



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 09:52 AM UTC

PDB ID : 8OHQ / pdb_00008ohq
Title : Crystal structure of human heparanase in complex with competitive inhibitor derived from siastatin B
Authors : Wu, L.; Davies, G.J.; Overkleeft, H.S.; Armstrong, Z.; Yurong, C.
Deposited on : 2023-03-21
Resolution : 1.70 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

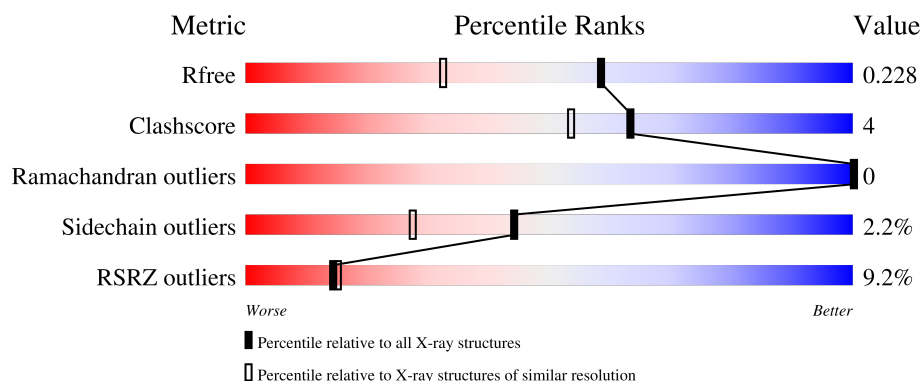
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	AAA	385	9% 92% 8%
2	BBB	74	9% 88% 12%
3	AeA	2	100%

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	EDO	AAA	610	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 4030 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 Heparanase 50 kDa subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	385	Total	C	N	O	S	0	3	0
			3079	1986	527	554	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	159	LYS	-	expression tag	UNP Q9Y251
AAA	307	ARG	LYS	variant	UNP Q9Y251

- Molecule 2 is a protein called Heparanase 8 kDa subunit.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	BBB	74	Total	C	N	O	0	1	0
			595	388	97	110			

- Molecule 3 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



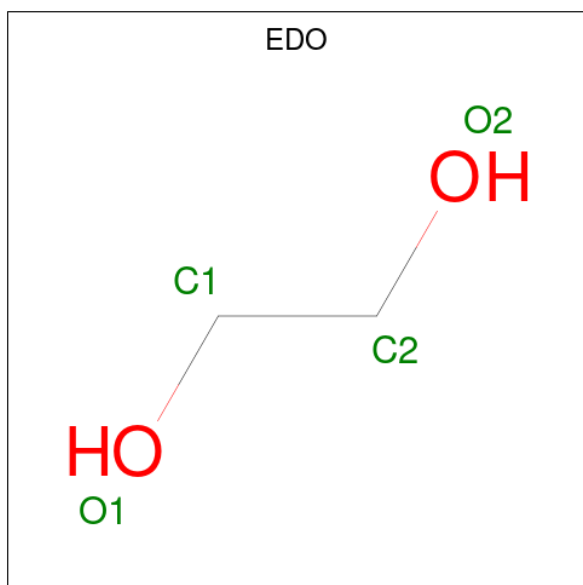
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	AeA	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

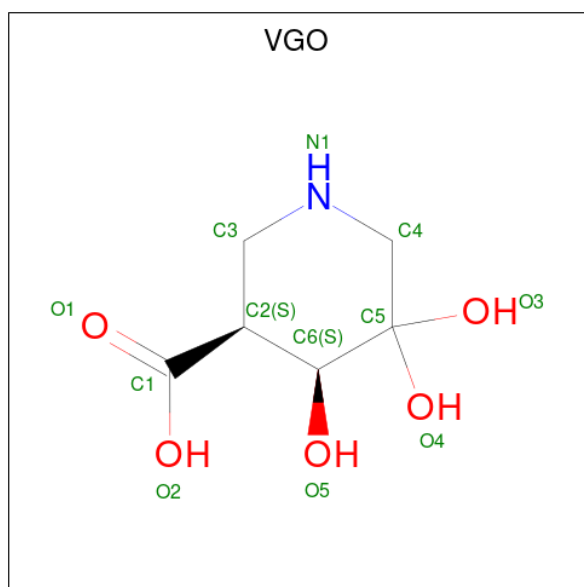


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAA	1	Total C O 4 2 2	0	0
5	AAA	1	Total C O 4 2 2	0	0
5	BBB	1	Total C O 4 2 2	0	0

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	AAA	3	Total Cl 3 3	0	0

- Molecule 7 is (3 {S},4 {S})-4,5,5-tris(oxidanyl)piperidine-3-carboxylic acid (CCD ID: VGO) (formula: C₆H₁₁NO₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	AAA	1	Total C N O 12 6 1 5	0	0

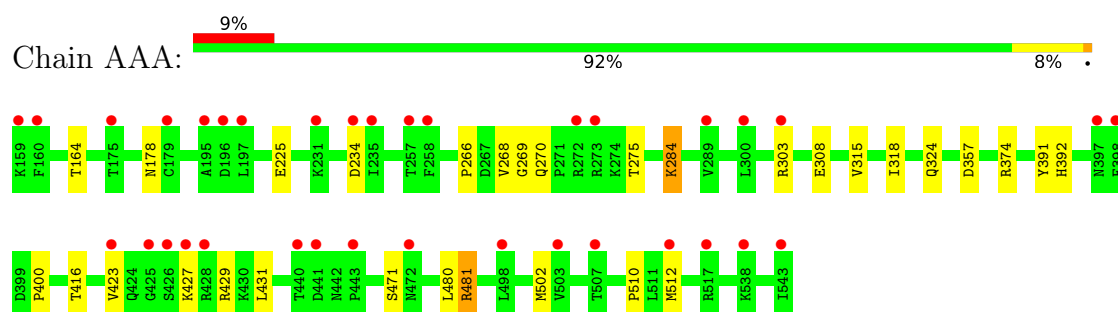
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	AAA	212	Total O 212 212	0	0
8	BBB	37	Total O 37 37	0	0

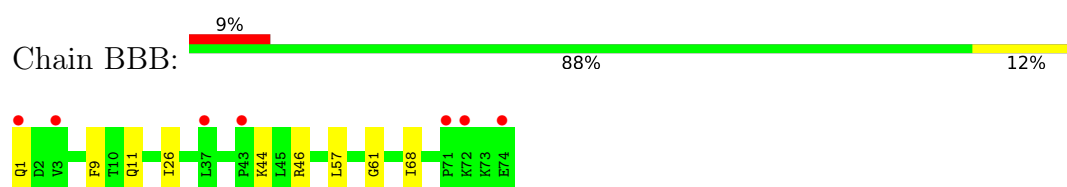
3 Residue-property plots [i](#)

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: Heparanase 50 kDa subunit



- Molecule 2: Heparanase 8 kDa subunit



- Molecule 3: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.11Å 70.92Å 78.56Å 90.00° 95.53° 90.00°	Depositor
Resolution (Å)	45.94 – 1.70 45.94 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.94-1.70) 99.6 (45.94-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.174 , 0.208 0.202 , 0.228	Depositor DCC
R_{free} test set	2756 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 29.9	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	0.95	EDS
Total number of atoms	4030	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.93% 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: EDO, VGO, FUC, CL, 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	AAA	1.08	1/3153 (0.0%)	1.25	4/4263 (0.1%)
2	BBB	1.06	0/609	1.15	1/826 (0.1%)
All	All	1.08	1/3762 (0.0%)	1.23	5/5089 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	480	LEU	C-O	5.01	1.30	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	481	ARG	CG-CD-NE	6.46	126.22	112.00
2	BBB	61	GLY	CA-C-O	-5.28	116.37	121.86
1	AAA	357	ASP	CA-CB-CG	5.23	117.83	112.60
1	AAA	324	GLN	CB-CG-CD	5.15	121.35	112.60
1	AAA	225	GLU	CB-CA-C	5.01	115.36	111.00

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	AAA	3079	0	3104	24	0
2	BBB	595	0	607	11	0
3	AeA	24	0	22	0	0
4	AAA	56	0	52	2	0
5	AAA	8	0	12	5	0
5	BBB	4	0	6	2	0
6	AAA	3	0	0	1	0
7	AAA	12	0	0	0	0
8	AAA	212	0	0	5	0
8	BBB	37	0	0	0	0
All	All	4030	0	3803	30	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.

The worst 5 of 30 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)
4:AAA:601:NAG:H62	8:AAA:791:HOH:O	1.85	0.75
1:AAA:374:ARG:HH22	5:AAA:610:EDO:H21	1.55	0.71
4:AAA:601:NAG:H3	8:AAA:865:HOH:O	1.95	0.67
2:BBB:26:ILE:HG12	2:BBB:57:LEU:HD11	1.83	0.60
1:AAA:502[A]:MET:HE3	2:BBB:44:LYS:CE	2.33	0.58

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	AAA	386/385 (100%)	377 (98%)	9 (2%)	0	100	100
2	BBB	73/74 (99%)	73 (100%)	0	0	100	100
All	All	459/459 (100%)	450 (98%)	9 (2%)	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	AAA	337/335 (101%)	329 (98%)	8 (2%)	43	26
2	BBB	67/66 (102%)	66 (98%)	1 (2%)	57	43
All	All	404/401 (101%)	395 (98%)	9 (2%)	44	29

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	481	ARG
2	BBB	1	GLN
1	AAA	392	HIS
1	AAA	427	LYS
1	AAA	429	ARG

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 [i](#)

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

5.5 Carbohydrates [i](#)

2 monosaccharides 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	NAG	AeA	1	1,3	14,14,15	0.48	0	17,19,21	1.85	5 (29%)
3	FUC	AeA	2	3	10,10,11	0.72	0	14,14,16	1.55	4 (28%)

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	AeA	1	1,3	-	0/6/23/26	0/1/1/1
3	FUC	AeA	2	3	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	AeA	1	NAG	C1-C2-N2	-5.25	102.16	110.43
3	AeA	2	FUC	C3-C4-C5	3.36	114.92	109.81
3	AeA	1	NAG	O3-C3-C4	-2.44	104.62	110.38
3	AeA	2	FUC	O5-C1-C2	2.39	116.48	110.79
3	AeA	2	FUC	O5-C5-C4	2.25	113.61	109.55

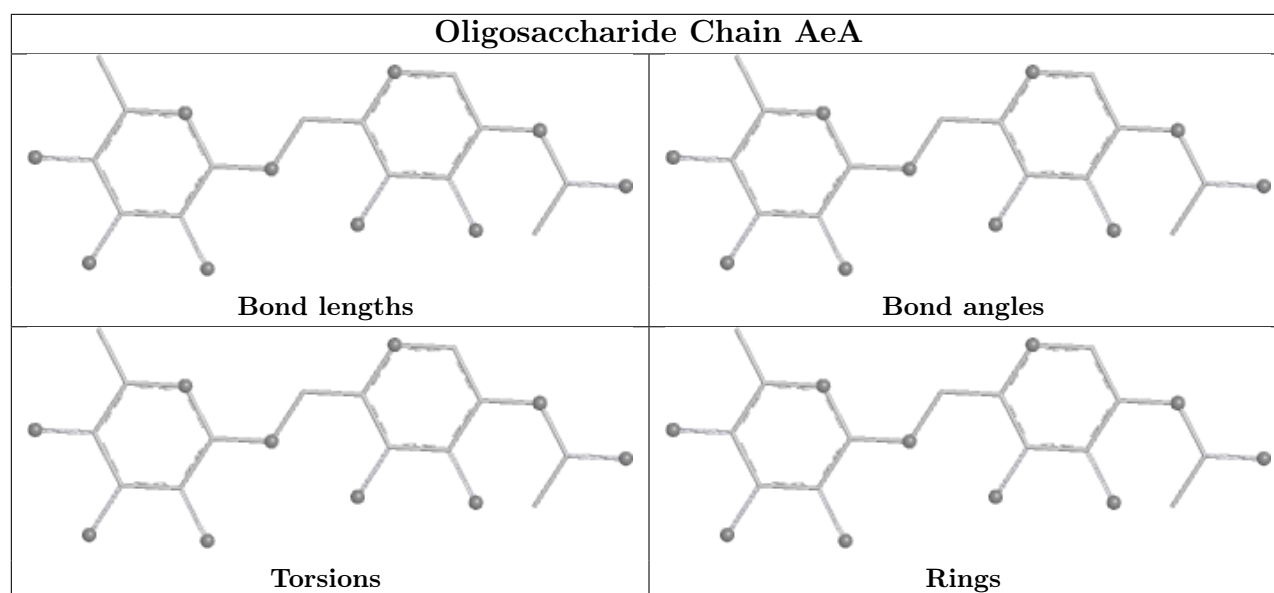
There are no chirality outliers.

There are no torsion outliers.

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 oligosaccharide.



5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 3 are monoatomic - leaving 8 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	$\# Z > 2$
5	EDO	AAA	605	-	3,3,3	0.20	0	2,2,2	0.18	0
4	NAG	AAA	603	1	14,14,15	0.48	0	17,19,21	1.98	5 (29%)
4	NAG	AAA	601	1	14,14,15	0.63	0	17,19,21	0.73	0
5	EDO	AAA	610	-	3,3,3	0.18	0	2,2,2	1.32	0
5	EDO	BBB	101	-	3,3,3	0.25	0	2,2,2	0.29	0
7	VGO	AAA	609	-	11,12,12	1.03	1 (9%)	13,18,18	1.37	2 (15%)
4	NAG	AAA	604	1	14,14,15	0.52	0	17,19,21	1.13	2 (11%)
4	NAG	AAA	602	1	14,14,15	0.52	0	17,19,21	0.64	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
5	EDO	AAA	605	-	-	1/1/1/1	-
4	NAG	AAA	603	1	-	1/6/23/26	0/1/1/1
4	NAG	AAA	601	1	-	3/6/23/26	0/1/1/1
5	EDO	AAA	610	-	-	1/1/1/1	-
5	EDO	BBB	101	-	-	1/1/1/1	-
7	VGO	AAA	609	-	-	4/4/21/21	0/1/1/1
4	NAG	AAA	604	1	-	0/6/23/26	0/1/1/1
4	NAG	AAA	602	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	AAA	609	VGO	O2-C1	-2.05	1.24	1.30

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AAA	603	NAG	C2-N2-C7	-4.52	116.84	122.90
4	AAA	603	NAG	C4-C3-C2	-3.51	105.87	111.02
4	AAA	603	NAG	C3-C4-C5	-2.89	104.99	110.23
4	AAA	603	NAG	O5-C1-C2	-2.86	106.87	111.29
4	AAA	603	NAG	C1-O5-C5	2.62	115.69	112.19

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

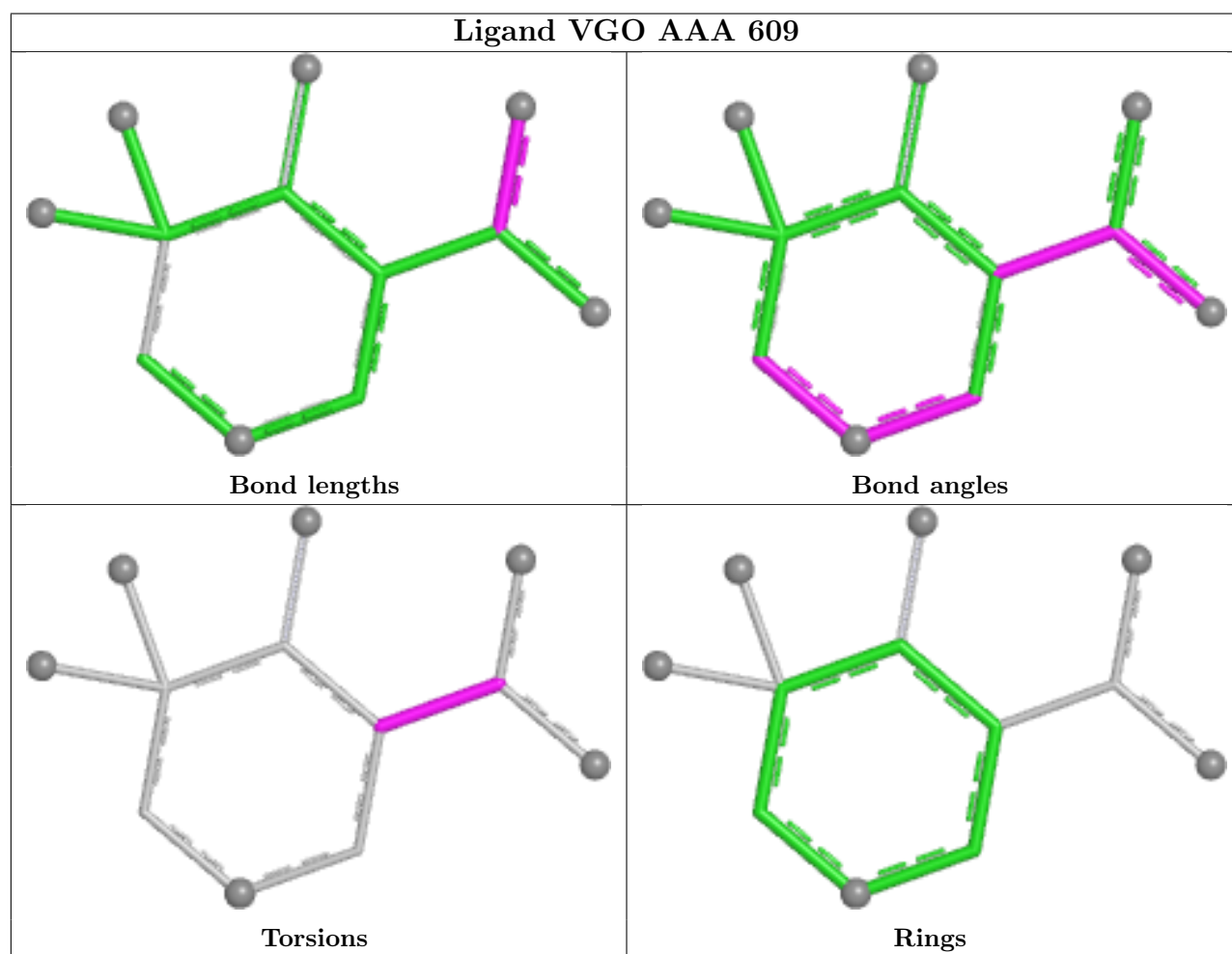
Mol	Chain	Res	Type	Atoms
4	AAA	601	NAG	C8-C7-N2-C2
4	AAA	601	NAG	O5-C5-C6-O6
4	AAA	602	NAG	C4-C5-C6-O6
5	AAA	605	EDO	O1-C1-C2-O2
5	BBB	101	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	AAA	605	EDO	1	0
4	AAA	601	NAG	2	0
5	AAA	610	EDO	4	0
5	BBB	101	EDO	2	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 ⓘ

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	AAA	385/385 (100%)	0.66	35 (9%) 15 15	12, 26, 49, 112	3 (0%)
2	BBB	74/74 (100%)	0.72	7 (9%) 14 14	13, 27, 44, 78	1 (1%)
All	All	459/459 (100%)	0.67	42 (9%) 14 15	12, 27, 49, 112	4 (0%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	160	PHE	5.9
1	AAA	425	GLY	4.7
1	AAA	426	SER	4.4
1	AAA	428	ARG	4.4
1	AAA	427	LYS	4.1

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

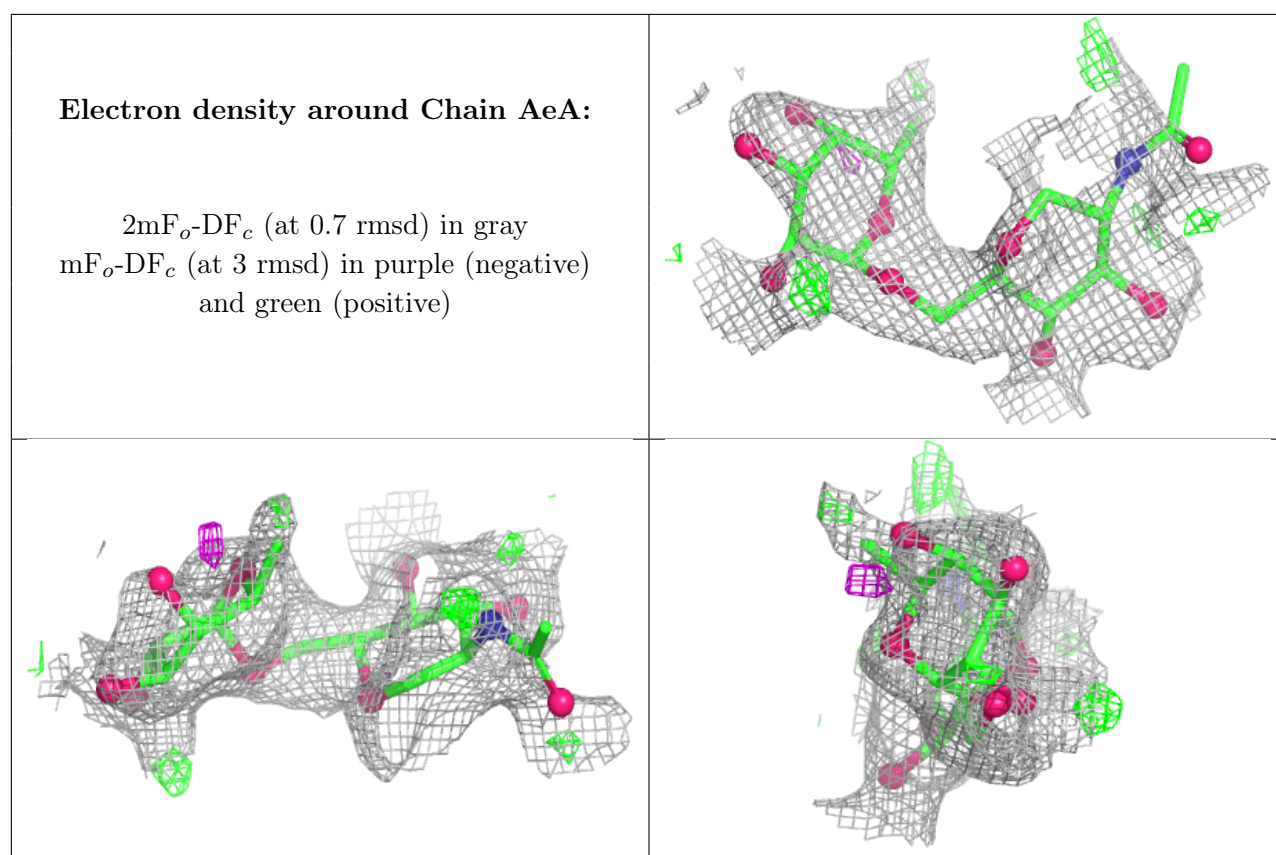
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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	AeA	1	14/15	-	-	61,68,82,86	0
3	FUC	AeA	2	10/11	-	-	64,72,74,76	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



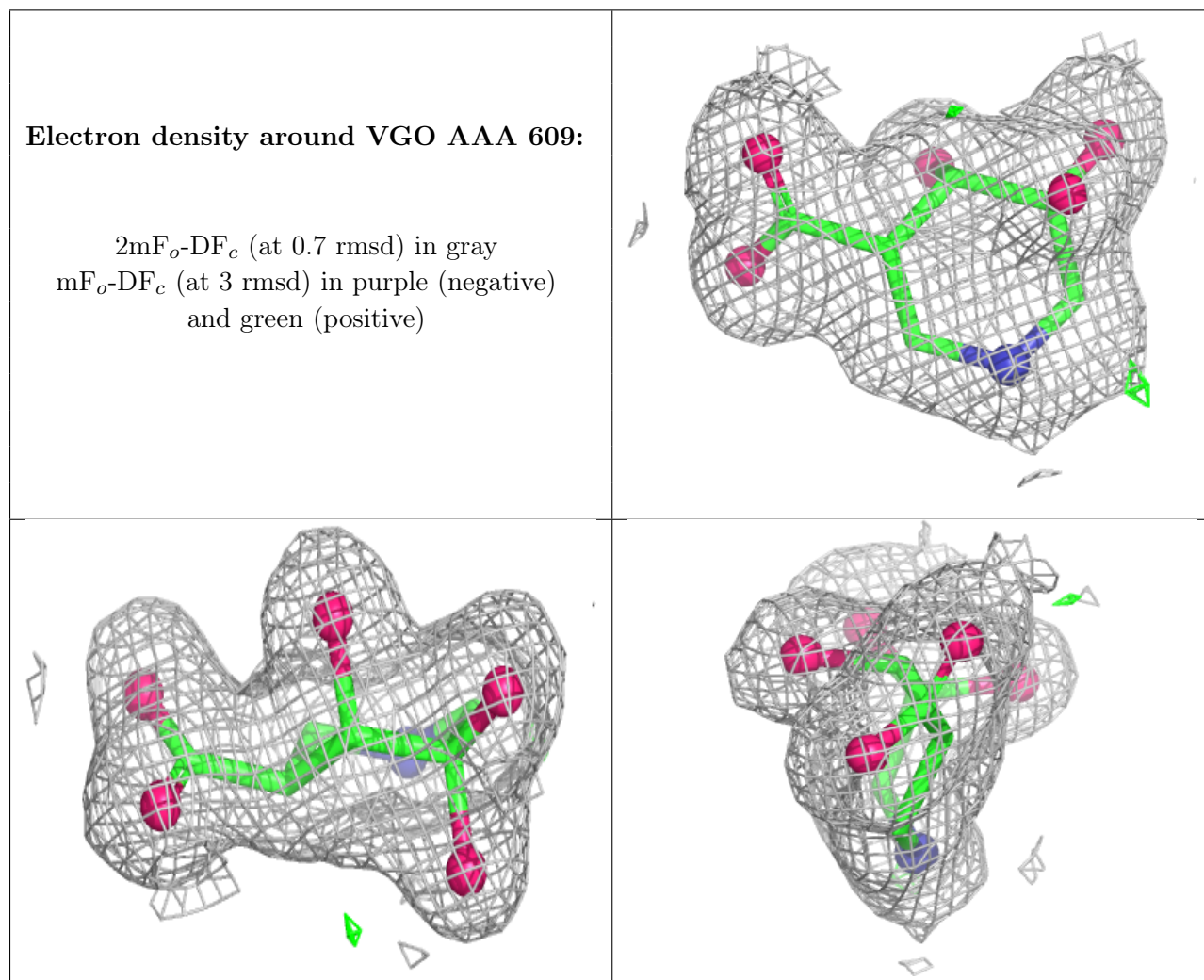
6.4 Ligands [i](#)

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	AAA	601	14/15	0.52	0.23	73,84,90,91	0
4	NAG	AAA	603	14/15	0.62	0.19	58,76,84,89	0
4	NAG	AAA	602	14/15	0.69	0.15	51,59,64,67	0
5	EDO	BBB	101	4/4	0.73	0.18	52,53,56,56	0
4	NAG	AAA	604	14/15	0.76	0.14	44,55,61,62	0
5	EDO	AAA	605	4/4	0.86	0.15	38,39,49,54	0
5	EDO	AAA	610	4/4	0.92	0.10	25,27,31,34	0
7	VGO	AAA	609	12/12	0.92	0.08	23,28,30,30	0
6	CL	AAA	606	1/1	0.96	0.17	43,43,43,43	0
6	CL	AAA	608	1/1	0.98	0.08	35,35,35,35	0
6	CL	AAA	607	1/1	0.98	0.04	27,27,27,27	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.