Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 11:42 PM EDT

PDB ID	:	5IS7
Title	:	Crystal structure of mouse CARM1 in complex with decarboxylated SAH
Authors	:	Cura, V.; Marechal, N.; Mailliot, J.; Troffer-Charlier, N.; Hassenboehler, P.; Wurtz, J.M.; Bonnefond, L.; Cavarelli, J.
Deposited on	:	2016-03-15
Resolution	:	2.29 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 (i) 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 (i)) were used in the production of this report:

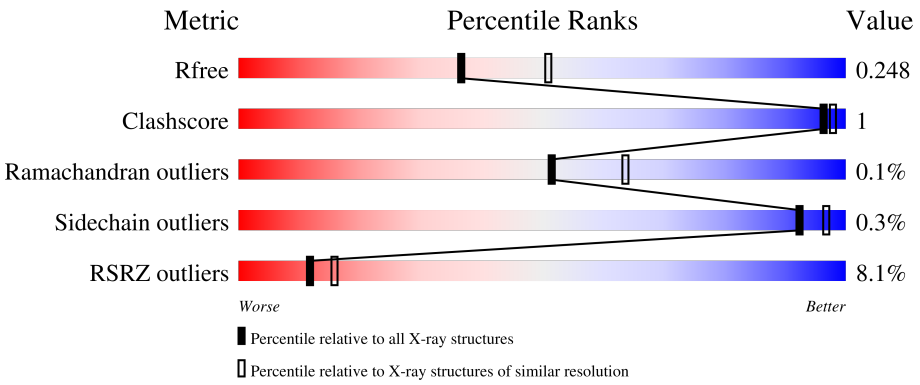
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	361	4% 93% • 5%
1	B	361	5% 92% • 5%
1	C	361	12% 91% • 6%
1	D	361	9% 91% • 6%

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
2	EDO	A	501	-	-	-	X
2	EDO	D	501	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 22214 atoms, of which 10946 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

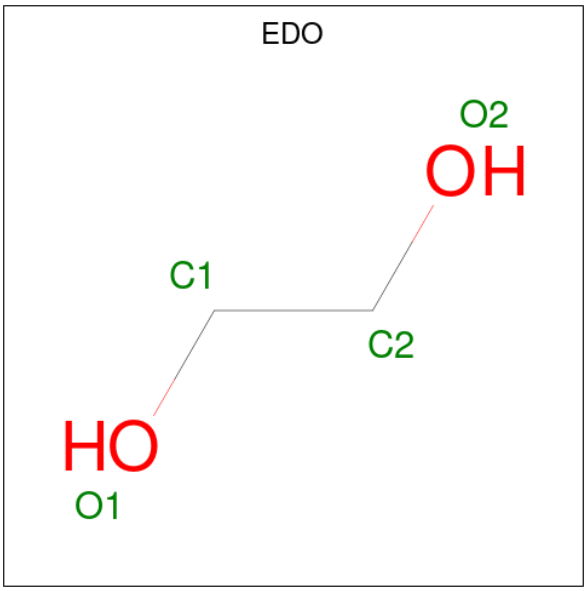
- Molecule 1 is a protein called Histone-arginine methyltransferase CARM1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	343	5530	1808	2736	458	513	15	0	5	0
1	B	342	5474	1786	2710	455	508	15	0	2	0
1	C	341	5425	1769	2687	452	503	14	0	0	0
1	D	340	5405	1760	2679	451	501	14	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

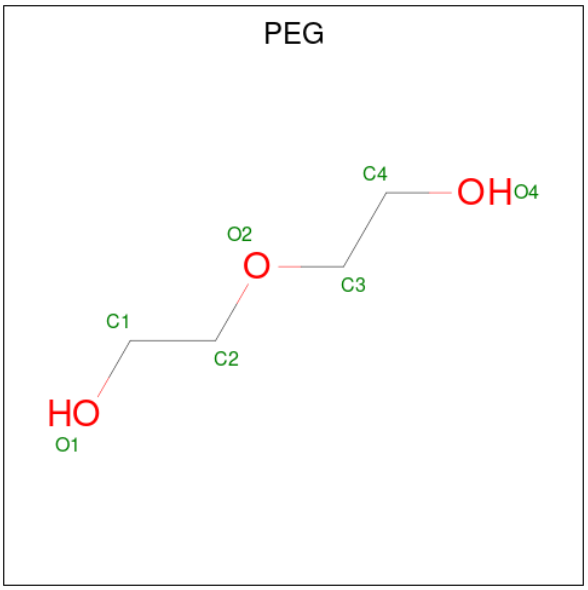
Chain	Residue	Modelled	Actual	Comment	Reference
A	127	GLY	-	expression tag	UNP Q9WVG6
A	128	HIS	-	expression tag	UNP Q9WVG6
A	129	MET	-	expression tag	UNP Q9WVG6
B	127	GLY	-	expression tag	UNP Q9WVG6
B	128	HIS	-	expression tag	UNP Q9WVG6
B	129	MET	-	expression tag	UNP Q9WVG6
C	127	GLY	-	expression tag	UNP Q9WVG6
C	128	HIS	-	expression tag	UNP Q9WVG6
C	129	MET	-	expression tag	UNP Q9WVG6
D	127	GLY	-	expression tag	UNP Q9WVG6
D	128	HIS	-	expression tag	UNP Q9WVG6
D	129	MET	-	expression tag	UNP Q9WVG6

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



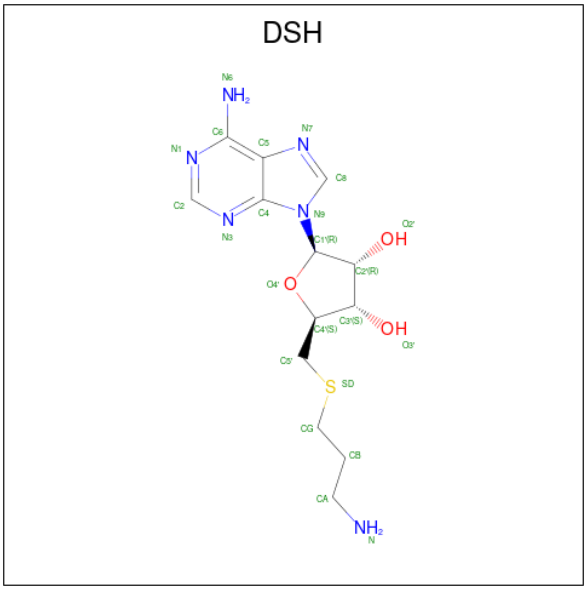
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	10	2	6	2	0	0
2	B	1	10	2	6	2	0	0
2	B	1	10	2	6	2	0	0
2	C	1	10	2	6	2	0	0
2	D	1	10	2	6	2	0	0

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	A	1	17	4	10	3	0	0
			Total	C	H	O		
3	A	1	17	4	10	3	0	0

- Molecule 4 is 5'-S-(3-aminopropyl)-5'-thioadenosine (three-letter code: DSH) (formula: $C_{13}H_{20}N_6O_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	H	N	O	S		
4	A	1	44	13	21	6	3	1	0	0
			Total	C	H	N	O	S		
4	B	1	44	13	21	6	3	1	0	0
			Total	C	H	N	O	S		
4	C	1	44	13	21	6	3	1	0	0
			Total	C	H	N	O	S		
4	D	1	44	13	21	6	3	1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	61	61	61	0	0
			Total	O		
5	B	44	44	44	0	0
			Total	O		
5	C	11	11	11	0	0

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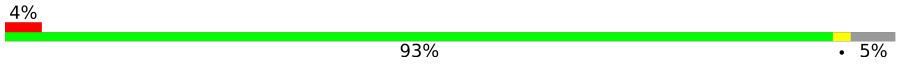
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	D	4	4	4	0	0

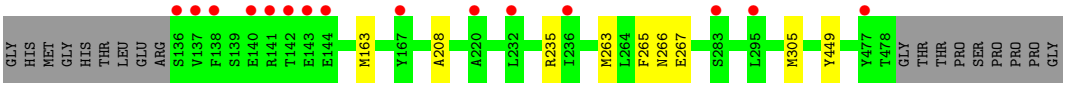
3 Residue-property plots (i)

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: Histone-arginine methyltransferase CARM1

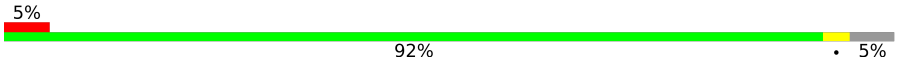
Chain A:





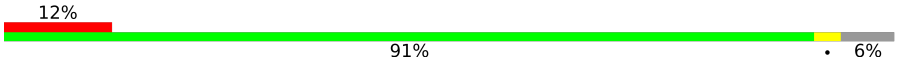
• Molecule 1: Histone-arginine methyltransferase CARM1

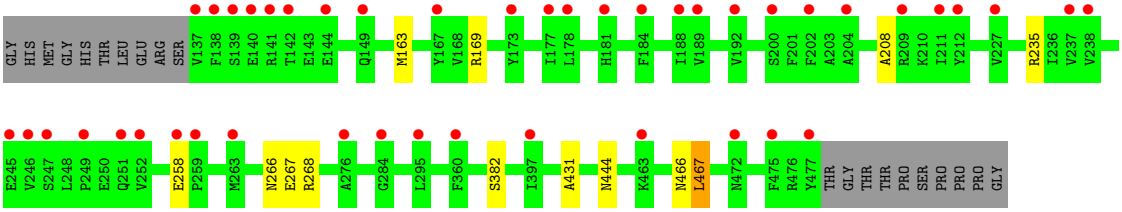
Chain B:



• Molecule 1: Histone-arginine methyltransferase CARM1

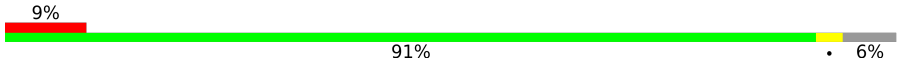
Chain C:

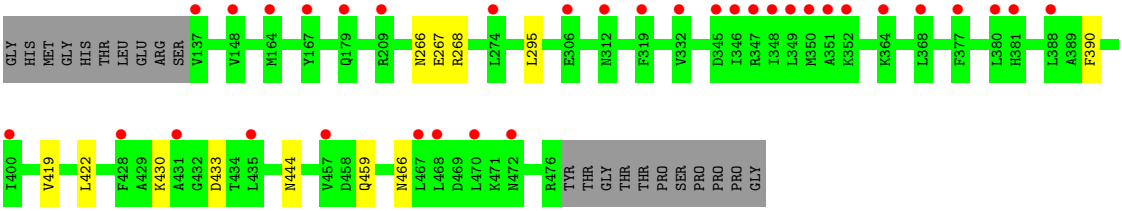




• Molecule 1: Histone-arginine methyltransferase CARM1

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	74.53Å 98.94Å 206.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.11 – 2.29 48.11 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.11-2.29) 99.5 (48.11-2.29)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.42 (at 2.29Å)	Xtriage
Refinement program	PHENIX dev_1980	Depositor
R, R_{free}	0.209 , 0.247 0.210 , 0.248	Depositor DCC
R_{free} test set	3434 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å^2)	59.7	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 55.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	22214	wwPDB-VP
Average B, all atoms (Å^2)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.46 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2590e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: EDO, DSH, 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	0.24	0/2876	0.39	0/3897
1	B	0.23	0/2835	0.36	0/3841
1	C	0.22	0/2808	0.35	0/3805
1	D	0.22	0/2795	0.34	0/3787
All	All	0.23	0/11314	0.36	0/15330

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 (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2794	2736	2726	4	0
1	B	2764	2710	2708	6	0
1	C	2738	2687	2687	7	0
1	D	2726	2679	2678	6	0
2	A	4	6	6	0	0
2	B	8	12	12	0	0
2	C	4	6	6	0	0
2	D	4	6	6	0	0
3	A	14	20	20	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	23	21	20	1	0
4	B	23	21	20	0	0
4	C	23	21	20	1	0
4	D	23	21	20	0	0
5	A	61	0	0	0	0
5	B	44	0	0	0	0
5	C	11	0	0	0	0
5	D	4	0	0	0	0
All	All	11268	10946	10929	23	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 1.

All (23) 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:C:169:ARG:NH2	1:C:258:GLU:OE2	2.43	0.52
1:D:430:LYS:NZ	1:D:433:ASP:OD1	2.42	0.52
1:A:163:MET:HE1	4:A:504:DSH:HB	1.94	0.51
1:C:466:ASN:OD1	1:C:467:LEU:N	2.42	0.51
1:A:208:ALA:O	1:A:235:ARG:NH2	2.40	0.50
1:C:163:MET:HE2	4:C:502:DSH:HB	1.92	0.50
1:C:208:ALA:O	1:C:235:ARG:NH1	2.39	0.50
1:B:459:GLN:OE1	1:B:459:GLN:N	2.46	0.49
1:C:268:ARG:NH1	1:C:444:ASN:O	2.46	0.48
1:D:268:ARG:NH1	1:D:444:ASN:O	2.44	0.47
1:C:382:SER:OG	1:C:431:ALA:N	2.48	0.46
1:B:263:MET:O	1:B:264:LEU:HB3	2.15	0.46
1:D:459:GLN:OE1	1:D:459:GLN:N	2.49	0.46
1:A:265:PHE:HB3	1:A:449:TYR:CE1	2.52	0.45
1:D:390:PHE:N	1:D:419:VAL:O	2.43	0.45
1:A:266:ASN:O	1:A:267:GLU:HB2	2.17	0.45
1:B:179:GLN:HB3	1:B:401[B]:MET:HE3	2.00	0.44
1:B:266:ASN:O	1:B:267:GLU:HB2	2.18	0.44
1:D:422:LEU:O	1:D:466:ASN:ND2	2.49	0.43
1:C:266:ASN:O	1:C:267:GLU:HB2	2.18	0.43
1:D:266:ASN:O	1:D:267:GLU:HB2	2.20	0.41
1:B:422:LEU:O	1:B:466:ASN:ND2	2.45	0.41
1:B:261:GLY:O	1:B:264:LEU:N	2.51	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	346/361 (96%)	335 (97%)	10 (3%)	1 (0%)	41	50
1	B	342/361 (95%)	332 (97%)	10 (3%)	0	100	100
1	C	339/361 (94%)	323 (95%)	16 (5%)	0	100	100
1	D	338/361 (94%)	326 (96%)	12 (4%)	0	100	100
All	All	1365/1444 (94%)	1316 (96%)	48 (4%)	1 (0%)	51	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	263	MET

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	304/313 (97%)	302 (99%)	2 (1%)	84	92
1	B	300/313 (96%)	299 (100%)	1 (0%)	92	97
1	C	297/313 (95%)	296 (100%)	1 (0%)	92	97
1	D	296/313 (95%)	295 (100%)	1 (0%)	92	97
All	All	1197/1252 (96%)	1192 (100%)	5 (0%)	92	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	305[A]	MET
1	A	305[B]	MET
1	B	295	LEU
1	C	467	LEU
1	D	295	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

11 ligands are modelled in this entry.

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	$\#\|Z\| > 2$
2	EDO	D	501	-	3,3,3	0.48	0	2,2,2	0.35	0
2	EDO	B	501	-	3,3,3	0.47	0	2,2,2	0.33	0
3	PEG	A	503	-	6,6,6	0.49	0	5,5,5	0.44	0
2	EDO	A	501	-	3,3,3	0.47	0	2,2,2	0.33	0
3	PEG	A	502	-	6,6,6	0.48	0	5,5,5	0.46	0
4	DSH	B	503	-	22,25,25	0.59	0	22,35,35	0.82	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	EDO	C	501	-	3,3,3	0.48	0	2,2,2	0.33	0
4	DSH	A	504	-	22,25,25	0.58	0	22,35,35	0.87	1 (4%)
2	EDO	B	502	-	3,3,3	0.47	0	2,2,2	0.33	0
4	DSH	C	502	-	22,25,25	0.58	0	22,35,35	0.91	2 (9%)
4	DSH	D	502	-	22,25,25	0.58	0	22,35,35	0.73	1 (4%)

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
2	EDO	D	501	-	-	1/1/1/1	-
2	EDO	B	501	-	-	0/1/1/1	-
3	PEG	A	503	-	-	1/4/4/4	-
2	EDO	A	501	-	-	1/1/1/1	-
3	PEG	A	502	-	-	1/4/4/4	-
4	DSH	B	503	-	-	3/6/26/26	0/3/3/3
2	EDO	C	501	-	-	1/1/1/1	-
4	DSH	A	504	-	-	3/6/26/26	0/3/3/3
2	EDO	B	502	-	-	0/1/1/1	-
4	DSH	C	502	-	-	4/6/26/26	0/3/3/3
4	DSH	D	502	-	-	2/6/26/26	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	502	DSH	C5-C6-N6	2.33	123.89	120.35
4	B	503	DSH	C5-C6-N6	2.31	123.86	120.35
4	A	504	DSH	C5-C6-N6	2.29	123.83	120.35
4	D	502	DSH	C5-C6-N6	2.25	123.78	120.35
4	C	502	DSH	C5'-C4'-C3'	-2.14	109.70	115.06

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	504	DSH	C3'-C4'-C5'-SD

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Mol	Chain	Res	Type	Atoms
4	A	504	DSH	O4'-C4'-C5'-SD
4	B	503	DSH	C3'-C4'-C5'-SD
4	B	503	DSH	O4'-C4'-C5'-SD
4	C	502	DSH	CA-CB-CG-SD
4	C	502	DSH	C3'-C4'-C5'-SD
4	C	502	DSH	O4'-C4'-C5'-SD
3	A	503	PEG	O2-C3-C4-O4
4	B	503	DSH	CA-CB-CG-SD
4	D	502	DSH	N-CA-CB-CG
3	A	502	PEG	O1-C1-C2-O2
2	C	501	EDO	O1-C1-C2-O2
2	D	501	EDO	O1-C1-C2-O2
4	C	502	DSH	CB-CG-SD-C5'
4	D	502	DSH	CA-CB-CG-SD
2	A	501	EDO	O1-C1-C2-O2
4	A	504	DSH	N-CA-CB-CG

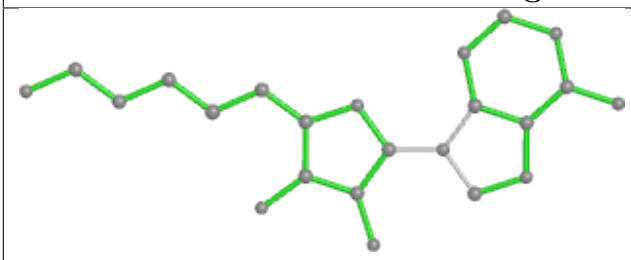
There are no ring outliers.

2 monomers are involved in 2 short contacts:

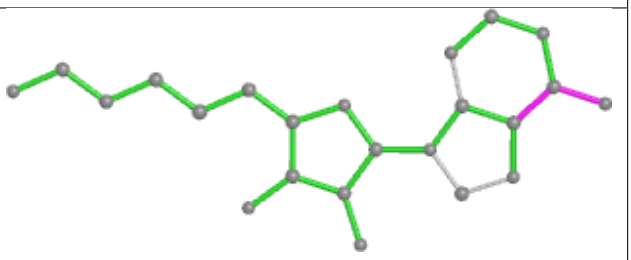
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504	DSH	1	0
4	C	502	DSH	1	0

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 then 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.

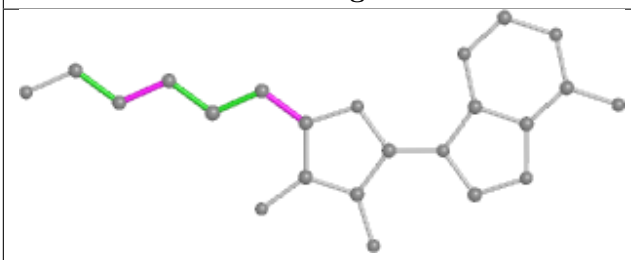
Ligand DSH B 503



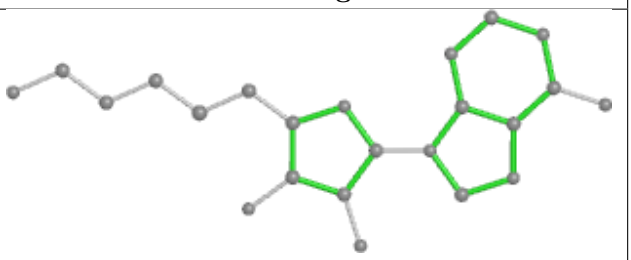
Bond lengths



Bond angles

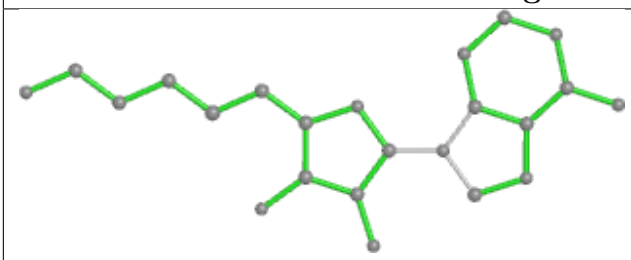


Torsions

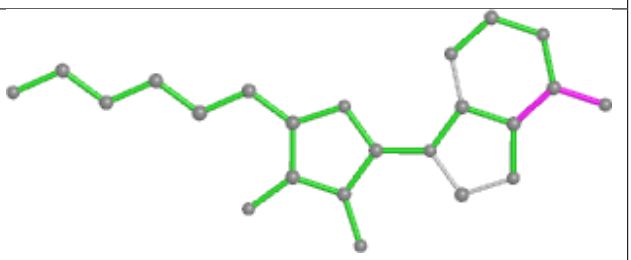


Rings

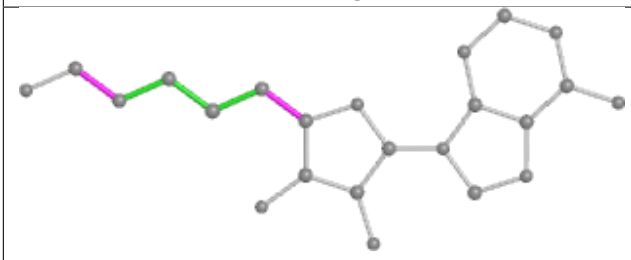
Ligand DSH A 504



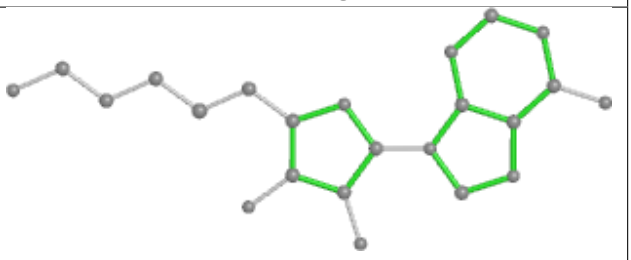
Bond lengths



Bond angles

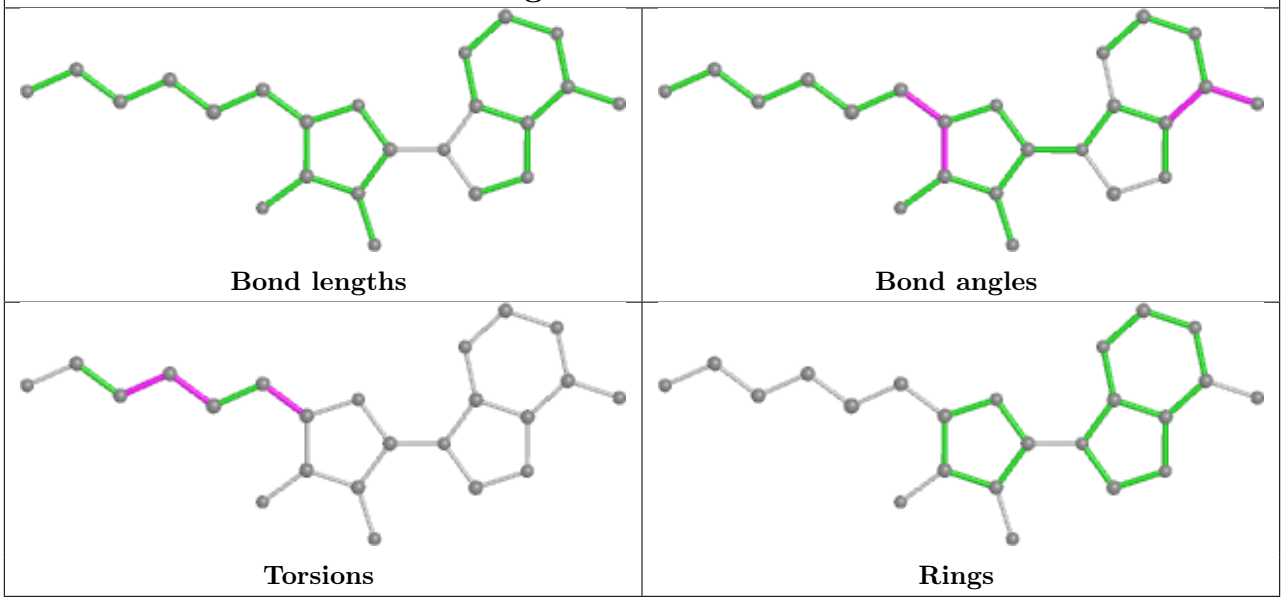


Torsions

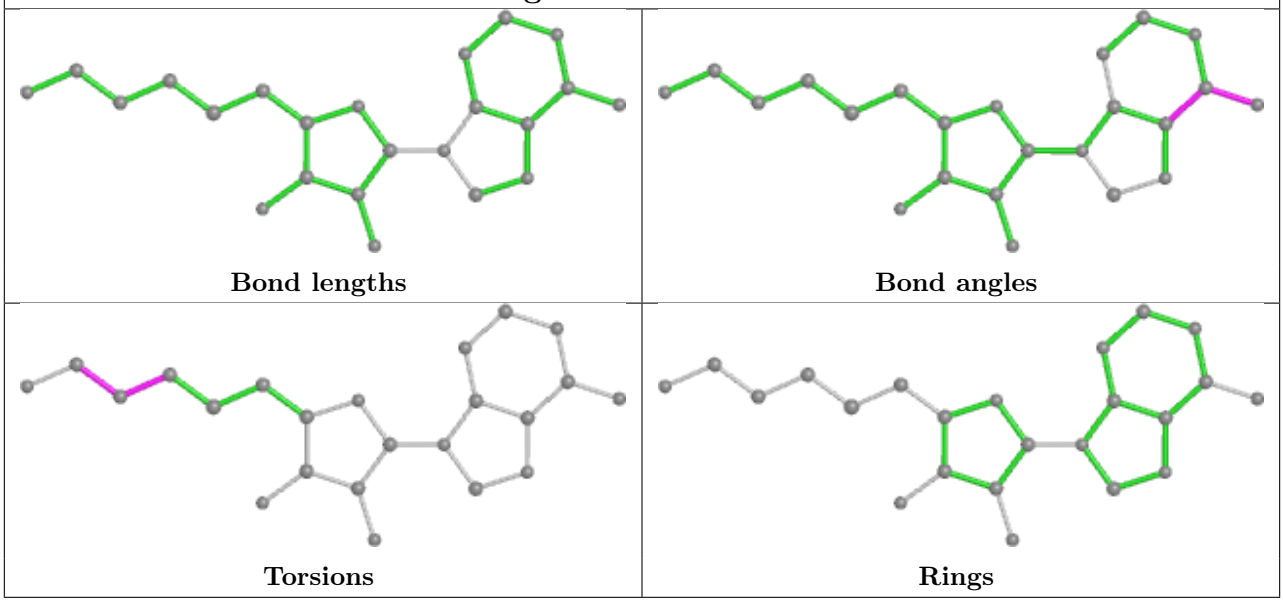


Rings

Ligand DSH C 502



Ligand DSH D 502



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	343/361 (95%)	0.37	15 (4%)	34	41	36, 62, 91, 138	0
1	B	342/361 (94%)	0.45	17 (4%)	28	35	39, 70, 102, 124	0
1	C	341/361 (94%)	0.76	44 (12%)	3	5	63, 96, 132, 161	0
1	D	340/361 (94%)	0.80	34 (10%)	7	10	66, 100, 128, 185	0
All	All	1366/1444 (94%)	0.60	110 (8%)	12	16	36, 82, 123, 185	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	137	VAL	7.9
1	D	380	LEU	5.9
1	C	138	PHE	5.3
1	A	136	SER	5.2
1	D	347	ARG	5.0
1	D	167	TYR	4.8
1	C	246	VAL	4.6
1	C	477	TYR	4.6
1	D	381	HIS	4.4
1	C	167	TYR	4.2
1	B	381	HIS	4.2
1	A	140	GLU	4.1
1	C	209	ARG	4.0
1	C	475	PHE	4.0
1	C	284	GLY	3.9
1	D	346	ILE	3.7
1	C	200	SER	3.7
1	B	350	MET	3.7
1	C	238	VAL	3.7
1	A	142	THR	3.6
1	B	347	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	212	TYR	3.4
1	D	350	MET	3.4
1	C	204	ALA	3.3
1	B	140	GLU	3.3
1	C	140	GLU	3.3
1	B	380	LEU	3.2
1	C	252	VAL	3.2
1	C	178	LEU	3.2
1	C	177	ILE	3.2
1	C	142	THR	3.1
1	C	139	SER	3.1
1	B	145	SER	3.1
1	C	184	PHE	3.1
1	B	167[A]	TYR	3.0
1	A	167[A]	TYR	3.0
1	B	477	TYR	3.0
1	C	251	GLN	3.0
1	C	144	GLU	3.0
1	C	149	GLN	3.0
1	C	249	PRO	2.9
1	D	209	ARG	2.9
1	C	472	ASN	2.9
1	D	364	LYS	2.9
1	C	276	ALA	2.8
1	B	435	LEU	2.8
1	C	173	TYR	2.8
1	D	472	ASN	2.8
1	D	470	LEU	2.7
1	C	295	LEU	2.7
1	D	349	LEU	2.7
1	D	457	VAL	2.7
1	C	237	VAL	2.6
1	D	352	LYS	2.6
1	D	351	ALA	2.6
1	D	332	VAL	2.6
1	B	345	ASP	2.6
1	A	236	ILE	2.5
1	C	181	HIS	2.5
1	B	467	LEU	2.5
1	D	148	VAL	2.5
1	A	477[A]	TYR	2.5
1	B	312	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	227	VAL	2.4
1	D	319	PHE	2.4
1	D	431	ALA	2.4
1	D	345	ASP	2.4
1	A	295	LEU	2.4
1	D	467	LEU	2.4
1	B	332	VAL	2.4
1	C	247	SER	2.4
1	A	232	LEU	2.4
1	D	368	LEU	2.4
1	D	435	LEU	2.4
1	C	192	VAL	2.4
1	C	245	GLU	2.4
1	C	259	PRO	2.4
1	C	211	ILE	2.3
1	C	258	GLU	2.3
1	D	468	LEU	2.3
1	C	137	VAL	2.3
1	B	136	SER	2.3
1	C	188	ILE	2.3
1	C	397	ILE	2.3
1	D	400	ILE	2.3
1	C	141	ARG	2.2
1	A	141	ARG	2.2
1	C	463	LYS	2.2
1	C	189	VAL	2.2
1	B	428	PHE	2.2
1	D	377	PHE	2.2
1	D	274	LEU	2.2
1	A	144	GLU	2.2
1	C	263	MET	2.2
1	C	360	PHE	2.1
1	A	143	GLU	2.1
1	A	220	ALA	2.1
1	D	428	PHE	2.1
1	D	179	GLN	2.1
1	D	164	MET	2.1
1	D	312	ASN	2.1
1	A	283	SER	2.1
1	C	202	PHE	2.1
1	D	388	LEU	2.1
1	D	137	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	306	GLU	2.0
1	D	348	ILE	2.0
1	B	263	MET	2.0
1	A	138	PHE	2.0
1	B	430	LYS	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)

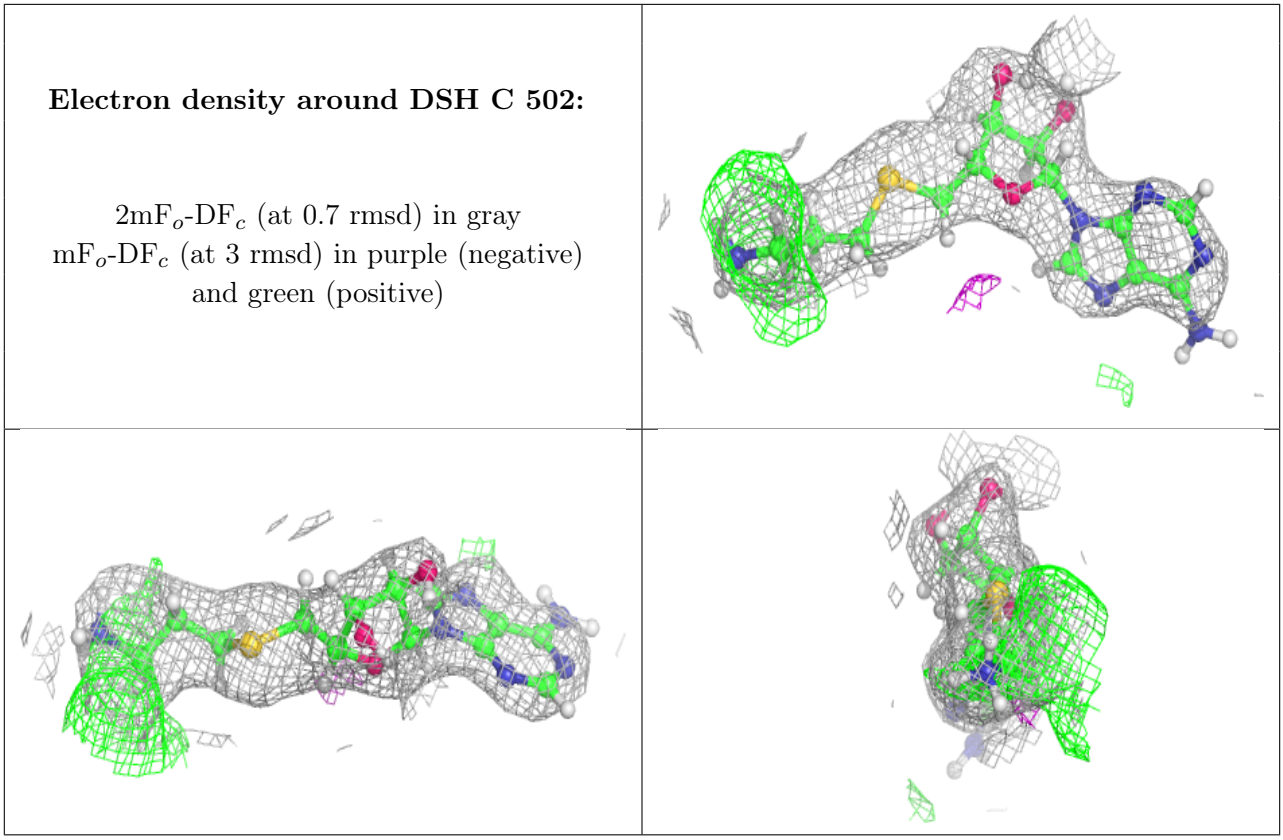
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	EDO	D	501	4/4	-0.01	0.86	256,307,307,308	0
2	EDO	A	501	4/4	0.44	0.82	230,276,276,277	0
4	DSH	C	502	23/23	0.63	0.21	107,122,146,148	0
2	EDO	B	501	4/4	0.73	0.14	77,92,95,97	0
4	DSH	D	502	23/23	0.76	0.25	117,126,151,151	0
4	DSH	A	504	23/23	0.78	0.17	57,73,92,93	0
2	EDO	C	501	4/4	0.79	0.17	88,105,107,109	0
3	PEG	A	502	7/7	0.79	0.28	85,102,109,109	0
3	PEG	A	503	7/7	0.79	0.22	84,101,114,114	0
4	DSH	B	503	23/23	0.87	0.18	65,80,102,105	0
2	EDO	B	502	4/4	0.89	0.33	86,103,106,107	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.

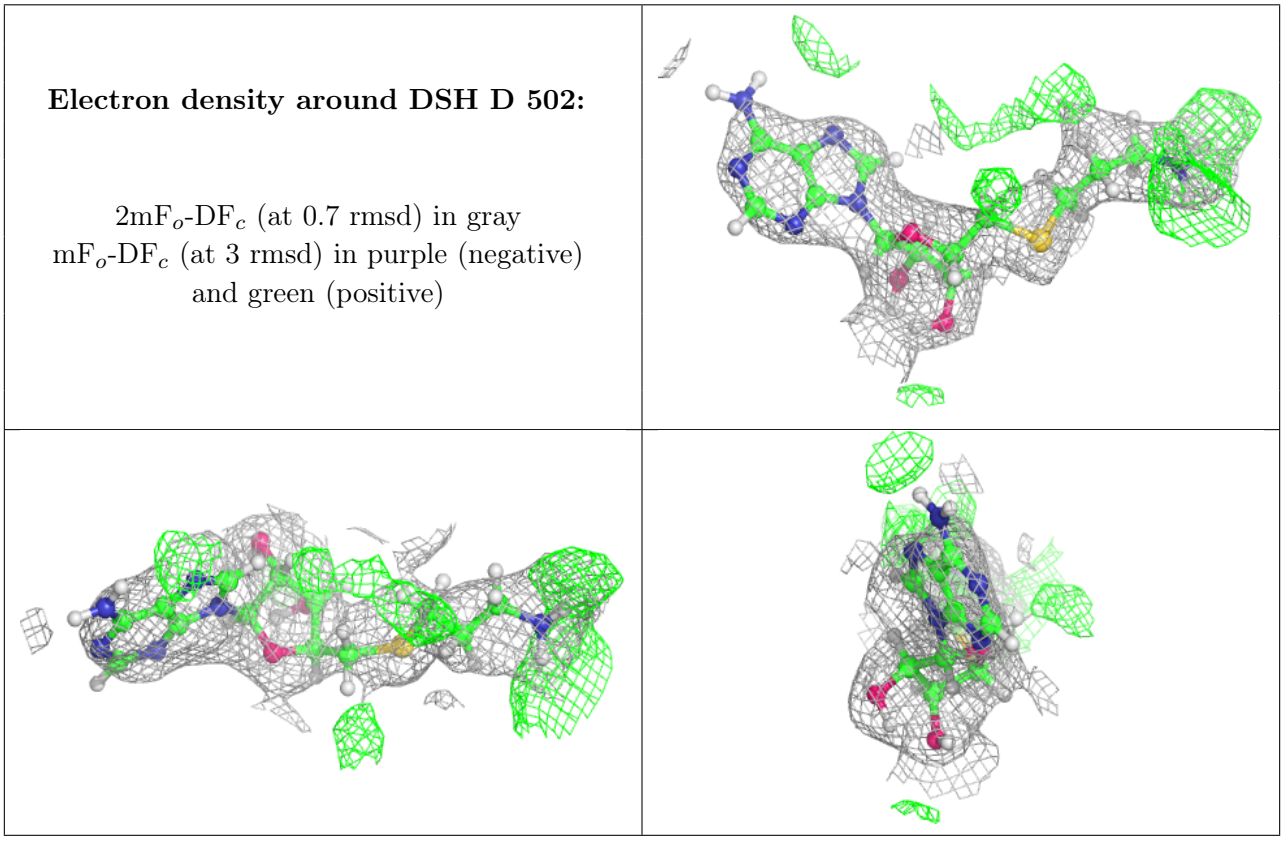
Electron density around DSH C 502:

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



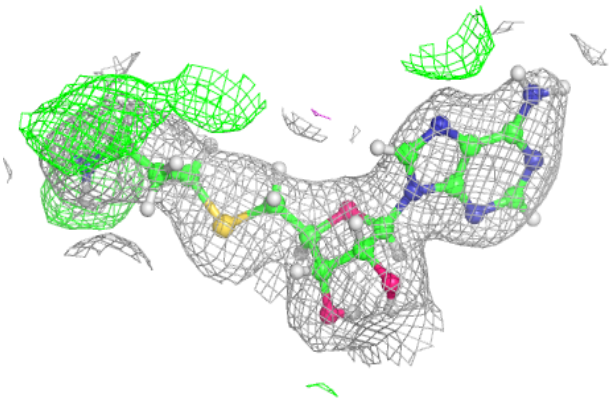
Electron density around DSH D 502:

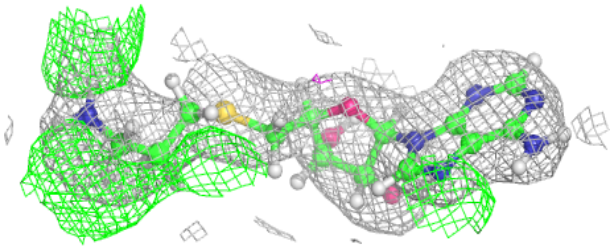
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

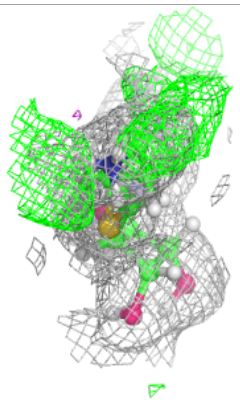


Electron density around DSH A 504:

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

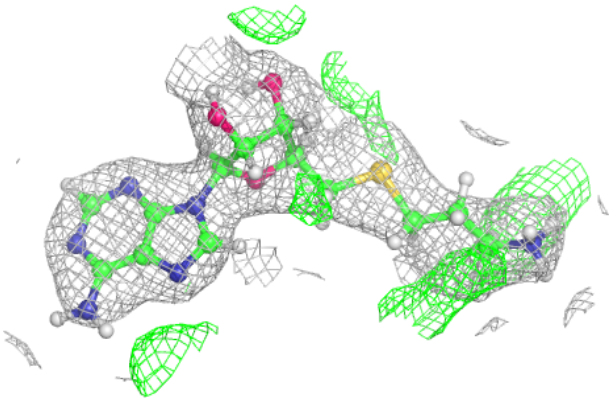


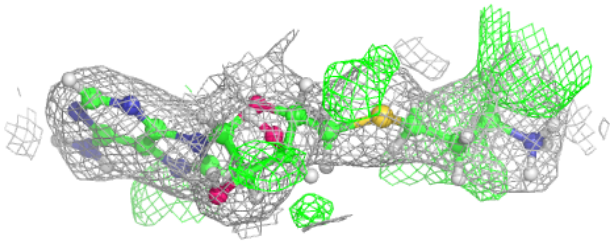


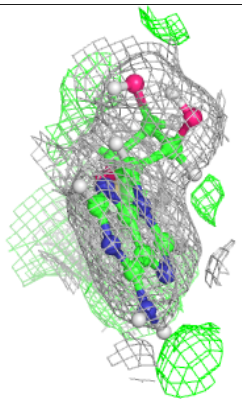


Electron density around DSH B 503:

$2mF_o$-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.