



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 2, 2025 – 01:34 am GMT

PDB ID : 8RTN
Title : Human thrombin in complex with a trivalent inhibitor
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Deposited on : 2024-01-26
Resolution : 2.51 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

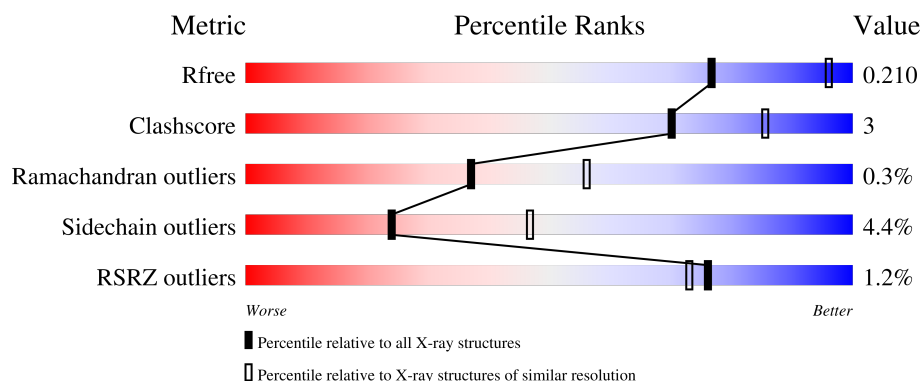
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)

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	H	622	 35% 5% 60%
1	L	622	 95%
2	I	48	 2% 71% 10% 19%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2744 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.

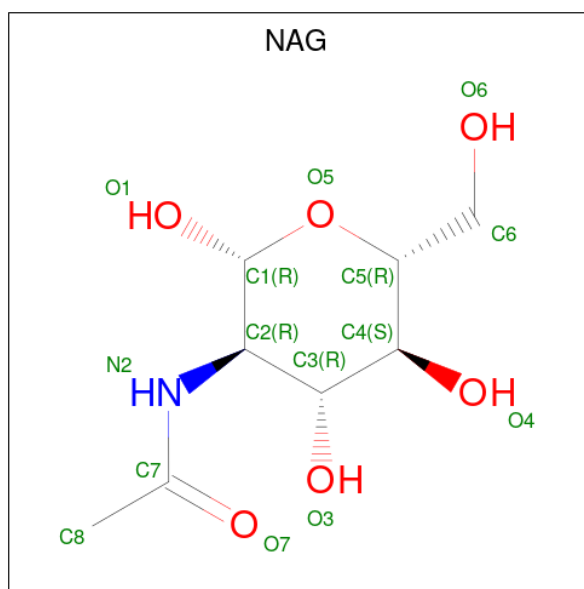
- Molecule 1 is a protein called Prothrombin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	34	Total	C	N	O	S	0	0	0
			268	167	43	57	1			
1	H	251	Total	C	N	O	S	0	0	0
			2029	1294	359	362	14			

- Molecule 2 is a protein called Synthetic trivalent inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	39	Total	C	N	O	S	0	0	0
			315	189	47	75	4			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total 1	Na 1	0	0

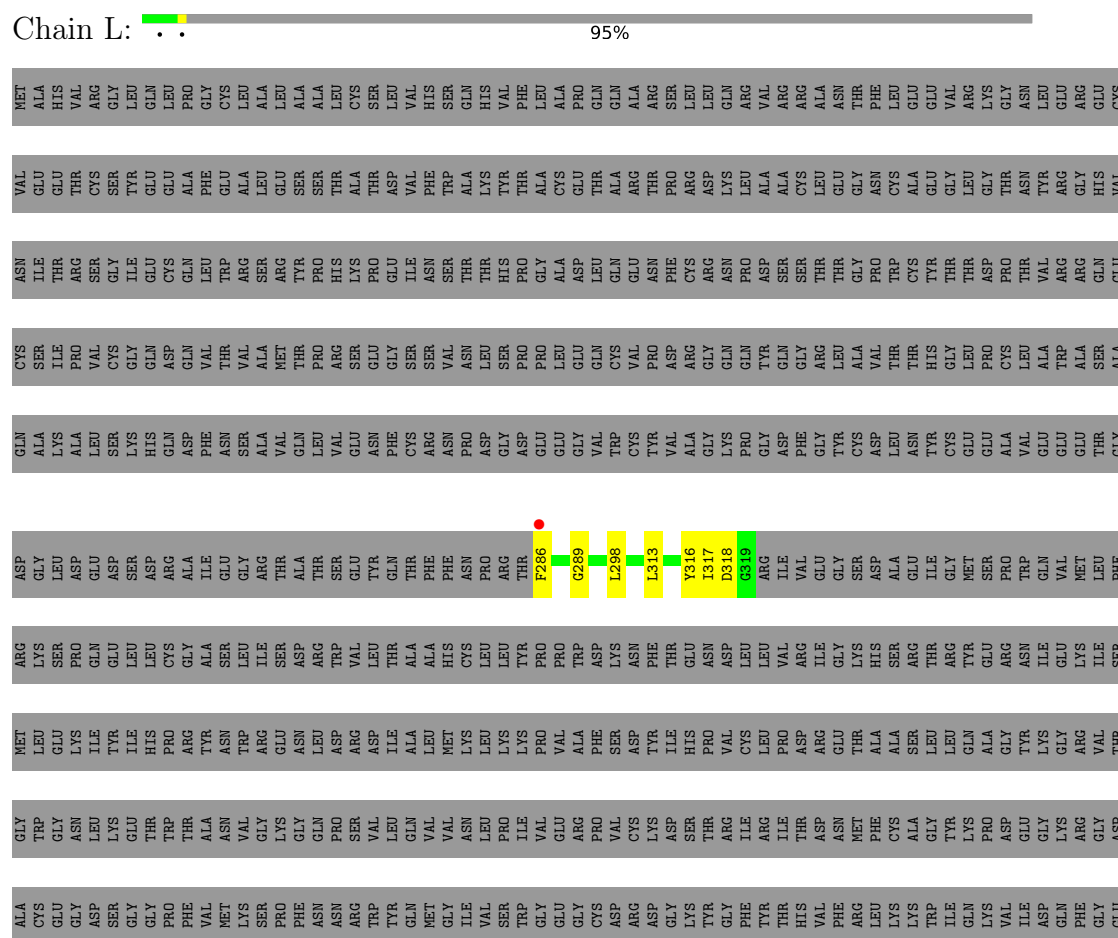
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	5	Total 5	O 5	0	0
5	H	95	Total 95	O 95	0	0
5	I	17	Total 17	O 17	0	0

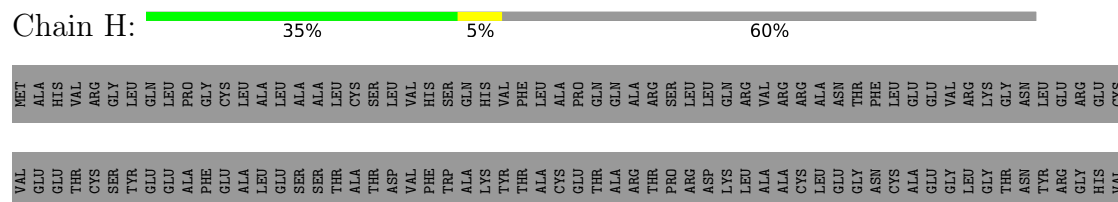
3 Residue-property plots

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: Prothrombin



• Molecule 1: Prothrombin



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

ASP	GLY	ARG	I321	G330	V336	F339	Q344	L347	A350	R356	H363	T375	D378	R382	I395	I398	K403	T404	Y405	D419	Y434	L464	K465	E466	T467	THR	THR	ALA	ASN	VAL	GLY	LYS	G475	Q476	P477	C507	P534	F535	N536	N537
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I544	K556	T561	H562	V563	R565	L566	K572	Q576	F577	G578	GLU
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● Molecule 2: Synthetic trivalent inhibitor



G1	A5	D8	Y9	Y12	GLY	ASP	SER	SER	GLU	GLU	VAL	GLY	GLY	A22	Y46	L47	Q48
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4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	82.19Å 82.19Å 271.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	68.86 – 2.51 68.86 – 2.51	Depositor EDS
% Data completeness (in resolution range)	99.9 (68.86-2.51) 100.0 (68.86-2.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.168 , 0.213 0.166 , 0.210	Depositor DCC
R_{free} test set	664 reflections (5.30%)	wwPDB-VP
Wilson B-factor (Å ²)	44.9	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2744	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.07% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TYS, NA, 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	H	0.32	0/2081	0.55	0/2811
1	L	0.32	0/271	0.54	0/360
2	I	0.27	0/269	0.49	0/358
All	All	0.31	0/2621	0.55	0/3529

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	H	2029	0	2003	16	1
1	L	268	0	255	3	0
2	I	315	0	266	3	0
3	H	14	0	13	0	0
4	H	1	0	0	0	0
5	H	95	0	0	0	0
5	I	17	0	0	0	0
5	L	5	0	0	0	0
All	All	2744	0	2537	17	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 3.

The worst 5 of 17 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:H:565:ARG:NH1	2:I:8:ASP:OD1	2.30	0.54
1:H:336:VAL:HB	1:H:350:ALA:HB3	1.90	0.53
1:H:562:HIS:CD2	1:H:565:ARG:HG3	2.47	0.49
1:L:298:LEU:HD12	1:H:330:GLY:HA3	1.96	0.48
1:L:316:TYR:CD2	1:H:534:PRO:HG3	2.47	0.47

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)
1:H:434:TYR:OH	1:H:434:TYR:OH[6_555]	2.09	0.11

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	H	247/622 (40%)	236 (96%)	11 (4%)	0	100	100
1	L	32/622 (5%)	28 (88%)	3 (9%)	1 (3%)	3	5
2	I	33/48 (69%)	30 (91%)	3 (9%)	0	100	100
All	All	312/1292 (24%)	294 (94%)	17 (5%)	1 (0%)	37	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	317	ILE

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	H	219/531 (41%)	209 (95%)	10 (5%)	23	45
1	L	29/531 (6%)	27 (93%)	2 (7%)	13	26
2	I	27/33 (82%)	27 (100%)	0	100	100
All	All	275/1095 (25%)	263 (96%)	12 (4%)	24	47

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	507	CYS
1	H	537	ASN
1	H	566	LEU
1	H	556	LYS
1	H	356	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	386	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

3 non-standard protein/DNA/RNA residues 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	TYS	I	46	2	15,16,17	0.94	1 (6%)	18,22,24	0.69	0
2	TYS	I	12	2	15,16,17	1.04	1 (6%)	18,22,24	0.70	0
2	TYS	I	9	2	15,16,17	0.95	1 (6%)	18,22,24	0.72	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	TYS	I	46	2	-	1/10/11/13	0/1/1/1
2	TYS	I	12	2	-	3/10/11/13	0/1/1/1
2	TYS	I	9	2	-	3/10/11/13	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	12	TYS	OH-S	3.61	1.63	1.58
2	I	9	TYS	OH-S	3.21	1.63	1.58
2	I	46	TYS	OH-S	3.17	1.63	1.58

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	9	TYS	CZ-OH-S-O3
2	I	12	TYS	CZ-OH-S-O3
2	I	46	TYS	O-C-CA-CB
2	I	9	TYS	CZ-OH-S-O1
2	I	9	TYS	CZ-OH-S-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
3	NAG	H	601	1	14,14,15	0.33	0	17,19,21	0.87	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	H	601	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	601	NAG	C1-O5-C5	3.17	116.49	112.19

There are no chirality outliers.

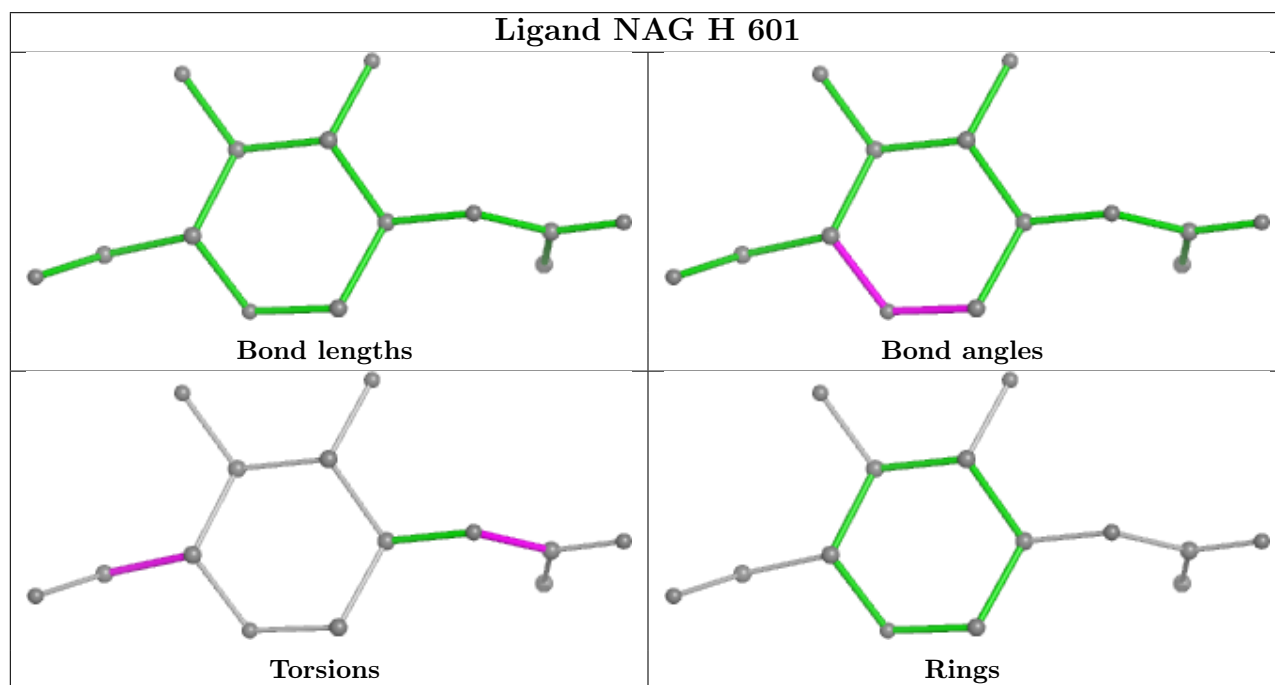
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	601	NAG	C4-C5-C6-O6
3	H	601	NAG	O5-C5-C6-O6
3	H	601	NAG	C8-C7-N2-C2
3	H	601	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	H	251/622 (40%)	-0.50	2 (0%) 82 79	33, 46, 69, 87	0
1	L	34/622 (5%)	-0.01	1 (2%) 54 50	46, 55, 100, 118	0
2	I	36/48 (75%)	-0.08	1 (2%) 55 51	35, 58, 103, 116	0
All	All	321/1292 (24%)	-0.40	4 (1%) 76 73	33, 48, 81, 118	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	286	PHE	3.3
1	H	578	GLY	2.3
2	I	1	GLY	2.3
1	H	535	PHE	2.1

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
2	TYS	I	12	16/17	0.74	0.15	83,88,100,101	0
2	TYS	I	9	16/17	0.89	0.10	80,84,99,102	0
2	TYS	I	46	16/17	0.97	0.06	56,61,77,77	0

6.3 Carbohydrates [i](#)

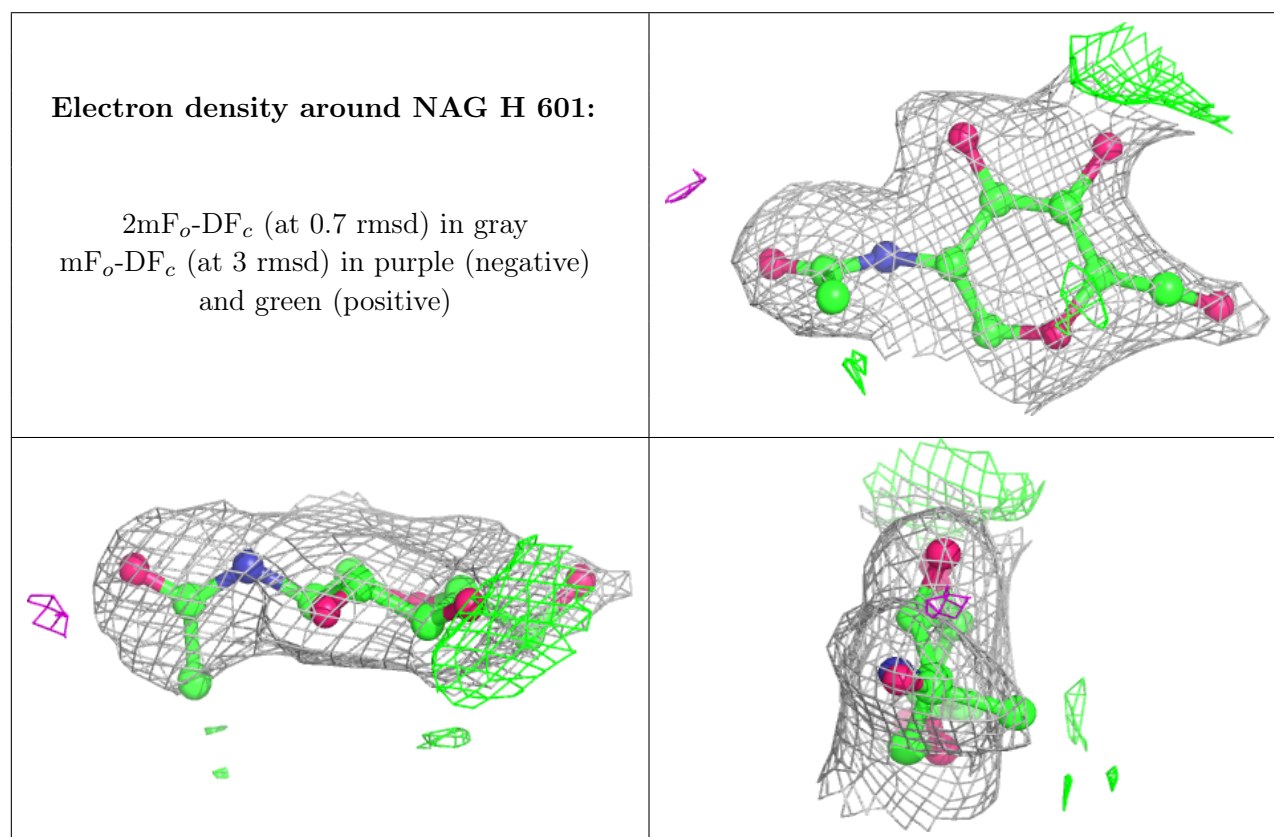
There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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	H	601	14/15	0.81	0.11	53,63,69,74	0
4	NA	H	602	1/1	0.87	0.16	45,45,45,45	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 ⓘ

There are no such residues in this entry.