



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 29, 2022 – 12:11 am GMT

PDB ID : 6TME
Title : Monomeric LRX8 in complex with RALF4
Authors : Moussu, S.; Caroline, C.; Santos-Fernandez, G.; Wehrle, S.; Grossniklaus, U.;
Santiago, J.
Deposited on : 2019-12-04
Resolution : 2.33 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.3
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

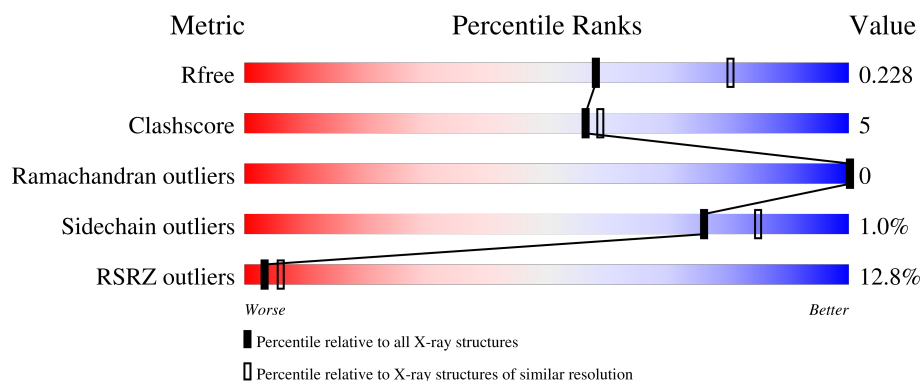
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	372	<div> <div>6%</div> <div>79%</div> <div>8%</div> <div>13%</div> </div>
1	B	372	<div> <div>15%</div> <div>76%</div> <div>12%</div> <div>13%</div> </div>
2	C	50	<div> <div>12%</div> <div>80%</div> <div>14%</div> <div>6%</div> </div>
2	D	50	<div> <div>22%</div> <div>80%</div> <div>12%</div> <div>8%</div> </div>
3	E	2	<div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	2	<div><div></div><div>50%</div><div></div><div>50%</div></div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	F	2	-	-	-	X
4	NAG	B	501	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6090 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 Pollen-specific leucine-rich repeat extensin-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	324	Total	C	N	O	S	0	0	0
			2494	1597	411	474	12			
1	B	324	Total	C	N	O	S	0	0	0
			2456	1574	402	468	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	MET	-	initiating methionine	UNP Q9LJ64
A	30	GLU	-	expression tag	UNP Q9LJ64
A	133	PHE	ALA	conflict	UNP Q9LJ64
B	29	MET	-	initiating methionine	UNP Q9LJ64
B	30	GLU	-	expression tag	UNP Q9LJ64
B	133	PHE	ALA	conflict	UNP Q9LJ64

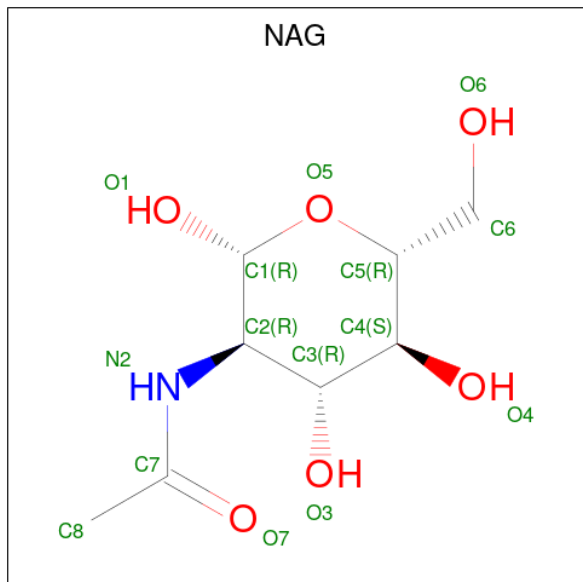
- Molecule 2 is a protein called Protein RALF-like 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	47	Total	C	N	O	S	0	0	0
			389	235	85	65	4			
2	D	46	Total	C	N	O	S	0	0	0
			372	226	78	64	4			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(3-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

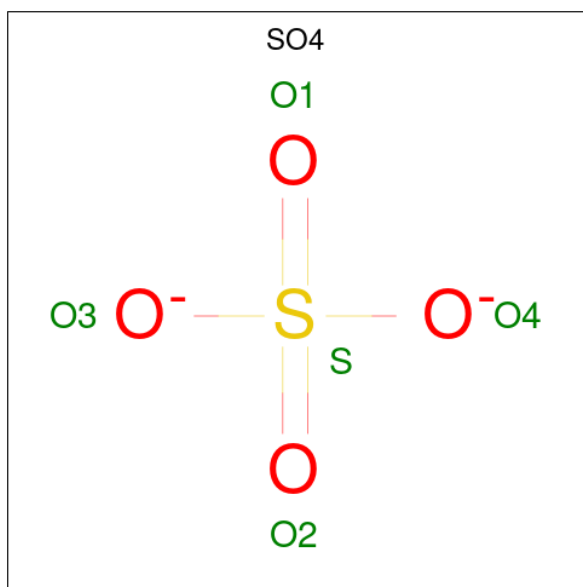
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



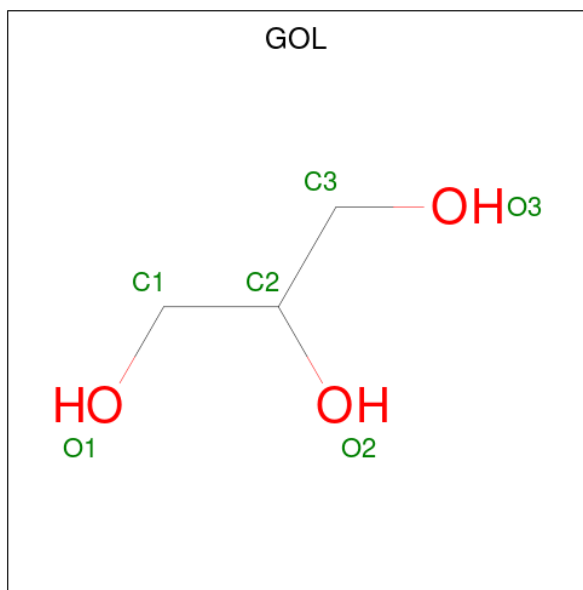
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			13	8	1	4		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



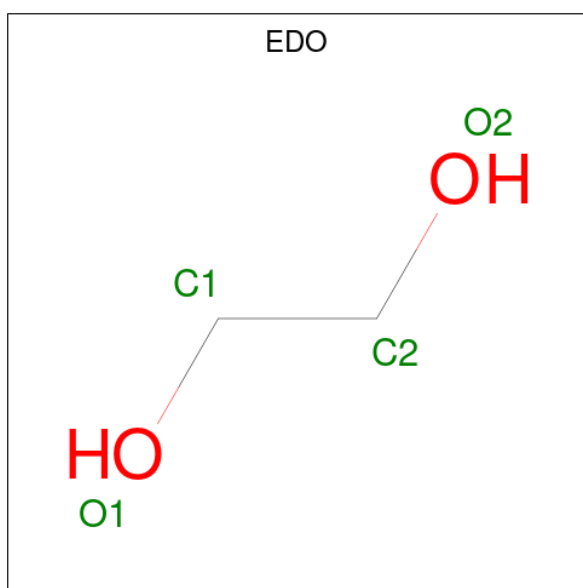
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	104	Total O 104 104	0	0
8	B	75	Total O 75 75	0	0

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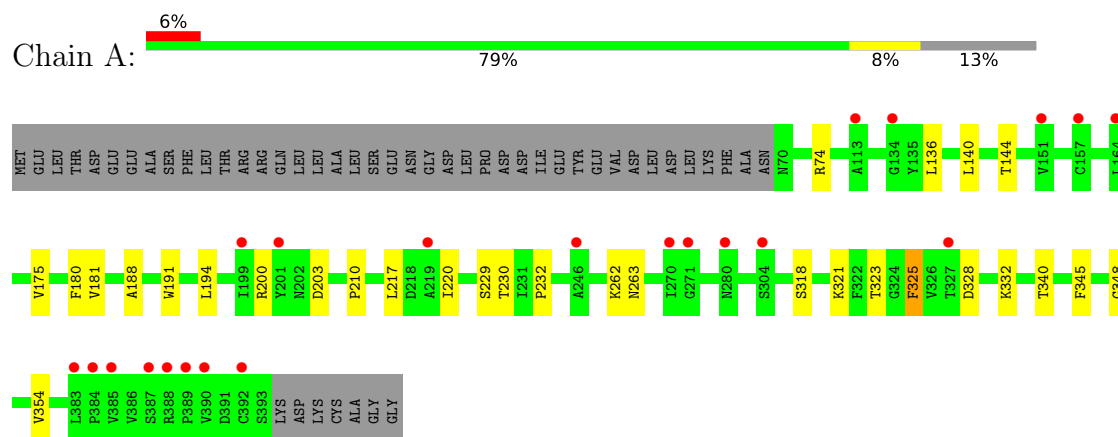
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	9	Total	O	0	0
			9	9		
8	D	8	Total	O	0	0
			8	8		

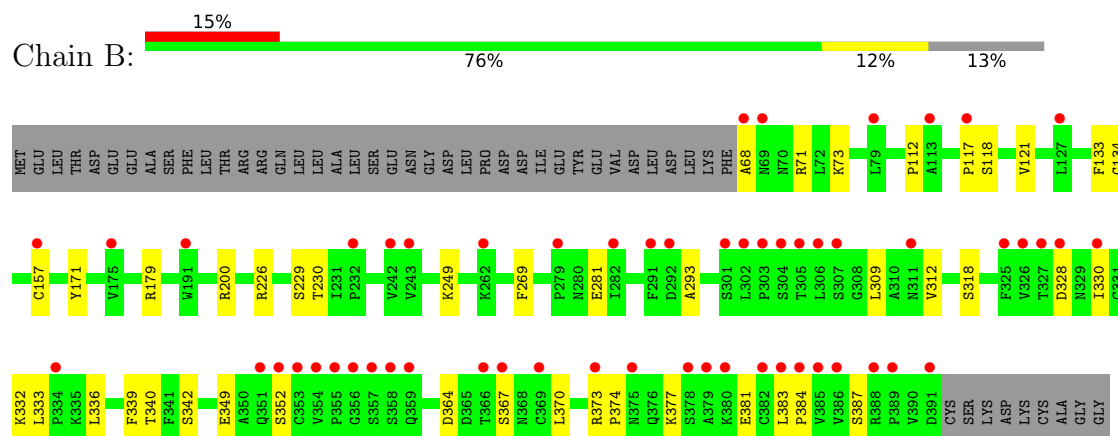
3 Residue-property plots [i](#)

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.

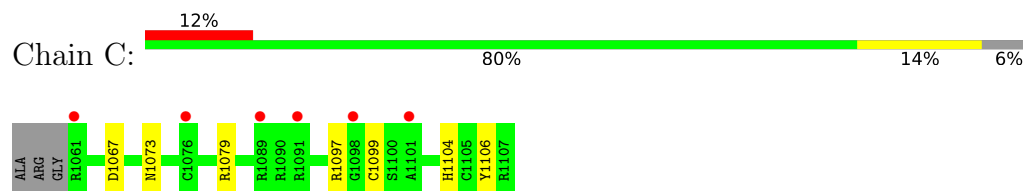
- Molecule 1: Pollen-specific leucine-rich repeat extensin-like protein 1



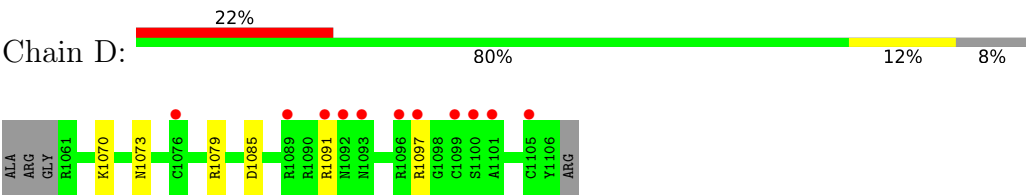
- Molecule 1: Pollen-specific leucine-rich repeat extensin-like protein 1



- Molecule 2: Protein RALF-like 4



- Molecule 2: Protein RALF-like 4



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(3-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(3-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.81Å 65.54Å 83.70Å 72.12° 87.62° 68.36°	Depositor
Resolution (Å)	48.00 – 2.33 48.00 – 2.33	Depositor EDS
% Data completeness (in resolution range)	97.2 (48.00-2.33) 97.3 (48.00-2.33)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.32Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.172 , 0.229 0.171 , 0.228	Depositor DCC
R_{free} test set	2017 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6090	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.94% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, EDO, SO4, GOL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	0/2557	0.60	0/3481
1	B	0.42	0/2519	0.56	0/3437
2	C	0.39	0/397	0.57	0/531
2	D	0.40	0/380	0.50	0/510
All	All	0.44	0/5853	0.58	0/7959

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	2494	0	2402	19	0
1	B	2456	0	2329	31	0
2	C	389	0	367	5	0
2	D	372	0	343	8	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
4	A	13	0	11	2	0
4	B	14	0	13	0	0
5	A	50	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	10	0	0	0	0
6	A	12	0	16	1	0
6	B	6	0	8	3	0
6	C	6	0	8	0	0
7	A	8	0	12	0	0
7	C	8	0	12	1	0
8	A	104	0	0	2	0
8	B	75	0	0	0	0
8	C	9	0	0	1	0
8	D	8	0	0	2	0
All	All	6090	0	5571	57	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.

All (57) 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:333:LEU:H	1:B:333:LEU:HD12	1.60	0.66
1:B:68:ALA:N	1:B:73:LYS:HZ3	1.94	0.66
1:A:328:ASP:HB2	1:A:332:LYS:HD3	1.80	0.64
1:B:229:SER:OG	1:B:230:THR:N	2.30	0.64
2:D:1097:ARG:NH1	8:D:1201:HOH:O	1.93	0.62
1:B:330:ILE:HA	1:B:333:LEU:HD11	1.81	0.61
1:B:171:TYR:CE2	2:D:1097:ARG:HD2	2.35	0.61
1:B:133:PHE:HE1	1:B:157:CYS:HG	1.49	0.59
1:B:226:ARG:HH12	6:B:504:GOL:H12	1.67	0.58
1:A:181:VAL:HG12	1:A:203:ASP:HB3	1.84	0.57
1:A:194:LEU:HG	1:A:217:LEU:HD21	1.88	0.56
1:B:249:LYS:NZ	6:B:504:GOL:H32	2.21	0.56
1:A:318:SER:HB3	1:A:340:THR:HG22	1.87	0.55
1:B:171:TYR:CZ	2:D:1097:ARG:HD2	2.41	0.55
1:A:321:LYS:NZ	8:A:602:HOH:O	2.40	0.54
1:B:328:ASP:O	1:B:332:LYS:N	2.40	0.52
1:B:340:THR:HG23	1:B:364:ASP:HB3	1.92	0.52
1:B:171:TYR:CE2	2:D:1097:ARG:CD	2.93	0.51
1:B:373:ARG:NE	1:B:374:PRO:HD2	2.26	0.50
1:A:354:VAL:HG11	6:A:512:GOL:H32	1.93	0.50
2:D:1085:ASP:HB2	2:D:1097:ARG:HA	1.94	0.49
1:B:309:LEU:HB3	1:B:312:VAL:HB	1.95	0.48
1:B:281:GLU:OE1	1:B:281:GLU:N	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:ARG:NH2	2:D:1073:ASN:O	2.46	0.48
1:B:318:SER:HA	1:B:342:SER:O	2.14	0.47
2:D:1070:LYS:HA	2:D:1070:LYS:HD2	1.61	0.47
8:A:675:HOH:O	2:C:1079:ARG:HD2	2.13	0.47
1:A:262:LYS:HA	4:A:501:NAG:H81	1.96	0.47
1:A:325:PHE:CE1	1:A:348:GLY:HA3	2.51	0.46
1:B:112:PRO:HB3	1:B:117:PRO:HA	1.98	0.46
1:B:367:SER:O	1:B:377:LYS:NZ	2.49	0.46
1:B:336:LEU:HD21	1:B:339:PHE:HB2	1.98	0.46
1:B:349:GLU:OE2	1:B:370:LEU:HD13	2.16	0.45
2:C:1104:HIS:NE2	7:C:1202:EDO:H21	2.31	0.45
1:A:136:LEU:HB3	1:A:140:LEU:HD12	1.99	0.45
1:A:203:ASP:OD2	1:B:134:GLY:HA2	2.16	0.45
2:C:1067:ASP:OD2	2:C:1106:TYR:OH	2.17	0.44
1:A:263:ASN:H	4:A:501:NAG:C8	2.30	0.44
1:A:217:LEU:HD13	1:A:220:ILE:HG12	2.00	0.44
1:A:210:PRO:HB3	1:A:232:PRO:HB3	2.00	0.44
1:B:249:LYS:HZ2	6:B:504:GOL:H32	1.83	0.43
1:A:175:VAL:HB	1:A:180:PHE:CE2	2.53	0.43
2:D:1079:ARG:HD3	8:D:1202:HOH:O	2.18	0.43
1:A:74:ARG:NH2	1:A:144:THR:OG1	2.52	0.43
1:B:71:ARG:HD3	1:B:121:VAL:HG12	2.00	0.43
1:B:383:LEU:O	1:B:387:SER:HB2	2.20	0.42
1:A:188:ALA:HA	1:A:191:TRP:CE3	2.56	0.41
1:A:200:ARG:NH2	2:C:1073:ASN:O	2.53	0.41
1:B:330:ILE:CA	1:B:333:LEU:HD11	2.49	0.41
1:B:373:ARG:CZ	1:B:374:PRO:HD2	2.50	0.41
1:B:373:ARG:HE	1:B:373:ARG:HB3	1.57	0.41
1:B:381:GLU:O	1:B:384:PRO:HD2	2.20	0.41
1:A:323:THR:HG22	1:A:345:PHE:HB2	2.01	0.41
1:A:229:SER:HB3	1:A:230:THR:H	1.66	0.41
2:C:1073:ASN:HB2	8:C:1306:HOH:O	2.19	0.41
1:B:157:CYS:SG	1:B:179:ARG:HB2	2.62	0.40
1:B:269:PHE:HB2	1:B:293:ALA:HA	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	322/372 (87%)	302 (94%)	20 (6%)	0	100	100
1	B	322/372 (87%)	295 (92%)	27 (8%)	0	100	100
2	C	45/50 (90%)	41 (91%)	4 (9%)	0	100	100
2	D	44/50 (88%)	41 (93%)	3 (7%)	0	100	100
All	All	733/844 (87%)	679 (93%)	54 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	279/326 (86%)	278 (100%)	1 (0%)	91	95
1	B	269/326 (82%)	267 (99%)	2 (1%)	84	90
2	C	39/43 (91%)	37 (95%)	2 (5%)	24	29
2	D	37/43 (86%)	36 (97%)	1 (3%)	44	55
All	All	624/738 (85%)	618 (99%)	6 (1%)	76	85

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	325	PHE
1	B	118	SER

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Mol	Chain	Res	Type
1	B	352	SER
2	C	1097	ARG
2	C	1099	CYS
2	D	1091	ARG

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	273	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

4 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	$\# Z > 2$
3	NAG	E	1	1,3	14,14,15	0.21	0	17,19,21	1.18	1 (5%)
3	NAG	E	2	3	14,14,15	0.28	0	19,19,21	0.38	0
3	NAG	F	1	1,3	14,14,15	0.38	0	17,19,21	1.19	1 (5%)
3	NAG	F	2	3	14,14,15	0.51	0	19,19,21	0.50	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	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/22/26	0/1/1/1
3	NAG	F	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/22/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1	NAG	C1-O5-C5	4.31	118.03	112.19
3	F	1	NAG	C1-O5-C5	4.17	117.84	112.19

There are no chirality outliers.

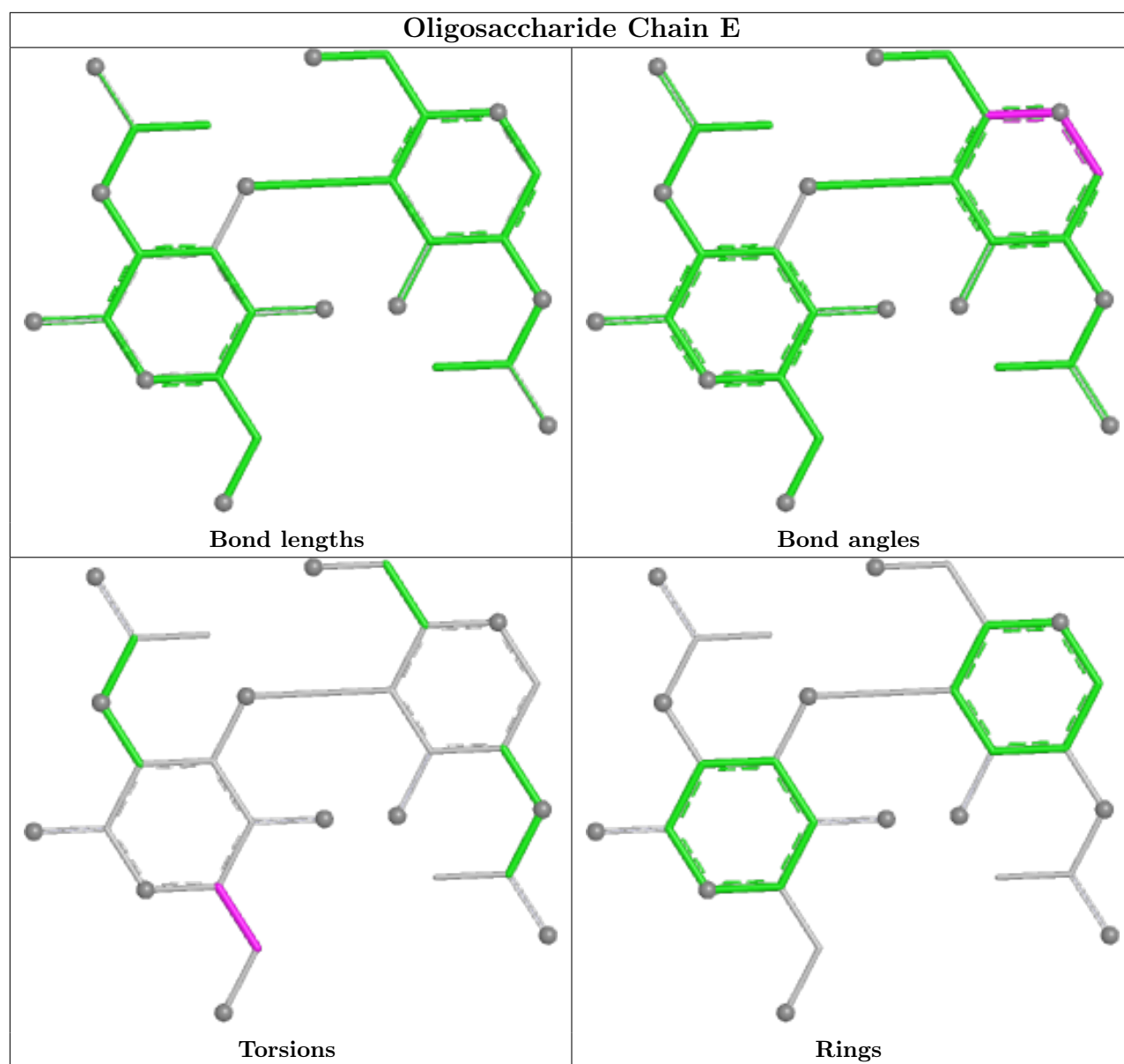
All (6) torsion outliers are listed below:

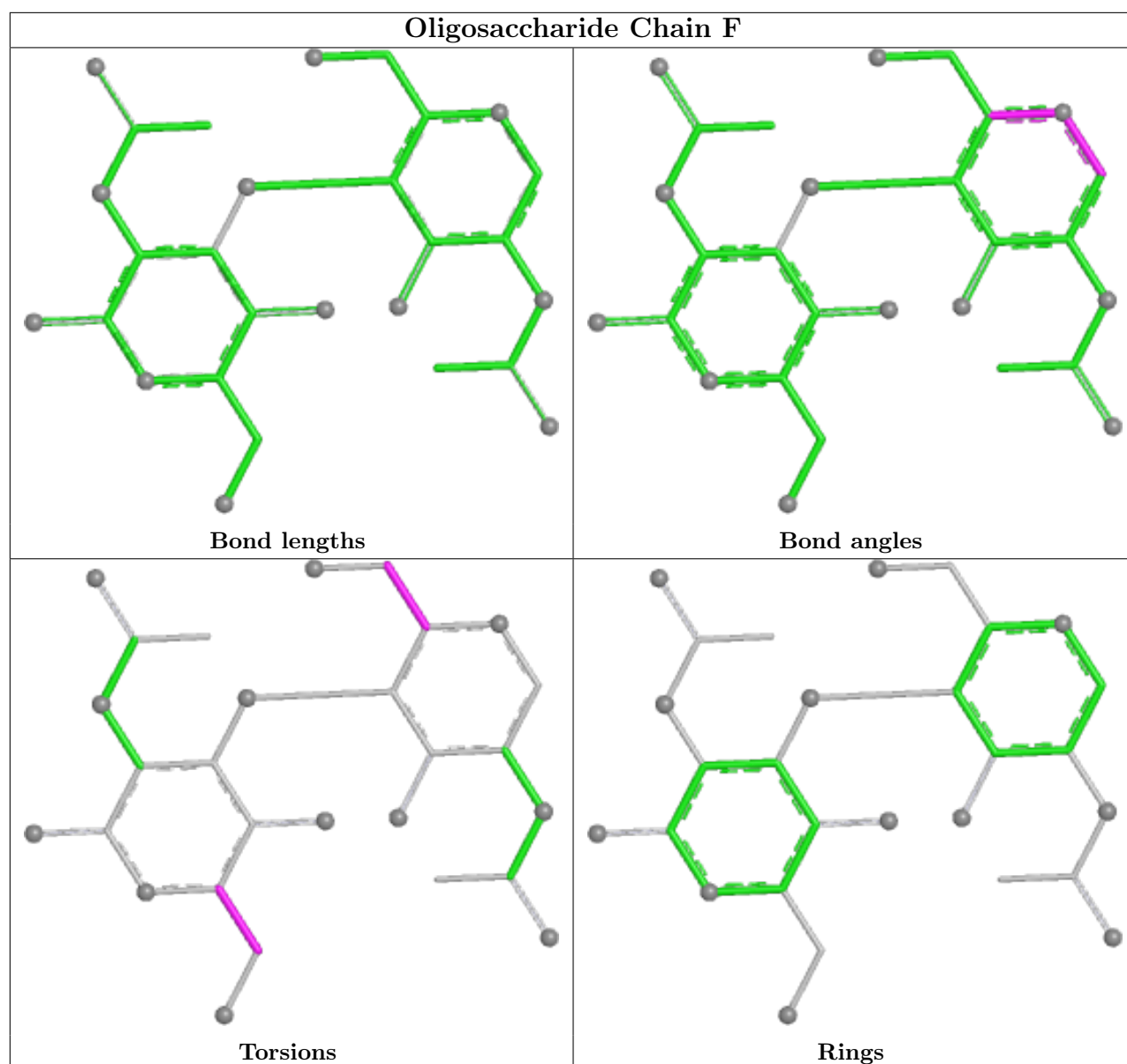
Mol	Chain	Res	Type	Atoms
3	F	2	NAG	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

22 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
5	SO4	A	509	-	4,4,4	0.14	0	6,6,6	0.07	0
4	NAG	B	501	1	14,14,15	0.71	0	17,19,21	0.87	1 (5%)
5	SO4	A	503	-	4,4,4	0.17	0	6,6,6	0.06	0
5	SO4	A	504	-	4,4,4	0.13	0	6,6,6	0.30	0
6	GOL	A	513	-	5,5,5	1.26	1 (20%)	5,5,5	0.89	0
5	SO4	A	510	-	4,4,4	0.13	0	6,6,6	0.09	0
5	SO4	A	505	-	4,4,4	0.15	0	6,6,6	0.08	0
4	NAG	A	501	1	13,13,15	0.41	0	16,17,21	0.72	1 (6%)
5	SO4	B	503	-	4,4,4	0.20	0	6,6,6	0.31	0
6	GOL	A	512	-	5,5,5	1.14	0	5,5,5	0.65	0
7	EDO	C	1203	-	3,3,3	0.56	0	2,2,2	0.18	0
5	SO4	A	506	-	4,4,4	0.14	0	6,6,6	0.13	0
7	EDO	C	1202	-	3,3,3	0.51	0	2,2,2	0.26	0
5	SO4	B	502	-	4,4,4	0.14	0	6,6,6	0.12	0
6	GOL	B	504	-	5,5,5	1.01	0	5,5,5	0.96	0
6	GOL	C	1201	-	5,5,5	1.22	0	5,5,5	0.99	0
5	SO4	A	508	-	4,4,4	0.12	0	6,6,6	0.13	0
7	EDO	A	514	-	3,3,3	0.44	0	2,2,2	0.32	0
5	SO4	A	502	-	4,4,4	0.18	0	6,6,6	0.53	0
5	SO4	A	507	-	4,4,4	0.13	0	6,6,6	0.10	0
5	SO4	A	511	-	4,4,4	0.16	0	6,6,6	0.17	0
7	EDO	A	515	-	3,3,3	0.54	0	2,2,2	0.26	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
4	NAG	A	501	1	-	4/6/19/26	0/1/1/1
4	NAG	B	501	1	-	2/6/23/26	0/1/1/1
6	GOL	A	512	-	-	4/4/4/4	-
7	EDO	A	515	-	-	0/1/1/1	-
6	GOL	B	504	-	-	4/4/4/4	-
7	EDO	C	1203	-	-	0/1/1/1	-
6	GOL	C	1201	-	-	2/4/4/4	-
6	GOL	A	513	-	-	2/4/4/4	-
7	EDO	A	514	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	C	1202	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	513	GOL	C1-C2	2.30	1.61	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	501	NAG	C1-O5-C5	3.16	116.48	112.19
4	A	501	NAG	C4-C3-C2	-2.22	109.79	112.53

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	513	GOL	O1-C1-C2-C3
6	C	1201	GOL	O1-C1-C2-C3
4	A	501	NAG	C8-C7-N2-C2
4	A	501	NAG	O7-C7-N2-C2
4	A	501	NAG	O5-C5-C6-O6
6	A	512	GOL	O1-C1-C2-C3
6	A	512	GOL	C1-C2-C3-O3
6	B	504	GOL	C1-C2-C3-O3
6	A	512	GOL	O1-C1-C2-O2
6	A	513	GOL	O1-C1-C2-O2
6	C	1201	GOL	O1-C1-C2-O2
4	B	501	NAG	O5-C5-C6-O6
4	B	501	NAG	C4-C5-C6-O6
6	A	512	GOL	O2-C2-C3-O3
4	A	501	NAG	C4-C5-C6-O6
6	B	504	GOL	O1-C1-C2-O2
6	B	504	GOL	O2-C2-C3-O3
6	B	504	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 7 short contacts:

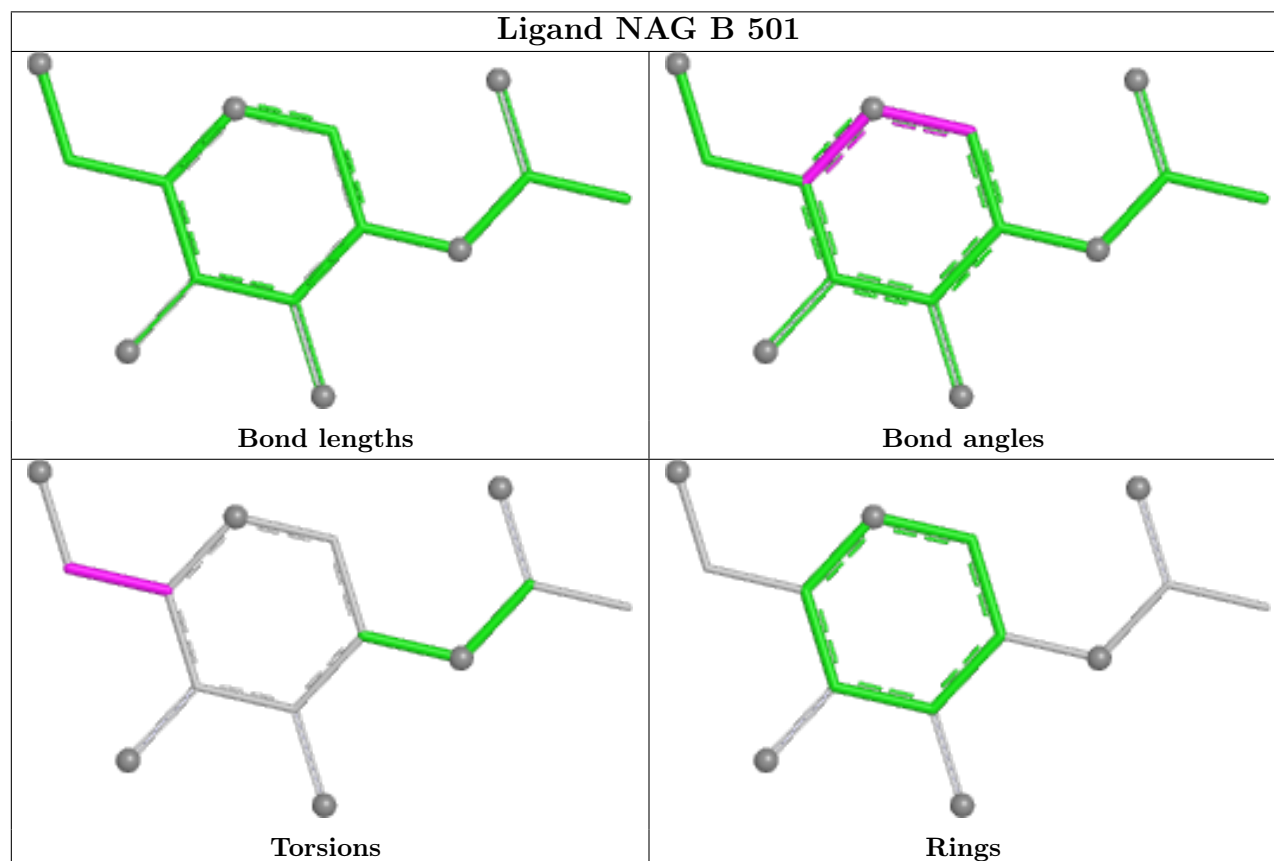
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	NAG	2	0

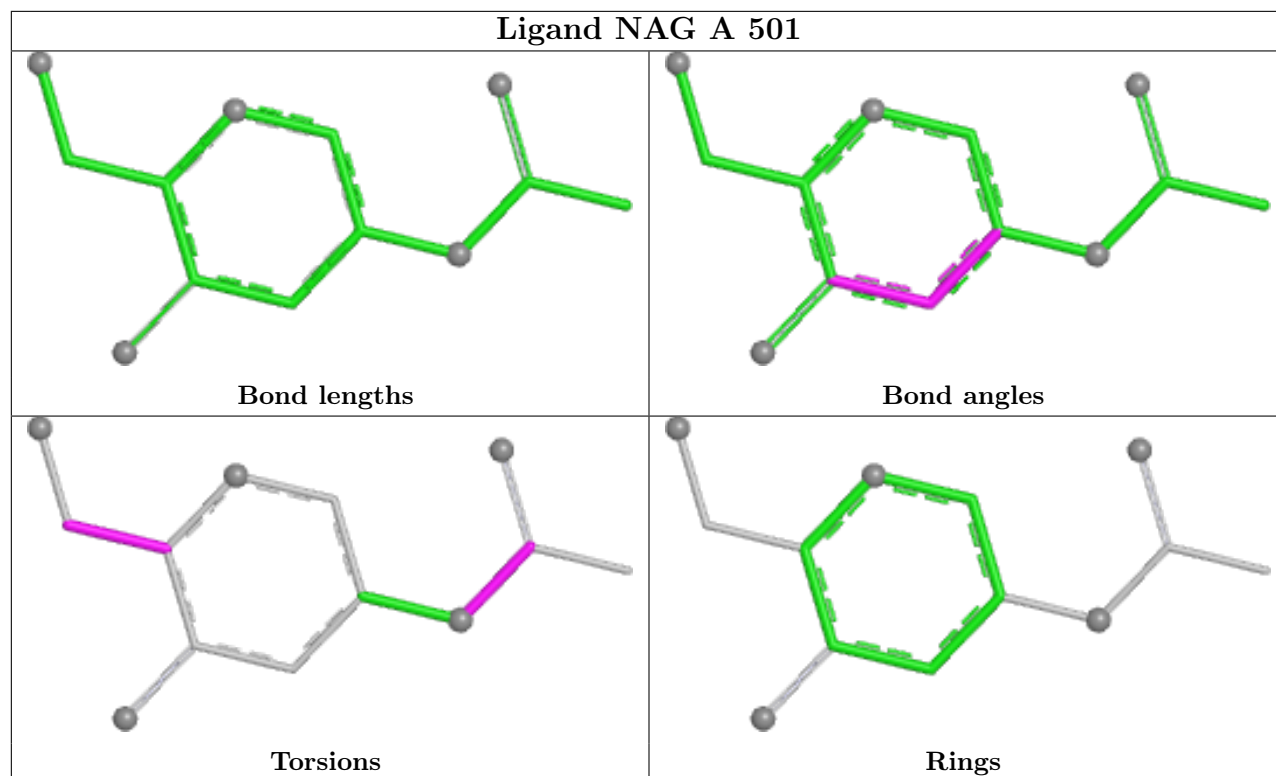
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	512	GOL	1	0
7	C	1202	EDO	1	0
6	B	504	GOL	3	0

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.





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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	324/372 (87%)	0.93	22 (6%) 17 25	20, 33, 54, 102	0
1	B	324/372 (87%)	1.20	56 (17%) 1 2	22, 42, 83, 108	0
2	C	47/50 (94%)	1.12	6 (12%) 3 6	25, 41, 88, 94	0
2	D	46/50 (92%)	1.41	11 (23%) 0 1	31, 50, 92, 108	0
All	All	741/844 (87%)	1.09	95 (12%) 3 6	20, 38, 78, 108	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	392	CYS	7.9
1	B	357	SER	6.9
1	B	384	PRO	6.8
1	B	378	SER	6.4
1	B	304	SER	5.7
1	B	326	VAL	5.7
1	B	69	ASN	5.3
1	B	351	GLN	5.1
1	B	375	ASN	5.1
2	D	1101	ALA	5.0
1	B	68	ALA	4.8
1	B	330	ILE	4.8
2	D	1091	ARG	4.7
1	B	306	LEU	4.6
1	B	334	PRO	4.5
1	B	311	ASN	4.3
1	B	359	GLN	4.2
1	B	325	PHE	4.2
2	C	1091	ARG	4.2
1	B	352	SER	4.1
1	B	328	ASP	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	291	PHE	3.9
2	D	1093	ASN	3.8
1	B	379	ALA	3.7
1	B	383	LEU	3.7
1	B	358	SER	3.6
1	A	388	ARG	3.6
1	B	380	LYS	3.5
1	B	389	PRO	3.5
1	B	355	PRO	3.4
1	B	302	LEU	3.3
1	A	387	SER	3.3
1	B	113	ALA	3.2
1	B	385	VAL	3.2
1	B	373	ARG	3.2
1	B	262	LYS	3.2
1	B	354	VAL	3.2
1	B	303	PRO	3.1
1	A	390	VAL	3.1
1	A	389	PRO	3.1
1	B	382	CYS	3.1
2	D	1097	ARG	3.0
1	B	279	PRO	3.0
2	D	1092	ASN	3.0
1	B	307	SER	2.9
1	B	282	ILE	2.9
1	A	327	THR	2.9
1	B	388	ARG	2.9
1	B	366	THR	2.8
2	C	1101	ALA	2.8
1	B	353	CYS	2.8
1	B	292	ASP	2.7
2	C	1098	GLY	2.7
1	B	386	VAL	2.7
1	B	327	THR	2.7
1	A	383	LEU	2.6
1	B	305	THR	2.6
1	B	191	TRP	2.5
1	A	271	GLY	2.5
1	B	243	VAL	2.5
2	D	1105	CYS	2.5
2	D	1076	CYS	2.5
1	B	242	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	270	ILE	2.4
1	A	385	VAL	2.4
1	A	201	TYR	2.3
1	B	301	SER	2.3
2	D	1099	CYS	2.3
2	D	1089	ARG	2.3
1	A	384	PRO	2.2
2	C	1089	ARG	2.2
1	B	356	GLY	2.2
1	A	199	ILE	2.2
1	A	280	ASN	2.2
1	B	391	ASP	2.2
1	B	157	CYS	2.2
2	C	1076	CYS	2.1
1	B	117	PRO	2.1
1	B	127	LEU	2.1
2	C	1061	ARG	2.1
1	A	113	ALA	2.1
1	A	246	ALA	2.1
1	A	304	SER	2.1
1	A	134	GLY	2.1
1	B	232	PRO	2.1
2	D	1096	ARG	2.1
1	B	175	VAL	2.1
1	B	367	SER	2.1
1	B	79	LEU	2.0
1	A	151	VAL	2.0
1	A	157	CYS	2.0
1	A	164	LEU	2.0
1	B	369	CYS	2.0
2	D	1100	SER	2.0
1	A	219	ALA	2.0

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

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

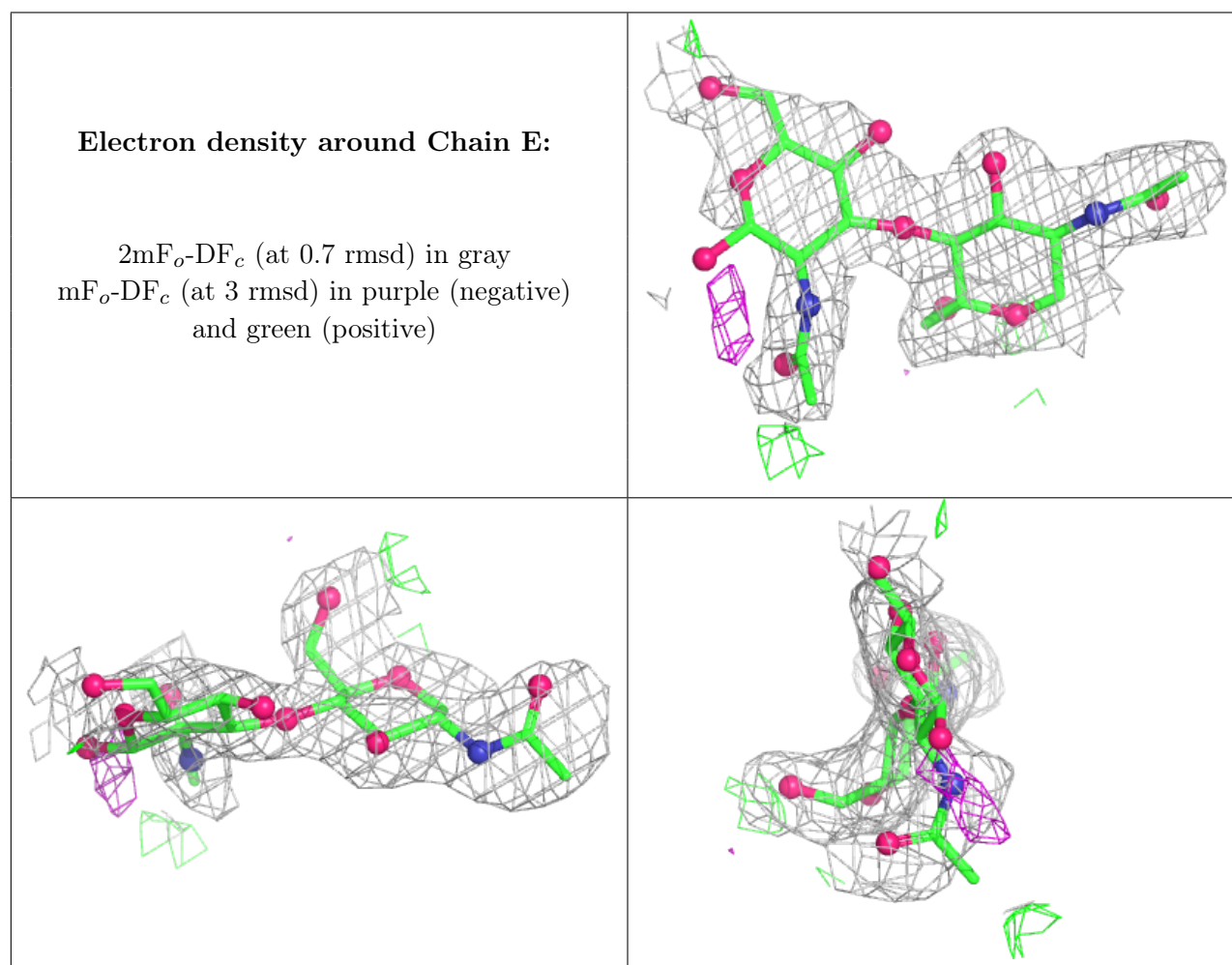
6.3 Carbohydrates [i](#)

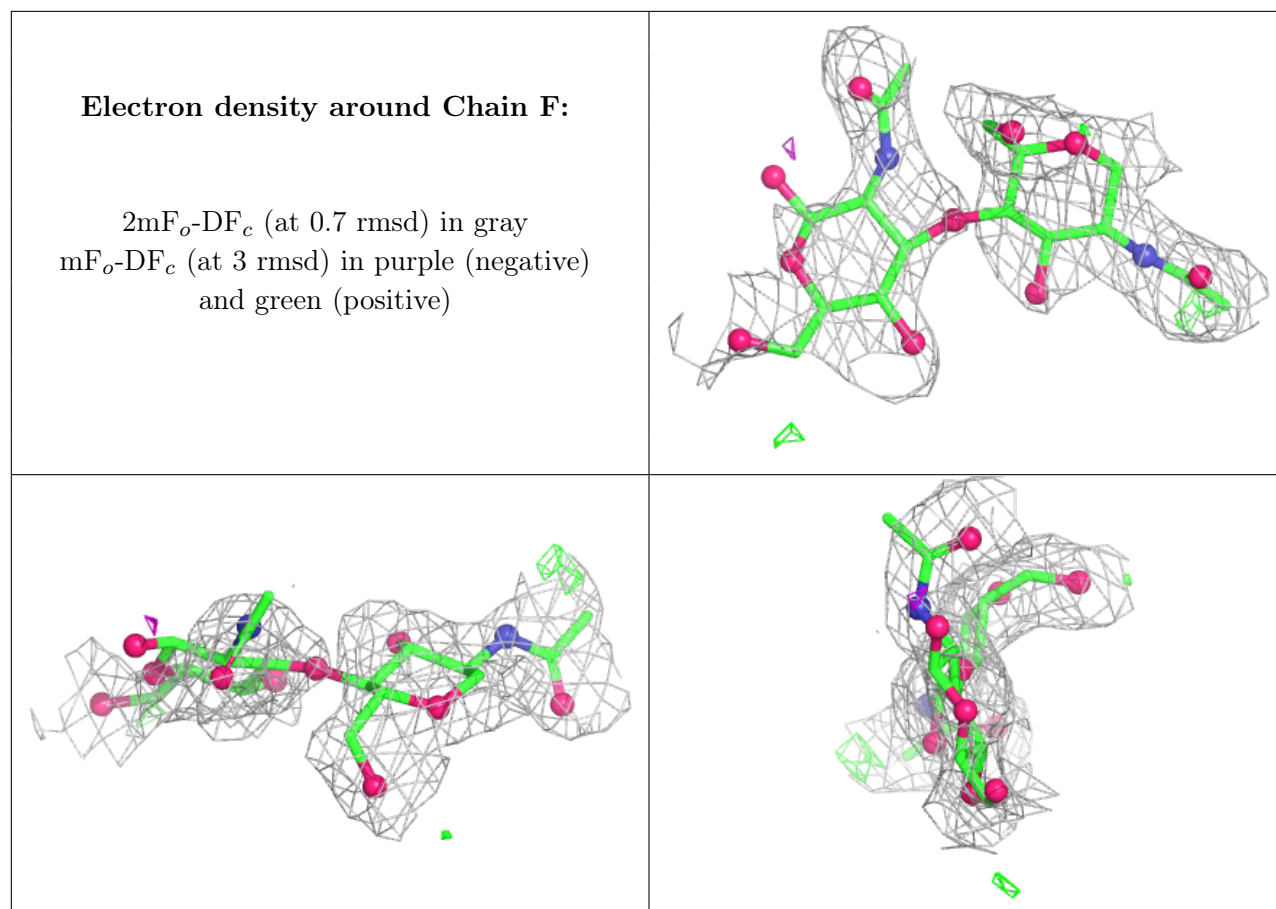
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	F	2	14/15	0.53	0.43	84,90,96,99	0
3	NAG	F	1	14/15	0.64	0.28	55,65,72,86	0
3	NAG	E	2	14/15	0.68	0.30	66,74,88,98	0
3	NAG	E	1	14/15	0.84	0.16	34,44,51,52	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.





6.4 Ligands [i](#)

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

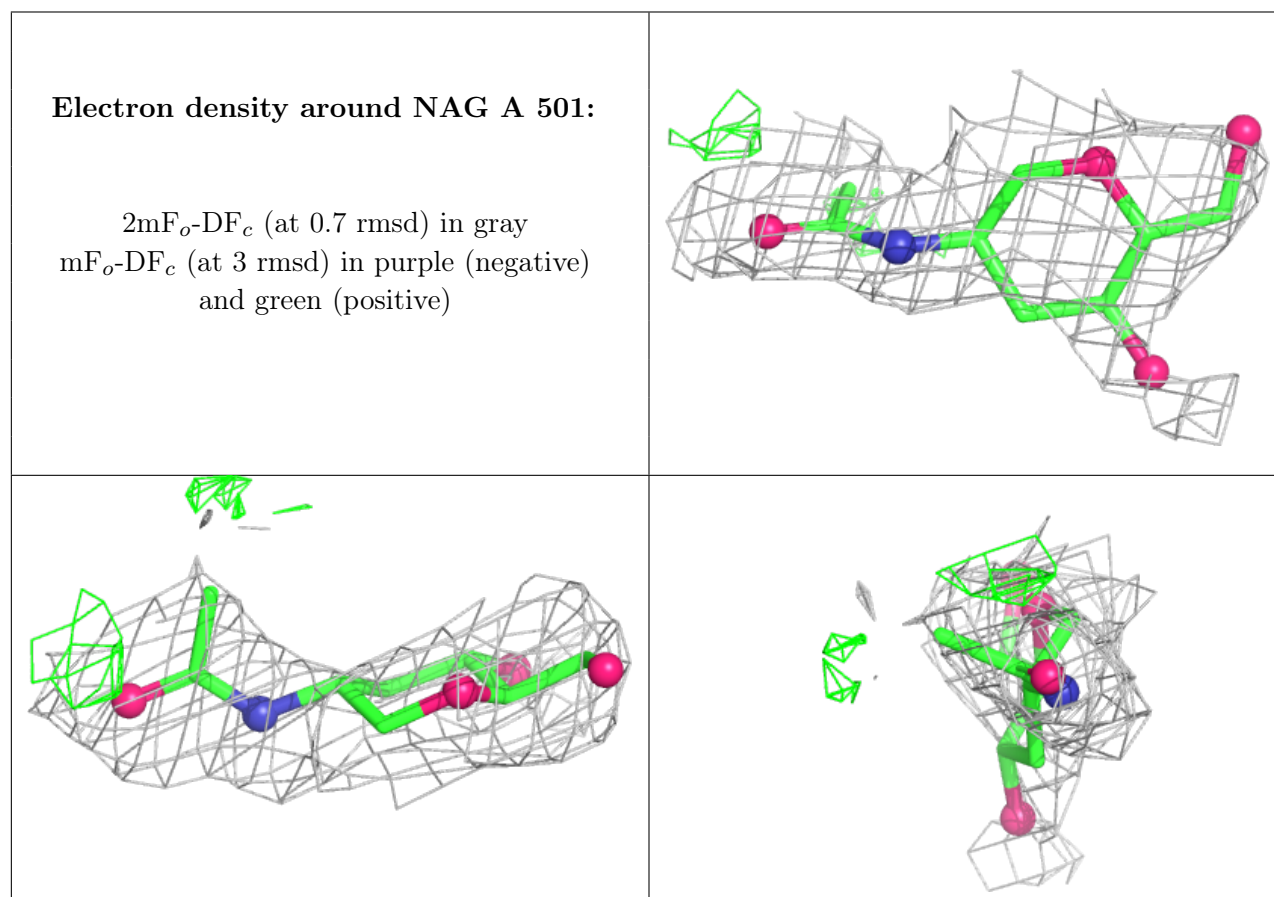
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	GOL	C	1201	6/6	0.46	0.30	48,73,76,78	0
7	EDO	C	1202	4/4	0.54	0.22	62,67,70,72	0
4	NAG	A	501	13/15	0.67	0.26	73,82,89,90	0
7	EDO	C	1203	4/4	0.71	0.30	52,63,66,66	0
5	SO4	A	506	5/5	0.76	0.25	108,109,114,122	0
5	SO4	A	510	5/5	0.77	0.21	107,113,116,116	0
4	NAG	B	501	14/15	0.77	0.42	72,91,101,101	0
5	SO4	A	511	5/5	0.80	0.23	95,95,97,102	0
5	SO4	A	505	5/5	0.82	0.40	92,92,98,105	0
7	EDO	A	515	4/4	0.82	0.29	43,50,61,68	0
5	SO4	A	509	5/5	0.83	0.28	127,130,131,134	0
5	SO4	B	503	5/5	0.85	0.16	59,69,84,88	0

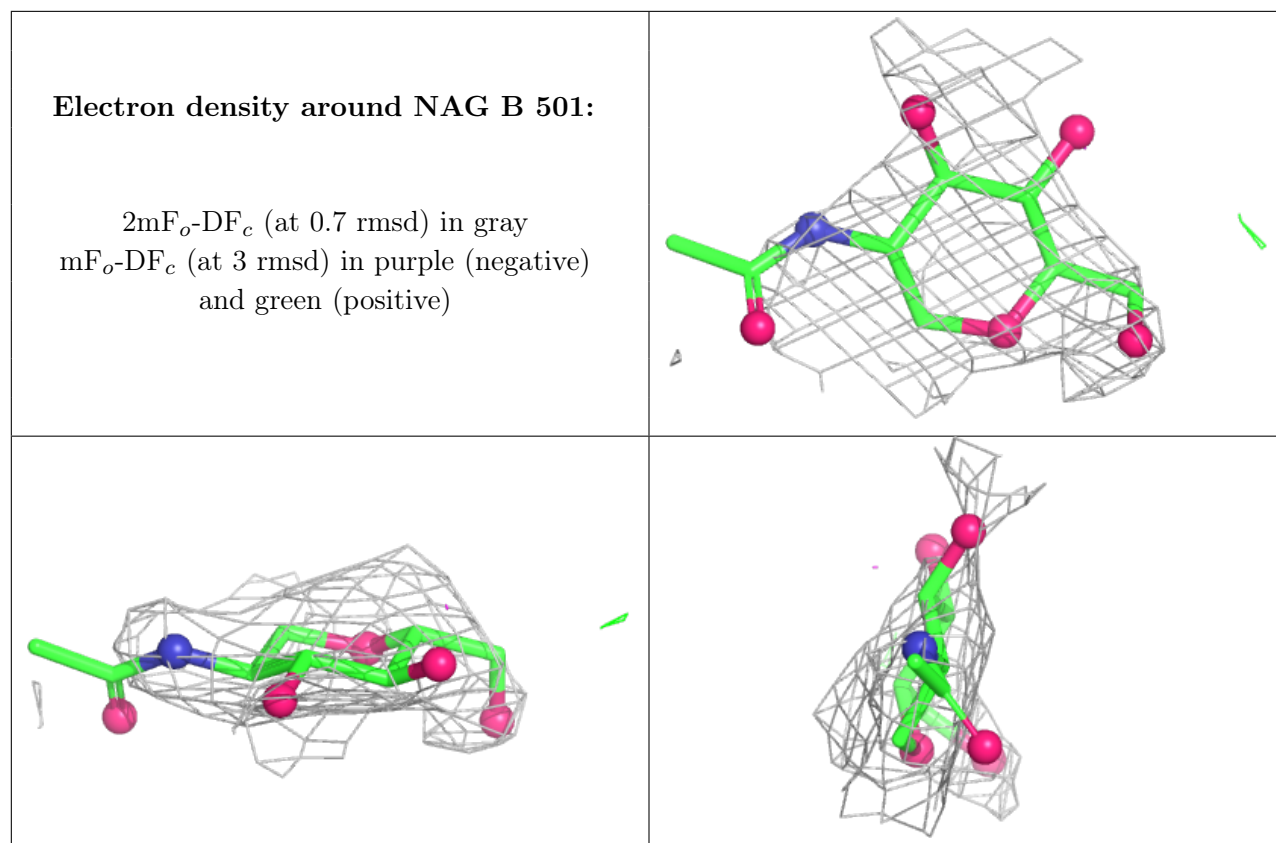
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	GOL	B	504	6/6	0.86	0.22	54,63,67,68	0
6	GOL	A	513	6/6	0.87	0.24	31,50,55,56	0
5	SO4	B	502	5/5	0.88	0.21	95,101,101,107	0
5	SO4	A	504	5/5	0.88	0.16	65,67,76,88	0
5	SO4	A	503	5/5	0.89	0.19	77,80,86,86	0
5	SO4	A	507	5/5	0.90	0.18	103,104,107,108	0
5	SO4	A	508	5/5	0.91	0.28	110,113,116,119	0
6	GOL	A	512	6/6	0.91	0.25	46,55,63,72	0
7	EDO	A	514	4/4	0.93	0.28	38,39,41,52	0
5	SO4	A	502	5/5	0.96	0.21	31,35,50,67	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.