



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 17, 2021 – 12:10 PM JST

PDB ID : 7CEE  
Title : Crystal structure of mouse neuroligin-3  
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Deposited on : 2020-06-23  
Resolution : 2.76 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](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 : 2.16  
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) : 2.16

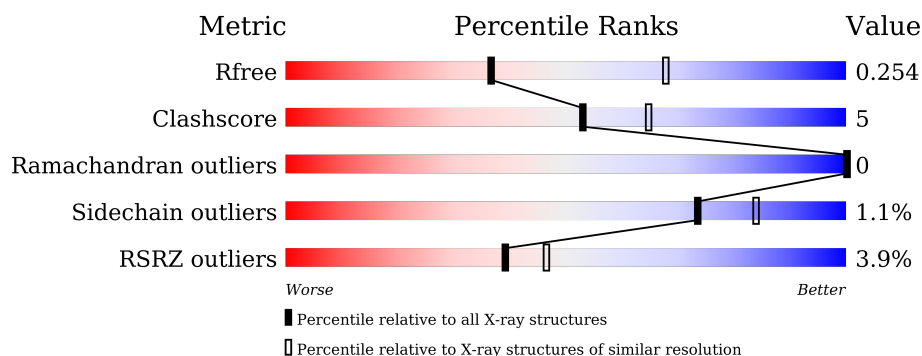
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.76 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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

Mol	Chain	Length	Quality of chain
1	A	655	<div> <div>3%</div> <div>69%</div> <div>12%</div> <div>18%</div> </div>
1	B	655	<div> <div>3%</div> <div>69%</div> <div>11%</div> <div>19%</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
2	NAG	B	1002	-	-	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8489 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 Neuroligin-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	S	0	0	0
			4190	2695	698	778	19			
1	B	533	Total	C	N	O	S	0	0	0
			4184	2692	697	776	19			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	685	HIS	-	expression tag	UNP Q8BYM5
A	686	HIS	-	expression tag	UNP Q8BYM5
A	687	HIS	-	expression tag	UNP Q8BYM5
A	688	HIS	-	expression tag	UNP Q8BYM5
A	689	HIS	-	expression tag	UNP Q8BYM5
A	690	HIS	-	expression tag	UNP Q8BYM5
B	685	HIS	-	expression tag	UNP Q8BYM5
B	686	HIS	-	expression tag	UNP Q8BYM5
B	687	HIS	-	expression tag	UNP Q8BYM5
B	688	HIS	-	expression tag	UNP Q8BYM5
B	689	HIS	-	expression tag	UNP Q8BYM5
B	690	HIS	-	expression tag	UNP Q8BYM5

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	31	Total	O	0	0
			31	31		
3	B	28	Total	O	0	0
			28	28		

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.

[illegible]

Chain B:

Category	Percentage
Green	69%
Yellow	11%
Grey	19%

ASN  
GLY  
LYS  
THR  
TRP  
SER  
THR  
LYS  
ARG  
PRO  
ALA  
ILE  
SER  
PRO  
ALA  
TYR  
SER  
ASN  
GLU  
ASN  
ALA  
PRO  
GLY  
SER  
TRP  
ASN  
GLY  
ASP  
GLN  
ASP  
ALA  
GLY  
PRO  
LEU  
LEU  
VAL  
GLU  
ASN  
PRO  
ARG  
ASP  
TYR  
SER  
THR  
GLU  
HIS  
HIS  
HIS  
HIS  
HIS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.84Å 167.14Å 177.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.66 – 2.76 49.66 – 2.76	Depositor EDS
% Data completeness (in resolution range)	98.3 (49.66-2.76) 98.3 (49.66-2.76)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.217 , 0.251 0.222 , 0.254	Depositor DCC
$R_{free}$ test set	2501 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.7	Xtriage
Anisotropy	0.665	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 34.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	8489	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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



## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.23	0/4316	0.44	0/5899
1	B	0.23	0/4310	0.45	0/5891
All	All	0.23	0/8626	0.45	0/11790

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

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	4190	0	4042	46	0
1	B	4184	0	4038	44	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
3	A	31	0	0	1	0
3	B	28	0	0	1	0
All	All	8489	0	8132	90	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 (90) 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:420:TYR:HA	1:A:424:LYS:HD2	1.57	0.86
1:B:420:TYR:HA	1:B:424:LYS:HD2	1.55	0.85
1:B:178:PRO:HG2	1:B:543:LYS:HG2	1.68	0.75
1:B:414:VAL:HG12	1:B:424:LYS:HE2	1.72	0.71
1:B:319:VAL:HG22	1:B:325:MET:HB3	1.74	0.69
1:B:95:ASN:OD1	1:B:97:THR:OG1	2.13	0.64
1:A:205:GLY:HA3	1:A:539:THR:HG21	1.80	0.64
1:A:238:GLN:HE22	1:A:270:CYS:HB3	1.63	0.64
1:B:205:GLY:HA3	1:B:539:THR:HG21	1.78	0.63
1:B:373:PHE:H	1:B:373:PHE:HD2	1.49	0.60
1:B:68:GLY:HA2	1:B:100:PRO:HG3	1.84	0.59
1:A:178:PRO:HG2	1:A:543:LYS:HG2	1.84	0.58
1:A:322:THR:HA	1:A:325:MET:HG2	1.86	0.57
1:B:425:ASP:OD1	1:B:428:ARG:NH2	2.36	0.57
1:B:56:PRO:HG3	1:B:513:VAL:HG13	1.87	0.57
1:A:68:GLY:HA2	1:A:100:PRO:HG3	1.89	0.55
1:A:399:ASP:O	1:A:448:ARG:NH1	2.40	0.55
1:A:373:PHE:HD2	1:A:373:PHE:H	1.53	0.54
1:B:592:HIS:HB3	1:B:595:ALA:HB2	1.90	0.54
1:B:473:ARG:HD3	1:B:474:TYR:CZ	2.44	0.53
1:A:539:THR:O	1:A:543:LYS:HG3	2.07	0.53
1:B:55:LEU:HD21	1:B:199:SER:HB3	1.91	0.53
1:A:117:PRO:HG2	1:A:120:PHE:HB2	1.91	0.53
1:A:319:VAL:HG22	1:A:325:MET:HB3	1.91	0.52
1:A:181:VAL:HB	1:A:261:VAL:HG12	1.93	0.51
1:B:51:ALA:HB2	1:B:97:THR:HG22	1.92	0.51
1:B:117:PRO:HG2	1:B:120:PHE:HB2	1.91	0.51
1:A:183:ILE:HD13	1:A:238:GLN:HE21	1.75	0.50
1:B:582:HIS:ND1	3:B:1101:HOH:O	2.34	0.49
1:B:539:THR:O	1:B:543:LYS:HG3	2.13	0.49
1:A:55:LEU:HD21	1:A:199:SER:HB3	1.94	0.49
1:A:378:ILE:HD12	1:A:471:HIS:CD2	2.47	0.49
1:B:399:ASP:O	1:B:448:ARG:NH1	2.44	0.49
1:A:268:ALA:HB1	1:A:289:ILE:HG23	1.95	0.48
1:A:592:HIS:HB3	1:A:595:ALA:HB2	1.96	0.48
1:B:526:ASN:HB3	1:B:585:LEU:HD23	1.95	0.48
1:A:378:ILE:HB	1:A:471:HIS:CE1	2.48	0.48
1:A:401:VAL:O	1:A:447:ARG:HD2	2.14	0.48
1:B:181:VAL:HB	1:B:261:VAL:HG12	1.95	0.48
1:B:311:LEU:O	1:B:315:VAL:HG22	2.14	0.48
1:B:364:PRO:O	1:B:368:MET:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:427:LEU:O	1:B:431:ILE:HG12	2.14	0.47
1:A:391:VAL:HG11	1:A:451:LEU:HB3	1.96	0.47
1:A:314:LYS:NZ	1:A:341:ASP:O	2.48	0.46
1:B:215:ARG:HB3	1:B:220:GLY:HA2	1.97	0.46
1:A:215:ARG:HB3	1:A:220:GLY:HA2	1.97	0.46
1:A:425:ASP:OD1	1:A:428:ARG:NH2	2.44	0.46
1:A:396:ASP:HB2	1:A:397:PRO:HD2	1.98	0.46
1:A:427:LEU:O	1:A:431:ILE:HG12	2.17	0.45
1:A:56:PRO:HG3	1:A:513:VAL:HG13	1.97	0.45
1:A:443:ASN:HA	1:A:444:PRO:HD3	1.84	0.45
1:A:311:LEU:O	1:A:315:VAL:HG22	2.16	0.45
1:B:315:VAL:HB	1:B:332:LYS:HE3	1.98	0.45
1:B:511:PRO:HG3	1:B:523:PHE:CD1	2.51	0.44
1:A:505:PRO:HG3	1:A:519:PHE:CE1	2.52	0.44
1:A:521:CYS:HB2	1:A:523:PHE:CZ	2.53	0.44
1:A:183:ILE:HD13	1:A:238:GLN:NE2	2.32	0.44
1:B:262:PHE:HB3	1:B:288:ILE:HB	1.99	0.44
1:B:505:PRO:HG3	1:B:519:PHE:CE1	2.52	0.44
1:A:596:THR:OG1	3:A:1101:HOH:O	2.20	0.43
1:B:396:ASP:HB2	1:B:397:PRO:HD2	2.01	0.43
1:A:415:ASP:OD1	1:A:424:LYS:NZ	2.41	0.43
1:B:415:ASP:OD1	1:B:424:LYS:NZ	2.42	0.43
1:B:465:VAL:HG11	1:B:598:VAL:HG11	2.00	0.43
1:A:177:LYS:HA	1:A:178:PRO:HD3	1.89	0.42
1:A:380:LEU:O	1:A:480:PHE:HA	2.19	0.42
1:A:205:GLY:O	1:A:543:LYS:NZ	2.53	0.42
1:B:394:VAL:HG12	1:B:394:VAL:O	2.20	0.42
1:B:462:GLU:HG3	1:B:601:TRP:HB2	2.00	0.42
1:A:394:VAL:O	1:A:394:VAL:HG12	2.19	0.42
1:B:325:MET:O	1:B:329:LEU:HG	2.19	0.42
1:B:422:GLU:HB2	1:B:610:ASN:OD1	2.19	0.42
1:B:187:SER:O	1:B:188:TYR:HB2	2.20	0.42
1:B:177:LYS:HA	1:B:178:PRO:HD3	1.94	0.41
1:B:87:PRO:HA	1:B:88:PRO:HD3	1.94	0.41
1:A:274:LEU:O	1:A:280:SER:OG	2.21	0.41
1:B:391:VAL:HG11	1:B:451:LEU:HB3	2.02	0.41
1:A:262:PHE:HB3	1:A:288:ILE:HB	2.03	0.41
1:A:76:ILE:N	1:A:79:LYS:HB2	2.35	0.41
1:A:579:LEU:HD23	1:A:591:ASP:HB3	2.03	0.41
1:B:235:LEU:O	1:B:239:ILE:HG12	2.21	0.41
1:A:410:VAL:O	1:A:414:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:378:ILE:HB	1:B:471:HIS:CE1	2.56	0.41
1:B:242:LEU:HD23	1:B:242:LEU:HA	1.94	0.40
1:B:53:VAL:HA	1:B:54:PRO:HD3	1.94	0.40
1:A:179:VAL:HG21	1:A:249:ILE:HG12	2.03	0.40
1:A:462:GLU:HB3	1:A:463:PRO:HD3	2.03	0.40
1:A:315:VAL:HB	1:A:332:LYS:HE3	2.03	0.40
1:B:335:LYS:O	1:B:339:GLU:HG2	2.21	0.40
1:A:145:VAL:HA	1:A:146:PRO:HD3	1.90	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.

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	528/655 (81%)	513 (97%)	15 (3%)	0	100	100
1	B	527/655 (80%)	512 (97%)	15 (3%)	0	100	100
All	All	1055/1310 (80%)	1025 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	456/561 (81%)	451 (99%)	5 (1%)	73	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	455/561 (81%)	450 (99%)	5 (1%)	73	84
All	All	911/1122 (81%)	901 (99%)	10 (1%)	73	84

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	262	PHE
1	A	278	HIS
1	A	298	TRP
1	A	321	ASP
1	A	373	PHE
1	B	262	PHE
1	B	325	MET
1	B	373	PHE
1	B	486	HIS
1	B	596	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	ASN
1	A	238	GLN
1	A	375	ASN
1	A	416	ASN
1	A	582	HIS
1	B	194	ASN
1	B	416	ASN
1	B	488	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NAG	A	1002	1	14,14,15	0.53	0	17,19,21	0.70	0
2	NAG	B	1002	1	14,14,15	0.39	0	17,19,21	0.27	0
2	NAG	B	1001	1	14,14,15	0.75	0	17,19,21	0.66	0
2	NAG	A	1001	1	14,14,15	0.21	0	17,19,21	0.43	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1002	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1002	1	-	0/6/23/26	0/1/1/1
2	NAG	B	1001	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1001	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

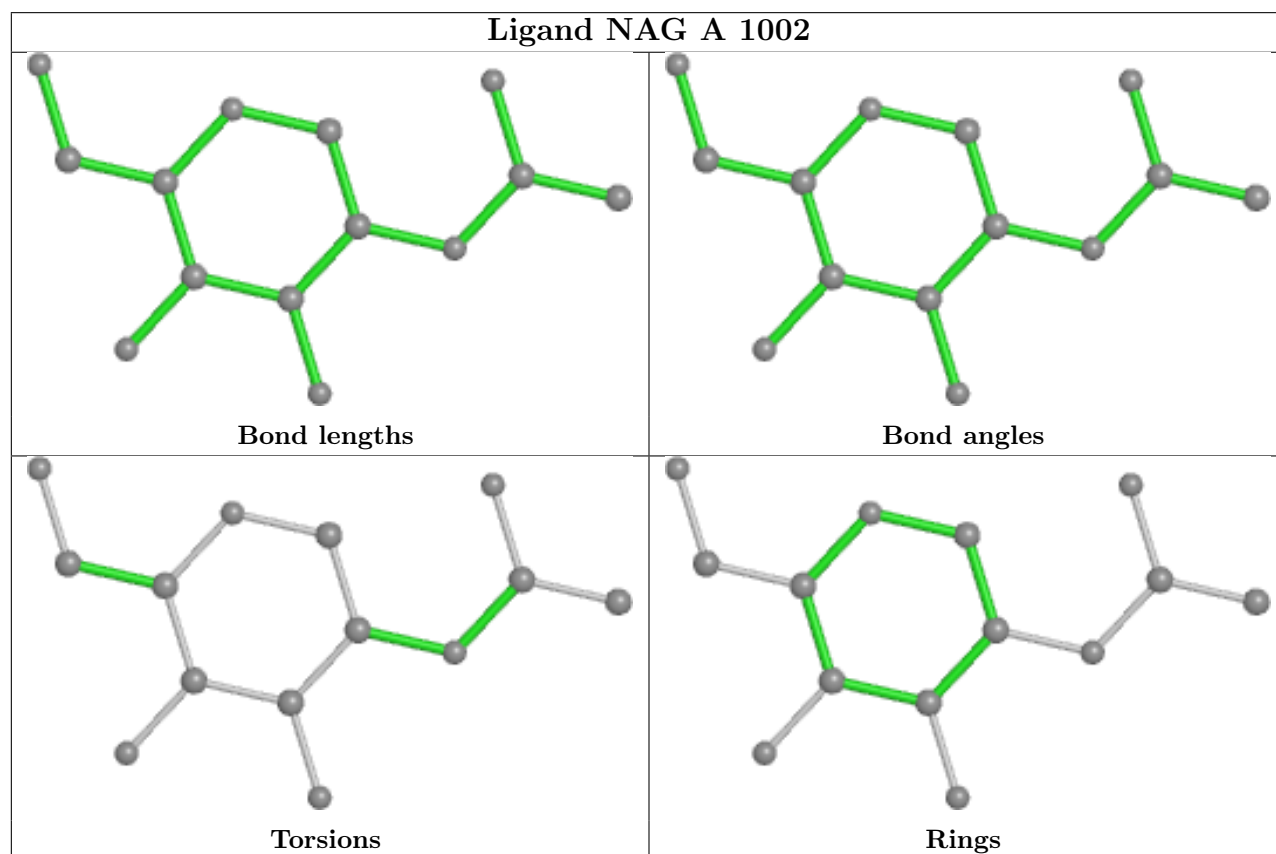
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1001	NAG	O5-C5-C6-O6
2	B	1001	NAG	C4-C5-C6-O6

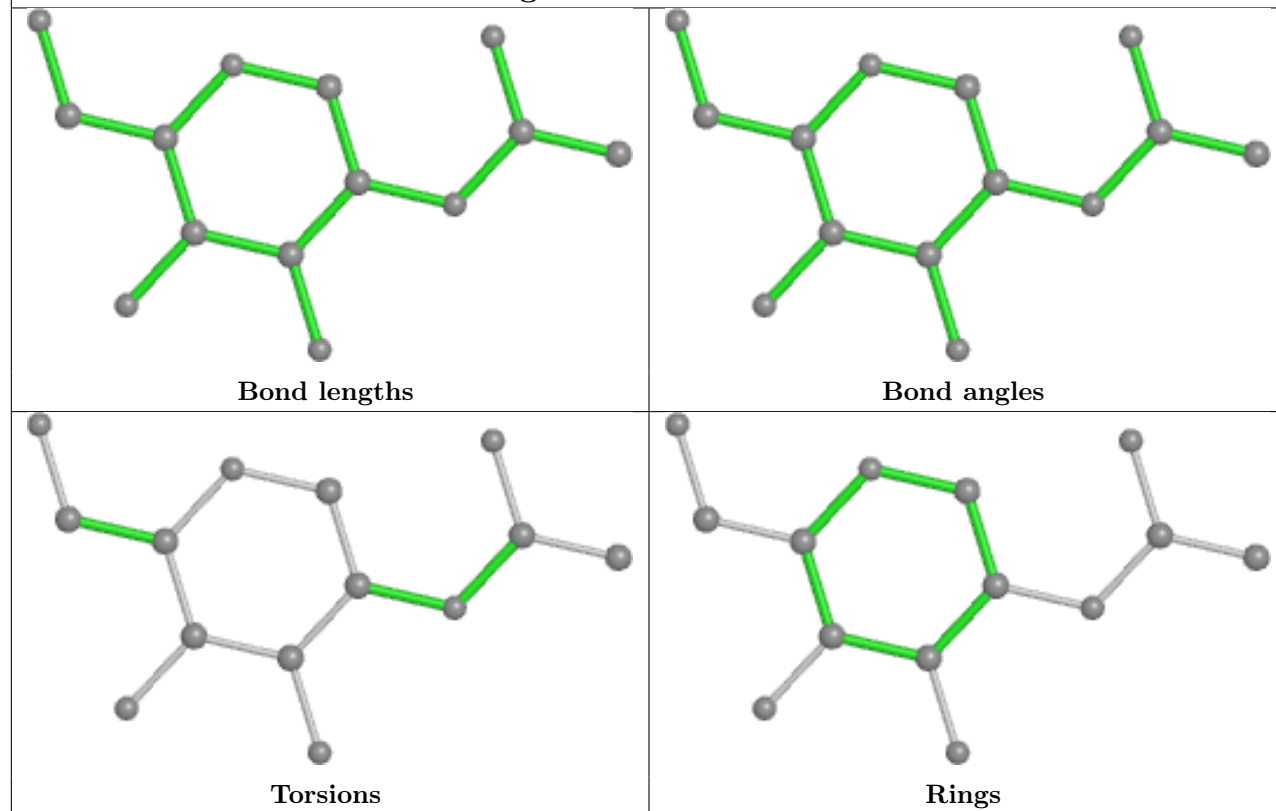
There are no ring outliers.

No monomer is involved in short contacts.

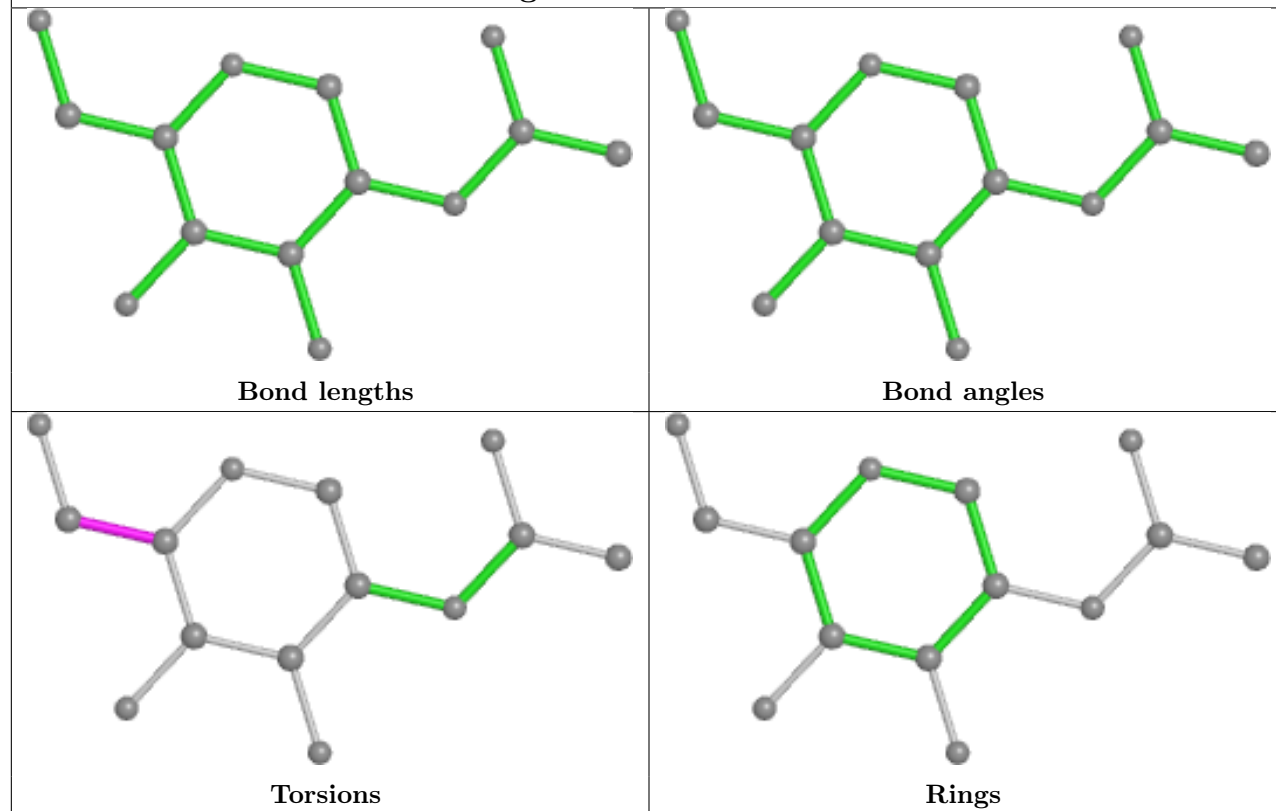
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



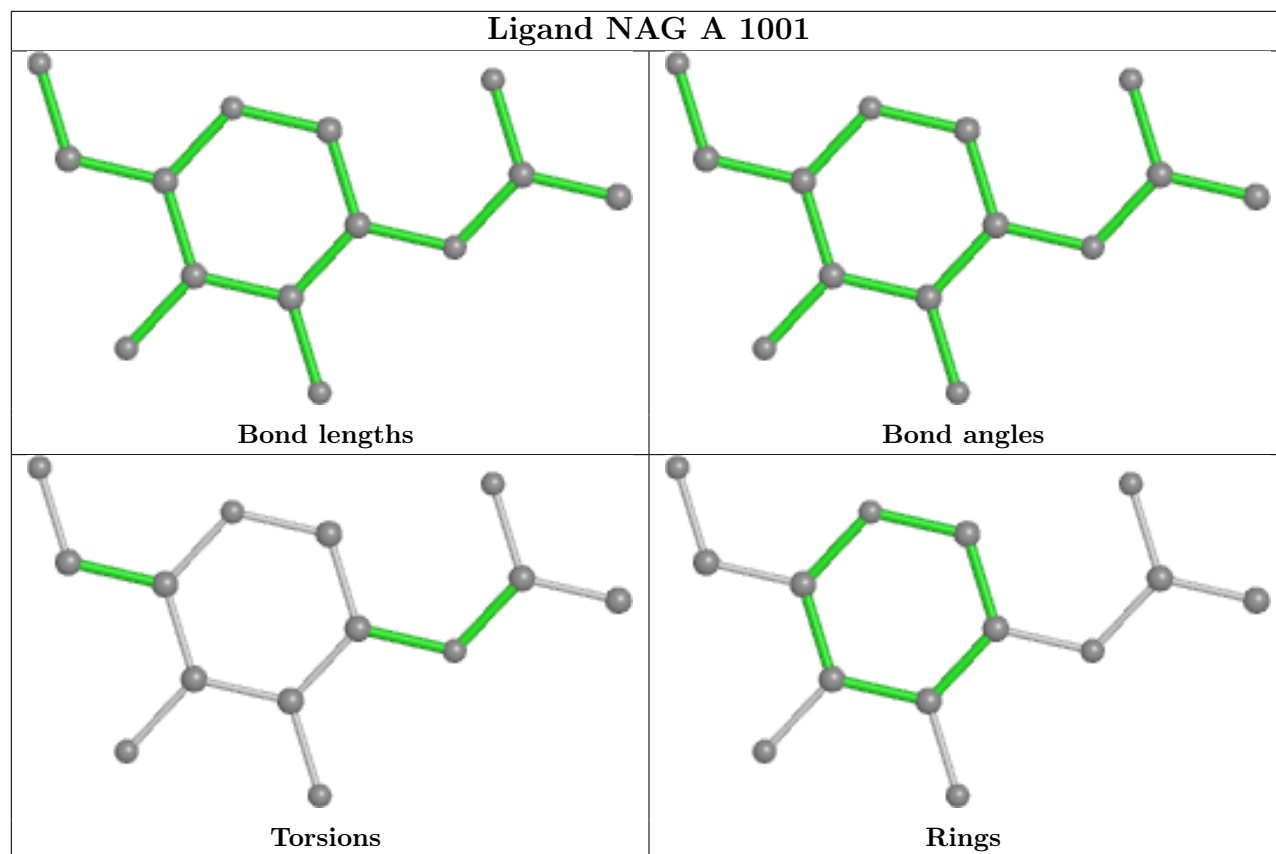
## Ligand NAG B 1002



## Ligand NAG B 1001







## 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

### 6.1 Protein, DNA and RNA chains

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	534/655 (81%)	0.20	20 (3%) 41 49	44, 62, 104, 152	0
1	B	533/655 (81%)	0.31	22 (4%) 37 44	47, 69, 121, 179	0
All	All	1067/1310 (81%)	0.25	42 (3%) 39 46	44, 65, 111, 179	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	554	ASP	5.9
1	B	422	GLU	4.9
1	B	420	TYR	4.9
1	A	422	GLU	4.4
1	A	568	VAL	4.3
1	B	320	LEU	4.2
1	B	108	HIS	4.1
1	B	609	TYR	3.8
1	A	421	PRO	3.8
1	A	420	TYR	3.7
1	B	38	ALA	3.7
1	A	66	TYR	3.6
1	A	609	TYR	3.6
1	B	585	LEU	3.6
1	A	49	ARG	3.5
1	B	490	LEU	3.4
1	B	424	LYS	3.4
1	B	421	PRO	3.3
1	A	47	LYS	3.2
1	A	554	ASP	3.1
1	A	553	GLN	3.0
1	A	38	ALA	2.8
1	B	308	THR	2.7
1	B	608	LEU	2.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	93	ILE	2.4
1	A	576	ARG	2.4
1	A	608	LEU	2.4
1	A	50	GLY	2.4
1	B	610	ASN	2.4
1	B	228	ALA	2.4
1	A	424	LYS	2.3
1	A	551	VAL	2.3
1	B	318	ASN	2.3
1	B	307	TYR	2.2
1	B	222	LEU	2.2
1	B	319	VAL	2.1
1	A	610	ASN	2.1
1	A	398	GLU	2.1
1	B	568	VAL	2.1
1	B	224	THR	2.1
1	B	442	ASP	2.0
1	A	108	HIS	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](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

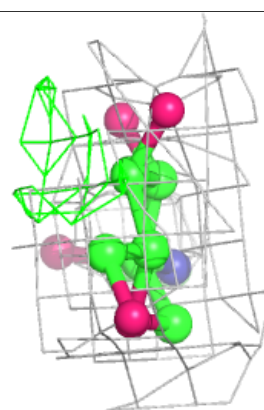
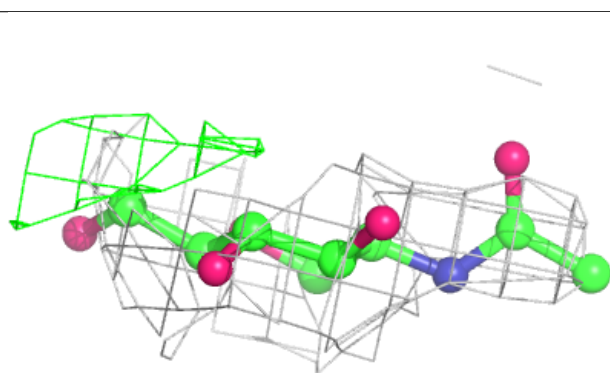
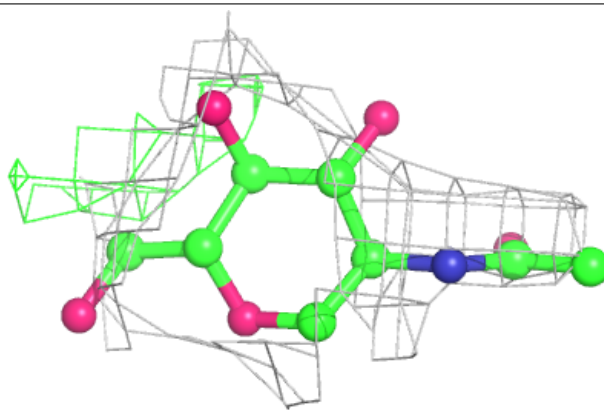
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	A	1002	14/15	0.73	0.34	122,132,135,136	0
2	NAG	B	1002	14/15	0.78	0.54	148,161,171,172	0
2	NAG	A	1001	14/15	0.78	0.31	98,106,109,112	0
2	NAG	B	1001	14/15	0.87	0.23	92,108,135,138	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.

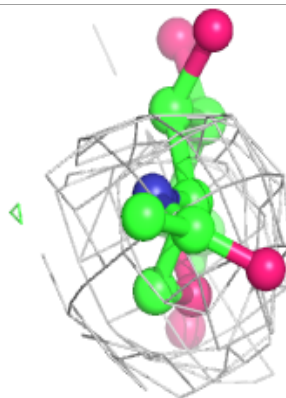
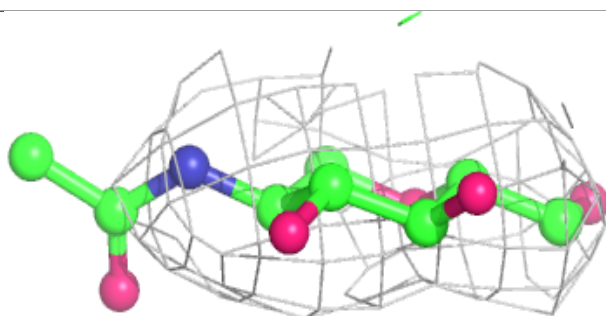
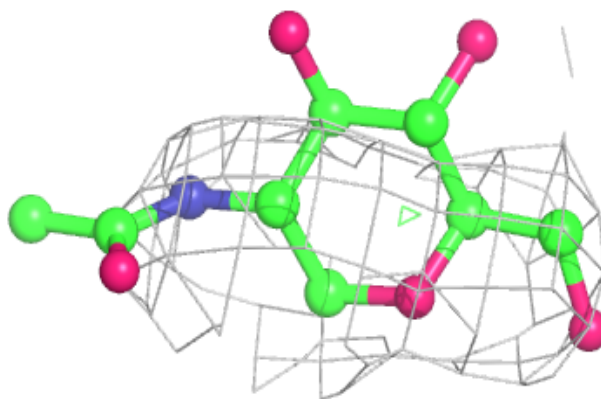
**Electron density around NAG A 1002:**

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

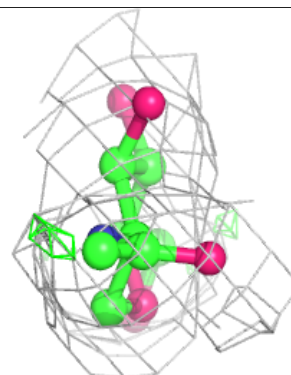
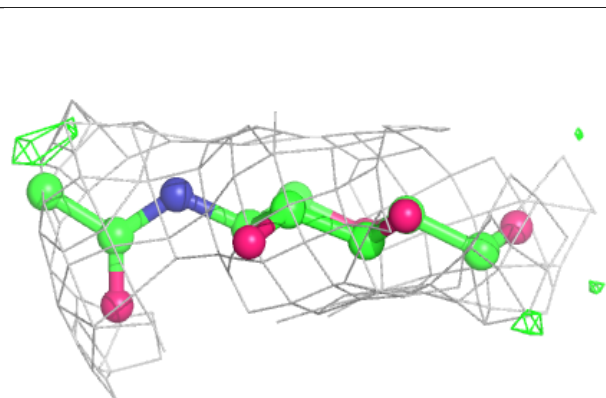
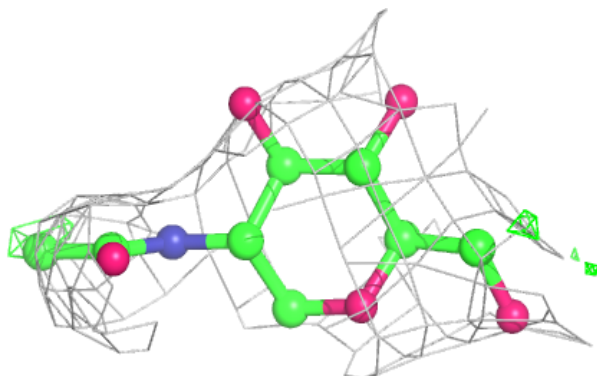


**Electron density around NAG B 1002:**

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

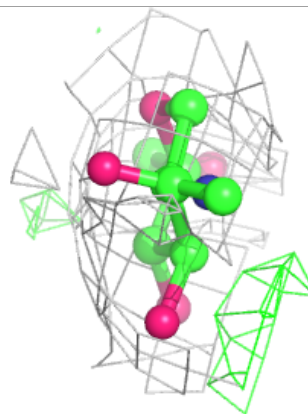
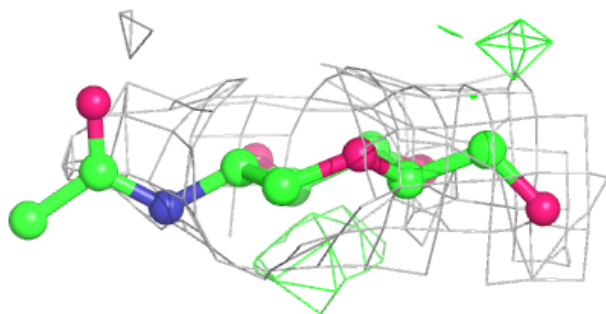
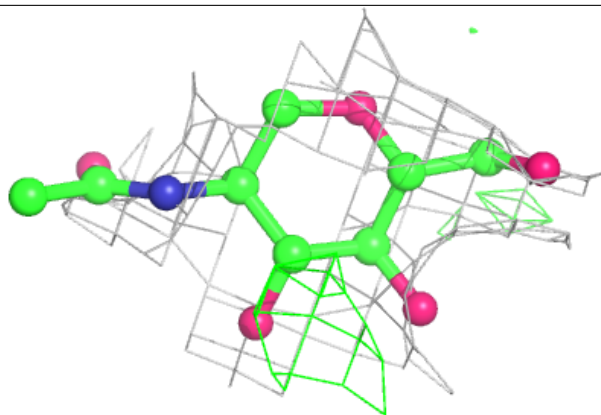
**Electron density around NAG A 1001:**

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



**Electron density around NAG B 1001:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.