Full wwPDB X-ray Structure Validation Report (i)

Jan 7, 2024 – 07:17 am GMT

PDB ID	:	6H4Y
Title	:	Crystal structure of human KDM4A in complex with compound 17e
Authors	:	Le Bihan, Y.V.; van Montfort, R.L.M.
Deposited on	:	2018-07-23
Resolution	:	2.38 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:

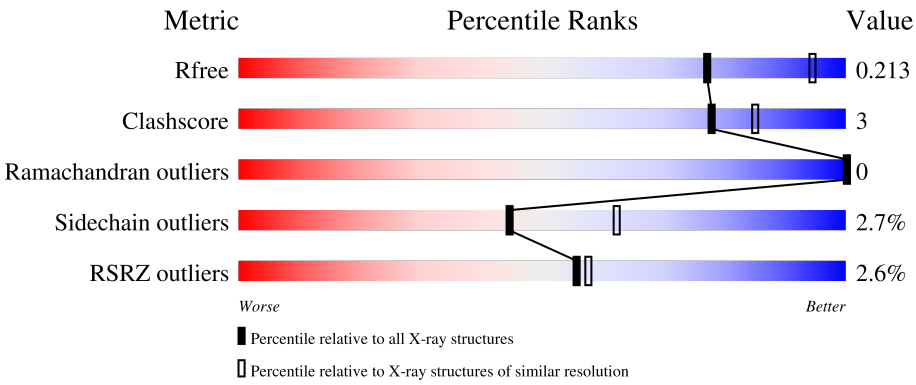
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.38 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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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 <=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	360	4% 87% 7% 6%
1	B	360	% 89% 6% 5%
1	C	360	2% 86% 8% 6%
1	D	360	3% 86% 8% 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
6	GOL	C	405	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 11366 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Lysine-specific demethylase 4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	337	2646	1730	425	477	14	0	1	0
1	B	341	2754	1785	460	495	14	0	2	0
1	C	339	2677	1746	432	484	15	0	1	0
1	D	339	2668	1739	436	479	14	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

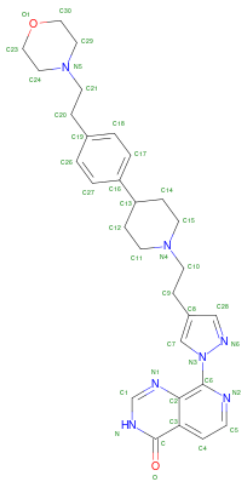
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O75164
B	0	SER	-	expression tag	UNP O75164
C	0	SER	-	expression tag	UNP O75164
D	0	SER	-	expression tag	UNP O75164

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	2	2	2	0	0
2	B	2	2	2	0	0
2	C	2	2	2	0	0
2	D	2	2	2	0	0

- Molecule 3 is 8-[4-[2-[4-[4-(2-morpholin-4-ylethyl)phenyl]piperidin-1-yl]ethyl]pyrazol-1-yl]-3{H}-pyrido[3,4-d]pyrimidin-4-one (three-letter code: FO8) (formula: $C_{29}H_{35}N_7O_2$) (labeled as "Ligand of Interest" by depositor).

FO8

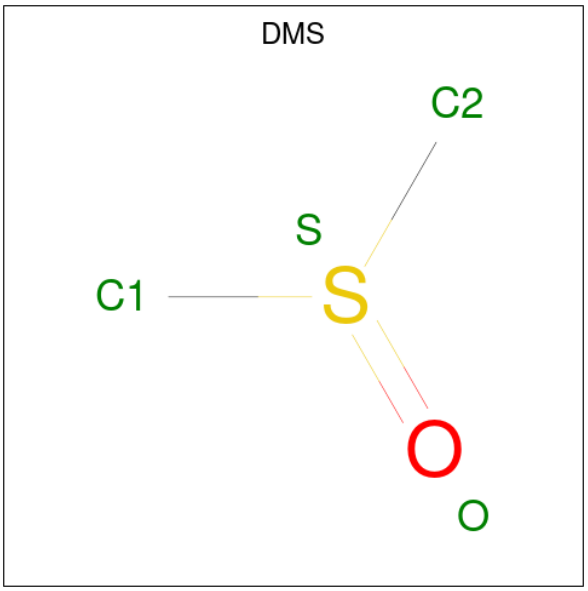


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	19	12	6	1	0	0
3	B	1	30	23	6	1	0	0
3	C	1	19	12	6	1	0	0
3	D	1	25	18	6	1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

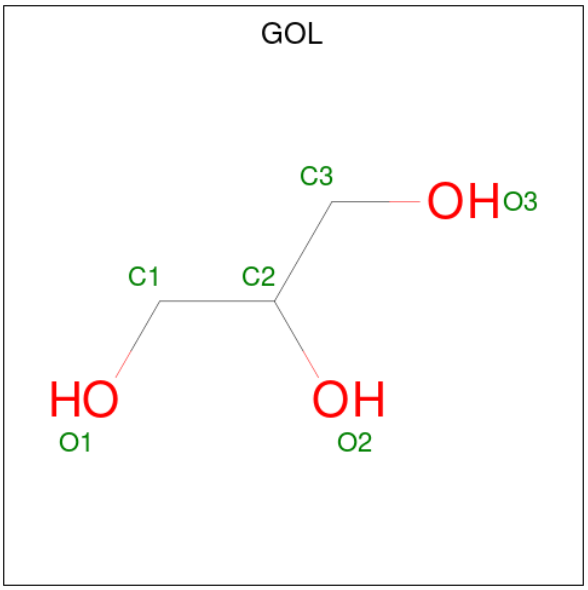
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	1	1	1	0	0
4	B	1	1	1	0	0
4	C	1	1	1	0	0

- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is water.

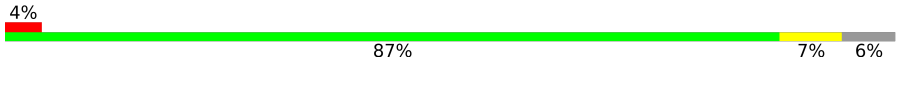
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	130	130	130	0	0
			Total	O		
7	B	149	149	149	0	0
			Total	O		
7	C	109	109	109	0	0
			Total	O		
7	D	107	107	107	0	0

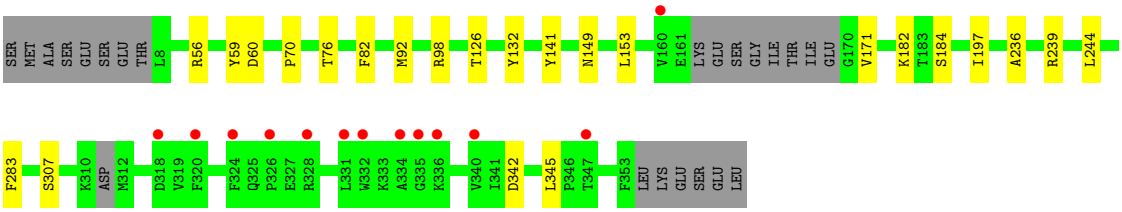
3 Residue-property plots (i)

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: Lysine-specific demethylase 4A

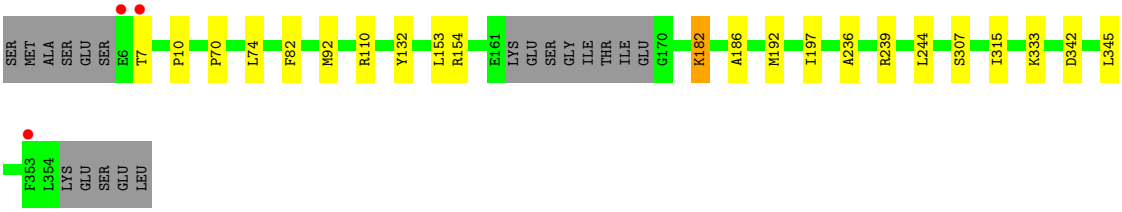
Chain A:





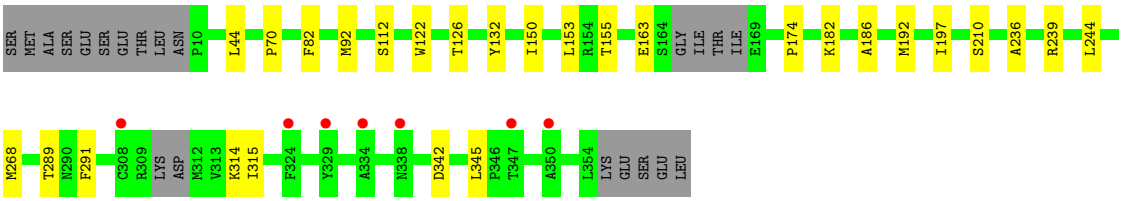
• Molecule 1: Lysine-specific demethylase 4A

Chain B:



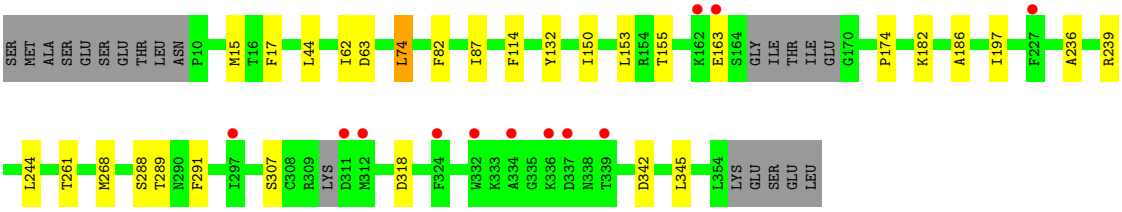
• Molecule 1: Lysine-specific demethylase 4A

Chain C:



• Molecule 1: Lysine-specific demethylase 4A

Chain D:


SER
MET
ALA
SER
GLU
SER
GLU
THR
LEU
ASN
P10
M15
T16
F17
L44
I62
D63
L74
F82
I87
F114
Y132
I150
L153
R154
T155
K162
E163
S164
GLY
ILE
THR
ILE
GLU
G170
P174
K182
A186
I197
F227
A236
R239
L244
T261
M268
S288
T289
N290
F291
I297
S307
C308
R309
LYS
D311
M312
D318
F324
W332
K333
A334
G335
K336
D337
N338
T339
D342
L345
L354
LYS
GLU
SER
GLU
LEU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	58.05Å 100.76Å 143.17Å 90.00° 99.56° 90.00°	Depositor
Resolution (Å)	57.24 – 2.38 57.24 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.8 (57.24-2.38) 99.8 (57.24-2.38)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 2.37Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.174 , 0.209 0.180 , 0.213	Depositor DCC
R_{free} test set	3112 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å^2)	59.2	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 62.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.024 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	11366	wwPDB-VP
Average B, all atoms (Å^2)	70.0	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 22.42 % 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 5.7165e-03. 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: GOL, ZN, DMS, CL, FO8

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	0.51	0/2730	0.68	0/3716
1	B	0.53	0/2839	0.69	0/3856
1	C	0.50	0/2762	0.67	0/3758
1	D	0.51	0/2754	0.67	0/3749
All	All	0.51	0/11085	0.68	0/15079

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	2646	0	2383	14	0
1	B	2754	0	2557	12	0
1	C	2677	0	2435	16	0
1	D	2668	0	2399	13	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	19	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	30	0	0	1	0
3	C	19	0	0	1	0
3	D	25	0	0	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	B	4	0	6	0	0
5	C	4	0	6	1	0
5	D	8	0	12	0	0
6	C	6	0	8	7	0
7	A	130	0	0	0	0
7	B	149	0	0	1	0
7	C	109	0	0	0	0
7	D	107	0	0	0	0
All	All	11366	0	9806	59	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 3.

All (59) 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:126:THR:HB	6:C:405:GOL:H2	1.27	1.08
1:C:192:MET:CE	1:C:314:LYS:HA	1.84	1.07
1:C:192:MET:HE3	1:C:314:LYS:HA	1.40	0.98
1:A:76:THR:HA	6:C:405:GOL:H32	1.67	0.75
1:A:76:THR:HA	6:C:405:GOL:C3	2.17	0.74
1:B:110:ARG:H	1:B:110:ARG:CD	2.11	0.63
1:B:110:ARG:H	1:B:110:ARG:NE	2.01	0.59
1:C:192:MET:HE1	1:C:314:LYS:HA	1.81	0.57
1:D:153:LEU:HD11	1:D:197:ILE:HG21	1.88	0.56
1:B:70:PRO:HG3	1:B:92:MET:HG2	1.88	0.55
1:C:192:MET:CE	1:C:315:ILE:H	2.20	0.55
1:C:153:LEU:HD11	1:C:197:ILE:HG21	1.89	0.54
1:A:70:PRO:HG3	1:A:92:MET:HG2	1.90	0.54
1:C:192:MET:HE3	1:C:314:LYS:CA	2.28	0.53
1:D:74:LEU:CD1	1:D:87:ILE:CD1	2.87	0.53
3:C:403:FO8:C7	3:C:403:FO8:N1	2.72	0.52
1:A:98:ARG:HG3	1:A:283:PHE:CE2	2.45	0.52
1:A:76:THR:HA	6:C:405:GOL:H31	1.90	0.52
3:A:403:FO8:N1	3:A:403:FO8:C7	2.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:403:FO8:C7	3:D:403:FO8:N1	2.72	0.51
3:B:403:FO8:C7	3:B:403:FO8:N1	2.73	0.51
1:A:153:LEU:HD11	1:A:197:ILE:HG21	1.91	0.51
1:B:153:LEU:HD11	1:B:197:ILE:HG21	1.94	0.50
1:C:150:ILE:HG22	1:C:174:PRO:HB3	1.94	0.49
1:C:70:PRO:HG3	1:C:92:MET:HG2	1.95	0.49
1:A:126:THR:HB	6:C:405:GOL:H12	1.95	0.49
1:B:192:MET:HG3	1:B:315:ILE:HD12	1.95	0.49
1:C:342:ASP:HB3	1:C:345:LEU:HD12	1.94	0.49
1:A:126:THR:CB	6:C:405:GOL:H12	2.44	0.47
1:D:15:MET:HE1	1:D:17:PHE:HZ	1.79	0.47
1:B:236:ALA:HB1	1:B:239:ARG:HG3	1.97	0.47
1:B:182:LYS:HE3	7:B:550:HOH:O	2.15	0.46
1:B:342:ASP:HB3	1:B:345:LEU:HD12	1.98	0.45
1:A:82:PHE:HB2	1:A:244:LEU:HB2	1.98	0.44
1:B:82:PHE:HB2	1:B:244:LEU:HB2	1.98	0.44
1:A:126:THR:OG1	6:C:405:GOL:H12	2.16	0.44
1:D:114[B]:PHE:CE2	1:D:261:THR:HG21	2.53	0.44
1:A:141:TYR:CE2	1:A:149:ASN:HA	2.52	0.44
1:D:150:ILE:HG22	1:D:174:PRO:HB3	2.00	0.43
1:D:186:ALA:HA	1:D:244:LEU:HD23	2.00	0.43
1:C:122:TRP:CD1	5:C:406:DMS:H12	2.54	0.43
1:B:7:THR:O	1:B:10:PRO:HD3	2.18	0.43
1:C:236:ALA:HB1	1:C:239:ARG:HG3	2.01	0.43
1:A:56:ARG:HD3	1:A:59:TYR:CD1	2.54	0.42
1:D:82:PHE:HB2	1:D:244:LEU:HB2	2.00	0.42
1:D:342:ASP:HB3	1:D:345:LEU:HD12	2.00	0.42
1:D:74:LEU:CD1	1:D:87:ILE:HD12	2.50	0.42
1:A:342:ASP:HB3	1:A:345:LEU:HD12	2.00	0.42
1:D:236:ALA:HB1	1:D:239:ARG:HG3	2.01	0.42
1:B:110:ARG:CD	1:B:110:ARG:N	2.81	0.41
1:D:74:LEU:HD13	1:D:87:ILE:HD11	2.01	0.41
1:B:186:ALA:HA	1:B:244:LEU:HD23	2.02	0.41
1:C:186:ALA:HA	1:C:244:LEU:HD23	2.01	0.41
1:A:236:ALA:HB1	1:A:239:ARG:HG3	2.02	0.40
1:D:44:LEU:HG	1:D:268:MET:CE	2.51	0.40
1:D:155:THR:HG21	1:D:291:PHE:HB2	2.03	0.40
1:C:44:LEU:HG	1:C:268:MET:CE	2.50	0.40
1:C:155:THR:HG21	1:C:291:PHE:HB2	2.03	0.40
1:C:82:PHE:HB2	1:C:244:LEU:HB2	2.03	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	332/360 (92%)	327 (98%)	5 (2%)	0	100	100
1	B	337/360 (94%)	332 (98%)	5 (2%)	0	100	100
1	C	334/360 (93%)	329 (98%)	5 (2%)	0	100	100
1	D	334/360 (93%)	329 (98%)	5 (2%)	0	100	100
All	All	1337/1440 (93%)	1317 (98%)	20 (2%)	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	247/316 (78%)	241 (98%)	6 (2%)	49	66
1	B	272/316 (86%)	266 (98%)	6 (2%)	52	69
1	C	257/316 (81%)	251 (98%)	6 (2%)	50	68
1	D	249/316 (79%)	239 (96%)	10 (4%)	31	47
All	All	1025/1264 (81%)	997 (97%)	28 (3%)	44	62

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ASP
1	A	132	TYR

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Mol	Chain	Res	Type
1	A	171	VAL
1	A	182	LYS
1	A	184	SER
1	A	307	SER
1	B	74	LEU
1	B	132	TYR
1	B	154	ARG
1	B	182	LYS
1	B	307	SER
1	B	333	LYS
1	C	112	SER
1	C	132	TYR
1	C	163	GLU
1	C	182	LYS
1	C	210	SER
1	C	289	THR
1	D	62	ILE
1	D	63	ASP
1	D	74	LEU
1	D	132	TYR
1	D	163	GLU
1	D	182	LYS
1	D	288	SER
1	D	289	THR
1	D	307	SER
1	D	318	ASP

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)

Of 20 ligands modelled in this entry, 11 are monoatomic - leaving 9 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	FO8	C	403	2	19,21,43	0.71	0	20,29,59	0.88	1 (5%)
6	GOL	C	405	-	5,5,5	0.44	0	5,5,5	0.50	0
3	FO8	B	403	2	33,34,43	0.56	1 (3%)	39,47,59	0.67	1 (2%)
5	DMS	C	406	-	3,3,3	0.35	0	3,3,3	0.19	0
5	DMS	D	405	-	3,3,3	0.19	0	3,3,3	0.30	0
5	DMS	D	404	-	3,3,3	0.29	0	3,3,3	0.35	0
3	FO8	D	403	2	27,28,43	0.61	1 (3%)	31,39,59	0.75	1 (3%)
3	FO8	A	403	2	19,21,43	0.73	1 (5%)	20,29,59	0.90	1 (5%)
5	DMS	B	405	-	3,3,3	0.30	0	3,3,3	0.15	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	FO8	C	403	2	-	0/3/7/36	0/3/3/6
6	GOL	C	405	-	-	1/4/4/4	-
3	FO8	B	403	2	-	1/9/23/36	0/5/5/6
3	FO8	D	403	2	-	1/5/19/36	0/4/4/6
3	FO8	A	403	2	-	0/3/7/36	0/3/3/6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	FO8	C-N	-2.19	1.34	1.38
3	D	403	FO8	C-N	-2.15	1.34	1.38
3	B	403	FO8	C-N	-2.08	1.34	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	403	FO8	C2-C6-N2	2.95	125.27	118.67
3	B	403	FO8	C2-C6-N2	2.59	124.45	118.67
3	D	403	FO8	C2-C6-N2	2.54	124.35	118.67
3	A	403	FO8	C2-C6-N2	2.48	124.21	118.67

There are no chirality outliers.

All (3) torsion outliers are listed below:

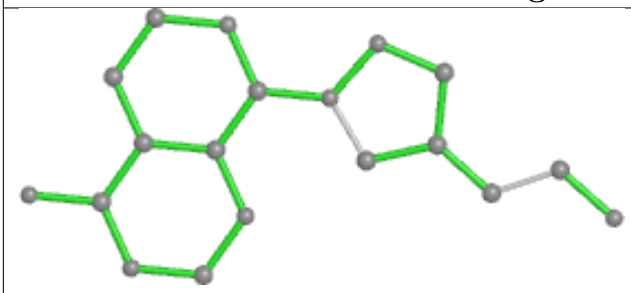
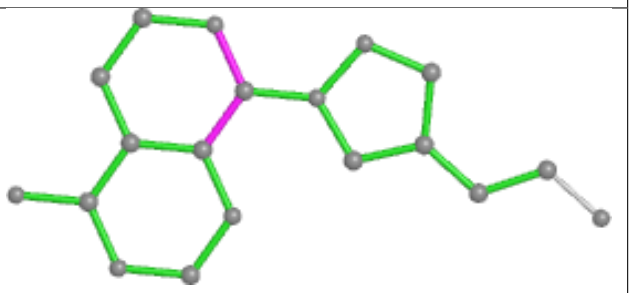
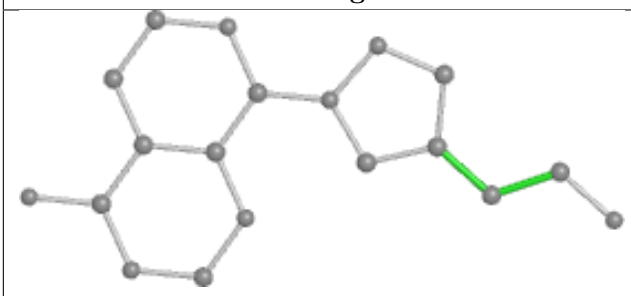
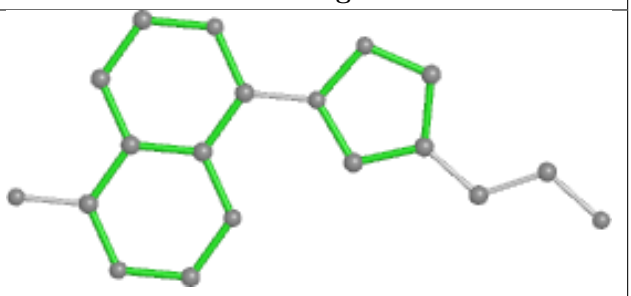
Mol	Chain	Res	Type	Atoms
3	D	403	FO8	C9-C10-N4-C15
6	C	405	GOL	O1-C1-C2-O2
3	B	403	FO8	C9-C10-N4-C15

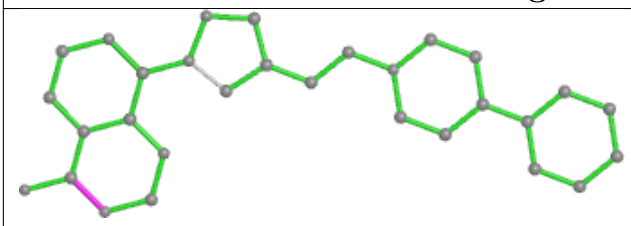
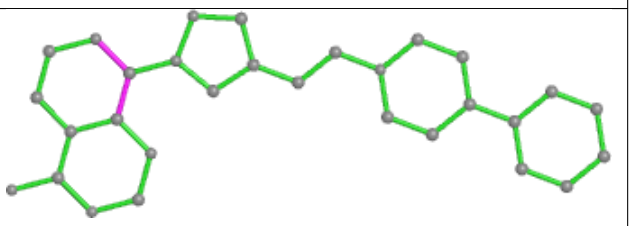
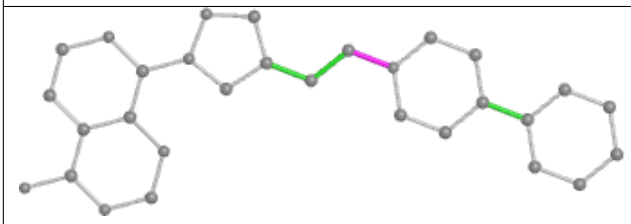
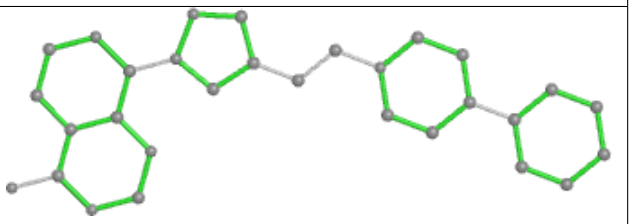
There are no ring outliers.

6 monomers are involved in 12 short contacts:

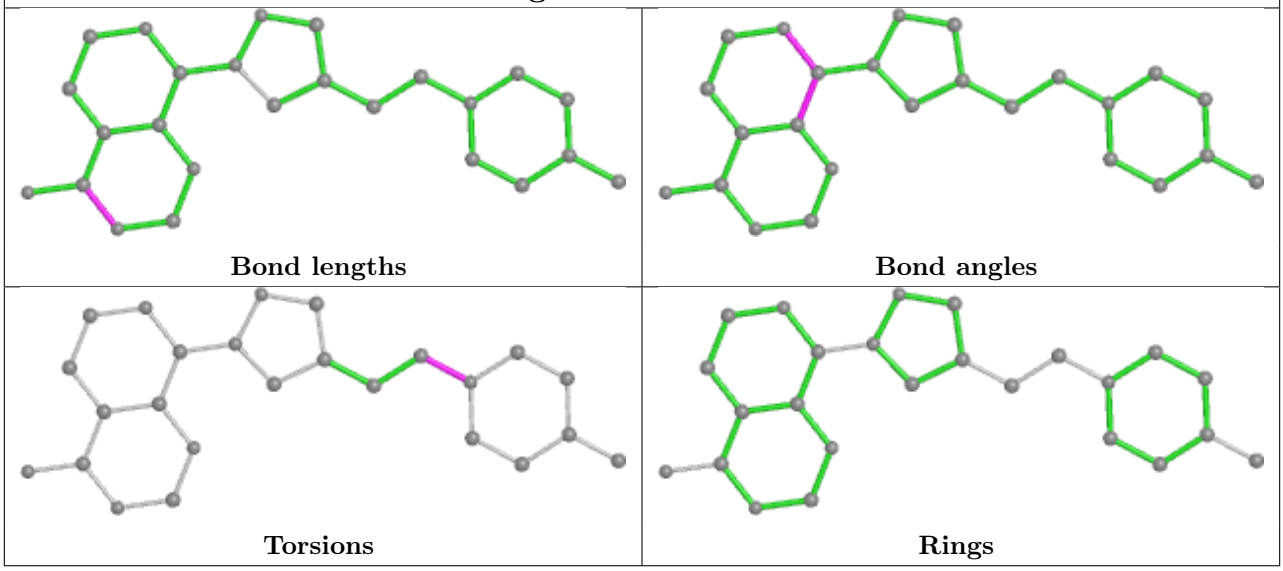
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	403	FO8	1	0
6	C	405	GOL	7	0
3	B	403	FO8	1	0
5	C	406	DMS	1	0
3	D	403	FO8	1	0
3	A	403	FO8	1	0

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.

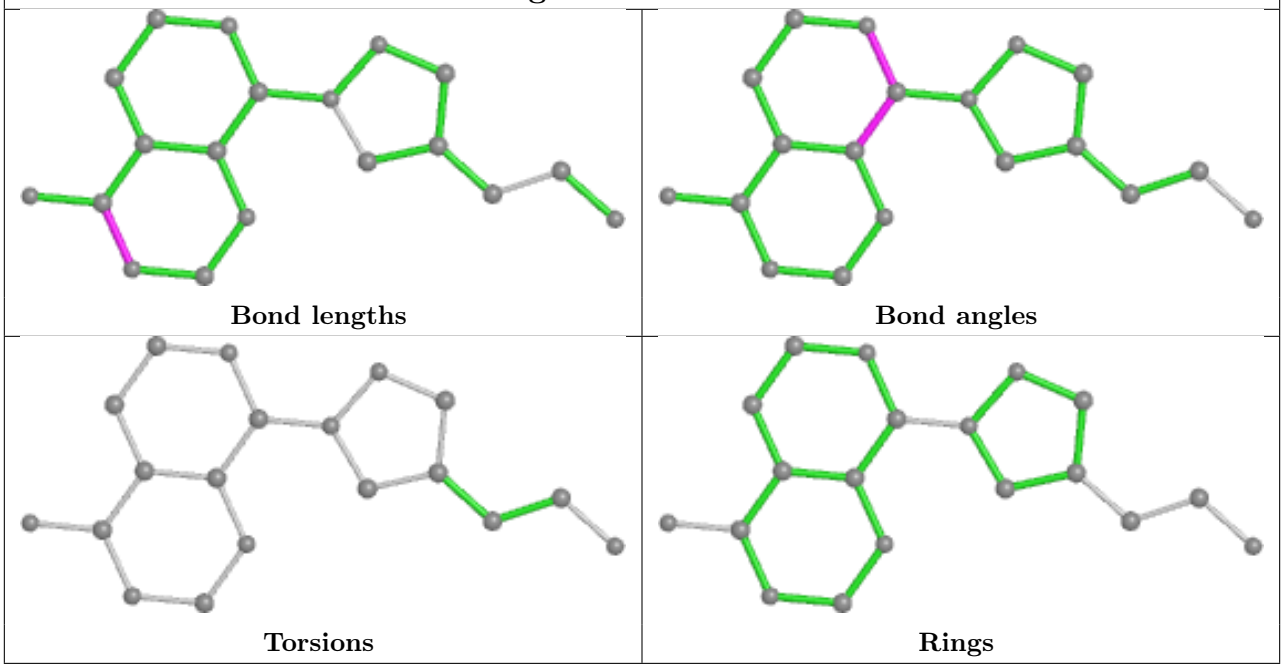
Ligand FO8 C 403	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand FO8 B 403	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand FO8 D 403



Ligand FO8 A 403



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	337/360 (93%)	0.29	13 (3%)	39	42	43, 67, 109, 135	0
1	B	341/360 (94%)	-0.02	3 (0%)	84	84	43, 58, 88, 134	0
1	C	339/360 (94%)	0.20	7 (2%)	63	65	44, 70, 119, 139	0
1	D	339/360 (94%)	0.21	12 (3%)	44	47	44, 70, 123, 150	0
All	All	1356/1440 (94%)	0.17	35 (2%)	56	57	43, 66, 111, 150	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	ALA	6.1
1	D	163	GLU	4.4
1	D	311	ASP	4.0
1	A	328	ARG	3.7
1	A	335	GLY	3.5
1	A	340	VAL	3.4
1	D	334	ALA	3.4
1	C	308	CYS	3.4
1	A	160	VAL	3.2
1	A	332	TRP	3.2
1	A	324	PHE	3.0
1	C	334	ALA	2.9
1	D	162	LYS	2.9
1	D	336	LYS	2.8
1	D	337	ASP	2.8
1	A	320	PHE	2.7
1	A	347	THR	2.7
1	B	7	THR	2.7
1	D	332	TRP	2.6
1	C	347	THR	2.6
1	D	324	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	353	PHE	2.5
1	A	331	LEU	2.5
1	D	312	MET	2.4
1	C	350	ALA	2.4
1	A	326	PRO	2.4
1	A	318	ASP	2.3
1	C	324	PHE	2.3
1	C	329	TYR	2.2
1	A	336	LYS	2.2
1	B	6	GLU	2.1
1	D	227	PHE	2.1
1	C	338	ASN	2.0
1	D	297	ILE	2.0
1	D	339	THR	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
4	CL	A	404	1/1	0.73	0.25	102,102,102,102	0
5	DMS	B	405	4/4	0.84	0.18	112,112,113,113	0
6	GOL	C	405	6/6	0.84	0.46	32,42,42,47	6
5	DMS	C	406	4/4	0.85	0.20	116,117,117,118	0
5	DMS	D	404	4/4	0.86	0.29	123,124,124,125	4
5	DMS	D	405	4/4	0.88	0.17	101,102,103,104	0
3	FO8	A	403	19/38	0.89	0.17	56,65,75,75	19
4	CL	B	404	1/1	0.91	0.31	107,107,107,107	0
3	FO8	D	403	25/38	0.93	0.15	62,71,83,84	25

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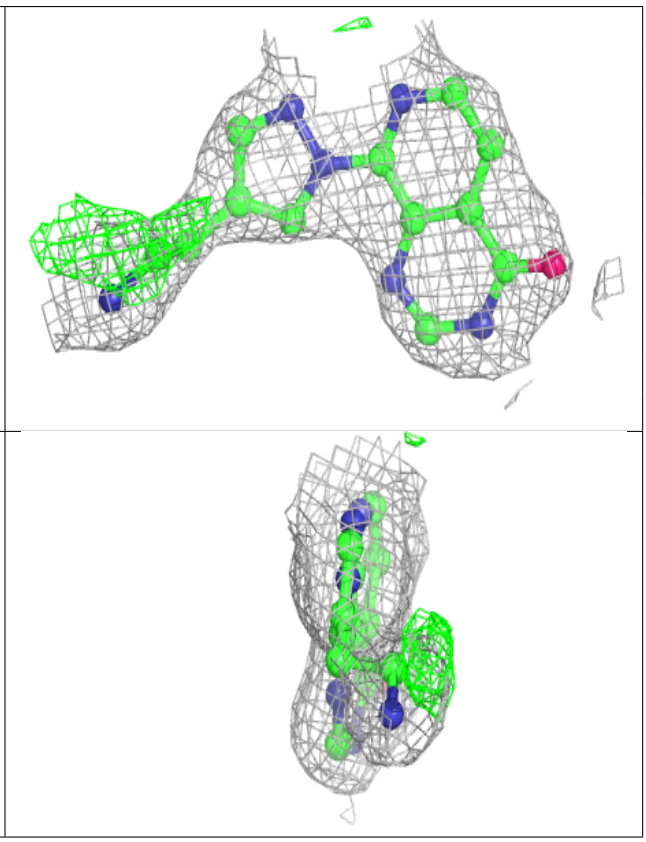
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FO8	C	403	19/38	0.93	0.15	63,67,76,79	19
4	CL	C	404	1/1	0.95	0.29	86,86,86,86	0
2	ZN	D	402	1/1	0.96	0.14	62,62,62,62	1
3	FO8	B	403	30/38	0.96	0.18	42,49,84,85	30
2	ZN	C	401	1/1	0.98	0.14	69,69,69,69	0
2	ZN	C	402	1/1	0.99	0.14	67,67,67,67	1
2	ZN	D	401	1/1	0.99	0.10	68,68,68,68	0
2	ZN	A	402	1/1	0.99	0.14	73,73,73,73	0
2	ZN	B	401	1/1	0.99	0.14	48,48,48,48	1
2	ZN	A	401	1/1	0.99	0.12	73,73,73,73	0
2	ZN	B	402	1/1	1.00	0.16	54,54,54,54	1

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.

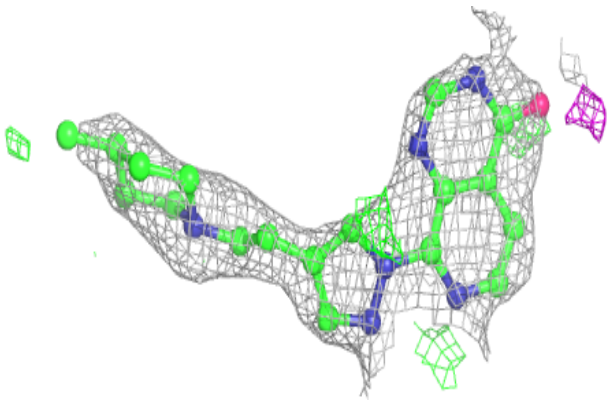
Electron density around FO8 A 403:

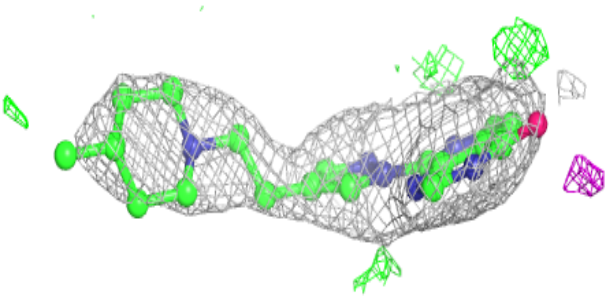
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

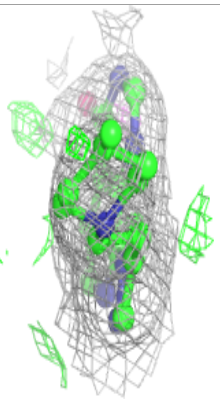


Electron density around FO8 D 403:

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

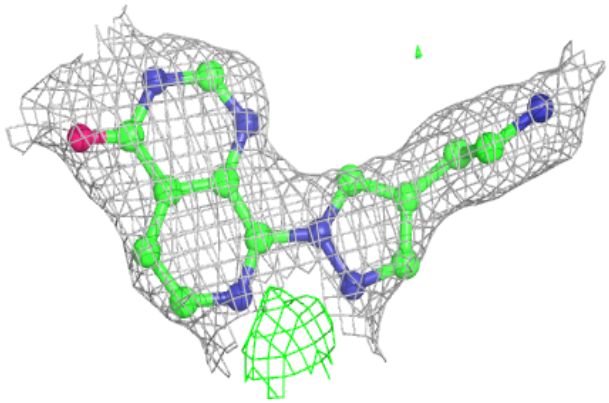


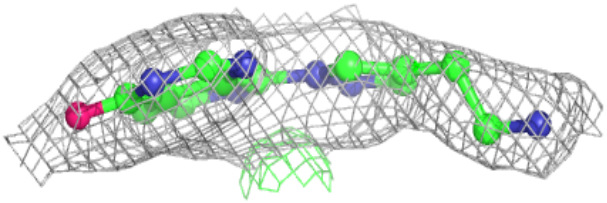


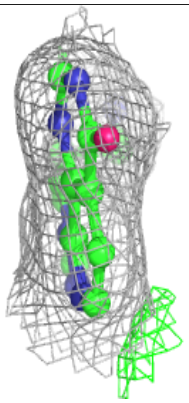


Electron density around FO8 C 403:

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

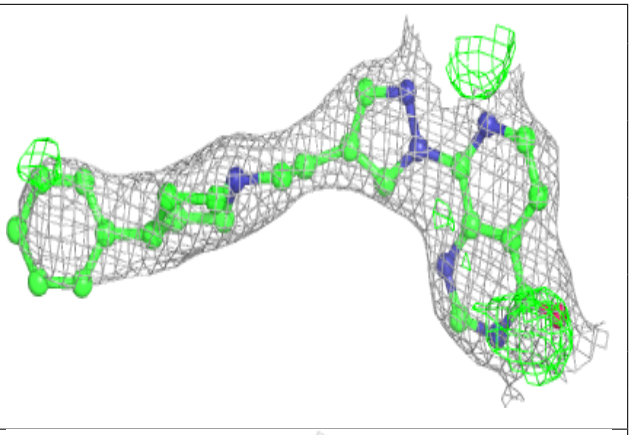


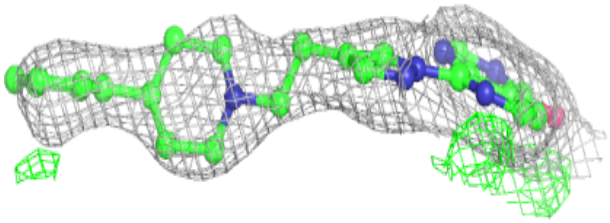


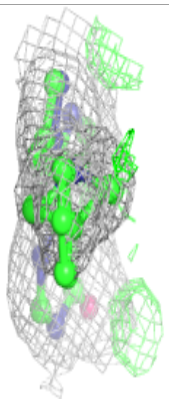


Electron density around FO8 B 403:

$2mF_o$-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.