



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 03:59 PM BST

PDB ID : 6Q1Z  
Title : Crystal structure of human 1G04 Fab in complex with influenza virus neuraminidase from A/Hunan/02650/2016 (H7N9)  
Authors : Zhu, X.; Wilson, I.A.  
Deposited on : 2019-08-06  
Resolution : 3.45 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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

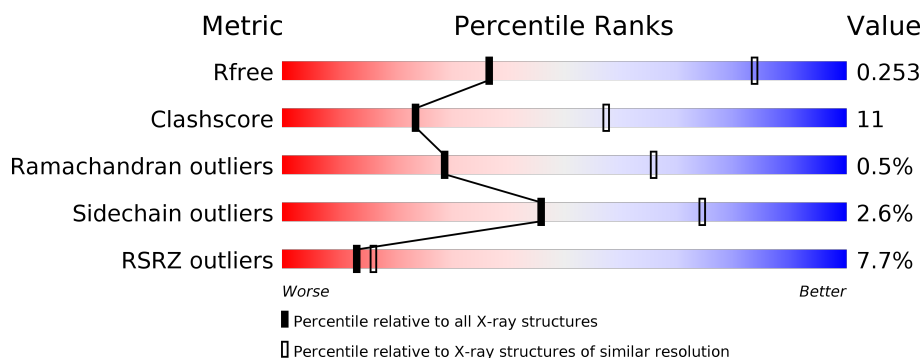
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.45 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.




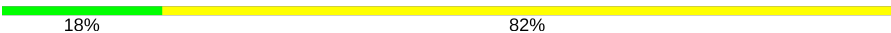
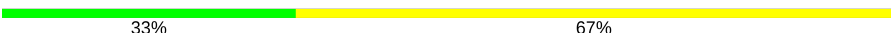
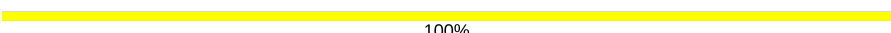
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1278 (3.50-3.38)
Clashscore	141614	1361 (3.50-3.38)
Ramachandran outliers	138981	1327 (3.50-3.38)
Sidechain outliers	138945	1328 (3.50-3.38)
RSRZ outliers	127900	1192 (3.50-3.38)

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 on 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	393	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 78%, yellow 78%, yellow 99%, grey 99%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>78%</span> <span>20%</span> </div> </div>
1	B	393	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 2%, green 2%, green 76%, yellow 76%, yellow 98%, grey 98%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>76%</span> <span>22%</span> </div> </div>
2	C	216	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 21%, green 21%, green 70%, yellow 70%, yellow 99%, grey 99%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>70%</span> <span>29%</span> </div> </div>
2	L	216	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 5%, green 5%, green 73%, yellow 73%, yellow 99%, grey 99%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>73%</span> <span>26%</span> </div> </div>
3	D	240	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 21%, green 21%, green 62%, yellow 62%, yellow 92%, grey 92%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>62%</span> <span>30%</span> </div> </div>
3	H	240	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 4%, green 4%, green 68%, yellow 68%, yellow 93%, grey 93%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>68%</span> <span>25%</span> </div> </div>

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Mol	Chain	Length	Quality of chain
4	E	11	 18%82%
4	G	11	 18%82%
5	F	3	 33%67%
5	I	3	 100%

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
6	NAG	A	501	-	-	-	X
6	NAG	B	501	-	-	-	X
7	CA	B	516	-	-	-	X

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 13236 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 Neuraminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	0	0
			3051	1899	542	587	23			
1	B	388	Total	C	N	O	S	0	0	0
			3051	1899	542	587	23			

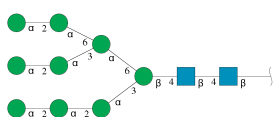
- Molecule 2 is a protein called 1G04 Fab kappa light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	215	Total	C	N	O	S	0	0	0
			1650	1039	273	333	5			
2	C	215	Total	C	N	O	S	0	0	0
			1650	1039	273	333	5			

- Molecule 3 is a protein called 1G04 Fab IgG1 heavy chain.

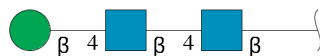
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	227	Total	C	N	O	S	0	0	0
			1736	1098	298	334	6			
3	D	227	Total	C	N	O	S	0	0	0
			1736	1098	298	334	6			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



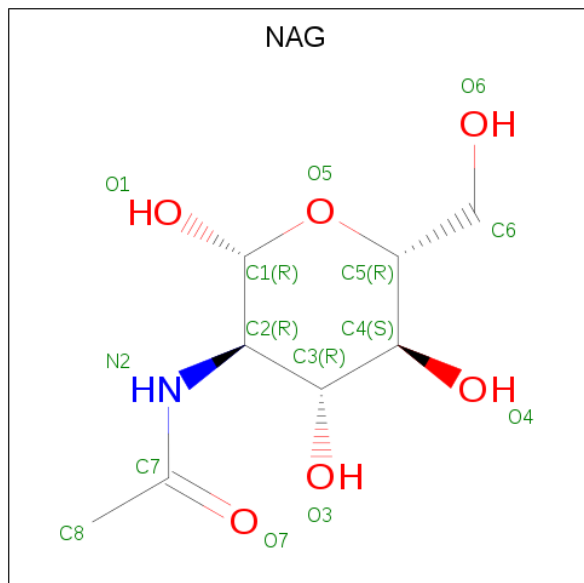
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	11	Total	C	N	O	0	0	0
			127	70	2	55			
4	G	11	Total	C	N	O	0	0	0
			127	70	2	55			

- Molecule 5 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
5	F	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ) (labeled as "Ligand of Interest" by author).



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

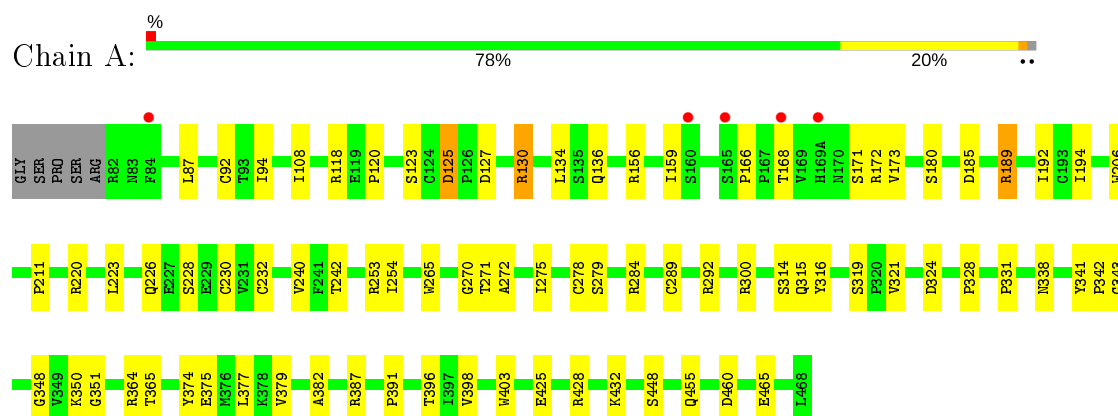
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total 1	Ca 1	0	0
7	A	1	Total 1	Ca 1	0	0

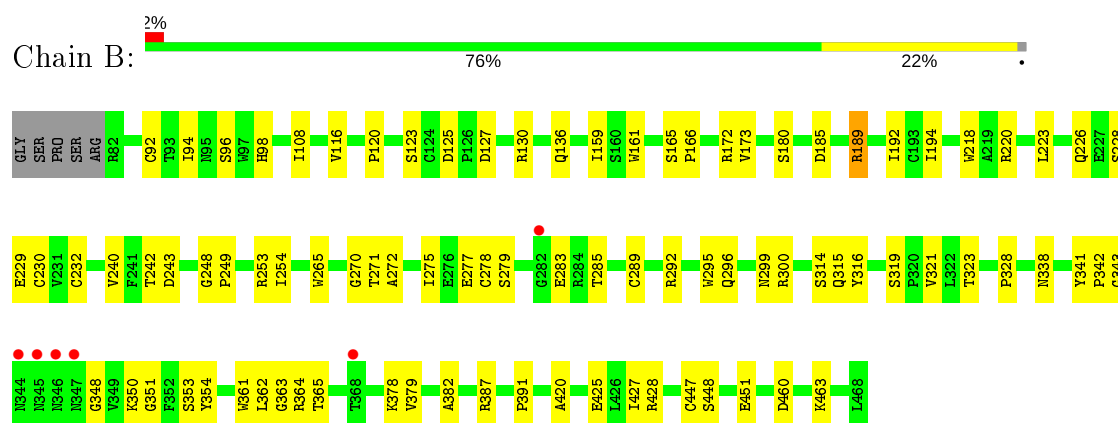
### 3 Residue-property plots [i](#)

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.

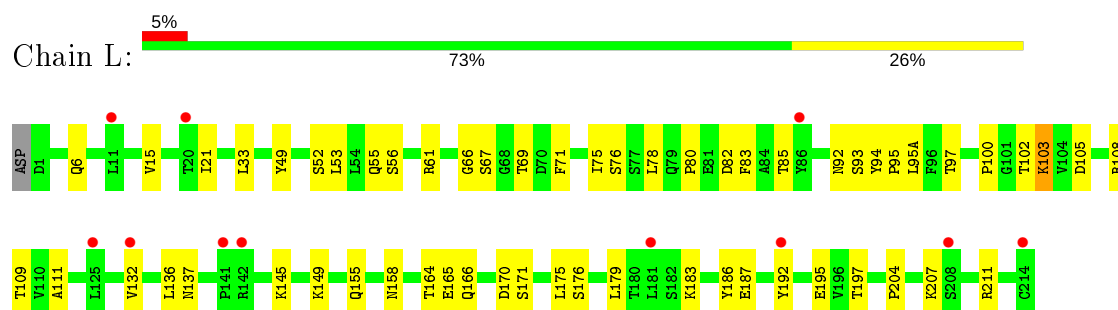
- Molecule 1: Neuraminidase



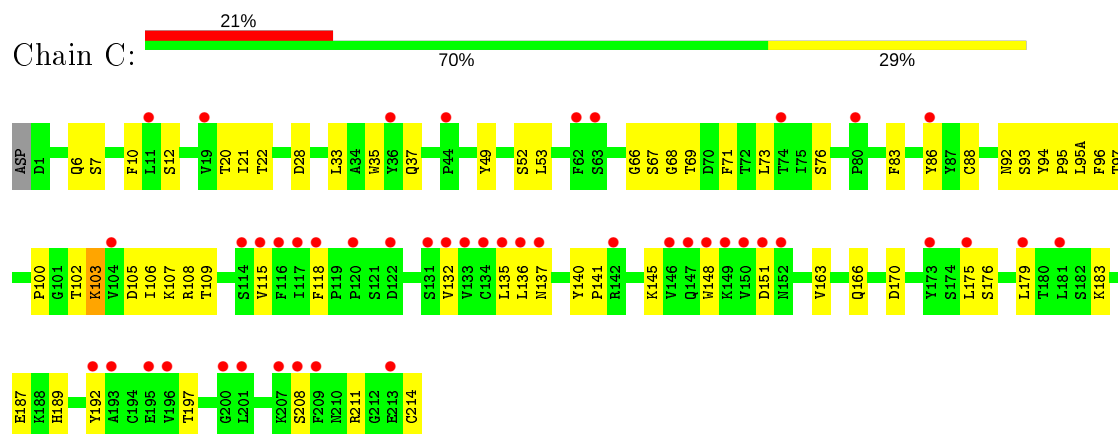
- Molecule 1: Neuraminidase



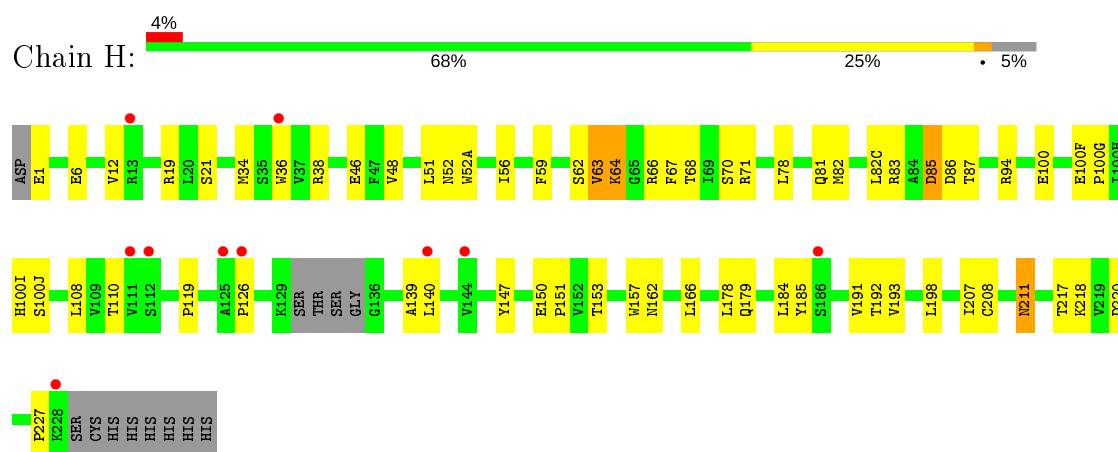
- Molecule 2: 1G04 Fab kappa light chain



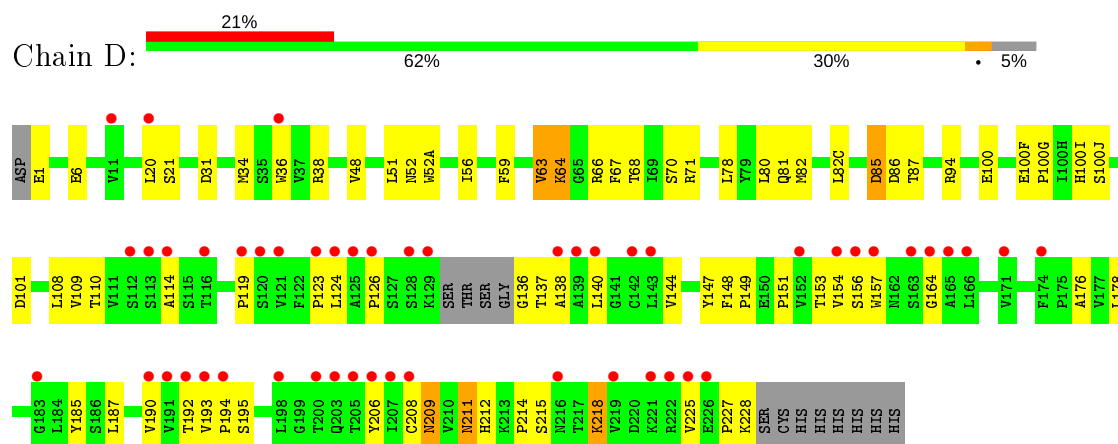
- Molecule 2: 1G04 Fab kappa light chain



- Molecule 3: 1G04 Fab IgG1 heavy chain



- Molecule 3: 1G04 Fab IgG1 heavy chain



- Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose







- Molecule 4:  $\alpha$ -D-mannopyranose-(1-2)- $\alpha$ -D-mannopyranose-(1-2)- $\alpha$ -D-mannopyranose-(1-3)-[ $\alpha$ -D-mannopyranose-(1-2)- $\alpha$ -D-mannopyranose-(1-3)-[ $\alpha$ -D-mannopyranose-(1-2)- $\alpha$ -D-mannopyranose-(1-6)] $\alpha$ -D-mannopyranose-(1-6)] $\beta$ -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose

Chain G: 18% 82%



- Molecule 5:  $\beta$ -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose

Chain F: 33% 67%



- Molecule 5:  $\beta$ -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- $\beta$ -D-glucopyranose

Chain I: 100%



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	180.24Å 180.24Å 148.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.37 – 3.45 47.37 – 3.45	Depositor EDS
% Data completeness (in resolution range)	98.9 (47.37-3.45) 99.0 (47.37-3.45)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.77 (at 3.48Å)	Xtriage
Refinement program	PHENIX (1.12_2829)	Depositor
R, $R_{free}$	0.197 , 0.247 0.209 , 0.253	Depositor DCC
$R_{free}$ test set	1494 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	117.7	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 101.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.046 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	13236	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	136.0	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 29.89 % 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 1.4340e-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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, BMA, NAG, MAN

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	0.51	0/3134	0.71	0/4268
1	B	0.47	1/3134 (0.0%)	0.68	0/4268
2	C	0.38	0/1687	0.63	0/2294
2	L	0.41	0/1687	0.67	0/2294
3	D	0.38	0/1780	0.63	0/2422
3	H	0.44	0/1780	0.69	0/2422
All	All	0.45	1/13202 (0.0%)	0.67	0/17968

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	296	GLN	C-N	-6.52	1.21	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	3051	0	2874	54	0
1	B	3051	0	2874	66	0
2	C	1650	0	1604	43	0
2	L	1650	0	1604	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	1736	0	1689	53	0
3	H	1736	0	1689	47	0
4	E	127	0	106	0	0
4	G	127	0	106	0	0
5	F	39	0	34	0	0
5	I	39	0	34	0	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
All	All	13236	0	12640	290	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 11.

The worst 5 of 290 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)
3:D:153:THR:HG22	3:D:211:ASN:HB3	1.50	0.94
2:C:214:CYS:SG	3:D:228:LYS:NZ	2.49	0.85
1:B:271:THR:HG21	1:B:338:ASN:HA	1.58	0.84
2:C:21:ILE:HG12	2:C:102:THR:HG21	1.59	0.84
1:A:379:VAL:HG23	1:A:382:ALA:HB2	1.59	0.83

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	386/393 (98%)	365 (95%)	20 (5%)	1 (0%)	41 75
1	B	386/393 (98%)	363 (94%)	22 (6%)	1 (0%)	41 75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	213/216 (99%)	196 (92%)	16 (8%)	1 (0%)	29	66
2	L	213/216 (99%)	196 (92%)	16 (8%)	1 (0%)	29	66
3	D	223/240 (93%)	210 (94%)	11 (5%)	2 (1%)	17	54
3	H	223/240 (93%)	209 (94%)	12 (5%)	2 (1%)	17	54
All	All	1644/1698 (97%)	1539 (94%)	97 (6%)	8 (0%)	29	66

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	342	PRO
1	B	342	PRO
2	L	92	ASN
2	C	92	ASN
3	H	63	VAL

### 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	339/343 (99%)	334 (98%)	5 (2%)	65	84
1	B	339/343 (99%)	335 (99%)	4 (1%)	71	87
2	C	189/190 (100%)	183 (97%)	6 (3%)	39	69
2	L	189/190 (100%)	184 (97%)	5 (3%)	46	74
3	D	192/204 (94%)	183 (95%)	9 (5%)	26	59
3	H	192/204 (94%)	184 (96%)	8 (4%)	30	61
All	All	1440/1474 (98%)	1403 (97%)	37 (3%)	46	74

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	70	SER
3	H	211	ASN

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Mol	Chain	Res	Type
3	D	209	ASN
3	H	85	ASP
3	H	100(J)	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	345	ASN
1	B	136	GLN
3	H	203	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

28 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	$\# Z  > 2$
4	NAG	E	1	1,4	14,14,15	0.49	0	17,19,21	0.53	0
4	MAN	E	10	4	11,11,12	1.36	1 (9%)	15,15,17	1.23	2 (13%)
4	MAN	E	11	4	11,11,12	1.17	1 (9%)	15,15,17	1.20	1 (6%)
4	NAG	E	2	4	14,14,15	0.21	0	17,19,21	0.66	0
4	BMA	E	3	4	11,11,12	1.37	1 (9%)	15,15,17	1.35	3 (20%)
4	MAN	E	4	4	11,11,12	0.91	0	15,15,17	1.79	5 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	MAN	E	5	4	11,11,12	1.16	2 (18%)	15,15,17	1.73	3 (20%)
4	MAN	E	6	4	11,11,12	1.04	0	15,15,17	1.40	2 (13%)
4	MAN	E	7	4	11,11,12	0.99	1 (9%)	15,15,17	1.04	1 (6%)
4	MAN	E	8	4	11,11,12	1.07	1 (9%)	15,15,17	1.11	1 (6%)
4	MAN	E	9	4	11,11,12	1.56	3 (27%)	15,15,17	1.11	0
5	NAG	F	1	1,5	14,14,15	0.37	0	17,19,21	0.83	1 (5%)
5	NAG	F	2	5	14,14,15	0.26	0	17,19,21	0.56	0
5	BMA	F	3	5	11,11,12	1.47	2 (18%)	15,15,17	0.76	0
4	NAG	G	1	1,4	14,14,15	0.66	0	17,19,21	0.65	0
4	MAN	G	10	4	11,11,12	1.72	4 (36%)	15,15,17	1.05	2 (13%)
4	MAN	G	11	4	11,11,12	1.58	2 (18%)	15,15,17	1.63	1 (6%)
4	NAG	G	2	4	14,14,15	0.44	0	17,19,21	0.62	0
4	BMA	G	3	4	11,11,12	0.88	0	15,15,17	1.04	1 (6%)
4	MAN	G	4	4	11,11,12	1.09	1 (9%)	15,15,17	1.65	2 (13%)
4	MAN	G	5	4	11,11,12	0.98	0	15,15,17	1.54	1 (6%)
4	MAN	G	6	4	11,11,12	1.81	2 (18%)	15,15,17	1.53	2 (13%)
4	MAN	G	7	4	11,11,12	0.89	0	15,15,17	1.13	3 (20%)
4	MAN	G	8	4	11,11,12	0.87	0	15,15,17	1.25	1 (6%)
4	MAN	G	9	4	11,11,12	1.34	2 (18%)	15,15,17	1.23	1 (6%)
5	NAG	I	1	1,5	14,14,15	0.84	2 (14%)	17,19,21	0.95	1 (5%)
5	NAG	I	2	5	14,14,15	0.60	0	17,19,21	1.03	2 (11%)
5	BMA	I	3	5	11,11,12	1.70	2 (18%)	15,15,17	1.07	2 (13%)

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	E	1	1,4	-	2/6/23/26	0/1/1/1
4	MAN	E	10	4	-	0/2/19/22	0/1/1/1
4	MAN	E	11	4	-	0/2/19/22	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	BMA	E	3	4	-	0/2/19/22	0/1/1/1
4	MAN	E	4	4	-	0/2/19/22	0/1/1/1
4	MAN	E	5	4	-	0/2/19/22	0/1/1/1
4	MAN	E	6	4	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MAN	E	7	4	-	2/2/19/22	0/1/1/1
4	MAN	E	8	4	-	1/2/19/22	0/1/1/1
4	MAN	E	9	4	-	0/2/19/22	0/1/1/1
5	NAG	F	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	F	2	5	-	2/6/23/26	0/1/1/1
5	BMA	F	3	5	-	2/2/19/22	0/1/1/1
4	NAG	G	1	1,4	-	1/6/23/26	0/1/1/1
4	MAN	G	10	4	-	2/2/19/22	0/1/1/1
4	MAN	G	11	4	-	0/2/19/22	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	BMA	G	3	4	-	0/2/19/22	0/1/1/1
4	MAN	G	4	4	-	2/2/19/22	0/1/1/1
4	MAN	G	5	4	-	2/2/19/22	0/1/1/1
4	MAN	G	6	4	-	2/2/19/22	0/1/1/1
4	MAN	G	7	4	-	0/2/19/22	0/1/1/1
4	MAN	G	8	4	-	0/2/19/22	0/1/1/1
4	MAN	G	9	4	-	2/2/19/22	0/1/1/1
5	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	3/6/23/26	0/1/1/1
5	BMA	I	3	5	-	2/2/19/22	0/1/1/1

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	6	MAN	C2-C3	4.26	1.58	1.52
5	I	3	BMA	C1-C2	3.89	1.61	1.52
4	G	11	MAN	O5-C5	3.26	1.50	1.43
4	E	10	MAN	C4-C5	3.21	1.59	1.53
4	E	3	BMA	C2-C3	-3.04	1.48	1.52

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	5	MAN	C1-O5-C5	4.90	118.83	112.19
4	G	4	MAN	C1-O5-C5	4.60	118.43	112.19
4	G	11	MAN	C1-O5-C5	4.40	118.15	112.19
4	G	6	MAN	C1-O5-C5	4.29	118.00	112.19
4	E	4	MAN	C1-O5-C5	3.99	117.60	112.19



There are no chirality outliers.

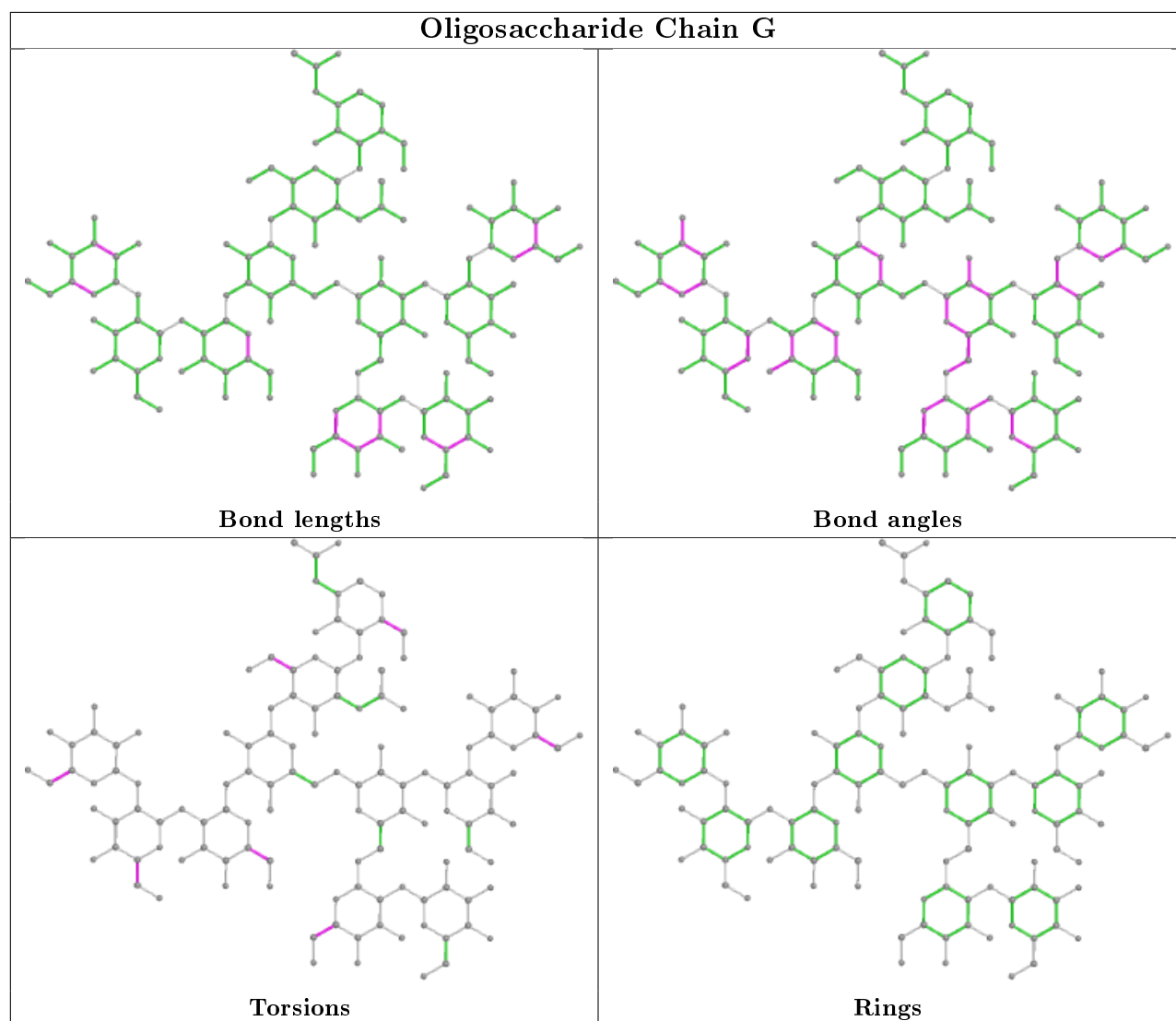
5 of 35 torsion outliers are listed below:

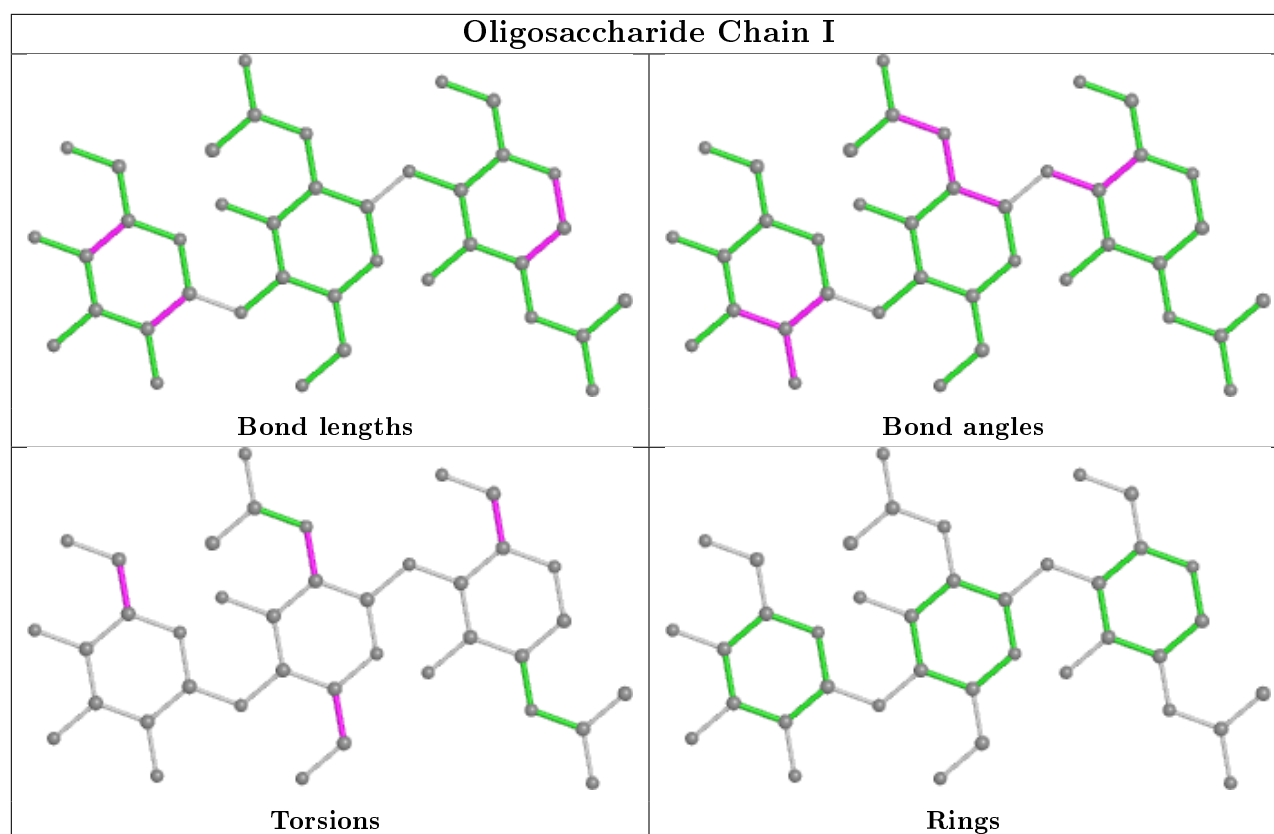
Mol	Chain	Res	Type	Atoms
4	G	6	MAN	O5-C5-C6-O6
4	G	10	MAN	O5-C5-C6-O6
5	I	3	BMA	C4-C5-C6-O6
5	I	3	BMA	O5-C5-C6-O6
5	I	1	NAG	C4-C5-C6-O6

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
6	NAG	A	501	1	14,14,15	0.88	1 (7%)	17,19,21	1.23	1 (5%)
6	NAG	B	501	1	14,14,15	0.74	1 (7%)	17,19,21	1.04	1 (5%)

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	NAG	A	501	1	-	1/6/23/26	0/1/1/1
6	NAG	B	501	1	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	501	NAG	O5-C1	3.08	1.48	1.43
6	B	501	NAG	O5-C1	2.31	1.47	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	501	NAG	C1-O5-C5	4.42	118.18	112.19
6	B	501	NAG	C1-O5-C5	3.64	117.12	112.19

There are no chirality outliers.

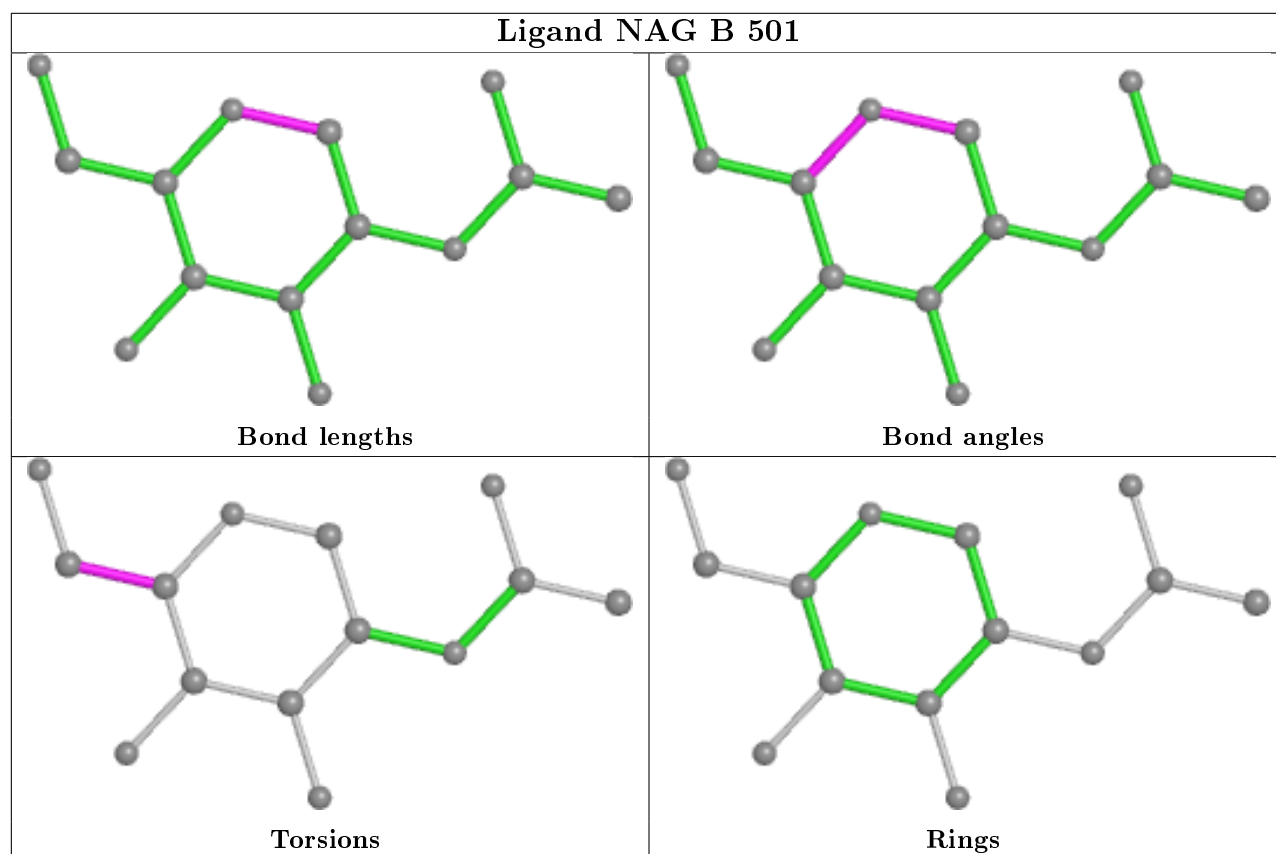
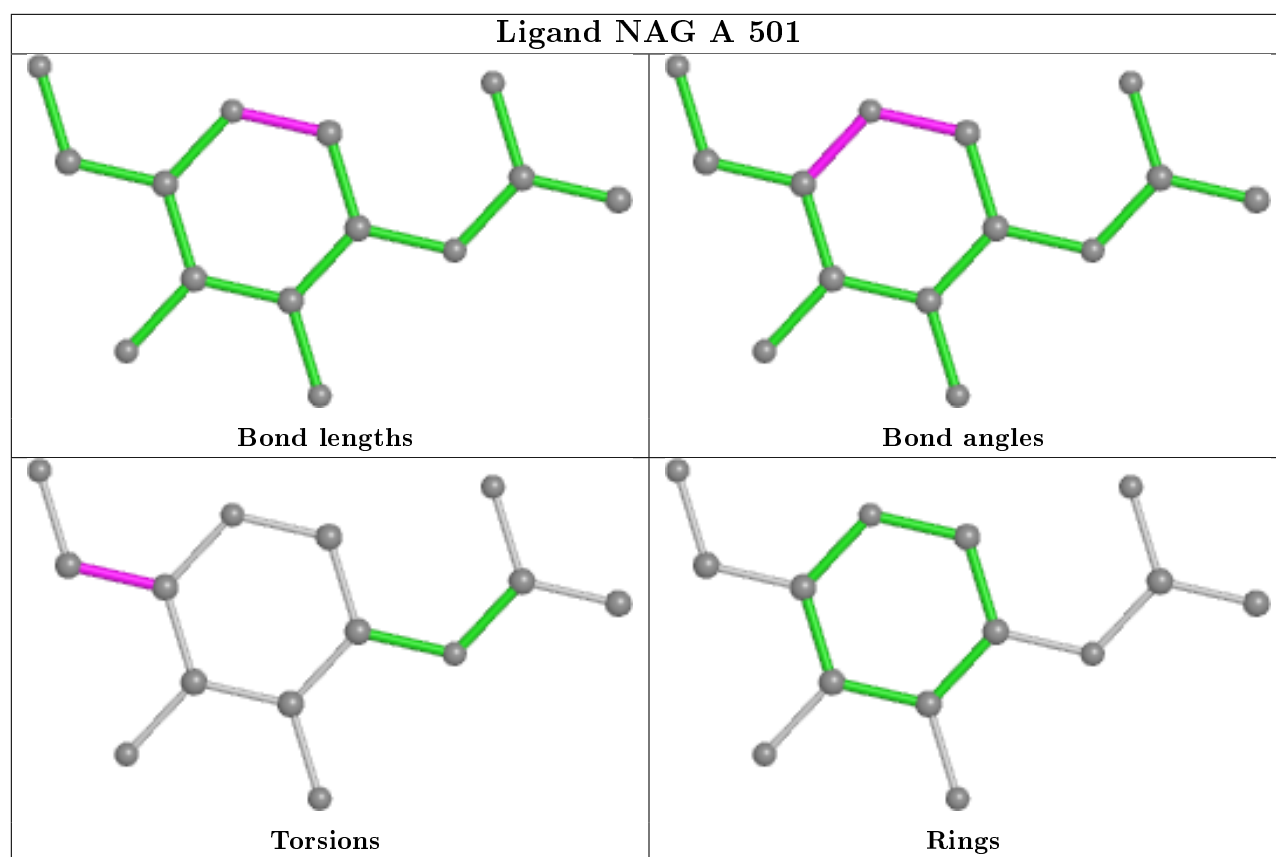
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	501	NAG	C4-C5-C6-O6
6	B	501	NAG	O5-C5-C6-O6
6	A	501	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 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, 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	388/393 (98%)	0.25	5 (1%) 77 74	69, 101, 134, 182	0
1	B	388/393 (98%)	0.29	6 (1%) 73 71	87, 120, 150, 208	0
2	C	215/216 (99%)	1.07	46 (21%) 0 1	101, 181, 216, 229	0
2	L	215/216 (99%)	0.33	11 (5%) 28 28	89, 141, 181, 192	0
3	D	227/240 (94%)	0.99	50 (22%) 0 1	113, 173, 223, 243	0
3	H	227/240 (94%)	0.28	10 (4%) 34 33	76, 141, 162, 175	0
All	All	1660/1698 (97%)	0.48	128 (7%) 13 16	69, 132, 206, 243	0

The worst 5 of 128 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	115	VAL	7.8
2	C	135	LEU	7.1
3	D	125	ALA	6.9
3	D	206	TYR	6.2
2	C	147	GLN	5.9

### 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](#)

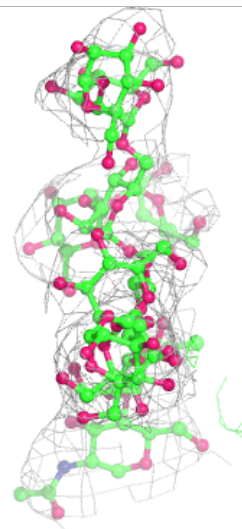
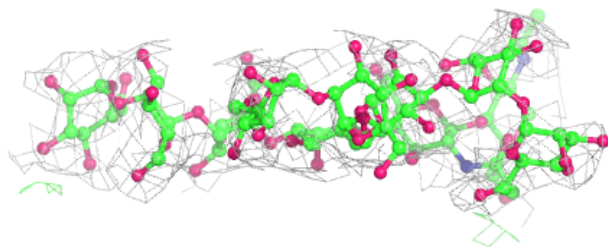
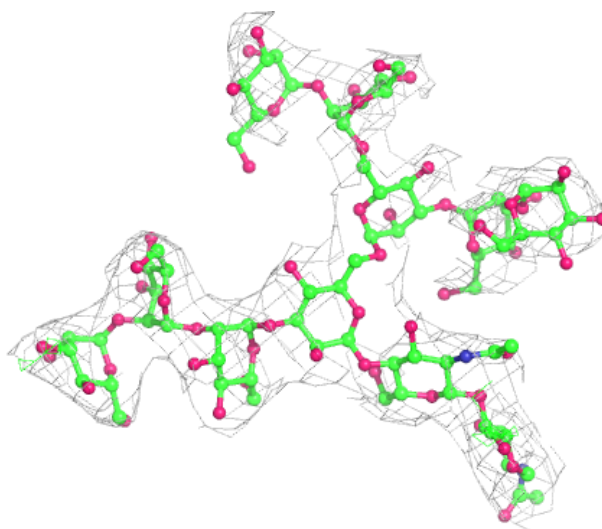
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MAN	E	9	11/12	0.73	0.34	126,155,180,187	0
5	BMA	F	3	11/12	0.76	0.18	153,198,211,211	0
5	BMA	I	3	11/12	0.84	0.16	128,175,191,196	0
4	MAN	G	11	11/12	0.85	0.30	132,165,182,183	0
4	MAN	E	11	11/12	0.86	0.26	131,156,177,184	0
4	MAN	G	9	11/12	0.87	0.30	138,172,194,199	0
4	MAN	E	10	11/12	0.90	0.12	120,136,152,153	0
4	MAN	E	6	11/12	0.90	0.20	110,122,146,149	0
4	MAN	G	6	11/12	0.91	0.30	118,129,150,152	0
4	MAN	G	4	11/12	0.91	0.22	117,136,142,147	0
4	BMA	G	3	11/12	0.93	0.11	128,140,150,159	0
5	NAG	F	2	14/15	0.93	0.17	106,176,206,227	0
4	MAN	G	10	11/12	0.93	0.15	137,158,173,183	0
4	NAG	E	1	14/15	0.93	0.21	100,113,129,143	0
4	NAG	G	2	14/15	0.93	0.19	115,128,149,151	0
5	NAG	F	1	14/15	0.94	0.14	113,131,150,156	0
5	NAG	I	1	14/15	0.94	0.14	100,126,142,165	0
4	MAN	G	5	11/12	0.94	0.23	98,125,143,151	0
5	NAG	I	2	14/15	0.94	0.16	151,179,198,203	0
4	MAN	E	8	11/12	0.94	0.14	126,133,148,155	0
4	MAN	G	8	11/12	0.95	0.13	140,159,167,167	0
4	MAN	E	5	11/12	0.95	0.22	104,108,124,133	0
4	MAN	E	7	11/12	0.95	0.10	100,113,126,148	0
4	MAN	E	4	11/12	0.96	0.13	93,110,124,130	0
4	MAN	G	7	11/12	0.96	0.07	141,154,163,170	0
4	BMA	E	3	11/12	0.96	0.11	101,113,130,137	0
4	NAG	G	1	14/15	0.96	0.16	109,122,135,144	0
4	NAG	E	2	14/15	0.97	0.17	93,104,121,128	0

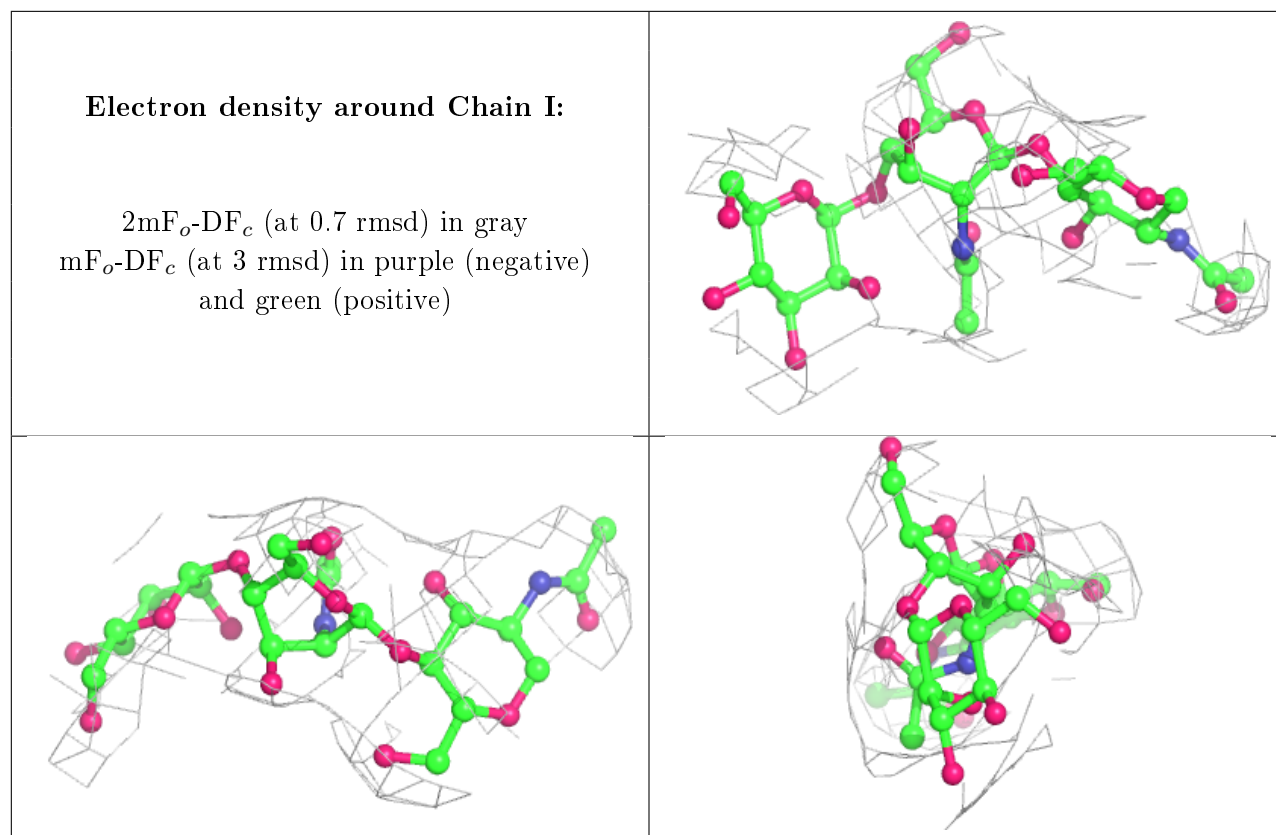
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around Chain G:**

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







## 6.4 Ligands [i](#)

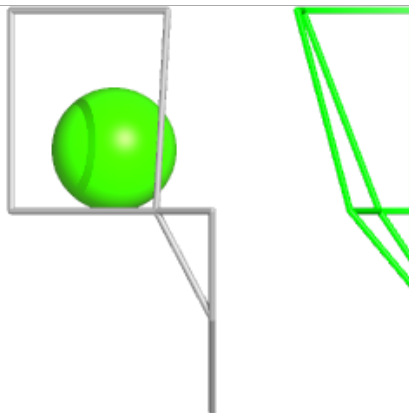
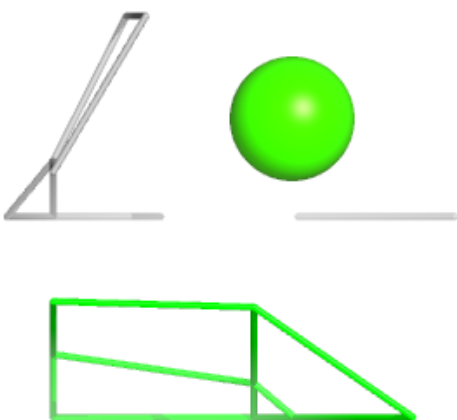
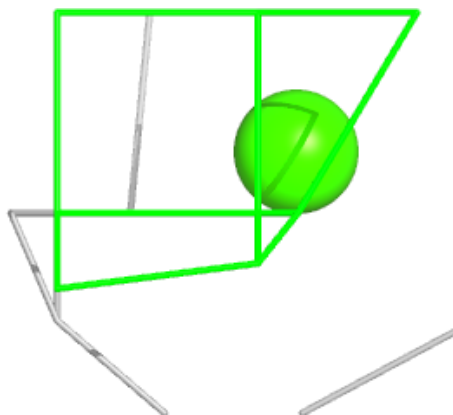
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
7	CA	B	516	1/1	0.48	0.62	154,154,154,154	0
6	NAG	A	501	14/15	0.60	0.56	134,203,219,220	0
6	NAG	B	501	14/15	0.66	0.47	151,206,215,219	0
7	CA	A	516	1/1	0.82	0.34	146,146,146,146	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.

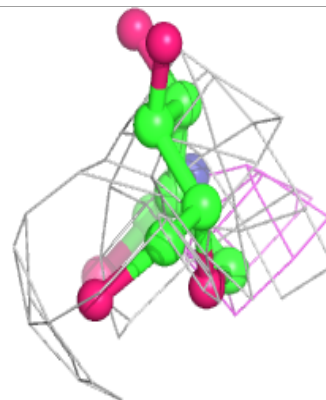
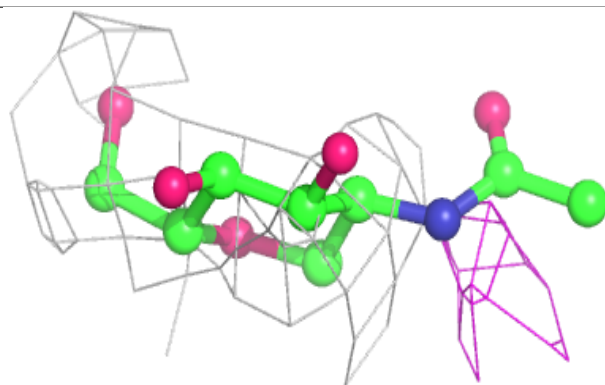
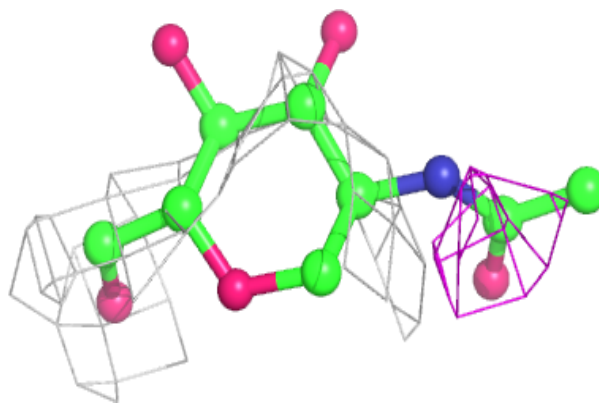
**Electron density around CA B 516:**

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

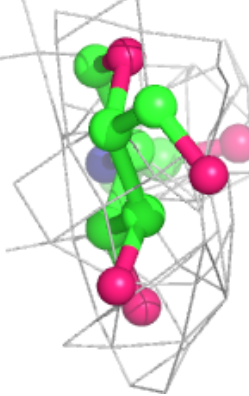
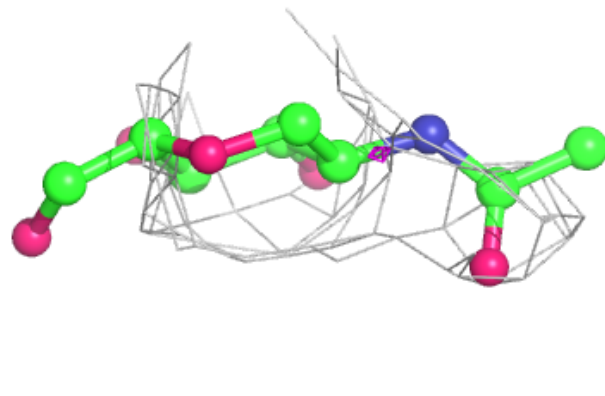
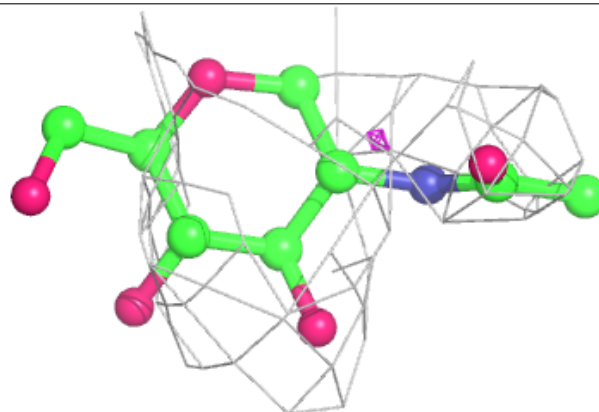


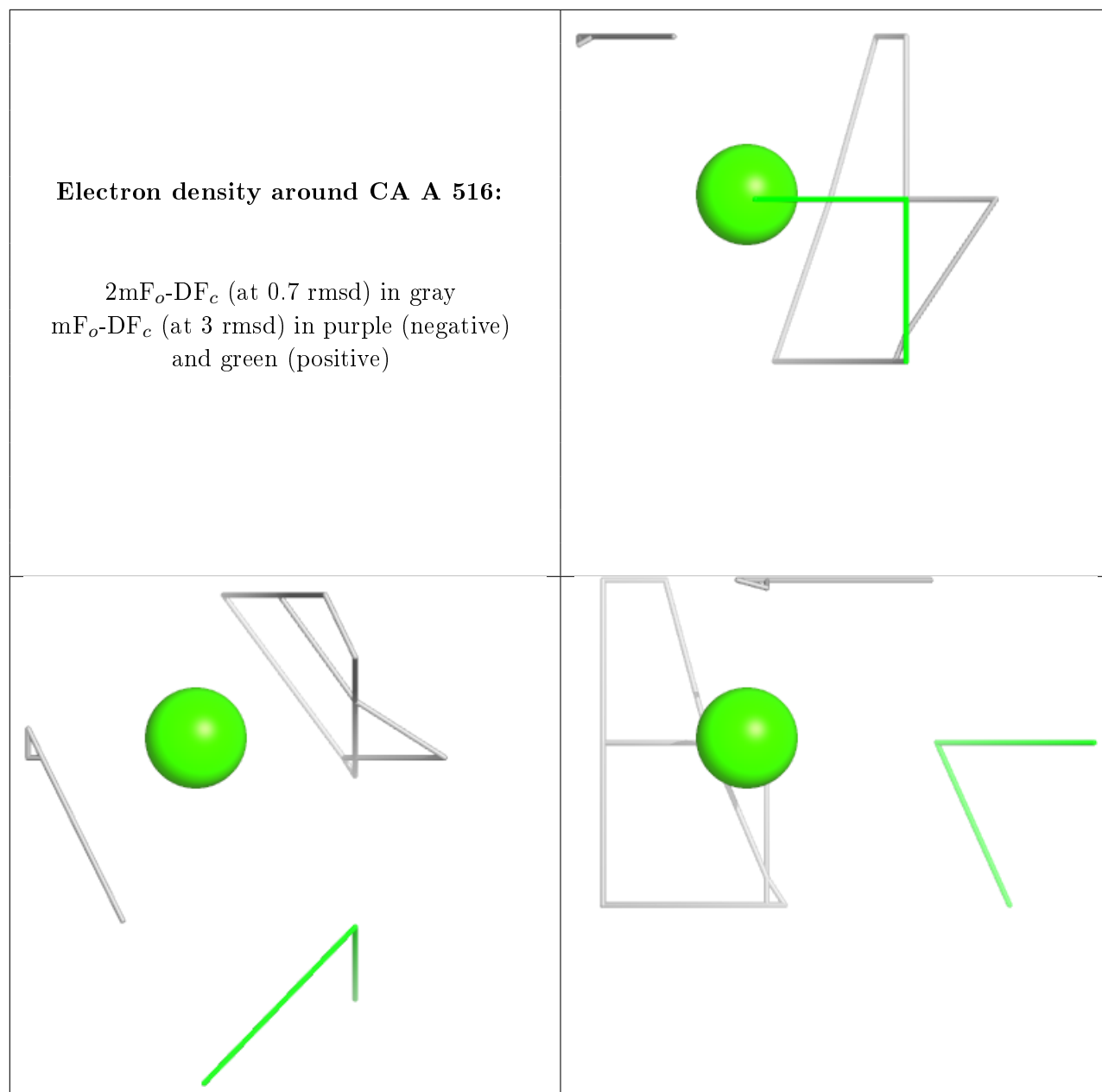
**Electron density around NAG A 501:**

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

**Electron density around NAG B 501:**

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





## 6.5 Other polymers ⓘ

There are no such residues in this entry.