

Full wwPDB X-ray Structure Validation Report (i)

Feb 7, 2024 – 02:16 PM EST

PDB ID	:	8TJ9
Title	:	CRYSTAL STRUCTURE OF THE A/Michigan/15/2014(H3N2) IN-
		FLUENZA VIRUS HEMAGGLUTININ WITH HUMAN RECEPTOR ANA-
		LOG 6'-SLNLN
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Deposited on	:	2023-07-20
Resolution	:	1.90 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 (i) 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 (i)) were used in the production of this report:

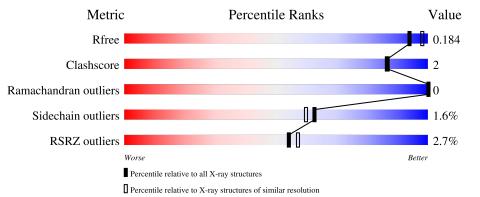
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.90 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	А	323	91%	7% ••
2	В	174	% 	••
3	С	3	67% 33%	
3	D	3	67% 33%	

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Mol	Chain	Length	Quality of chain				
3	Е	3	67%	33%			
4	F	5	40%	60%			

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	BMA	D	3	-	-	-	Х
3	BMA	Е	3	-	-	-	Х



Entry composition (i) $\mathbf{2}$

There are 11 unique types of molecules in this entry. The entry contains 4642 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 Hemagglutinin HA1 chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	317	Total 2474	C 1553	N 439	0 470	S 12	0	0	0

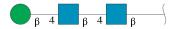
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	7	ALA	-	expression tag	UNP A0A0Y0S9M3
А	8	ASP	-	expression tag	UNP A0A0Y0S9M3
А	9	PRO	-	expression tag	UNP A0A0Y0S9M3
А	10	GLY	-	expression tag	UNP A0A0Y0S9M3

• Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	173	Total 1396	C 869	N 247	0 274	S 6	0	0	0

• Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	С	3	Total C N O 39 22 2 15	0	0	0
3	D	3	Total C N O 39 22 2 15	0	0	0
3	Е	3	Total C N O 39 22 2 15	0	0	0



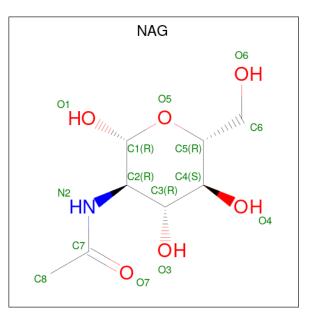


• Molecule 4 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galacto pyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	F	5	Total C N O 71 39 3 29	0	0	0

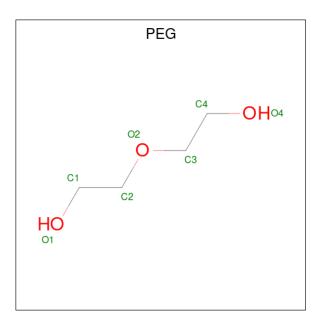
• Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



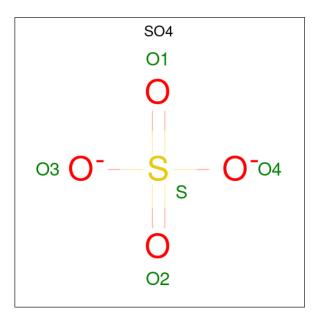
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	1	Total C N O 14 8 1 5	0	0
5	А	1	Total C N O 14 8 1 5	0	0
5	А	1	Total C N O 14 8 1 5	0	0

• Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 7 & 4 & 3 \end{array}$	0	0
6	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 7 4 3 \end{array}$	0	0
6	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 7 4 3 \end{array}$	0	0



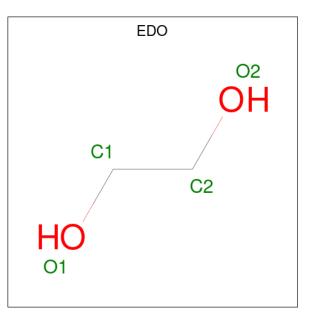
Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
7	А	1	Total 5	0 4	S 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
7	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
7	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0



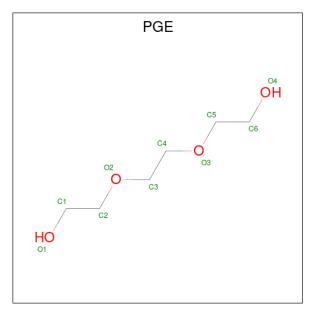
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
8	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
8	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 9 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



PG4	
C_{1} C_{2} C_{3} C_{4} C_{7} C_{7	

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
9	В	1	Total	C 8	0 5	0	0
			13	8	\mathbf{b}		



Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
10	В	1	Total 10	С 6	0 4	0	0

• Molecule 11 is water.

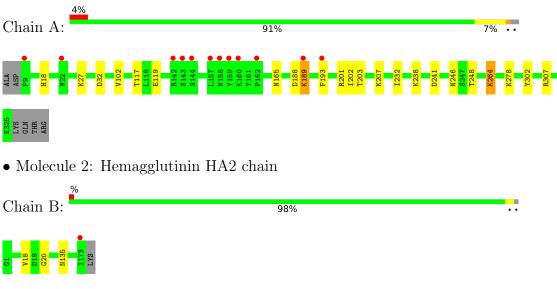


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	А	246	Total O 246 246	0	0
11	В	220	Total O 220 220	0	0



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: Hemagglutinin HA1 chain

• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:	67%	33%
(G1 (A3 (A3		

 \bullet Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:	67%	33%

NAG1 NAG2 BMA3

N/ BN

• Molecule 3: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 67% 33%



NAG1 NAG2 BMA3

 \bullet Molecule 4: N-acetyl-alpha-neuraminic acid-(2-6)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 40%

60%

NAG1 GAL2 NAG3 GAL4 SIA5



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants	100.59Å 100.59Å 394.89Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.53 - 1.90	Depositor
Resolution (A)	42.95 - 1.90	EDS
% Data completeness	99.9 (42.53-1.90)	Depositor
(in resolution range)	99.9 (42.95-1.90)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.09	Depositor
$< I/\sigma(I) > 1$	$3.05 (at 1.89 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
D D.	0.161 , 0.185	Depositor
R, R_{free}	0.161 , 0.184	DCC
R_{free} test set	3136 reflections $(5.13%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	28.2	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35 , 55.2	EDS
L-test for twinning ²	$ \langle L \rangle = 0.50, \langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4642	wwPDB-VP
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.53% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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, PG4, SO4, NAG, SIA, PEG, PGE, GAL, EDO

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).

Mal	Chain	Bond	lengths	Bond angles	
Mol Chain		RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.43	0/2532	0.62	0/3441
2	В	0.50	0/1420	0.69	0/1906
All	All	0.46	0/3952	0.65	0/5347

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	А	2474	0	2430	12	0
2	В	1396	0	1330	3	0
3	С	39	0	34	0	0
3	D	39	0	34	2	0
3	Е	39	0	34	0	0
4	F	71	0	61	0	0
5	А	42	0	39	0	0
6	А	14	0	20	1	0
6	В	7	0	10	0	0
7	А	10	0	0	0	0
7	В	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	В	12	0	18	1	0
9	В	13	0	18	1	0
10	В	10	0	14	3	0
11	А	246	0	0	3	0
11	В	220	0	0	1	0
All	All	4642	0	4042	17	0

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The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (17) 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:117:THR:OG1	1:A:119:GLU:HG3	1.94	0.68
1:A:203:THR:HG22	11:A:527:HOH:O	2.01	0.60
2:B:135:ASN:HB3	8:B:205:EDO:H21	1.84	0.59
1:A:189:LYS:HG2	1:A:193:PHE:CZ	2.44	0.53
2:B:20:GLY:O	10:B:206:PGE:H6	2.10	0.51
1:A:27:LYS:HE3	1:A:32:ASP:OD1	2.11	0.50
1:A:264:LYS:HG3	11:A:578:HOH:O	2.13	0.49
1:A:264:LYS:HD2	1:A:302:TYR:OH	2.15	0.47
1:A:165:ASN:HB2	3:D:1:NAG:O5	2.16	0.46
1:A:307:ARG:HD2	9:B:202:PG4:H12	1.97	0.46
2:B:18:VAL:C	10:B:206:PGE:H62	2.36	0.46
1:A:102:VAL:HG22	1:A:232:ILE:HB	1.99	0.44
1:A:201:ARG:C	1:A:202:ILE:HD12	2.37	0.44
1:A:207:LYS:HG3	1:A:241:ASP:OD1	2.18	0.43
1:A:248:THR:HG23	3:D:1:NAG:O7	2.19	0.43
6:A:405:PEG:H41	11:A:683:HOH:O	2.18	0.42
10:B:206:PGE:H42	11:B:437:HOH:O	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	А	315/323~(98%)	307~(98%)	8 (2%)	0	100	100
2	В	171/174~(98%)	163~(95%)	8 (5%)	0	100	100
All	All	486/497~(98%)	470 (97%)	16 (3%)	0	100	100

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

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	А	280/285~(98%)	273~(98%)	7 (2%)	47 41
2	В	146/147~(99%)	146 (100%)	0	100 100
All	All	426/432 (99%)	419 (98%)	7 (2%)	62 60

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	18	HIS
1	А	188	ASP
1	А	189	LYS
1	А	238	LYS
1	А	246	ASN
1	А	264	LYS
1	А	278	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	154	ASN
2	В	172	GLN



5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

14 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	Bo	ond leng	ths	В	ond ang	les
	туре	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
3	NAG	С	1	3,1	$14,\!14,\!15$	0.54	0	$17,\!19,\!21$	0.52	0
3	NAG	С	2	3	14,14,15	0.48	0	17,19,21	0.58	0
3	BMA	С	3	3	11,11,12	0.89	1 (9%)	$15,\!15,\!17$	1.35	3 (20%)
3	NAG	D	1	3,1	14,14,15	0.33	0	17,19,21	0.55	0
3	NAG	D	2	3	14,14,15	0.53	0	17,19,21	0.51	0
3	BMA	D	3	3	11,11,12	0.85	0	$15,\!15,\!17$	0.73	0
3	NAG	Е	1	3,1	14,14,15	0.62	0	17,19,21	0.46	0
3	NAG	Е	2	3	$14,\!14,\!15$	0.30	0	$17,\!19,\!21$	0.43	0
3	BMA	Е	3	3	11,11,12	0.80	0	$15,\!15,\!17$	0.85	1 (6%)
4	NAG	F	1	4	$15,\!15,\!15$	0.82	1 (6%)	21,21,21	1.07	1 (4%)
4	GAL	F	2	4	11,11,12	1.17	1 (9%)	$15,\!15,\!17$	1.18	1 (6%)
4	NAG	F	3	4	14,14,15	0.52	0	17,19,21	0.36	0
4	GAL	F	4	4	11,11,12	0.47	0	$15,\!15,\!17$	0.87	0
4	SIA	F	5	4	20,20,21	2.15	2 (10%)	24,28,31	1.53	4 (16%)

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	С	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	С	2	3	-	0/6/23/26	0/1/1/1
3	BMA	С	3	3	-	2/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	1/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	NAG	Е	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	Ε	2	3	-	0/6/23/26	0/1/1/1
3	BMA	Е	3	3	-	0/2/19/22	0/1/1/1
4	NAG	F	1	4	-	0/6/26/26	0/1/1/1
4	GAL	F	2	4	-	1/2/19/22	0/1/1/1
4	NAG	F	3	4	-	0/6/23/26	0/1/1/1
4	GAL	F	4	4	-	0/2/19/22	0/1/1/1
4	SIA	F	5	4	-	1/18/34/38	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
4	F	5	SIA	C2-C1	8.36	1.59	1.52
4	F	2	GAL	O5-C1	-2.57	1.39	1.43
4	F	5	SIA	O6-C2	2.54	1.47	1.43
4	F	1	NAG	C1-C2	2.30	1.55	1.52
3	С	3	BMA	C1-C2	2.08	1.56	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	F	5	SIA	O1A-C1-C2	-3.70	113.84	122.57
4	F	2	GAL	C1-C2-C3	3.51	113.98	109.67
4	F	1	NAG	C4-C3-C2	3.01	114.75	110.34
3	С	3	BMA	C1-O5-C5	2.80	115.98	112.19
4	F	5	SIA	C6-O6-C2	2.64	116.99	111.34
4	F	5	SIA	C8-C7-C6	-2.52	108.25	113.03
3	С	3	BMA	C1-C2-C3	2.29	112.48	109.67
3	С	3	BMA	O5-C1-C2	2.19	114.16	110.77
4	F	5	SIA	O1B-C1-O1A	2.13	128.94	124.09
3	Е	3	BMA	C1-O5-C5	2.02	114.93	112.19

There are no chirality outliers.

All (9) torsion outliers are listed below:



ОП	
δJ	L J 9

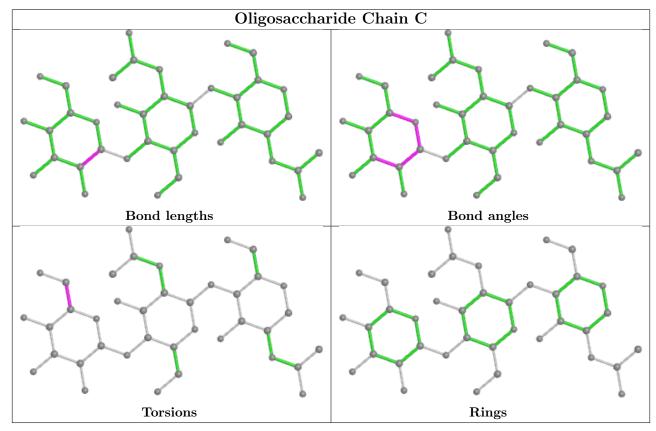
Mol	Chain	Res	Type	Atoms
3	С	3	BMA	C4-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6
3	D	3	BMA	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
3	С	3	BMA	O5-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
4	F	2	GAL	O5-C5-C6-O6
3	D	2	NAG	C3-C2-N2-C7
4	F	5	SIA	O1A-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

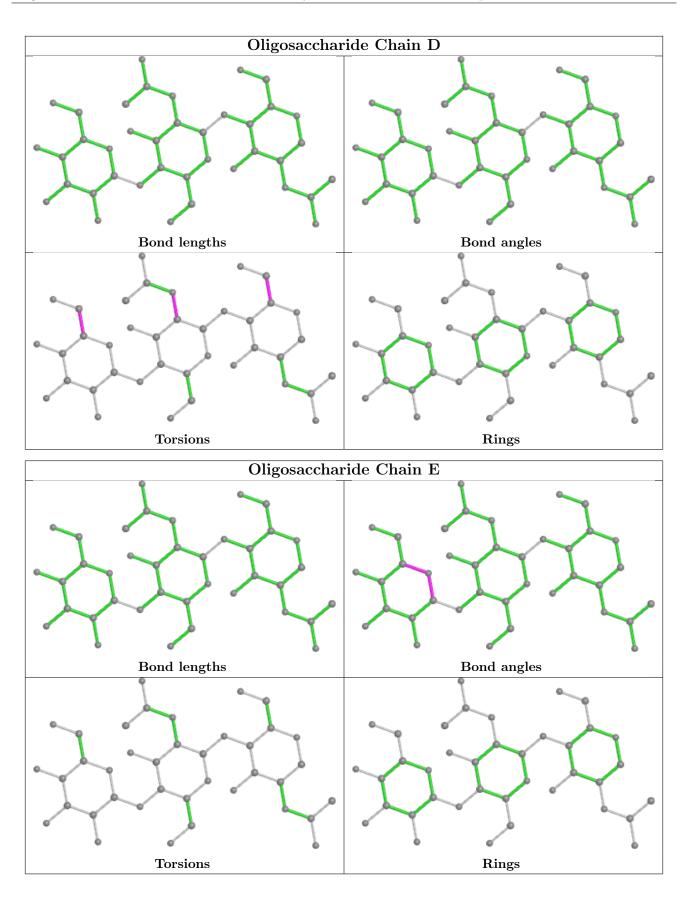
Ν	/Iol	Chain	Res	Type	Clashes	Symm-Clashes
	3	D	1	NAG	2	0

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

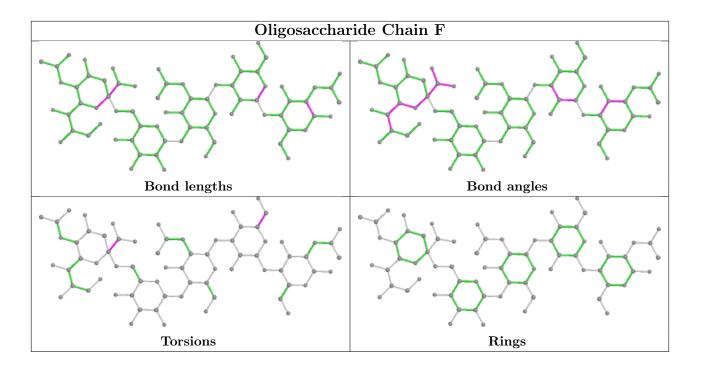












5.6 Ligand geometry (i)

15 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
6	PEG	А	405	-	$6,\!6,\!6$	0.15	0	$5,\!5,\!5$	0.07	0
5	NAG	А	401	1	$14,\!14,\!15$	0.45	0	$17,\!19,\!21$	0.61	1 (5%)
7	SO4	А	406	-	4,4,4	0.13	0	6,6,6	0.08	0
7	SO4	В	207	-	4,4,4	0.13	0	6,6,6	0.39	0
7	SO4	В	208	-	4,4,4	0.23	0	$6,\!6,\!6$	0.39	0
6	PEG	А	404	-	$6,\!6,\!6$	0.14	0	$5,\!5,\!5$	0.16	0
8	EDO	В	201	-	3,3,3	0.52	0	2,2,2	0.24	0
10	PGE	В	206	-	$9,\!9,\!9$	0.34	0	8,8,8	0.34	0
9	PG4	В	202	-	12,12,12	0.12	0	11,11,11	0.72	0
5	NAG	А	403	1	14,14,15	0.57	0	17,19,21	0.48	0
6	PEG	В	204	-	$6,\!6,\!6$	0.17	0	$5,\!5,\!5$	0.20	0
8	EDO	В	203	-	3,3,3	0.59	0	2,2,2	0.16	0
8	EDO	В	205	-	3,3,3	0.45	0	2,2,2	0.31	0
5	NAG	А	402	1	14,14,15	0.48	0	17,19,21	0.56	0



Mol Type Cha		Chain	Chain Res 1		Bond lengths			Bond angles		
IVIOI	Moi Type Chain Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2		
7	SO4	А	407	-	4,4,4	0.14	0	$6,\!6,\!6$	0.13	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
6	PEG	А	405	-	-	3/4/4/4	-
5	NAG	А	401	1	-	0/6/23/26	0/1/1/1
6	PEG	А	404	-	-	1/4/4/4	-
8	EDO	В	201	-	-	0/1/1/1	-
10	PGE	В	206	-	-	4/7/7/7	-
9	PG4	В	202	-	-	5/10/10/10	-
5	NAG	А	403	1	-	2/6/23/26	0/1/1/1
6	PEG	В	204	-	-	2/4/4/4	-
8	EDO	В	203	-	-	1/1/1/1	-
8	EDO	В	205	-	-	0/1/1/1	-
5	NAG	А	402	1	_	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
5	А	401	NAG	C1-O5-C5	2.12	115.07	112.19

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	В	206	PGE	O2-C3-C4-O3
6	А	405	PEG	O2-C3-C4-O4
9	В	202	PG4	O1-C1-C2-O2
9	В	202	PG4	O2-C3-C4-O3
6	А	405	PEG	O1-C1-C2-O2
6	В	204	PEG	O2-C3-C4-O4
8	В	203	EDO	O1-C1-C2-O2
6	А	404	PEG	O1-C1-C2-O2
6	В	204	PEG	C4-C3-O2-C2
6	А	405	PEG	C1-C2-O2-C3

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Mol	Chain	Res	Type	Atoms
10	В	206	PGE	C4-C3-O2-C2
10	В	206	PGE	C6-C5-O3-C4
9	В	202	PG4	C8-C7-O4-C6
10	В	206	PGE	C3-C4-O3-C5
5	А	403	NAG	C4-C5-C6-O6
9	В	202	PG4	C1-C2-O2-C3
5	А	403	NAG	O5-C5-C6-O6
9	В	202	PG4	C5-C6-O4-C7

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There are no ring outliers.

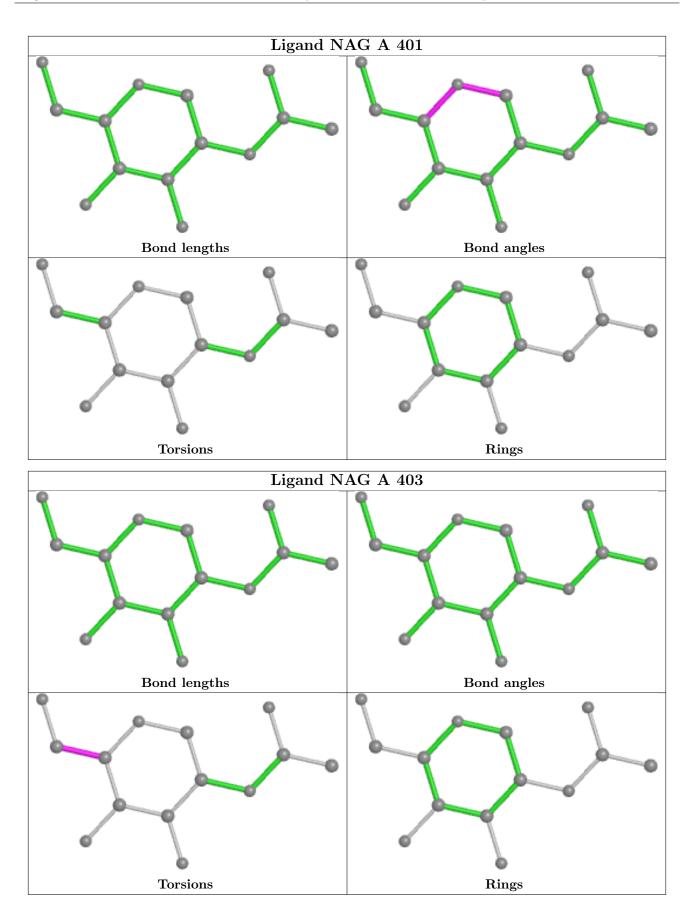
4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	А	405	PEG	1	0
10	В	206	PGE	3	0
9	В	202	PG4	1	0
8	В	205	EDO	1	0

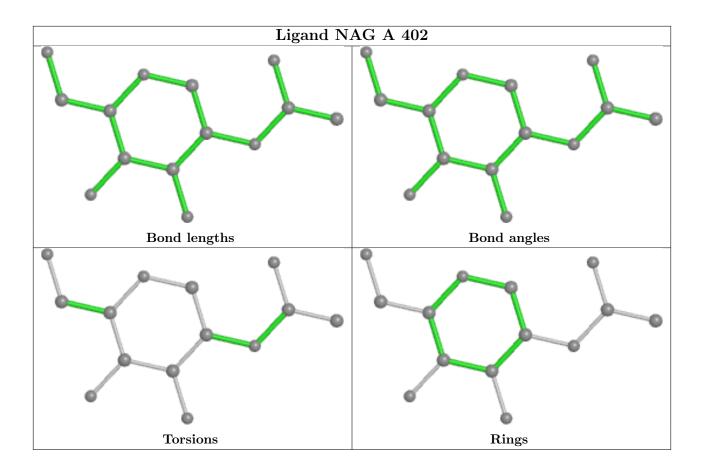
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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 sup 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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	317/323~(98%)	-0.23	12 (3%) 40 43	17, 37, 63, 87	0
2	В	173/174~(99%)	-0.29	1 (0%) 89 90	17, 26, 43, 75	0
All	All	490/497~(98%)	-0.25	13 (2%) 54 57	17, 32, 61, 87	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	173	ILE	4.0
1	А	9	PRO	3.7
1	А	159	TYR	3.2
1	А	160	LYS	3.1
1	А	193	PHE	3.0
1	А	143	SER	2.7
1	А	158	ASN	2.7
1	А	157	LEU	2.4
1	А	142	ARG	2.4
1	А	22	ASN	2.2
1	А	162	PRO	2.1
1	А	144	SER	2.0
1	А	189	LYS	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,

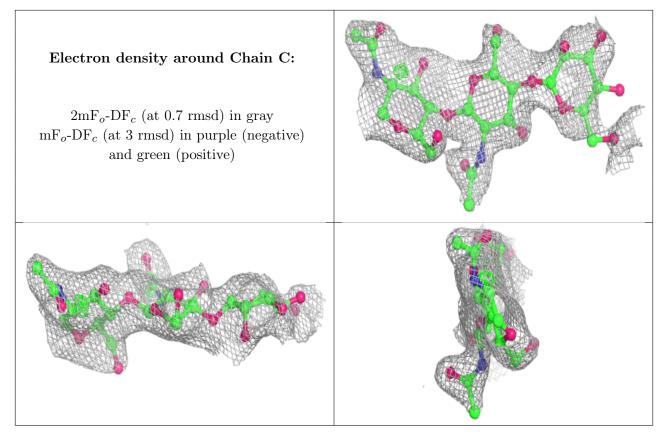


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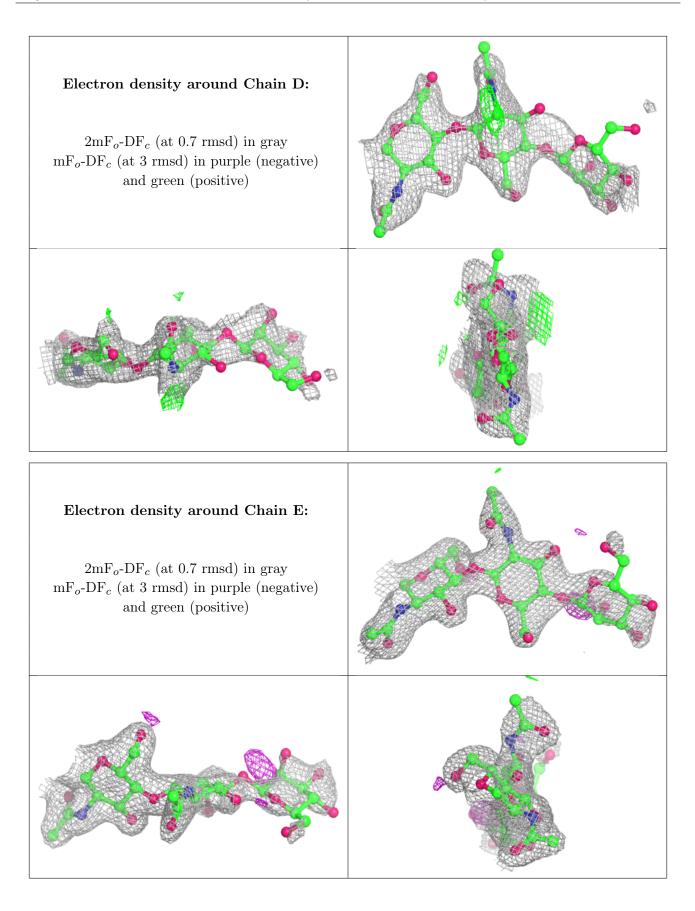
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(A^2)$	Q<0.9
3	BMA	D	3	11/12	0.56	0.45	104,119,136,136	0
3	BMA	Е	3	11/12	0.63	0.45	82,89,98,99	0
3	BMA	С	3	11/12	0.69	0.33	100,111,131,139	0
3	NAG	D	2	14/15	0.82	0.27	82,90,105,105	0
4	NAG	F	1	15/15	0.82	0.30	$63,\!81,\!101,\!107$	0
3	NAG	D	1	14/15	0.86	0.16	52,64,82,90	0
3	NAG	Ε	2	14/15	0.87	0.31	65, 76, 85, 101	0
4	NAG	F	3	14/15	0.89	0.20	44,48,60,65	0
4	GAL	F	2	11/12	0.90	0.33	$54,\!62,\!81,\!87$	0
3	NAG	С	2	14/15	0.92	0.24	48,74,91,98	0
4	GAL	F	4	11/12	0.93	0.15	$43,\!47,\!55,\!56$	0
3	NAG	С	1	14/15	0.95	0.13	46,54,71,77	0
3	NAG	Е	1	14/15	0.96	0.14	32,39,49,63	0
4	SIA	F	5	20/21	0.96	0.12	37,46,54,55	0

median, 95^{th} 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.

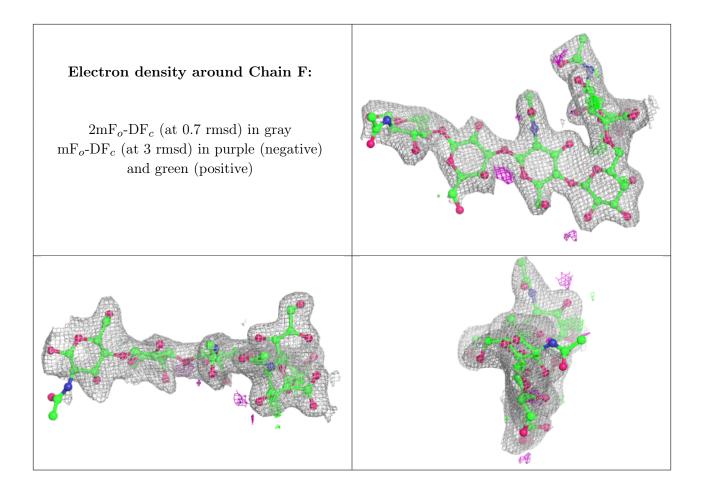
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.











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, 95^{th} 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	$B-factors(A^2)$	Q<0.9
6	PEG	А	404	7/7	0.73	0.15	$55,\!65,\!78,\!79$	0
6	PEG	В	204	7/7	0.76	0.18	52,61,64,65	0
6	PEG	А	405	7/7	0.77	0.35	61,73,77,80	0
8	EDO	В	201	4/4	0.81	0.12	45,50,54,56	0
10	PGE	В	206	10/10	0.81	0.36	44,57,73,76	0
5	NAG	А	403	14/15	0.85	0.14	$62,\!77,\!89,\!89$	0
5	NAG	А	401	14/15	0.86	0.21	$35,\!52,\!63,\!65$	0
8	EDO	В	203	4/4	0.87	0.20	$44,\!57,\!57,\!63$	0
7	SO4	А	406	5/5	0.89	0.20	72,86,112,116	0
9	PG4	В	202	13/13	0.90	0.12	$38,\!50,\!56,\!59$	0
5	NAG	А	402	14/15	0.90	0.25	53,71,75,81	0
7	SO4	А	407	5/5	0.92	0.16	75,78,89,107	0
8	EDO	В	205	4/4	0.95	0.17	49,53,60,61	0

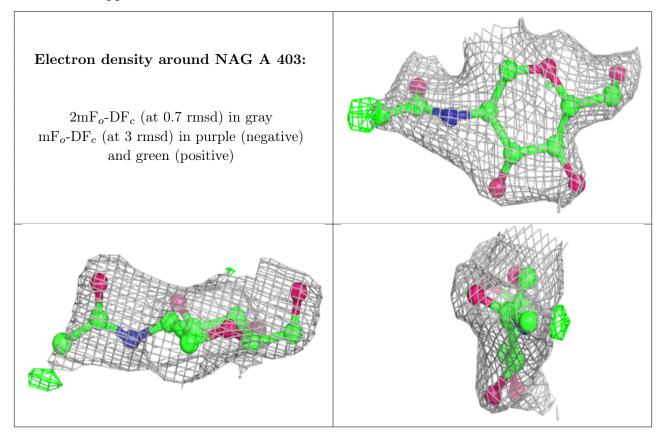
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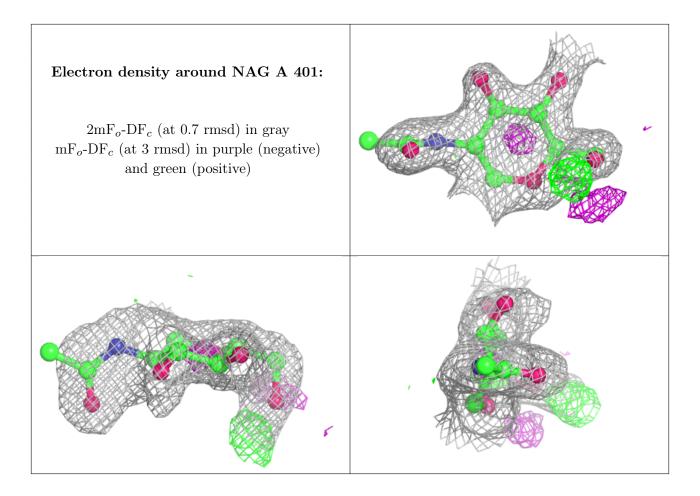
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
7	SO4	В	208	5/5	0.99	0.10	40,41,49,59	0
7	SO4	В	207	5/5	0.99	0.10	36,49,56,63	0

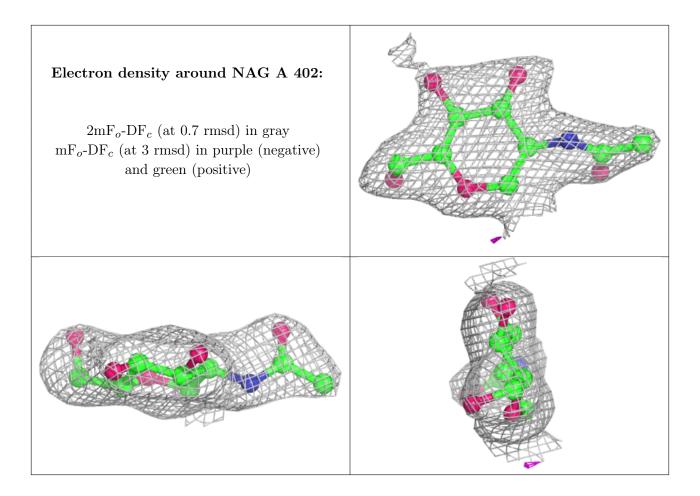
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.











6.5 Other polymers (i)

There are no such residues in this entry.

