



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 12:50 PM BST

PDB ID : 6L1Y
Title : structure of gp120/CD4 with a non-canonical surface
Authors : Liu, X.; Ning, W.
Deposited on : 2019-10-01
Resolution : 2.47 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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

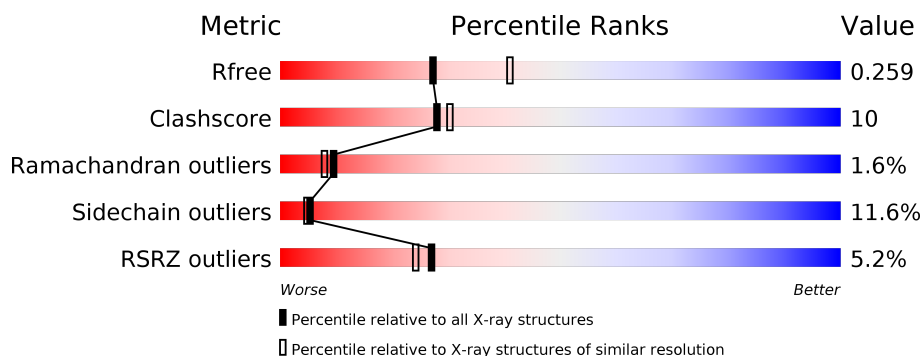
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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 ≥ 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	392	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 13%, orange 17%, yellow 17%, green 67%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 13% 67% 17% 13% </div> </div>
2	C	177	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 13%, orange 17%, yellow 32%, green 59%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 13% 59% 32% 8% </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	607	-	-	-	X
3	NAG	A	608	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4271 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.

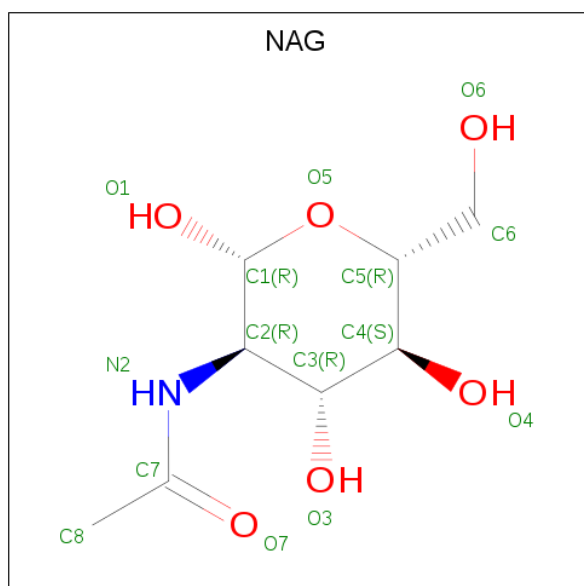
- Molecule 1 is a protein called gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2643	1656	460	506	21			

- Molecule 2 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	177	Total	C	N	O	S	0	0	0
			1378	862	241	271	4			

- Molecule 3 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).



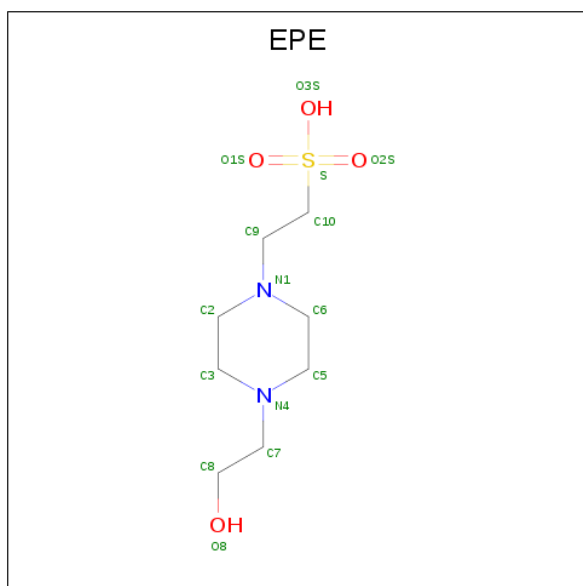
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	1
			15	8	2	4	1		

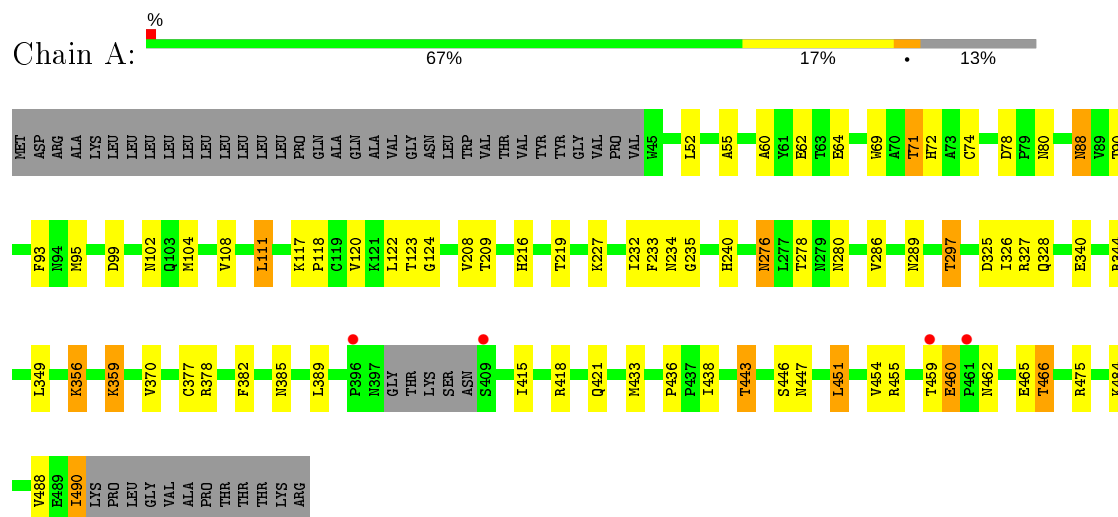
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	108	Total	O	0	0
			108	108		
5	C	15	Total	O	0	0
			15	15		

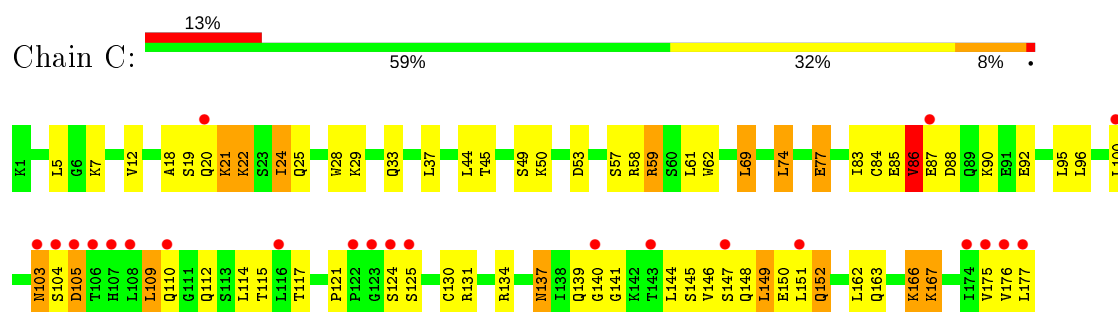
3 Residue-property plots [i](#)

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: gp120



• Molecule 2: T-cell surface glycoprotein CD4



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.44Å 66.47Å 73.85Å 90.00° 108.40° 90.00°	Depositor
Resolution (Å)	33.81 – 2.47 48.22 – 2.47	Depositor EDS
% Data completeness (in resolution range)	94.9 (33.81-2.47) 94.9 (48.22-2.47)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.203 , 0.257 0.203 , 0.259	Depositor DCC
R_{free} test set	1113 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	49.6	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4271	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EPE, 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	0.49	0/2700	0.67	0/3669
2	C	0.40	0/1397	0.66	0/1884
All	All	0.46	0/4097	0.67	0/5553

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2643	0	2575	43	0
2	C	1378	0	1409	40	0
3	A	112	0	104	4	0
4	A	15	0	17	0	0
5	A	108	0	0	5	0
5	C	15	0	0	1	0
All	All	4271	0	4105	82	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 10.

All (82) 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:356:LYS:HG2	1:A:465:GLU:HG2	1.55	0.86
2:C:109:LEU:HA	2:C:176:VAL:HG13	1.63	0.80
1:A:297:THR:HB	1:A:443:THR:HB	1.64	0.77
1:A:359:LYS:HE2	1:A:466:THR:HB	1.71	0.73
1:A:64:GLU:HA	1:A:209:THR:HG23	1.69	0.72
2:C:37:LEU:HG	2:C:44:LEU:HD11	1.69	0.72
2:C:18:ALA:O	2:C:20:GLN:N	2.23	0.72
2:C:115:THR:HG23	2:C:145:SER:HB3	1.74	0.69
2:C:162:LEU:HD23	2:C:167:LYS:HB3	1.77	0.66
1:A:90:THR:HG22	1:A:240:HIS:HA	1.79	0.64
2:C:12:VAL:HB	2:C:74:LEU:HD21	1.82	0.61
1:A:475:ARG:NE	5:A:707:HOH:O	2.28	0.61
1:A:289:ASN:HD21	3:A:604:NAG:C7	2.14	0.61
1:A:60:ALA:HA	1:A:71:THR:HG21	1.84	0.60
1:A:385:ASN:O	1:A:415:ILE:HG23	2.04	0.58
1:A:340:GLU:OE1	5:A:701:HOH:O	2.17	0.58
1:A:370:VAL:HG11	2:C:45:THR:HG22	1.86	0.57
2:C:103:ASN:HD21	2:C:117:THR:HB	1.69	0.57
1:A:327:ARG:NH1	1:A:421:GLN:OE1	2.38	0.56
2:C:18:ALA:HB2	2:C:86:VAL:HG11	1.88	0.56
2:C:109:LEU:HD23	2:C:110:GLN:HG2	1.89	0.54
2:C:112:GLN:O	2:C:149:LEU:HB2	2.08	0.54
1:A:436:PRO:O	5:A:702:HOH:O	2.19	0.54
1:A:325:ASP:OD2	1:A:418:ARG:NH2	2.41	0.54
1:A:74:CYS:HB2	5:A:727:HOH:O	2.08	0.54
1:A:286:VAL:HB	1:A:451:LEU:HB2	1.91	0.53
1:A:78:ASP:OD1	1:A:80:ASN:N	2.29	0.52
2:C:22:LYS:HD2	2:C:22:LYS:H	1.74	0.51
2:C:21:LYS:HB2	2:C:22:LYS:HD2	1.93	0.51
2:C:59:ARG:HA	2:C:62:TRP:CE2	2.46	0.50
2:C:28:TRP:CE2	2:C:69:LEU:HB2	2.46	0.50
1:A:93:PHE:HB2	1:A:233:PHE:HZ	1.78	0.49
2:C:85:GLU:HG2	2:C:90:LYS:HD2	1.95	0.49
1:A:389:LEU:HD13	1:A:415:ILE:HD11	1.95	0.48
2:C:131:ARG:NH1	2:C:137:ASN:OD1	2.47	0.47
2:C:37:LEU:HD21	2:C:57:SER:HB2	1.95	0.47
1:A:123:THR:HG22	1:A:124:GLY:N	2.29	0.47
2:C:121:PRO:HG2	2:C:124:SER:HB3	1.96	0.47
1:A:95:MET:SD	1:A:235:GLY:HA3	2.53	0.47
2:C:150:GLU:OE2	2:C:152:GLN:NE2	2.48	0.47
1:A:447:ASN:ND2	3:A:608:NAG:H4	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:59:ARG:HG3	2:C:59:ARG:H	1.54	0.46
2:C:18:ALA:HB1	2:C:21:LYS:HE2	1.98	0.46
2:C:21:LYS:HB2	2:C:22:LYS:H	1.48	0.46
2:C:5:LEU:HD11	2:C:166:LYS:HB3	1.97	0.46
1:A:377:CYS:HB3	1:A:382:PHE:CE2	2.51	0.45
1:A:447:ASN:HD21	3:A:608:NAG:H4	1.81	0.45
2:C:146:VAL:HG21	2:C:149:LEU:HD13	1.97	0.45
1:A:227:LYS:HA	1:A:484:LYS:O	2.17	0.44
2:C:83:ILE:HG13	2:C:92:GLU:HG2	2.00	0.44
2:C:50:LYS:HD2	2:C:50:LYS:HA	1.84	0.44
2:C:58:ARG:HD2	2:C:61:LEU:CD1	2.48	0.44
1:A:325:ASP:HB3	1:A:328:GLN:HB2	2.00	0.43
1:A:385:ASN:O	1:A:415:ILE:HD12	2.18	0.43
2:C:29:LYS:HD3	2:C:33:GLN:OE1	2.18	0.43
1:A:280:ASN:HB2	1:A:455:ARG:O	2.18	0.43
1:A:120:VAL:HB	1:A:433:MET:HB2	2.00	0.43
1:A:55:ALA:HB3	1:A:216:HIS:HB2	2.00	0.43
1:A:69:TRP:CD2	1:A:111:LEU:HD22	2.54	0.43
1:A:104:MET:O	1:A:108:VAL:HG23	2.18	0.43
1:A:276:ASN:HD21	3:A:603:NAG:C1	2.33	0.42
1:A:460:GLU:H	1:A:460:GLU:HG2	1.70	0.42
2:C:7:LYS:HG3	5:C:203:HOH:O	2.19	0.41
1:A:349:LEU:HD23	1:A:349:LEU:HA	1.80	0.41
1:A:490:ILE:HA	1:A:490:ILE:HD12	1.87	0.41
1:A:88:ASN:O	1:A:88:ASN:ND2	2.44	0.41
2:C:114:LEU:HB3	2:C:146:VAL:HG22	2.02	0.41
1:A:359:LYS:HE3	1:A:359:LYS:HB2	1.79	0.41
2:C:130:CYS:O	2:C:137:ASN:HA	2.20	0.41
1:A:340:GLU:O	1:A:344:ARG:HG3	2.20	0.41
2:C:114:LEU:HD22	2:C:115:THR:N	2.36	0.41
2:C:53:ASP:N	2:C:53:ASP:OD1	2.54	0.41
1:A:99:ASP:OD1	1:A:102:ASN:ND2	2.46	0.41
2:C:134:ARG:HE	2:C:152:GLN:HB2	1.85	0.41
2:C:77:GLU:HG3	2:C:77:GLU:H	1.52	0.41
1:A:378:ARG:NH1	5:A:721:HOH:O	2.52	0.41
1:A:62:GLU:HG3	1:A:64:GLU:H	1.85	0.41
2:C:140:GLY:HA3	2:C:144:LEU:HB3	2.02	0.41
1:A:117:LYS:HA	1:A:118:PRO:HD3	1.89	0.40
2:C:24:ILE:HB	2:C:87:GLU:OE1	2.22	0.40
2:C:163:GLN:O	2:C:166:LYS:HB3	2.22	0.40
2:C:28:TRP:CE2	2:C:84:CYS:HB2	2.56	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	337/392 (86%)	317 (94%)	18 (5%)	2 (1%)	25	29
2	C	175/177 (99%)	154 (88%)	15 (9%)	6 (3%)	3	1
All	All	512/569 (90%)	471 (92%)	33 (6%)	8 (2%)	9	8

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	19	SER
1	A	438	ILE
2	C	105	ASP
1	A	276	ASN
2	C	147	SER
2	C	166	LYS
2	C	86	VAL
2	C	141	GLY

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	297/341 (87%)	272 (92%)	25 (8%)	11	12
2	C	161/161 (100%)	133 (83%)	28 (17%)	2	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	458/502 (91%)	405 (88%)	53 (12%)	5 5

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	A	71	THR
1	A	72	HIS
1	A	88	ASN
1	A	111	LEU
1	A	122	LEU
1	A	208	VAL
1	A	219	THR
1	A	232	ILE
1	A	234	ASN
1	A	278	THR
1	A	297	THR
1	A	326	ILE
1	A	356	LYS
1	A	359	LYS
1	A	443	THR
1	A	446	SER
1	A	451	LEU
1	A	454	VAL
1	A	459	THR
1	A	460	GLU
1	A	462	ASN
1	A	466	THR
1	A	488	VAL
1	A	490	ILE
2	C	21	LYS
2	C	22	LYS
2	C	24	ILE
2	C	25	GLN
2	C	49	SER
2	C	59	ARG
2	C	69	LEU
2	C	74	LEU
2	C	77	GLU
2	C	86	VAL
2	C	88	ASP
2	C	95	LEU

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Mol	Chain	Res	Type
2	C	96	LEU
2	C	100	LEU
2	C	103	ASN
2	C	104	SER
2	C	105	ASP
2	C	109	LEU
2	C	125	SER
2	C	137	ASN
2	C	139	GLN
2	C	148	GLN
2	C	149	LEU
2	C	151	LEU
2	C	152	GLN
2	C	167	LYS
2	C	175	VAL
2	C	177	LEU

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

Mol	Chain	Res	Type
1	A	289	ASN
1	A	385	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

9 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	EPE	A	609[A]	-	15,15,15	0.95	1 (6%)	18,20,20	1.86	4 (22%)
3	NAG	A	607	-	14,14,15	0.24	0	17,19,21	0.48	0
3	NAG	A	605	-	14,14,15	0.35	0	17,19,21	0.59	0
3	NAG	A	608	-	14,14,15	0.54	0	17,19,21	0.58	0
3	NAG	A	601	-	14,14,15	0.41	0	17,19,21	0.55	0
3	NAG	A	606	-	14,14,15	1.06	1 (7%)	17,19,21	0.55	0
3	NAG	A	602	-	14,14,15	0.25	0	17,19,21	0.81	0
3	NAG	A	603	-	14,14,15	0.27	0	17,19,21	0.59	0
3	NAG	A	604	-	14,14,15	0.65	1 (7%)	17,19,21	0.44	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EPE	A	609[A]	-	-	6/9/19/19	0/1/1/1
3	NAG	A	607	-	-	3/6/23/26	0/1/1/1
3	NAG	A	605	-	-	0/6/23/26	0/1/1/1
3	NAG	A	608	-	-	0/6/23/26	0/1/1/1
3	NAG	A	601	-	-	0/6/23/26	0/1/1/1
3	NAG	A	606	-	-	2/6/23/26	0/1/1/1
3	NAG	A	602	-	-	0/6/23/26	0/1/1/1
3	NAG	A	603	-	-	0/6/23/26	0/1/1/1
3	NAG	A	604	-	-	4/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	606	NAG	O5-C1	-3.86	1.37	1.43
4	A	609[A]	EPE	C10-S	2.78	1.81	1.77
3	A	604	NAG	O5-C1	-2.37	1.39	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	609[A]	EPE	C5-N4-C3	4.79	119.62	108.83
4	A	609[A]	EPE	C7-N4-C5	3.79	120.92	111.23
4	A	609[A]	EPE	C7-N4-C3	2.89	118.64	111.23
4	A	609[A]	EPE	C6-N1-C2	2.63	114.76	108.83

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	609[A]	EPE	C10-C9-N1-C2
4	A	609[A]	EPE	C8-C7-N4-C5
4	A	609[A]	EPE	S-C10-C9-N1
4	A	609[A]	EPE	C9-C10-S-O2S
3	A	606	NAG	O5-C5-C6-O6
3	A	606	NAG	C4-C5-C6-O6
3	A	607	NAG	C8-C7-N2-C2
3	A	607	NAG	O7-C7-N2-C2
3	A	604	NAG	C8-C7-N2-C2
3	A	604	NAG	O7-C7-N2-C2
4	A	609[A]	EPE	C9-C10-S-O3S
3	A	604	NAG	O5-C5-C6-O6
4	A	609[A]	EPE	C9-C10-S-O1S
3	A	607	NAG	O5-C5-C6-O6
3	A	604	NAG	C4-C5-C6-O6

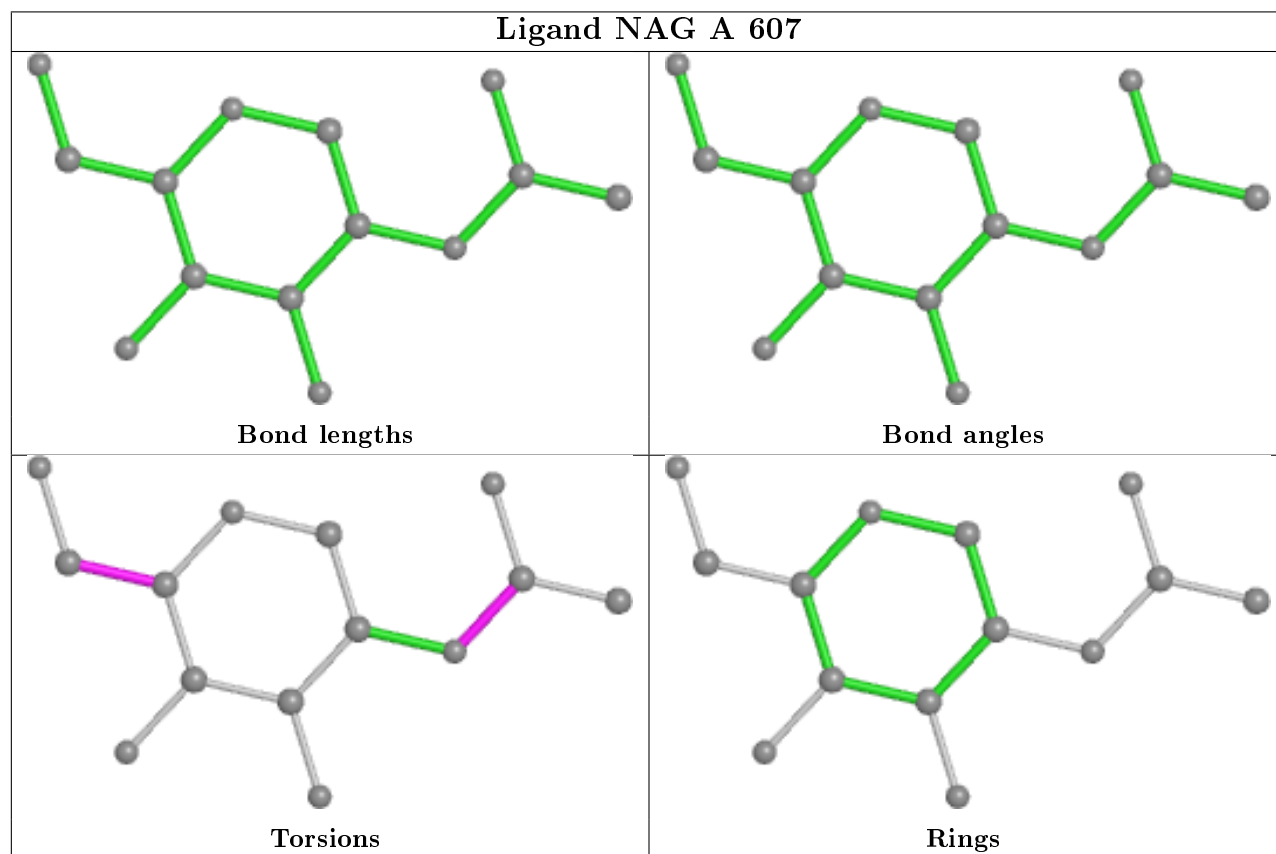
There are no ring outliers.

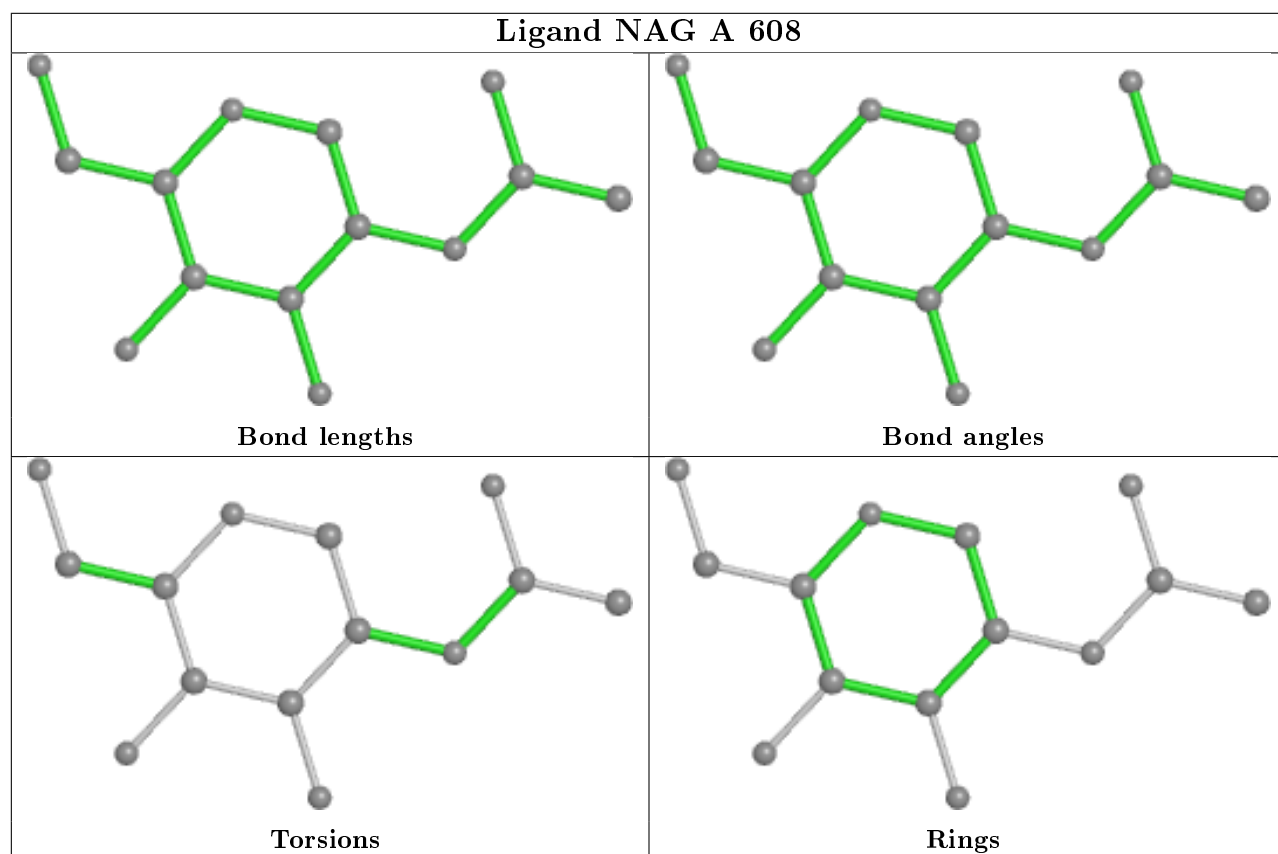
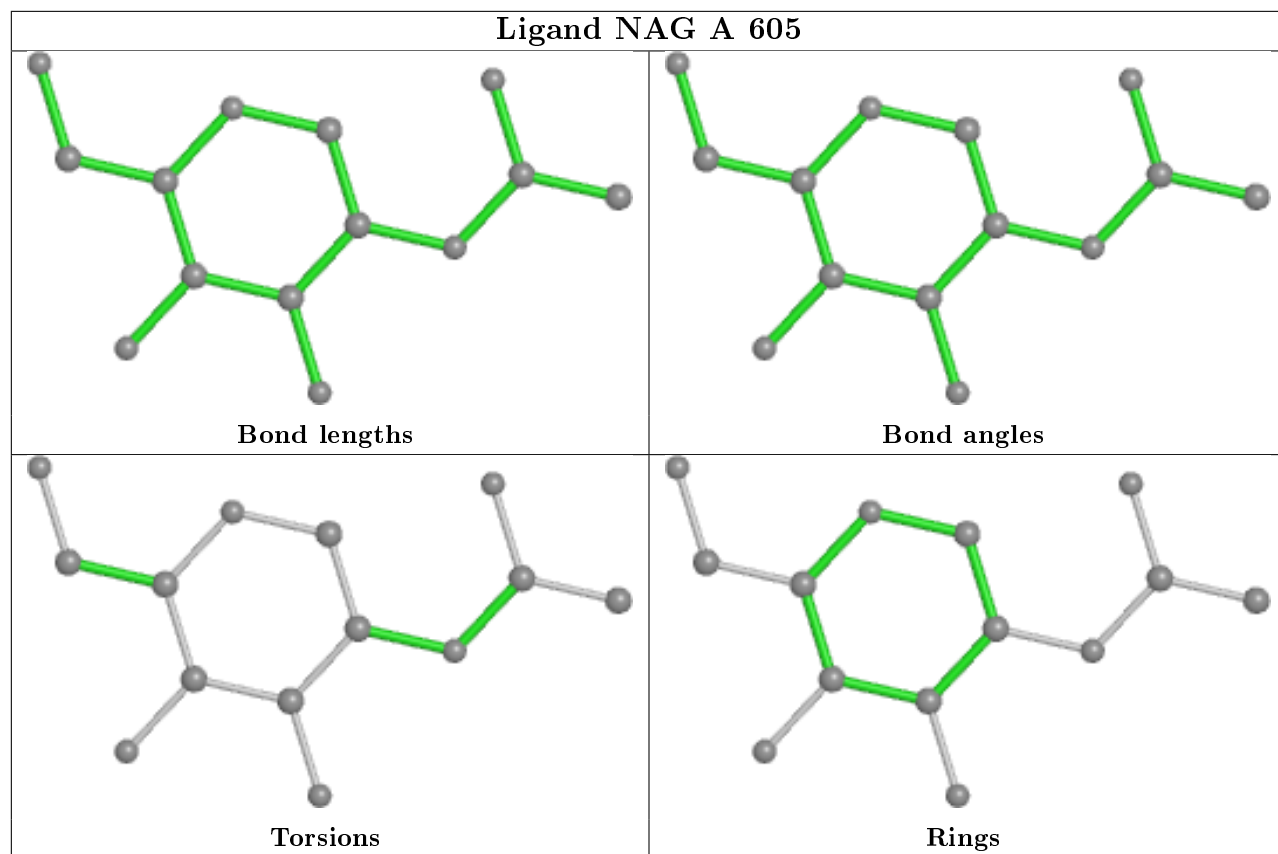
3 monomers are involved in 4 short contacts:

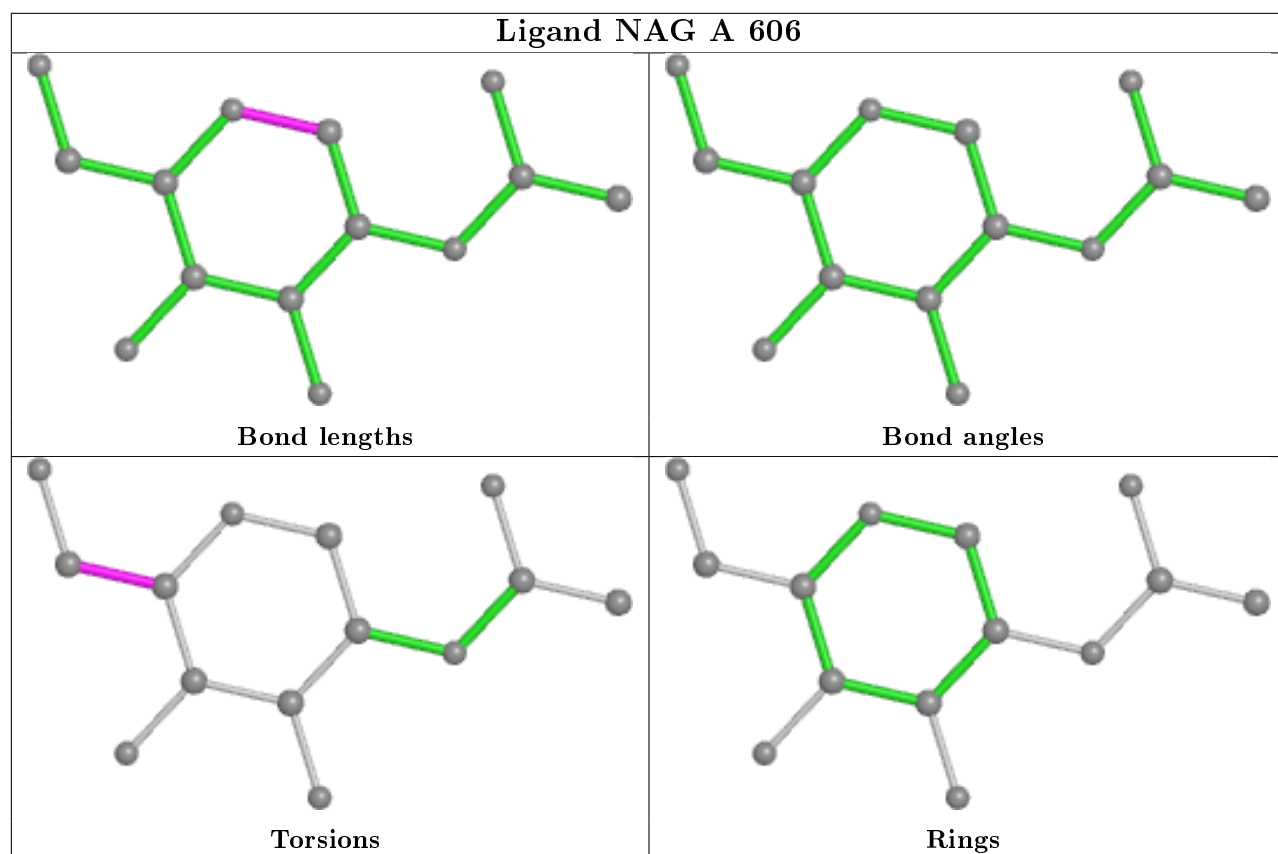
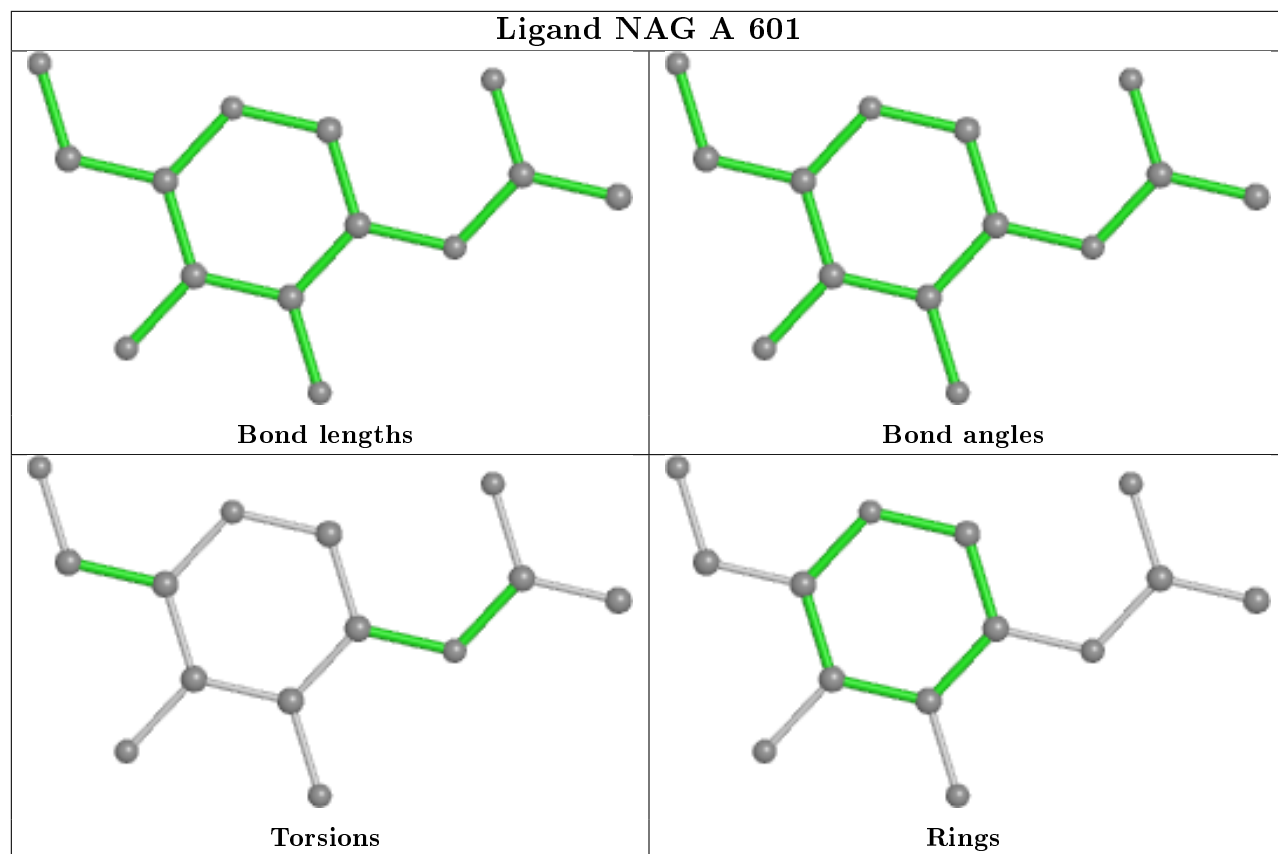
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	608	NAG	2	0
3	A	603	NAG	1	0
3	A	604	NAG	1	0

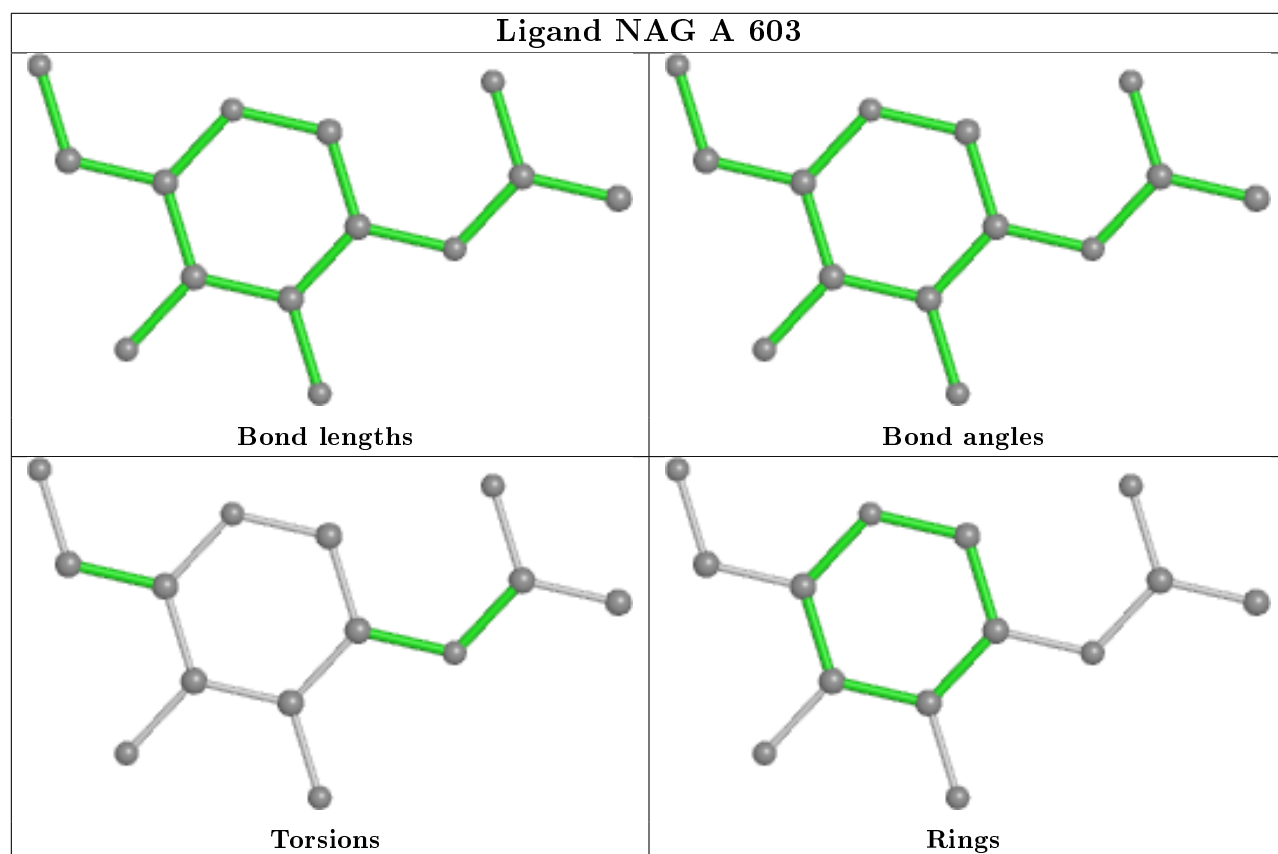
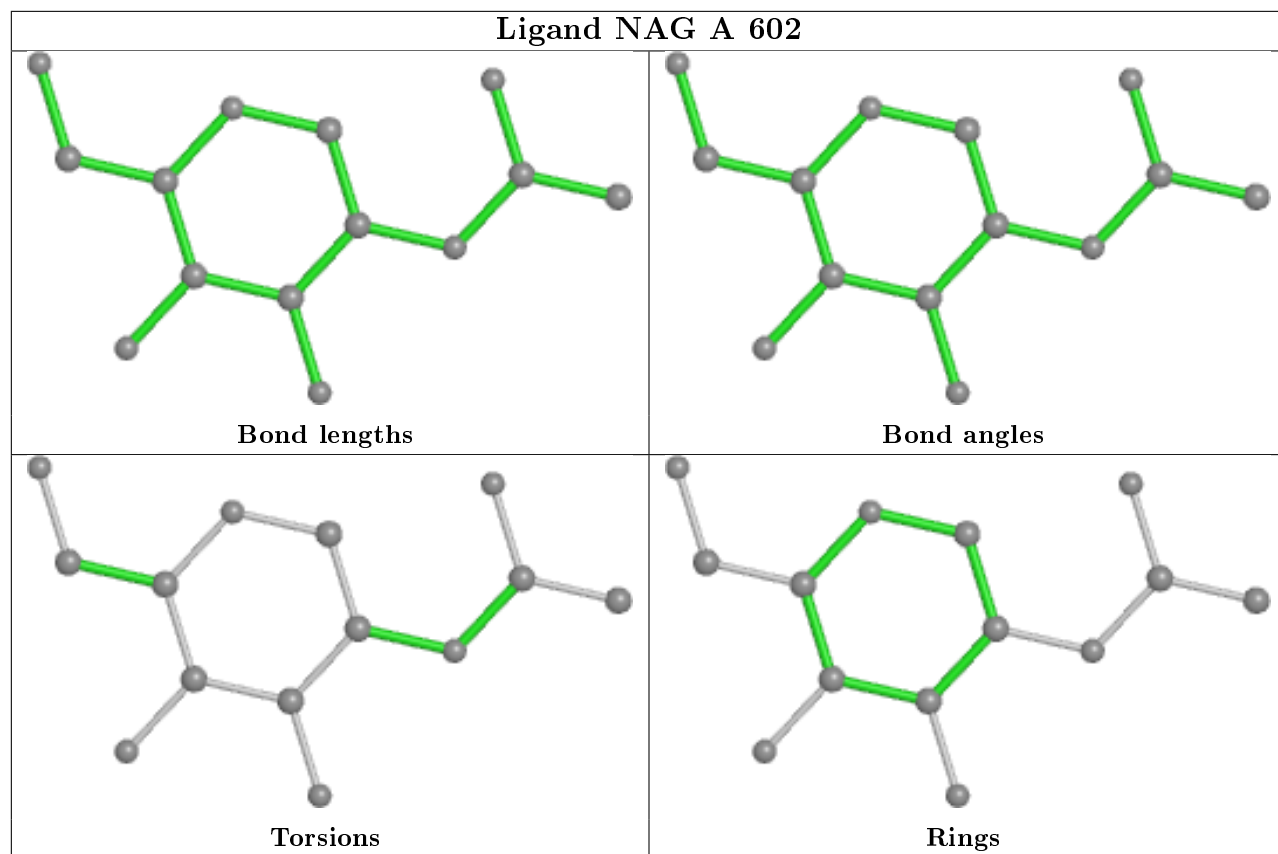
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

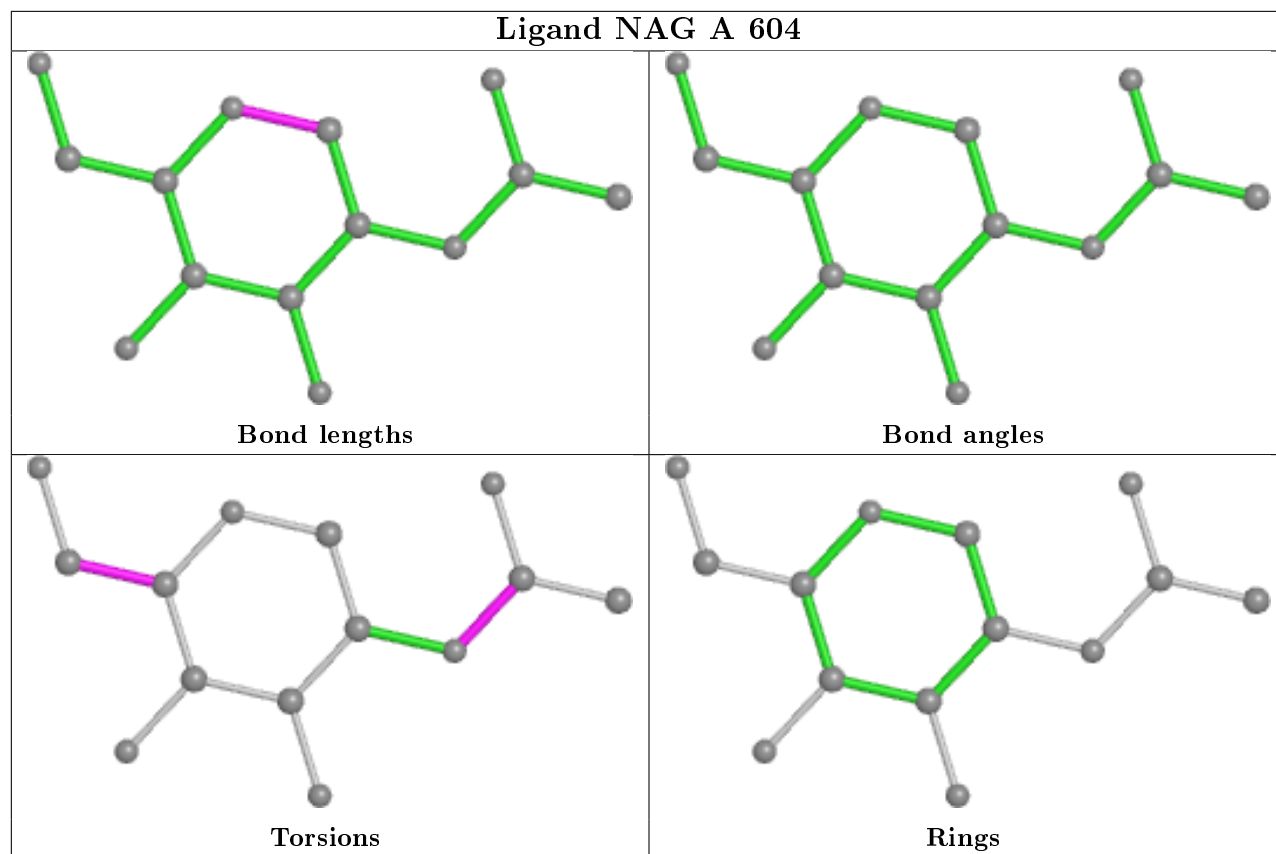
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents 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 ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	341/392 (86%)	-0.07	4 (1%) 79 77	28, 40, 67, 95	0
2	C	177/177 (100%)	0.57	23 (12%) 3 2	32, 61, 96, 114	0
All	All	518/569 (91%)	0.15	27 (5%) 27 24	28, 45, 85, 114	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	177	LEU	7.4
2	C	107	HIS	6.9
2	C	103	ASN	6.5
2	C	106	THR	6.2
2	C	124	SER	5.7
1	A	409	SER	4.2
2	C	123	GLY	3.8
2	C	174	ILE	3.5
2	C	175	VAL	3.4
2	C	176	VAL	3.4
2	C	105	ASP	3.3
2	C	108	LEU	3.3
2	C	122	PRO	3.2
2	C	125	SER	2.8
2	C	147	SER	2.7
2	C	140	GLY	2.7
1	A	461	PRO	2.6
2	C	100	LEU	2.6
2	C	143	THR	2.5
2	C	116	LEU	2.5
2	C	110	GLN	2.5
1	A	396	PRO	2.4
2	C	87	GLU	2.4
2	C	20	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	459	THR	2.4
2	C	151	LEU	2.3
2	C	104	SER	2.2

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](#)

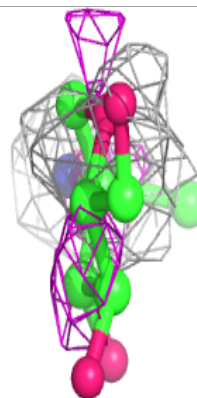
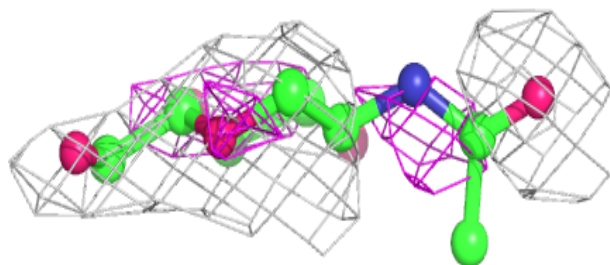
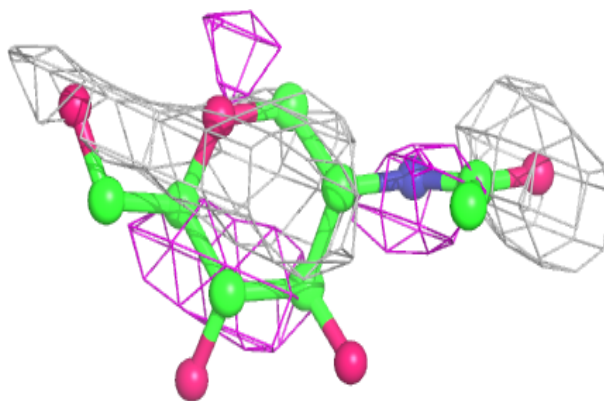
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	A	607	14/15	0.55	0.57	57,79,87,88	0
3	NAG	A	608	14/15	0.70	0.53	52,73,78,80	0
3	NAG	A	605	14/15	0.71	0.21	71,82,87,90	0
3	NAG	A	606	14/15	0.75	0.31	65,79,91,95	0
3	NAG	A	603	14/15	0.81	0.28	65,74,82,83	0
3	NAG	A	601	14/15	0.89	0.17	49,56,63,65	0
3	NAG	A	604	14/15	0.90	0.16	53,58,65,70	0
4	EPE	A	609[A]	15/15	0.96	0.19	29,37,45,48	0
3	NAG	A	602	14/15	0.96	0.16	33,37,39,40	0

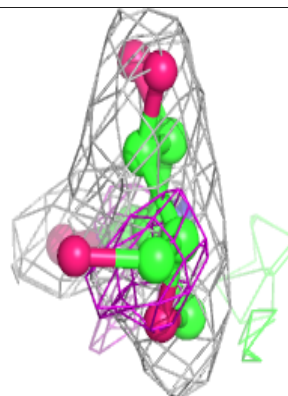
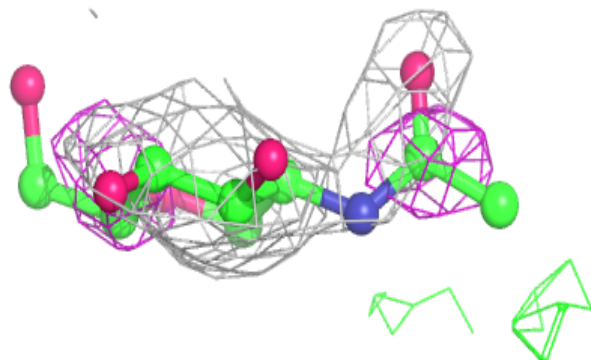
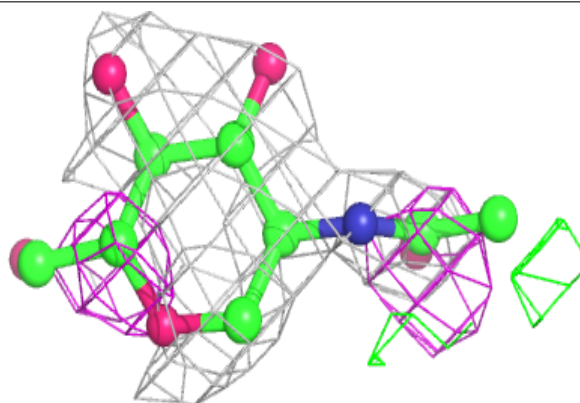
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAG A 607:

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

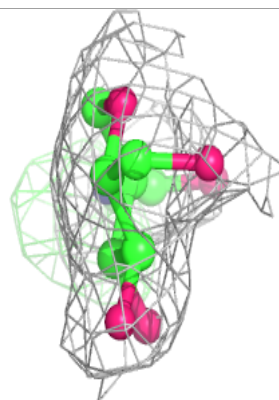
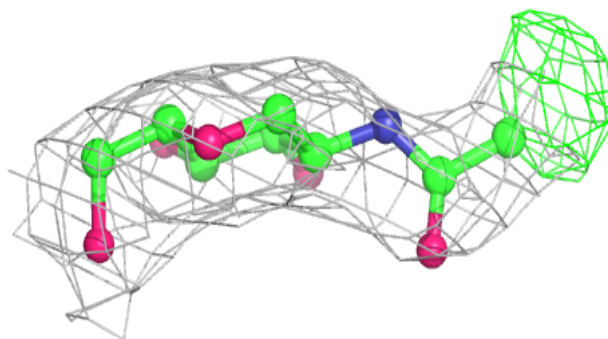
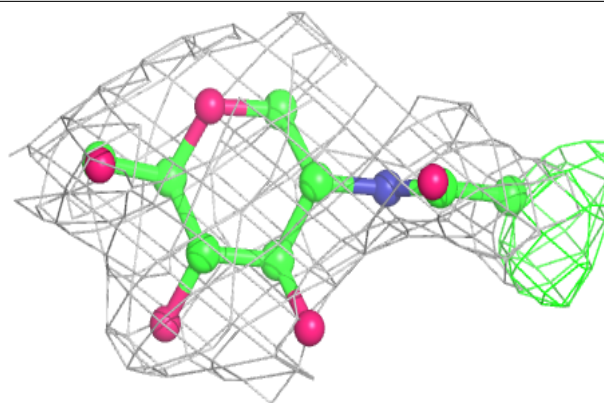
**Electron density around NAG A 608:**

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

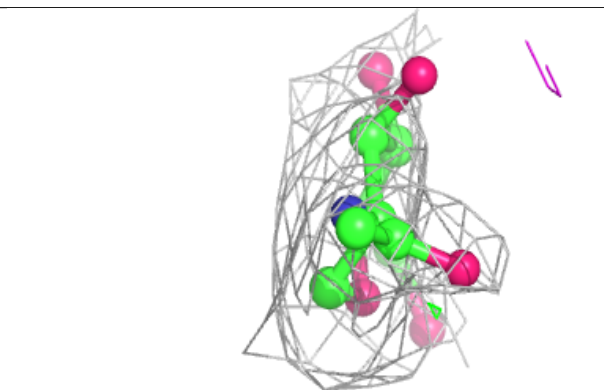
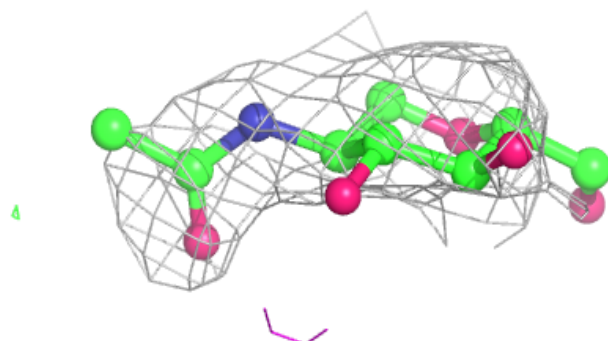
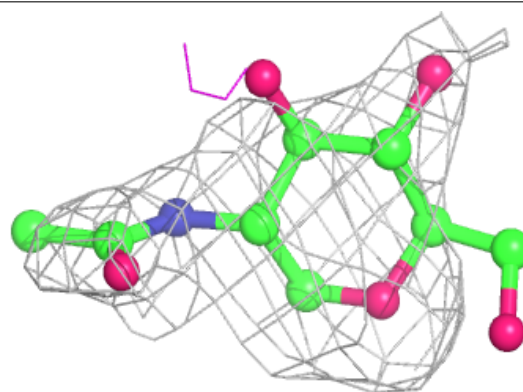


Electron density around NAG A 605:

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

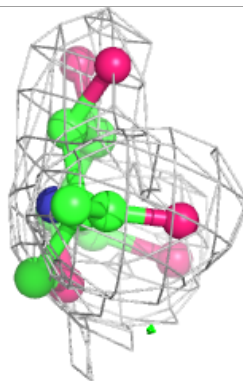
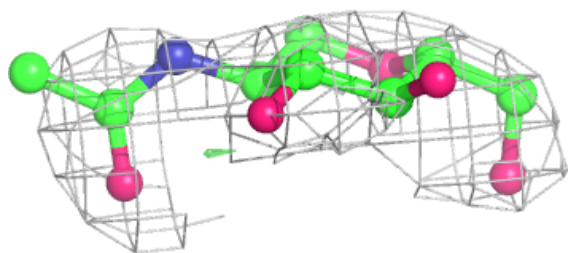
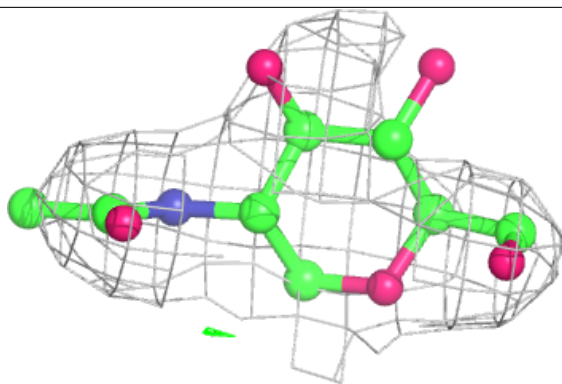
**Electron density around NAG A 606:**

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

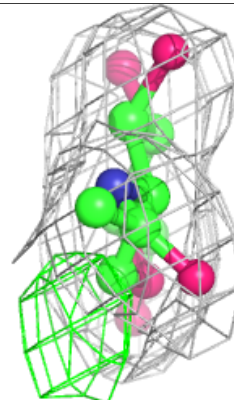
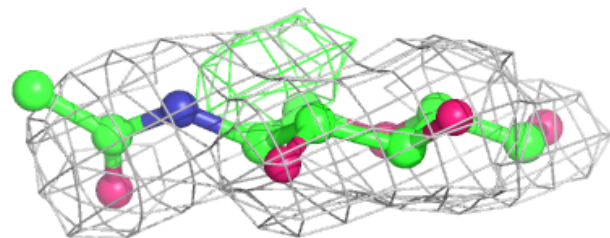
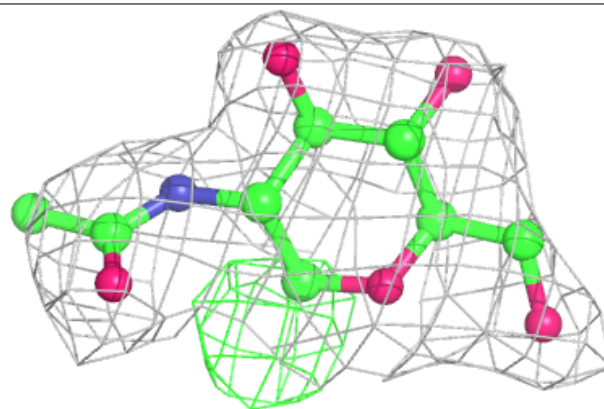


Electron density around NAG A 603:

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

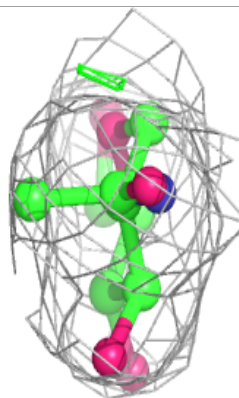
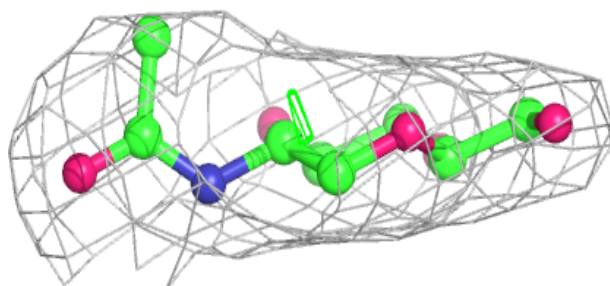
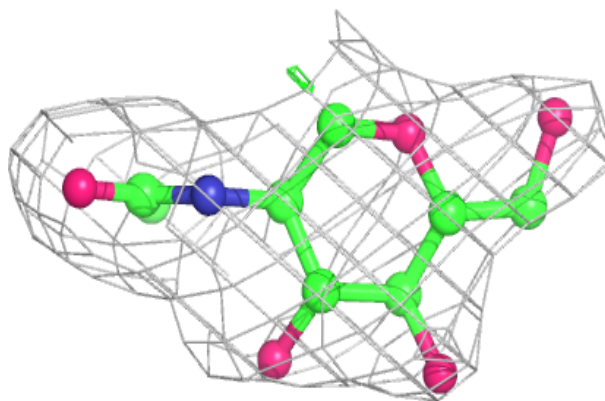
**Electron density around NAG A 601:**

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

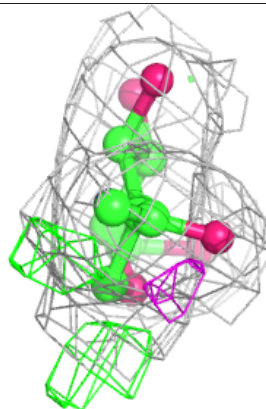
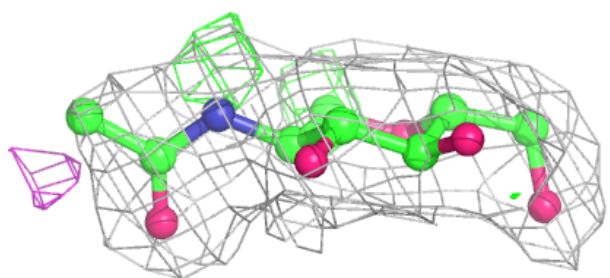
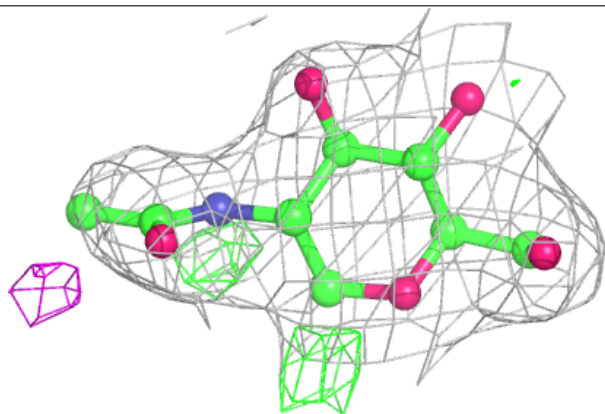


Electron density around NAG A 604:

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

**Electron density around NAG A 602:**

$2mF_o-DF_c$ (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.