



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:11 AM UTC

PDB ID : 7CD0 / pdb_00007cd0
Title : Crystal structure of the 2-iodoporphobilinogen-bound ES2 intermediate form of human hydroxymethylbilane synthase
Authors : Sato, H.; Sugishima, M.; Wada, K.; Hirabayashi, K.; Tsukaguchi, M.
Deposited on : 2020-06-18
Resolution : 2.31 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)
Xtrriage (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

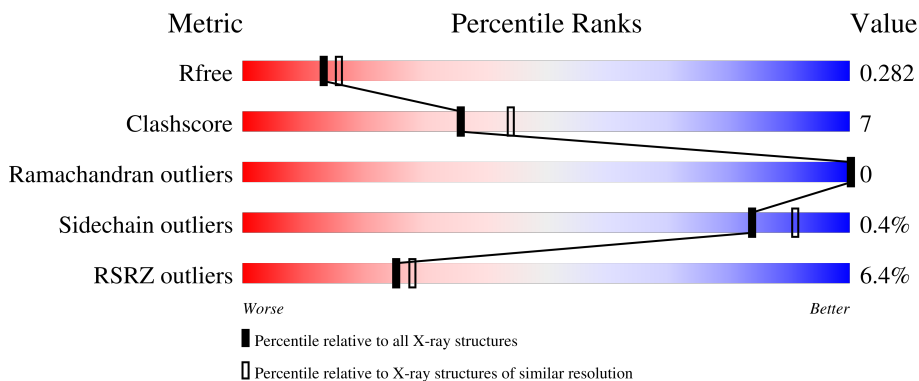
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.31 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	7754 (2.34-2.30)
Clashscore	190562	8383 (2.34-2.30)
Ramachandran outliers	187476	8303 (2.34-2.30)
Sidechain outliers	187428	8303 (2.34-2.30)
RSRZ outliers	180081	7760 (2.34-2.30)

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 $\leq 5\%$. 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	361	 5% 77% 12% 11%
1	B	361	 7% 72% 16% 11%

2 Entry composition [i](#)

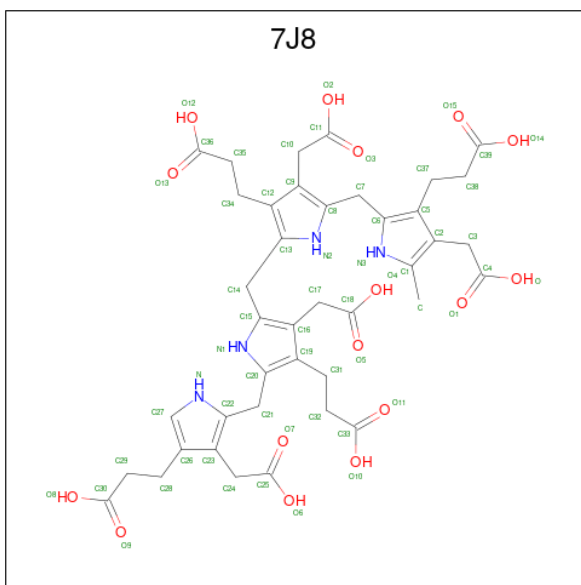
There are 4 unique types of molecules in this entry. The entry contains 5107 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Porphobilinogen deaminase.

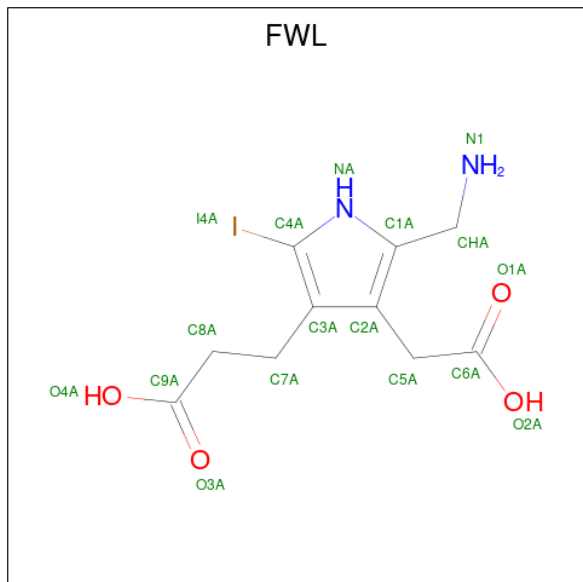
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	323	Total	C	N	O	S	0	0	0
			2460	1549	449	453	9			
1	B	320	Total	C	N	O	S	0	0	0
			2434	1533	446	446	9			

- Molecule 2 is 3-[4-(2-hydroxy-2-oxoethyl)-5-[[4-(2-hydroxy-2-oxoethyl)-5-[[4-(2-hydroxy-2-oxoethyl)-5-[[4-(2-hydroxy-2-oxoethyl)-3-(3-hydroxy-3-oxopropyl)-5-methyl-1 {H}-pyrrol-2-yl]methyl]-3-(3-hydroxy-3-oxopropyl)-1 {H}-pyrrol-2-yl]methyl]-3-(3-hydroxy-3-oxopropyl)-1 {H}-pyrrol-2-yl]methyl]-1 {H}-pyrrol-3-yl]propanoic acid (CCD ID: 7J8) (formula: C₄₀H₄₆N₄O₁₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total	C	N	O	0	0
			60	40	4	16		
2	B	1	Total	C	N	O	0	0
			60	40	4	16		

- Molecule 3 is 3-[5-(aminomethyl)-4-(carboxymethyl)-2-iodo-1H-pyrrol-3-yl]propanoic acid (CCD ID: FWL) (formula: C₁₀H₁₃IN₂O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	I	N			O
3	B	1	17	10	1	2	4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	54	Total	O	0	0
			54	54		
4	B	22	Total	O	0	0
			22	22		

4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.42Å 81.37Å 108.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.25 – 2.31 45.25 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.25-2.31) 99.6 (45.25-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.32Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.227 , 0.277 0.235 , 0.282	Depositor DCC
R_{free} test set	1614 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.8	Xtrriage
Anisotropy	0.312	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5107	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.76 % 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 6.5549e-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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FWL, 7J8

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	0.16	0/2502	0.43	0/3394
1	B	0.33	0/2476	0.60	7/3360 (0.2%)
All	All	0.26	0/4978	0.53	7/6754 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	115	LYS	CG-CD-CE	-6.46	96.43	111.30
1	B	132	LYS	CB-CG-CD	-5.69	98.22	111.30
1	B	132	LYS	CA-CB-CG	5.53	125.15	114.10
1	B	56	MET	CB-CG-SD	-5.48	96.25	112.70
1	B	162	GLU	CB-CA-C	-5.16	101.39	109.70
1	B	161	LEU	CA-C-N	5.11	128.10	120.90
1	B	161	LEU	C-N-CA	5.11	128.10	120.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	26	ARG	Sidechain

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	2460	0	2490	36	0
1	B	2434	0	2461	38	0
2	A	60	0	0	2	0
2	B	60	0	0	2	0
3	B	17	0	0	1	0
4	A	54	0	0	1	0
4	B	22	0	0	1	0
All	All	5107	0	4951	73	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 7.

All (73) 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:142:VAL:HG13	1:B:162:GLU:HG2	1.25	1.15
1:A:194:GLN:HE21	1:A:199:HIS:HD2	1.10	0.94
1:B:251:ARG:NH1	1:B:316:VAL:O	2.12	0.81
1:B:142:VAL:HA	1:B:162:GLU:HB3	1.62	0.81
1:A:194:GLN:HE21	1:A:199:HIS:CD2	2.02	0.73
1:A:295:MET:HE1	1:A:337:SER:HB2	1.74	0.70
1:B:352:ASP:O	1:B:356:GLN:HG2	1.92	0.69
1:A:245:LEU:HB2	1:A:271:MET:HE1	1.74	0.68
1:A:255:ARG:NH1	4:A:502:HOH:O	2.26	0.67
1:B:29:GLN:NE2	4:B:501:HOH:O	2.29	0.66
1:B:172:THR:HA	1:B:175:ARG:HE	1.62	0.65
1:A:352:ASP:OD1	1:A:355:ARG:NH2	2.31	0.64
1:A:139:GLU:OE2	1:A:140:LYS:NZ	2.32	0.60
1:A:126:HIS:ND1	1:A:128:LYS:HG2	2.16	0.60
1:A:194:GLN:NE2	1:A:199:HIS:HD2	1.92	0.58
1:B:101:PRO:O	1:B:251:ARG:NH2	2.36	0.58
1:A:139:GLU:CG	1:A:140:LYS:HG3	2.34	0.57
1:A:139:GLU:HG3	1:A:140:LYS:HG3	1.85	0.57
1:A:246:ARG:HG3	1:A:271:MET:HE3	1.86	0.57
1:A:275:GLN:NE2	1:A:296:GLN:OE1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:348:LYS:NZ	1:B:352:ASP:OD1	2.33	0.55
1:A:98:LYS:O	2:A:401:7J8:N2	2.38	0.55
1:B:127:PRO:HA	1:B:130:VAL:HG23	1.88	0.55
1:B:285:LEU:HD12	1:B:357:LEU:HD22	1.88	0.55
1:B:126:HIS:HD2	1:B:127:PRO:N	2.07	0.52
1:A:265:VAL:HG22	1:A:282:VAL:HG12	1.90	0.52
1:B:112:ALA:HB1	1:B:238:LEU:HB2	1.92	0.51
1:B:142:VAL:HA	1:B:162:GLU:CB	2.36	0.50
1:B:347:ALA:O	1:B:351:LEU:HG	2.11	0.50
1:B:22:ARG:NH2	1:B:88:ASN:O	2.44	0.50
1:B:191:ALA:O	1:B:195:ARG:HG3	2.12	0.49
1:A:295:MET:HE1	1:A:337:SER:CB	2.42	0.49
1:A:170:LEU:HD21	1:A:193:LEU:HD23	1.94	0.48
1:A:315:LEU:HD11	1:A:329:LEU:HD12	1.94	0.48
1:A:139:GLU:HG2	1:A:140:LYS:NZ	2.29	0.47
1:A:348:LYS:HE3	1:A:352:ASP:OD2	2.14	0.47
1:B:117:GLU:OE1	1:B:195:ARG:NH2	2.48	0.47
1:B:142:VAL:CG1	1:B:162:GLU:HG2	2.19	0.47
1:B:154:LEU:HB3	1:B:163:PHE:CE2	2.50	0.46
1:A:112:ALA:HB1	1:A:238:LEU:HB2	1.96	0.46
1:A:146:SER:HB2	2:A:401:7J8:O11	2.16	0.46
1:B:26:ARG:HG3	1:B:81:LEU:HD21	1.97	0.46
1:A:26:ARG:HD2	1:A:77:PHE:CE1	2.50	0.46
1:B:147:SER:HB3	1:B:150:ARG:HB2	1.96	0.46
1:B:168:GLY:O	1:B:173:ARG:NE	2.47	0.45
1:A:105:PRO:HB2	1:A:108:PHE:CD2	2.51	0.45
1:B:104:LEU:HD11	1:B:110:ILE:HG13	1.98	0.45
1:B:98:LYS:NZ	2:B:401:7J8:O5	2.49	0.45
1:B:265:VAL:HG22	1:B:282:VAL:HG12	1.99	0.45
1:B:56:MET:HE2	1:B:56:MET:HB3	1.53	0.44
1:B:275:GLN:NE2	1:B:296:GLN:OE1	2.49	0.44
1:B:169:ASN:HB2	3:B:402:FWL:O2A	2.18	0.44
1:A:245:LEU:HB2	1:A:271:MET:CE	2.43	0.43
1:B:117:GLU:OE1	1:B:195:ARG:NE	2.51	0.43
1:B:123:VAL:CG1	1:B:204:GLN:HB3	2.49	0.43
1:A:128:LYS:NZ	1:A:129:PHE:CE2	2.87	0.43
1:A:39:VAL:HG12	1:A:43:LYS:HD2	2.01	0.42
1:B:259:GLY:O	1:B:355:ARG:HD3	2.18	0.42
1:A:139:GLU:HG2	1:A:140:LYS:HZ3	1.83	0.42
1:A:105:PRO:HB2	1:A:108:PHE:HD2	1.85	0.42
1:B:86:GLU:HB2	1:B:108:PHE:HZ	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:SER:HB3	1:A:289:ASP:HB2	2.01	0.42
1:A:215:VAL:HG21	1:A:254:LEU:HB2	2.02	0.42
1:B:174:LEU:HD23	1:B:186:ILE:HD11	2.01	0.42
1:A:86:GLU:HG3	1:A:87:LYS:HG3	2.02	0.41
1:A:193:LEU:HD23	1:A:193:LEU:HA	1.87	0.41
1:B:126:HIS:HE1	1:B:181:GLN:HG2	1.85	0.41
1:B:149:ARG:HH21	2:B:401:7J8:C18	2.34	0.41
1:A:179:GLU:HB3	1:B:53:ILE:HD13	2.01	0.41
1:B:263:VAL:HA	1:B:264:PRO:HD3	1.93	0.41
1:A:22:ARG:HB3	1:A:54:ILE:HD13	2.02	0.40
1:A:147:SER:HB3	1:A:150:ARG:HD2	2.03	0.40
1:B:255:ARG:CZ	1:B:316:VAL:HG12	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	319/361 (88%)	311 (98%)	8 (2%)	0	100	100
1	B	316/361 (88%)	306 (97%)	10 (3%)	0	100	100
All	All	635/722 (88%)	617 (97%)	18 (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	263/299 (88%)	263 (100%)	0	100	100
1	B	259/299 (87%)	257 (99%)	2 (1%)	73	85
All	All	522/598 (87%)	520 (100%)	2 (0%)	84	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	27	LYS
1	B	88	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	199	HIS
1	A	300	HIS
1	A	305	HIS
1	B	88	ASN
1	B	126	HIS
1	B	305	HIS
1	B	332	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	7J8	A	401	1	63,63,63	1.43	7 (11%)	83,89,89	1.45	19 (22%)
3	FWL	B	402	-	16,17,17	1.69	2 (12%)	17,23,23	1.40	1 (5%)
2	7J8	B	401	1	63,63,63	1.44	8 (12%)	83,89,89	1.39	12 (14%)

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	7J8	A	401	1	-	10/48/48/48	0/4/4/4
3	FWL	B	402	-	-	0/9/11/11	0/1/1/1
2	7J8	B	401	1	-	10/48/48/48	0/4/4/4

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402	FWL	C1A-C2A	4.24	1.50	1.39
2	B	401	7J8	C22-N	3.66	1.42	1.37
3	B	402	FWL	C4A-I4A	3.66	2.15	2.06
2	A	401	7J8	C22-N	3.52	1.42	1.37
2	A	401	7J8	C27-N	3.23	1.42	1.36
2	B	401	7J8	C27-N	3.18	1.42	1.36
2	A	401	7J8	C15-N1	2.73	1.43	1.37
2	B	401	7J8	C15-N1	2.62	1.42	1.37
2	A	401	7J8	C6-N3	2.33	1.42	1.37
2	B	401	7J8	C6-N3	2.30	1.42	1.37
2	A	401	7J8	C-C1	2.25	1.53	1.49
2	B	401	7J8	C20-N1	2.23	1.42	1.37
2	A	401	7J8	C20-N1	2.22	1.42	1.37
2	B	401	7J8	C-C1	2.20	1.53	1.49
2	A	401	7J8	C17-C16	2.16	1.54	1.51
2	B	401	7J8	C17-C16	2.12	1.54	1.51
2	B	401	7J8	C24-C23	2.02	1.54	1.51

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	FWL	CHA-C1A-NA	3.49	125.93	121.49
2	A	401	7J8	C8-C7-C6	-3.46	102.45	115.77
2	B	401	7J8	C20-N1-C15	-3.36	107.54	110.53
2	A	401	7J8	C20-N1-C15	-3.16	107.73	110.53
2	A	401	7J8	C34-C35-C36	-2.95	105.84	113.67
2	B	401	7J8	C-C1-C2	-2.95	126.23	131.20
2	A	401	7J8	C-C1-C2	-2.92	126.28	131.20
2	A	401	7J8	C14-C15-C16	-2.79	124.73	130.07
2	B	401	7J8	C14-C15-C16	-2.79	124.74	130.07
2	A	401	7J8	C14-C15-N1	2.58	127.28	122.04
2	A	401	7J8	C21-C20-C19	-2.51	125.28	130.07
2	A	401	7J8	C31-C32-C33	-2.50	107.03	113.67
2	B	401	7J8	C31-C32-C33	-2.50	107.04	113.67
2	B	401	7J8	C14-C15-N1	2.48	127.09	122.04
2	B	401	7J8	C37-C38-C39	-2.43	107.21	113.67
2	B	401	7J8	C21-C20-C19	-2.34	125.59	130.07
2	A	401	7J8	C21-C20-N1	2.34	126.79	122.04
2	B	401	7J8	C11-C10-C9	-2.30	107.97	113.76
2	B	401	7J8	C8-C7-C6	-2.28	106.96	115.77
2	A	401	7J8	C37-C38-C39	-2.23	107.74	113.67
2	B	401	7J8	O14-C39-C38	2.11	120.67	114.00
2	A	401	7J8	O2-C11-C10	2.09	121.00	114.51
2	B	401	7J8	C-C1-N3	2.09	125.61	121.36
2	A	401	7J8	O14-C39-C38	2.08	120.56	114.00
2	A	401	7J8	C-C1-N3	2.07	125.58	121.36
2	A	401	7J8	O12-C36-C35	2.07	120.53	114.00
2	A	401	7J8	C7-C8-C9	-2.05	126.15	130.07
2	B	401	7J8	C21-C20-N1	2.04	126.19	122.04
2	A	401	7J8	C7-C6-C5	-2.03	126.20	130.07
2	A	401	7J8	C7-C6-N3	2.02	126.14	122.04
2	A	401	7J8	O8-C30-C29	2.01	120.36	114.00
2	A	401	7J8	O-C4-C3	2.01	120.74	114.51

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	7J8	N2-C13-C14-C15
2	A	401	7J8	N2-C13-C14-C15
2	A	401	7J8	C12-C13-C14-C15
2	B	401	7J8	C12-C13-C14-C15

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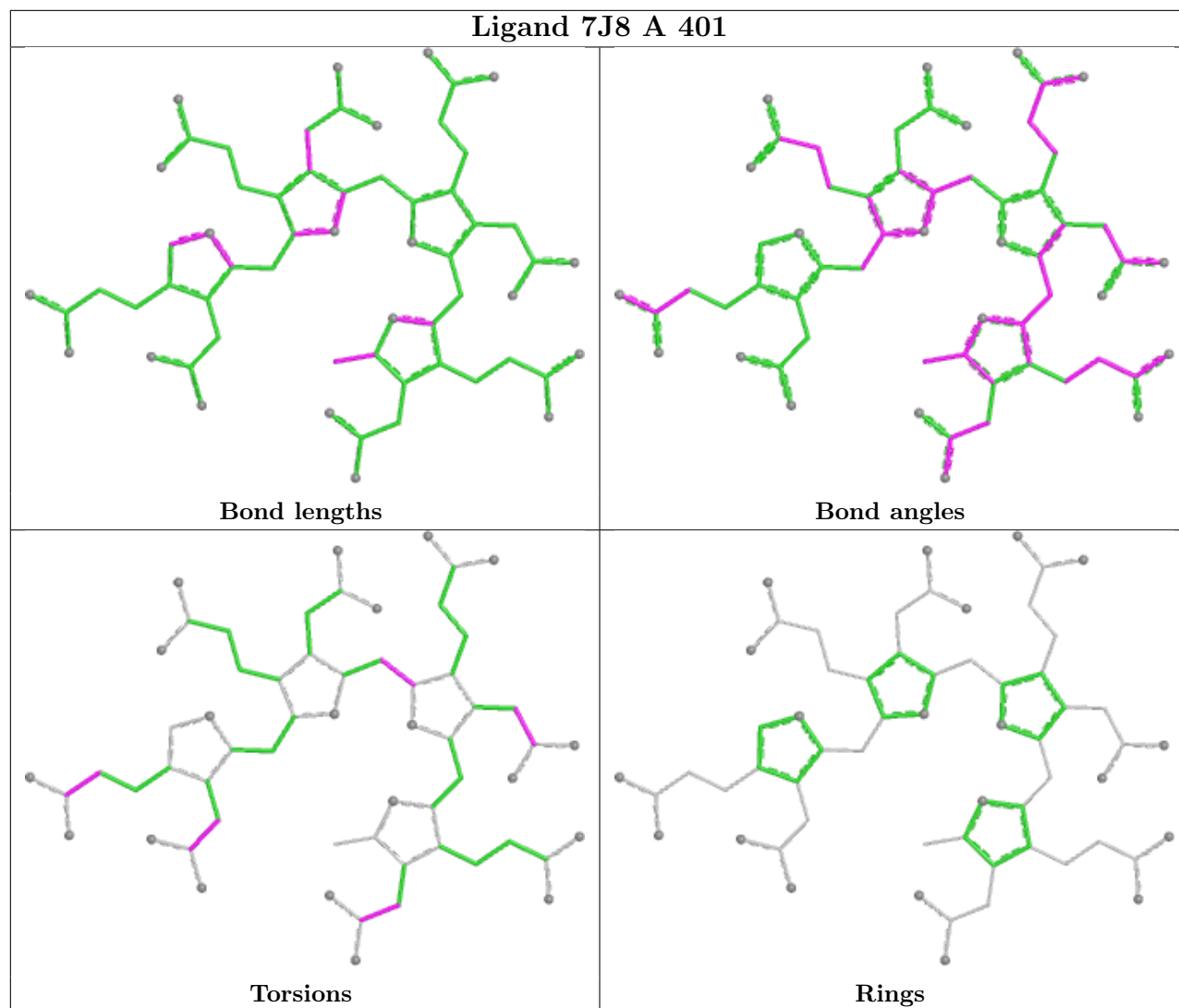
Mol	Chain	Res	Type	Atoms
2	A	401	7J8	C2-C3-C4-O1
2	A	401	7J8	C2-C3-C4-O
2	A	401	7J8	C23-C24-C25-O7
2	A	401	7J8	C23-C24-C25-O6
2	B	401	7J8	C9-C10-C11-O3
2	B	401	7J8	C23-C24-C25-O7
2	B	401	7J8	C23-C24-C25-O6
2	A	401	7J8	C9-C10-C11-O3
2	A	401	7J8	C9-C10-C11-O2
2	B	401	7J8	C9-C10-C11-O2
2	B	401	7J8	C28-C29-C30-O9
2	A	401	7J8	C28-C29-C30-O9
2	B	401	7J8	C28-C29-C30-O8
2	A	401	7J8	C28-C29-C30-O8
2	B	401	7J8	C31-C32-C33-O10
2	B	401	7J8	C31-C32-C33-O11

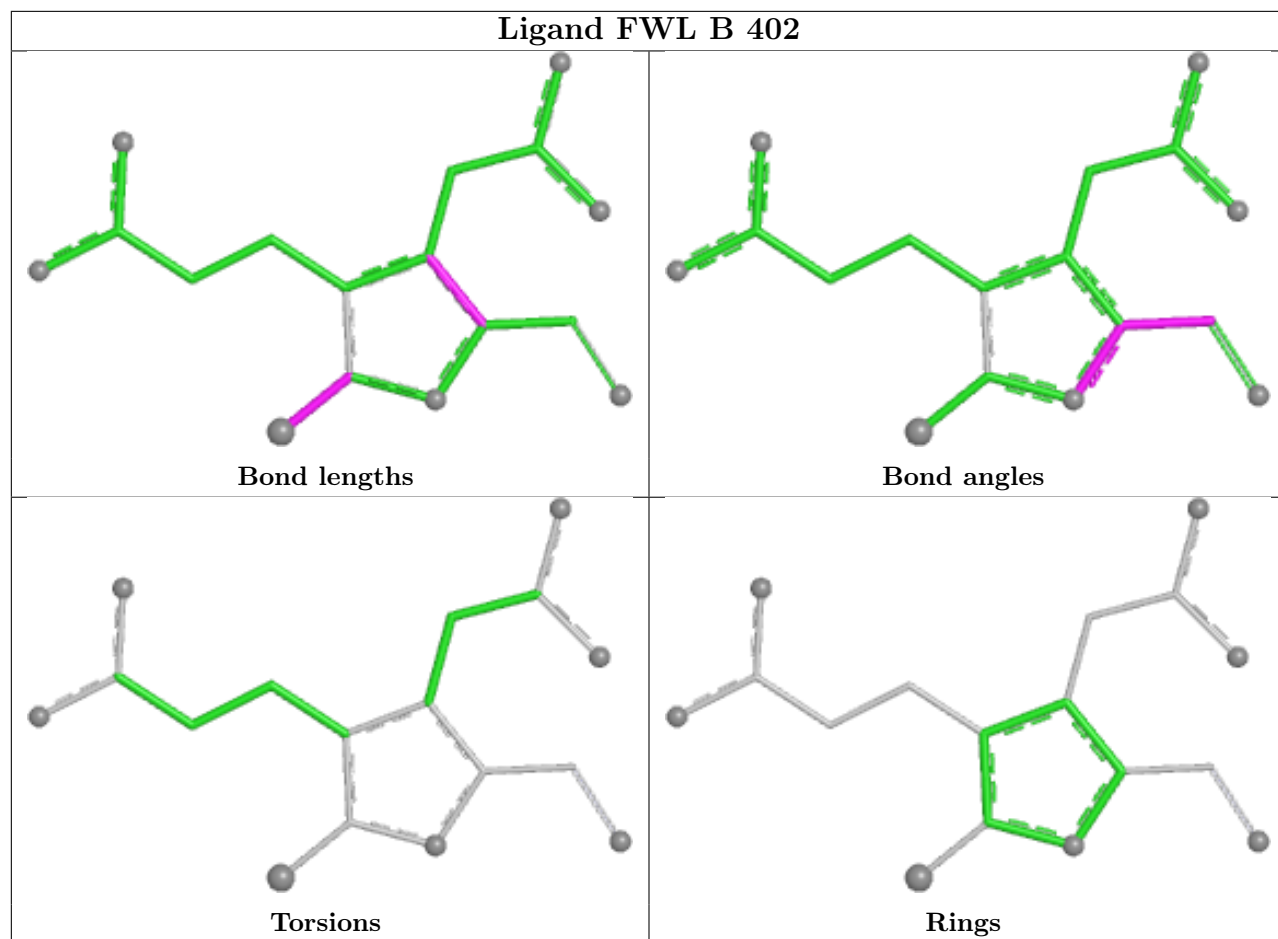
There are no ring outliers.

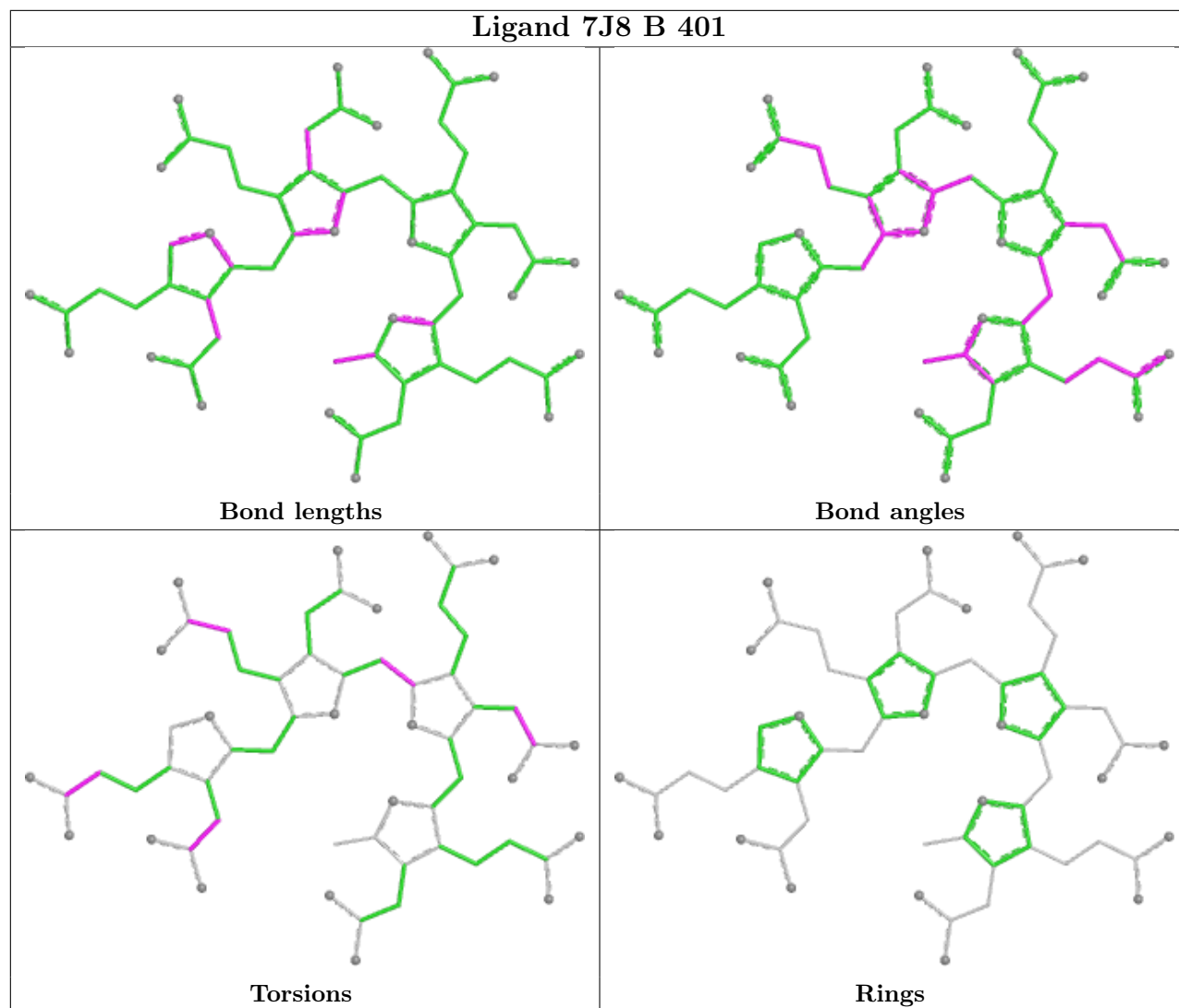
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	7J8	2	0
3	B	402	FWL	1	0
2	B	401	7J8	2	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	323/361 (89%)	0.75	17 (5%) 32 34	26, 51, 80, 108	0
1	B	320/361 (88%)	0.81	24 (7%) 20 23	38, 58, 91, 115	0
All	All	643/722 (89%)	0.78	41 (6%) 25 28	26, 55, 85, 115	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	77	PHE	4.9
1	A	24	GLY	4.2
1	B	154	LEU	4.2
1	A	76	LEU	3.9
1	B	142	VAL	3.7
1	B	301	VAL	3.4
1	A	19	ARG	2.9
1	B	162	GLU	2.9
1	B	129	PHE	2.8
1	B	263	VAL	2.8
1	B	164	ARG	2.7
1	A	331	ALA	2.7
1	B	163	PHE	2.6
1	B	357	LEU	2.5
1	B	160	HIS	2.5
1	A	191	ALA	2.5
1	B	210	GLU	2.5
1	A	20	VAL	2.4
1	A	77	PHE	2.4
1	B	100	LEU	2.4
1	B	193	LEU	2.4
1	A	56	MET	2.4
1	B	259	GLY	2.3
1	B	139	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	247	CYS	2.2
1	A	89	GLU	2.2
1	B	300	HIS	2.2
1	B	57	SER	2.2
1	A	231	ILE	2.2
1	B	262	SER	2.2
1	B	202	VAL	2.1
1	A	209	GLU	2.1
1	A	57	SER	2.1
1	B	299	ILE	2.1
1	A	259	GLY	2.1
1	A	188	LEU	2.1
1	A	114	CYS	2.1
1	B	185	ALA	2.1
1	A	152	ALA	2.0
1	B	84	ALA	2.0
1	B	247	CYS	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.

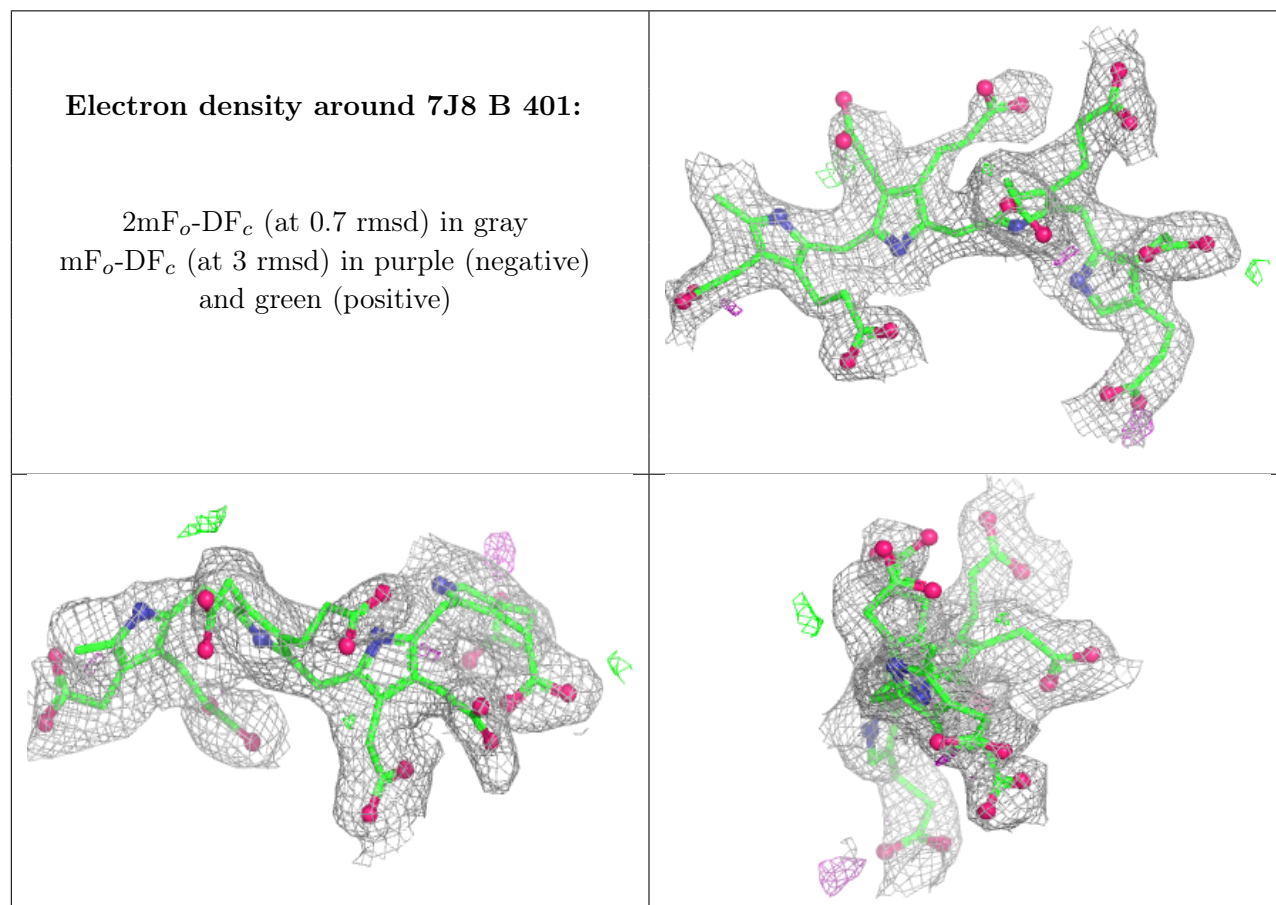
6.4 Ligands [i](#)

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
2	7J8	B	401	60/60	0.79	0.12	41,56,72,79	0
2	7J8	A	401	60/60	0.81	0.11	34,45,66,69	0
3	FWL	B	402	17/17	0.87	0.14	55,61,65,107	17

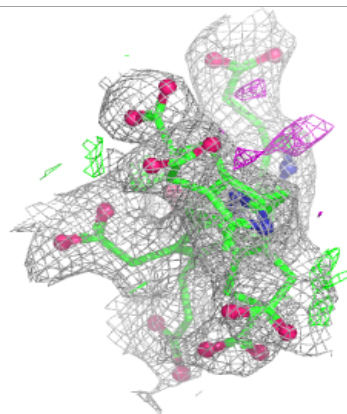
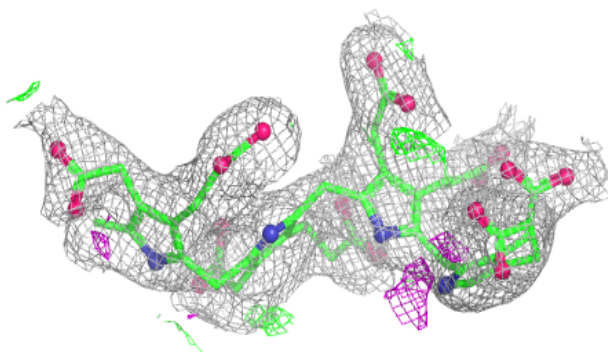
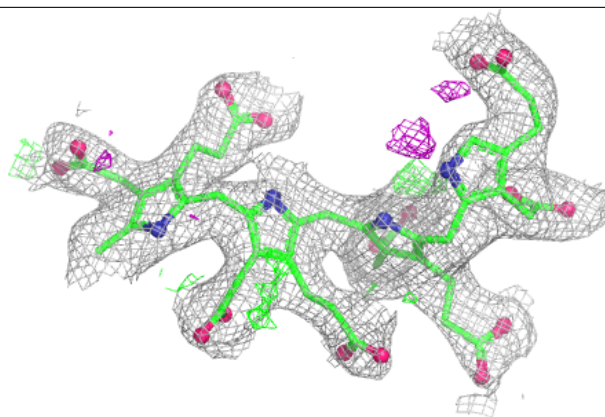
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

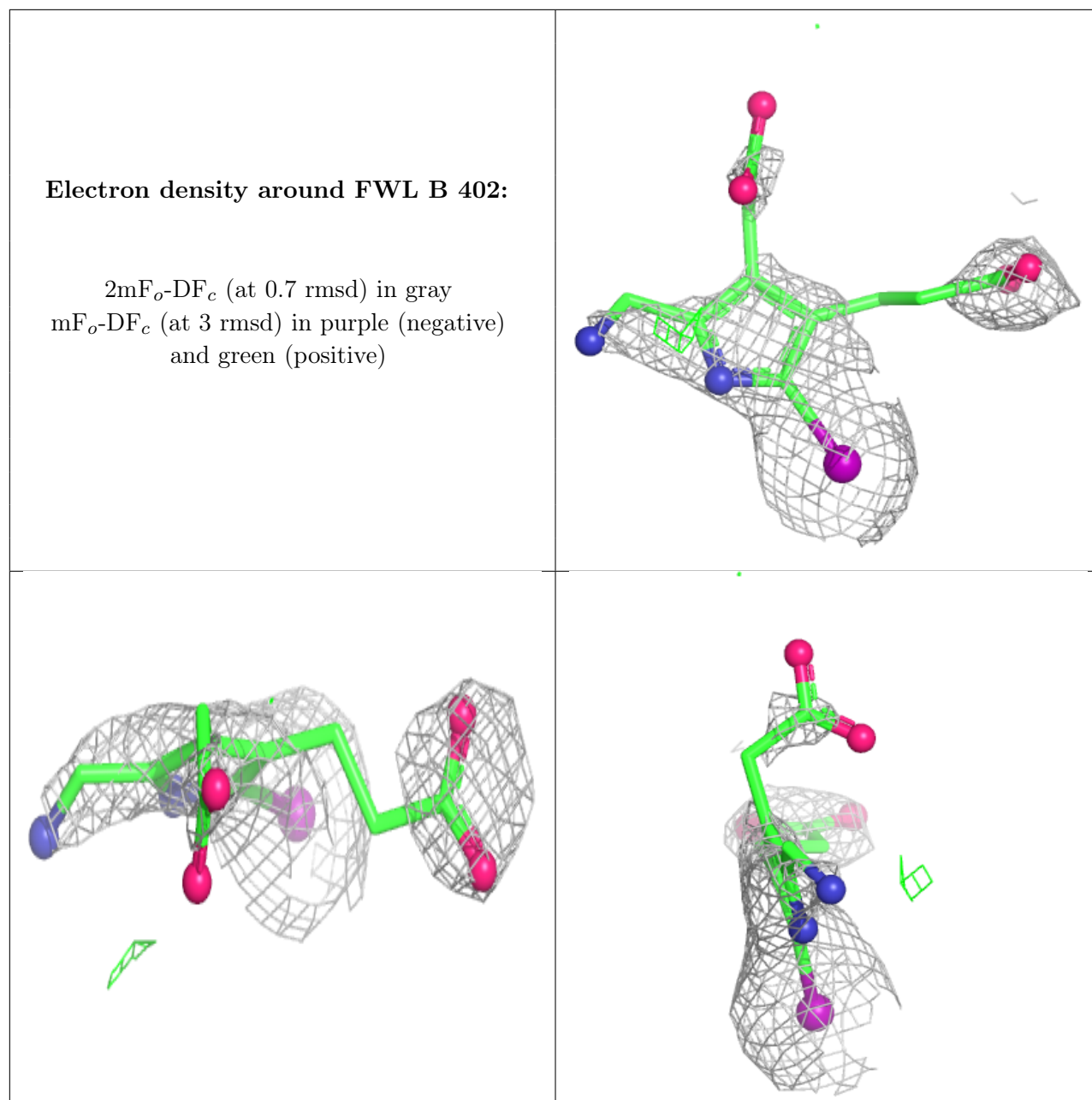
as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around 7J8 A 401:

$2mF_o-DF_c$ (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.