



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 14, 2023 – 12:14 am BST

PDB ID : 8BZP  
Title : JNK3 (Mitogen-activated protein kinase 10) in Complex with Compound 23 bearing a C(sp<sup>3</sup>)F<sub>2</sub>Br moiety  
Authors : Stahlecker, J.; Vaas, S.; Stehle, T.; Boeckler, F.M.  
Deposited on : 2022-12-15  
Resolution : 1.86 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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

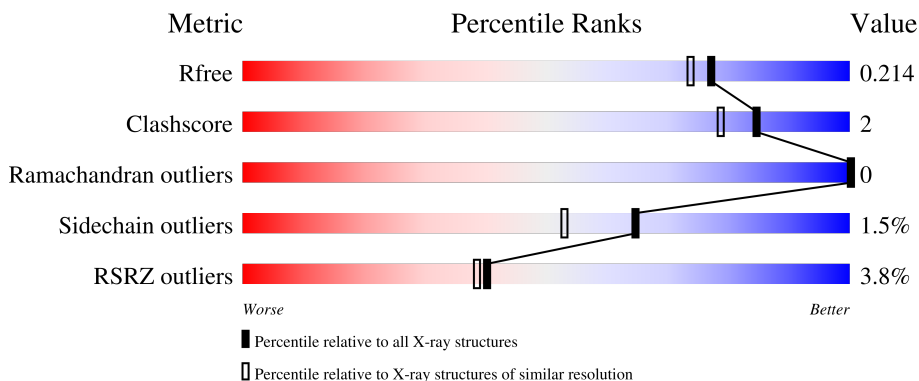
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

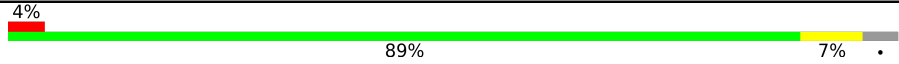
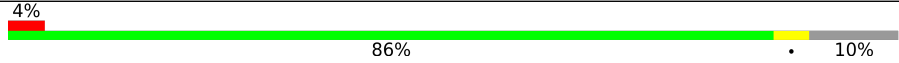
The reported resolution of this entry is 1.86 Å.

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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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  $\geq 3$ , 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	364	
1	B	364	

## 2 Entry composition i

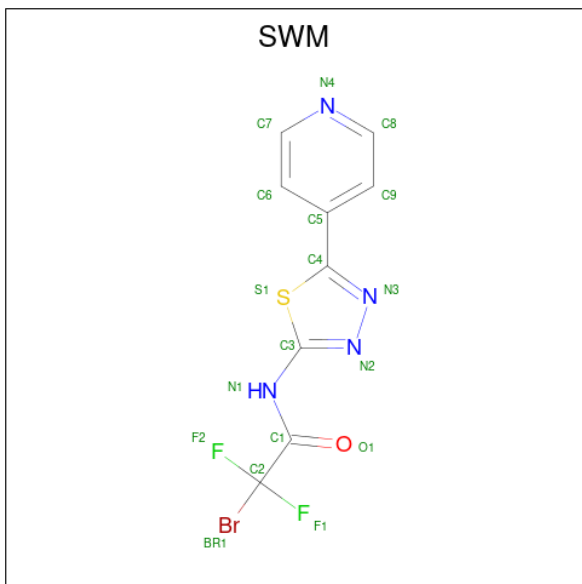
There are 9 unique types of molecules in this entry. The entry contains 5834 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Mitogen-activated protein kinase 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	350	Total	C	N	O	S	0	6	0
			2772	1788	465	495	24			
1	B	326	Total	C	N	O	S	0	7	0
			2585	1670	430	462	23			

- Molecule 2 is 2-bromanyl-2,2-bis(fluoranyl)- {N}-(5-pyridin-4-yl-1,3,4-thiadiazol-2-yl)ethanamide (three-letter code: SWM) (formula: C<sub>9</sub>H<sub>5</sub>BrF<sub>2</sub>N<sub>4</sub>OS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf		
			Total	Br	C	F	N	O			S	
2	A	1	Total	Br	C	F	N	O	S	0	1	
			36	2	18	4	8	2	2			
2	B	1	Total	C	N	S					0	0
			13	8	4	1						

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



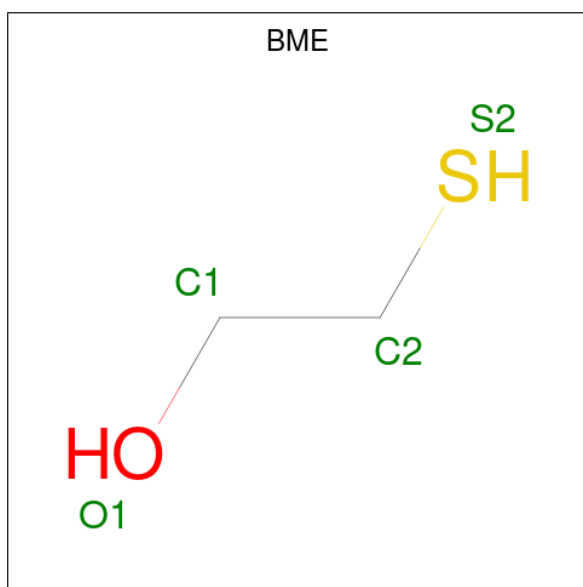
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



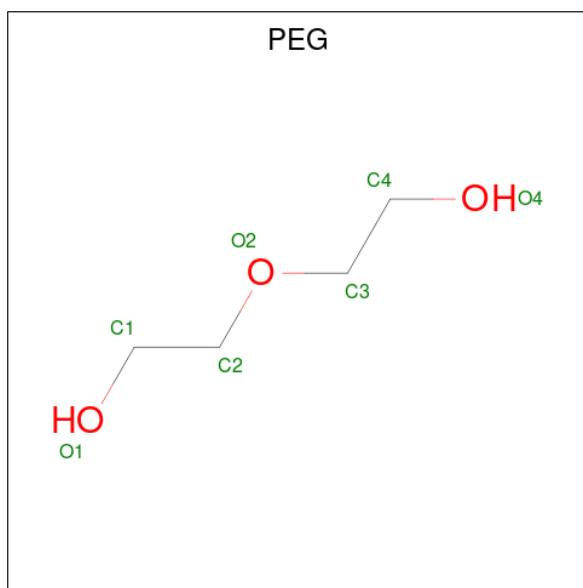
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

- Molecule 5 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C<sub>2</sub>H<sub>6</sub>OS).



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

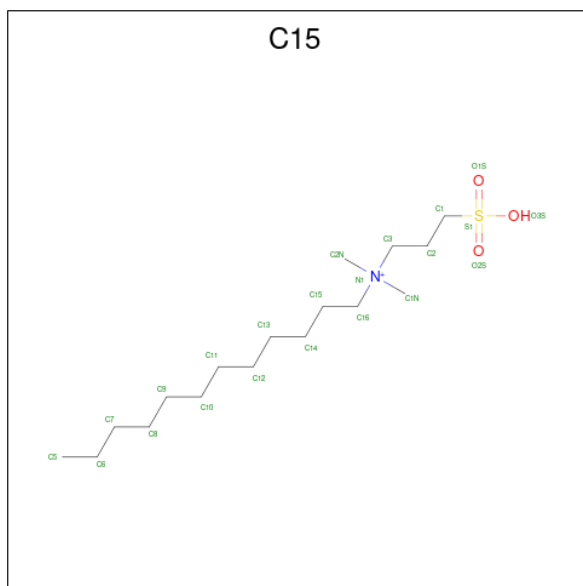
- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	7	4	3	0	0
6	A	1	7	4	3	0	0

- Molecule 7 is N-DODECYL-N,N-DIMETHYL-3-AMMONIO-1-PROPANESULFONATE

(three-letter code: C15) (formula: C<sub>17</sub>H<sub>38</sub>NO<sub>3</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
7	A	1	Total	C	N	O	S	0	0
			22	17	1	3	1		
7	B	1	Total	C	N	O	S	0	0
			16	11	1	3	1		
7	B	1	Total	C	N			0	0
			12	11	1				

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Cl	0	0
			1	1		

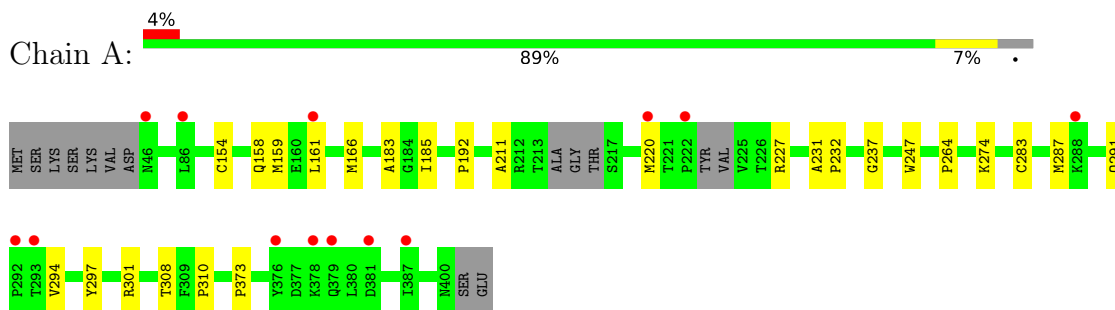
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	169	Total	O	0	0
			169	169		
9	B	118	Total	O	0	0
			118	118		

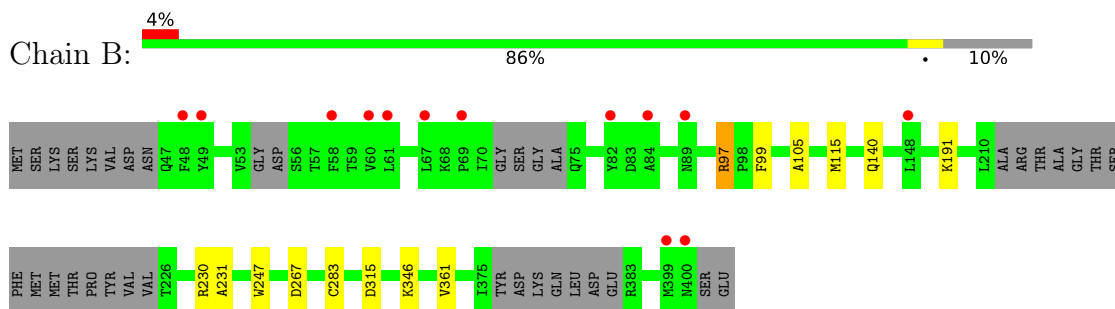
### 3 Residue-property plots [i](#)

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: Mitogen-activated protein kinase 10



- Molecule 1: Mitogen-activated protein kinase 10





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.80Å 155.38Å 43.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.84 – 1.86 46.84 – 1.86	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.84-1.86) 99.4 (46.84-1.86)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.14 (at 1.86Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.189 , 0.216 0.189 , 0.214	Depositor DCC
$R_{free}$ test set	1501 reflections (2.35%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.4	Xtrriage
Anisotropy	0.200	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 56.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	5834	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SWM, BME, EDO, PEG, C15, GOL, CL

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	0.42	0/2836	0.61	0/3854
1	B	0.41	0/2644	0.58	0/3597
All	All	0.41	0/5480	0.59	0/7451

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	2772	0	2697	16	0
1	B	2585	0	2481	6	0
2	A	36	0	0	2	0
2	B	13	0	0	0	0
3	A	16	0	24	0	0
3	B	8	0	12	1	0
4	A	18	0	24	2	0
4	B	30	0	40	1	0
5	A	4	0	5	0	0
6	A	14	0	20	0	0
7	A	22	0	38	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	28	0	39	1	0
8	B	1	0	0	0	0
9	A	169	0	0	5	0
9	B	118	0	0	0	0
All	All	5834	0	5380	25	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 2.

All (25) 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:A:159:MET:HB2	4:A:511:GOL:H32	1.70	0.73
1:A:185:ILE:HG23	1:A:211:ALA:HA	1.70	0.71
1:A:291:GLN:HB3	1:A:294:VAL:HG12	1.75	0.68
2:A:501[A]:SWM:S1	9:A:605:HOH:O	2.54	0.65
2:A:501[B]:SWM:S1	9:A:605:HOH:O	2.54	0.65
1:A:154[B]:CYS:SG	9:A:706:HOH:O	2.54	0.64
1:A:264:PRO:HD2	1:A:274:LYS:HD2	1.80	0.62
1:B:283[A]:CYS:SG	1:B:346:LYS:NZ	2.78	0.57
1:A:166[A]:MET:HG2	4:A:511:GOL:H12	1.86	0.56
1:A:183:ALA:HB2	1:A:373:PRO:HD2	1.89	0.55
1:A:237:GLY:HA3	7:A:512:C15:H132	1.88	0.54
1:A:283[B]:CYS:SG	9:A:762:HOH:O	2.59	0.53
1:B:97:ARG:HG3	1:B:140:GLN:HG2	1.91	0.53
1:B:361[A]:VAL:HG11	3:B:504:EDO:H12	1.92	0.52
1:A:308:THR:HB	1:A:310:PRO:HD2	1.92	0.52
1:A:297:TYR:CZ	1:A:301:ARG:HD3	2.45	0.52
1:B:267:ASP:HA	4:B:506:GOL:H2	1.94	0.50
1:A:161:LEU:HB2	1:A:166[A]:MET:SD	2.56	0.46
1:B:231:ALA:HA	1:B:247:TRP:CD1	2.51	0.46
1:A:154[A]:CYS:SG	1:A:192:PRO:HB2	2.58	0.43
1:A:231:ALA:HA	1:A:247:TRP:CD1	2.54	0.42
1:B:99:PHE:HA	1:B:105:ALA:HB2	2.02	0.42
7:B:510:C15:H161	7:B:510:C15:H131	1.84	0.41
1:A:232:PRO:HD3	1:A:247:TRP:CE2	2.55	0.41
1:A:227:ARG:NH1	9:A:613:HOH:O	2.53	0.41

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	350/364 (96%)	344 (98%)	6 (2%)	0	100	100
1	B	323/364 (89%)	318 (98%)	5 (2%)	0	100	100
All	All	673/728 (92%)	662 (98%)	11 (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	292/329 (89%)	289 (99%)	3 (1%)	76	69
1	B	269/329 (82%)	264 (98%)	5 (2%)	57	43
All	All	561/658 (85%)	553 (99%)	8 (1%)	65	55

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	GLN
1	A	220	MET
1	A	287	MET
1	B	97	ARG
1	B	115	MET
1	B	191	LYS
1	B	230	ARG
1	B	315	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 24 ligands modelled in this entry, 1 is monoatomic - leaving 23 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	BME	A	505	1	3,3,3	0.38	0	1,2,2	0.39	0
2	SWM	A	501[B]	-	12,19,19	1.14	1 (8%)	14,27,27	1.60	2 (14%)
4	GOL	B	505	-	5,5,5	1.01	0	5,5,5	0.97	0
3	EDO	A	503	-	3,3,3	0.57	0	2,2,2	0.30	0
3	EDO	A	502	-	3,3,3	0.49	0	2,2,2	0.27	0
4	GOL	B	501	-	5,5,5	0.99	0	5,5,5	0.70	0
4	GOL	A	504	-	5,5,5	1.07	0	5,5,5	0.97	0
4	GOL	A	507	-	5,5,5	1.12	0	5,5,5	0.71	0
4	GOL	A	511	-	5,5,5	0.75	0	5,5,5	1.51	1 (20%)
4	GOL	B	506	-	5,5,5	0.69	0	5,5,5	1.02	0
6	PEG	A	510	-	6,6,6	0.21	0	5,5,5	0.08	0
7	C15	B	510	-	11,11,21	0.28	0	13,13,26	0.30	0
6	PEG	A	506	-	6,6,6	0.19	0	5,5,5	0.11	0
7	C15	B	509	-	14,14,21	0.61	0	17,18,26	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	B	503	-	3,3,3	0.56	0	2,2,2	0.32	0
4	GOL	B	507	-	5,5,5	0.83	0	5,5,5	0.91	0
3	EDO	A	509	-	3,3,3	0.45	0	2,2,2	0.36	0
7	C15	A	512	-	21,21,21	0.60	0	25,26,26	0.84	2 (8%)
4	GOL	B	508	-	5,5,5	0.79	0	5,5,5	0.91	0
2	SWM	B	502	-	9,14,19	1.59	1 (11%)	8,18,27	1.42	1 (12%)
3	EDO	B	504	-	3,3,3	0.38	0	2,2,2	0.56	0
3	EDO	A	508	-	3,3,3	0.54	0	2,2,2	0.15	0
2	SWM	A	501[A]	-	12,19,19	0.97	1 (8%)	14,27,27	1.45	2 (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
5	BME	A	505	1	-	0/1/1/1	-
2	SWM	A	501[B]	-	-	0/10/14/14	0/2/2/2
4	GOL	B	505	-	-	0/4/4/4	-
3	EDO	A	503	-	-	1/1/1/1	-
3	EDO	A	502	-	-	0/1/1/1	-
4	GOL	B	501	-	-	1/4/4/4	-
4	GOL	A	504	-	-	0/4/4/4	-
4	GOL	A	507	-	-	0/4/4/4	-
4	GOL	A	511	-	-	2/4/4/4	-
4	GOL	B	506	-	-	4/4/4/4	-
6	PEG	A	510	-	-	0/4/4/4	-
7	C15	B	510	-	-	8/9/9/21	-
6	PEG	A	506	-	-	2/4/4/4	-
7	C15	B	509	-	-	3/8/8/21	-
3	EDO	B	503	-	-	0/1/1/1	-
4	GOL	B	507	-	-	3/4/4/4	-
3	EDO	A	509	-	-	1/1/1/1	-
7	C15	A	512	-	-	5/21/21/21	-
4	GOL	B	508	-	-	2/4/4/4	-
2	SWM	B	502	-	-	0/4/6/14	0/2/2/2
3	EDO	B	504	-	-	0/1/1/1	-
3	EDO	A	508	-	-	0/1/1/1	-
2	SWM	A	501[A]	-	-	5/10/14/14	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	SWM	C1-N1	-4.73	1.36	1.45
2	A	501[B]	SWM	C2-C1	-3.81	1.49	1.54
2	A	501[A]	SWM	C2-C1	-3.15	1.50	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501[B]	SWM	O1-C1-C2	4.03	121.55	118.48
2	A	501[A]	SWM	C4-N3-N2	3.89	113.30	105.29
2	A	501[B]	SWM	C4-N3-N2	3.79	113.09	105.29
2	B	502	SWM	C4-N3-N2	3.71	112.92	105.29
2	A	501[A]	SWM	O1-C1-C2	3.42	121.09	118.48
4	A	511	GOL	C3-C2-C1	-2.75	101.02	111.70
7	A	512	C15	O2S-S1-C1	-2.19	104.27	106.92
7	A	512	C15	C2-C1-S1	-2.04	110.12	113.25

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501[A]	SWM	N1-C1-C2-F1
2	A	501[A]	SWM	N1-C1-C2-F2
2	A	501[A]	SWM	O1-C1-C2-F1
2	A	501[A]	SWM	O1-C1-C2-F2
4	A	511	GOL	O1-C1-C2-O2
4	B	506	GOL	C1-C2-C3-O3
4	B	508	GOL	O1-C1-C2-O2
4	B	508	GOL	O1-C1-C2-C3
7	B	510	C15	C14-C15-C16-N1
4	A	511	GOL	O1-C1-C2-C3
4	B	506	GOL	O1-C1-C2-C3
4	B	507	GOL	O1-C1-C2-C3
4	B	507	GOL	C1-C2-C3-O3
4	B	506	GOL	O2-C2-C3-O3
4	B	507	GOL	O1-C1-C2-O2
3	A	503	EDO	O1-C1-C2-O2
3	A	509	EDO	O1-C1-C2-O2
7	A	512	C15	C10-C11-C12-C13
7	B	510	C15	C15-C16-N1-C3
7	A	512	C15	C11-C12-C13-C14
7	B	510	C15	C10-C11-C12-C13

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Mol	Chain	Res	Type	Atoms
7	B	510	C15	C15-C16-N1-C2N
4	B	501	GOL	C1-C2-C3-O3
7	B	510	C15	C13-C14-C15-C16
7	A	512	C15	C12-C13-C14-C15
7	B	510	C15	C15-C16-N1-C1N
6	A	506	PEG	O1-C1-C2-O2
7	B	510	C15	C9-C10-C11-C12
7	B	509	C15	C15-C16-N1-C2N
7	A	512	C15	S1-C1-C2-C3
2	A	501[A]	SWM	C2-C1-N1-C3
7	B	509	C15	C15-C16-N1-C1N
7	B	510	C15	C12-C13-C14-C15
4	B	506	GOL	O1-C1-C2-O2
6	A	506	PEG	C1-C2-O2-C3
7	B	509	C15	C15-C16-N1-C3
7	A	512	C15	C13-C14-C15-C16

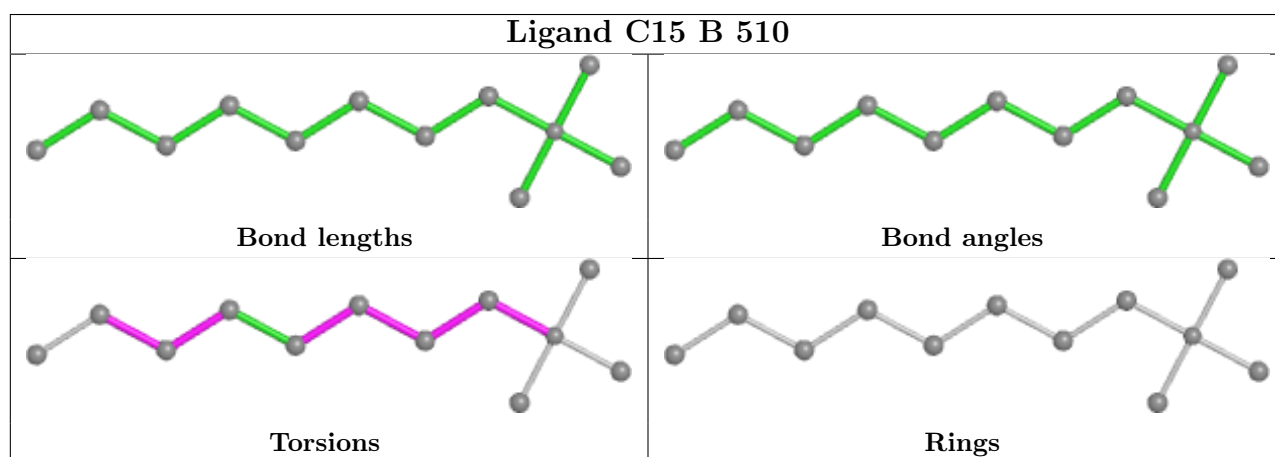
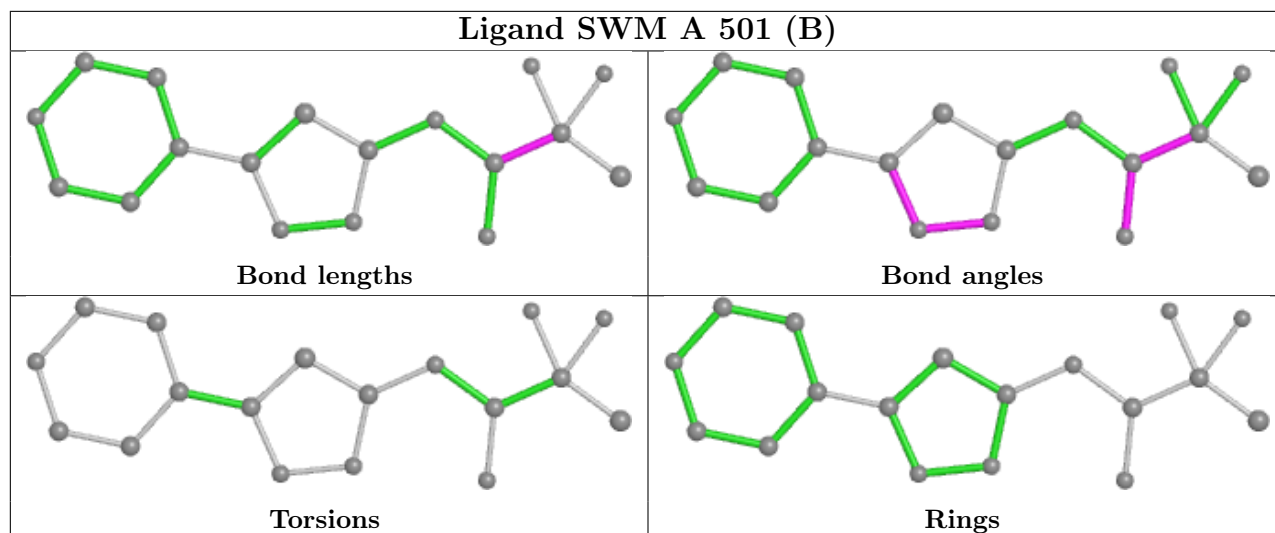
There are no ring outliers.

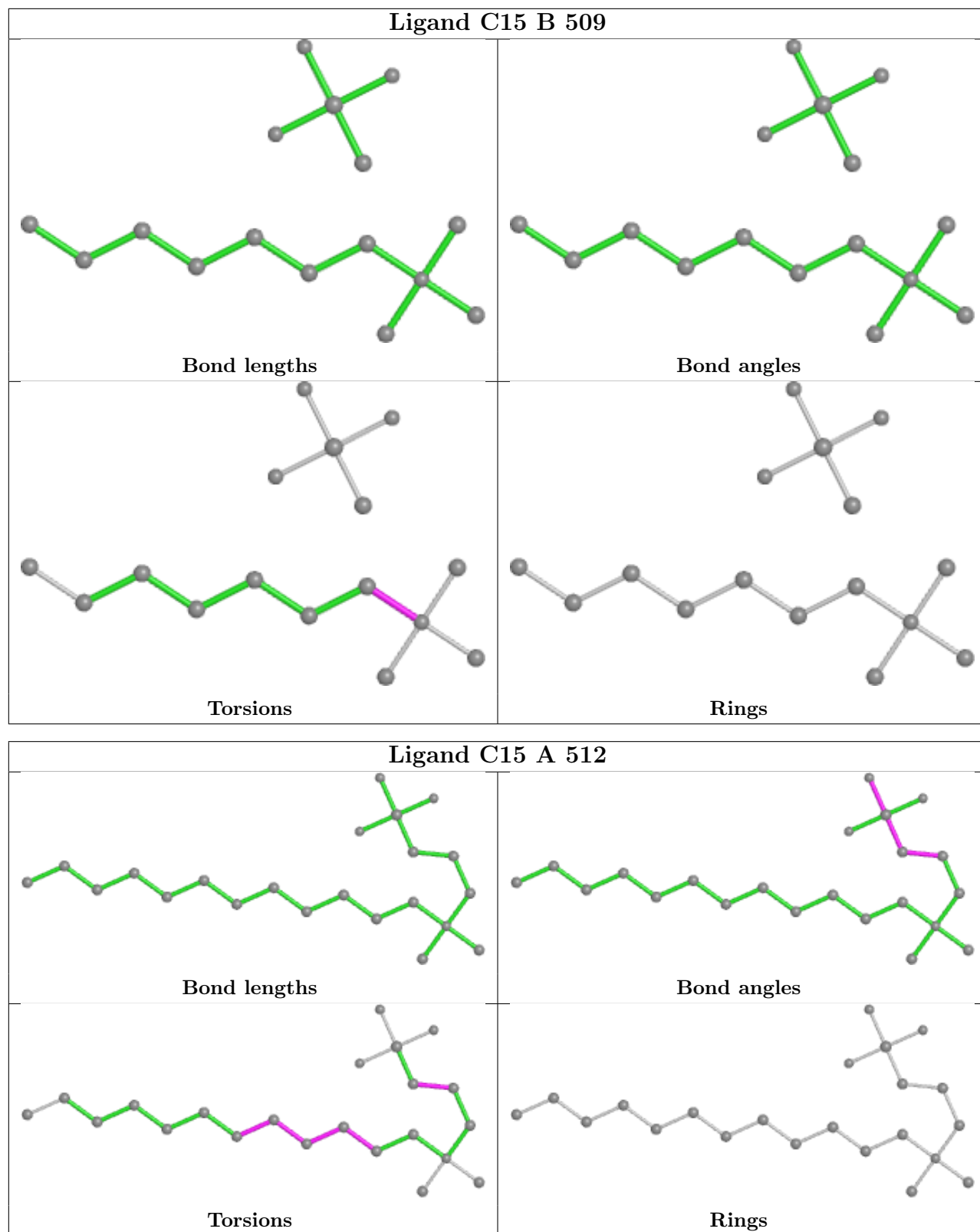
7 monomers are involved in 8 short contacts:

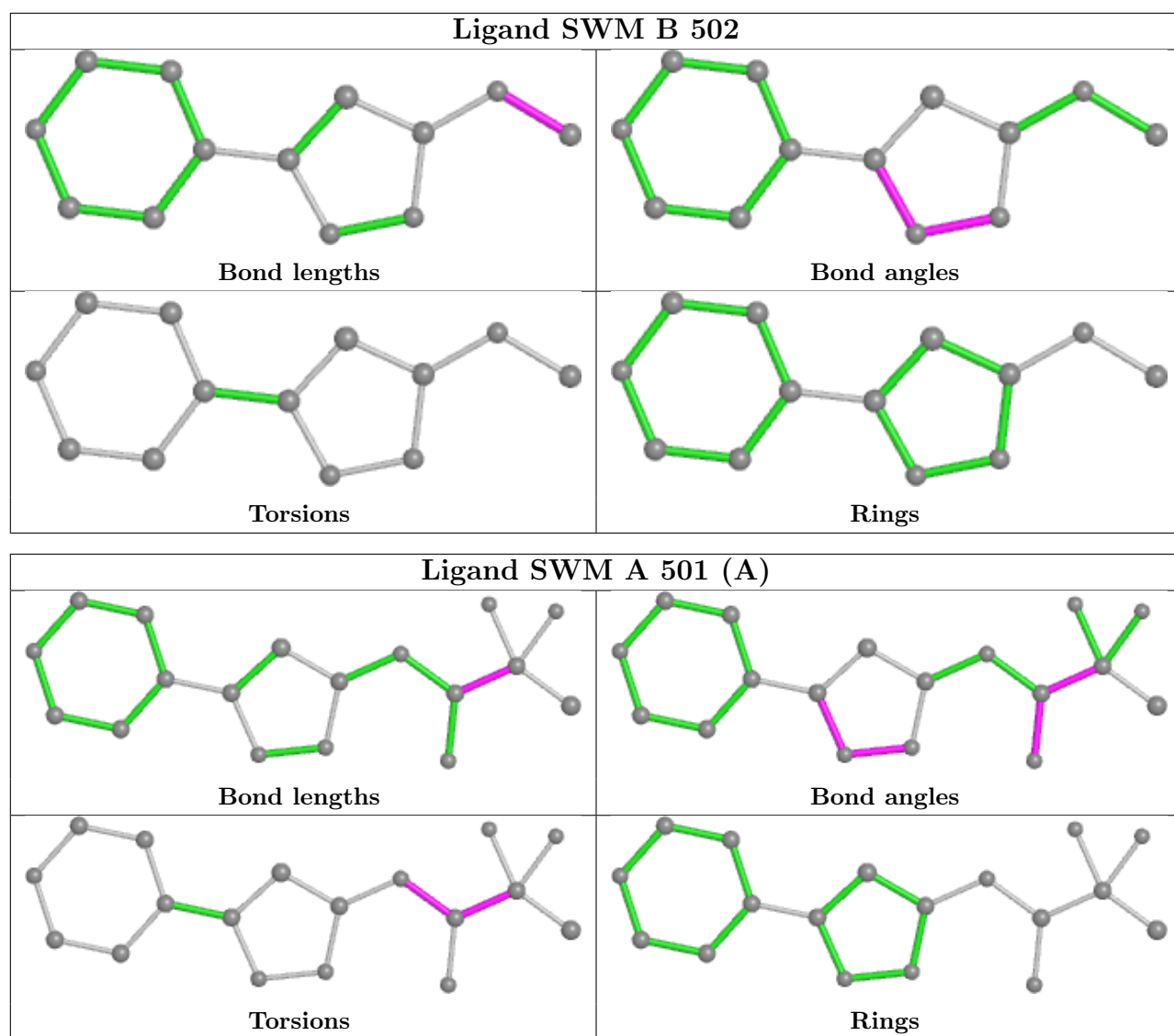
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501[B]	SWM	1	0
4	A	511	GOL	2	0
4	B	506	GOL	1	0
7	B	510	C15	1	0
7	A	512	C15	1	0
3	B	504	EDO	1	0
2	A	501[A]	SWM	1	0

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	350/364 (96%)	0.03	13 (3%) 41 39	27, 42, 71, 104	0
1	B	326/364 (89%)	0.09	13 (3%) 38 36	28, 45, 79, 97	0
All	All	676/728 (92%)	0.06	26 (3%) 40 38	27, 44, 76, 104	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	84	ALA	6.3
1	A	292	PRO	4.1
1	B	69	PRO	3.8
1	B	48	PHE	3.8
1	B	60	VAL	3.6
1	B	82	TYR	3.5
1	A	379	GLN	3.3
1	A	161	LEU	3.0
1	B	67	LEU	3.0
1	A	86	LEU	2.9
1	A	387	ILE	2.9
1	B	399	MET	2.9
1	A	378	LYS	2.9
1	B	49	TYR	2.8
1	A	376	TYR	2.8
1	B	89	ASN	2.6
1	A	220	MET	2.5
1	A	293	THR	2.5
1	A	222	PRO	2.4
1	A	381	ASP	2.2
1	B	400	ASN	2.2
1	B	58	PHE	2.1
1	B	148	LEU	2.1
1	A	288	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	61	LEU	2.1
1	A	46	ASN	2.1

## 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, 95<sup>th</sup> 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.

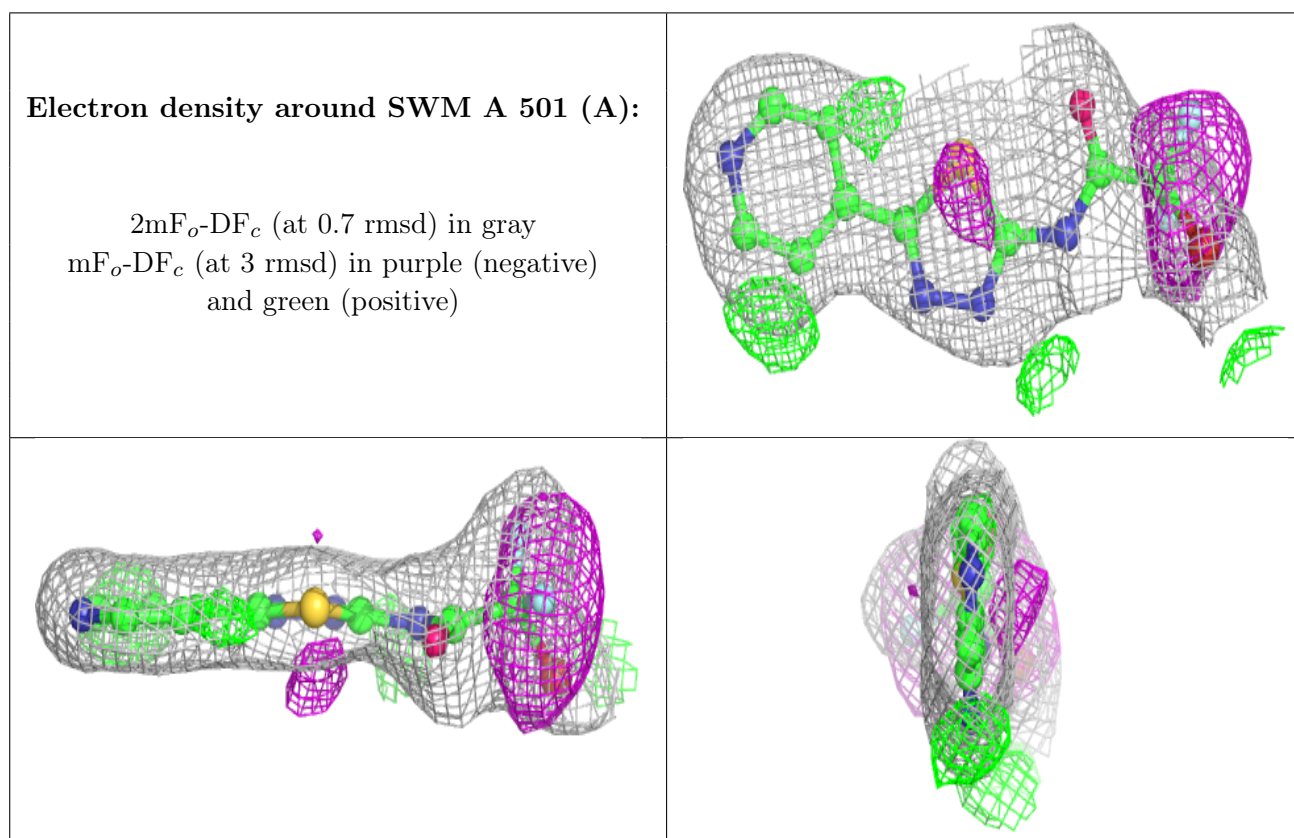
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	B	505	6/6	0.74	0.20	50,52,64,69	0
6	PEG	A	510	7/7	0.75	0.29	50,53,59,64	0
4	GOL	B	508	6/6	0.76	0.20	60,61,74,75	0
4	GOL	A	507	6/6	0.76	0.21	56,64,66,68	0
4	GOL	B	506	6/6	0.78	0.18	50,57,64,68	0
2	SWM	A	501[A]	18/18	0.78	0.18	38,49,78,93	18
2	SWM	A	501[B]	18/18	0.78	0.18	39,49,78,90	18
4	GOL	A	511	6/6	0.81	0.21	49,56,59,60	0
7	C15	B	510	12/22	0.81	0.28	52,57,65,66	0
4	GOL	A	504	6/6	0.83	0.22	57,58,65,73	0
4	GOL	B	501	6/6	0.83	0.21	48,57,61,67	0
4	GOL	B	507	6/6	0.83	0.19	62,69,72,72	0
3	EDO	A	503	4/4	0.84	0.14	42,53,53,63	0
7	C15	B	509	16/22	0.85	0.33	53,63,87,88	0
3	EDO	A	509	4/4	0.86	0.26	58,63,63,65	0
3	EDO	B	503	4/4	0.87	0.12	44,50,53,64	0
3	EDO	A	508	4/4	0.87	0.15	43,63,63,72	0
2	SWM	B	502	13/18	0.88	0.12	44,53,67,67	0
6	PEG	A	506	7/7	0.89	0.40	44,60,66,67	0
3	EDO	A	502	4/4	0.91	0.11	43,48,53,56	0
3	EDO	B	504	4/4	0.92	0.18	39,51,53,69	0

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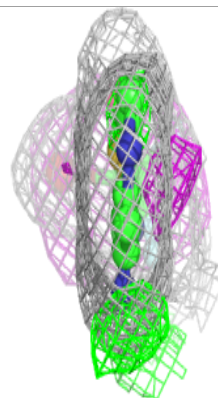
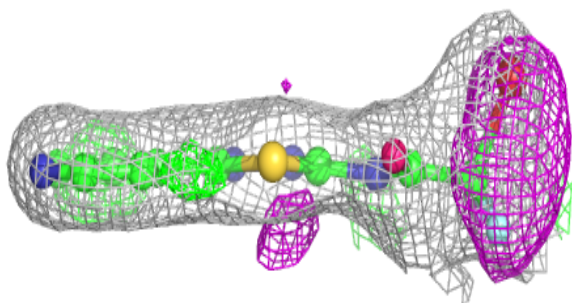
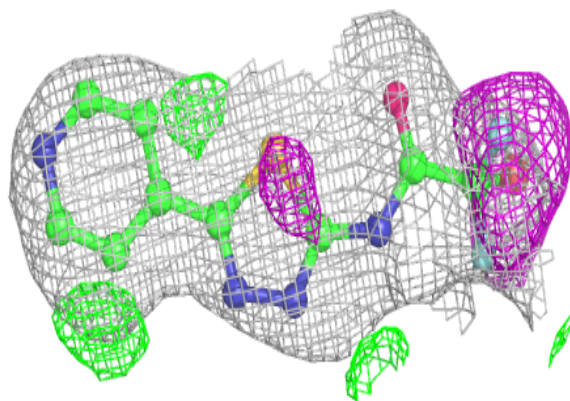
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	C15	A	512	22/22	0.95	0.11	43,51,56,64	0
5	BME	A	505	4/4	0.96	0.10	51,55,57,64	0
8	CL	B	511	1/1	0.98	0.08	36,36,36,36	0

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.

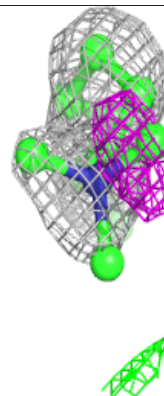
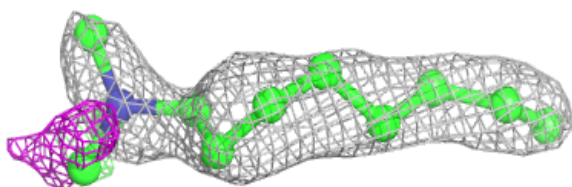
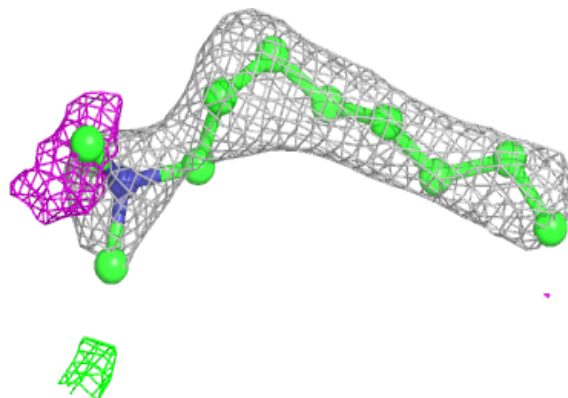


**Electron density around SWM A 501 (B):**

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

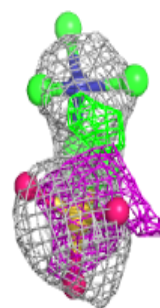
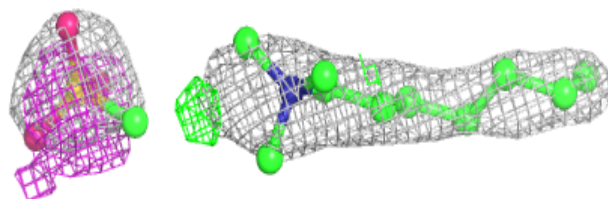
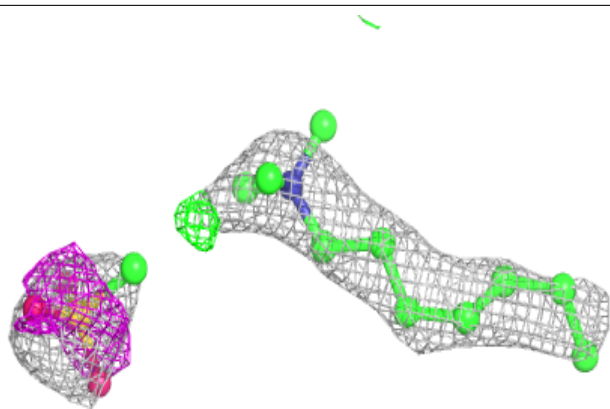
**Electron density around C15 B 510:**

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

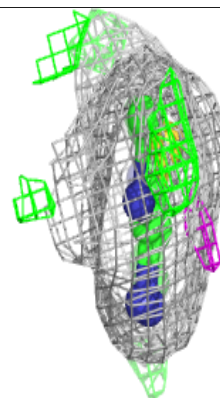
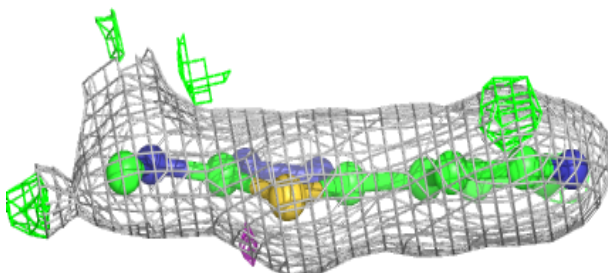
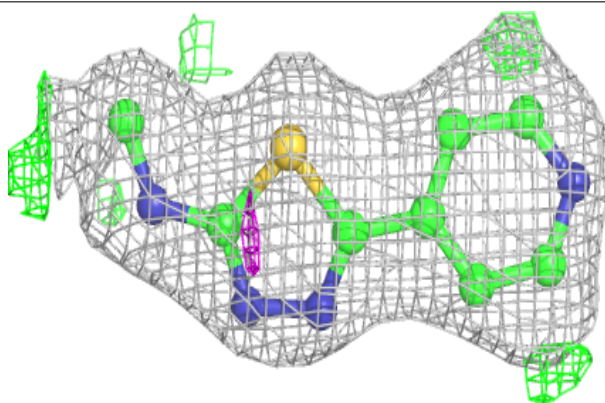


**Electron density around C15 B 509:**

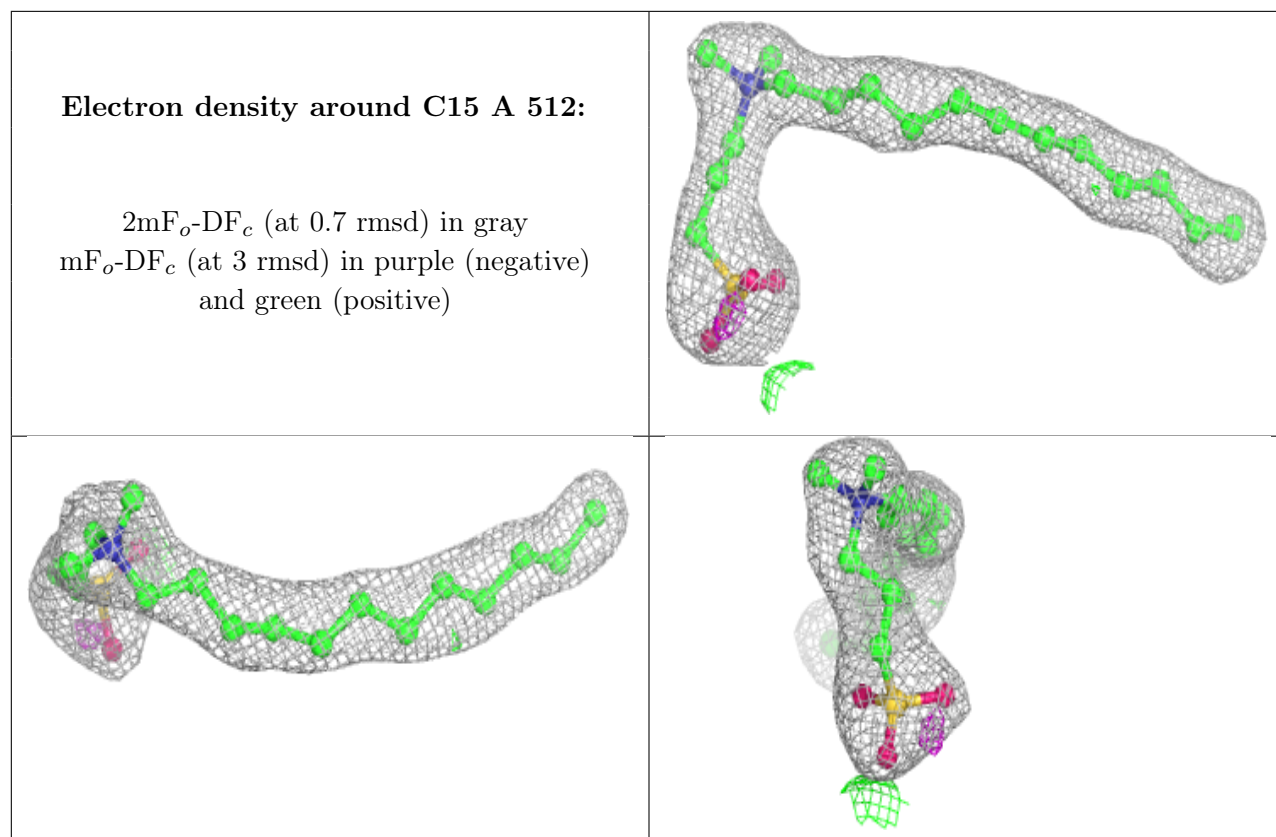
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around SWM B 502:**

$2mF_o-DF_c$  (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.