A	912	D3U	NAM-CAN-NAP	-2.61	114.27	119.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	912	D3U	OBH-PBF-O5'	-2.52	96.06	107.75
8	A	912	D3U	CAZ-CAX-CAV	-2.50	107.38	112.20
8	A	912	D3U	CCH-CCG-CCF	2.48	123.97	120.19
8	A	912	D3U	C5-C6-N6	-2.47	116.60	120.35
8	A	912	D3U	O4'-C4'-C5'	-2.45	101.31	109.37
8	A	912	D3U	OAU-CAT-CAV	-2.30	103.51	109.10
3	A	901[A]	CW0	C27-C26-C25	-2.15	115.94	119.93
3	A	901[A]	CW0	C28-C23-C21	2.13	125.11	121.08
8	A	912	D3U	OBH-PBF-OBG	2.10	122.62	112.24
8	A	912	D3U	CAS-CAT-CAV	2.09	115.64	109.79
3	A	901[A]	CW0	C28-C23-C24	-2.08	115.70	118.29
5	A	903	ACT	O-C-CH3	-2.04	114.38	122.33
8	A	912	D3U	OAW-CAV-CAX	-2.04	103.88	108.81

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	901[A]	CW0	C5-C4-C7-O8
3	A	901[A]	CW0	C3-C4-C7-O8
3	A	901[A]	CW0	N10-C9-O8-C7
3	A	901[A]	CW0	O11-C9-O8-C7
4	A	902	DTT	S1-C1-C2-O2
4	A	902	DTT	S1-C1-C2-C3
4	A	902	DTT	C2-C3-C4-S4
4	A	902	DTT	O3-C3-C4-S4
7	A	910	GOL	C1-C2-C3-O3
7	A	910	GOL	O2-C2-C3-O3
7	A	910	GOL	O1-C1-C2-O2
10	A	925	PEG	O1-C1-C2-O2
10	A	926	PEG	O2-C3-C4-O4
10	A	926	PEG	O1-C1-C2-O2
7	A	909	GOL	O1-C1-C2-C3
7	A	909	GOL	C1-C2-C3-O3
7	A	910	GOL	O1-C1-C2-C3
7	A	911	GOL	C1-C2-C3-O3
7	A	909	GOL	O2-C2-C3-O3
10	A	925	PEG	O2-C3-C4-O4
9	A	913	EDO	O1-C1-C2-O2
9	A	914	EDO	O1-C1-C2-O2
9	A	915	EDO	O1-C1-C2-O2
9	A	921	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
9	A	920	EDO	O1-C1-C2-O2
9	A	922	EDO	O1-C1-C2-O2
3	A	901[A]	CW0	C13-C14-C17-N19
8	A	912	D3U	O4'-C4'-C5'-O5'
7	A	911	GOL	O1-C1-C2-O2
7	A	911	GOL	O2-C2-C3-O3
3	A	901[A]	CW0	C15-C14-C17-N19
10	A	927	PEG	C1-C2-O2-C3
10	A	927	PEG	O2-C3-C4-O4
6	A	906	MLA	O1A-C1-C2-C3
9	A	924	EDO	O1-C1-C2-O2
6	A	905	MLA	C1-C2-C3-O3B
6	A	907	MLA	C1-C2-C3-O3A
6	A	905	MLA	C1-C2-C3-O3A
6	A	906	MLA	O1B-C1-C2-C3
6	A	907	MLA	C1-C2-C3-O3B
7	A	911	GOL	O1-C1-C2-C3
9	A	923	EDO	O1-C1-C2-O2

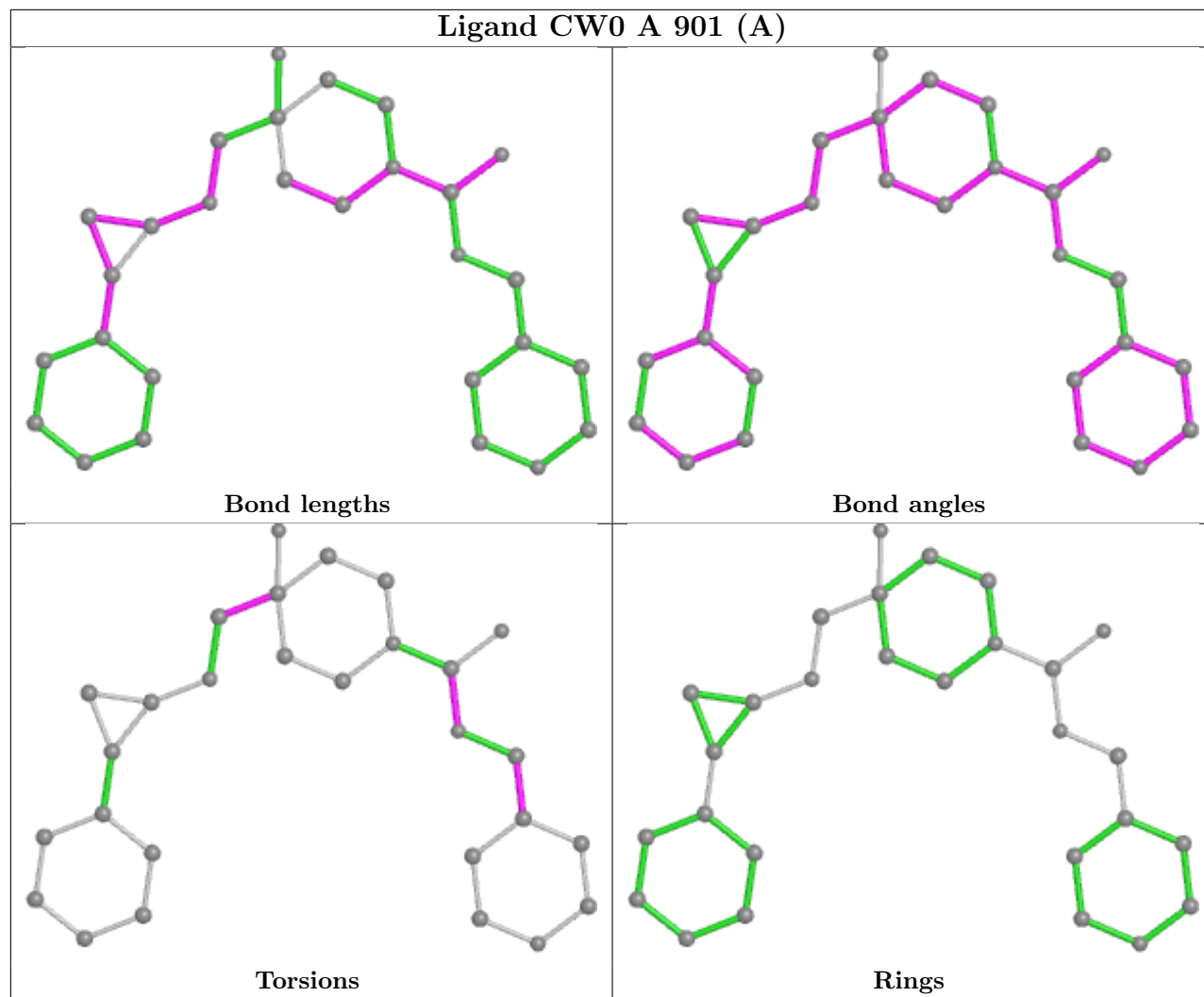
There are no ring outliers.

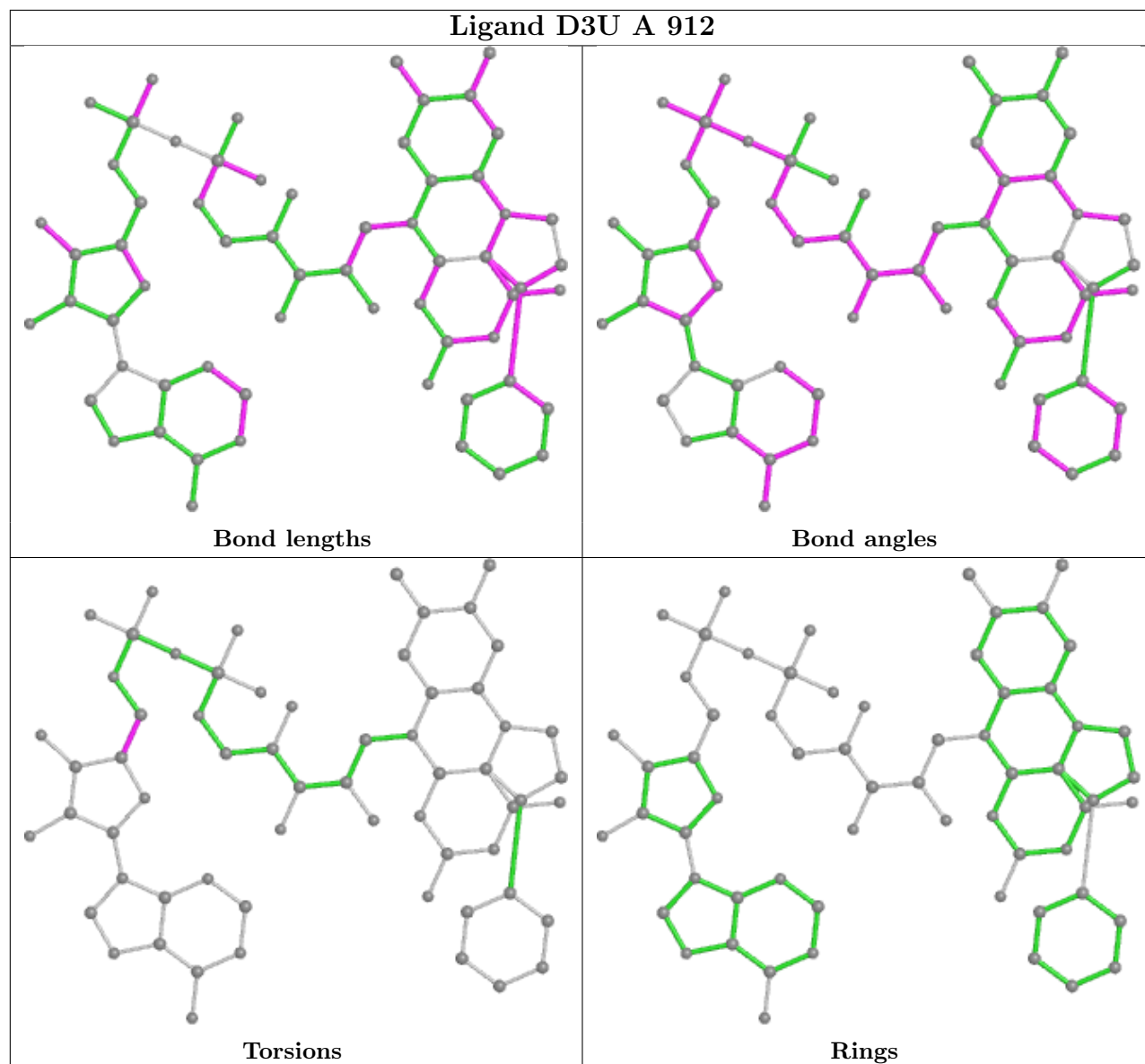
7 monomers are involved in 7 short contacts:

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





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%)	0.34	11 (1%) 70 70	68, 105, 150, 199	0
2	B	133/140 (95%)	0.23	5 (3%) 40 36	96, 140, 170, 208	0
All	All	794/802 (99%)	0.32	16 (2%) 65 63	68, 112, 158, 208	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	376	ILE	3.7
1	A	508	LEU	2.9
2	B	402	PHE	2.8
2	B	375	VAL	2.6
1	A	431	TRP	2.4
2	B	383	TRP	2.4
1	A	398	PHE	2.4
2	B	395	ILE	2.3
1	A	516	PRO	2.2
1	A	668	ARG	2.2
1	A	691	LEU	2.2
1	A	740	VAL	2.2
1	A	670	PHE	2.1
1	A	242	TYR	2.1
1	A	455	ILE	2.0
1	A	703	LEU	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 monosaccharides 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.

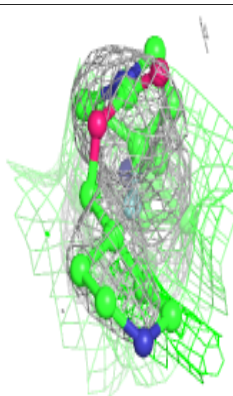
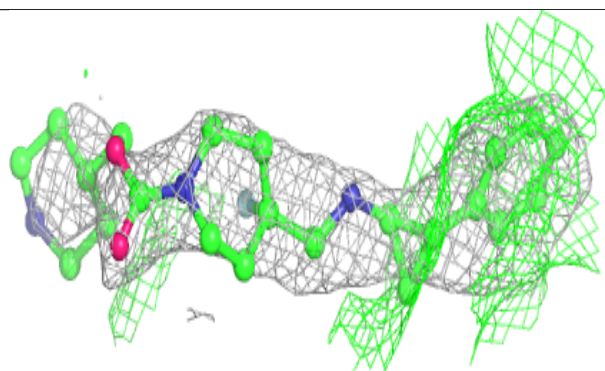
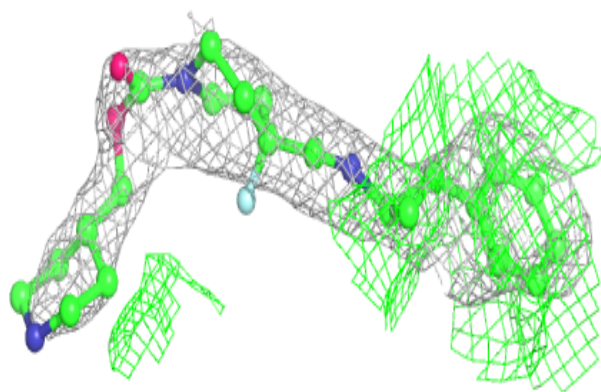
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
10	PEG	A	925	7/7	0.28	0.67	146,155,166,166	0
10	PEG	A	927	7/7	0.38	0.51	146,164,179,195	0
9	EDO	A	915	4/4	0.39	0.57	147,151,152,155	0
9	EDO	A	916	4/4	0.47	0.40	135,135,139,140	0
9	EDO	A	920	4/4	0.48	0.60	118,128,141,147	0
4	DTT	A	902	8/8	0.49	0.39	159,196,217,226	0
9	EDO	A	919	4/4	0.50	0.71	138,141,151,151	0
10	PEG	A	926	7/7	0.53	0.59	146,167,179,182	0
9	EDO	A	923	4/4	0.54	0.59	122,128,134,138	0
7	GOL	A	911	6/6	0.56	0.45	145,176,184,189	0
9	EDO	A	922	4/4	0.59	0.30	141,147,150,151	0
5	ACT	A	904	4/4	0.64	0.42	129,140,148,152	0
6	MLA	A	907	7/7	0.65	0.49	149,174,180,180	0
9	EDO	A	913	4/4	0.67	0.46	117,120,129,137	0
3	CW0	A	901[A]	28/28	0.69	0.50	132,168,191,195	0
9	EDO	A	921	4/4	0.72	0.54	131,133,137,139	0
9	EDO	A	917	4/4	0.72	0.66	113,139,140,145	0
9	EDO	A	924	4/4	0.73	0.27	133,135,137,140	0
9	EDO	A	914	4/4	0.74	0.60	112,128,132,147	0
7	GOL	A	908	6/6	0.76	0.35	104,118,144,145	0
11	CL	A	928	1/1	0.76	0.21	143,143,143,143	0
9	EDO	A	918	4/4	0.78	0.42	146,148,157,163	0
7	GOL	A	910	6/6	0.81	0.34	115,139,150,158	6
6	MLA	A	906	7/7	0.81	0.27	96,109,127,139	0
7	GOL	A	909	6/6	0.83	0.27	118,139,153,162	0
6	MLA	A	905	7/7	0.85	0.39	120,124,131,133	0
11	CL	A	929	1/1	0.85	0.63	140,140,140,140	0
5	ACT	A	903	4/4	0.93	0.26	85,88,94,104	0
8	D3U	A	912	62/62	0.98	0.21	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.

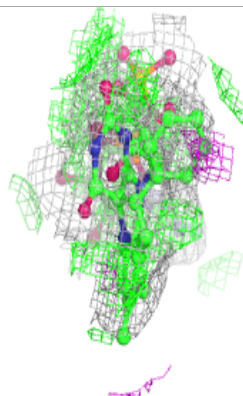
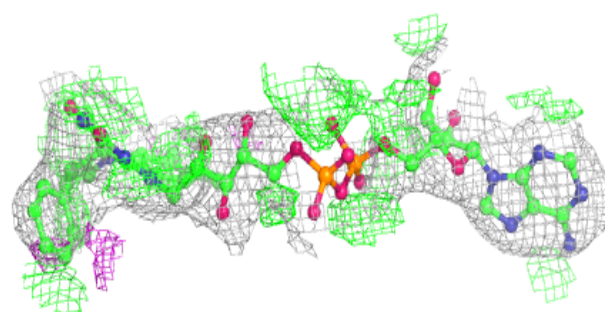
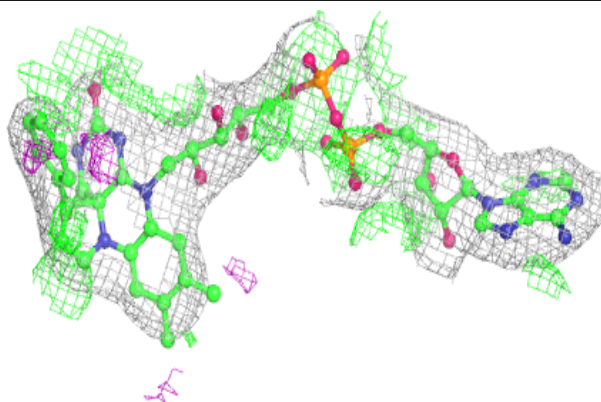
Electron density around CW0 A 901 (A):

$2mF_o-DF_c$ (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.