



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 1, 2025 – 03:17 pm GMT

PDB ID : 9RO7 / pdb\_00009ro7  
Title : Crystal structure of human CD22 Ig domains 1-3 in complex with modified sialoside 7-012  
Authors : Ereno-Orbea, J.; Sicard, T.; Julien, J.-P.  
Deposited on : 2025-06-20  
Resolution : 3.15 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

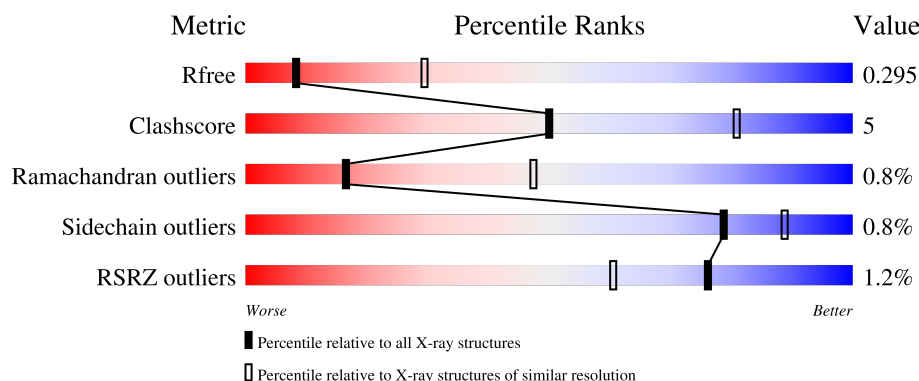
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 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))
$R_{free}$	164625	2168 (3.20-3.12)
Clashscore	180529	2333 (3.20-3.12)
Ramachandran outliers	177936	2266 (3.20-3.12)
Sidechain outliers	177891	2265 (3.20-3.12)
RSRZ outliers	164620	2169 (3.20-3.12)

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	324	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 11%, green 83%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>83%</span> <span>11%</span> <span>5%</span> </div> </div>
1	B	324	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 80%, grey 6%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>80%</span> <span>14%</span> <span>6%</span> </div> </div>
1	C	324	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 2%, yellow 14%, green 74%, grey 12%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>74%</span> <span>14%</span> <span>12%</span> </div> </div>
1	D	324	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 77%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>77%</span> <span>14%</span> <span>9%</span> </div> </div>
2	E	3	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 33%, yellow 67%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>33%</span> <span>67%</span> </div> </div>

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Mol	Chain	Length	Quality of chain
2	H	3	 67%33%
2	J	3	 100%
2	L	3	 100%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9883 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 B-cell receptor CD22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	0	0
			2438	1543	413	469	13			
1	B	306	Total	C	N	O	S	0	0	0
			2432	1540	412	467	13			
1	C	286	Total	C	N	O	S	0	0	0
			2277	1444	382	438	13			
1	D	295	Total	C	N	O	S	0	0	0
			2343	1486	395	449	13			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLU	-	expression tag	UNP P20273
A	18	THR	-	expression tag	UNP P20273
A	19	GLY	-	expression tag	UNP P20273
A	67	ALA	ASN	engineered mutation	UNP P20273
A	112	ALA	ASN	engineered mutation	UNP P20273
A	135	ALA	ASN	engineered mutation	UNP P20273
A	164	ALA	ASN	engineered mutation	UNP P20273
A	231	ALA	ASN	engineered mutation	UNP P20273
A	331	GLY	-	expression tag	UNP P20273
A	332	GLY	-	expression tag	UNP P20273
A	333	THR	-	expression tag	UNP P20273
A	334	LYS	-	expression tag	UNP P20273
A	335	HIS	-	expression tag	UNP P20273
A	336	HIS	-	expression tag	UNP P20273
A	337	HIS	-	expression tag	UNP P20273
A	338	HIS	-	expression tag	UNP P20273
A	339	HIS	-	expression tag	UNP P20273
A	340	HIS	-	expression tag	UNP P20273
B	17	GLU	-	expression tag	UNP P20273
B	18	THR	-	expression tag	UNP P20273
B	19	GLY	-	expression tag	UNP P20273

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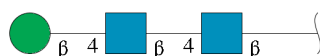
Chain	Residue	Modelled	Actual	Comment	Reference
B	67	ALA	ASN	engineered mutation	UNP P20273
B	112	ALA	ASN	engineered mutation	UNP P20273
B	135	ALA	ASN	engineered mutation	UNP P20273
B	164	ALA	ASN	engineered mutation	UNP P20273
B	231	ALA	ASN	engineered mutation	UNP P20273
B	331	GLY	-	expression tag	UNP P20273
B	332	GLY	-	expression tag	UNP P20273
B	333	THR	-	expression tag	UNP P20273
B	334	LYS	-	expression tag	UNP P20273
B	335	HIS	-	expression tag	UNP P20273
B	336	HIS	-	expression tag	UNP P20273
B	337	HIS	-	expression tag	UNP P20273
B	338	HIS	-	expression tag	UNP P20273
B	339	HIS	-	expression tag	UNP P20273
B	340	HIS	-	expression tag	UNP P20273
C	17	GLU	-	expression tag	UNP P20273
C	18	THR	-	expression tag	UNP P20273
C	19	GLY	-	expression tag	UNP P20273
C	67	ALA	ASN	engineered mutation	UNP P20273
C	112	ALA	ASN	engineered mutation	UNP P20273
C	135	ALA	ASN	engineered mutation	UNP P20273
C	164	ALA	ASN	engineered mutation	UNP P20273
C	231	ALA	ASN	engineered mutation	UNP P20273
C	331	GLY	-	expression tag	UNP P20273
C	332	GLY	-	expression tag	UNP P20273
C	333	THR	-	expression tag	UNP P20273
C	334	LYS	-	expression tag	UNP P20273
C	335	HIS	-	expression tag	UNP P20273
C	336	HIS	-	expression tag	UNP P20273
C	337	HIS	-	expression tag	UNP P20273
C	338	HIS	-	expression tag	UNP P20273
C	339	HIS	-	expression tag	UNP P20273
C	340	HIS	-	expression tag	UNP P20273
D	17	GLU	-	expression tag	UNP P20273
D	18	THR	-	expression tag	UNP P20273
D	19	GLY	-	expression tag	UNP P20273
D	67	ALA	ASN	engineered mutation	UNP P20273
D	112	ALA	ASN	engineered mutation	UNP P20273
D	135	ALA	ASN	engineered mutation	UNP P20273
D	164	ALA	ASN	engineered mutation	UNP P20273
D	231	ALA	ASN	engineered mutation	UNP P20273
D	331	GLY	-	expression tag	UNP P20273

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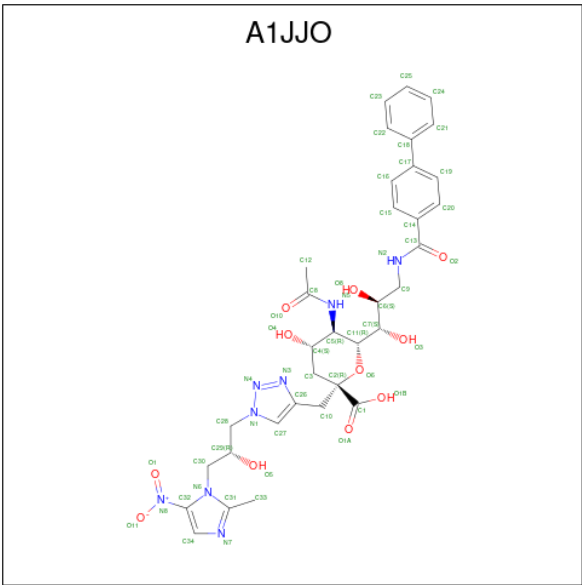
Chain	Residue	Modelled	Actual	Comment	Reference
D	332	GLY	-	expression tag	UNP P20273
D	333	THR	-	expression tag	UNP P20273
D	334	LYS	-	expression tag	UNP P20273
D	335	HIS	-	expression tag	UNP P20273
D	336	HIS	-	expression tag	UNP P20273
D	337	HIS	-	expression tag	UNP P20273
D	338	HIS	-	expression tag	UNP P20273
D	339	HIS	-	expression tag	UNP P20273
D	340	HIS	-	expression tag	UNP P20273

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



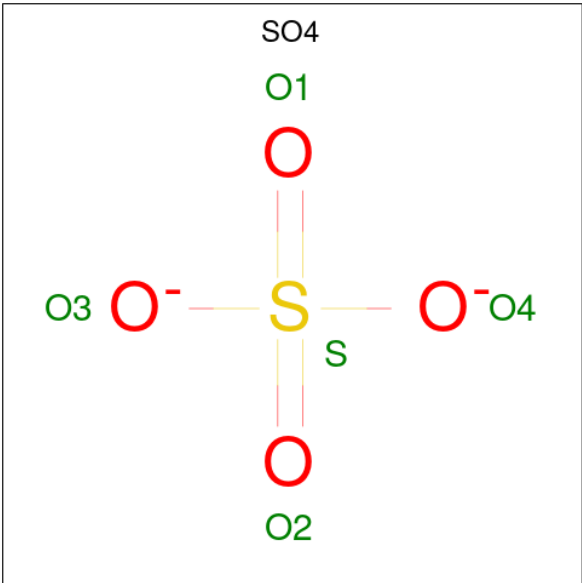
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	L	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is (2R,4S,5R,6R)-5-acetamido-6-[(1S,2S)-1,2-bis(oxidanyl)-3-[(4-phenylphenyl)carbonylamino]propyl]-2-[[1-[(2R)-3-(2-methyl-5-nitro-imidazol-1-yl)-2-oxidanyl-propyl]-1,2,3-triazol-4-yl]methyl]-4-oxidanyl-oxane-2-carboxylic acid (CCD ID: A1JJO) (formula: C<sub>34</sub>H<sub>40</sub>N<sub>8</sub>O<sub>11</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			53	34	8	11		
3	B	1	Total	C	N	O	0	0
			53	34	8	11		
3	C	1	Total	C	N	O	0	0
			53	34	8	11		
3	D	1	Total	C	N	O	0	0
			53	34	8	11		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O<sub>4</sub>S) (labeled as "Ligand of Interest" by depositor).



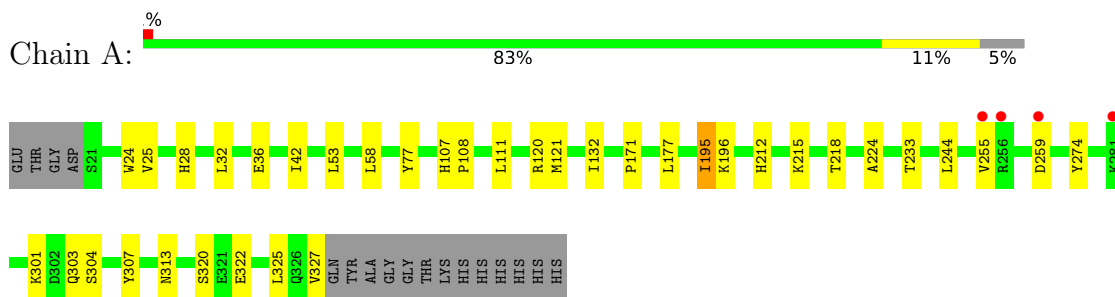
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		



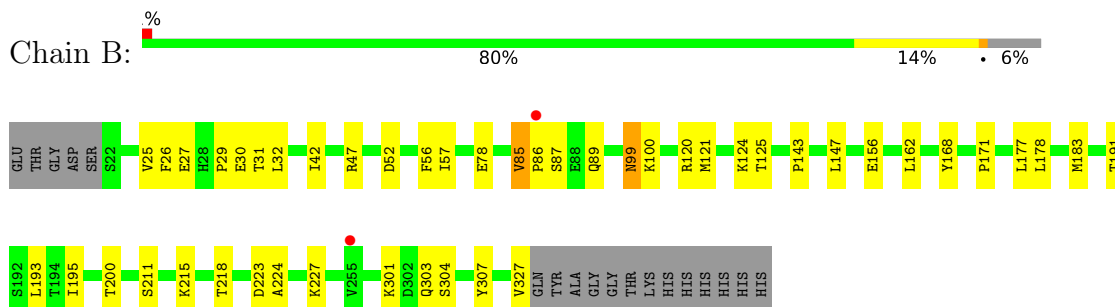
### 3 Residue-property plots

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.

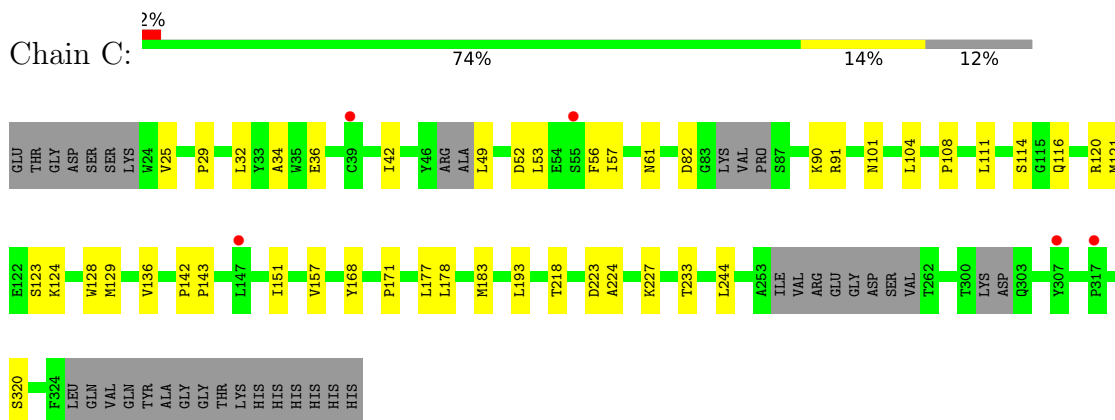
#### • Molecule 1: B-cell receptor CD22



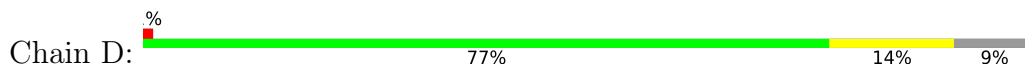
#### • Molecule 1: B-cell receptor CD22

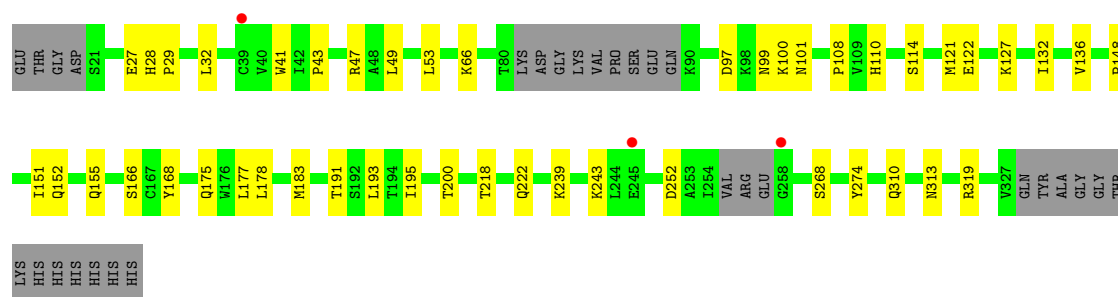


#### • Molecule 1: B-cell receptor CD22



#### • Molecule 1: B-cell receptor CD22





- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 33% 67%



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H: 67% 33%



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J: 100%



- Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L: 100%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.39Å 113.29Å 138.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.42 – 3.15 39.42 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.42-3.15) 99.8 (39.42-3.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 3.12Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.239 , 0.298 0.238 , 0.295	Depositor DCC
$R_{free}$ test set	1425 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	61.6	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 38.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	9883	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	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 30.24 % 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 1.3511e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: BMA, SO4, A1JJO, NAG

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	0.21	0/2497	0.39	0/3390
1	B	0.22	0/2491	0.40	0/3382
1	C	0.19	0/2331	0.44	3/3161 (0.1%)
1	D	0.18	0/2399	0.35	0/3256
All	All	0.20	0/9718	0.40	3/13189 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	123	SER	CA-C-O	8.72	123.82	118.33
1	C	123	SER	CB-CA-C	-8.58	103.92	116.53
1	C	123	SER	N-CA-C	6.67	115.16	108.75

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	2438	0	2391	23	0
1	B	2432	0	2386	27	0
1	C	2277	0	2212	25	0
1	D	2343	0	2293	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	39	0	34	0	0
2	H	39	0	34	2	0
2	J	39	0	34	0	0
2	L	39	0	34	0	0
3	A	53	0	0	3	0
3	B	53	0	0	2	0
3	C	53	0	0	3	0
3	D	53	0	0	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	10	0	0	0	0
4	D	5	0	0	0	0
All	All	9883	0	9418	100	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 5.

The worst 5 of 100 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:85:VAL:HB	1:B:86:PRO:HD3	1.70	0.73
1:B:178:LEU:HB2	1:B:183:MET:HE2	1.72	0.70
1:B:177:LEU:HB2	1:B:218:THR:HB	1.74	0.68
1:D:175:GLN:OE1	1:D:222:GLN:NE2	2.27	0.67
1:C:57:ILE:HB	1:C:120:ARG:HB3	1.76	0.67

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	305/324 (94%)	276 (90%)	28 (9%)	1 (0%)	37	66
1	B	304/324 (94%)	277 (91%)	23 (8%)	4 (1%)	10	37
1	C	276/324 (85%)	257 (93%)	18 (6%)	1 (0%)	30	61
1	D	289/324 (89%)	270 (93%)	16 (6%)	3 (1%)	13	43
All	All	1174/1296 (91%)	1080 (92%)	85 (7%)	9 (1%)	16	47

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	85	VAL
1	A	303	GLN
1	B	147	LEU
1	D	99	ASN
1	D	166	SER

### 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	279/292 (96%)	277 (99%)	2 (1%)	81	90
1	B	278/292 (95%)	274 (99%)	4 (1%)	62	80
1	C	260/292 (89%)	257 (99%)	3 (1%)	67	82
1	D	268/292 (92%)	268 (100%)	0	100	100
All	All	1085/1168 (93%)	1076 (99%)	9 (1%)	79	89

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	49	LEU
1	C	101	ASN
1	B	30	GLU
1	B	156	GLU
1	B	162	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	303	GLN
1	D	116	GLN
1	C	99	ASN
1	B	144	HIS
1	D	60	HIS

### 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 ⓘ

12 monosaccharides 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	NAG	E	1	1,2	14,14,15	0.59	1 (7%)	17,19,21	0.52	0
2	NAG	E	2	2	14,14,15	0.35	0	17,19,21	0.84	1 (5%)
2	BMA	E	3	2	11,11,12	0.91	0	15,15,17	0.85	0
2	NAG	H	1	1,2	14,14,15	0.39	0	17,19,21	0.49	0
2	NAG	H	2	2	14,14,15	0.46	0	17,19,21	1.39	2 (11%)
2	BMA	H	3	2	11,11,12	0.80	1 (9%)	15,15,17	1.10	1 (6%)
2	NAG	J	1	1,2	14,14,15	0.49	0	17,19,21	0.56	0
2	NAG	J	2	2	14,14,15	0.25	0	17,19,21	0.49	0
2	BMA	J	3	2	11,11,12	0.88	0	15,15,17	0.87	0
2	NAG	L	1	1,2	14,14,15	0.32	0	17,19,21	0.59	0
2	NAG	L	2	2	14,14,15	0.34	0	17,19,21	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	BMA	L	3	2	11,11,12	0.87	0	15,15,17	0.83	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
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	3/6/23/26	0/1/1/1
2	BMA	E	3	2	-	0/2/19/22	0/1/1/1
2	NAG	H	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	H	2	2	-	3/6/23/26	0/1/1/1
2	BMA	H	3	2	-	2/2/19/22	0/1/1/1
2	NAG	J	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	J	2	2	-	1/6/23/26	0/1/1/1
2	BMA	J	3	2	-	1/2/19/22	0/1/1/1
2	NAG	L	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	L	2	2	-	2/6/23/26	0/1/1/1
2	BMA	L	3	2	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	NAG	O5-C1	-2.02	1.40	1.43
2	H	3	BMA	C4-C3	2.01	1.57	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	2	NAG	C2-N2-C7	4.13	128.79	122.90
2	H	3	BMA	C1-O5-C5	2.54	115.63	112.19
2	E	2	NAG	C1-O5-C5	2.44	115.50	112.19
2	H	2	NAG	C1-O5-C5	2.39	115.43	112.19

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	2	NAG	O5-C5-C6-O6

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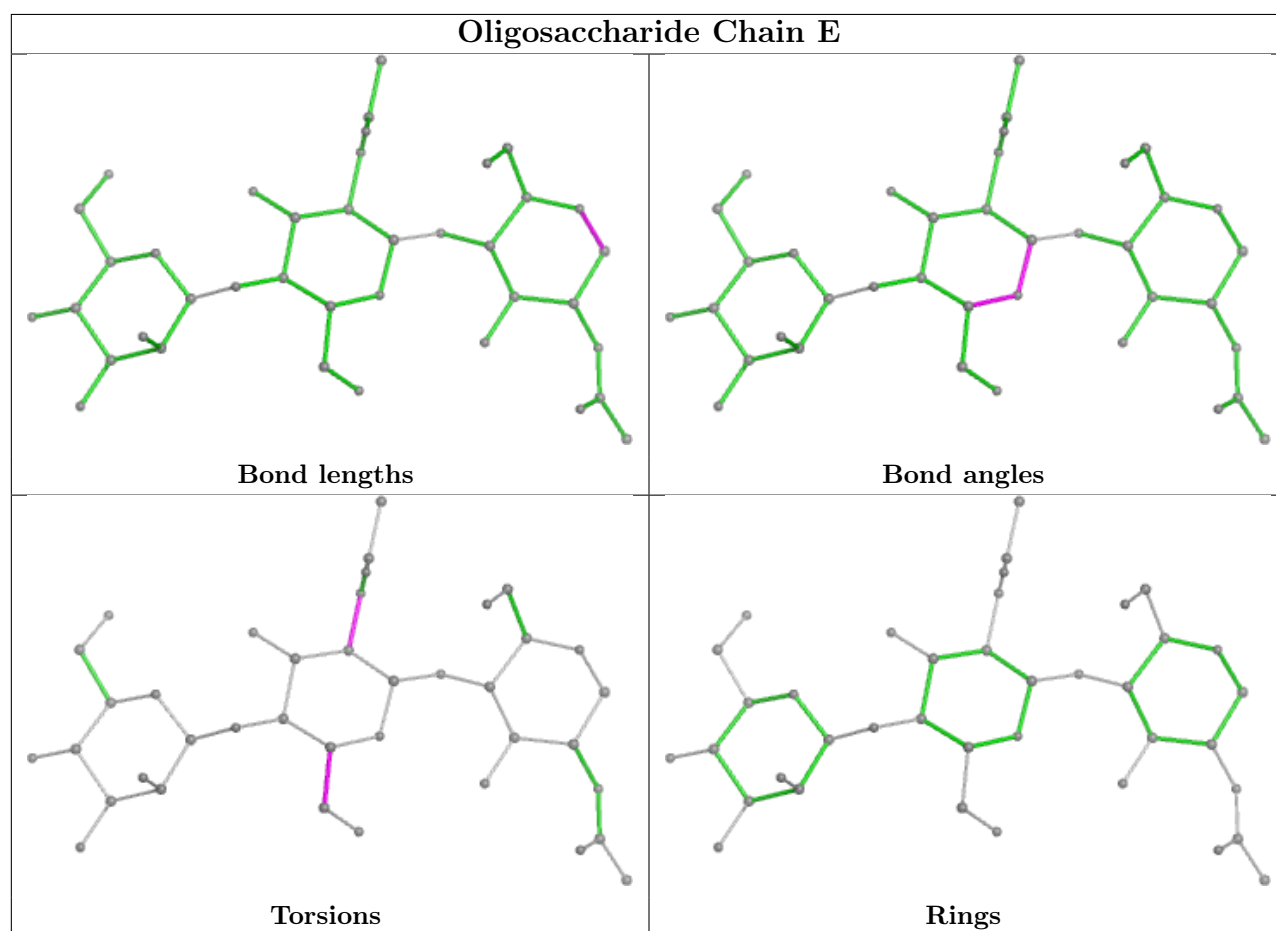
Mol	Chain	Res	Type	Atoms
2	L	2	NAG	C4-C5-C6-O6
2	L	2	NAG	O5-C5-C6-O6
2	L	1	NAG	O5-C5-C6-O6
2	L	1	NAG	C4-C5-C6-O6

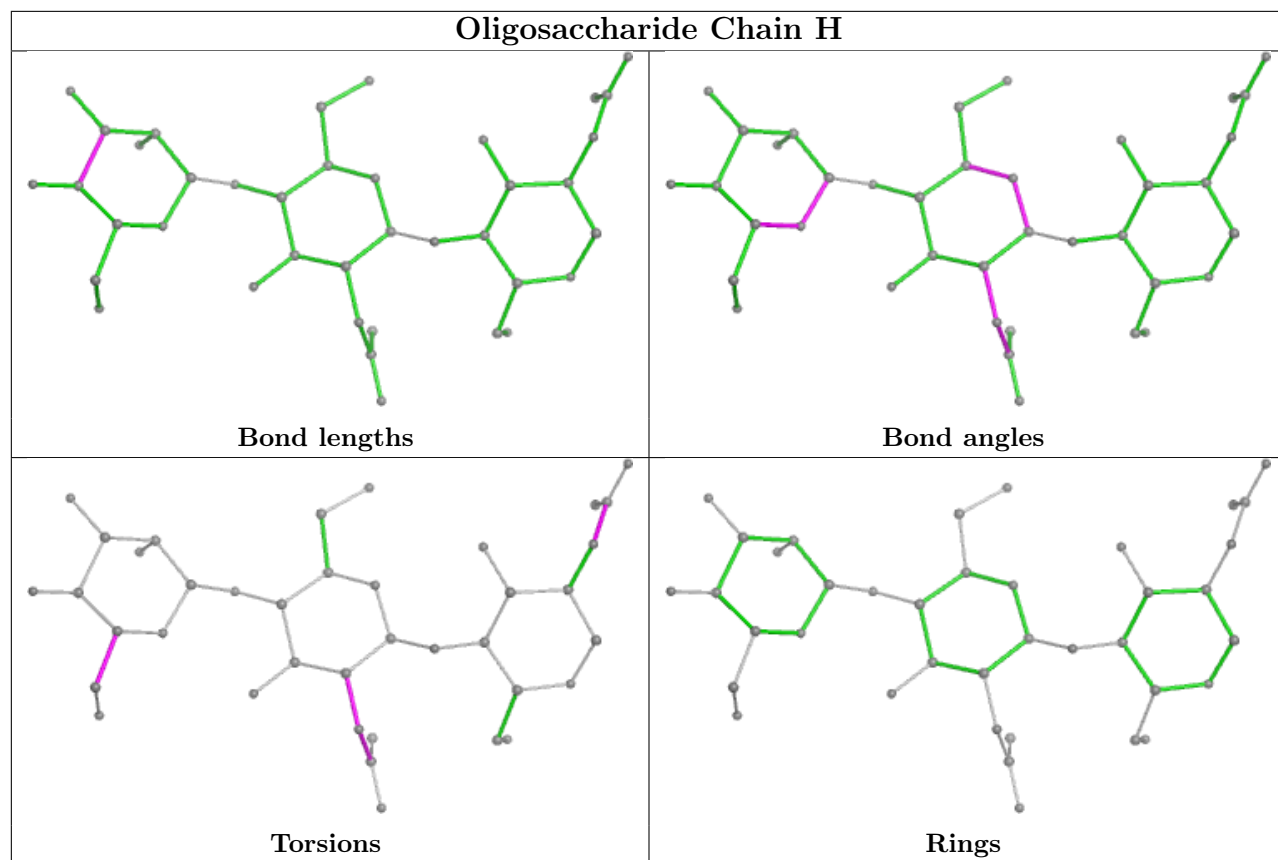
There are no ring outliers.

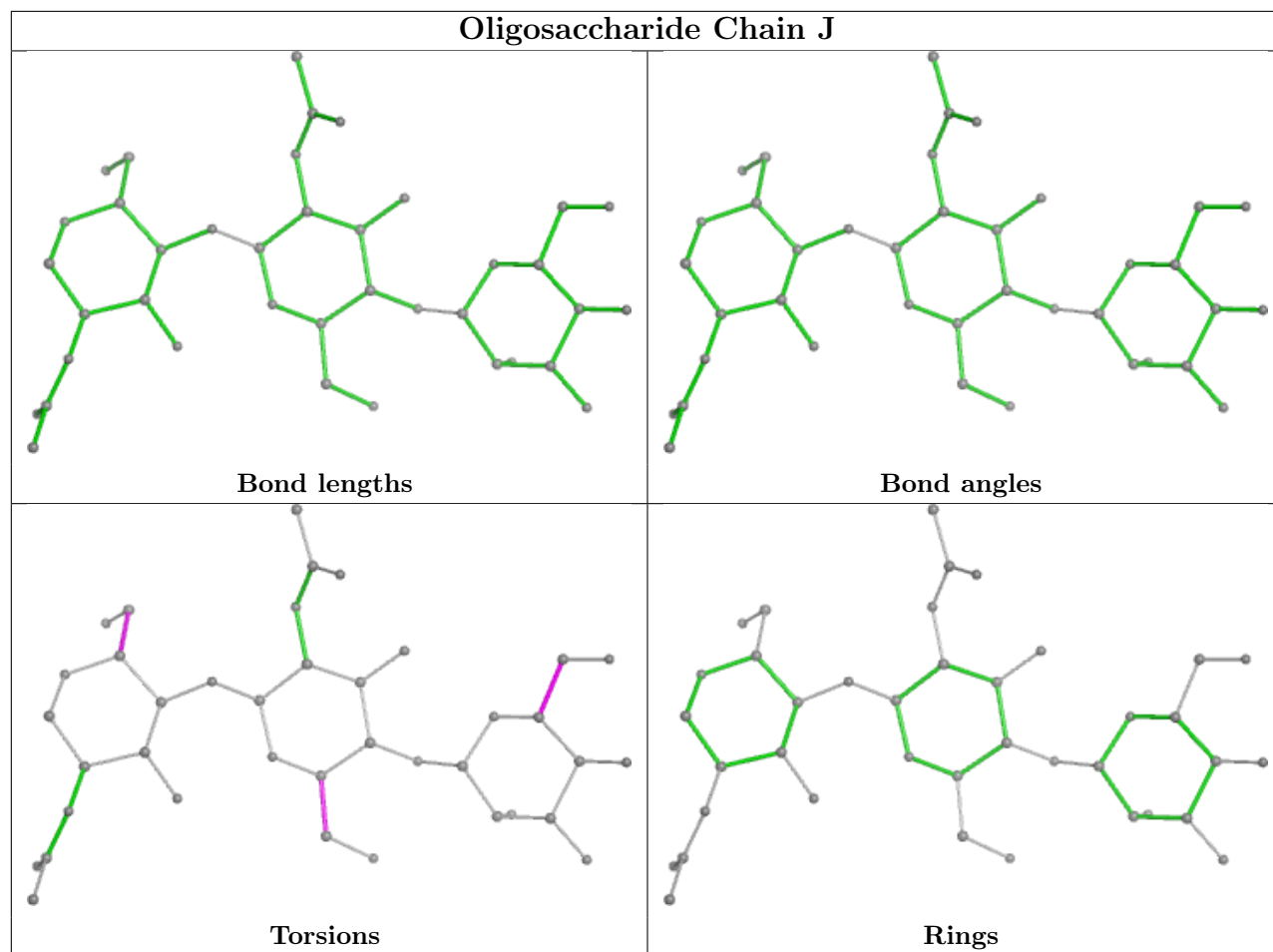
2 monomers are involved in 2 short contacts:

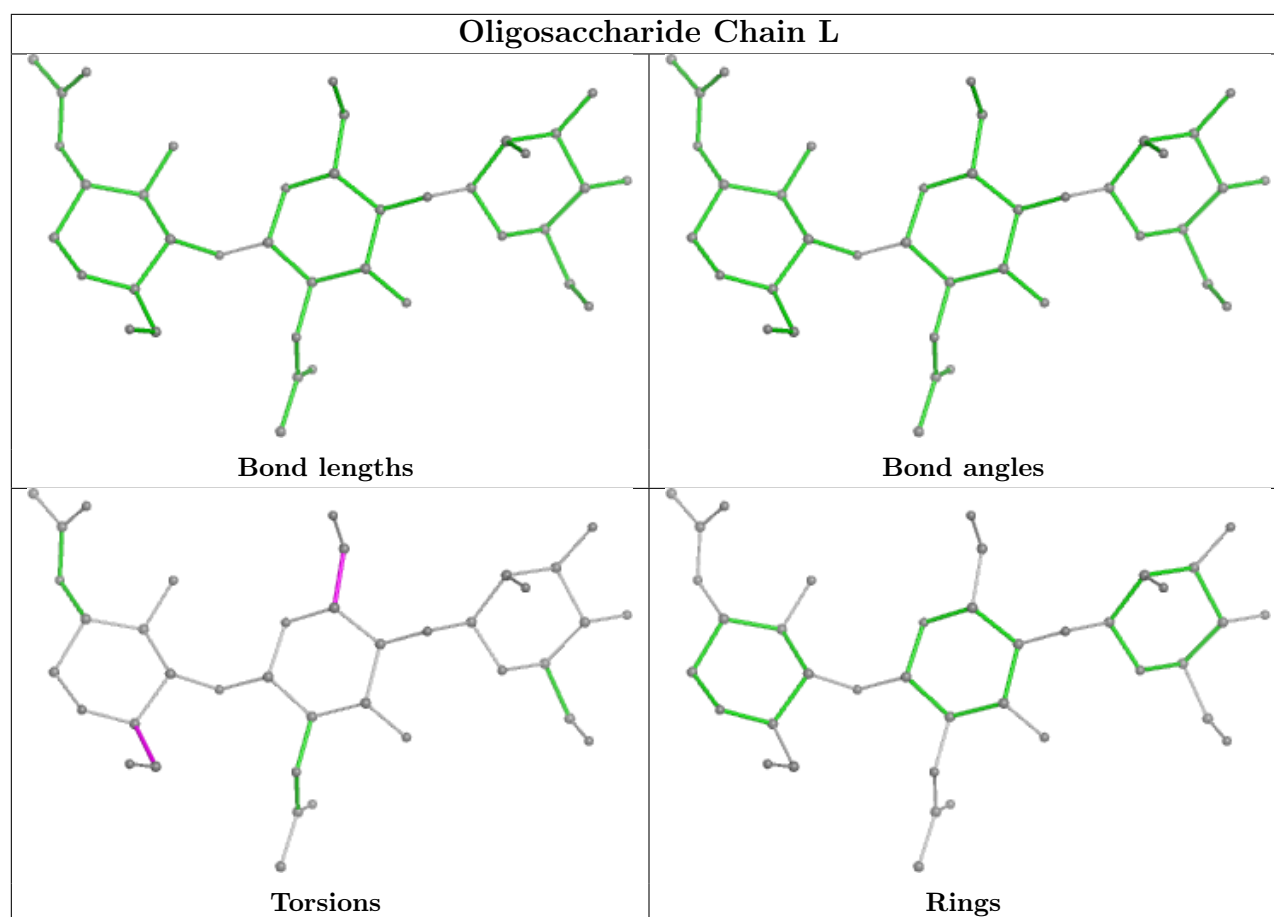
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1	NAG	1	0
2	H	2	NAG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.









## 5.6 Ligand geometry [i](#)

9 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
4	SO4	B	402	-	4,4,4	0.15	0	6,6,6	0.13	0
4	SO4	A	402	-	4,4,4	0.15	0	6,6,6	0.20	0
4	SO4	C	402	-	4,4,4	0.13	0	6,6,6	0.14	0
4	SO4	D	402	-	4,4,4	0.15	0	6,6,6	0.11	0
3	A1JJO	B	401	-	54,57,57	0.68	1 (1%)	59,82,82	1.06	4 (6%)
3	A1JJO	C	401	-	54,57,57	0.66	1 (1%)	59,82,82	0.90	5 (8%)
3	A1JJO	D	401	-	54,57,57	0.65	1 (1%)	59,82,82	0.94	4 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	A1JJO	A	401	-	54,57,57	0.68	1 (1%)	59,82,82	0.98	4 (6%)
4	SO4	C	403	-	4,4,4	0.14	0	6,6,6	0.38	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	A1JJO	B	401	-	-	12/39/66/66	0/5/5/5
3	A1JJO	D	401	-	-	14/39/66/66	0/5/5/5
3	A1JJO	C	401	-	-	14/39/66/66	0/5/5/5
3	A1JJO	A	401	-	-	13/39/66/66	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	A1JJO	C2-C1	2.21	1.54	1.52
3	B	401	A1JJO	C2-C1	2.17	1.54	1.52
3	C	401	A1JJO	C2-C1	2.15	1.54	1.52
3	D	401	A1JJO	C2-C1	2.14	1.54	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	A1JJO	O6-C11-C5	4.93	114.59	109.78
3	A	401	A1JJO	C2-C10-C26	4.80	122.92	115.36
3	D	401	A1JJO	C2-C10-C26	4.56	122.55	115.36
3	B	401	A1JJO	C2-C10-C26	4.10	121.81	115.36
3	C	401	A1JJO	C2-C10-C26	3.18	120.37	115.36

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

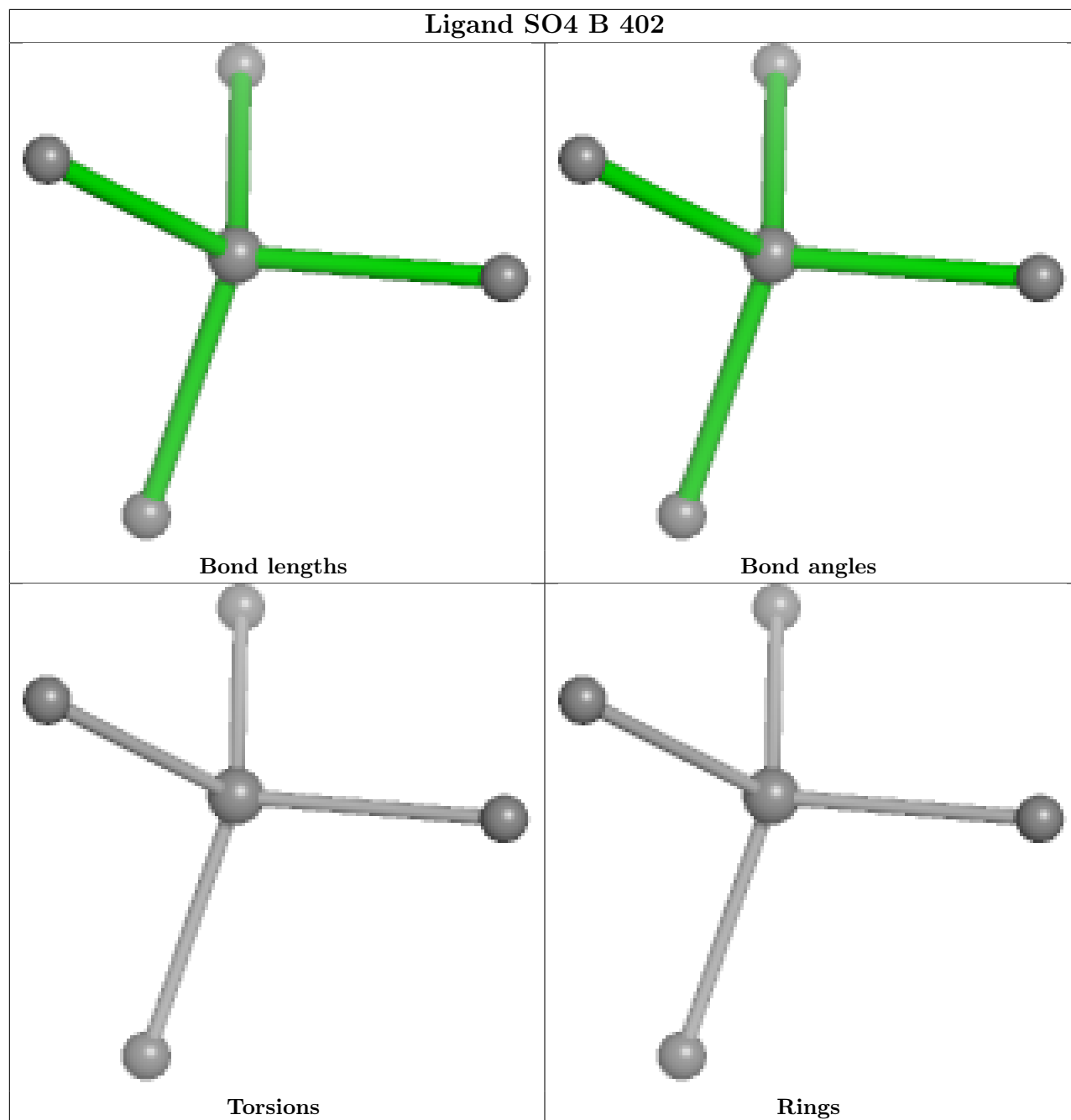
Mol	Chain	Res	Type	Atoms
3	A	401	A1JJO	C5-C11-C7-C6
3	A	401	A1JJO	C5-C11-C7-O3
3	A	401	A1JJO	O6-C11-C7-C6
3	A	401	A1JJO	O6-C11-C7-O3
3	A	401	A1JJO	C26-C10-C2-C1

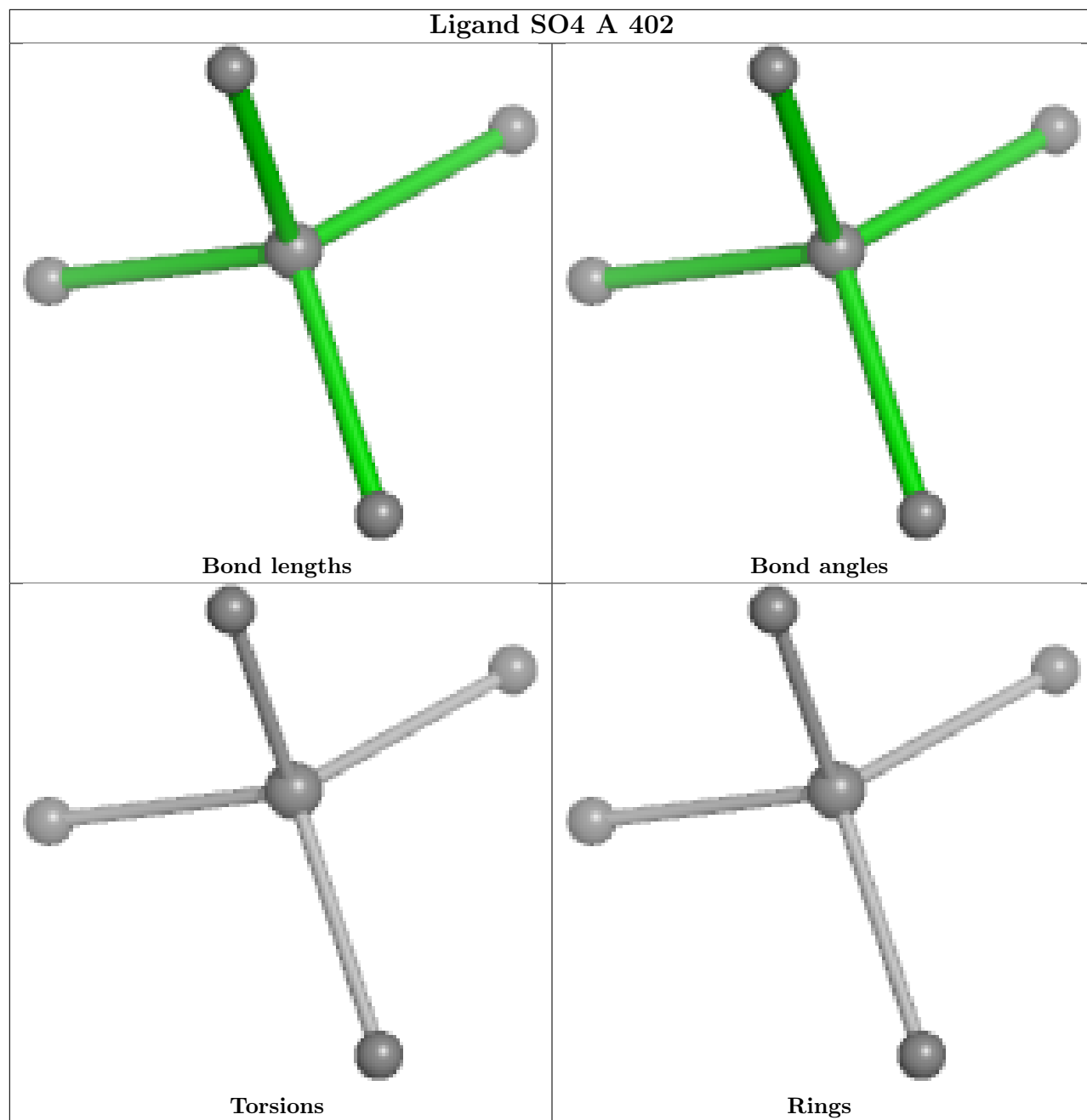
There are no ring outliers.

3 monomers are involved in 8 short contacts:

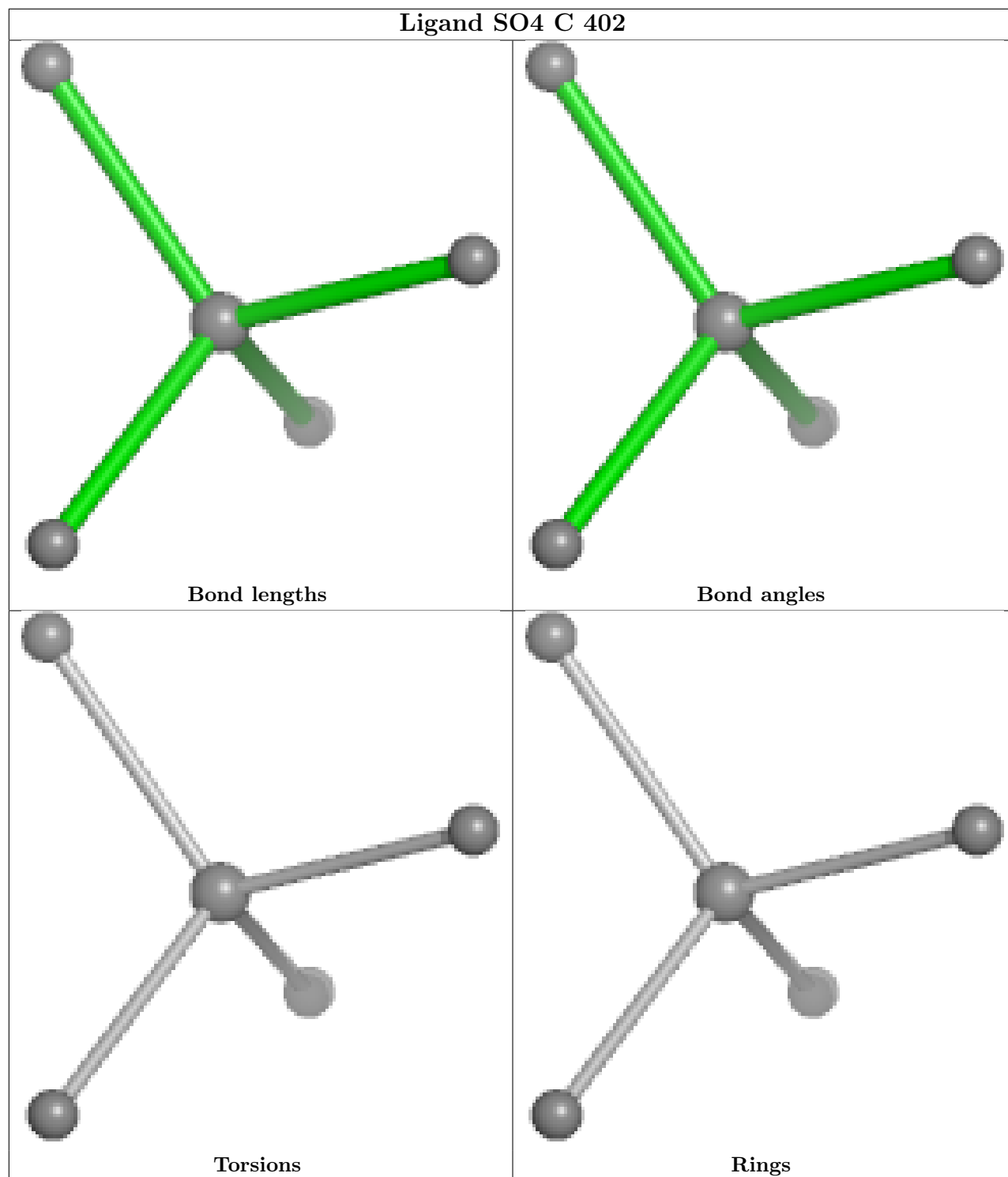
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	A1JJO	2	0
3	C	401	A1JJO	3	0
3	A	401	A1JJO	3	0

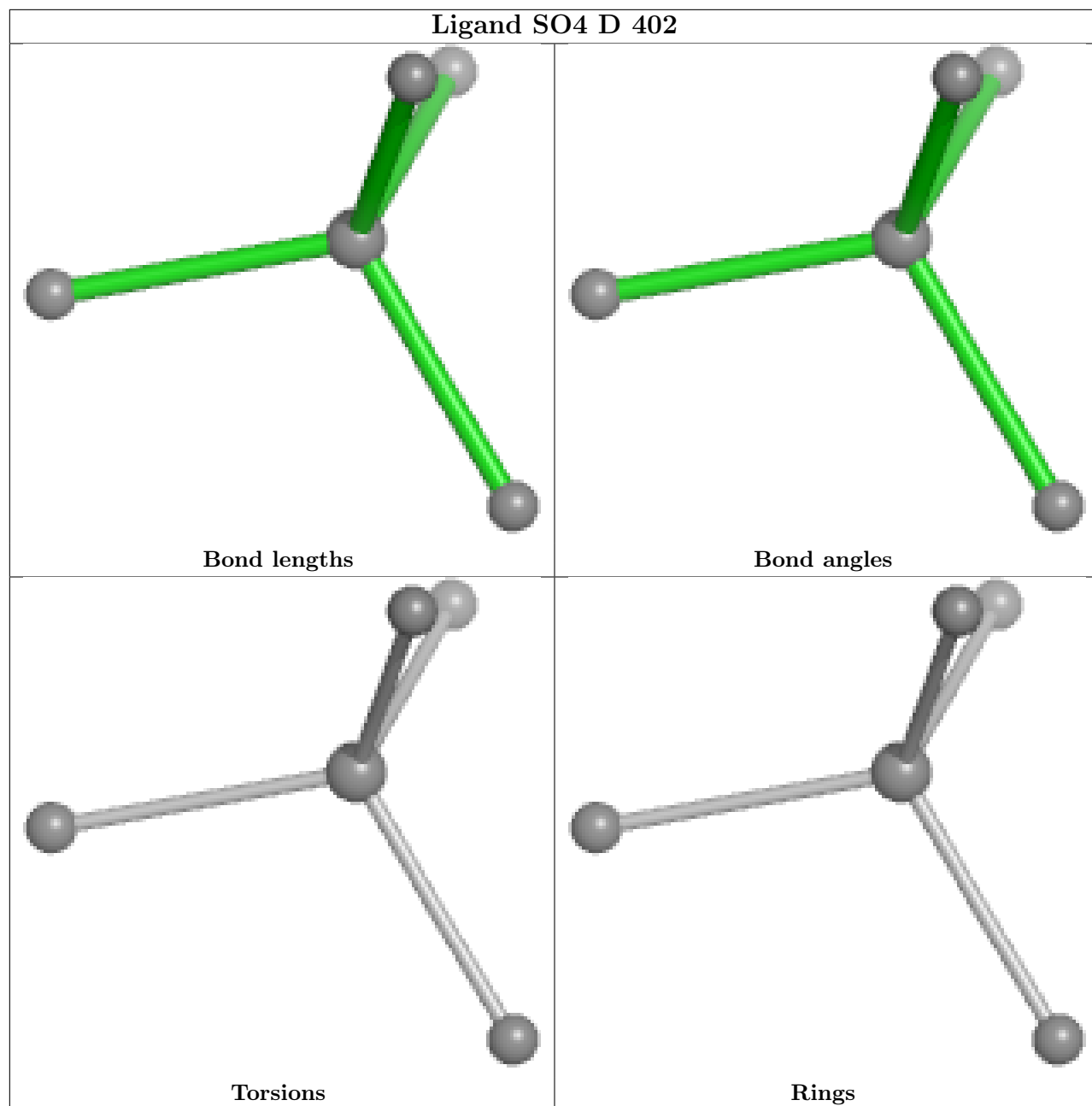
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



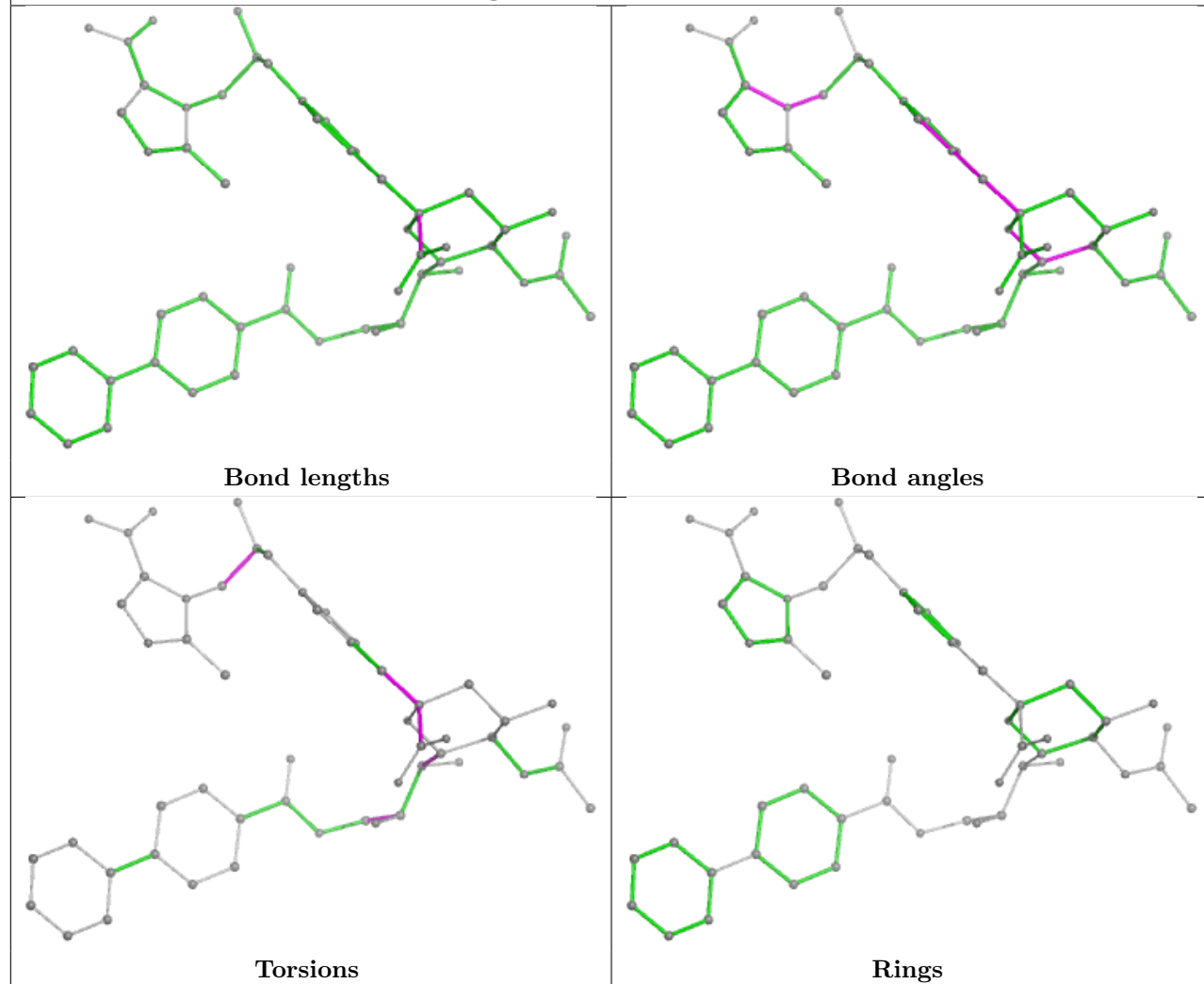




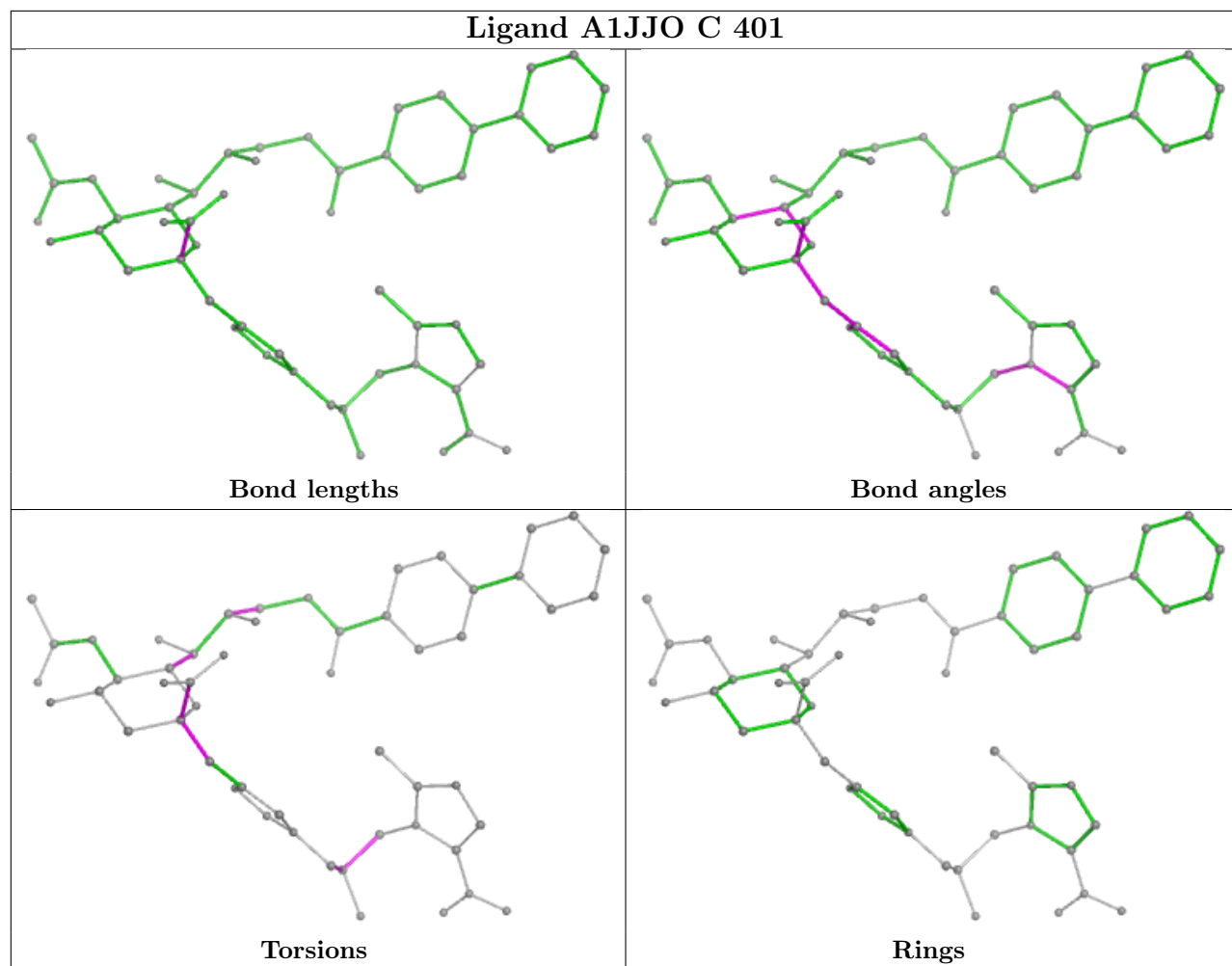




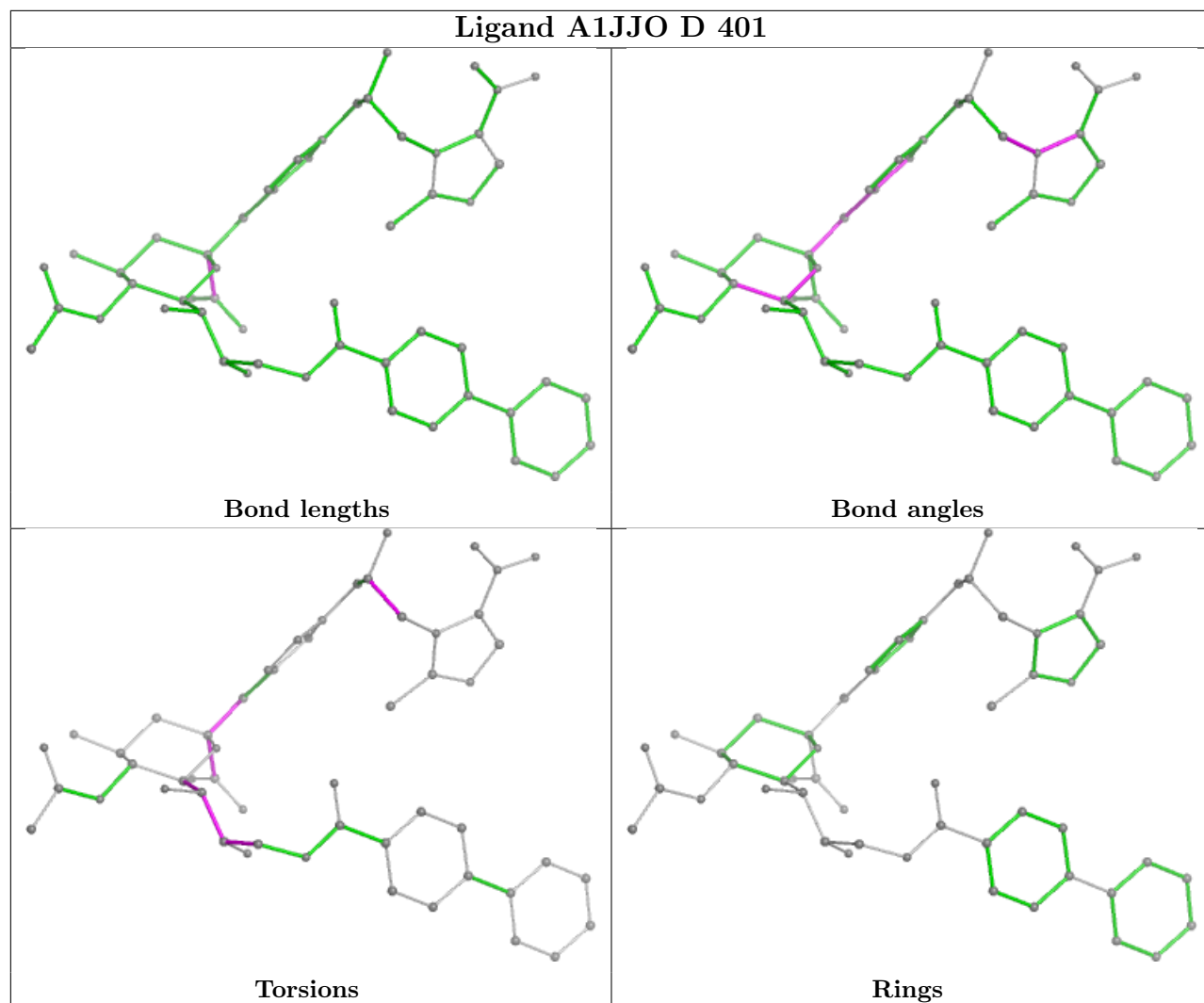
## Ligand A1JJO B 401



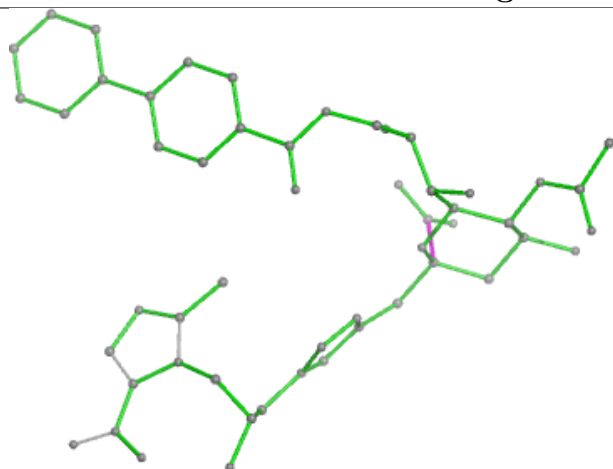
## Ligand A1JJO C 401



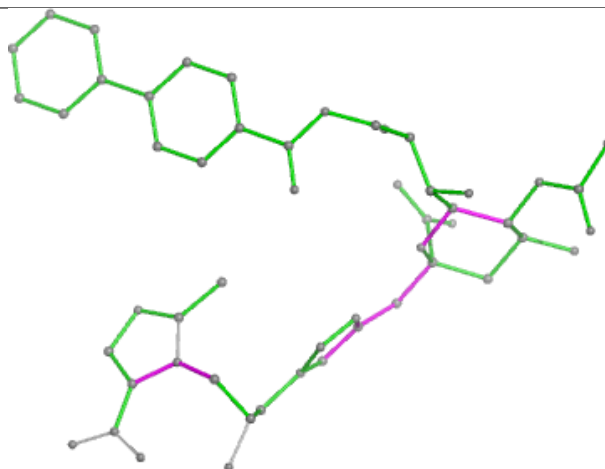
## Ligand A1JJO D 401



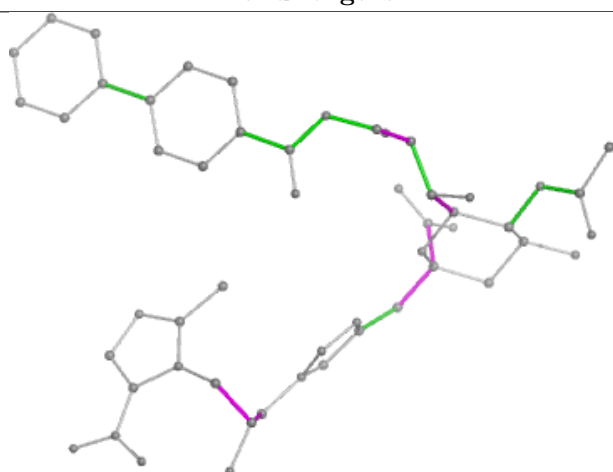
## Ligand A1JJO A 401



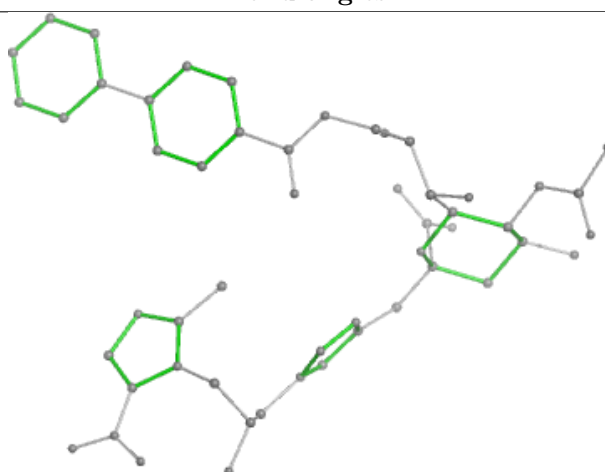
Bond lengths



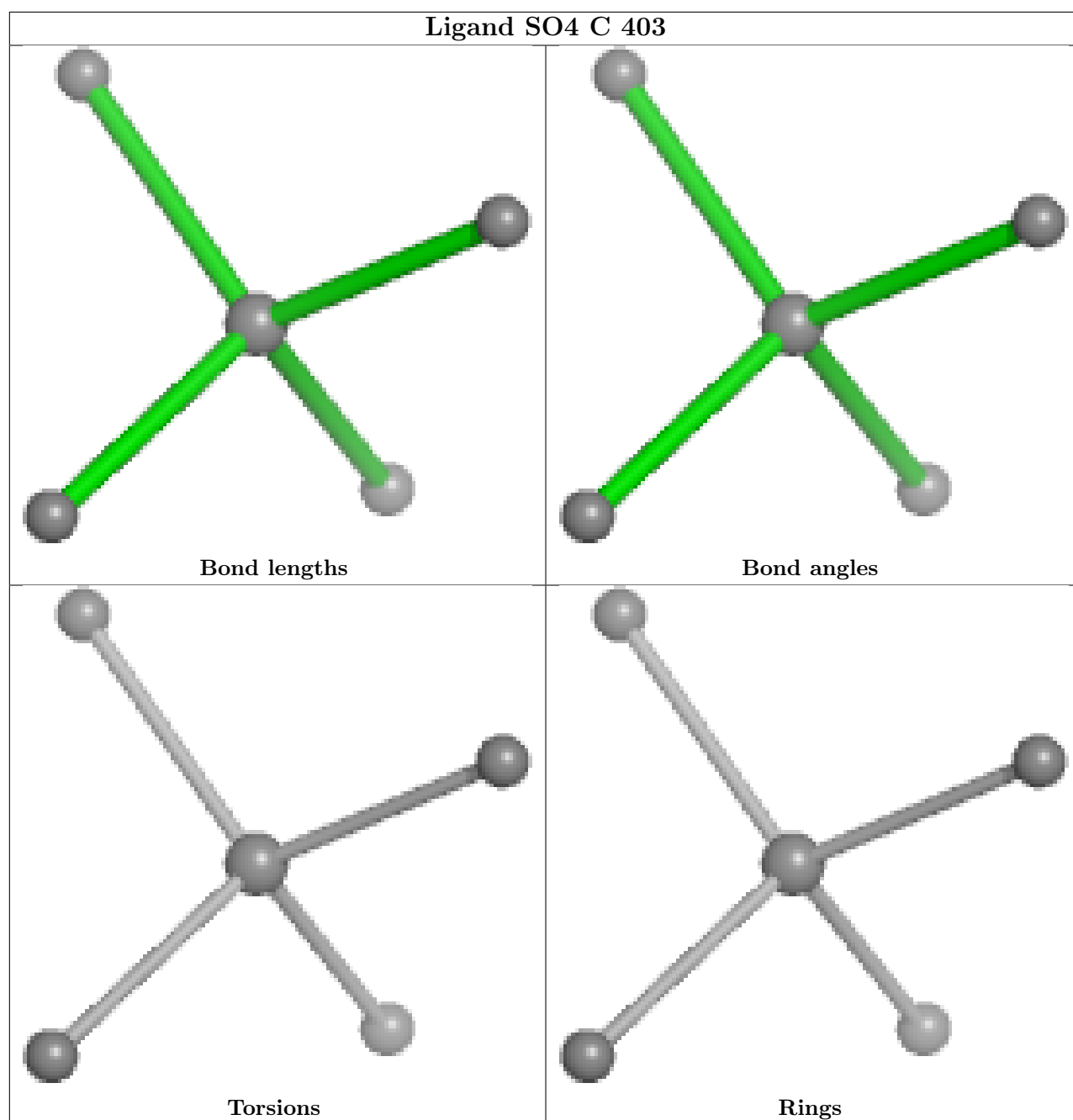
Bond angles



Torsions



Rings



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	307/324 (94%)	-0.13	4 (1%) 74 59	31, 55, 90, 116	0
1	B	306/324 (94%)	-0.07	2 (0%) 84 72	31, 56, 100, 126	0
1	C	286/324 (88%)	0.33	5 (1%) 69 53	44, 74, 128, 149	0
1	D	295/324 (91%)	0.06	3 (1%) 79 65	37, 65, 94, 118	0
All	All	1194/1296 (92%)	0.04	14 (1%) 76 60	31, 62, 113, 149	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	LYS	2.7
1	D	258	GLY	2.7
1	C	317	PRO	2.5
1	C	307	TYR	2.5
1	B	86	PRO	2.5

### 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](#)

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	BMA	H	3	11/12	0.58	0.13	47,50,63,73	0
2	BMA	E	3	11/12	0.84	0.09	45,53,58,58	0

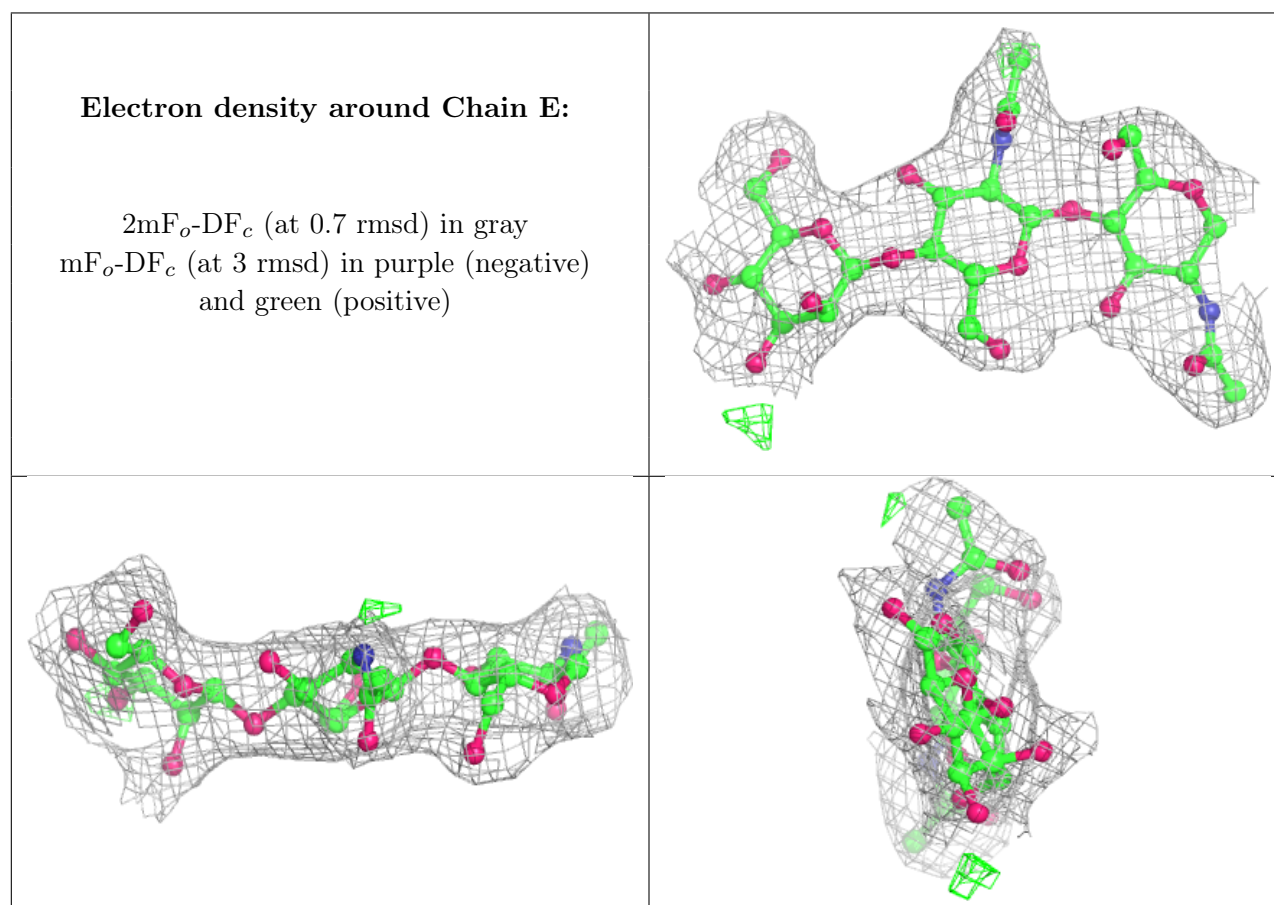
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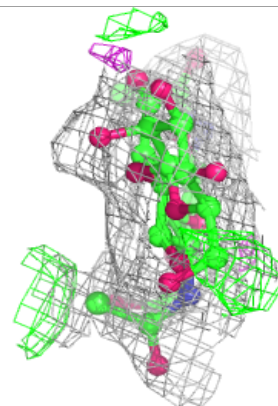
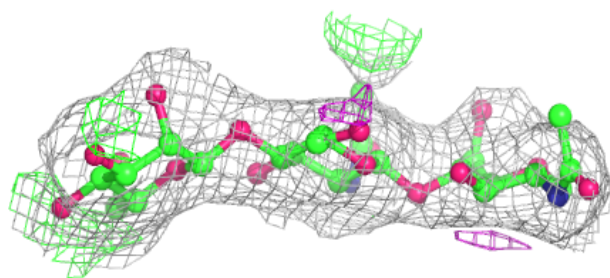
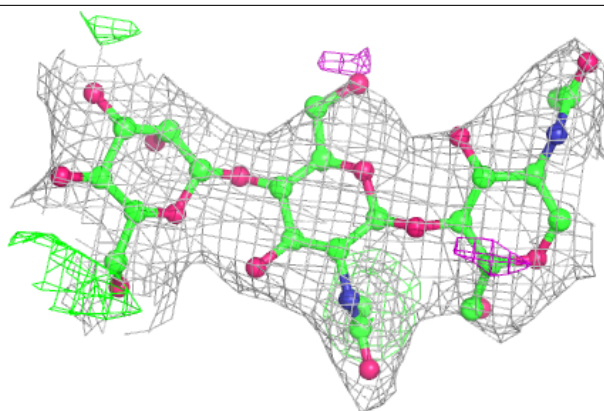
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	H	2	14/15	0.85	0.10	45,54,61,62	0
2	NAG	H	1	14/15	0.85	0.10	40,48,53,55	0
2	NAG	E	2	14/15	0.88	0.10	33,48,50,52	0
2	NAG	E	1	14/15	0.94	0.09	31,41,45,47	0
2	NAG	J	1	14/15	-	-	45,64,74,76	0
2	NAG	J	2	14/15	-	-	65,72,77,83	0
2	BMA	J	3	11/12	-	-	63,70,81,82	0
2	NAG	L	1	14/15	-	-	43,61,69,82	0
2	NAG	L	2	14/15	-	-	60,78,80,82	0
2	BMA	L	3	11/12	-	-	59,75,84,85	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

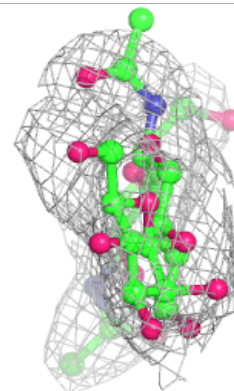
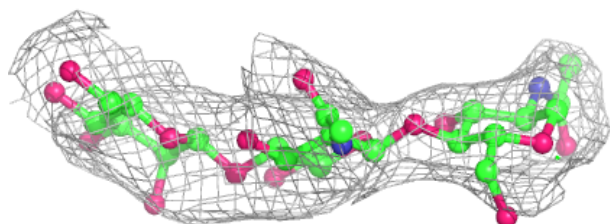
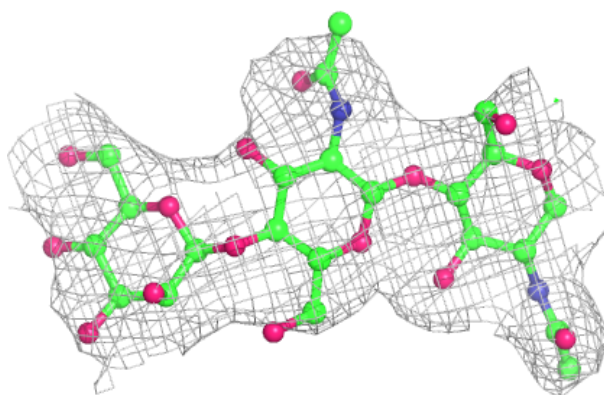


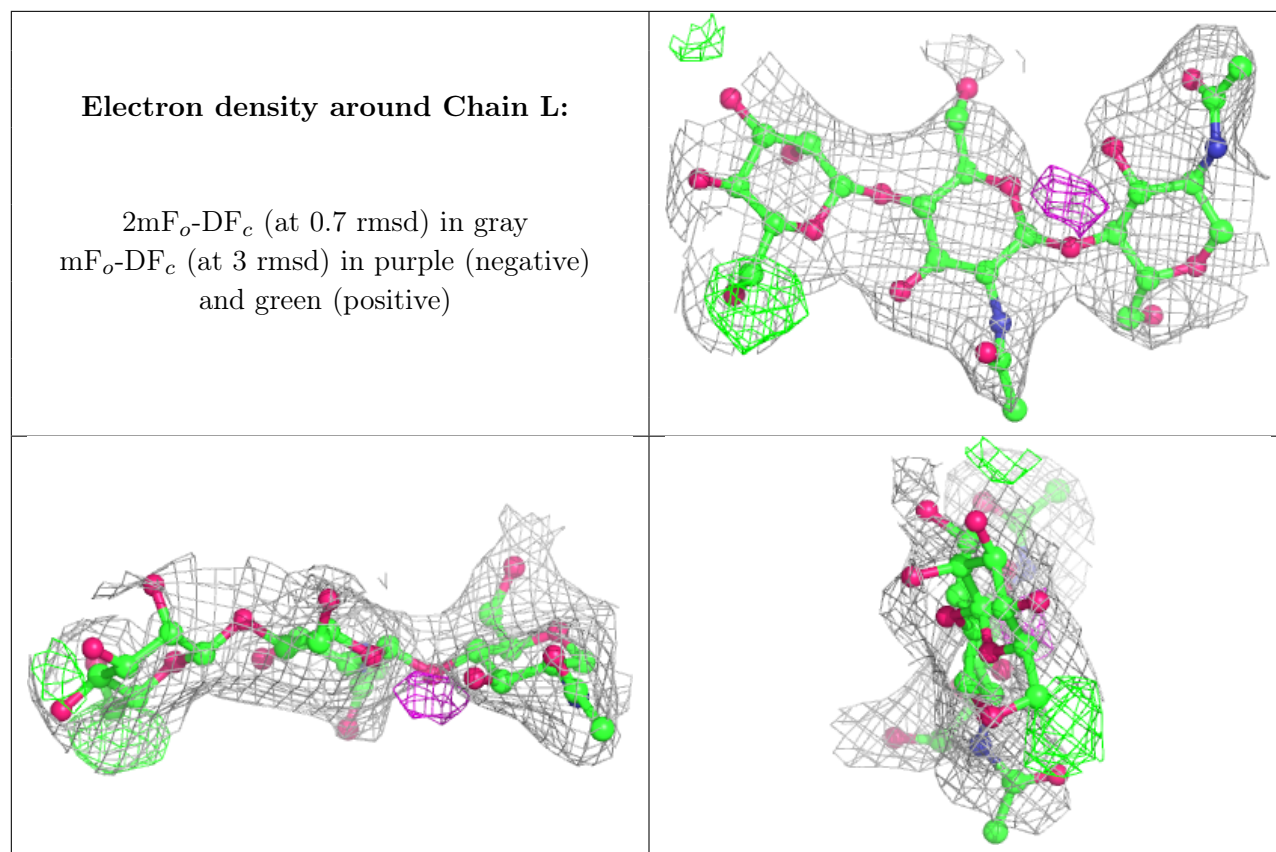
**Electron density around Chain H:**

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

**Electron density around Chain J:**

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





## 6.4 Ligands [i](#)

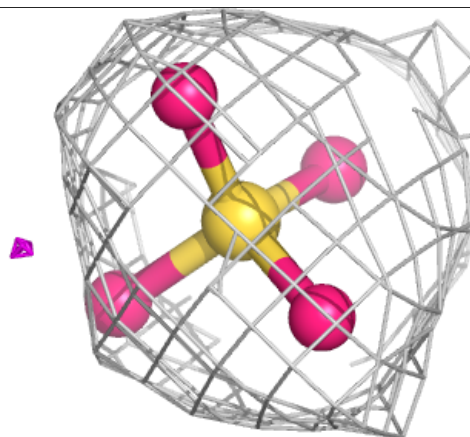
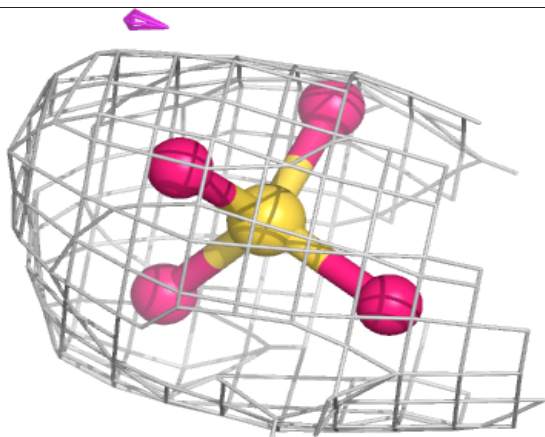
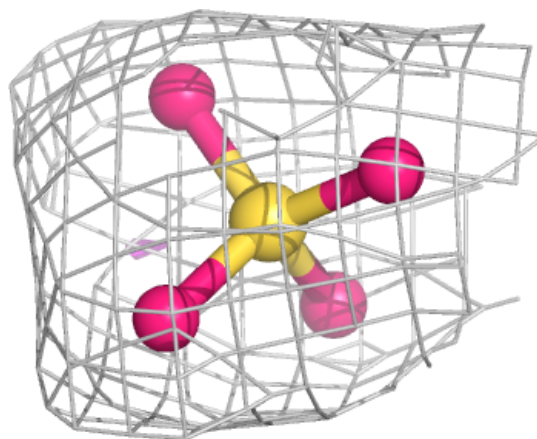
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 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	SO4	C	403	5/5	0.73	0.14	63,74,100,108	0
4	SO4	C	402	5/5	0.74	0.27	84,102,113,128	0
4	SO4	D	402	5/5	0.78	0.27	90,107,123,130	0
4	SO4	B	402	5/5	0.81	0.18	68,70,94,96	0
3	A1JJO	D	401	53/53	0.84	0.14	46,66,82,86	0
3	A1JJO	C	401	53/53	0.87	0.11	53,64,74,79	0
4	SO4	A	402	5/5	0.88	0.21	74,76,96,103	0
3	A1JJO	A	401	53/53	0.89	0.11	32,47,63,78	0
3	A1JJO	B	401	53/53	0.90	0.11	26,42,56,61	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.

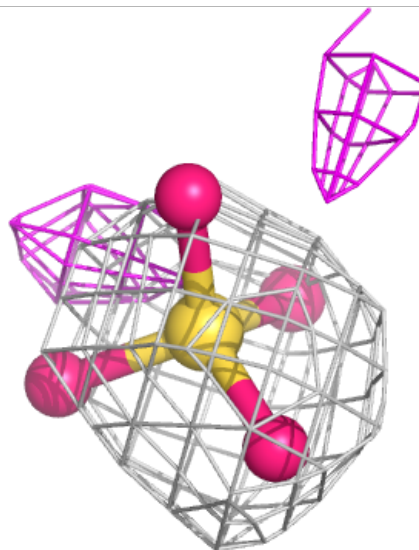
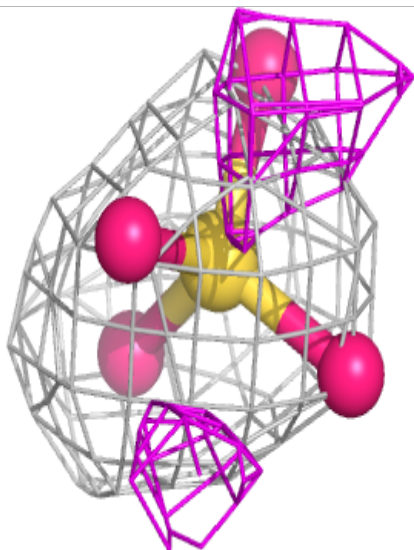
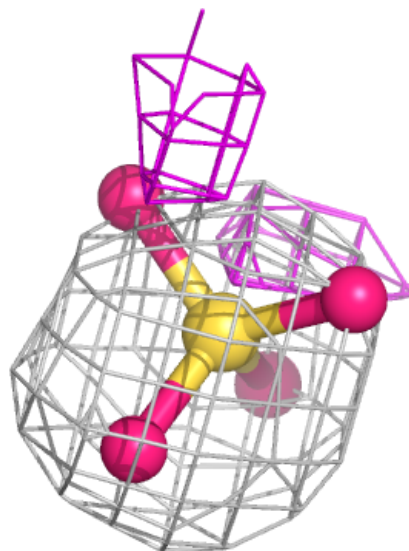
**Electron density around SO4 C 403:**

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



**Electron density around SO4 C 402:**

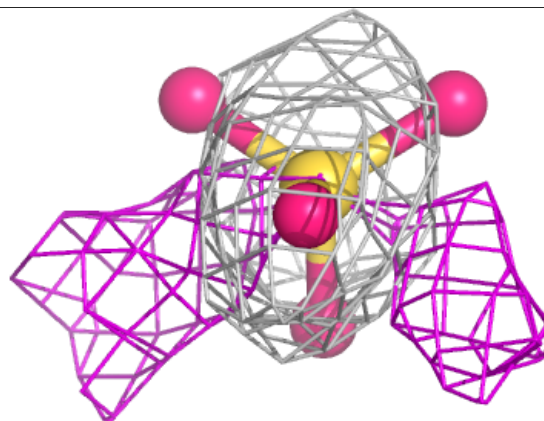
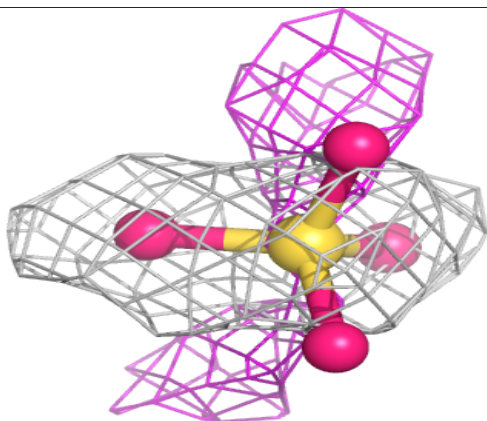
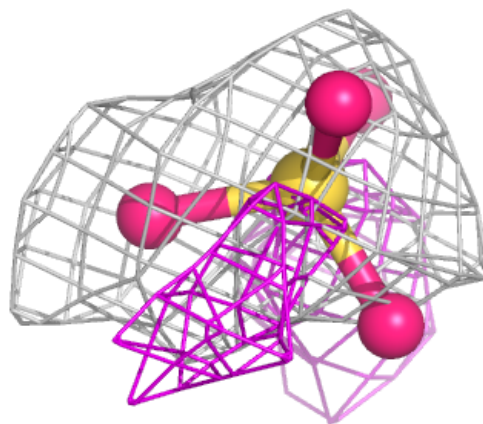
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



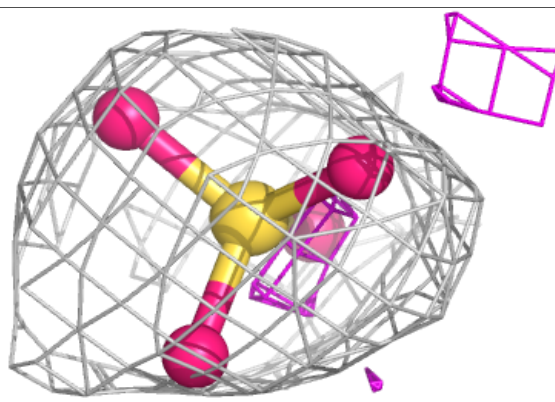
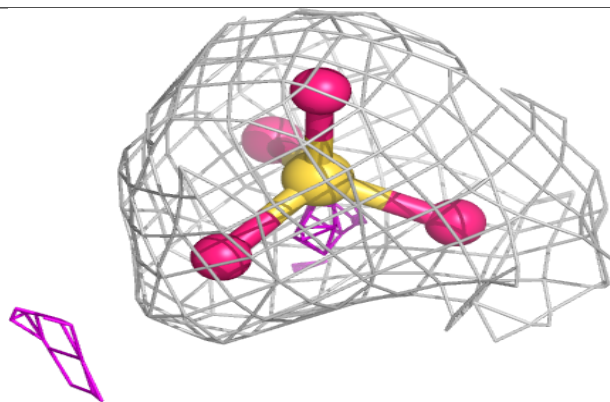
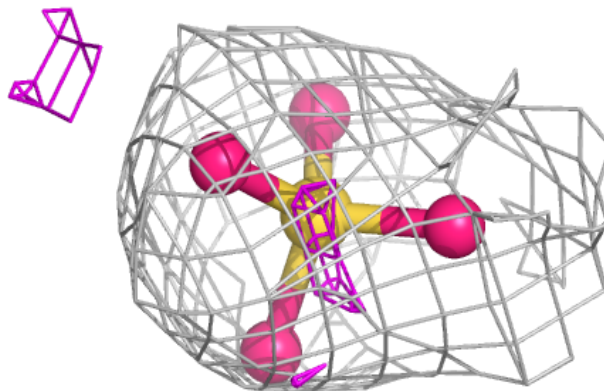


**Electron density around SO4 D 402:**

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

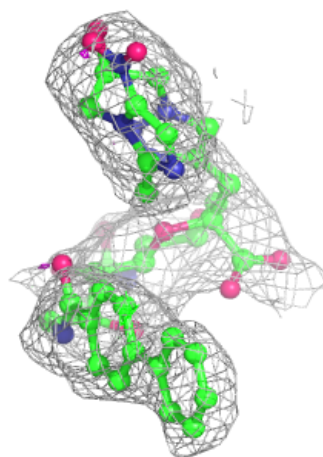
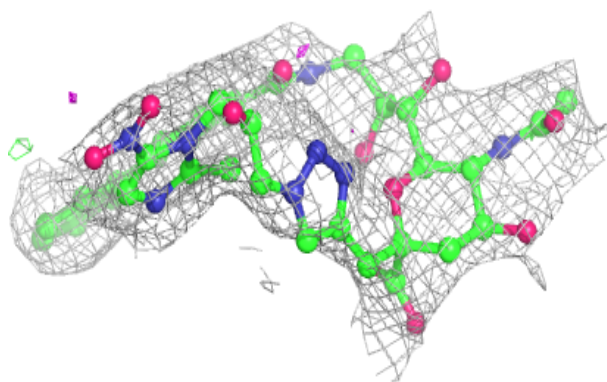
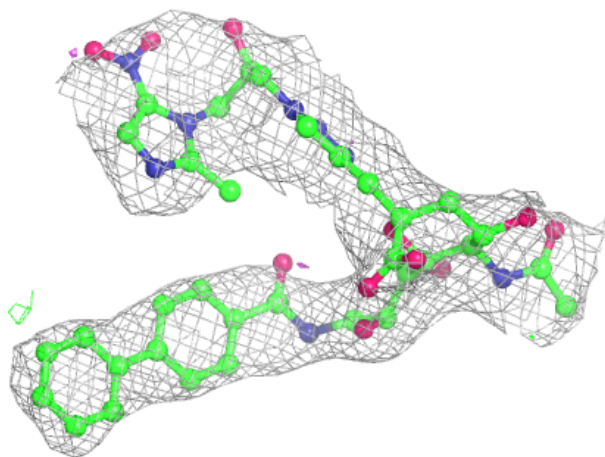
**Electron density around SO4 B 402:**

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



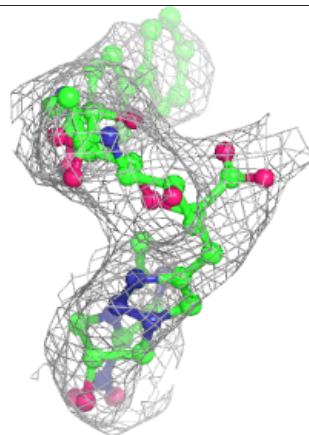
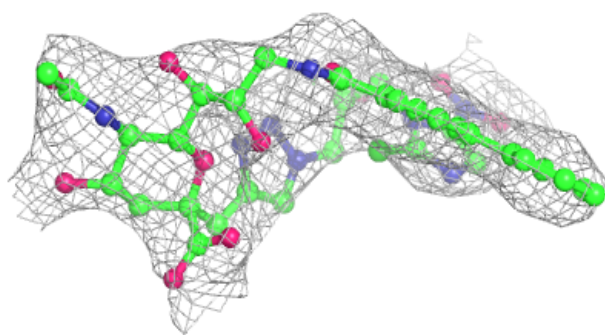
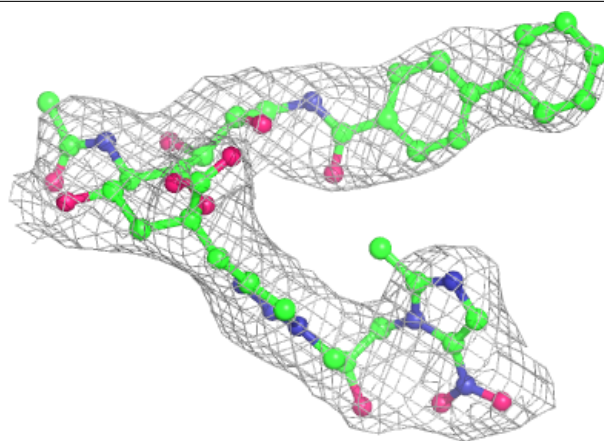
**Electron density around A1JJO D 401:**

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



**Electron density around A1JJO C 401:**

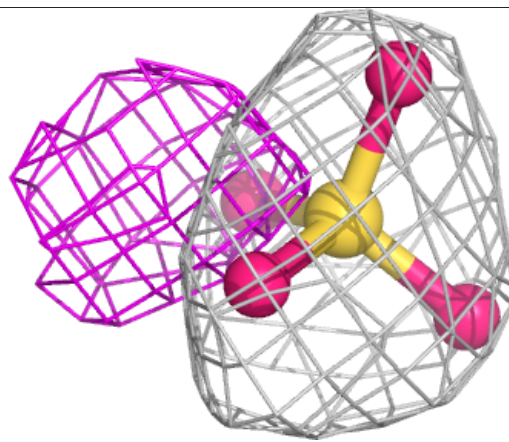
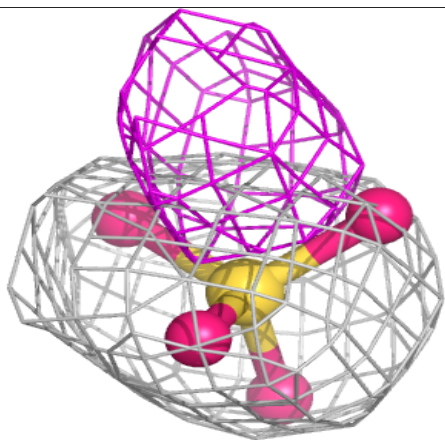
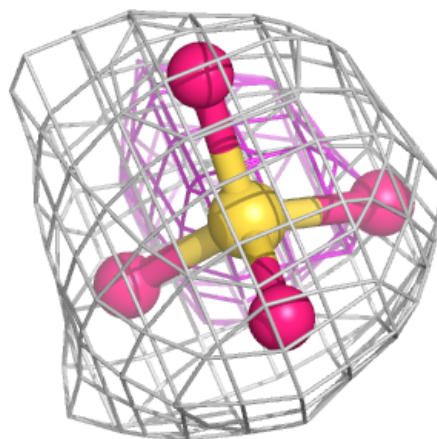
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





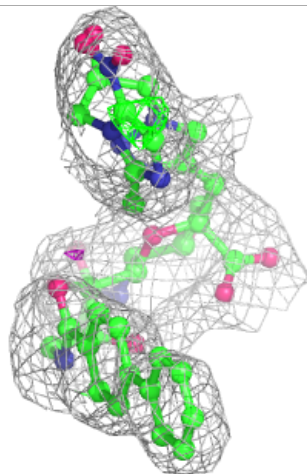
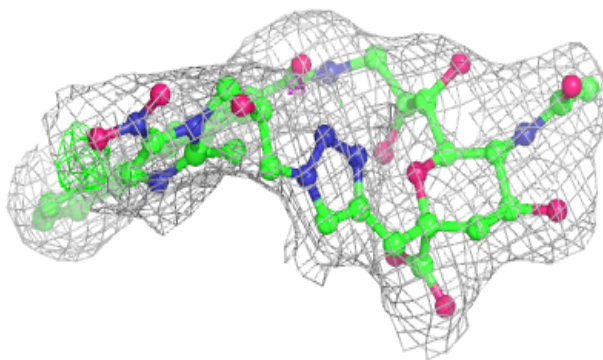
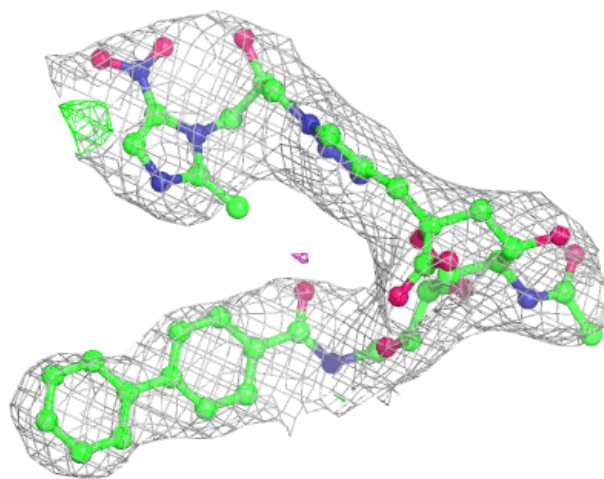
**Electron density around SO4 A 402:**

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



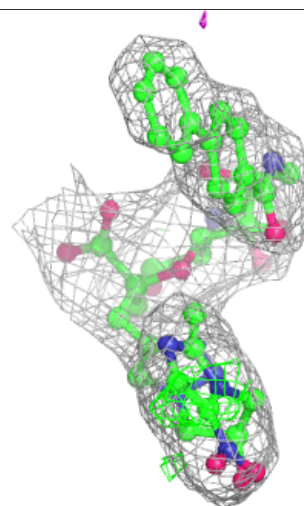
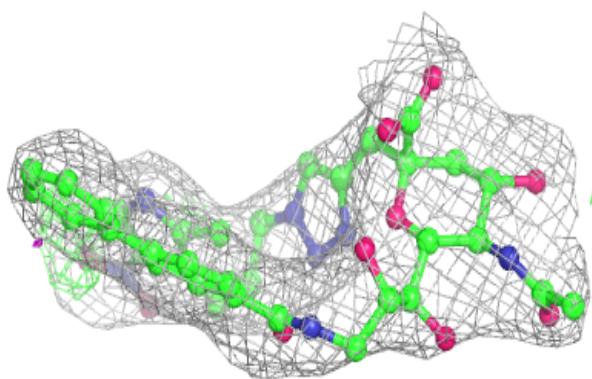
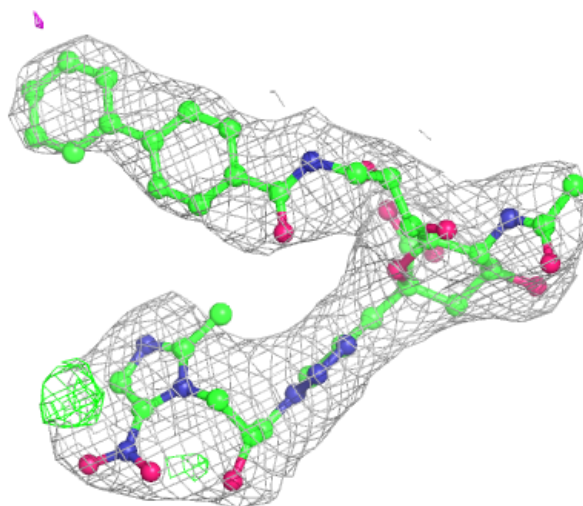
**Electron density around A1JJO A 401:**

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



**Electron density around A1JJO B 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.