



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 5, 2026 – 02:15 AM UTC

PDB ID : 9R1C / pdb\_00009r1c  
Title : Keap1 - inhibitor complex - 1  
Authors : Talapatra, S.K.; Kozielski, F.; Wells, G.  
Deposited on : 2025-04-26  
Resolution : 1.69 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4-5-2 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

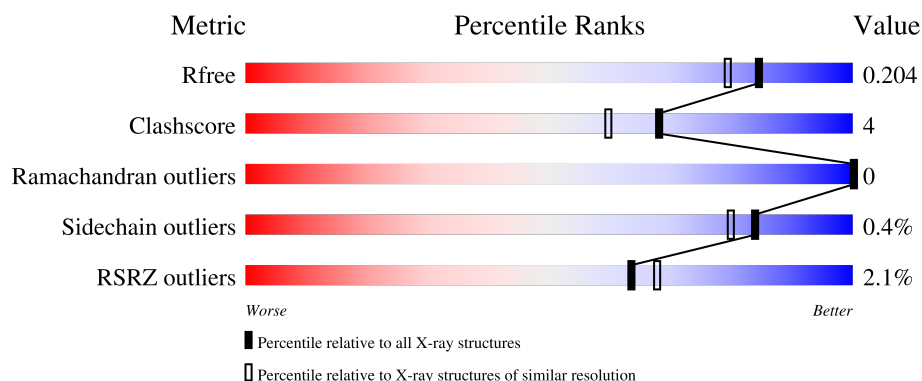
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 1.69 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	414	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2698 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 Kelch-like ECH-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	286	2220	1381	402	422	15	0	4	0

There are 125 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	196	MET	-	initiating methionine	UNP Q14145
A	197	ALA	-	expression tag	UNP Q14145
A	198	MET	-	expression tag	UNP Q14145
A	199	GLY	-	expression tag	UNP Q14145
A	200	SER	-	expression tag	UNP Q14145
A	201	SER	-	expression tag	UNP Q14145
A	202	HIS	-	expression tag	UNP Q14145
A	203	HIS	-	expression tag	UNP Q14145
A	204	HIS	-	expression tag	UNP Q14145
A	205	HIS	-	expression tag	UNP Q14145
A	206	HIS	-	expression tag	UNP Q14145
A	207	HIS	-	expression tag	UNP Q14145
A	208	HIS	-	expression tag	UNP Q14145
A	209	HIS	-	expression tag	UNP Q14145
A	210	SER	-	expression tag	UNP Q14145
A	211	SER	-	expression tag	UNP Q14145
A	212	GLY	-	expression tag	UNP Q14145
A	213	LEU	-	expression tag	UNP Q14145
A	214	VAL	-	expression tag	UNP Q14145
A	215	PRO	-	expression tag	UNP Q14145
A	216	ARG	-	expression tag	UNP Q14145
A	217	GLY	-	expression tag	UNP Q14145
A	218	SER	-	expression tag	UNP Q14145
A	219	HIS	-	expression tag	UNP Q14145
A	220	MET	-	expression tag	UNP Q14145
A	221	ALA	-	expression tag	UNP Q14145
A	222	SER	-	expression tag	UNP Q14145

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Chain	Residue	Modelled	Actual	Comment	Reference
A	223	MET	-	expression tag	UNP Q14145
A	224	SER	-	expression tag	UNP Q14145
A	225	ASP	-	expression tag	UNP Q14145
A	226	SER	-	expression tag	UNP Q14145
A	227	GLU	-	expression tag	UNP Q14145
A	228	VAL	-	expression tag	UNP Q14145
A	229	ASN	-	expression tag	UNP Q14145
A	230	GLN	-	expression tag	UNP Q14145
A	231	GLU	-	expression tag	UNP Q14145
A	232	ALA	-	expression tag	UNP Q14145
A	233	LYS	-	expression tag	UNP Q14145
A	234	PRO	-	expression tag	UNP Q14145
A	235	GLU	-	expression tag	UNP Q14145
A	236	VAL	-	expression tag	UNP Q14145
A	237	LYS	-	expression tag	UNP Q14145
A	238	PRO	-	expression tag	UNP Q14145
A	239	GLU	-	expression tag	UNP Q14145
A	240	VAL	-	expression tag	UNP Q14145
A	241	LYS	-	expression tag	UNP Q14145
A	242	PRO	-	expression tag	UNP Q14145
A	243	GLU	-	expression tag	UNP Q14145
A	244	THR	-	expression tag	UNP Q14145
A	245	HIS	-	expression tag	UNP Q14145
A	246	ILE	-	expression tag	UNP Q14145
A	247	ASN	-	expression tag	UNP Q14145
A	248	LEU	-	expression tag	UNP Q14145
A	249	LYS	-	expression tag	UNP Q14145
A	250	VAL	-	expression tag	UNP Q14145
A	251	SER	-	expression tag	UNP Q14145
A	252	ASP	-	expression tag	UNP Q14145
A	253	GLY	-	expression tag	UNP Q14145
A	254	SER	-	expression tag	UNP Q14145
A	255	SER	-	expression tag	UNP Q14145
A	256	GLU	-	expression tag	UNP Q14145
A	257	ILE	-	expression tag	UNP Q14145
A	258	PHE	-	expression tag	UNP Q14145
A	259	PHE	-	expression tag	UNP Q14145
A	260	LYS	-	expression tag	UNP Q14145
A	261	ILE	-	expression tag	UNP Q14145
A	262	LYS	-	expression tag	UNP Q14145
A	263	LYS	-	expression tag	UNP Q14145
A	264	THR	-	expression tag	UNP Q14145

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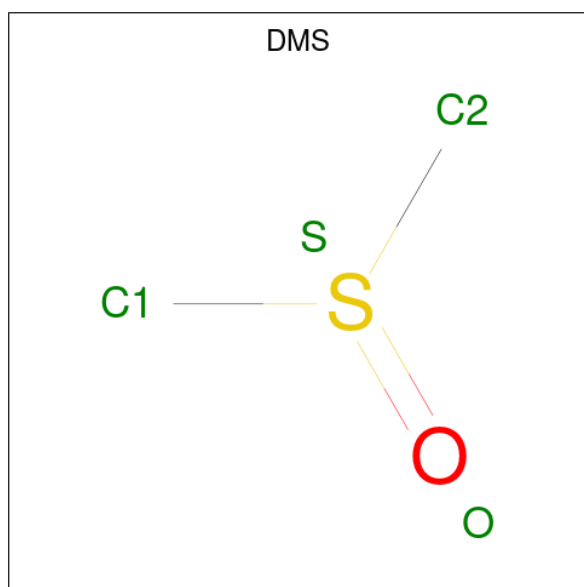
Chain	Residue	Modelled	Actual	Comment	Reference
A	265	THR	-	expression tag	UNP Q14145
A	266	PRO	-	expression tag	UNP Q14145
A	267	LEU	-	expression tag	UNP Q14145
A	268	ARG	-	expression tag	UNP Q14145
A	269	ARG	-	expression tag	UNP Q14145
A	270	LEU	-	expression tag	UNP Q14145
A	271	MET	-	expression tag	UNP Q14145
A	272	GLU	-	expression tag	UNP Q14145
A	273	ALA	-	expression tag	UNP Q14145
A	274	PHE	-	expression tag	UNP Q14145
A	275	ALA	-	expression tag	UNP Q14145
A	276	LYS	-	expression tag	UNP Q14145
A	277	ARG	-	expression tag	UNP Q14145
A	278	GLN	-	expression tag	UNP Q14145
A	279	GLY	-	expression tag	UNP Q14145
A	280	LYS	-	expression tag	UNP Q14145
A	281	GLU	-	expression tag	UNP Q14145
A	282	MET	-	expression tag	UNP Q14145
A	283	ASP	-	expression tag	UNP Q14145
A	284	SER	-	expression tag	UNP Q14145
A	285	LEU	-	expression tag	UNP Q14145
A	286	ARG	-	expression tag	UNP Q14145
A	287	PHE	-	expression tag	UNP Q14145
A	288	LEU	-	expression tag	UNP Q14145
A	289	TYR	-	expression tag	UNP Q14145
A	290	ASP	-	expression tag	UNP Q14145
A	291	GLY	-	expression tag	UNP Q14145
A	292	ILE	-	expression tag	UNP Q14145
A	293	ARG	-	expression tag	UNP Q14145
A	294	ILE	-	expression tag	UNP Q14145
A	295	GLN	-	expression tag	UNP Q14145
A	296	ALA	-	expression tag	UNP Q14145
A	297	ASP	-	expression tag	UNP Q14145
A	298	GLN	-	expression tag	UNP Q14145
A	299	THR	-	expression tag	UNP Q14145
A	300	PRO	-	expression tag	UNP Q14145
A	301	GLU	-	expression tag	UNP Q14145
A	302	ASP	-	expression tag	UNP Q14145
A	303	LEU	-	expression tag	UNP Q14145
A	304	ASP	-	expression tag	UNP Q14145
A	305	MET	-	expression tag	UNP Q14145
A	306	GLU	-	expression tag	UNP Q14145

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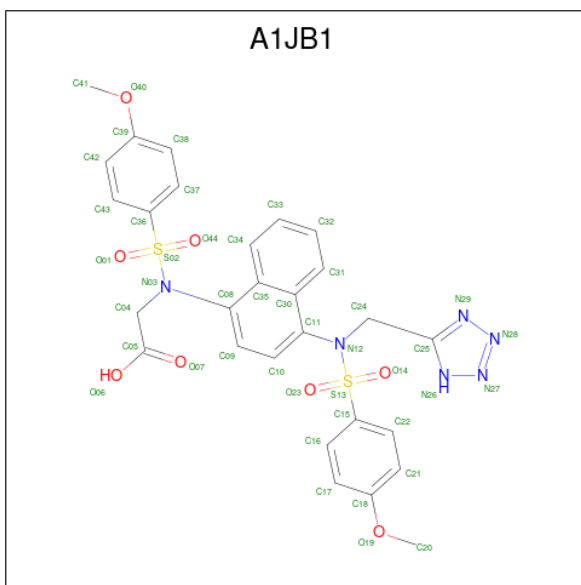
Chain	Residue	Modelled	Actual	Comment	Reference
A	307	ASP	-	expression tag	UNP Q14145
A	308	ASN	-	expression tag	UNP Q14145
A	309	ASP	-	expression tag	UNP Q14145
A	310	ILE	-	expression tag	UNP Q14145
A	311	ILE	-	expression tag	UNP Q14145
A	312	GLU	-	expression tag	UNP Q14145
A	313	ALA	-	expression tag	UNP Q14145
A	314	HIS	-	expression tag	UNP Q14145
A	315	ARG	-	expression tag	UNP Q14145
A	316	GLU	-	expression tag	UNP Q14145
A	317	GLN	-	expression tag	UNP Q14145
A	318	ILE	-	expression tag	UNP Q14145
A	319	GLY	-	expression tag	UNP Q14145
A	320	GLY	-	expression tag	UNP Q14145

- Molecule 2 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is 2-[(4-methoxyphenyl)sulfonyl]-4-[(4-methoxyphenyl)sulfonyl-(1 {H}-1,2,3,4-tetrazol-5-ylmethyl)amino]naphthalen-1-yl]amino]ethanoic acid (CCD ID: A1JB1) (formula: C<sub>28</sub>H<sub>26</sub>N<sub>6</sub>O<sub>8</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			44	28	6	8	2		

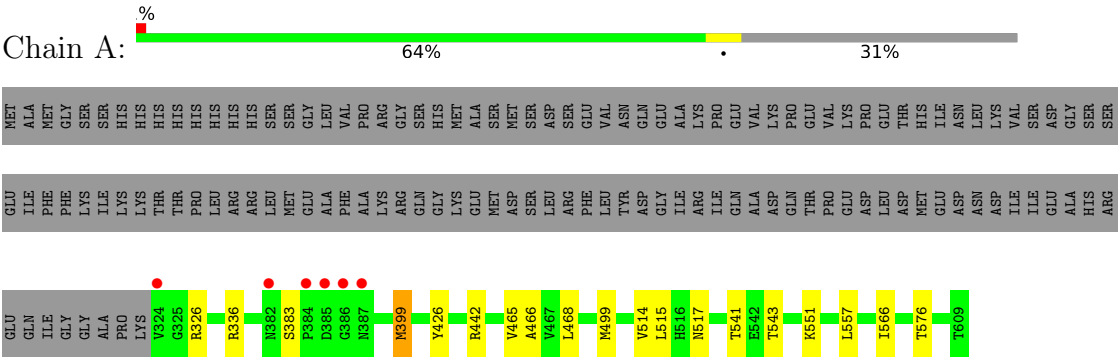
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	426	Total O 426 426	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: Kelch-like ECH-associated protein 1





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.42Å 75.58Å 48.68Å 90.00° 106.19° 90.00°	Depositor
Resolution (Å)	60.70 – 1.69 60.70 – 1.69	Depositor EDS
% Data completeness (in resolution range)	99.8 (60.70-1.69) 99.8 (60.70-1.69)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 1.69Å)	Xtriage
Refinement program	PHENIX (1.19.1_4122: ???)	Depositor
R, $R_{free}$	0.166 , 0.202 0.168 , 0.204	Depositor DCC
$R_{free}$ test set	2437 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.5	Xtriage
Anisotropy	0.090	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 42.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2698	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.36% 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: A1JB1, DMS

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	0.54	0/2276	0.68	1/3099 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	399	MET	CB-CG-SD	-5.77	95.40	112.70

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	2220	0	2113	16	0
2	A	8	0	12	1	0
3	A	44	0	0	0	0
4	A	426	0	0	5	2
All	All	2698	0	2125	16	2

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 4.

The worst 5 of 16 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:517[A]:ASN:ND2	4:A:801:HOH:O	1.91	1.01
1:A:383:SER:O	4:A:802:HOH:O	2.08	0.72
1:A:465:VAL:O	4:A:803:HOH:O	2.17	0.57
1:A:399:MET:SD	2:A:701:DMS:H13	2.46	0.55
1:A:557:LEU:H	1:A:557:LEU:HD23	1.74	0.52

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:928:HOH:O	4:A:1162:HOH:O[2_556]	2.08	0.12
4:A:1161:HOH:O	4:A:1213:HOH:O[4_446]	2.15	0.05

## 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	288/414 (70%)	282 (98%)	6 (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	234/344 (68%)	233 (100%)	1 (0%)	84 80

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	576	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	528	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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	DMS	A	701	-	3,3,3	0.31	0	3,3,3	0.20	0
3	A1JB1	A	703	-	46,48,48	1.96	10 (21%)	64,70,70	2.63	22 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	DMS	A	702	-	3,3,3	0.37	0	3,3,3	0.51	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	A1JB1	A	703	-	-	5/44/44/44	0/5/5/5

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	703	A1JB1	S13-N12	5.03	1.72	1.65
3	A	703	A1JB1	S02-N03	4.73	1.71	1.65
3	A	703	A1JB1	O23-S13	4.61	1.48	1.43
3	A	703	A1JB1	C24-C25	4.22	1.54	1.49
3	A	703	A1JB1	C36-S02	4.02	1.81	1.76

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	703	A1JB1	C36-S02-N03	-9.25	94.88	106.97
3	A	703	A1JB1	O44-S02-O01	-6.60	109.29	119.59
3	A	703	A1JB1	O23-S13-O14	-6.24	109.86	119.59
3	A	703	A1JB1	O01-S02-N03	6.15	113.85	106.69
3	A	703	A1JB1	C09-C08-N03	-5.48	113.33	119.75

There are no chirality outliers.

All (5) torsion outliers are listed below:

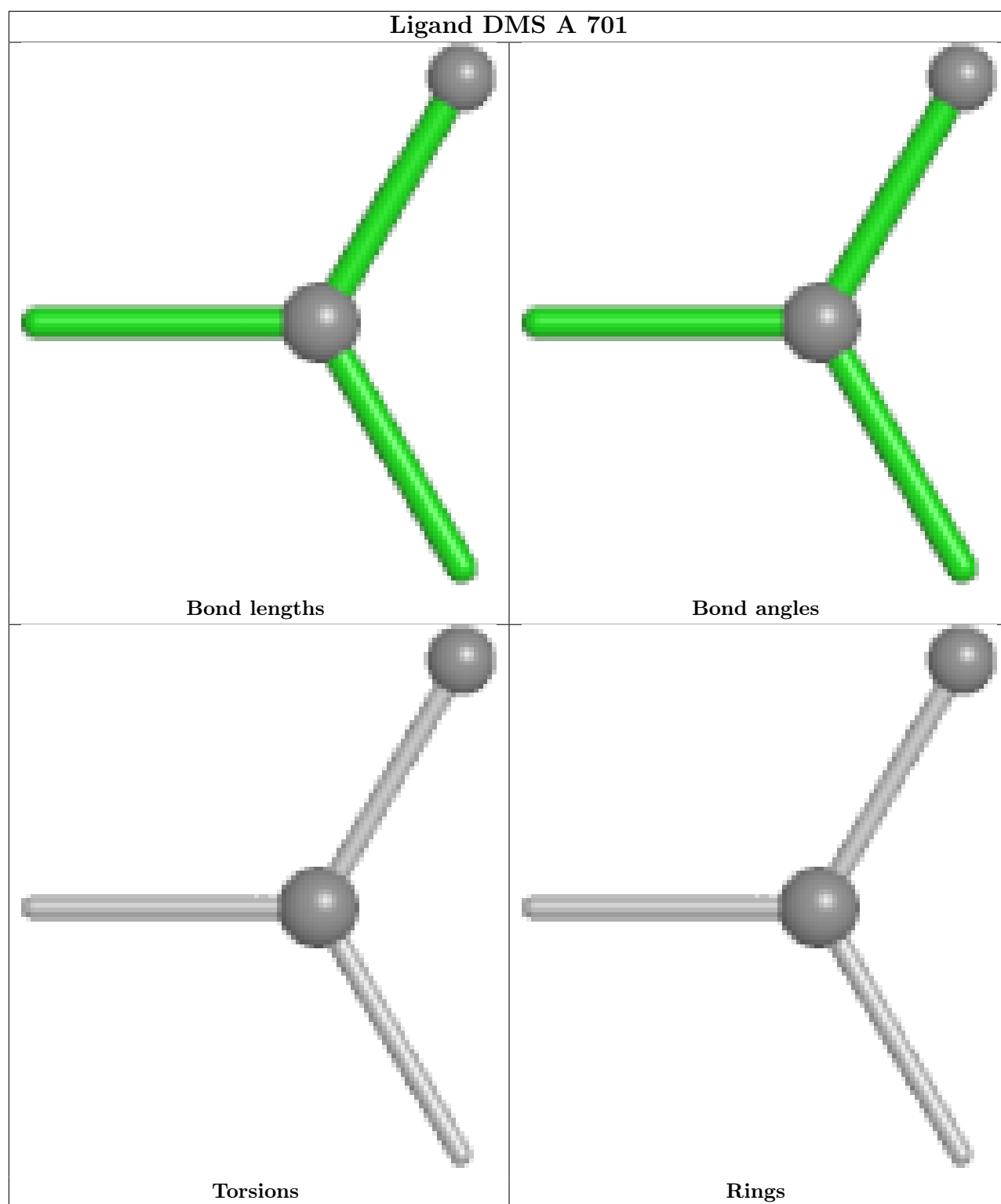
Mol	Chain	Res	Type	Atoms
3	A	703	A1JB1	C25-C24-N12-S13
3	A	703	A1JB1	N03-C04-C05-O06
3	A	703	A1JB1	N03-C04-C05-O07
3	A	703	A1JB1	C05-C04-N03-C08
3	A	703	A1JB1	C35-C08-N03-S02

There are no ring outliers.

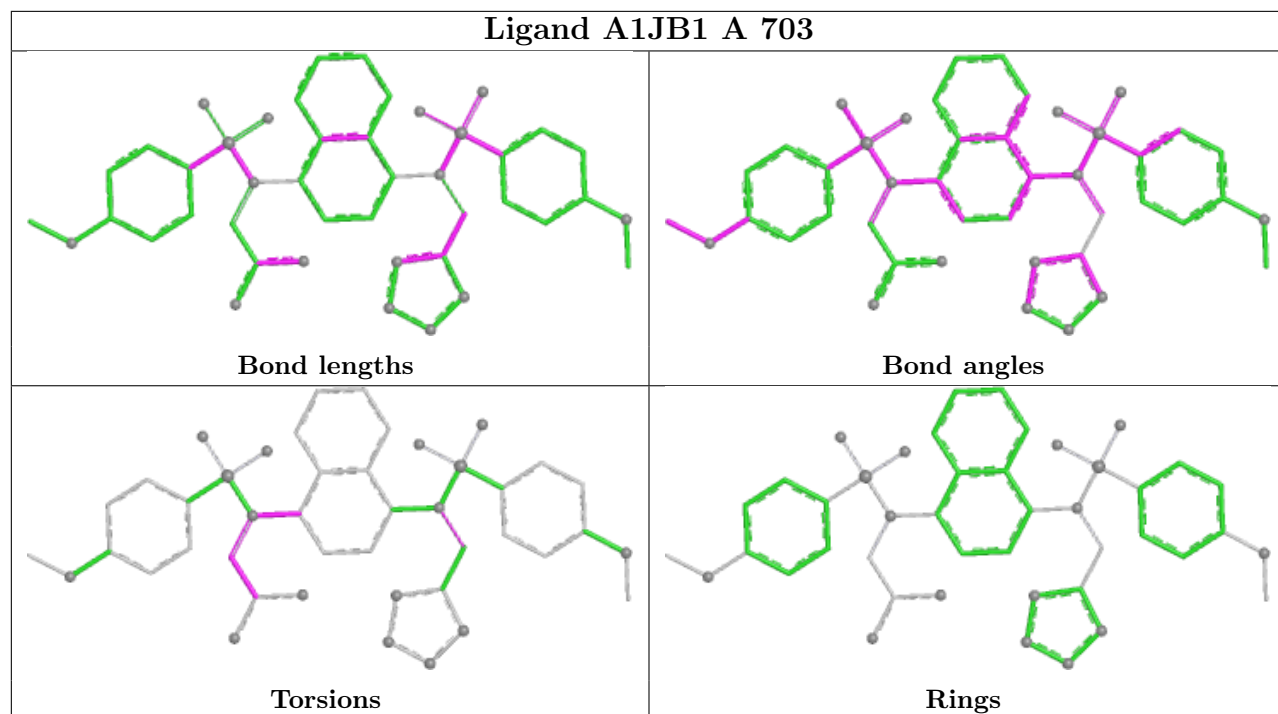
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	DMS	1	0

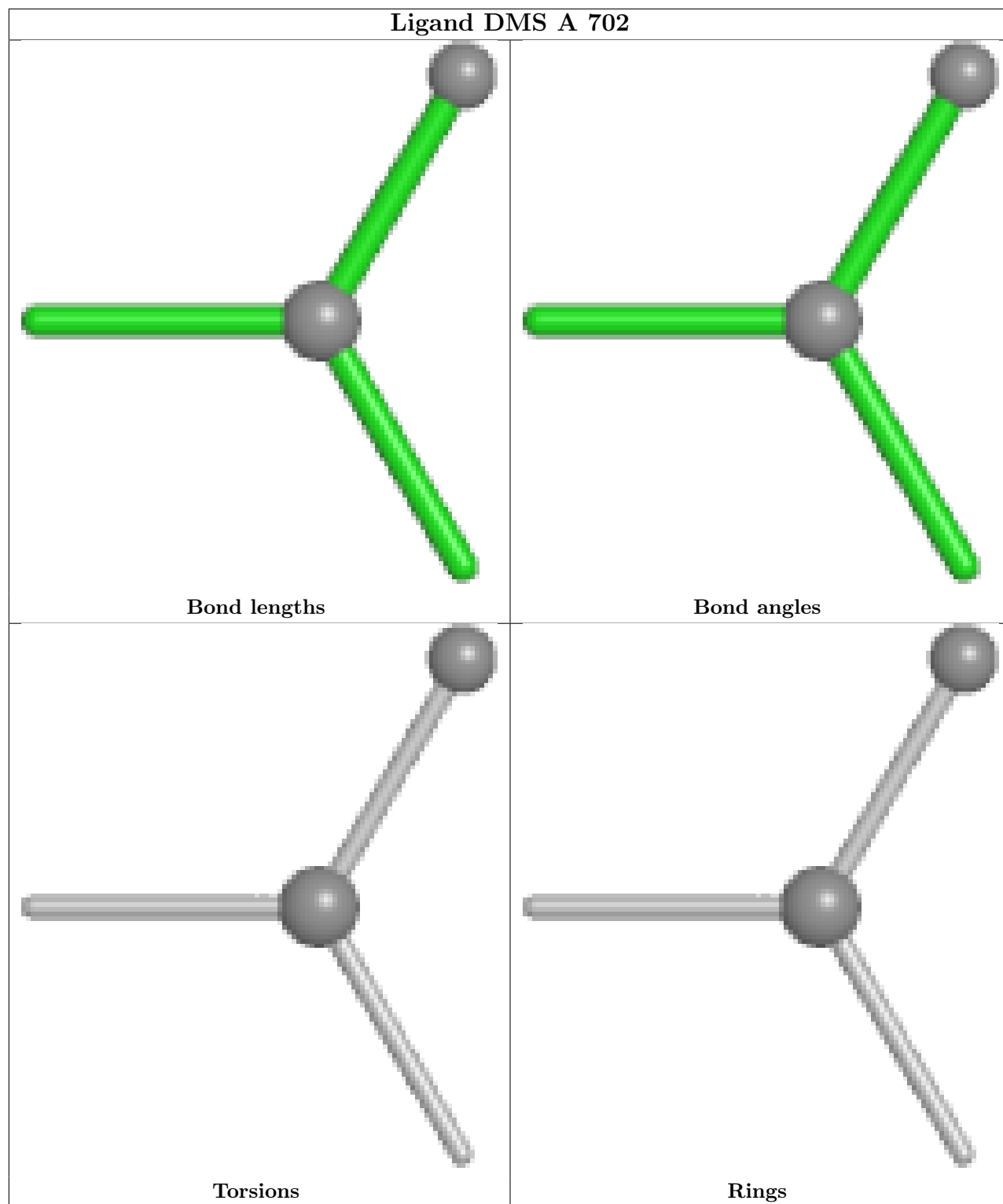
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



## Ligand A1JB1 A 703







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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, 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	286/414 (69%)	-0.46	6 (2%) 63 68	9, 16, 32, 59	4 (1%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	324	VAL	7.3
1	A	385	ASP	4.2
1	A	384	PRO	3.3
1	A	387	ASN	3.2
1	A	386	GLY	3.0

### 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](#)

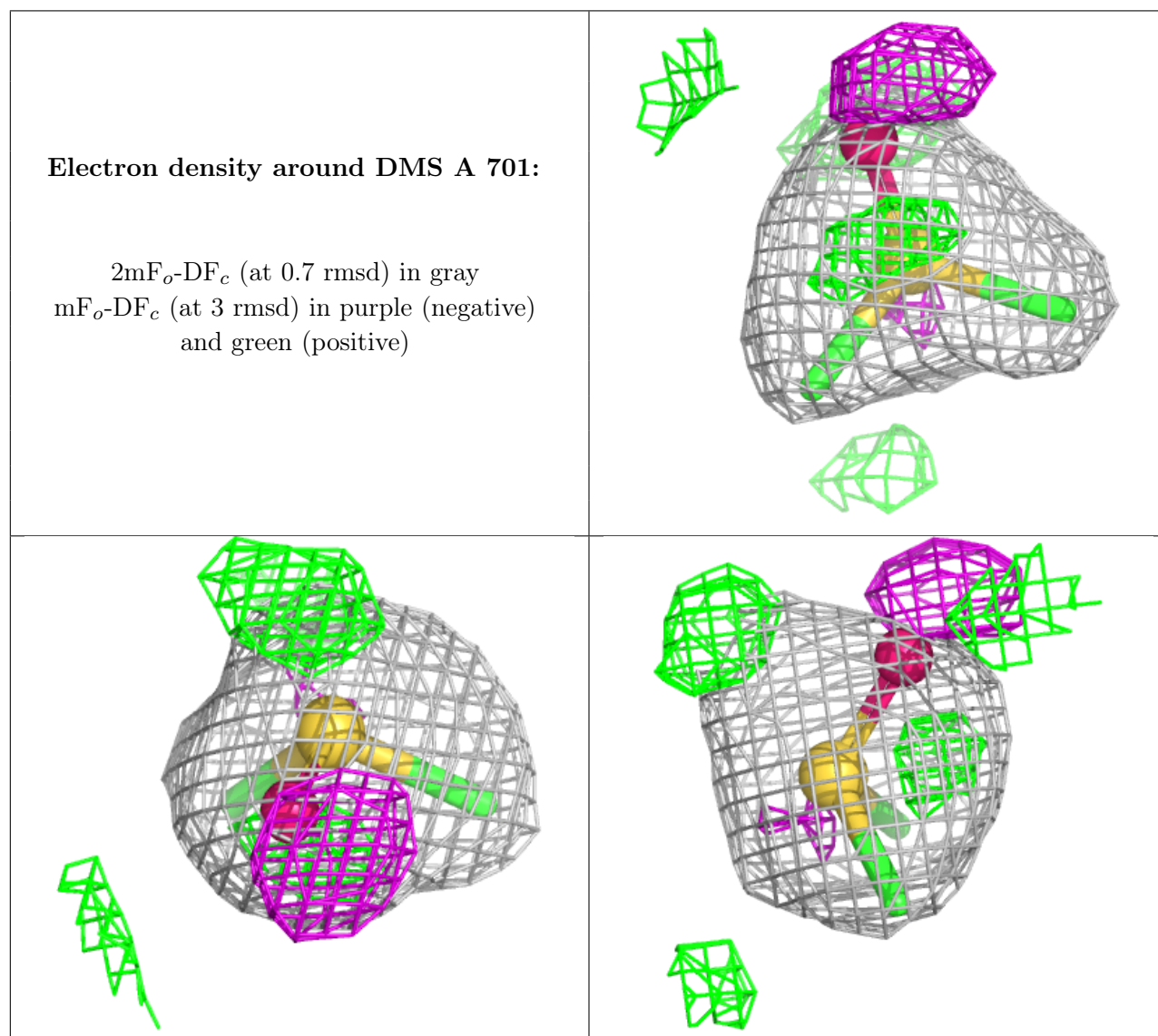
There are no oligosaccharides in this entry.

### 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, 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.

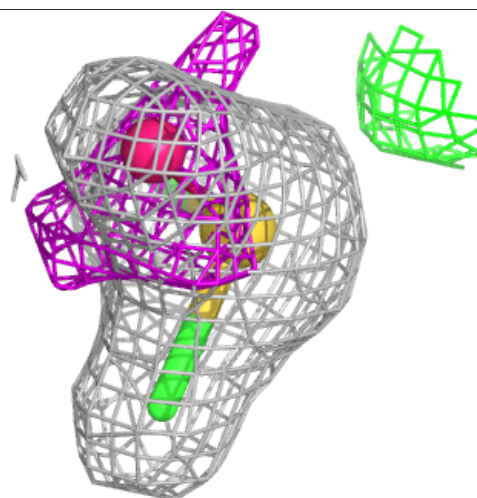
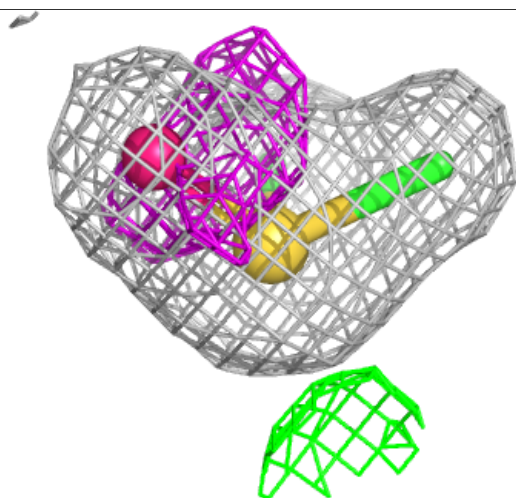
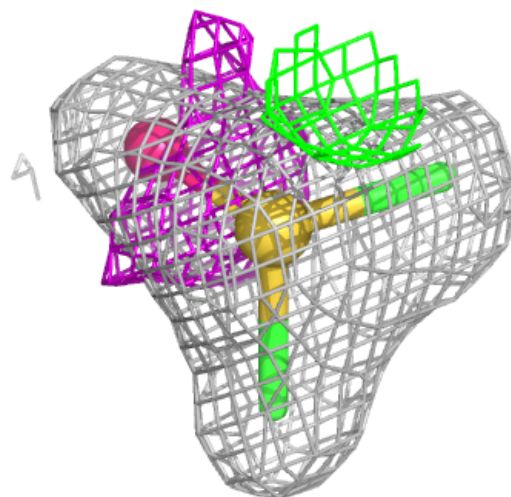
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	DMS	A	701	4/4	0.91	0.17	36,45,48,48	0
2	DMS	A	702	4/4	0.96	0.13	23,26,27,33	0
3	A1JB1	A	703	44/44	0.97	0.07	15,22,30,36	0

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.



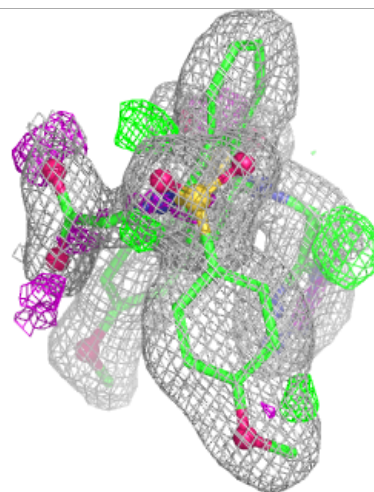
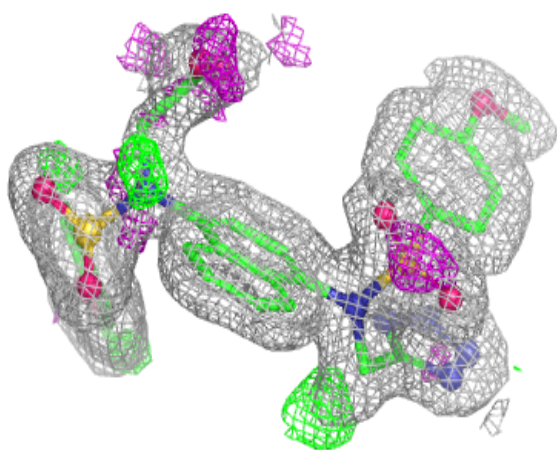
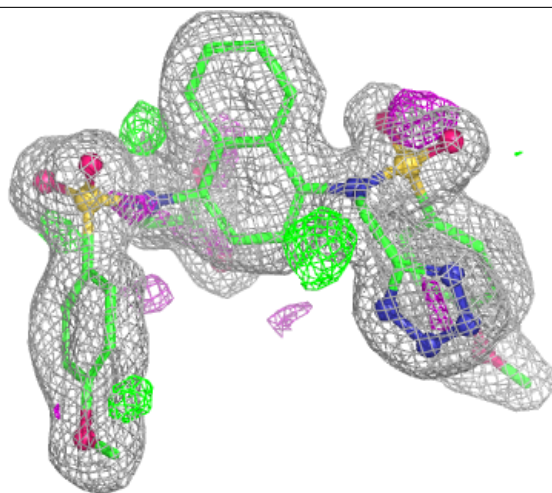
**Electron density around DMS A 702:**

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



**Electron density around A1JB1 A 703:**

$2mF_o-DF_c$  (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.