



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 24, 2022 – 12:45 PM EST

PDB ID : 7RY7
Title : Structure of Plasmepsin X (PM10, PMX) from Plasmodium falciparum 3D7
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2021-08-24
Resolution : 2.10 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 : 2.26
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) : 2.26

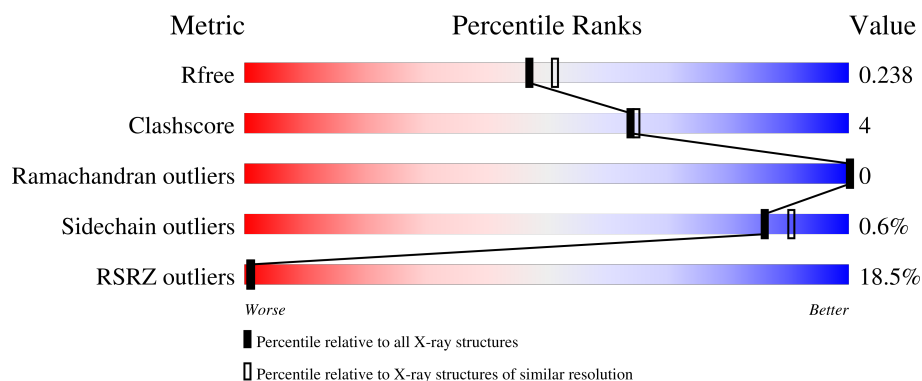
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	467	<div> <div>17%</div> <div>83%</div> <div>9%</div> <div>7%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3307 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 Plasmepsin X.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	433	Total	C	N	O	S	0	1	0
			3225	2066	529	609	21			

There are 91 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LEU	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	PHE	deletion	UNP Q8IAS0
A	?	-	THR	deletion	UNP Q8IAS0
A	?	-	THR	deletion	UNP Q8IAS0
A	?	-	TYR	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	LYS	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	LYS	deletion	UNP Q8IAS0
A	?	-	ALA	deletion	UNP Q8IAS0
A	?	-	GLN	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ILE	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	HIS	deletion	UNP Q8IAS0
A	?	-	LEU	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ILE	deletion	UNP Q8IAS0
A	?	-	GLN	deletion	UNP Q8IAS0
A	?	-	LYS	deletion	UNP Q8IAS0
A	?	-	HIS	deletion	UNP Q8IAS0
A	?	-	VAL	deletion	UNP Q8IAS0
A	?	-	TYR	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0

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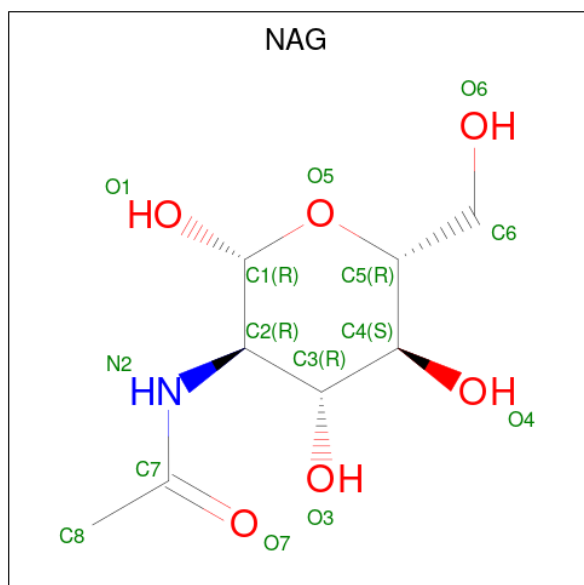
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ALA	deletion	UNP Q8IAS0
A	?	-	GLN	deletion	UNP Q8IAS0
A	?	-	LYS	deletion	UNP Q8IAS0
A	?	-	GLY	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	LYS	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	PHE	deletion	UNP Q8IAS0
A	?	-	THR	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	LEU	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	LEU	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0

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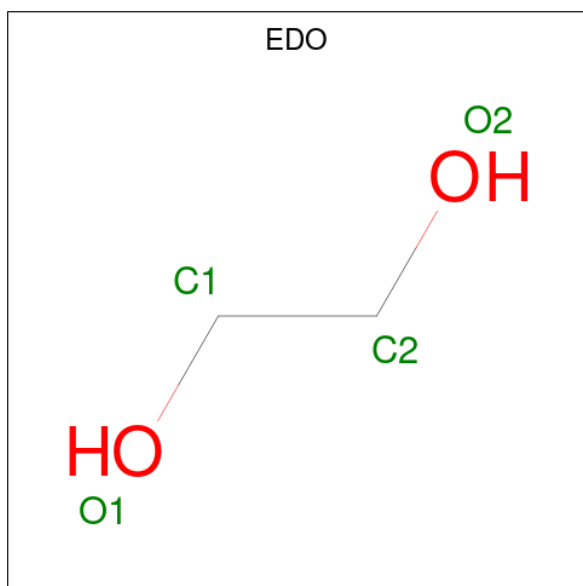
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	ASP	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	SER	deletion	UNP Q8IAS0
A	?	-	ILE	deletion	UNP Q8IAS0
A	?	-	GLU	deletion	UNP Q8IAS0
A	?	-	LYS	deletion	UNP Q8IAS0
A	?	-	ASN	deletion	UNP Q8IAS0
A	?	-	PHE	deletion	UNP Q8IAS0
A	?	-	ILE	deletion	UNP Q8IAS0
A	?	-	ALA	deletion	UNP Q8IAS0
A	574	GLU	-	expression tag	UNP Q8IAS0
A	575	ASN	-	expression tag	UNP Q8IAS0
A	576	LEU	-	expression tag	UNP Q8IAS0
A	577	TYR	-	expression tag	UNP Q8IAS0
A	578	PHE	-	expression tag	UNP Q8IAS0
A	579	GLN	-	expression tag	UNP Q8IAS0

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



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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

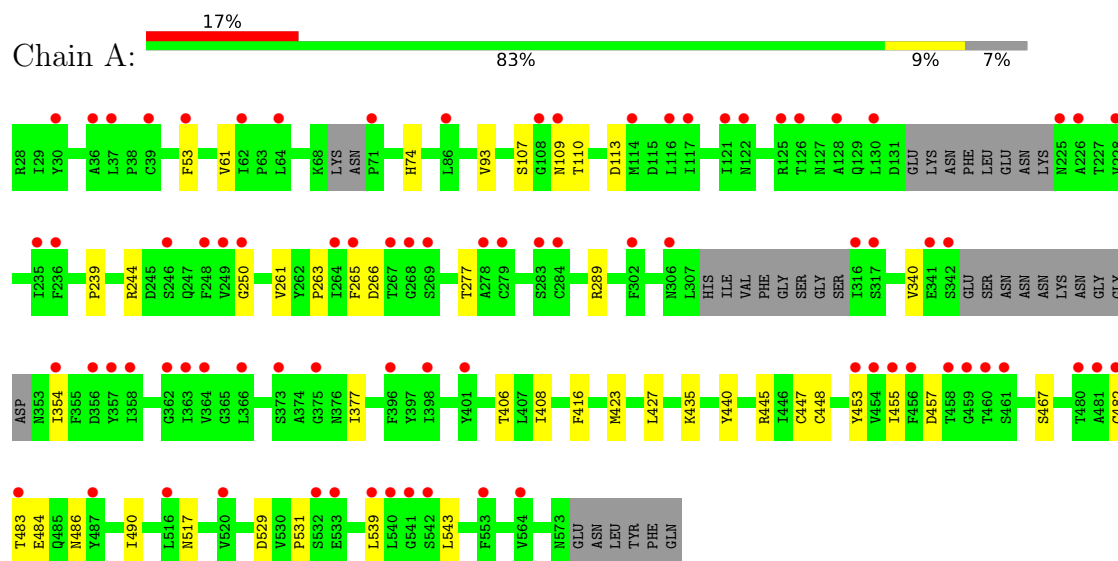
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	60	Total	O	0	0
			60	60		

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: Plasmepsin X



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	192.30Å 50.88Å 49.92Å 90.00° 93.15° 90.00°	Depositor
Resolution (Å)	35.26 – 2.10 35.26 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (35.26-2.10) 99.9 (35.26-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.19 dev 4329	Depositor
R, R_{free}	0.206 , 0.238 0.205 , 0.238	Depositor DCC
R_{free} test set	2129 reflections (7.50%)	wwPDB-VP
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.468	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 60.1	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	0.96	EDS
Total number of atoms	3307	wwPDB-VP
Average B, all atoms (Å ²)	69.0	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: NAG, EDO

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.38	0/3299	0.56	0/4490

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	265	PHE	Peptide

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	3225	0	2986	26	0
2	A	14	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	8	0	12	0	0
4	A	60	0	0	0	0
All	All	3307	0	3011	26	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 4.

All (26) 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:377:ILE:HG12	2:A:601:NAG:H61	1.69	0.74
1:A:53:PHE:HB2	1:A:423:MET:SD	2.40	0.62
1:A:455:ILE:HB	1:A:539:LEU:HD23	1.87	0.56
1:A:61:VAL:HG13	1:A:406:THR:CG2	2.37	0.55
1:A:261:VAL:HG23	1:A:263:PRO:HD3	1.87	0.54
1:A:440:TYR:CE2	1:A:445:ARG:HB2	2.43	0.54
1:A:277:THR:O	1:A:289:ARG:HD3	2.08	0.53
1:A:427:LEU:HD23	1:A:453:TYR:HE1	1.74	0.52
1:A:244:ARG:NH1	1:A:266:ASP:OD1	2.43	0.52
1:A:427:LEU:HD22	1:A:435:LYS:HB2	1.92	0.50
1:A:61:VAL:HG13	1:A:406:THR:HG23	1.95	0.49
1:A:486:ASN:O	1:A:490:ILE:HG12	2.15	0.47
1:A:340:VAL:HG12	1:A:354:ILE:HD11	1.97	0.47
1:A:109:ASN:HB2	1:A:239:PRO:O	2.15	0.47
1:A:244:ARG:HH11	1:A:266:ASP:CG	2.20	0.46
1:A:543:LEU:HD23	1:A:543:LEU:HA	1.73	0.45
1:A:93:VAL:O	1:A:531:PRO:HD2	2.17	0.45
1:A:467:SER:N	1:A:529:ASP:OD1	2.50	0.44
1:A:427:LEU:HD23	1:A:453:TYR:CE1	2.52	0.43
1:A:408:ILE:HD11	1:A:416:PHE:CE2	2.55	0.42
1:A:483:THR:OG1	1:A:484:GLU:N	2.52	0.42
1:A:250:GLY:O	1:A:263:PRO:HD2	2.20	0.41
1:A:110:THR:HG22	1:A:113:ASP:OD2	2.19	0.41
1:A:447:CYS:HA	1:A:448:CYS:HA	1.78	0.41
1:A:244:ARG:NH2	1:A:457:ASP:OD2	2.36	0.41
1:A:74:HIS:HB2	1:A:517:ASN:OD1	2.21	0.41

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	424/467 (91%)	408 (96%)	16 (4%)	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	335/423 (79%)	333 (99%)	2 (1%)	86	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	SER
1	A	482	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

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 ⓘ

3 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	$\# Z > 2$
3	EDO	A	603	-	3,3,3	0.50	0	2,2,2	0.29	0
2	NAG	A	601	1	14,14,15	0.65	0	17,19,21	0.55	0
3	EDO	A	602	-	3,3,3	0.48	0	2,2,2	0.51	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
3	EDO	A	603	-	-	0/1/1/1	-
2	NAG	A	601	1	-	2/6/23/26	0/1/1/1
3	EDO	A	602	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

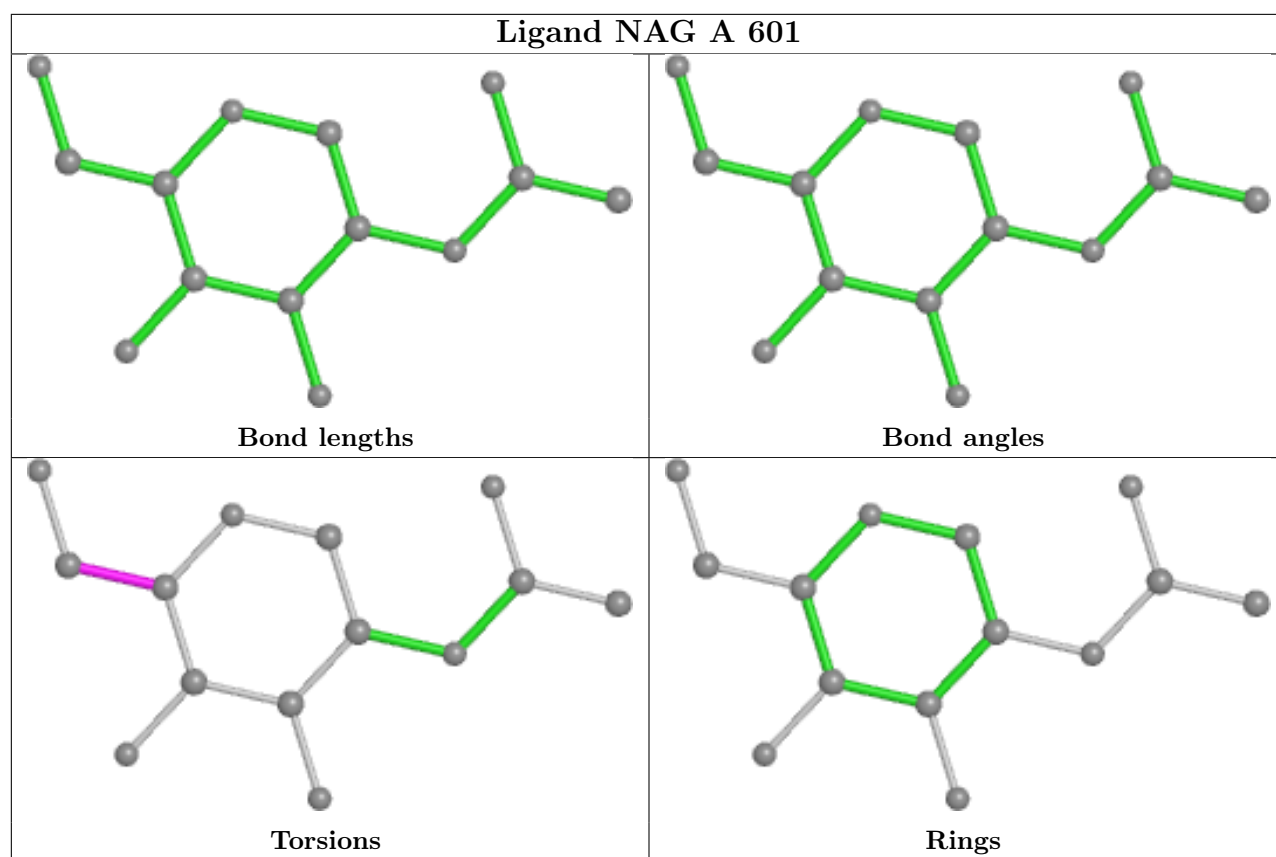
Mol	Chain	Res	Type	Atoms
2	A	601	NAG	C4-C5-C6-O6
2	A	601	NAG	O5-C5-C6-O6
3	A	602	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	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	433/467 (92%)	0.89	80 (18%) 1 1	44, 66, 114, 145	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	354	ILE	7.3
1	A	487	TYR	6.0
1	A	130	LEU	5.9
1	A	357	TYR	4.9
1	A	108	GLY	4.8
1	A	316	ILE	4.8
1	A	302	PHE	4.7
1	A	236	PHE	4.6
1	A	480	THR	4.4
1	A	516	LEU	4.3
1	A	483	THR	4.3
1	A	126	THR	4.3
1	A	532	SER	4.2
1	A	520	VAL	4.1
1	A	458	THR	4.1
1	A	117	ILE	4.1
1	A	459	GLY	4.0
1	A	279	CYS	3.9
1	A	356	ASP	3.8
1	A	246	SER	3.8
1	A	541	GLY	3.8
1	A	460	THR	3.6
1	A	455	ILE	3.5
1	A	539	LEU	3.5
1	A	358	ILE	3.4
1	A	401	TYR	3.4
1	A	284	CYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	249	VAL	3.4
1	A	125	ARG	3.4
1	A	226	ALA	3.3
1	A	540	LEU	3.3
1	A	37	LEU	3.3
1	A	121	ILE	3.3
1	A	453	TYR	3.2
1	A	264	ILE	3.2
1	A	122	ASN	3.2
1	A	267	THR	3.2
1	A	30	TYR	3.2
1	A	116	LEU	3.1
1	A	248	PHE	3.0
1	A	342	SER	3.0
1	A	482	CYS	2.9
1	A	306	ASN	2.8
1	A	228	VAL	2.7
1	A	86	LEU	2.7
1	A	283	SER	2.7
1	A	363	ILE	2.7
1	A	268	GLY	2.6
1	A	64	LEU	2.6
1	A	235	ILE	2.6
1	A	366	LEU	2.6
1	A	542	SER	2.6
1	A	53	PHE	2.6
1	A	373	SER	2.5
1	A	128	ALA	2.5
1	A	114	MET	2.4
1	A	533	GLU	2.3
1	A	364	VAL	2.3
1	A	265	PHE	2.2
1	A	39[A]	CYS	2.2
1	A	396	PHE	2.2
1	A	317	SER	2.2
1	A	461	SER	2.2
1	A	454	VAL	2.2
1	A	109	ASN	2.2
1	A	36	ALA	2.2
1	A	278	ALA	2.2
1	A	481	ALA	2.2
1	A	362	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	456	PHE	2.2
1	A	553	PHE	2.2
1	A	375	GLY	2.1
1	A	269	SER	2.1
1	A	71	PRO	2.1
1	A	250	GLY	2.1
1	A	62	ILE	2.1
1	A	341	GLU	2.1
1	A	225	ASN	2.0
1	A	398	ILE	2.0
1	A	564	VAL	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](#)

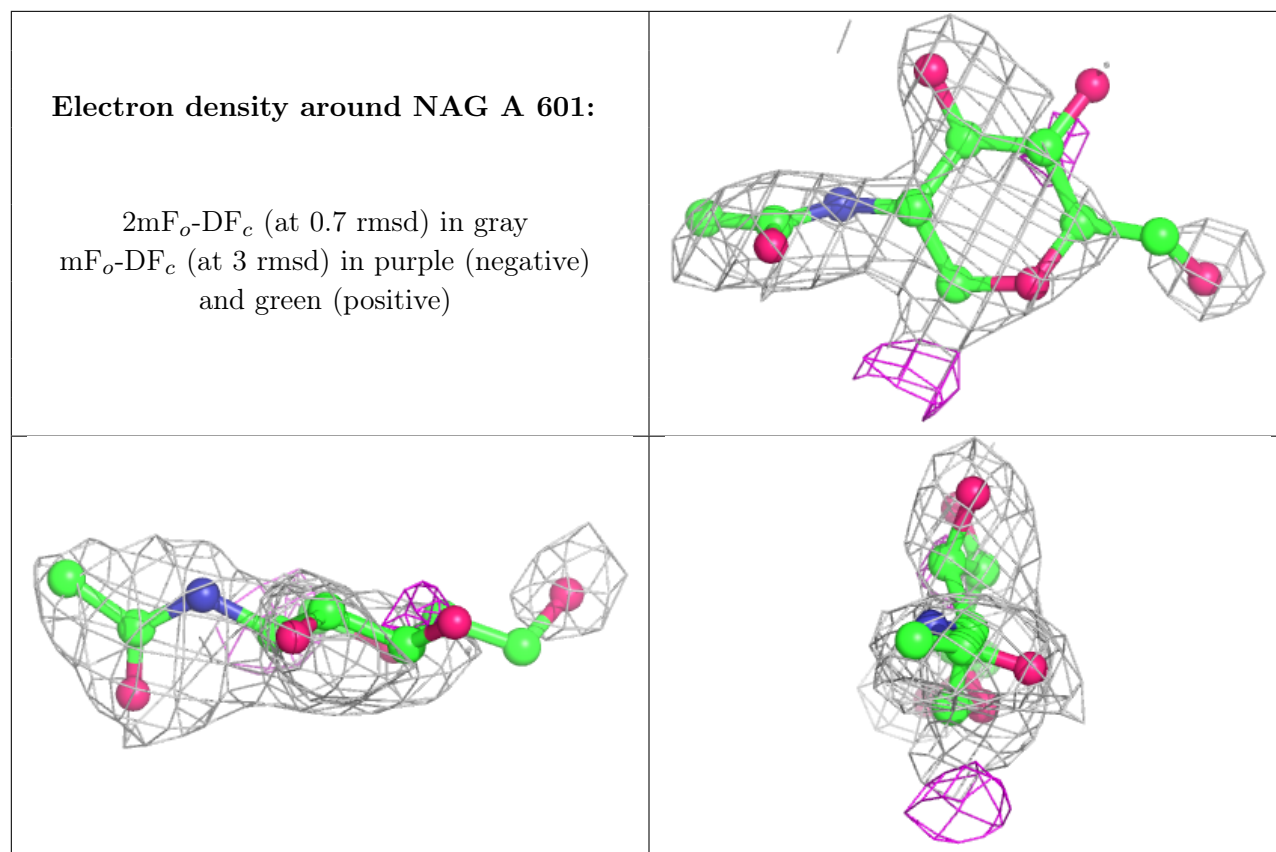
There are no monosaccharides in this entry.

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, 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
2	NAG	A	601	14/15	0.64	0.37	76,80,81,82	14
3	EDO	A	603	4/4	0.85	0.12	83,85,87,87	0
3	EDO	A	602	4/4	0.97	0.30	49,52,53,56	0

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



6.5 Other polymers [i](#)

There are no such residues in this entry.