



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 19, 2019 – 11:30 AM EDT

PDB ID : 6KMK
Title : Crystal structure of hydrogen peroxide bound bovine lactoperoxidase at 2.3 Å resolution
Authors : Singh, P.K.; Sirohi, H.V.; Bhusan, A.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2019-07-31
Resolution : 2.30 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 : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.4
buster-report : 1.1.7 (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

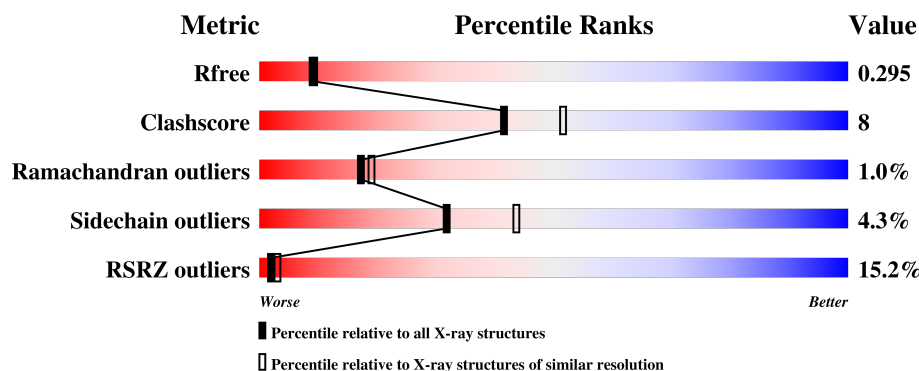
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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. 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	595	<div> <div>15%</div> <div>82%</div> <div>17%</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
5	IOD	A	616	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	IOD	A	621	-	-	X	-

2 Entry composition [i](#)

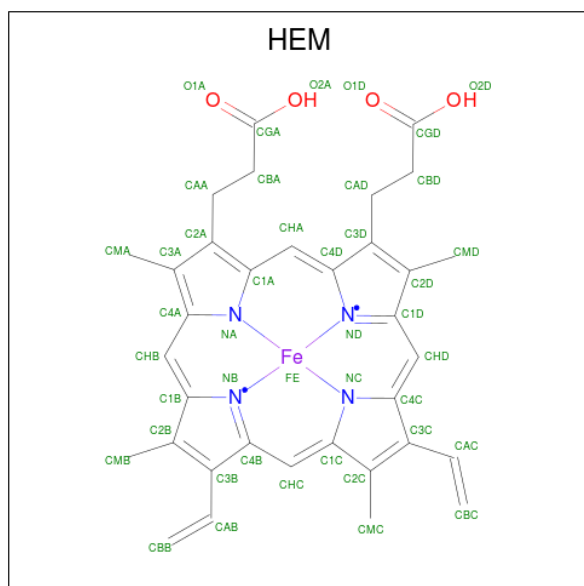
There are 7 unique types of molecules in this entry. The entry contains 5144 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

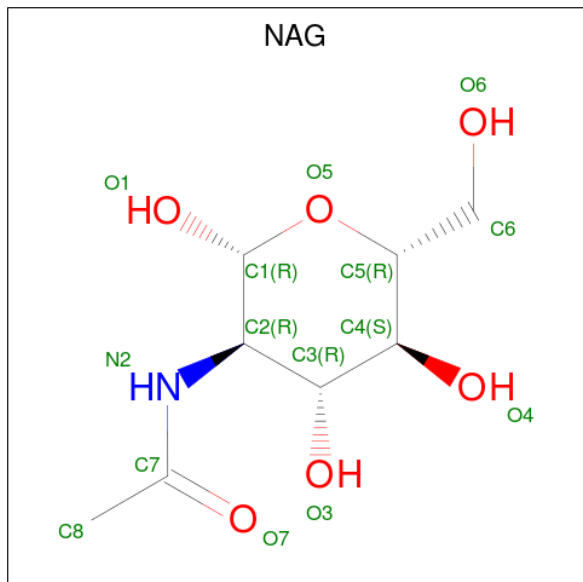
- Molecule 1 is a protein called Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	P	S	0	0	0
			4774	3037	847	863	1	26			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by author).



- Molecule 4 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by author).

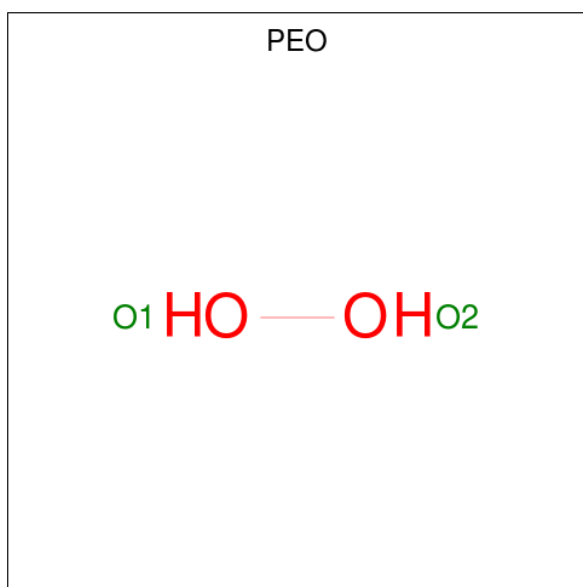


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	15	Total	I	0	0
			15	15		

- Molecule 6 is HYDROGEN PEROXIDE (three-letter code: PEO) (formula: H_2O_2).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	O	0	0
			2	2		
6	A	1	Total	O	0	0
			2	2		

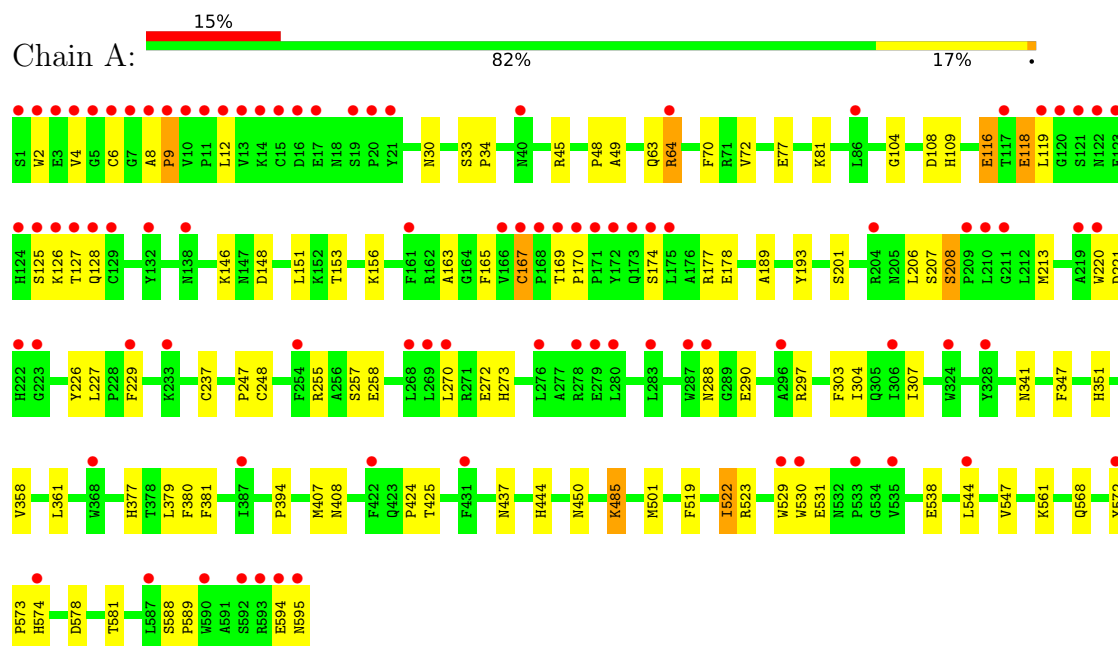
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	251	Total	O	0	0
			251	251		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Lactoperoxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.83Å 80.42Å 75.82Å 90.00° 102.58° 90.00°	Depositor
Resolution (Å)	54.46 – 2.30 54.46 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.7 (54.46-2.30) 98.7 (54.46-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.245 , 0.295 0.249 , 0.295	Depositor DCC
R_{free} test set	1405 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	38.2	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 44.6	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	0.85	EDS
Total number of atoms	5144	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, SEP, CA, PEO, HEM, IOD

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	0.68	0/4891	0.79	0/6634

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	4774	0	4687	68	0
2	A	43	0	30	12	0
3	A	1	0	0	0	0
4	A	56	0	52	4	0
5	A	15	0	0	5	1
6	A	4	0	0	1	0
7	A	251	0	0	6	1
All	All	5144	0	4769	73	1

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 8.

All (73) 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:258:GLU:OE2	2:A:601:HEM:CMB	1.77	1.33
1:A:108:ASP:OD2	2:A:601:HEM:CMD	1.82	1.28
1:A:258:GLU:OE2	2:A:601:HEM:HMB1	1.00	1.16
1:A:108:ASP:OD2	2:A:601:HEM:HMD1	0.94	1.10
1:A:64:ARG:NH1	7:A:702:HOH:O	2.10	0.83
1:A:126:LYS:N	1:A:127:THR:HA	1.97	0.78
1:A:77:GLU:OE2	1:A:81:LYS:NZ	2.16	0.75
1:A:48:PRO:HD3	5:A:621:IOD:I	2.56	0.75
2:A:601:HEM:HBC2	2:A:601:HEM:HMC1	1.72	0.71
1:A:351:HIS:HD1	1:A:437:ASN:HD21	1.37	0.70
1:A:127:THR:N	1:A:128:GLN:HA	2.07	0.69
1:A:407:MET:HB3	1:A:501:MET:CE	2.23	0.69
2:A:601:HEM:HMB2	2:A:601:HEM:HBB2	1.76	0.67
1:A:288:ASN:HD21	1:A:290:GLU:HB3	1.60	0.66
4:A:606:NAG:O6	7:A:701:HOH:O	1.71	0.65
1:A:220:TRP:HB2	7:A:878:HOH:O	1.96	0.65
1:A:8:ALA:HB3	1:A:9:PRO:HD3	1.77	0.65
1:A:568:GLN:NE2	4:A:606:NAG:C1	2.61	0.64
1:A:126:LYS:N	1:A:127:THR:CA	2.63	0.62
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.35	0.62
1:A:424:PRO:O	1:A:425:THR:OG1	2.16	0.61
1:A:206:LEU:O	1:A:208:SER:N	2.34	0.61
1:A:588:SER:HB2	1:A:589:PRO:HD3	1.84	0.60
1:A:30:ASN:O	1:A:34:PRO:HA	2.03	0.58
1:A:193:TYR:OH	1:A:297:ARG:HA	2.04	0.58
1:A:568:GLN:NE2	4:A:606:NAG:O5	2.37	0.57
1:A:544:LEU:O	1:A:547:VAL:HG22	2.04	0.57
2:A:601:HEM:HBC2	2:A:601:HEM:CMC	2.35	0.57
1:A:193:TYR:CZ	1:A:297:ARG:HA	2.41	0.56
1:A:148:ASP:O	1:A:151:LEU:HB2	2.06	0.55
1:A:237:CYS:HA	1:A:381:PHE:O	2.07	0.55
1:A:258:GLU:OE2	2:A:601:HEM:HMB2	1.96	0.55
1:A:167:CYS:O	1:A:169:THR:N	2.40	0.55
1:A:227:LEU:HD23	1:A:270:LEU:HD22	1.89	0.54
1:A:108:ASP:OD2	2:A:601:HEM:C2D	2.58	0.54
1:A:189:ALA:HB2	1:A:304:ILE:HD12	1.89	0.54
1:A:108:ASP:CG	2:A:601:HEM:CMD	2.70	0.54
1:A:561:LYS:HE2	5:A:611:IOD:I	2.79	0.52
2:A:601:HEM:CMB	2:A:601:HEM:HBB2	2.40	0.51
1:A:229:PHE:CD1	1:A:247:PRO:HG2	2.45	0.51
1:A:255:ARG:HD2	5:A:616:IOD:I	2.81	0.51
1:A:116:GLU:HA	1:A:163:ALA:HA	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.46	0.50
1:A:70:PHE:CD1	1:A:485:LYS:HG3	2.47	0.50
1:A:568:GLN:HE22	4:A:606:NAG:C1	2.23	0.49
1:A:341:ASN:OD1	1:A:444:HIS:ND1	2.29	0.49
1:A:255:ARG:HB3	5:A:616:IOD:I	2.81	0.49
1:A:519:PHE:CD1	1:A:522:ILE:HD11	2.48	0.49
1:A:109:HIS:NE2	6:A:622:PEO:O1	2.37	0.48
1:A:303:PHE:O	1:A:307:ILE:HG12	2.14	0.48
1:A:125:SER:C	1:A:127:THR:HA	2.34	0.48
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.49	0.48
1:A:530:TRP:CZ2	1:A:531:GLU:HG3	2.48	0.48
1:A:594:GLU:HB2	7:A:734:HOH:O	2.14	0.48
1:A:523:ARG:HG3	1:A:529:TRP:CE2	2.49	0.47
1:A:237:CYS:HB2	1:A:248:CYS:N	2.30	0.47
1:A:45:ARG:CZ	1:A:49:ALA:HB2	2.45	0.47
1:A:127:THR:N	1:A:128:GLN:CA	2.77	0.46
1:A:581:THR:HG22	1:A:581:THR:O	2.16	0.46
1:A:361:LEU:O	1:A:394:PRO:HA	2.15	0.46
1:A:272:GLU:HA	1:A:272:GLU:OE1	2.16	0.45
1:A:45:ARG:HA	5:A:608:IOD:I	2.88	0.44
1:A:116:GLU:O	1:A:119:LEU:CD2	2.66	0.44
1:A:450:ASN:N	7:A:724:HOH:O	2.48	0.44
1:A:407:MET:SD	1:A:408:ASN:N	2.91	0.43
1:A:257:SER:O	1:A:381:PHE:HA	2.19	0.43
1:A:104:GLY:HA3	2:A:601:HEM:CBC	2.47	0.43
1:A:165:PHE:CD1	1:A:165:PHE:N	2.85	0.43
1:A:358:VAL:HB	1:A:379:LEU:CD1	2.48	0.43
1:A:165:PHE:CD2	1:A:177:ARG:HD2	2.54	0.42
1:A:178:GLU:OE2	1:A:178:GLU:HA	2.20	0.41
1:A:220:TRP:CB	7:A:878:HOH:O	2.63	0.40
1:A:572:TYR:CD1	1:A:573:PRO:HA	2.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:621:IOD:I	7:A:925:HOH:O[2_646]	1.10	1.10

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	592/595 (100%)	545 (92%)	41 (7%)	6 (1%)	17 19

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	118	GLU
1	A	174	SER
1	A	207	SER
1	A	9	PRO
1	A	170	PRO
1	A	485	LYS

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	517/517 (100%)	495 (96%)	22 (4%)	32 43

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	TRP
1	A	4	VAL
1	A	6	CYS
1	A	12	LEU
1	A	33	SER

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Mol	Chain	Res	Type
1	A	63	GLN
1	A	64	ARG
1	A	72	VAL
1	A	116	GLU
1	A	118	GLU
1	A	146	LYS
1	A	153	THR
1	A	156	LYS
1	A	167	CYS
1	A	201	SER
1	A	208	SER
1	A	347	PHE
1	A	522	ILE
1	A	538	GLU
1	A	574	HIS
1	A	578	ASP
1	A	595	ASN

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

Mol	Chain	Res	Type
1	A	18	ASN
1	A	122	ASN
1	A	288	ASN
1	A	468	GLN
1	A	497	ASN
1	A	521	GLN
1	A	568	GLN
1	A	595	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
1	SEP	A	198	1	9,9,10	1.76	2 (22%)	9,12,14	1.01	1 (11%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	198	1	-	5/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	CA-C	3.31	1.54	1.50
1	A	198	SEP	P-OG	2.84	1.69	1.60

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	P-OG-CB	2.12	124.12	118.30

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	N-CA-CB-OG
1	A	198	SEP	CB-OG-P-O2P
1	A	198	SEP	CB-OG-P-O3P
1	A	198	SEP	CB-OG-P-O1P
1	A	198	SEP	CA-CB-OG-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 23 ligands modelled in this entry, 16 are monoatomic - leaving 7 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	$\# Z > 2$
2	HEM	A	601	1,6	27,50,50	1.06	2 (7%)	17,82,82	1.38	2 (11%)
4	NAG	A	603	1	14,14,15	0.62	0	17,19,21	1.55	3 (17%)
4	NAG	A	604	1	14,14,15	0.61	0	17,19,21	1.85	4 (23%)
4	NAG	A	605	1	14,14,15	0.53	0	17,19,21	1.69	4 (23%)
4	NAG	A	606	1	14,14,15	0.90	0	17,19,21	2.08	4 (23%)
6	PEO	A	622	2	1,1,1	0.44	0	-		
6	PEO	A	623	-	1,1,1	0.65	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	HEM	A	601	1,6	-	0/6/54/54	-
4	NAG	A	603	1	-	1/6/23/26	0/1/1/1
4	NAG	A	604	1	-	0/6/23/26	0/1/1/1
4	NAG	A	605	1	-	0/6/23/26	0/1/1/1
4	NAG	A	606	1	-	4/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	HEM	C4D-C3D	2.46	1.48	1.42
2	A	601	HEM	C3C-C2C	-2.43	1.37	1.40

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	606	NAG	C1-O5-C5	6.35	120.84	112.20
4	A	604	NAG	C1-O5-C5	5.20	119.27	112.20
4	A	605	NAG	C4-C3-C2	4.31	117.34	111.02
4	A	603	NAG	C3-C4-C5	-3.07	104.71	110.23
4	A	605	NAG	O5-C5-C6	3.00	111.90	107.15
2	A	601	HEM	CBA-CAA-C2A	-3.00	106.75	112.48
4	A	603	NAG	O5-C1-C2	-2.92	106.78	111.36
2	A	601	HEM	CBD-CAD-C3D	-2.91	106.91	112.47
4	A	606	NAG	O5-C5-C6	2.78	111.55	107.15
4	A	604	NAG	O5-C1-C2	-2.69	107.14	111.36
4	A	604	NAG	O4-C4-C5	2.61	115.81	109.29
4	A	605	NAG	C1-O5-C5	2.55	115.66	112.20
4	A	604	NAG	C6-C5-C4	-2.45	107.26	113.00
4	A	606	NAG	C8-C7-N2	2.29	120.05	116.10
4	A	606	NAG	C3-C4-C5	2.13	114.05	110.23
4	A	603	NAG	O4-C4-C3	2.06	115.13	110.34
4	A	605	NAG	C3-C4-C5	2.01	113.84	110.23

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	606	NAG	O5-C5-C6-O6
4	A	606	NAG	C8-C7-N2-C2
4	A	606	NAG	O7-C7-N2-C2
4	A	606	NAG	C4-C5-C6-O6
4	A	603	NAG	O5-C5-C6-O6

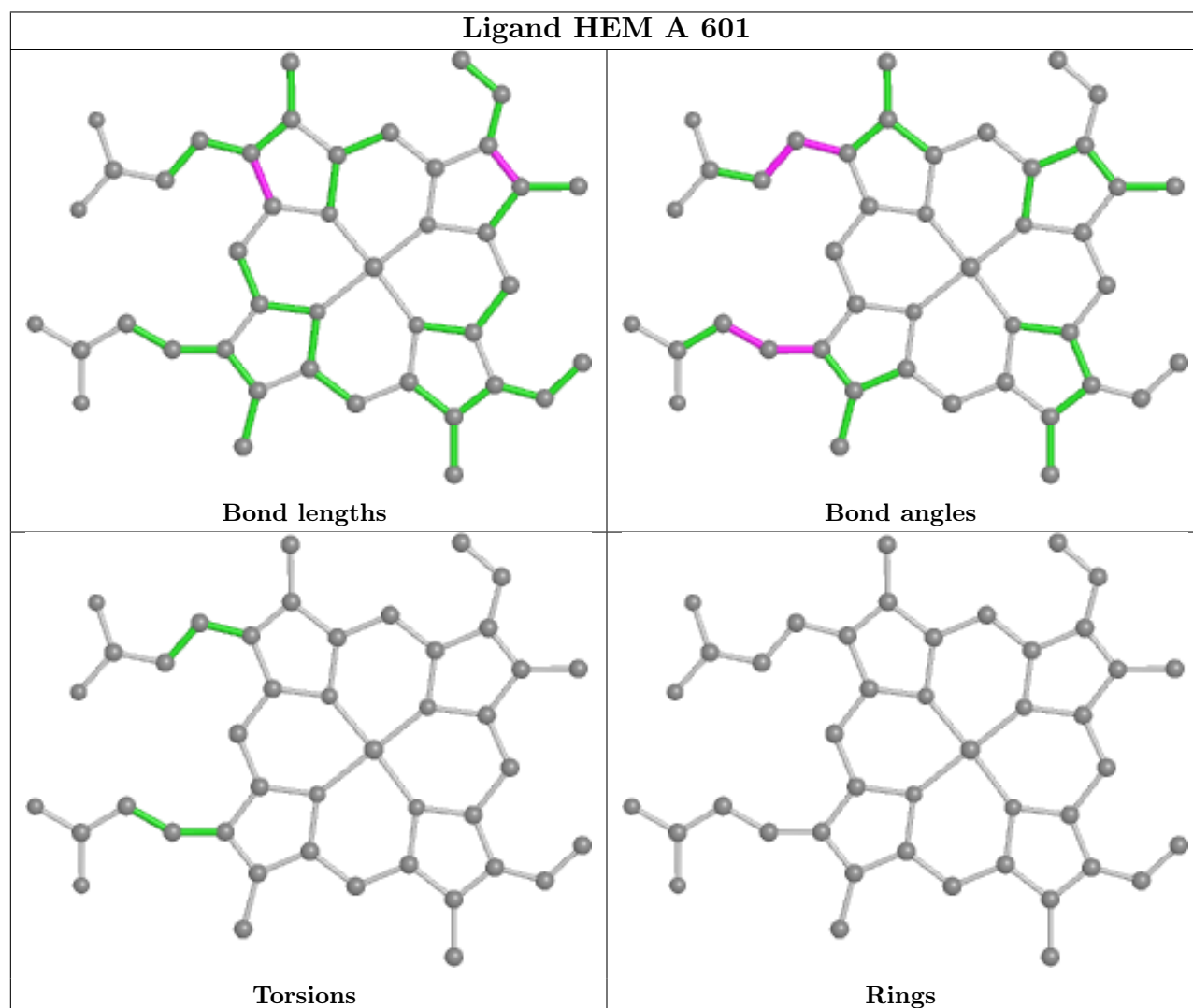
There are no ring outliers.

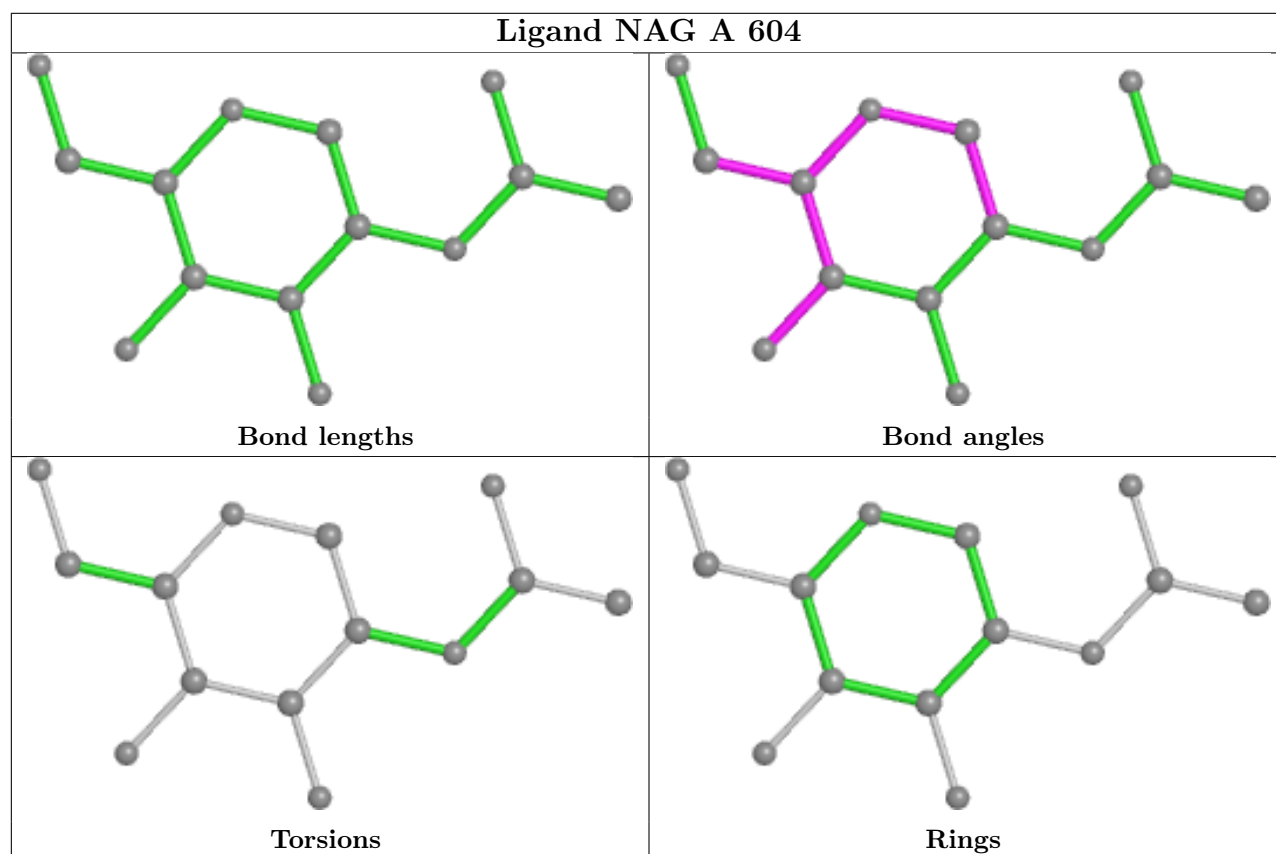
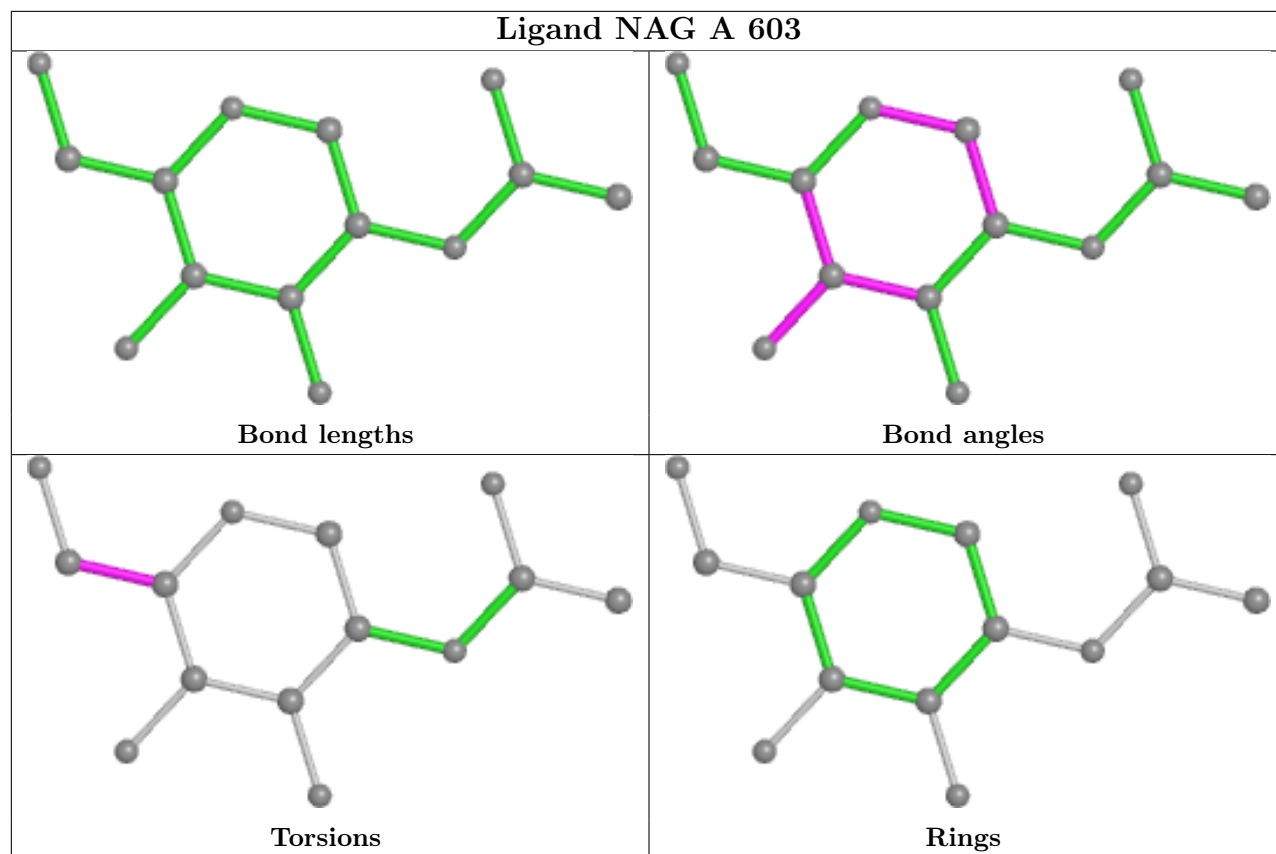
2 monomers are involved in 16 short contacts:

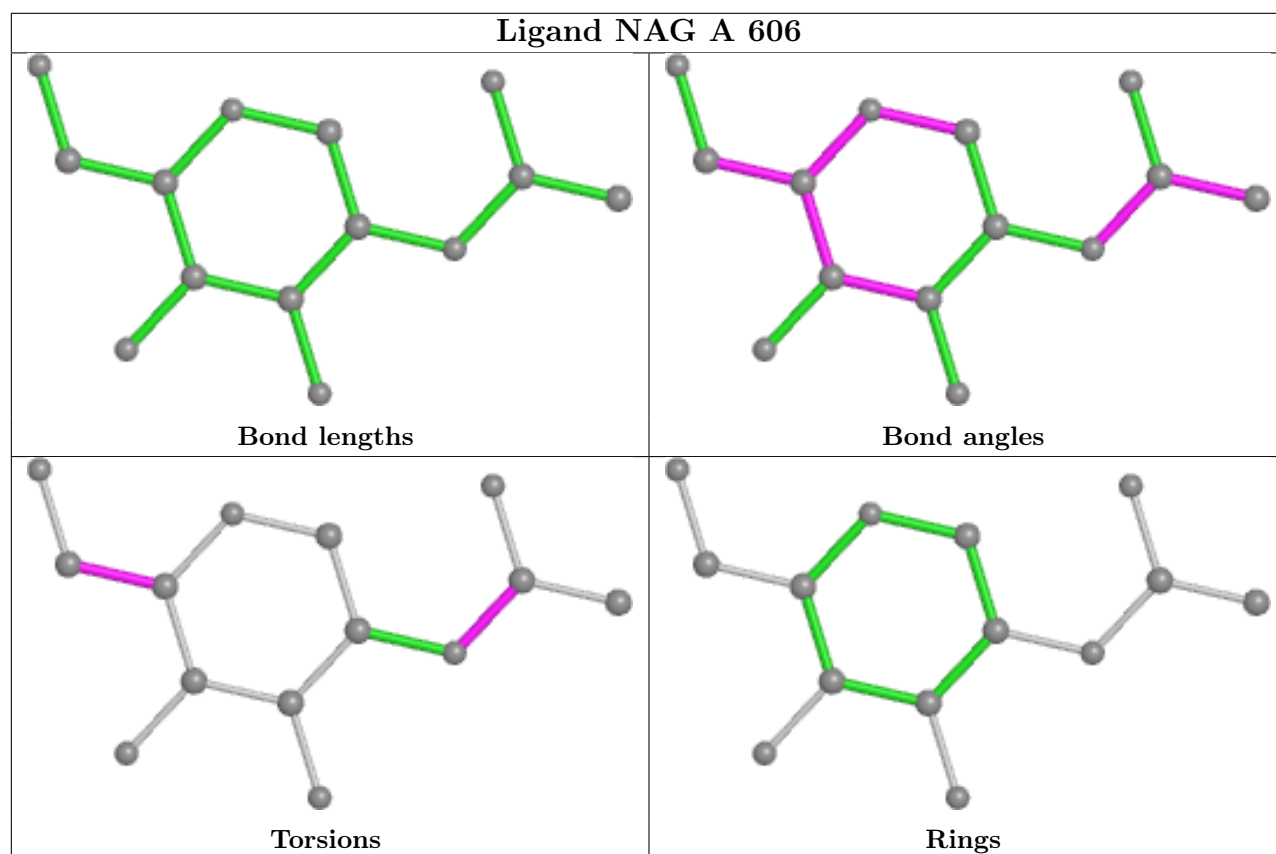
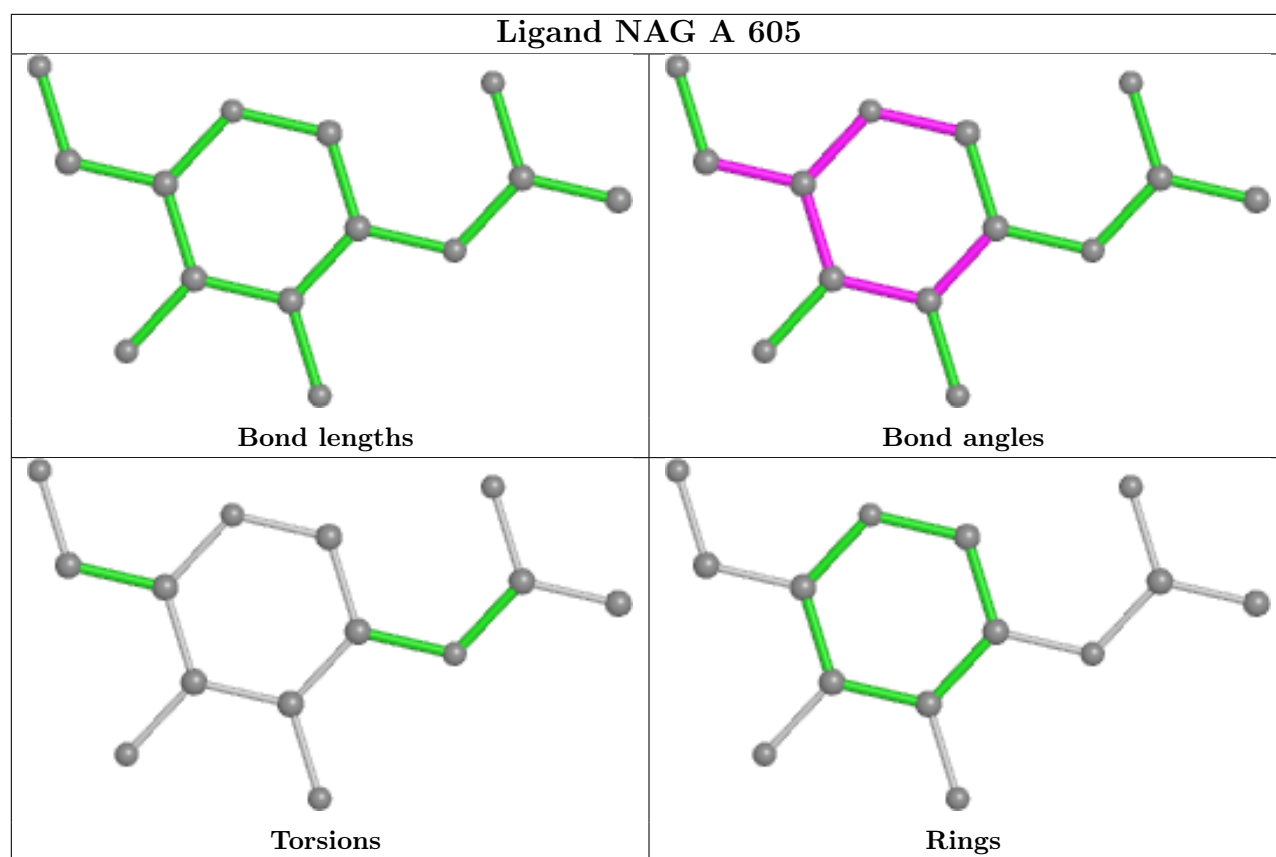
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEM	12	0
4	A	606	NAG	4	0

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	594/595 (99%)	1.24	90 (15%) 2 3	18, 37, 104, 148	0

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7	GLY	22.1
1	A	8	ALA	16.1
1	A	2	TRP	12.7
1	A	595	ASN	11.4
1	A	120	GLY	11.3
1	A	119	LEU	10.8
1	A	4	VAL	10.7
1	A	11	PRO	8.9
1	A	172	TYR	8.8
1	A	122	ASN	8.5
1	A	12	LEU	8.3
1	A	13	VAL	8.1
1	A	124	HIS	8.1
1	A	1	SER	8.0
1	A	5	GLY	7.9
1	A	173	GLN	7.1
1	A	121	SER	6.9
1	A	117	THR	6.7
1	A	6	CYS	6.1
1	A	10	VAL	5.9
1	A	126	LYS	5.9
1	A	174	SER	5.8
1	A	593	ARG	5.8
1	A	127	THR	5.0
1	A	280	LEU	4.9
1	A	211	GLY	4.8
1	A	128	GLN	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	9	PRO	4.7
1	A	170	PRO	4.7
1	A	125	SER	4.5
1	A	123	GLU	4.4
1	A	15	CYS	4.4
1	A	544	LEU	4.1
1	A	283	LEU	4.1
1	A	529	TRP	3.8
1	A	64	ARG	3.8
1	A	530	TRP	3.7
1	A	166	VAL	3.6
1	A	287	TRP	3.6
1	A	279	GLU	3.5
1	A	594	GLU	3.5
1	A	21	TYR	3.5
1	A	587	LEU	3.5
1	A	269	LEU	3.5
1	A	572	TYR	3.4
1	A	171	PRO	3.4
1	A	169	THR	3.4
1	A	254	PHE	3.3
1	A	590	TRP	3.3
1	A	17	GLU	3.3
1	A	288	ASN	3.2
1	A	3	GLU	3.2
1	A	233	LYS	3.2
1	A	220	TRP	3.1
1	A	219	ALA	3.0
1	A	161	PHE	3.0
1	A	168	PRO	2.9
1	A	223	GLY	2.9
1	A	20	PRO	2.8
1	A	387	ILE	2.8
1	A	210	LEU	2.7
1	A	535	VAL	2.7
1	A	132	TYR	2.6
1	A	328	TYR	2.6
1	A	592	SER	2.6
1	A	167	CYS	2.5
1	A	324	TRP	2.5
1	A	368	TRP	2.5
1	A	19	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	40	ASN	2.5
1	A	175	LEU	2.5
1	A	422	PHE	2.4
1	A	296	ALA	2.4
1	A	276	LEU	2.3
1	A	268	LEU	2.2
1	A	574	HIS	2.2
1	A	129	CYS	2.2
1	A	270	LEU	2.2
1	A	229	PHE	2.1
1	A	204	ARG	2.1
1	A	222	HIS	2.1
1	A	209	PRO	2.1
1	A	138	ASN	2.1
1	A	86	LEU	2.1
1	A	431	PHE	2.1
1	A	306	ILE	2.0
1	A	14	LYS	2.0
1	A	533	PRO	2.0
1	A	16	ASP	2.0
1	A	278	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	A	198	10/11	0.93	0.23	26,41,45,45	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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,

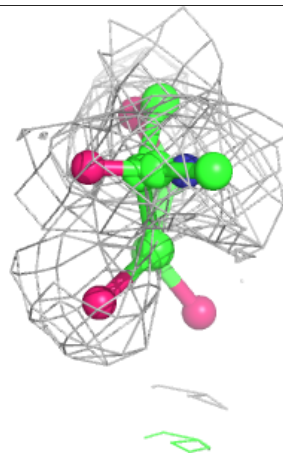
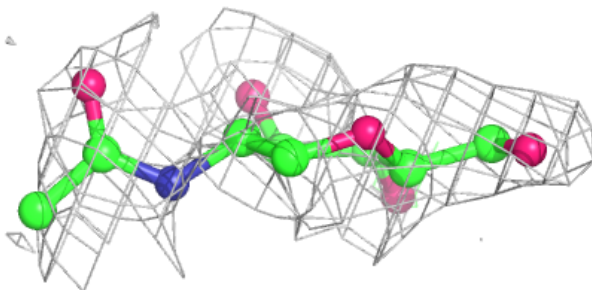
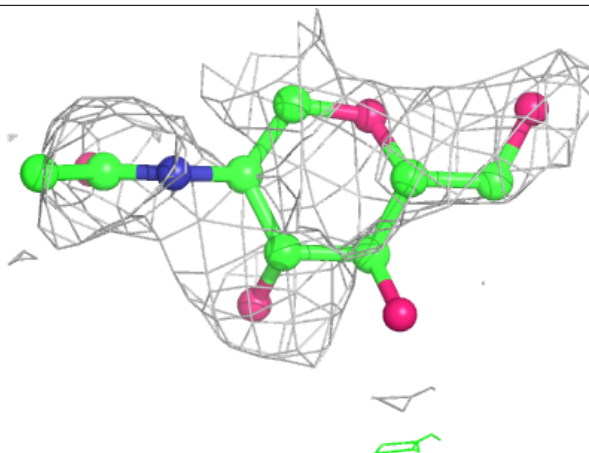
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	605	14/15	0.59	0.30	68,83,87,89	0
4	NAG	A	606	14/15	0.70	0.28	53,59,66,67	0
4	NAG	A	604	14/15	0.78	0.22	52,57,59,61	0
5	IOD	A	617	1/1	0.85	0.12	68,68,68,68	1
4	NAG	A	603	14/15	0.85	0.18	39,42,45,48	0
6	PEO	A	623	2/2	0.87	0.21	42,42,42,49	0
5	IOD	A	615	1/1	0.87	0.08	45,45,45,45	1
5	IOD	A	619	1/1	0.93	0.07	79,79,79,79	1
3	CA	A	602	1/1	0.94	0.07	29,29,29,29	0
2	HEM	A	601	43/43	0.94	0.14	16,21,28,30	0
5	IOD	A	620	1/1	0.94	0.10	62,62,62,62	1
5	IOD	A	613	1/1	0.95	0.07	61,61,61,61	0
5	IOD	A	607	1/1	0.95	0.06	55,55,55,55	0
6	PEO	A	622	2/2	0.96	0.21	36,36,36,41	0
5	IOD	A	609	1/1	0.97	0.09	44,44,44,44	0
5	IOD	A	612	1/1	0.97	0.10	43,43,43,43	1
5	IOD	A	616	1/1	0.98	0.06	55,55,55,55	1
5	IOD	A	618	1/1	0.98	0.07	48,48,48,48	1
5	IOD	A	611	1/1	0.98	0.10	42,42,42,42	1
5	IOD	A	610	1/1	0.98	0.06	51,51,51,51	0
5	IOD	A	614	1/1	0.99	0.09	57,57,57,57	0
5	IOD	A	621	1/1	0.99	0.08	81,81,81,81	1
5	IOD	A	608	1/1	0.99	0.04	36,36,36,36	1

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.

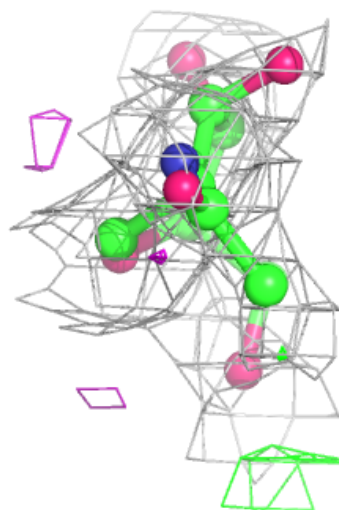
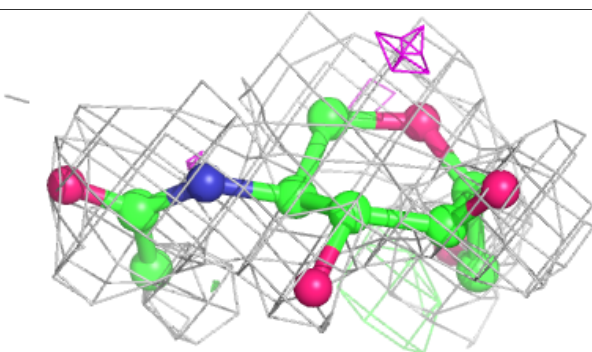
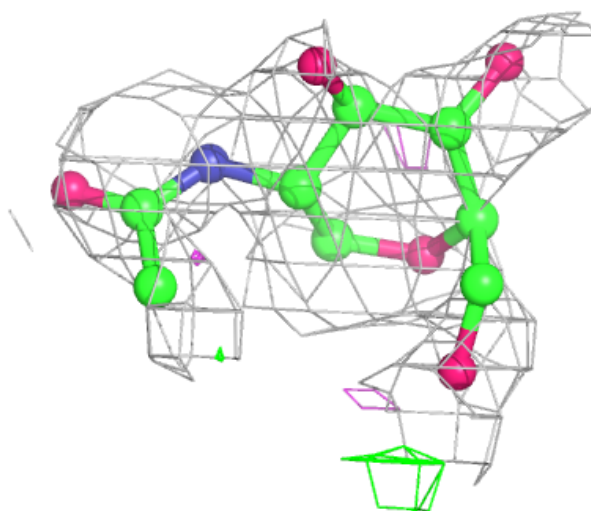
Electron density around NAG A 605:

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



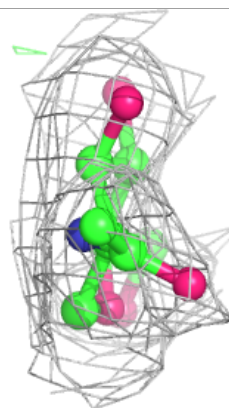
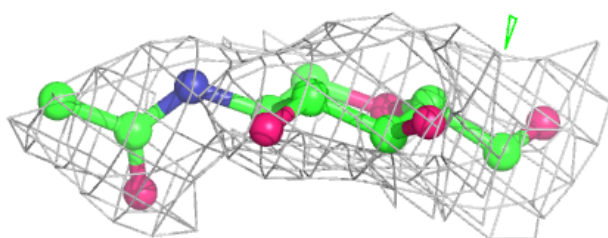
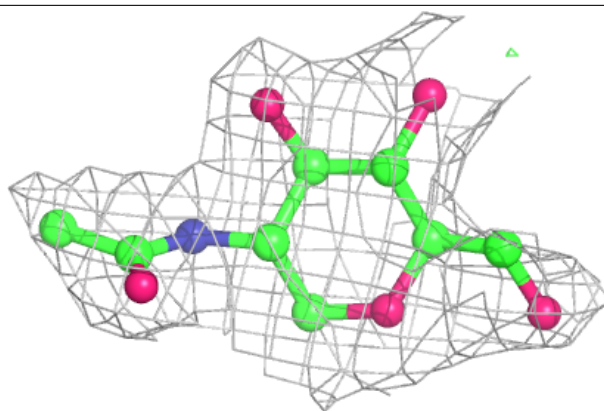
Electron density around NAG A 606:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

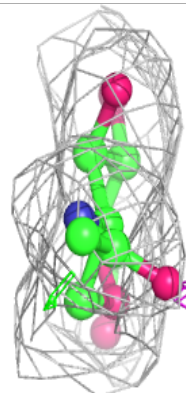
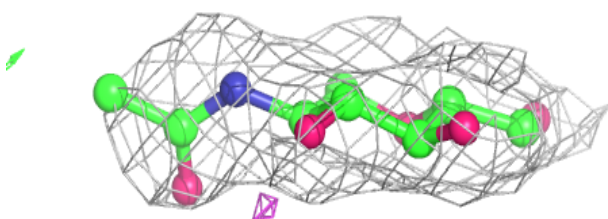
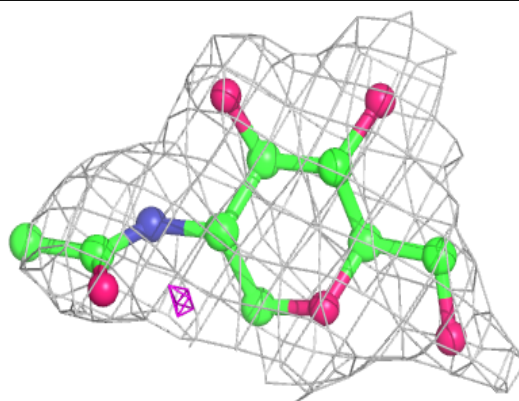


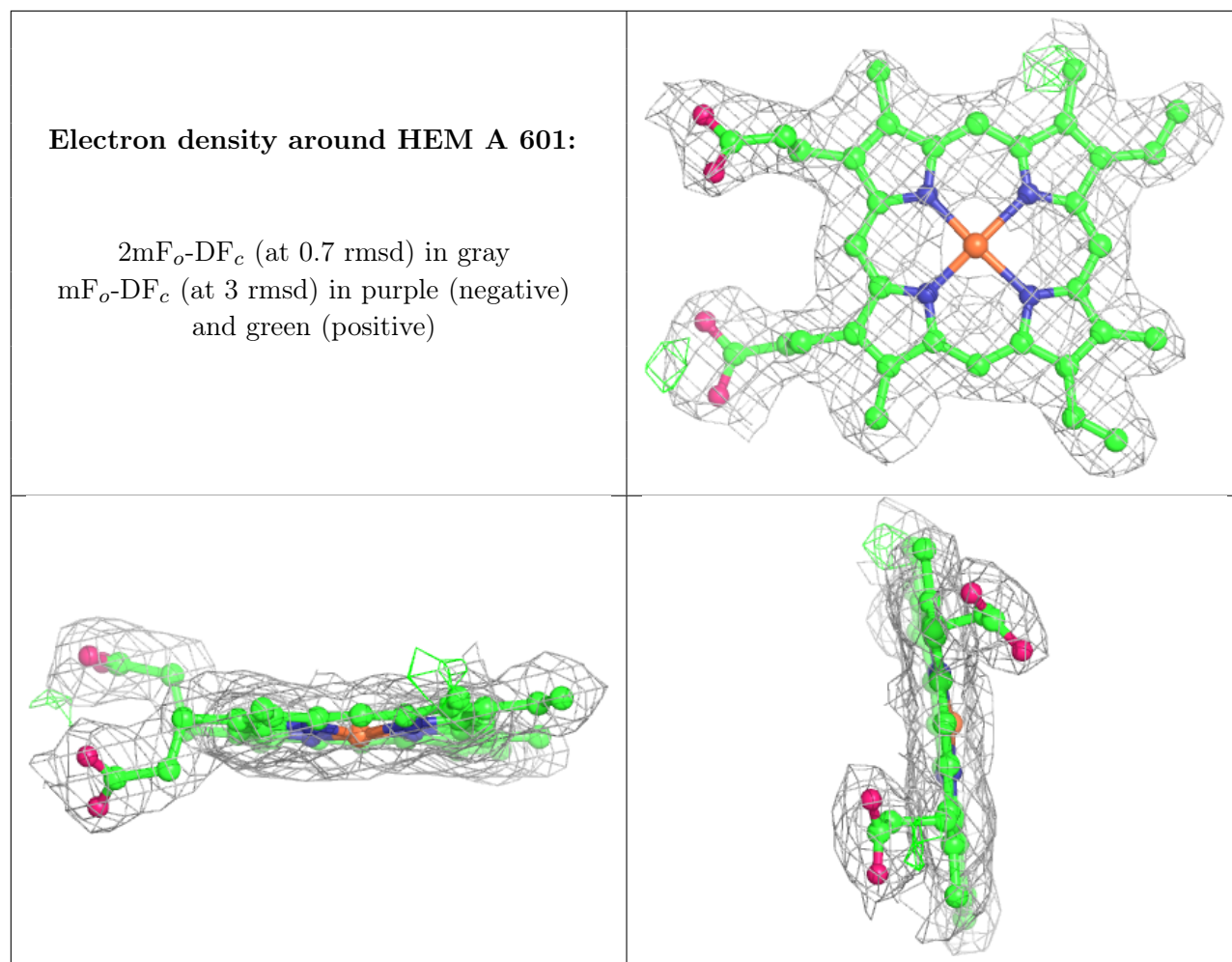
Electron density around NAG A 604:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
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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)





6.5 Other polymers [i](#)

There are no such residues in this entry.