

wwPDB X-ray Structure Validation Summary Report (i)

Jan 2, 2024 – 02:14 pm GMT

PDB ID	:	80HQ
Title	:	Crystal structure of human heparanase in complex with competitive inhibitor
		derrived 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 (i) 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 (1)) were used in the production of this report:

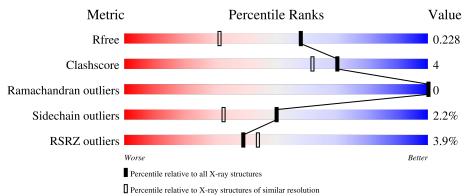
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (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 <=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	4% 94%	6% •
2	BBB	74	89%	11%
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	-	-	Х	-



2 Entry composition (i)

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		At	oms			ZeroOcc	AltConf	Trace
1	AAA	385	Total 3079	C 1986	N 527	0 554	S 12	0	3	0

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		Ator	\mathbf{ns}		ZeroOcc	AltConf	Trace
2	BBB	74	Total 595	C 388	N 97	O 110	0	1	0

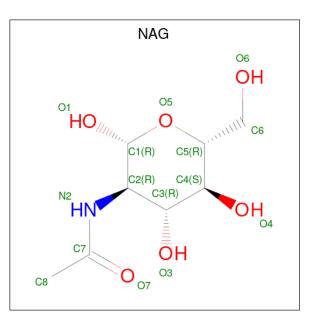
• Molecule 3 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-bet a-D-glucopyranose.



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

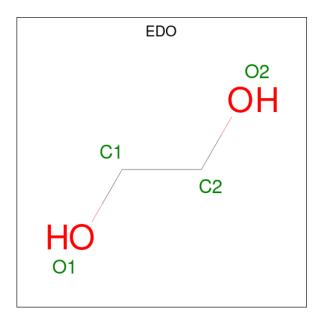
• Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





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

• Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



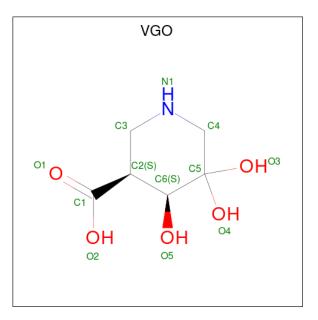


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	AAA	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
5	BBB	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 6 is CHLORIDE ION (three-letter code: 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 (three-letter code: VGO) (formula: $C_6H_{11}NO_5$) (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

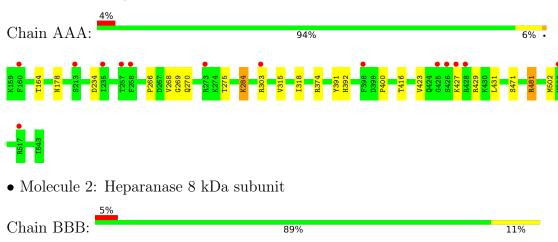
• Molecule 8 is water.

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

Q1 F9 Q11 126 126 137 K44 K44 K44 L57 L57 I68 K73 K73 K73

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

Chain AeA:

100%

NAG1 FUC2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	46.11Å 70.92Å 78.56Å	Depositor
a, b, c, α , β , γ	90.00° 95.53° 90.00°	Depositor
Resolution (Å)	45.94 - 1.70	Depositor
	45.90 - 1.70	EDS
% Data completeness	99.6 (45.94 - 1.70)	Depositor
(in resolution range)	99.6 (45.90 - 1.70)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.99 (at 1.70 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.174 , 0.208	Depositor
It, It _{free}	0.202 , 0.228	DCC
R_{free} test set	2756 reflections $(4.99%)$	wwPDB-VP
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 39.2	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.

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.



¹Intensities estimated from amplitudes.

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: FUC, NAG, VGO, CL, 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	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	AAA	0.76	0/3153	0.85	1/4263~(0.0%)
2	BBB	0.71	0/609	0.80	0/826
All	All	0.75	0/3762	0.84	1/5089~(0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	AAA	481	ARG	CG-CD-NE	6.87	126.22	111.80

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	21	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

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	3	Non-H	1 0	H(added)	Clashes	Symm-Clashes
8	AAA	212	0	0	5	0
8	BBB	37	0	0	0	0
All	All	4030	0	3803	27	0

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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 27 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:400:PRO:HD3	1:AAA:502[A]:MET:HE2	1.84	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	Perce	ntiles
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%)	49 31	
2	BBB	67/66~(102%)	66~(98%)	1 (2%)	65 51	
All	All	404/401 (101%)	395~(98%)	9~(2%)	50 34	

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 side chains can be flipped to improve hydrogen bonding and reduce clashes. There are no such side chains 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



Mal	Type	Chain	Res	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
	туре	Ullaili	nes	LIIIK	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	4 (23%)
3	FUC	AeA	2	3	10,10,11	0.72	0	14,14,16	1.72	4 (28%)

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).

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 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	AeA	1	NAG	C1-C2-N2	-4.88	102.16	110.49
3	AeA	2	FUC	O5-C1-C2	3.70	116.48	110.77
3	AeA	2	FUC	C3-C4-C5	3.30	114.92	109.77
3	AeA	1	NAG	O5-C5-C6	3.05	111.98	107.20
3	AeA	1	NAG	O3-C3-C4	-2.48	104.62	110.35

There are no chirality outliers.

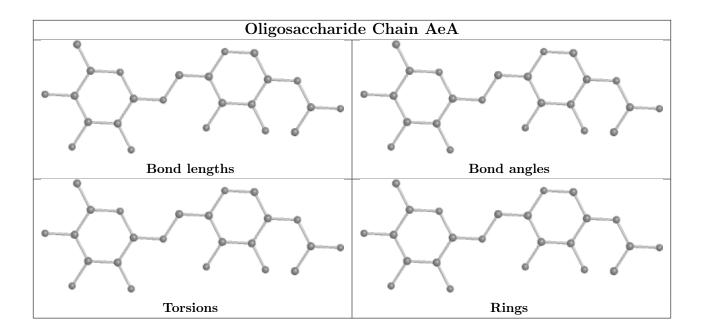
There are no torsion outliers.

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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Ullaili	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
4	NAG	AAA	601	1	14,14,15	0.63	0	17,19,21	0.72	0
4	NAG	AAA	602	1	$14,\!14,\!15$	0.50	0	$17,\!19,\!21$	0.68	0
5	EDO	AAA	605	-	3,3,3	0.20	0	2,2,2	0.26	0
7	VGO	AAA	609	-	10,12,12	1.05	0	10,18,18	1.24	0
4	NAG	AAA	604	1	$14,\!14,\!15$	0.52	0	$17,\!19,\!21$	1.12	2 (11%)
4	NAG	AAA	603	1	14,14,15	0.48	0	17,19,21	1.94	6 (35%)
5	EDO	BBB	101	-	3,3,3	0.25	0	2,2,2	0.33	0
5	EDO	AAA	610	-	3,3,3	0.18	0	2,2,2	1.46	0

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



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	AAA	601	1	-	3/6/23/26	0/1/1/1
4	NAG	AAA	602	1	-	2/6/23/26	0/1/1/1
5	EDO	AAA	605	-	-	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	603	1	-	1/6/23/26	0/1/1/1
5	EDO	BBB	101	-	-	1/1/1/1	-
5	EDO	AAA	610	-	-	1/1/1/1	-

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	AAA	603	NAG	C2-N2-C7	-4.26	116.84	122.90
4	AAA	603	NAG	C4-C3-C2	-3.51	105.87	111.02
4	AAA	603	NAG	C3-C4-C5	-2.94	104.99	110.24
4	AAA	603	NAG	O5-C1-C2	-2.80	106.87	111.29
4	AAA	603	NAG	C1-O5-C5	2.58	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
5	AAA	605	EDO	O1-C1-C2-O2
5	BBB	101	EDO	O1-C1-C2-O2
4	AAA	602	NAG	C4-C5-C6-O6

There are no ring outliers.

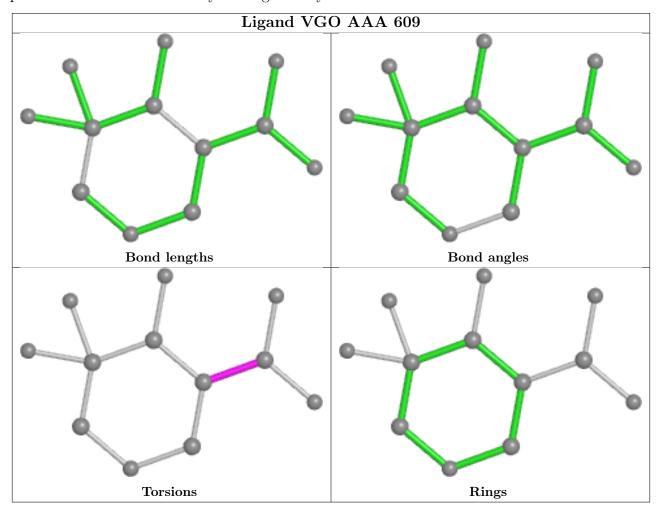
4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	601	NAG	2	0
5	AAA	605	EDO	1	0
5	BBB	101	EDO	2	0
5	AAA	610	EDO	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 then 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 similar 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 (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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	AAA	385/385~(100%)	0.29	14 (3%) 42 47	14, 26, 49, 112	0
2	BBB	74/74~(100%)	0.37	4 (5%) 25 28	17, 27, 44, 78	0
All	All	459/459~(100%)	0.30	18 (3%) 39 44	14, 27, 49, 112	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	160	PHE	7.8
1	AAA	428	ARG	5.9
1	AAA	427	LYS	5.2
1	AAA	425	GLY	4.5
1	AAA	426	SER	4.5

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

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

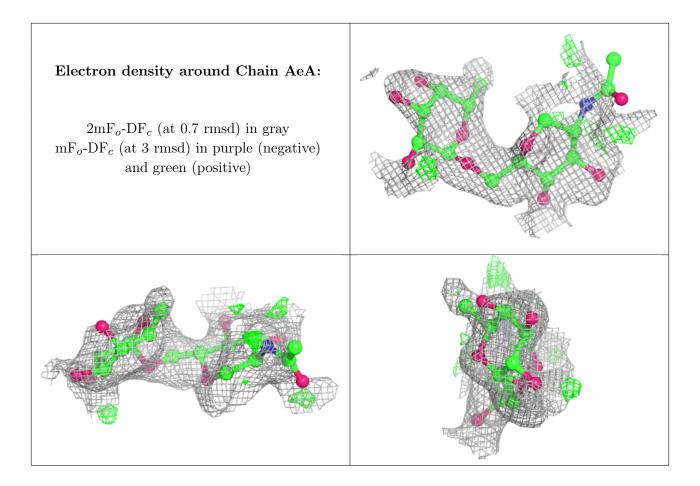
6.3 Carbohydrates (i)

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, 95^{th} 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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
3	NAG	AeA	1	14/15	0.65	0.27	$61,\!68,\!82,\!86$	0
3	FUC	AeA	2	10/11	0.65	0.31	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)

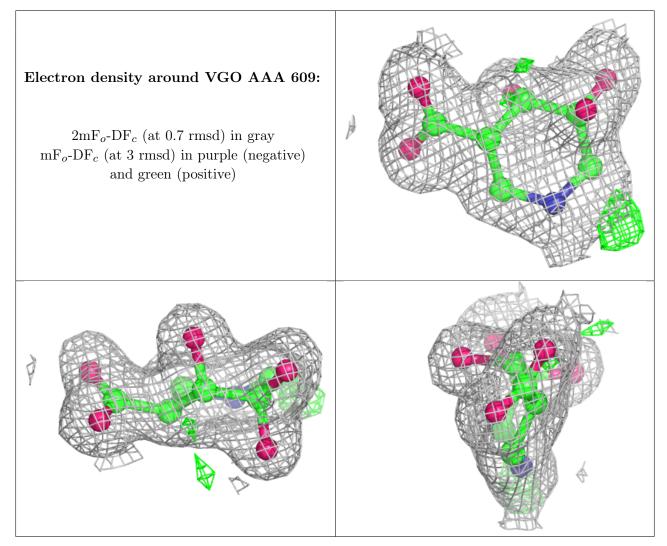
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	0.35	73,84,90,91	0
4	NAG	AAA	602	14/15	0.74	0.26	51,59,64,67	0
4	NAG	AAA	603	14/15	0.78	0.22	58,76,84,89	0
4	NAG	AAA	604	14/15	0.79	0.17	44,55,61,62	0
5	EDO	BBB	101	4/4	0.85	0.23	52,53,56,56	0
5	EDO	AAA	605	4/4	0.86	0.19	38,39,49,54	0
5	EDO	AAA	610	4/4	0.92	0.12	$25,\!27,\!31,\!34$	0
7	VGO	AAA	609	12/12	0.93	0.09	23,28,30,30	0
6	CL	AAA	608	1/1	0.97	0.04	$35,\!35,\!35,\!35$	0
6	CL	AAA	606	1/1	0.98	0.07	43,43,43,43	0
6	CL	AAA	607	1/1	0.99	0.08	$27,\!27,\!27,\!27$	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.

