



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:06 AM UTC

PDB ID : 6H4Y / pdb_00006h4y
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 ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

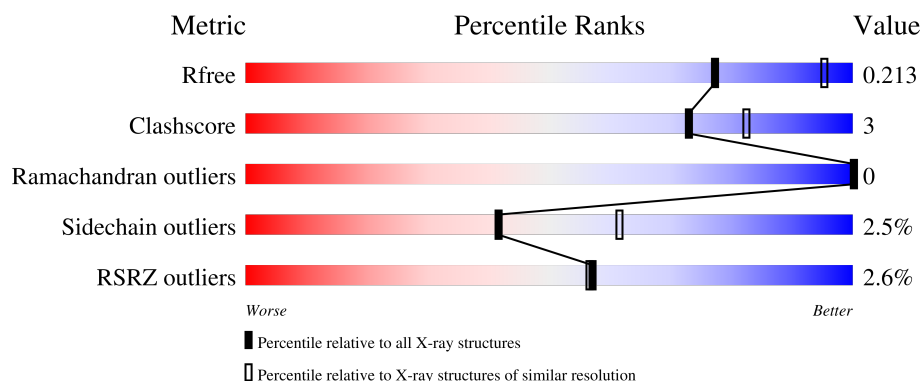
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	180053	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	360	2% 86% 7% 6%
1	B	360	% 87% 7% 5%
1	C	360	3% 84% 9% 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

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

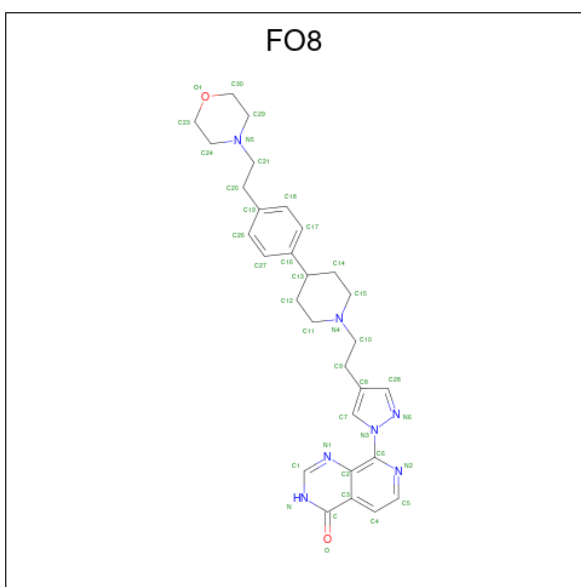
There are 4 discrepancies between the modelled and reference sequences:

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 (CCD ID: ZN) (formula: Zn).

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

- 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 (CCD ID: FO8) (formula: C₂₉H₃₅N₇O₂) (labeled as "Ligand of Interest" by depositor).

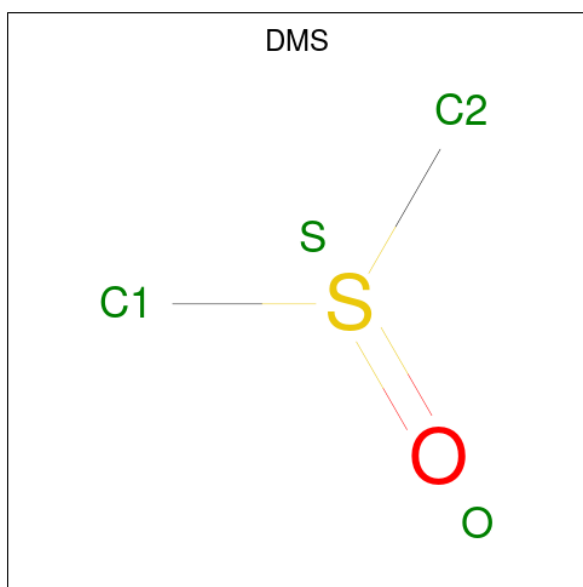


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	12	6	1		
3	B	1	Total	C	N	O	0	0
			30	23	6	1		
3	C	1	Total	C	N	O	0	0
			19	12	6	1		
3	D	1	Total	C	N	O	0	0
			25	18	6	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

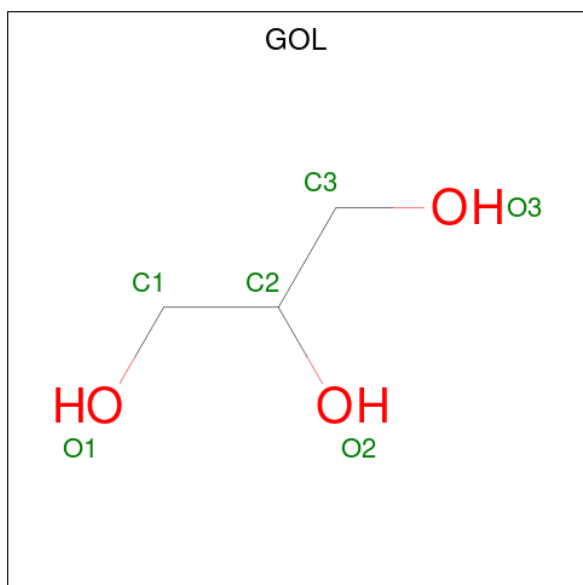
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		
4	B	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



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

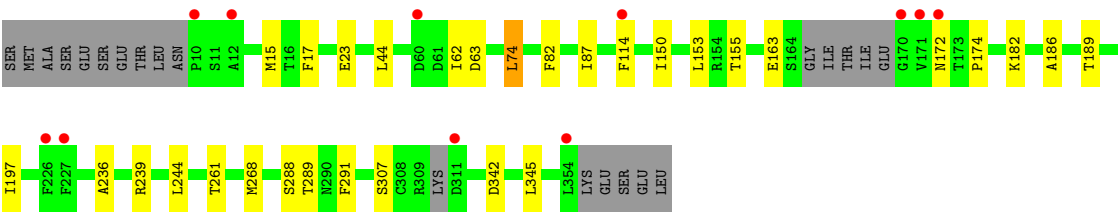
- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is water.

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



4 Data and refinement statistics

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
$\langle I/\sigma(I) \rangle$ 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)	0.32 , 66.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, DMS, ZN, FO8, GOL

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	0.86	0/2730	1.26	5/3716 (0.1%)
1	B	0.87	0/2839	1.26	5/3856 (0.1%)
1	C	0.84	0/2762	1.26	5/3758 (0.1%)
1	D	0.85	0/2754	1.25	4/3749 (0.1%)
All	All	0.86	0/11085	1.26	19/15079 (0.1%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	172	ASN	N-CA-C	-7.26	104.45	113.38
1	D	172	ASN	N-CA-C	-5.59	106.50	113.38
1	A	189	THR	N-CA-C	-5.56	101.97	110.14
1	A	97	PHE	CA-C-N	5.54	127.70	120.28
1	A	97	PHE	C-N-CA	5.54	127.70	120.28
1	C	189	THR	N-CA-C	-5.45	102.14	110.14
1	B	23	GLU	CA-C-N	5.34	127.98	120.28
1	B	23	GLU	C-N-CA	5.34	127.98	120.28
1	B	189	THR	N-CA-C	-5.33	102.31	110.14
1	C	23	GLU	CA-C-N	5.24	127.83	120.28
1	C	23	GLU	C-N-CA	5.24	127.83	120.28
1	D	189	THR	N-CA-C	-5.24	102.44	110.14
1	B	185	PHE	CA-CB-CG	5.19	118.99	113.80
1	B	293	THR	N-CA-C	-5.13	101.62	109.41
1	D	23	GLU	CA-C-N	5.12	127.65	120.28
1	D	23	GLU	C-N-CA	5.12	127.65	120.28
1	A	23	GLU	CA-C-N	5.07	127.58	120.28
1	A	23	GLU	C-N-CA	5.07	127.58	120.28
1	C	185	PHE	CA-CB-CG	5.03	118.83	113.80

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	2646	0	2383	14	0
1	B	2754	0	2557	14	0
1	C	2677	0	2435	20	0
1	D	2668	0	2399	14	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
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	1	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	66	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 (66) 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:192:MET:HE3	1:C:314:LYS:HA	1.35	1.08
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:315:ILE:H	1.35	0.90
1:D:15:MET:HE2	1:D:17:PHE:CZ	2.16	0.80
1:C:192:MET:HE3	1:C:314:LYS:CA	2.15	0.76
1:A:76:THR:HA	6:C:405:GOL:H32	1.67	0.75
1:C:192:MET:HE3	1:C:315:ILE:N	2.01	0.75
1:A:76:THR:HA	6:C:405:GOL:C3	2.17	0.74
1:D:15:MET:HE2	1:D:17:PHE:HZ	1.54	0.72
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:15:MET:HE2	1:C:17:PHE:CZ	2.40	0.56
1:C:248:LEU:HG	5:C:406:DMS:H11	1.88	0.56
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: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: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
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:B:236:ALA:HB1	1:B:239:ARG:HG3	1.97	0.47
1:C:15:MET:HE2	1:C:17:PHE:HZ	1.79	0.47
1:B:182:LYS:HE3	7:B:550:HOH:O	2.15	0.46
1:C:192:MET:HE2	1:C:314:LYS:HA	1.90	0.45
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:192:MET:HE3	1:C:314:LYS:C	2.42	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:B:333:LYS:HA	5:B:405:DMS:H22	2.01	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:B:63:ASP:CG	1:B:98:ARG:HH12	2.28	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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%)	242 (98%)	5 (2%)	48	68
1	B	272/316 (86%)	267 (98%)	5 (2%)	51	71
1	C	257/316 (81%)	249 (97%)	8 (3%)	35	54
1	D	249/316 (79%)	241 (97%)	8 (3%)	34	53
All	All	1025/1264 (81%)	999 (98%)	26 (2%)	42	61

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ASP
1	A	171	VAL
1	A	182	LYS
1	A	184	SER
1	A	307	SER
1	B	74	LEU
1	B	154	ARG
1	B	182	LYS
1	B	307	SER
1	B	333	LYS
1	C	112	SER
1	C	163	GLU
1	C	171	VAL

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Mol	Chain	Res	Type
1	C	182	LYS
1	C	210	SER
1	C	289	THR
1	C	307	SER
1	C	345	LEU
1	D	62	ILE
1	D	63	ASP
1	D	74	LEU
1	D	163	GLU
1	D	182	LYS
1	D	288	SER
1	D	289	THR
1	D	307	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	128	ASN
1	A	137	ASN
1	B	137	ASN
1	B	215	HIS
1	C	128	ASN
1	C	137	ASN
1	D	137	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 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
5	DMS	C	406	-	3,3,3	0.36	0	3,3,3	0.18	0
5	DMS	D	405	-	3,3,3	0.19	0	3,3,3	0.30	0
3	FO8	C	403	2	20,21,43	0.57	0	24,29,59	0.87	1 (4%)
6	GOL	C	405	-	5,5,5	0.44	0	5,5,5	0.51	0
5	DMS	D	404	-	3,3,3	0.30	0	3,3,3	0.35	0
3	FO8	D	403	2	27,28,43	0.55	1 (3%)	34,39,59	0.74	1 (2%)
3	FO8	A	403	2	20,21,43	0.63	1 (5%)	24,29,59	0.83	1 (4%)
5	DMS	B	405	-	3,3,3	0.30	0	3,3,3	0.16	0
3	FO8	B	403	2	33,34,43	0.49	1 (3%)	42,47,59	0.70	1 (2%)

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	-	4/7/7/36	0/3/3/6
6	GOL	C	405	-	-	1/4/4/4	-
3	FO8	D	403	2	-	5/9/19/36	0/4/4/6
3	FO8	A	403	2	-	4/7/7/36	0/3/3/6
3	FO8	B	403	2	-	4/13/23/36	0/5/5/6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	FO8	C-N	-2.23	1.34	1.38
3	D	403	FO8	C-N	-2.19	1.34	1.38
3	B	403	FO8	C-N	-2.12	1.34	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	403	FO8	C2-C6-N2	3.24	125.27	118.55
3	B	403	FO8	C2-C6-N2	2.85	124.45	118.55
3	D	403	FO8	C2-C6-N2	2.79	124.35	118.55
3	A	403	FO8	C2-C6-N2	2.73	124.21	118.55

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	403	FO8	N2-C6-N3-N6
3	A	403	FO8	C2-C6-N3-N6
3	B	403	FO8	N2-C6-N3-N6
3	B	403	FO8	C2-C6-N3-N6
3	C	403	FO8	N2-C6-N3-N6
3	C	403	FO8	C2-C6-N3-N6
3	D	403	FO8	N2-C6-N3-N6
3	D	403	FO8	C2-C6-N3-N6
3	D	403	FO8	C9-C10-N4-C15
6	C	405	GOL	O1-C1-C2-O2
3	A	403	FO8	N2-C6-N3-C7
3	B	403	FO8	N2-C6-N3-C7
3	C	403	FO8	N2-C6-N3-C7
3	D	403	FO8	N2-C6-N3-C7
3	A	403	FO8	C2-C6-N3-C7
3	B	403	FO8	C2-C6-N3-C7
3	C	403	FO8	C2-C6-N3-C7
3	D	403	FO8	C2-C6-N3-C7

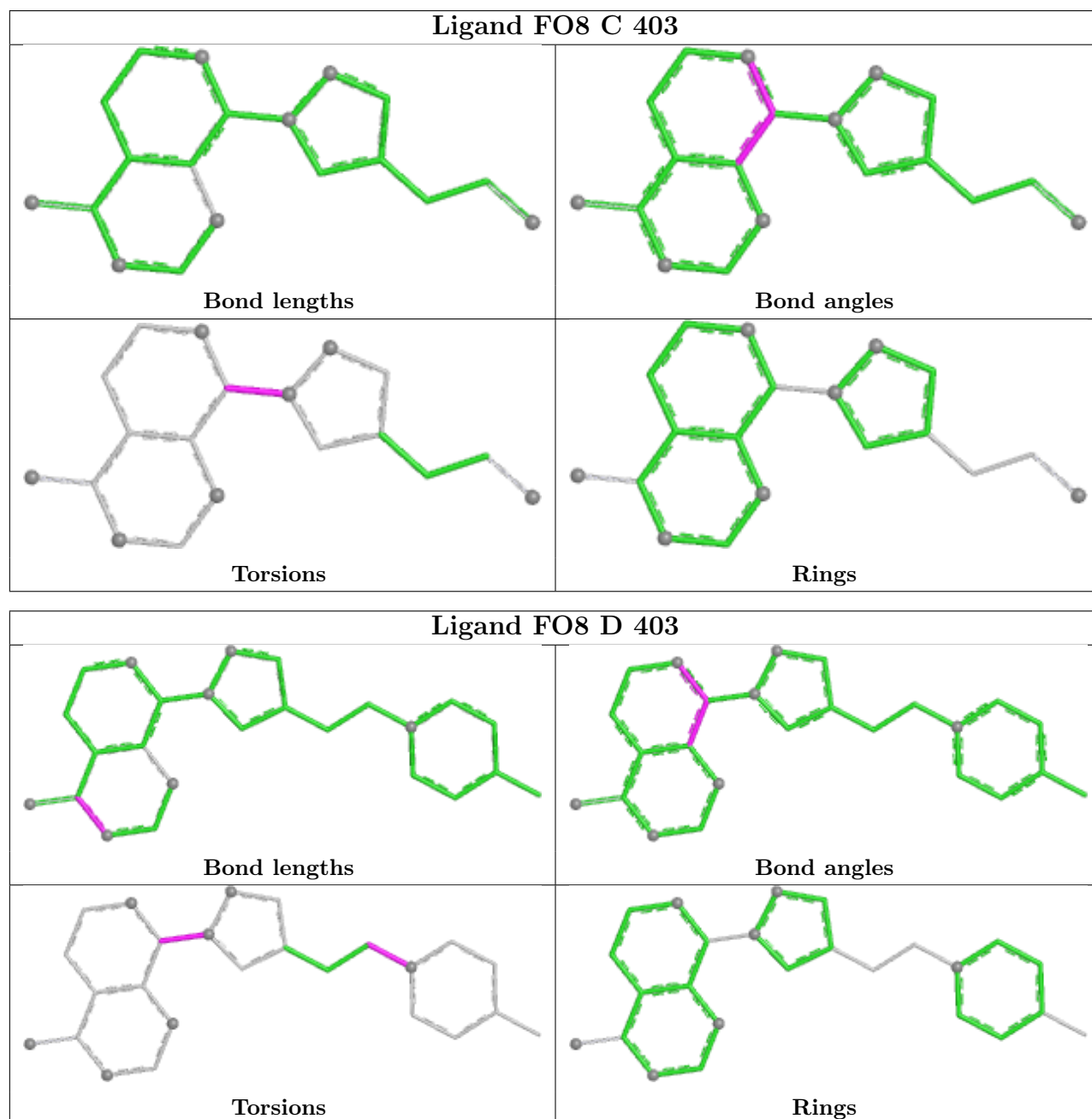
There are no ring outliers.

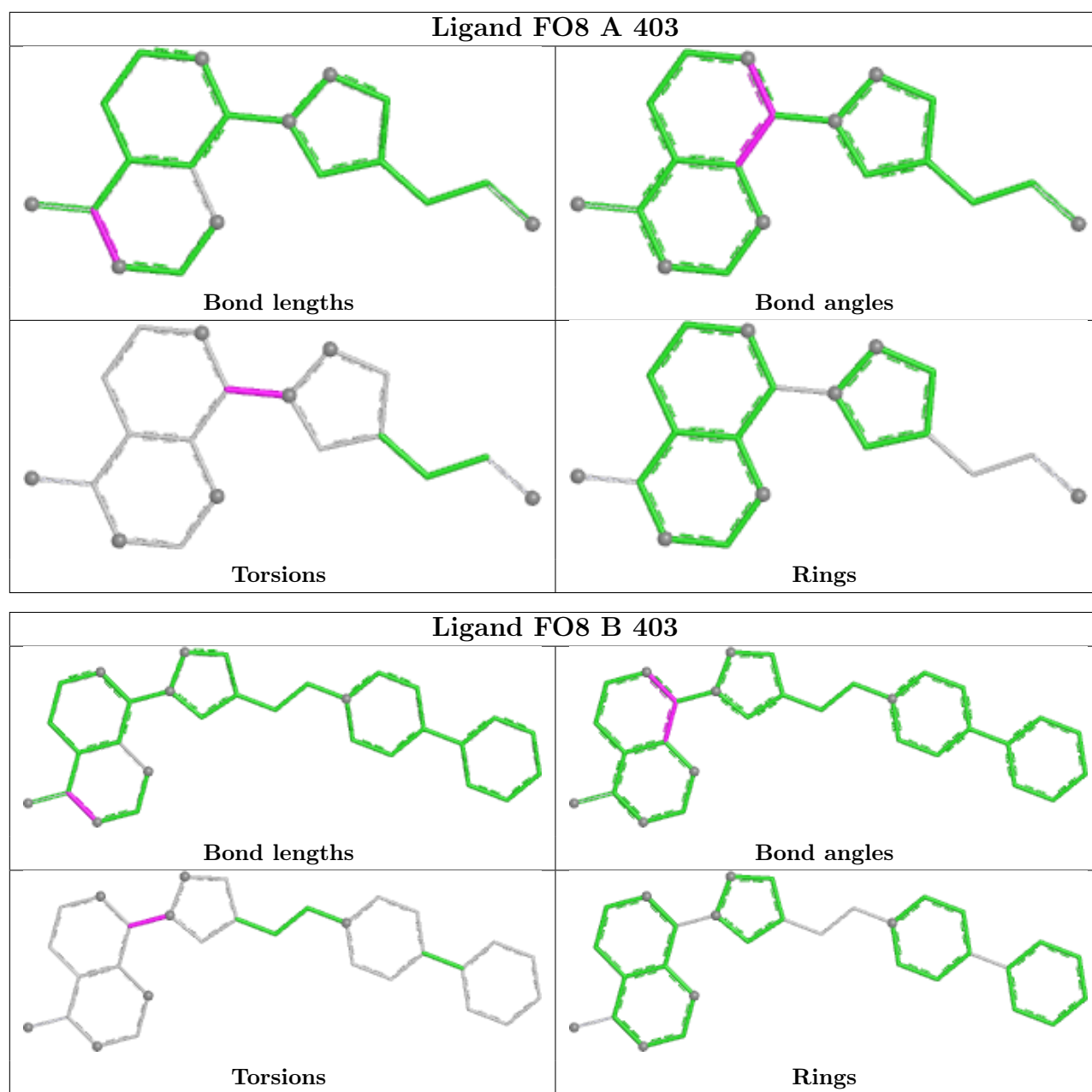
7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	406	DMS	1	0
3	C	403	FO8	1	0
6	C	405	GOL	7	0
3	D	403	FO8	1	0
3	A	403	FO8	1	0
5	B	405	DMS	1	0
3	B	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	337/360 (93%)	0.15	7 (2%) 63 62	37, 67, 109, 135	1 (0%)
1	B	341/360 (94%)	-0.13	5 (1%) 72 71	34, 58, 88, 134	2 (0%)
1	C	339/360 (94%)	0.17	12 (3%) 47 47	36, 70, 119, 139	1 (0%)
1	D	339/360 (94%)	0.21	11 (3%) 50 50	34, 70, 123, 150	1 (0%)
All	All	1356/1440 (94%)	0.10	35 (2%) 57 56	34, 66, 111, 150	5 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	170	GLY	5.7
1	D	227	PHE	4.9
1	C	10	PRO	4.8
1	D	10	PRO	4.7
1	C	164	SER	3.8
1	B	161	GLU	3.6
1	A	13[A]	ARG	3.4
1	C	354	LEU	3.3
1	D	12	ALA	3.2
1	B	354	LEU	3.1
1	A	353	PHE	2.9
1	C	170	GLY	2.8
1	D	311	ASP	2.7
1	D	354	LEU	2.7
1	B	7	THR	2.7
1	D	114[A]	PHE	2.6
1	C	171	VAL	2.6
1	A	232	GLN	2.5
1	D	226	PHE	2.5
1	D	171	VAL	2.5
1	C	313	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	144	HIS	2.4
1	C	227	PHE	2.4
1	A	338	ASN	2.3
1	D	60	ASP	2.3
1	D	172	ASN	2.2
1	A	328	ARG	2.2
1	C	226	PHE	2.2
1	C	338	ASN	2.2
1	B	170	GLY	2.2
1	A	8	LEU	2.1
1	A	170	GLY	2.1
1	C	318	ASP	2.1
1	C	308	CYS	2.1
1	B	312	MET	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	DMS	D	404	4/4	0.78	0.20	123,124,124,125	4
5	DMS	B	405	4/4	0.80	0.19	112,112,113,113	0
5	DMS	C	406	4/4	0.83	0.22	116,117,117,118	0
5	DMS	D	405	4/4	0.86	0.19	101,102,103,104	0
6	GOL	C	405	6/6	0.86	0.16	32,42,42,47	6
3	FO8	D	403	25/38	0.90	0.14	62,71,83,84	25
3	FO8	A	403	19/38	0.91	0.12	56,65,75,75	19
3	FO8	C	403	19/38	0.92	0.12	63,67,76,79	19
4	CL	B	404	1/1	0.93	0.15	107,107,107,107	0

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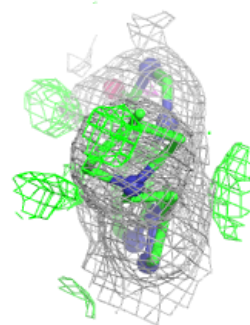
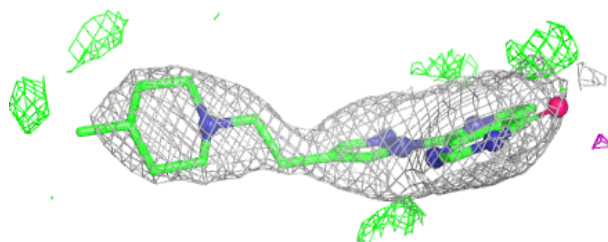
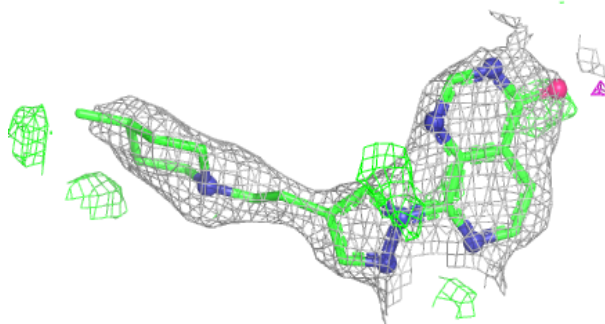
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	FO8	B	403	30/38	0.94	0.12	42,49,84,85	30
4	CL	A	404	1/1	0.94	0.16	102,102,102,102	0
4	CL	C	404	1/1	0.95	0.18	86,86,86,86	0
2	ZN	B	401	1/1	0.98	0.03	48,48,48,48	1
2	ZN	A	402	1/1	0.99	0.04	73,73,73,73	0
2	ZN	A	401	1/1	0.99	0.03	73,73,73,73	0
2	ZN	C	401	1/1	0.99	0.02	69,69,69,69	0
2	ZN	C	402	1/1	0.99	0.03	67,67,67,67	1
2	ZN	D	401	1/1	0.99	0.04	68,68,68,68	0
2	ZN	D	402	1/1	0.99	0.03	62,62,62,62	1
2	ZN	B	402	1/1	1.00	0.04	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.

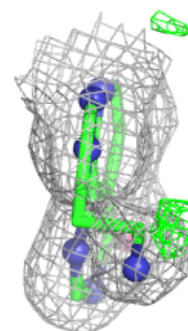
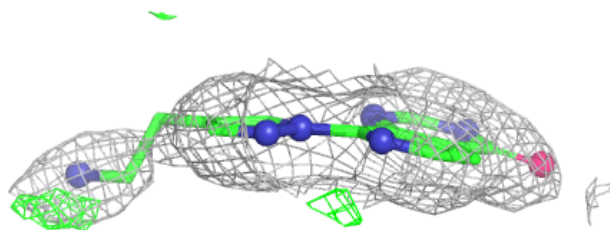
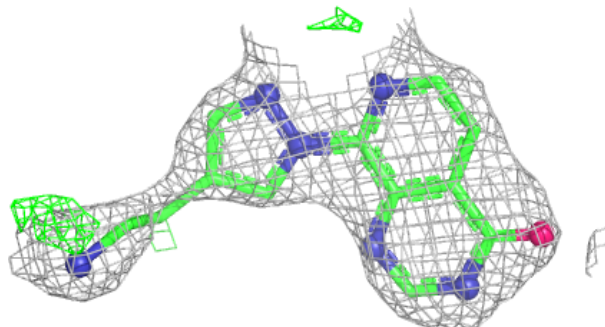
Electron density around FO8 D 403:

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

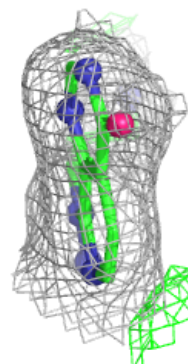
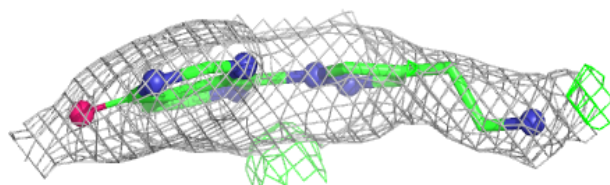
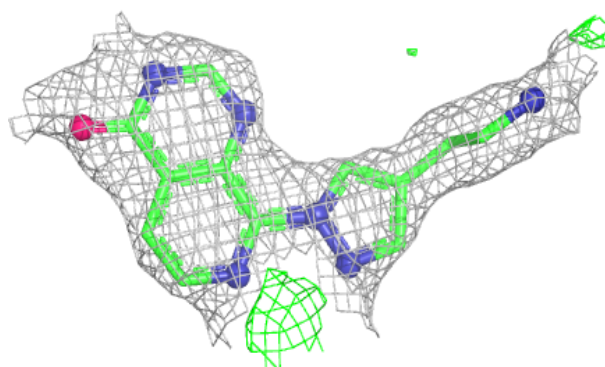


Electron density around FO8 A 403:

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

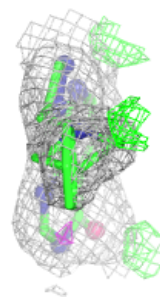
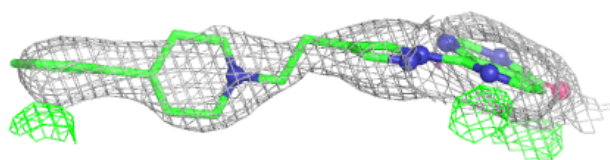
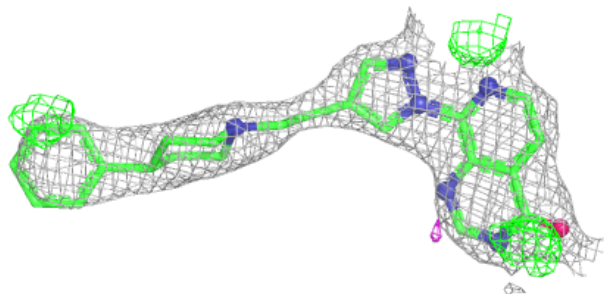
**Electron density around FO8 C 403:**

$2mF_o-DF_c$ (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.