



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:25 PM UTC

PDB ID : 3S1S / pdb_00003s1s
Title : Characterization and crystal structure of the type IIG restriction endonuclease BpuSI
Authors : Shen, B.W.; Xu, D.; Chan, S.-H.; Zheng, Y.; Zhu, Y.; Xu, S.-Y.; Stoddard, B.L.
Deposited on : 2011-05-16
Resolution : 2.35 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	:	4-5-2 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

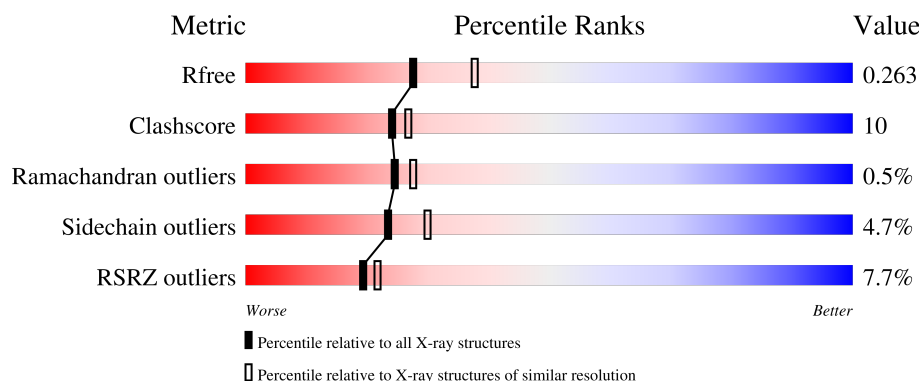
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

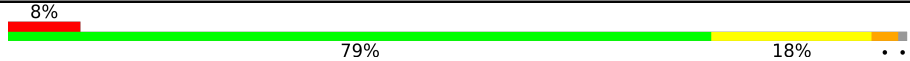
The reported resolution of this entry is 2.35 Å.

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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	878	

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
5	IOD	A	942	-	-	X	-
5	IOD	A	947	-	-	X	-
5	IOD	A	963	-	-	X	-

2 Entry composition [i](#)

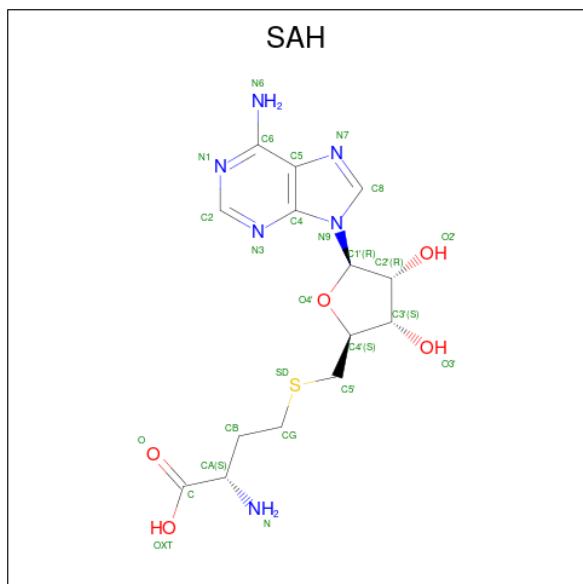
There are 6 unique types of molecules in this entry. The entry contains 7588 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 restriction endonuclease BpuSI.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	870	7127	4527	1205	1378	9	8	0	30	0

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	26	14	6	5	1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 4 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 5 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	38	Total I 38 38	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	316	Total O 316 316	0	0

3 Residue-property plots

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: restriction endonuclease BpuSI



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	213.47Å 215.73Å 73.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.35 30.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	92.8 (30.00-2.35) 92.7 (30.00-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.212 , 0.268 0.209 , 0.263	Depositor DCC
R_{free} test set	3581 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	40.2	Xtriage
Anisotropy	0.329	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7588	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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, SAH, IOD, MN

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	0.62	0/7344	0.86	0/9942

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	7127	0	7106	140	0
2	A	26	0	19	2	0
3	A	80	0	120	12	0
4	A	1	0	0	0	0
5	A	38	0	0	17	1
6	A	316	0	0	8	1
All	All	7588	0	7245	145	1

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 10.

All (145) 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:240:ASP:CG	1:A:241:PHE:H	1.34	1.23
5:A:952:IOD:I	6:A:1248:HOH:O	2.36	1.11
1:A:240:ASP:CG	1:A:241:PHE:N	2.11	0.99
1:A:763[B]:GLU:OE2	1:A:763[B]:GLU:HA	1.63	0.97
1:A:275:THR:HG22	1:A:277:ASP:H	1.31	0.93
1:A:288:THR:O	1:A:288:THR:HG23	1.74	0.86
1:A:273:ILE:HG13	1:A:278:GLU:HG3	1.57	0.85
1:A:331:GLY:HA3	2:A:900:SAH:HB2	1.56	0.85
5:A:939:IOD:I	6:A:1106:HOH:O	2.69	0.80
1:A:243:VAL:H	3:A:913:EDO:H11	1.45	0.79
1:A:593:ASN:OD1	1:A:854:LYS:HE2	1.83	0.79
1:A:7:ASN:HD21	1:A:39:ASN:HD21	1.30	0.78
1:A:624:ILE:HG12	1:A:668:LEU:HB2	1.67	0.76
1:A:624:ILE:CG1	1:A:668:LEU:HB2	2.15	0.76
1:A:706:GLU:H	1:A:706:GLU:CD	1.95	0.75
1:A:302:GLU:HA	1:A:302:GLU:OE1	1.88	0.73
1:A:275:THR:HG21	1:A:277:ASP:OD2	1.89	0.72
1:A:288:THR:O	1:A:288:THR:CG2	2.38	0.71
1:A:137:SER:O	1:A:174:LYS:HE2	1.89	0.71
2:A:900:SAH:N6	6:A:1235:HOH:O	2.23	0.71
1:A:143[B]:ASN:HD22	1:A:145:SER:H	1.36	0.70
1:A:763[B]:GLU:OE2	1:A:763[B]:GLU:CA	2.38	0.70
1:A:148:VAL:HG23	5:A:942:IOD:I	2.62	0.69
1:A:727:HIS:O	1:A:765:MSE:HG2	1.93	0.69
1:A:427:ILE:HD13	1:A:433:ARG:HA	1.75	0.68
1:A:423:ALA:O	1:A:427:ILE:HG12	1.95	0.67
1:A:729:VAL:HG13	1:A:757:VAL:HB	1.76	0.67
1:A:293:HIS:HE1	1:A:357:GLU:OE1	1.78	0.66
1:A:647:LEU:HD13	1:A:653:ILE:HD13	1.78	0.65
1:A:343:PHE:O	1:A:346:VAL:HG22	1.97	0.65
5:A:947:IOD:I	6:A:1250:HOH:O	2.85	0.64
1:A:349:ARG:HH22	3:A:904:EDO:H12	1.62	0.64
1:A:292:GLY:HA2	1:A:293:HIS:HB2	1.80	0.64
1:A:791:GLU:HG2	5:A:931:IOD:I	2.67	0.64
1:A:424:HIS:HB3	5:A:958:IOD:I	2.69	0.63
1:A:505:VAL:HG12	5:A:963:IOD:I	2.68	0.62
1:A:88:ARG:HE	1:A:92[A]:GLN:HE21	1.48	0.62
1:A:528:SER:HB2	1:A:558:MSE:HE3	1.83	0.60
1:A:427:ILE:CD1	1:A:433:ARG:HA	2.30	0.60
1:A:555:PRO:HG2	1:A:558:MSE:HB2	1.84	0.59
1:A:550:GLU:HG2	1:A:551:GLN:N	2.19	0.58
1:A:253:ASN:HD22	1:A:253:ASN:H	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:GLU:HG3	1:A:572:VAL:HG11	1.85	0.57
1:A:492:HIS:HB3	1:A:513:VAL:HB	1.87	0.57
1:A:251:ASN:HB3	1:A:253:ASN:ND2	2.20	0.56
1:A:223:ILE:HG22	3:A:910:EDO:H12	1.87	0.56
1:A:289:ARG:NE	1:A:289:ARG:O	2.39	0.55
1:A:729:VAL:HG11	1:A:768:LEU:HD23	1.88	0.55
1:A:837:LYS:O	1:A:841:LEU:HD13	2.06	0.55
1:A:504:GLU:O	5:A:963:IOD:I	2.96	0.54
1:A:758:PHE:HA	1:A:765:MSE:HE2	1.88	0.54
1:A:851:GLU:HG3	1:A:852:MSE:H	1.72	0.54
1:A:297:VAL:CG1	1:A:509[A]:THR:HG21	2.38	0.54
1:A:78:LYS:HE3	1:A:92[B]:GLN:HE22	1.73	0.54
1:A:223:ILE:CG2	3:A:910:EDO:H12	2.38	0.53
1:A:647:LEU:CD1	1:A:653:ILE:HD13	2.39	0.53
1:A:79:ARG:NH2	1:A:535:VAL:O	2.38	0.52
1:A:530:THR:HG23	1:A:534:GLN:HB2	1.91	0.52
1:A:291:ARG:HH11	1:A:291:ARG:HB3	1.74	0.51
1:A:810:ILE:HG23	1:A:814:LEU:HD23	1.93	0.51
1:A:355:ASP:O	1:A:386:GLY:HA2	2.10	0.51
1:A:275:THR:CG2	1:A:277:ASP:OD2	2.57	0.51
1:A:6:LEU:HD13	6:A:1253:HOH:O	2.10	0.51
1:A:230:GLY:H	3:A:907:EDO:H22	1.76	0.51
1:A:291:ARG:HB3	1:A:291:ARG:NH1	2.25	0.51
1:A:101:ASN:O	1:A:104:VAL:HB	2.10	0.50
1:A:416:PRO:HA	1:A:419:LYS:HE3	1.94	0.50
1:A:820:GLU:OE1	1:A:823:ARG:NH2	2.28	0.50
1:A:347:MSE:H	1:A:350:GLN:NE2	2.10	0.50
1:A:831:CYS:SG	1:A:873:GLY:HA3	2.51	0.50
1:A:624:ILE:HG13	1:A:668:LEU:HB2	1.94	0.49
1:A:240:ASP:OD2	1:A:241:PHE:N	2.33	0.49
1:A:495:LEU:HD23	1:A:510:VAL:HG23	1.95	0.49
1:A:39:ASN:HD22	1:A:160:GLN:NE2	2.10	0.49
1:A:851:GLU:HG3	1:A:852:MSE:N	2.27	0.49
1:A:491:GLU:OE2	1:A:515:ARG:CZ	2.61	0.49
1:A:240:ASP:OD1	1:A:381:ALA:CB	2.61	0.49
1:A:216:GLU:O	3:A:905:EDO:H12	2.13	0.49
1:A:143[B]:ASN:ND2	1:A:145:SER:H	2.07	0.49
1:A:699:LYS:NZ	5:A:940:IOD:I	3.02	0.49
1:A:240:ASP:OD1	6:A:1038:HOH:O	2.20	0.48
1:A:849:GLY:HA2	1:A:850:ASN:HA	1.57	0.48
1:A:650:VAL:HG21	1:A:732:PRO:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:624:ILE:HD13	1:A:643:LEU:CD2	2.44	0.48
1:A:487[B]:ASN:HA	3:A:916:EDO:H22	1.96	0.48
1:A:147:THR:HA	5:A:942:IOD:I	2.84	0.47
1:A:550:GLU:CG	1:A:551:GLN:N	2.77	0.47
1:A:706:GLU:CD	1:A:706:GLU:N	2.69	0.47
1:A:17:TYR:HE1	5:A:968:IOD:I	2.67	0.47
3:A:913:EDO:H12	6:A:1038:HOH:O	2.14	0.47
1:A:297:VAL:HG13	1:A:509[A]:THR:HG21	1.95	0.47
1:A:624:ILE:HD13	1:A:643:LEU:HD22	1.97	0.47
1:A:812:ASP:O	1:A:816:GLN:HG2	2.14	0.46
1:A:90:ARG:HH12	1:A:133:ILE:HD11	1.80	0.46
1:A:745:GLU:HG2	6:A:1162:HOH:O	2.14	0.46
1:A:807:LEU:H	1:A:807:LEU:HD12	1.81	0.46
1:A:429:LEU:HD11	1:A:454:LEU:HD13	1.98	0.46
1:A:291:ARG:HA	1:A:292:GLY:HA2	1.45	0.46
1:A:308:SER:HB2	1:A:339:VAL:HA	1.97	0.46
1:A:735:LEU:HD22	1:A:740:ARG:HD2	1.97	0.46
1:A:835:VAL:HG13	1:A:855:THR:CG2	2.46	0.46
1:A:564:LYS:HB3	1:A:566[B]:GLU:OE1	2.15	0.46
1:A:769:LEU:HD23	1:A:822:VAL:HG11	1.97	0.46
1:A:581:SER:O	1:A:585:VAL:HG12	2.16	0.45
1:A:611:GLY:HA3	1:A:751:SER:O	2.16	0.45
1:A:800:GLN:HG2	5:A:946:IOD:I	2.87	0.45
1:A:735:LEU:CD2	1:A:740:ARG:HD2	2.47	0.45
1:A:673:SER:HA	1:A:676:GLN:CD	2.42	0.45
1:A:120:PHE:CE1	1:A:133:ILE:HG12	2.51	0.44
1:A:550:GLU:OE1	1:A:550:GLU:N	2.39	0.44
1:A:567:GLU:HG2	5:A:947:IOD:I	2.87	0.44
1:A:645:PRO:HG3	1:A:660:GLU:HG2	1.98	0.44
1:A:835:VAL:HG13	1:A:855:THR:HG22	2.00	0.44
1:A:798:SER:OG	5:A:936:IOD:I	3.02	0.44
1:A:176:SER:HA	5:A:935:IOD:I	2.88	0.43
1:A:297:VAL:CG1	1:A:509[B]:THR:HG21	2.49	0.43
1:A:57:ILE:HA	1:A:504:GLU:HG2	2.01	0.43
1:A:275:THR:HG22	1:A:277:ASP:N	2.13	0.43
1:A:289:ARG:HD2	1:A:289:ARG:HA	1.80	0.43
1:A:576:TRP:O	1:A:579:ILE:HG12	2.17	0.43
1:A:732:PRO:HG2	1:A:740:ARG:HB2	1.99	0.43
1:A:521[B]:GLU:CD	1:A:521[B]:GLU:H	2.27	0.43
1:A:293:HIS:CE1	1:A:357:GLU:OE1	2.66	0.42
1:A:176:SER:HB2	5:A:962:IOD:I	2.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:PRO:HD3	5:A:933:IOD:I	2.88	0.42
1:A:704:LYS:HA	3:A:908:EDO:H21	2.01	0.42
1:A:253:ASN:HD22	1:A:253:ASN:N	2.16	0.42
1:A:228:ARG:O	1:A:231:ARG:HB2	2.19	0.42
1:A:593:ASN:HD21	3:A:901:EDO:H21	1.84	0.42
1:A:552:ILE:HD11	1:A:560:LEU:HG	2.02	0.42
1:A:292:GLY:HA3	1:A:294:GLU:H	1.85	0.42
1:A:147:THR:O	1:A:150[A]:GLU:HG2	2.20	0.42
1:A:251:ASN:HB3	1:A:253:ASN:HD22	1.85	0.42
1:A:29:CYS:HB2	1:A:114:LEU:HD21	2.02	0.41
1:A:347:MSE:H	1:A:350:GLN:HE21	1.68	0.41
1:A:655:THR:HG22	1:A:656:PRO:HD2	2.02	0.41
1:A:780:GLN:O	1:A:784:MSE:HG3	2.21	0.41
1:A:337:ALA:CB	3:A:906:EDO:H21	2.50	0.41
1:A:850:ASN:O	1:A:851:GLU:C	2.63	0.41
1:A:305:LYS:HE3	3:A:917:EDO:O2	2.20	0.41
1:A:434:PRO:HB2	1:A:437:LEU:HB2	2.03	0.40
1:A:494:PHE:HB3	1:A:511:VAL:HB	2.02	0.40
1:A:220:ARG:HD3	1:A:220:ARG:HA	1.92	0.40
1:A:429:LEU:CD1	1:A:454:LEU:HD13	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:959:IOD:I	6:A:1176:HOH:O[6_554]	1.91	0.29

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	898/878 (102%)	861 (96%)	33 (4%)	4 (0%)	30 34

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	ASP
1	A	548	SER
1	A	101	ASN
1	A	291	ARG

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	809/774 (104%)	771 (95%)	38 (5%)	23	30

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	LEU
1	A	104	VAL
1	A	129	VAL
1	A	210	LEU
1	A	253	ASN
1	A	288	THR
1	A	289	ARG
1	A	291	ARG
1	A	302	GLU
1	A	307	LEU
1	A	346	VAL
1	A	413	VAL
1	A	454	LEU
1	A	456	GLN
1	A	478	LYS
1	A	509[A]	THR
1	A	509[B]	THR
1	A	523	ILE
1	A	530	THR
1	A	551	GLN
1	A	553	ILE

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Mol	Chain	Res	Type
1	A	572	VAL
1	A	573	THR
1	A	585	VAL
1	A	624	ILE
1	A	650	VAL
1	A	652	GLU
1	A	655	THR
1	A	657	ILE
1	A	706	GLU
1	A	721	ASP
1	A	729	VAL
1	A	755	LEU
1	A	765	MSE
1	A	809	ASP
1	A	836	ARG
1	A	852	MSE
1	A	854	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	39	ASN
1	A	94	GLN
1	A	107	HIS
1	A	122	HIS
1	A	168	ASN
1	A	253	ASN
1	A	293	HIS
1	A	334	ASN
1	A	350	GLN
1	A	435	GLN
1	A	456	GLN
1	A	475	ASN
1	A	570	ASN
1	A	582	ASN
1	A	592	ASN
1	A	593	ASN
1	A	672	ASN
1	A	676	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 60 ligands modelled in this entry, 39 are monoatomic - leaving 21 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	$\# Z > 2$
3	EDO	A	921	-	3,3,3	0.57	0	2,2,2	0.11	0
2	SAH	A	900	-	27,28,28	1.64	5 (18%)	36,40,40	2.57	12 (33%)
3	EDO	A	920	-	3,3,3	0.54	0	2,2,2	0.18	0
3	EDO	A	909	-	3,3,3	0.36	0	2,2,2	0.50	0
3	EDO	A	913	-	3,3,3	0.42	0	2,2,2	0.39	0
3	EDO	A	906	-	3,3,3	0.59	0	2,2,2	0.48	0
3	EDO	A	912	-	3,3,3	0.35	0	2,2,2	0.54	0
3	EDO	A	916	-	3,3,3	0.43	0	2,2,2	0.48	0
3	EDO	A	905	-	3,3,3	0.47	0	2,2,2	0.51	0
3	EDO	A	918	-	3,3,3	0.45	0	2,2,2	0.46	0
3	EDO	A	919	-	3,3,3	0.47	0	2,2,2	0.36	0
3	EDO	A	904	-	3,3,3	0.50	0	2,2,2	0.30	0
3	EDO	A	915	-	3,3,3	0.52	0	2,2,2	0.33	0
3	EDO	A	910	-	3,3,3	0.35	0	2,2,2	0.37	0
3	EDO	A	908	-	3,3,3	0.39	0	2,2,2	0.45	0
3	EDO	A	911	-	3,3,3	0.47	0	2,2,2	0.29	0
3	EDO	A	917	-	3,3,3	0.32	0	2,2,2	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	907	-	3,3,3	0.39	0	2,2,2	0.49	0
3	EDO	A	903	-	3,3,3	0.71	0	2,2,2	0.11	0
3	EDO	A	914	-	3,3,3	0.53	0	2,2,2	0.28	0
3	EDO	A	901	-	3,3,3	0.44	0	2,2,2	0.35	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
3	EDO	A	921	-	-	1/1/1/1	-
2	SAH	A	900	-	-	8/15/31/31	0/3/3/3
3	EDO	A	920	-	-	1/1/1/1	-
3	EDO	A	909	-	-	1/1/1/1	-
3	EDO	A	913	-	-	1/1/1/1	-
3	EDO	A	906	-	-	0/1/1/1	-
3	EDO	A	912	-	-	1/1/1/1	-
3	EDO	A	916	-	-	0/1/1/1	-
3	EDO	A	905	-	-	0/1/1/1	-
3	EDO	A	918	-	-	0/1/1/1	-
3	EDO	A	919	-	-	1/1/1/1	-
3	EDO	A	904	-	-	1/1/1/1	-
3	EDO	A	915	-	-	1/1/1/1	-
3	EDO	A	910	-	-	1/1/1/1	-
3	EDO	A	908	-	-	1/1/1/1	-
3	EDO	A	911	-	-	1/1/1/1	-
3	EDO	A	917	-	-	1/1/1/1	-
3	EDO	A	907	-	-	1/1/1/1	-
3	EDO	A	903	-	-	1/1/1/1	-
3	EDO	A	914	-	-	1/1/1/1	-
3	EDO	A	901	-	-	1/1/1/1	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900	SAH	C5-C4	5.41	1.48	1.39
2	A	900	SAH	C5-N7	-2.62	1.34	1.39
2	A	900	SAH	OXT-C	-2.44	1.22	1.30
2	A	900	SAH	C4-N3	2.22	1.38	1.34
2	A	900	SAH	C5-C6	2.01	1.46	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	SAH	N3-C4-N9	6.92	138.94	127.17
2	A	900	SAH	C5-C4-N3	-6.72	117.47	126.72
2	A	900	SAH	CB-CG-SD	-4.94	102.43	113.45
2	A	900	SAH	C4-N9-C8	3.73	109.65	105.74
2	A	900	SAH	C2-N3-C4	3.65	120.74	111.83
2	A	900	SAH	N6-C6-N1	3.64	126.48	118.38
2	A	900	SAH	C5-C6-N6	-3.54	114.53	123.29
2	A	900	SAH	OXT-C-O	-3.34	116.51	124.08
2	A	900	SAH	N3-C2-N1	-3.02	124.01	128.58
2	A	900	SAH	C1'-N9-C8	-2.96	120.53	127.09
2	A	900	SAH	O4'-C1'-C2'	-2.33	101.64	106.62
2	A	900	SAH	C5-C4-N9	-2.04	103.59	105.81

There are no chirality outliers.

All (24) torsion outliers are listed below:

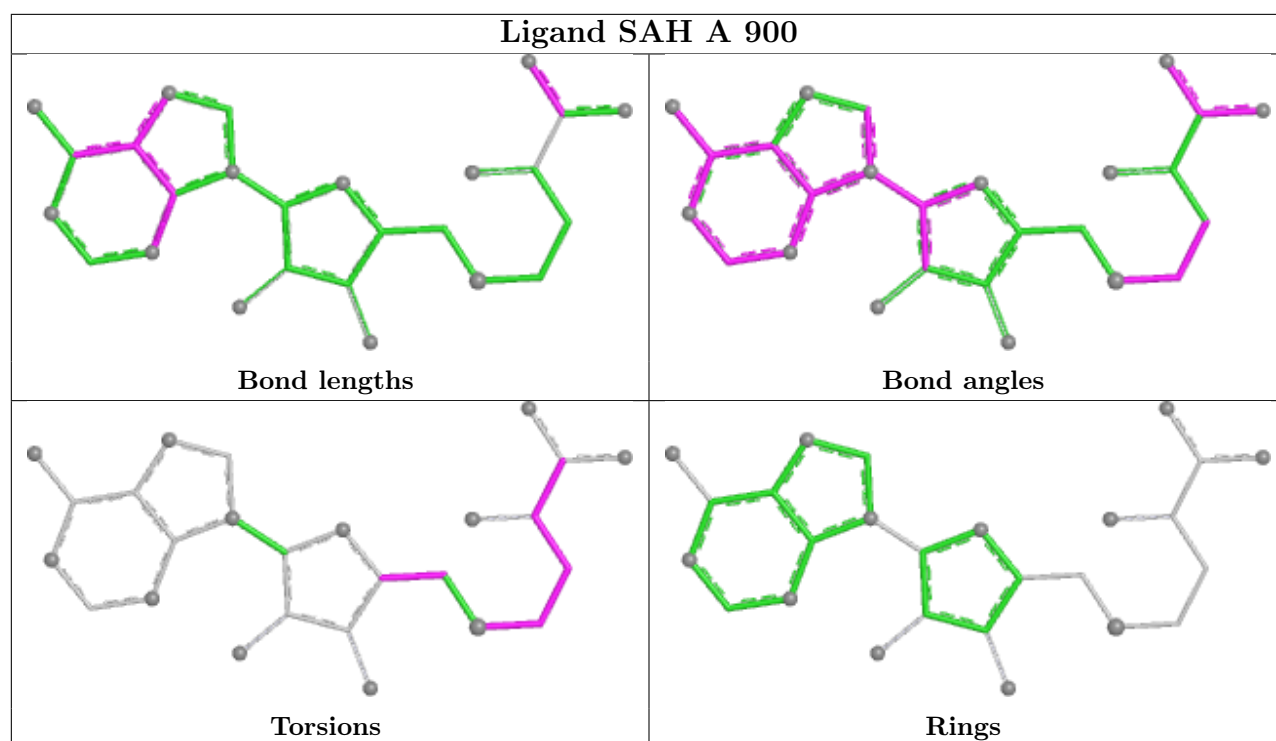
Mol	Chain	Res	Type	Atoms
2	A	900	SAH	O4'-C4'-C5'-SD
2	A	900	SAH	C3'-C4'-C5'-SD
2	A	900	SAH	CA-CB-CG-SD
3	A	908	EDO	O1-C1-C2-O2
3	A	919	EDO	O1-C1-C2-O2
2	A	900	SAH	C-CA-CB-CG
3	A	907	EDO	O1-C1-C2-O2
3	A	909	EDO	O1-C1-C2-O2
3	A	911	EDO	O1-C1-C2-O2
3	A	913	EDO	O1-C1-C2-O2
3	A	910	EDO	O1-C1-C2-O2
3	A	917	EDO	O1-C1-C2-O2
3	A	903	EDO	O1-C1-C2-O2
3	A	912	EDO	O1-C1-C2-O2
3	A	914	EDO	O1-C1-C2-O2
3	A	915	EDO	O1-C1-C2-O2
2	A	900	SAH	O-C-CA-CB
2	A	900	SAH	OXT-C-CA-CB
3	A	921	EDO	O1-C1-C2-O2
3	A	920	EDO	O1-C1-C2-O2
2	A	900	SAH	CB-CG-SD-C5'
3	A	904	EDO	O1-C1-C2-O2
2	A	900	SAH	N-CA-CB-CG
3	A	901	EDO	O1-C1-C2-O2

There are no ring outliers.

11 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	SAH	2	0
3	A	913	EDO	2	0
3	A	906	EDO	1	0
3	A	916	EDO	1	0
3	A	905	EDO	1	0
3	A	904	EDO	1	0
3	A	910	EDO	2	0
3	A	908	EDO	1	0
3	A	917	EDO	1	0
3	A	907	EDO	1	0
3	A	901	EDO	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 ⓘ

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	862/878 (98%)	0.55	66 (7%)	19 22	17, 40, 64, 76	30 (3%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	292	GLY	6.4
1	A	552	ILE	5.5
1	A	290	GLY	5.2
1	A	548	SER	4.9
1	A	549	ASN	4.5
1	A	617	GLY	4.5
1	A	551	GLN	4.4
1	A	550	GLU	4.3
1	A	677[A]	ASP	4.2
1	A	705	PHE	4.2
1	A	848	SER	4.1
1	A	624	ILE	4.0
1	A	291	ARG	3.8
1	A	504	GLU	3.6
1	A	684	ILE	3.6
1	A	706	GLU	3.6
1	A	6	LEU	3.5
1	A	807	LEU	3.5
1	A	413	VAL	3.5
1	A	847	TRP	3.5
1	A	505	VAL	3.4
1	A	763[A]	GLU	3.3
1	A	603	ALA	3.3
1	A	553	ILE	3.2
1	A	850	ASN	3.1
1	A	653	ILE	3.1
1	A	8	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	875	GLN	2.9
1	A	789	GLU	2.8
1	A	683	ILE	2.7
1	A	824	GLU	2.6
1	A	811[A]	ASP	2.6
1	A	709	LYS	2.5
1	A	678	GLY	2.5
1	A	293	HIS	2.5
1	A	499	GLU	2.5
1	A	657	ILE	2.4
1	A	835	VAL	2.4
1	A	440[A]	GLN	2.4
1	A	810	ILE	2.4
1	A	587	GLU	2.4
1	A	642	TRP	2.4
1	A	787	ASP	2.3
1	A	701	LYS	2.3
1	A	715	ILE	2.3
1	A	704	LYS	2.3
1	A	853	SER	2.3
1	A	711[A]	GLU	2.3
1	A	748	VAL	2.2
1	A	803	TYR	2.2
1	A	590	ILE	2.2
1	A	501	LEU	2.2
1	A	846	PHE	2.2
1	A	872	GLU	2.2
1	A	414	THR	2.2
1	A	809	ASP	2.2
1	A	597	HIS	2.2
1	A	676	GLN	2.2
1	A	56	SER	2.2
1	A	289	ARG	2.1
1	A	644	TYR	2.1
1	A	412	GLY	2.1
1	A	849	GLY	2.1
1	A	131[A]	GLN	2.1
1	A	128	VAL	2.1
1	A	125	ASN	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 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.

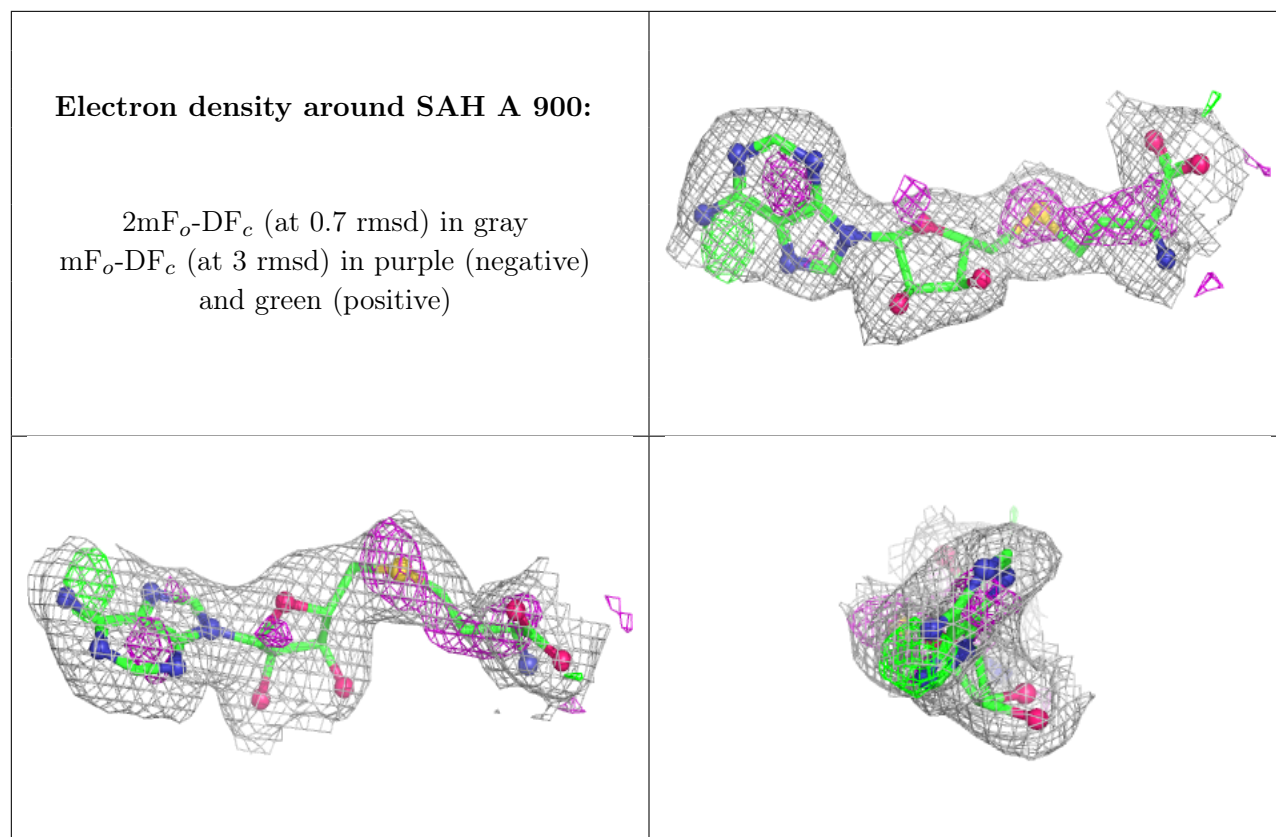
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	A	919	4/4	0.71	0.27	70,70,70,71	0
3	EDO	A	921	4/4	0.74	0.28	60,61,61,63	0
3	EDO	A	903	4/4	0.80	0.18	41,43,44,45	0
3	EDO	A	906	4/4	0.81	0.21	40,41,41,41	0
3	EDO	A	914	4/4	0.81	0.17	60,61,62,62	0
3	EDO	A	917	4/4	0.83	0.21	39,39,41,44	0
3	EDO	A	915	4/4	0.84	0.17	55,56,56,56	0
3	EDO	A	911	4/4	0.84	0.18	51,51,52,53	0
3	EDO	A	907	4/4	0.85	0.13	43,45,45,46	0
3	EDO	A	912	4/4	0.86	0.14	44,44,45,45	0
2	SAH	A	900	26/26	0.88	0.10	35,39,42,44	0
3	EDO	A	920	4/4	0.88	0.16	55,55,55,56	0
3	EDO	A	918	4/4	0.88	0.20	57,58,58,59	0
3	EDO	A	904	4/4	0.89	0.13	46,48,49,49	0
3	EDO	A	901	4/4	0.91	0.11	50,50,50,52	0
3	EDO	A	916	4/4	0.92	0.10	48,48,49,49	0
3	EDO	A	905	4/4	0.94	0.19	39,40,40,41	0
3	EDO	A	913	4/4	0.94	0.15	45,45,45,46	0
5	IOD	A	931	1/1	0.94	0.20	168,168,168,168	0
5	IOD	A	940	1/1	0.95	0.11	166,166,166,166	0
3	EDO	A	909	4/4	0.96	0.10	32,32,32,32	0
5	IOD	A	947	1/1	0.96	0.13	158,158,158,158	0
3	EDO	A	908	4/4	0.96	0.09	53,55,57,58	0
5	IOD	A	963	1/1	0.96	0.20	139,139,139,139	0
3	EDO	A	910	4/4	0.97	0.06	32,33,33,35	0
5	IOD	A	948	1/1	0.97	0.10	143,143,143,143	0
5	IOD	A	949	1/1	0.97	0.18	173,173,173,173	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	IOD	A	944	1/1	0.97	0.14	136,136,136,136	0
5	IOD	A	945	1/1	0.97	0.15	155,155,155,155	0
5	IOD	A	934	1/1	0.97	0.23	117,117,117,117	0
5	IOD	A	951	1/1	0.98	0.19	154,154,154,154	0
5	IOD	A	953	1/1	0.98	0.17	119,119,119,119	0
5	IOD	A	943	1/1	0.98	0.15	138,138,138,138	0
5	IOD	A	941	1/1	0.98	0.26	121,121,121,121	0
5	IOD	A	942	1/1	0.98	0.29	138,138,138,138	0
5	IOD	A	936	1/1	0.98	0.20	125,125,125,125	0
5	IOD	A	937	1/1	0.98	0.25	132,132,132,132	0
5	IOD	A	954	1/1	0.99	0.13	83,83,83,83	0
5	IOD	A	957	1/1	0.99	0.20	120,120,120,120	0
5	IOD	A	958	1/1	0.99	0.17	82,82,82,82	0
5	IOD	A	960	1/1	0.99	0.10	93,93,93,93	0
5	IOD	A	946	1/1	0.99	0.13	121,121,121,121	0
5	IOD	A	961	1/1	0.99	0.11	125,125,125,125	0
5	IOD	A	962	1/1	0.99	0.20	81,81,81,81	0
5	IOD	A	933	1/1	0.99	0.11	87,87,87,87	0
5	IOD	A	950	1/1	0.99	0.11	118,118,118,118	0
4	MN	A	930	1/1	0.99	0.03	27,27,27,27	0
5	IOD	A	952	1/1	0.99	0.08	104,104,104,104	0
5	IOD	A	966	1/1	0.99	0.15	78,78,78,78	0
5	IOD	A	939	1/1	0.99	0.10	90,90,90,90	0
5	IOD	A	938	1/1	0.99	0.10	108,108,108,108	0
5	IOD	A	964	1/1	1.00	0.04	79,79,79,79	1
5	IOD	A	935	1/1	1.00	0.03	51,51,51,51	0
5	IOD	A	965	1/1	1.00	0.13	72,72,72,72	0
5	IOD	A	955	1/1	1.00	0.01	40,40,40,40	0
5	IOD	A	956	1/1	1.00	0.04	74,74,74,74	0
5	IOD	A	959	1/1	1.00	0.03	54,54,54,54	0
5	IOD	A	967	1/1	1.00	0.07	65,65,65,65	0
5	IOD	A	932	1/1	1.00	0.08	66,66,66,66	0
5	IOD	A	968	1/1	1.00	0.15	65,65,65,65	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.