Full wwPDB X-ray Structure Validation Report (i)

Oct 7, 2023 – 11:52 PM EDT

PDB ID	:	6DYY
Title	:	Crystal structure of Helicobacter pylori 5'-methylthioadenosine/S-adenosyl homocysteine nucleosidase (MTAN) complexed with (3R,4S)-1-((4-amino-5H-pyrrolo[3,2-d]pyrimidin-7-yl)methyl)-4-(((3-(1-butyl-1H-1,2,3-triazol-4-yl)propyl)thio)methyl)pyrrolidin-3-ol
Authors	:	Harijan, R.K.; Ducati, R.G.; Bonanno, J.B.; Almo, S.C.; Schramm, V.L.
Deposited on	:	2018-07-02
Resolution	:	1.61 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 (1)) were used in the production of this report:

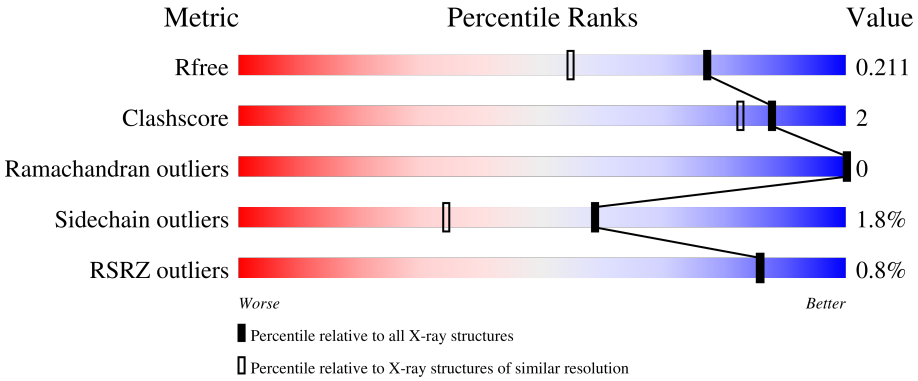
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance

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

The reported resolution of this entry is 1.61 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	4693 (1.64-1.60)
Clashscore	141614	5002 (1.64-1.60)
Ramachandran outliers	138981	4888 (1.64-1.60)
Sidechain outliers	138945	4887 (1.64-1.60)
RSRZ outliers	127900	4609 (1.64-1.60)

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	245	91% • • 5%
1	B	245	% 89% 5% 6%
1	C	245	88% 5% • 6%
1	D	245	2% 90% • 5%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 8147 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 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	1	0
			1771	1136	289	337	9			
1	B	230	Total	C	N	O	S	0	4	0
			1778	1140	289	339	10			
1	C	230	Total	C	N	O	S	0	4	0
			1780	1143	289	338	10			
1	D	232	Total	C	N	O	S	0	2	0
			1775	1140	289	337	9			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	expression tag	UNP A0A1W0VQJ9
A	-13	GLY	-	expression tag	UNP A0A1W0VQJ9
A	-12	HIS	-	expression tag	UNP A0A1W0VQJ9
A	-11	HIS	-	expression tag	UNP A0A1W0VQJ9
A	-10	HIS	-	expression tag	UNP A0A1W0VQJ9
A	-9	HIS	-	expression tag	UNP A0A1W0VQJ9
A	-8	HIS	-	expression tag	UNP A0A1W0VQJ9
A	-7	HIS	-	expression tag	UNP A0A1W0VQJ9
A	-6	GLU	-	expression tag	UNP A0A1W0VQJ9
A	-5	ASN	-	expression tag	UNP A0A1W0VQJ9
A	-4	LEU	-	expression tag	UNP A0A1W0VQJ9
A	-3	TYR	-	expression tag	UNP A0A1W0VQJ9
A	-2	PHE	-	expression tag	UNP A0A1W0VQJ9
A	-1	GLN	-	expression tag	UNP A0A1W0VQJ9
A	0	GLY	-	expression tag	UNP A0A1W0VQJ9
B	-14	MET	-	expression tag	UNP A0A1W0VQJ9
B	-13	GLY	-	expression tag	UNP A0A1W0VQJ9
B	-12	HIS	-	expression tag	UNP A0A1W0VQJ9
B	-11	HIS	-	expression tag	UNP A0A1W0VQJ9
B	-10	HIS	-	expression tag	UNP A0A1W0VQJ9
B	-9	HIS	-	expression tag	UNP A0A1W0VQJ9

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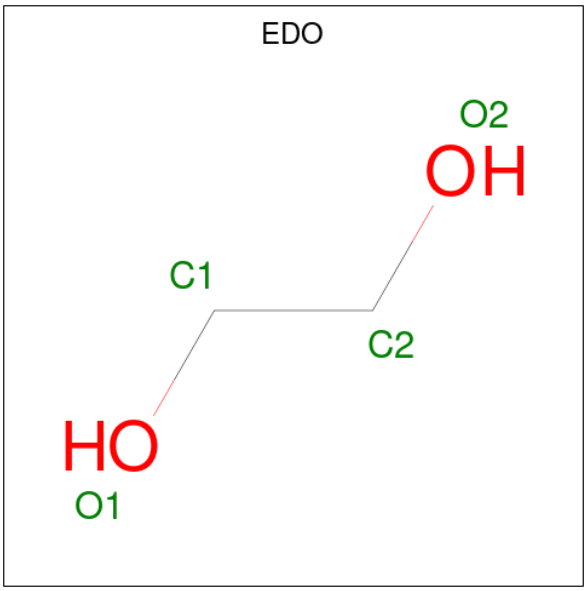
Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	HIS	-	expression tag	UNP A0A1W0VQJ9
B	-7	HIS	-	expression tag	UNP A0A1W0VQJ9
B	-6	GLU	-	expression tag	UNP A0A1W0VQJ9
B	-5	ASN	-	expression tag	UNP A0A1W0VQJ9
B	-4	LEU	-	expression tag	UNP A0A1W0VQJ9
B	-3	TYR	-	expression tag	UNP A0A1W0VQJ9
B	-2	PHE	-	expression tag	UNP A0A1W0VQJ9
B	-1	GLN	-	expression tag	UNP A0A1W0VQJ9
B	0	GLY	-	expression tag	UNP A0A1W0VQJ9
C	-14	MET	-	expression tag	UNP A0A1W0VQJ9
C	-13	GLY	-	expression tag	UNP A0A1W0VQJ9
C	-12	HIS	-	expression tag	UNP A0A1W0VQJ9
C	-11	HIS	-	expression tag	UNP A0A1W0VQJ9
C	-10	HIS	-	expression tag	UNP A0A1W0VQJ9
C	-9	HIS	-	expression tag	UNP A0A1W0VQJ9
C	-8	HIS	-	expression tag	UNP A0A1W0VQJ9
C	-7	HIS	-	expression tag	UNP A0A1W0VQJ9
C	-6	GLU	-	expression tag	UNP A0A1W0VQJ9
C	-5	ASN	-	expression tag	UNP A0A1W0VQJ9
C	-4	LEU	-	expression tag	UNP A0A1W0VQJ9
C	-3	TYR	-	expression tag	UNP A0A1W0VQJ9
C	-2	PHE	-	expression tag	UNP A0A1W0VQJ9
C	-1	GLN	-	expression tag	UNP A0A1W0VQJ9
C	0	GLY	-	expression tag	UNP A0A1W0VQJ9
D	-14	MET	-	expression tag	UNP A0A1W0VQJ9
D	-13	GLY	-	expression tag	UNP A0A1W0VQJ9
D	-12	HIS	-	expression tag	UNP A0A1W0VQJ9
D	-11	HIS	-	expression tag	UNP A0A1W0VQJ9
D	-10	HIS	-	expression tag	UNP A0A1W0VQJ9
D	-9	HIS	-	expression tag	UNP A0A1W0VQJ9
D	-8	HIS	-	expression tag	UNP A0A1W0VQJ9
D	-7	HIS	-	expression tag	UNP A0A1W0VQJ9
D	-6	GLU	-	expression tag	UNP A0A1W0VQJ9
D	-5	ASN	-	expression tag	UNP A0A1W0VQJ9
D	-4	LEU	-	expression tag	UNP A0A1W0VQJ9
D	-3	TYR	-	expression tag	UNP A0A1W0VQJ9
D	-2	PHE	-	expression tag	UNP A0A1W0VQJ9
D	-1	GLN	-	expression tag	UNP A0A1W0VQJ9
D	0	GLY	-	expression tag	UNP A0A1W0VQJ9

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

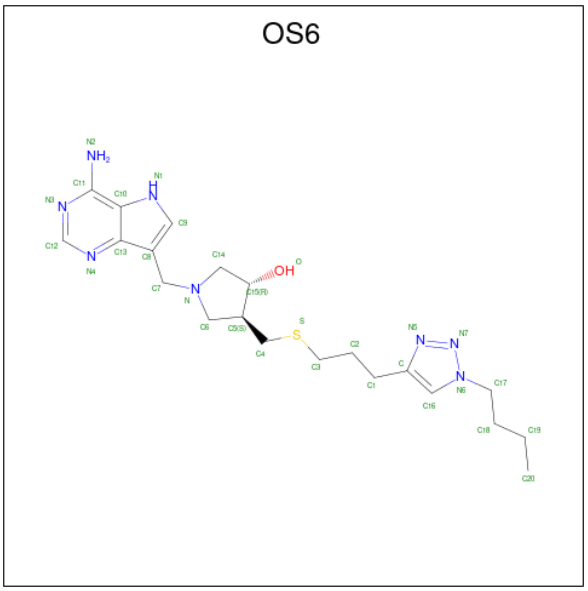


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is (3R,4S)-1-[(4-amino-5H-pyrrolo[3,2-d]pyrimidin-7-yl)methyl]-4-({[3-(1-butyl-1H-1,2,3-triazol-4-yl)propyl]sulfanyl}methyl)pyrrolidin-3-ol (three-letter code: OS6) (formula: $C_{21}H_{32}N_8OS$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			31	21	8	1	1		
4	B	1	Total	C	N	O	S	0	0
			31	21	8	1	1		
4	C	1	Total	C	N	O	S	0	0
			31	21	8	1	1		
4	D	1	Total	C	N	O	S	0	0
			31	21	8	1	1		

- Molecule 5 is water.

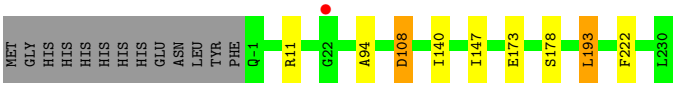
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	229	Total	O	0	0
			229	229		
5	B	242	Total	O	0	0
			242	242		
5	C	241	Total	O	0	0
			241	241		
5	D	177	Total	O	0	0
			177	177		

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: 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase

Chain A:

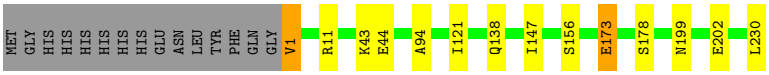


• Molecule 1: 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase

Chain B:

• Molecule 1: 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase

Chain C:



• Molecule 1: 5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	72.56Å 74.03Å 176.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.44 – 1.61 88.44 – 1.61	Depositor EDS
% Data completeness (in resolution range)	100.0 (88.44-1.61) 99.9 (88.44-1.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.29 (at 1.61Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.179 , 0.203 0.191 , 0.211	Depositor DCC
R_{free} test set	6265 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	19.4	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 34.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.176 for k,h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8147	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OS6, MG, EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.50	0/1806	0.69	3/2431 (0.1%)
1	B	0.52	0/1813	0.67	0/2440
1	C	0.51	0/1815	0.68	2/2443 (0.1%)
1	D	0.46	0/1810	0.64	0/2437
All	All	0.50	0/7244	0.67	5/9751 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	193	LEU	CA-CB-CG	7.16	131.77	115.30
1	C	11	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	108	ASP	CB-CG-OD1	-5.14	113.68	118.30
1	C	1	VAL	CA-CB-CG2	5.05	118.48	110.90
1	A	11	ARG	NE-CZ-NH2	5.01	122.81	120.30

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	1771	0	1792	3	0
1	B	1778	0	1797	7	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1780	0	1803	10	0
1	D	1775	0	1796	9	1
2	A	4	0	6	0	0
2	B	12	0	18	0	0
2	C	8	0	12	3	0
2	D	4	0	6	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	31	0	0	0	0
4	B	31	0	0	0	0
4	C	31	0	0	1	0
4	D	31	0	0	1	0
5	A	229	0	0	0	0
5	B	242	0	0	4	0
5	C	241	0	0	4	0
5	D	177	0	0	2	0
All	All	8147	0	7230	29	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 2.

All (29) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:184:GLN:NE2	5:B:402:HOH:O	1.99	0.95
1:B:133:LYS:NZ	5:B:401:HOH:O	1.98	0.95
1:D:184:GLN:NE2	5:D:401:HOH:O	2.03	0.92
1:C:44:GLU:OE2	5:C:401:HOH:O	2.08	0.72
1:C:121:ILE:HD11	5:C:402:HOH:O	1.91	0.71
1:C:202:GLU:HB3	2:C:302:EDO:H12	1.79	0.63
1:B:94:ALA:HB2	1:B:147:ILE:HD12	1.83	0.60
1:A:94:ALA:HB2	1:A:147:ILE:HD12	1.84	0.59
1:D:94:ALA:HB2	1:D:147:ILE:HD12	1.88	0.55
1:B:199:ASN:ND2	5:B:407:HOH:O	2.39	0.55
1:D:134:ILE:CG2	1:D:138:GLN:NE2	2.71	0.54
1:C:44:GLU:HG3	5:C:401:HOH:O	2.08	0.52
1:B:11:ARG:NH1	5:B:409:HOH:O	2.43	0.51
1:B:140:ILE:HD11	1:B:222:PHE:CD1	2.45	0.51
1:C:94:ALA:HB2	1:C:147:ILE:HD12	1.92	0.51
1:D:134:ILE:CG2	1:D:138:GLN:HE21	2.24	0.50
1:D:140:ILE:HD11	1:D:222:PHE:CD1	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:116:GLU:CD	5:D:402:HOH:O	2.51	0.49
1:C:199:ASN:ND2	5:C:404:HOH:O	2.46	0.49
1:A:140:ILE:HD11	1:A:222:PHE:CD1	2.48	0.48
1:C:43:LYS:CE	1:C:230:LEU:O	2.63	0.47
1:A:140:ILE:HD11	1:A:222:PHE:CE1	2.51	0.45
1:D:140:ILE:HD11	1:D:222:PHE:CE1	2.52	0.45
1:D:134:ILE:HG22	1:D:138:GLN:NE2	2.31	0.44
1:B:140:ILE:HD11	1:B:222:PHE:CE1	2.53	0.44
1:D:173:GLU:HA	4:D:302:OS6:N4	2.34	0.43
1:C:202:GLU:HB3	2:C:302:EDO:C1	2.49	0.41
1:C:173:GLU:HA	4:C:303:OS6:N4	2.36	0.40
1:C:156:SER:HA	2:C:302:EDO:H11	2.02	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)
1:B:42:ASN:ND2	1:D:42:ASN:ND2[4_465]	1.95	0.25

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	231/245 (94%)	224 (97%)	7 (3%)	0	100	100
1	B	232/245 (95%)	225 (97%)	7 (3%)	0	100	100
1	C	232/245 (95%)	225 (97%)	7 (3%)	0	100	100
1	D	232/245 (95%)	225 (97%)	7 (3%)	0	100	100
All	All	927/980 (95%)	899 (97%)	28 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	194/206 (94%)	190 (98%)	4 (2%)	53	27
1	B	196/206 (95%)	191 (97%)	5 (3%)	46	19
1	C	196/206 (95%)	192 (98%)	4 (2%)	55	29
1	D	194/206 (94%)	192 (99%)	2 (1%)	76	60
All	All	780/824 (95%)	765 (98%)	15 (2%)	59	32

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	ASP
1	A	173	GLU
1	A	178	SER
1	A	193	LEU
1	B	71	GLN
1	B	108	ASP
1	B	173	GLU
1	B	178[A]	SER
1	B	178[B]	SER
1	C	1	VAL
1	C	138	GLN
1	C	173	GLU
1	C	178	SER
1	D	173	GLU
1	D	178	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	128	ASN
1	B	128	ASN
1	C	42	ASN

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Mol	Chain	Res	Type
1	C	138	GLN
1	C	199	ASN
1	D	128	ASN
1	D	138	GLN
1	D	184	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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	$\#\|Z\| > 2$
2	EDO	B	302	-	3,3,3	0.49	0	2,2,2	0.12	0
4	OS6	B	305	-	32,34,34	1.10	3 (9%)	27,46,46	1.92	9 (33%)
2	EDO	C	302	-	3,3,3	0.36	0	2,2,2	0.44	0
2	EDO	D	301	-	3,3,3	0.42	0	2,2,2	0.56	0
2	EDO	B	303	-	3,3,3	0.49	0	2,2,2	0.23	0
4	OS6	A	303	-	32,34,34	1.27	4 (12%)	27,46,46	2.10	7 (25%)
4	OS6	C	303	-	32,34,34	1.18	2 (6%)	27,46,46	2.24	7 (25%)
2	EDO	C	301	-	3,3,3	0.48	0	2,2,2	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	OS6	D	302	-	32,34,34	1.27	4 (12%)	27,46,46	1.67	6 (22%)
2	EDO	A	301	-	3,3,3	0.54	0	2,2,2	0.73	0
2	EDO	B	301	-	3,3,3	0.46	0	2,2,2	0.50	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
2	EDO	B	302	-	-	0/1/1/1	-
4	OS6	B	305	-	-	3/15/28/28	0/4/4/4
2	EDO	C	302	-	-	1/1/1/1	-
2	EDO	D	301	-	-	0/1/1/1	-
2	EDO	B	303	-	-	1/1/1/1	-
4	OS6	A	303	-	-	2/15/28/28	0/4/4/4
4	OS6	C	303	-	-	1/15/28/28	0/4/4/4
2	EDO	C	301	-	-	0/1/1/1	-
4	OS6	D	302	-	-	3/15/28/28	0/4/4/4
2	EDO	A	301	-	-	1/1/1/1	-
2	EDO	B	301	-	-	0/1/1/1	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	302	OS6	N5-N7	3.79	1.41	1.34
4	A	303	OS6	N5-N7	3.70	1.41	1.34
4	D	302	OS6	N7-N6	3.61	1.41	1.34
4	C	303	OS6	N5-N7	3.35	1.40	1.34
4	C	303	OS6	N7-N6	3.35	1.40	1.34
4	A	303	OS6	N7-N6	2.89	1.40	1.34
4	B	305	OS6	N7-N6	2.77	1.39	1.34
4	A	303	OS6	C16-C	2.69	1.40	1.36
4	B	305	OS6	N5-N7	2.69	1.39	1.34
4	B	305	OS6	C16-C	2.34	1.39	1.36
4	D	302	OS6	C16-C	2.28	1.39	1.36
4	D	302	OS6	C-N5	2.07	1.36	1.34
4	A	303	OS6	C-N5	2.02	1.36	1.34

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	303	OS6	C12-N4-C13	5.74	119.28	114.81
4	C	303	OS6	C12-N4-C13	5.46	119.06	114.81
4	C	303	OS6	N4-C12-N3	-4.90	121.03	128.68
4	C	303	OS6	C8-C7-N	4.15	120.06	114.14
4	A	303	OS6	C8-C7-N	4.05	119.93	114.14
4	C	303	OS6	N5-N7-N6	-4.02	104.28	107.31
4	D	302	OS6	C8-C7-N	3.98	119.83	114.14
4	B	305	OS6	N4-C12-N3	-3.96	122.49	128.68
4	A	303	OS6	N4-C12-N3	-3.87	122.62	128.68
4	B	305	OS6	C12-N4-C13	3.86	117.81	114.81
4	D	302	OS6	N5-N7-N6	-3.56	104.63	107.31
4	A	303	OS6	C10-C13-N4	-3.54	120.81	124.92
4	A	303	OS6	N5-N7-N6	-3.35	104.79	107.31
4	C	303	OS6	C7-C8-C9	-3.12	122.62	127.48
4	A	303	OS6	C7-C8-C9	-3.11	122.62	127.48
4	B	305	OS6	C8-C7-N	3.11	118.59	114.14
4	D	302	OS6	N4-C12-N3	-3.11	123.82	128.68
4	B	305	OS6	C6-N-C14	2.88	108.47	104.19
4	B	305	OS6	C15-C14-N	-2.85	98.99	104.44
4	C	303	OS6	C3-C2-C1	-2.71	105.12	112.97
4	C	303	OS6	C10-C13-N4	-2.71	121.78	124.92
4	B	305	OS6	C10-C13-N4	-2.66	121.83	124.92
4	B	305	OS6	C17-N6-C16	2.60	135.93	129.82
4	B	305	OS6	C3-C2-C1	-2.50	105.73	112.97
4	D	302	OS6	C3-C2-C1	-2.36	106.14	112.97
4	B	305	OS6	N5-N7-N6	-2.30	105.58	107.31
4	D	302	OS6	C7-C8-C9	-2.20	124.04	127.48
4	A	303	OS6	C7-N-C6	2.03	116.72	113.27
4	D	302	OS6	C10-C13-N4	-2.00	122.59	124.92

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	302	OS6	C18-C17-N6-C16
4	C	303	OS6	N6-C17-C18-C19
2	C	302	EDO	O1-C1-C2-O2
4	B	305	OS6	C17-C18-C19-C20
2	B	303	EDO	O1-C1-C2-O2
4	A	303	OS6	C18-C17-N6-N7
4	B	305	OS6	C18-C17-N6-N7
4	D	302	OS6	C18-C17-N6-N7
2	A	301	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
4	D	302	OS6	C17-C18-C19-C20
4	A	303	OS6	S-C4-C5-C15
4	B	305	OS6	N-C7-C8-C9

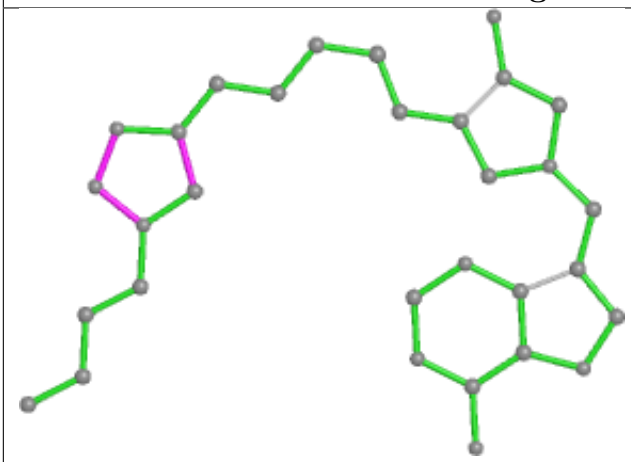
There are no ring outliers.

3 monomers are involved in 5 short contacts:

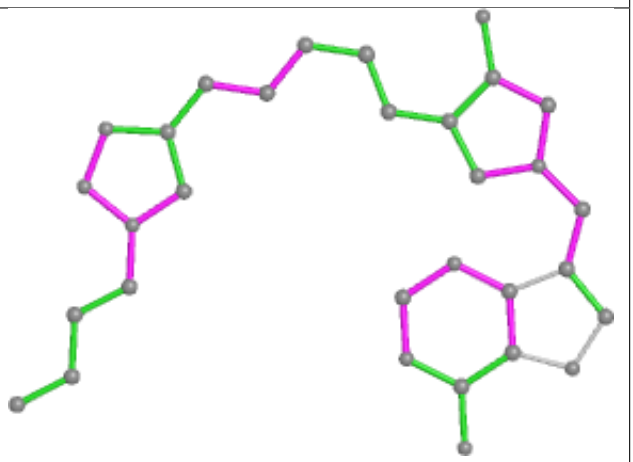
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	302	EDO	3	0
4	C	303	OS6	1	0
4	D	302	OS6	1	0

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.

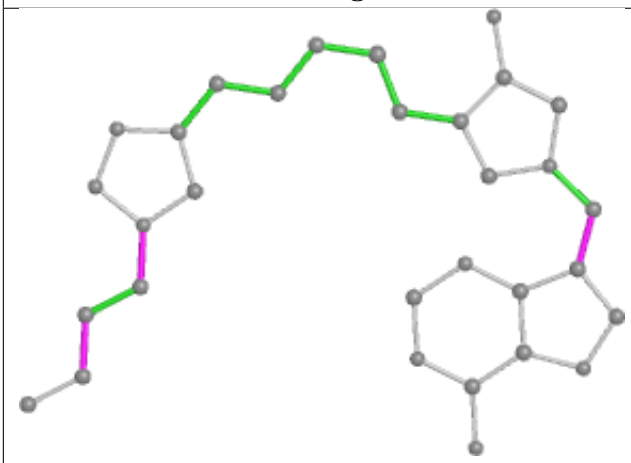
Ligand OS6 B 305



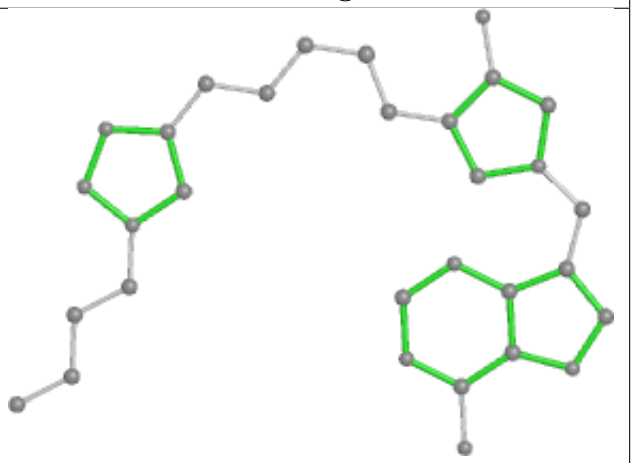
Bond lengths



Bond angles

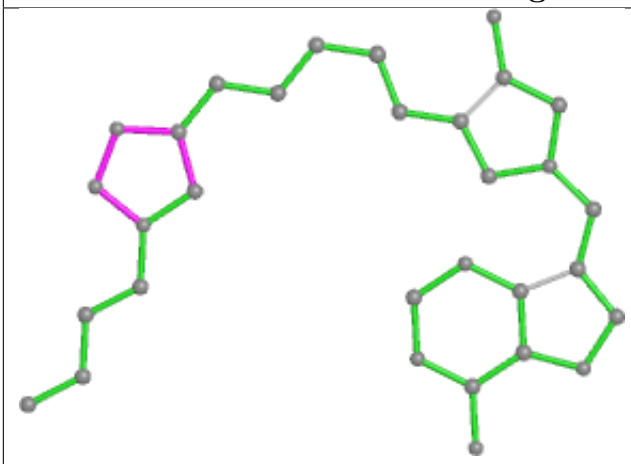


Torsions

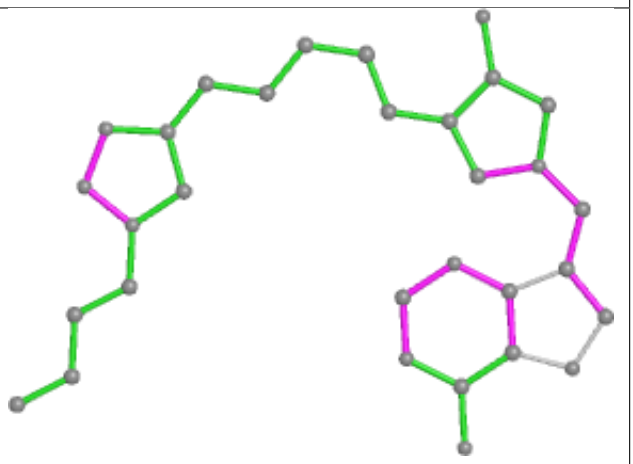


Rings

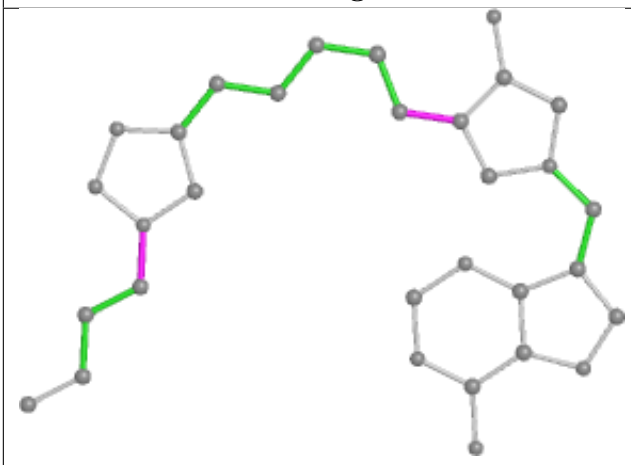
Ligand OS6 A 303



Bond lengths



Bond angles



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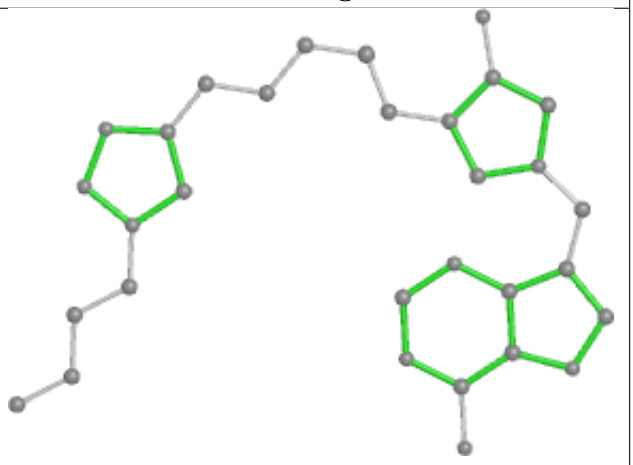
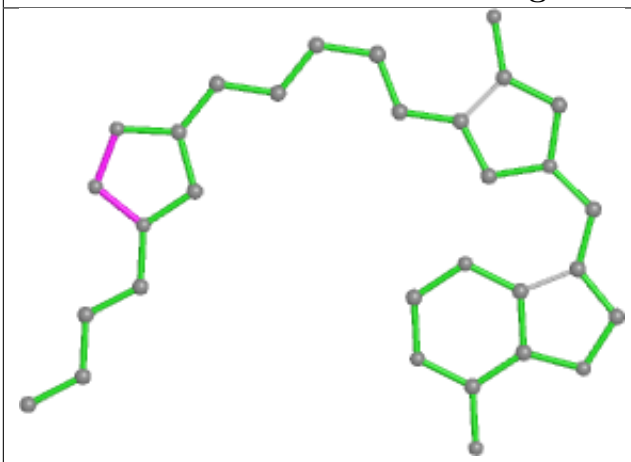
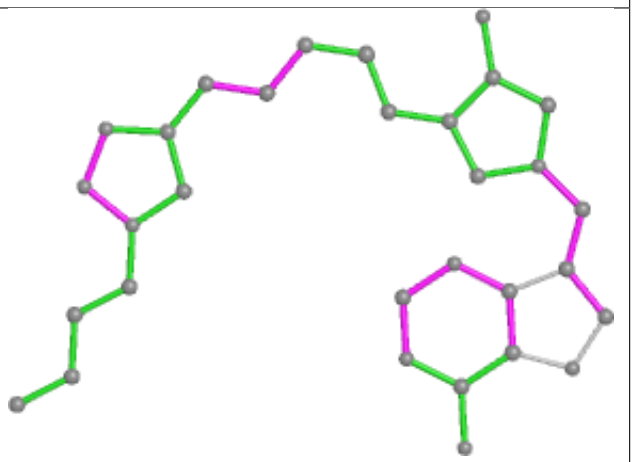


Rings

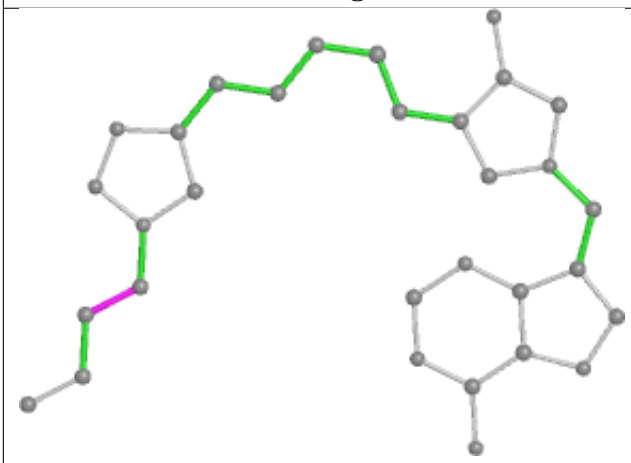
Ligand OS6 C 303



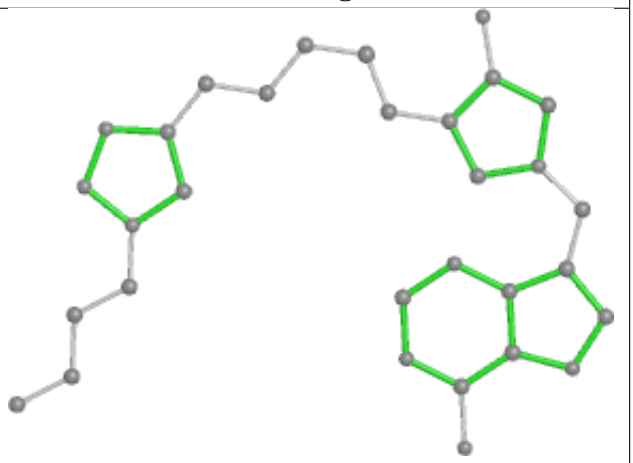
Bond lengths



Bond angles

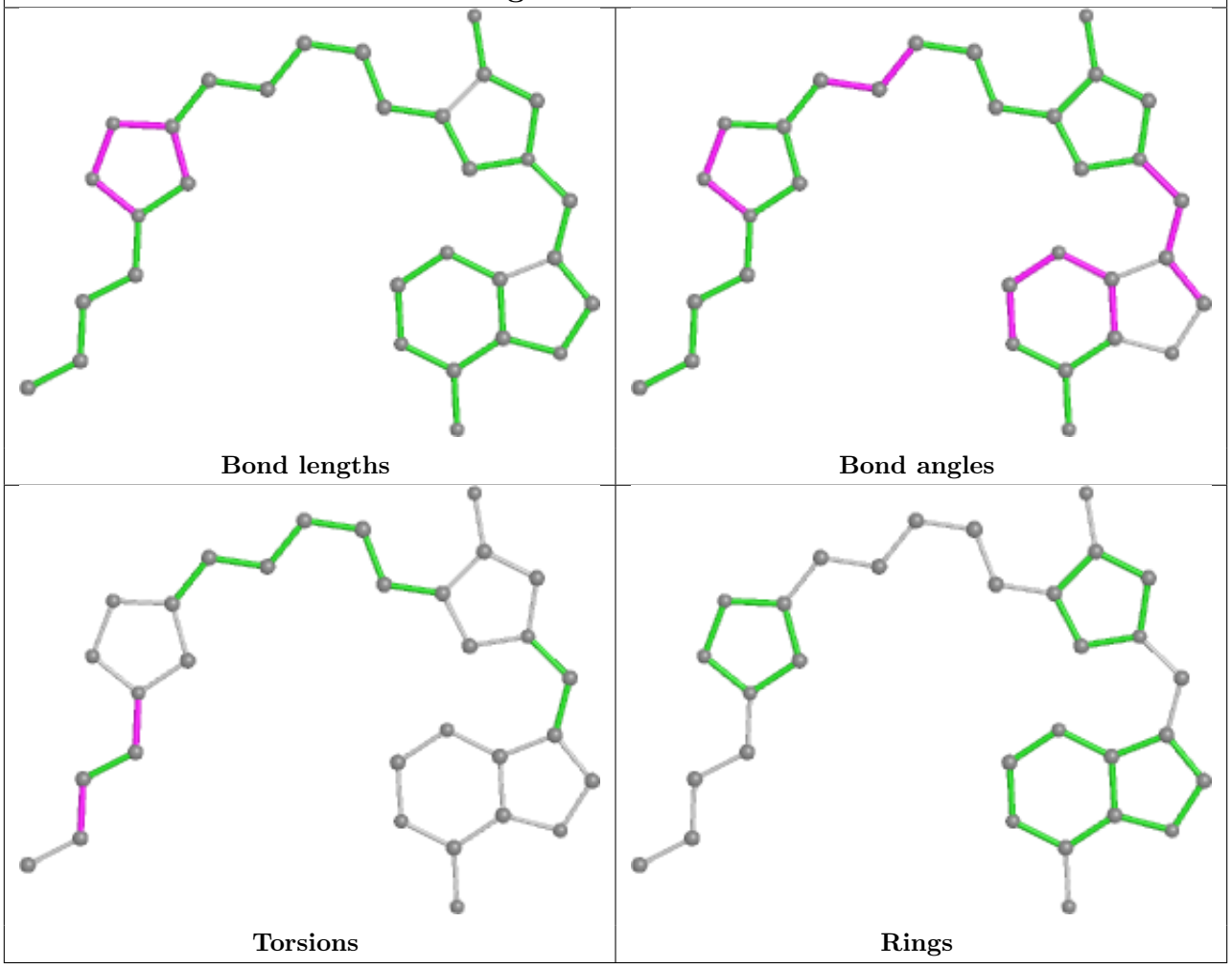


Torsions



Rings

Ligand OS6 D 302



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, 95^{th} 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	232/245 (94%)	-0.33	1 (0%) 92 92	12, 21, 36, 48	0
1	B	230/245 (93%)	-0.42	2 (0%) 84 84	12, 19, 34, 52	0
1	C	230/245 (93%)	-0.46	0 100 100	14, 20, 32, 47	0
1	D	232/245 (94%)	-0.23	4 (1%) 70 68	15, 24, 47, 71	0
All	All	924/980 (94%)	-0.36	7 (0%) 86 86	12, 21, 38, 71	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	VAL	4.6
1	D	42	ASN	3.4
1	D	139	HIS	3.3
1	D	1	VAL	3.1
1	B	42	ASN	2.2
1	A	22	GLY	2.1
1	D	-1	GLN	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

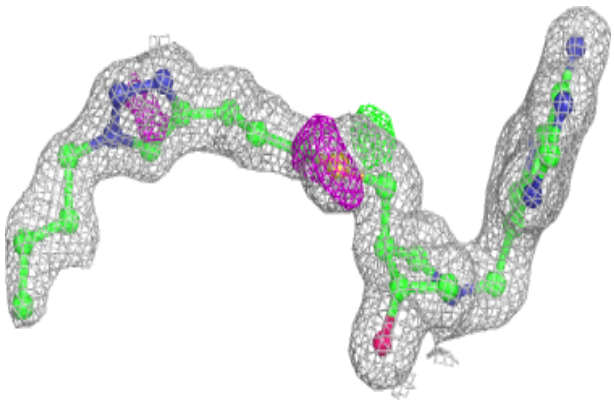
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

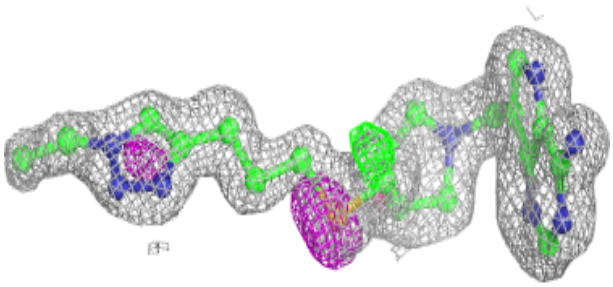
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	EDO	B	303	4/4	0.68	0.17	42,43,45,47	0
2	EDO	B	302	4/4	0.78	0.14	51,55,57,59	0
2	EDO	A	301	4/4	0.90	0.11	22,26,30,31	0
2	EDO	B	301	4/4	0.91	0.11	23,27,32,33	0
2	EDO	D	301	4/4	0.91	0.12	22,27,30,32	0
2	EDO	C	302	4/4	0.92	0.15	23,30,31,34	0
2	EDO	C	301	4/4	0.92	0.11	24,28,31,33	0
4	OS6	A	303	31/31	0.94	0.09	16,18,37,39	0
4	OS6	D	302	31/31	0.94	0.10	15,16,48,49	0
4	OS6	C	303	31/31	0.96	0.08	12,14,41,45	0
3	MG	A	302	1/1	0.97	0.21	31,31,31,31	0
4	OS6	B	305	31/31	0.97	0.07	13,15,30,34	0
3	MG	B	304	1/1	0.99	0.19	28,28,28,28	0

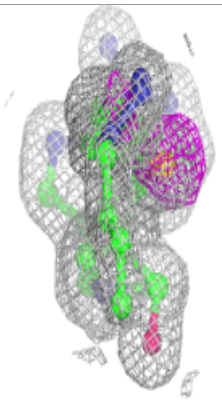
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around OS6 A 303:

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

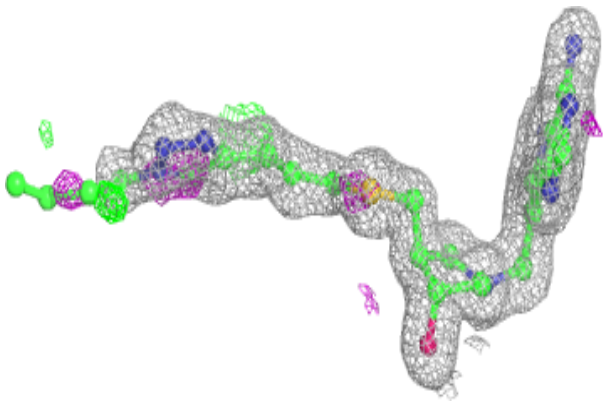


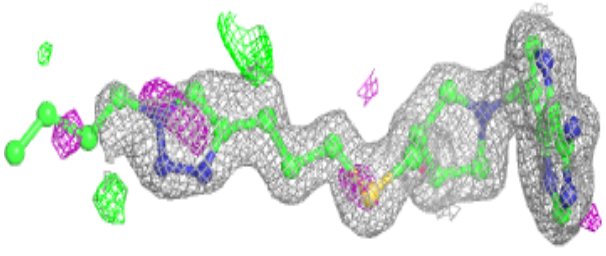


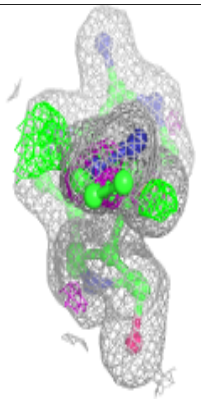


Electron density around OS6 D 302:

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

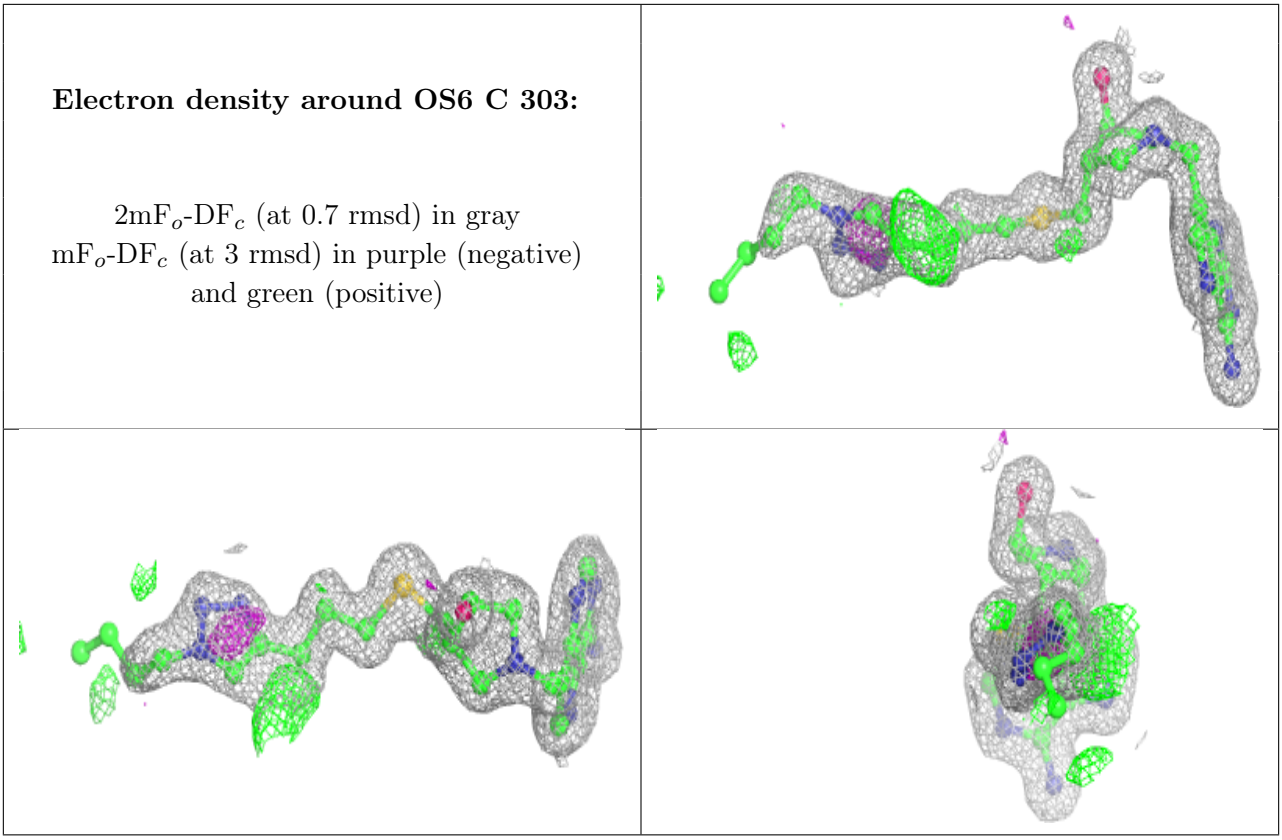






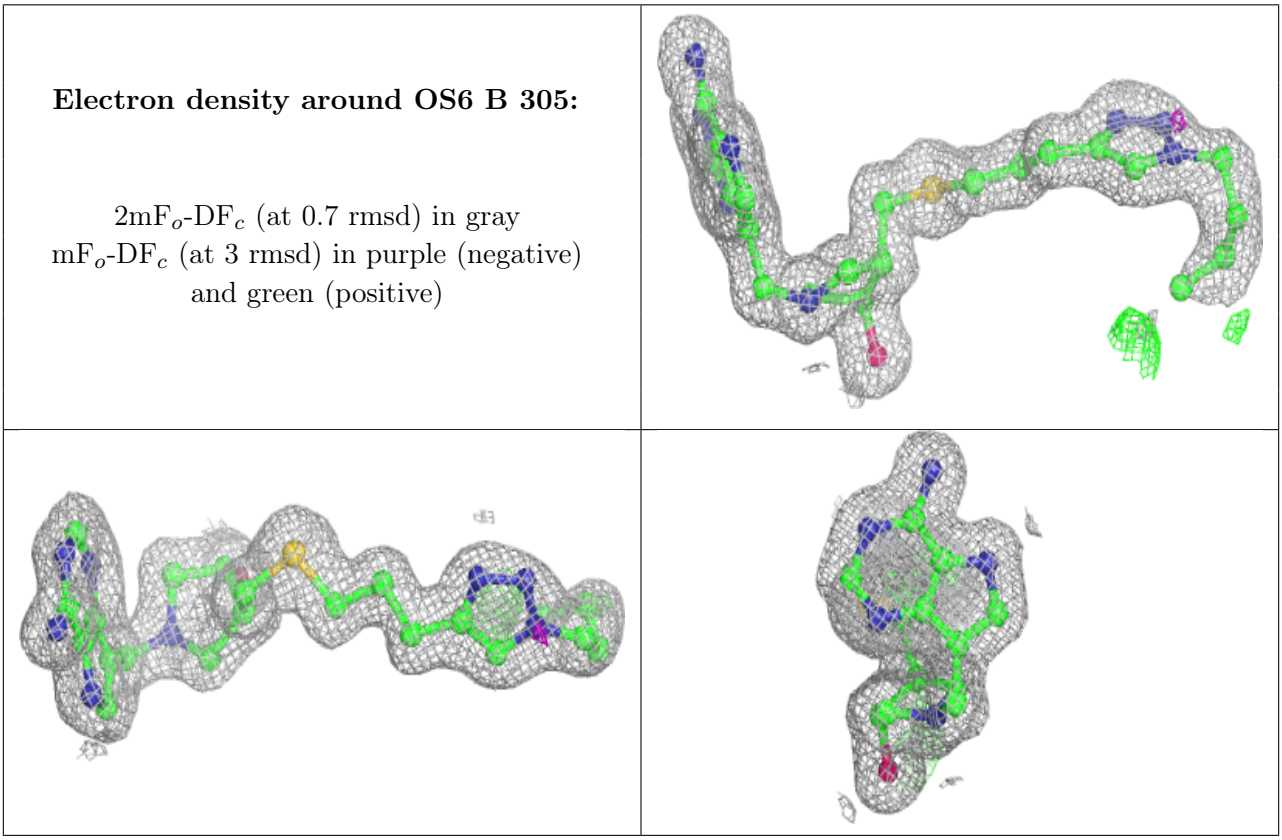
Electron density around OS6 C 303:

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



Electron density around OS6 B 305:

$2mF_o$-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.