



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 11:33 PM UTC

PDB ID : 8B0B / pdb_00008b0b
Title : Crystal structure of human heparanase in complex with covalent inhibitor VB151
Authors : Armstrong, Z.; Davies, G.J.
Deposited on : 2022-09-07
Resolution : 1.95 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 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

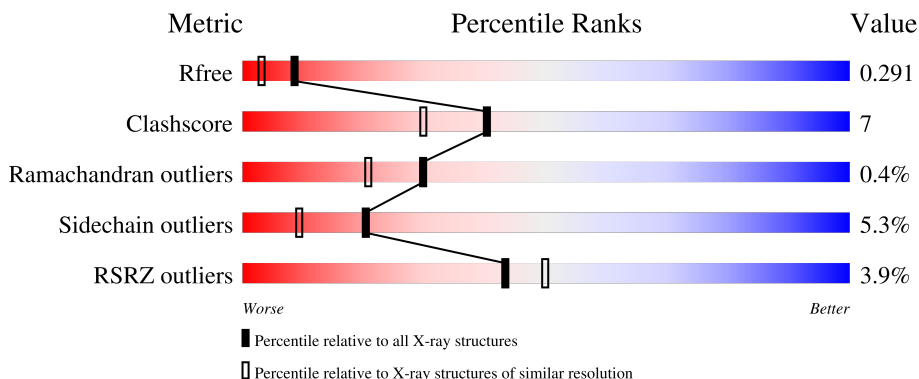
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	4% 81% 17% .
2	BBB	74	% 84% 14% ..

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7476 atoms, of which 3699 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
			Total	C	H	N	O	S			
1	AAA	384	6055	1944	3039	512	549	11	152	0	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.

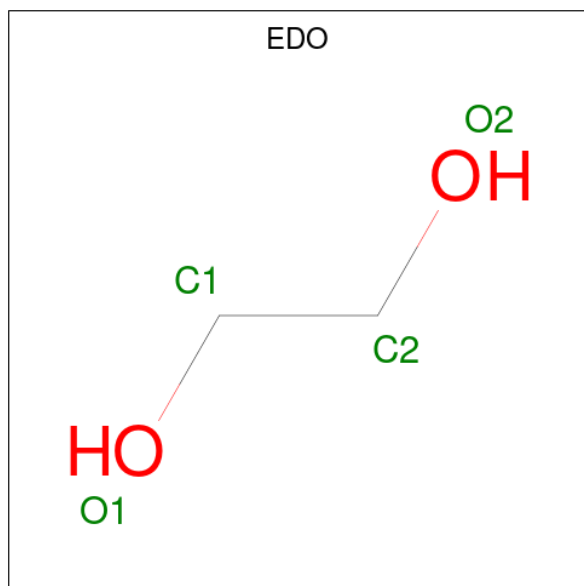
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	BBB	73	1171	378	595	94	104	20	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



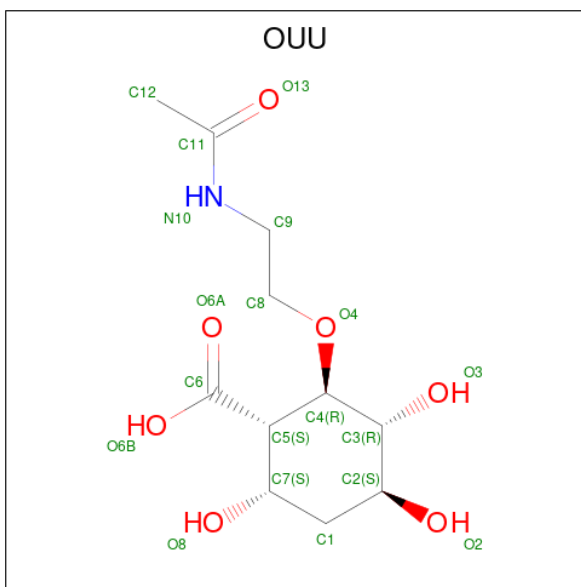
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	AAA	1	Total	C	H	N	O	3	0
			28	8	14	1	5		
3	AAA	1	Total	C	H	N	O	3	0
			28	8	14	1	5		
3	AAA	1	Total	C	H	N	O	3	0
			28	8	14	1	5		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	AAA	1	Total	C	H	O	1	0
			10	2	6	2		

- Molecule 5 is (1 {S},2 {R},3 {R},4 {S},6 {S})-2-(2-acetamidoethoxy)-3,4,6-tris(oxidanyl)cyclohexane-1-carboxylic acid (CCD ID: OUU) (formula: C₁₁H₁₉NO₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	AAA	1	Total	C	H	N	O	3	0
			36	11	17	1	7		

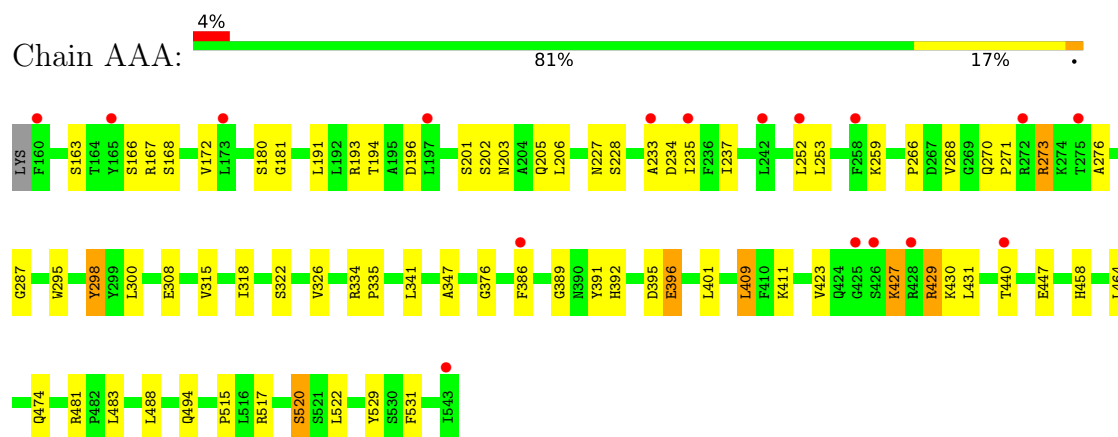
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	AAA	99	Total	O	0	0
			99	99		
6	BBB	21	Total	O	0	0
			21	21		

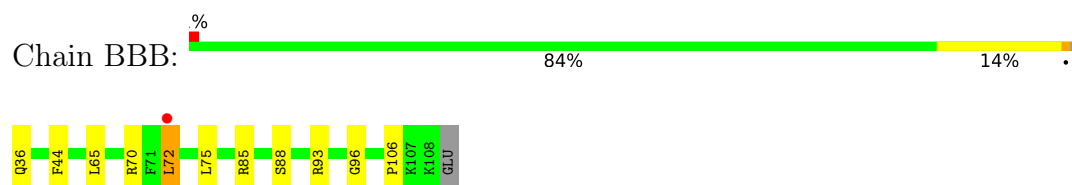
3 Residue-property plots [i](#)

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	44.44Å 70.85Å 78.29Å 90.00° 98.70° 90.00°	Depositor
Resolution (Å)	52.31 – 1.95 52.31 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (52.31-1.95) 99.9 (52.31-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.232 , 0.291 0.232 , 0.291	Depositor DCC
R_{free} test set	1711 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.642	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 37.1	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	7476	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.91% 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: OUU, EDO, 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	1.06	0/3088	1.44	5/4184 (0.1%)
2	BBB	1.02	0/590	1.34	1/802 (0.1%)
All	All	1.05	0/3678	1.42	6/4986 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	481	ARG	CG-CD-NE	6.00	125.19	112.00
2	BBB	44	PHE	CA-C-O	-5.54	114.22	120.43
1	AAA	389	GLY	CA-C-N	5.36	129.18	120.60
1	AAA	389	GLY	C-N-CA	5.36	129.18	120.60
1	AAA	488	LEU	N-CA-C	-5.20	106.89	113.18
1	AAA	440	THR	CA-CB-OG1	-5.18	101.82	109.60

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	AAA	3016	3039	3019	46	0
2	BBB	576	595	591	9	0
3	AAA	42	42	39	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AAA	4	6	6	0	0
5	AAA	19	17	0	1	0
6	AAA	99	0	0	4	0
6	BBB	21	0	0	2	0
All	All	3777	3699	3655	48	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 7.

All (48) 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:AAA:194:THR:OG1	1:AAA:196:ASP:OD1	2.01	0.76
1:AAA:427:LYS:HE3	1:AAA:427:LYS:HA	1.70	0.72
1:AAA:181:GLY:O	2:BBB:88:SER:OG	2.08	0.71
1:AAA:396:GLU:HB2	6:AAA:720:HOH:O	1.93	0.68
1:AAA:266:PRO:HG2	1:AAA:268:VAL:HG13	1.84	0.60
1:AAA:270:GLN:HE22	1:AAA:298:TYR:H	1.51	0.58
1:AAA:193:ARG:CZ	1:AAA:237:ILE:HD13	2.34	0.58
1:AAA:430:LYS:HD2	1:AAA:458:HIS:CD2	2.38	0.58
1:AAA:172:VAL:HG21	2:BBB:72:LEU:HG	1.87	0.56
1:AAA:253:LEU:O	1:AAA:259:LYS:HA	2.05	0.56
1:AAA:335:PRO:HA	6:AAA:776:HOH:O	2.06	0.56
1:AAA:483:LEU:CD1	1:AAA:494:GLN:NE2	2.71	0.54
1:AAA:196:ASP:OD1	1:AAA:196:ASP:N	2.41	0.54
1:AAA:474:GLN:NE2	1:AAA:515:PRO:HB3	2.25	0.52
2:BBB:93:ARG:NH1	6:BBB:201:HOH:O	2.37	0.52
1:AAA:483:LEU:CD1	1:AAA:494:GLN:HE21	2.23	0.51
1:AAA:205:GLN:HE22	1:AAA:252:LEU:HD22	1.76	0.51
1:AAA:409:LEU:HD13	1:AAA:531:PHE:CD1	2.45	0.51
1:AAA:203:ASN:HD22	1:AAA:206:LEU:HD12	1.77	0.50
1:AAA:427:LYS:HA	1:AAA:427:LYS:CE	2.35	0.50
1:AAA:180:SER:HA	2:BBB:85:ARG:HG3	1.92	0.50
1:AAA:517:ARG:O	1:AAA:520:SER:OG	2.30	0.48
1:AAA:308:GLU:N	1:AAA:308:GLU:OE1	2.47	0.47
1:AAA:270:GLN:NE2	1:AAA:298:TYR:H	2.11	0.47
1:AAA:172:VAL:CG1	2:BBB:75:LEU:HB2	2.44	0.47
1:AAA:483:LEU:HD13	1:AAA:494:GLN:HE21	1.80	0.47
1:AAA:315:VAL:O	1:AAA:318:ILE:HG12	2.16	0.46
5:AAA:605:OUU:O2	2:BBB:96:GLY:HA2	2.16	0.46
1:AAA:166:SER:OG	1:AAA:168:SER:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:167:ARG:NE	2:BBB:106:PRO:O	2.45	0.45
1:AAA:395:ASP:OD1	1:AAA:395:ASP:C	2.59	0.44
1:AAA:427:LYS:HD2	1:AAA:429:ARG:HG2	1.99	0.43
1:AAA:287:GLY:HA3	1:AAA:334:ARG:NE	2.34	0.43
1:AAA:427:LYS:HE2	1:AAA:429:ARG:HB3	2.01	0.42
1:AAA:376:GLY:HA2	6:AAA:718:HOH:O	2.18	0.42
1:AAA:295:TRP:O	1:AAA:341:LEU:HD23	2.20	0.42
1:AAA:386:PHE:CZ	2:BBB:65:LEU:HD21	2.54	0.42
1:AAA:300:LEU:O	1:AAA:347:ALA:HA	2.19	0.42
1:AAA:411:LYS:CG	6:BBB:205:HOH:O	2.66	0.41
1:AAA:464:LEU:HB2	1:AAA:522:LEU:HB2	2.02	0.41
1:AAA:191:LEU:HD23	1:AAA:191:LEU:HA	1.90	0.41
1:AAA:273:ARG:O	1:AAA:276:ALA:HB3	2.21	0.41
1:AAA:228:SER:HA	6:AAA:761:HOH:O	2.21	0.41
1:AAA:233:ALA:O	1:AAA:235:ILE:HG13	2.21	0.40
1:AAA:295:TRP:CD2	1:AAA:326:VAL:HG21	2.57	0.40
1:AAA:395:ASP:HB3	1:AAA:401:LEU:HD21	2.03	0.40
1:AAA:172:VAL:HG12	2:BBB:75:LEU:HB2	2.04	0.40
1:AAA:193:ARG:CZ	1:AAA:237:ILE:CD1	3.00	0.40

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	382/385 (99%)	366 (96%)	14 (4%)	2 (0%)	24	16
2	BBB	71/74 (96%)	69 (97%)	2 (3%)	0	100	100
All	All	453/459 (99%)	435 (96%)	16 (4%)	2 (0%)	30	21

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	271	PRO
1	AAA	447	GLU

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	AAA	328/335 (98%)	310 (94%)	18 (6%)	19	8
2	BBB	65/66 (98%)	62 (95%)	3 (5%)	24	13
All	All	393/401 (98%)	372 (95%)	21 (5%)	20	9

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	163	SER
1	AAA	201	SER
1	AAA	202	SER
1	AAA	227	ASN
1	AAA	234	ASP
1	AAA	273	ARG
1	AAA	298	TYR
1	AAA	322	SER
1	AAA	391	TYR
1	AAA	392	HIS
1	AAA	396	GLU
1	AAA	409	LEU
1	AAA	423	VAL
1	AAA	427	LYS
1	AAA	429	ARG
1	AAA	431	LEU
1	AAA	520	SER
1	AAA	529	TYR
2	BBB	36	GLN
2	BBB	70	ARG
2	BBB	72	LEU

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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	NAG	AAA	602	1	14,14,15	0.61	0	17,19,21	1.58	3 (17%)
5	OUU	AAA	605	1	19,19,19	0.92	1 (5%)	23,26,26	0.99	0
3	NAG	AAA	603	1	14,14,15	0.75	0	17,19,21	2.22	4 (23%)
4	EDO	AAA	604	-	3,3,3	0.09	0	2,2,2	0.08	0
3	NAG	AAA	601	1	14,14,15	1.08	1 (7%)	17,19,21	1.65	3 (17%)

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	AAA	602	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	OUU	AAA	605	1	-	3/11/31/31	0/1/1/1
3	NAG	AAA	603	1	-	4/6/23/26	0/1/1/1
4	EDO	AAA	604	-	-	1/1/1/1	-
3	NAG	AAA	601	1	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	AAA	605	OUU	O6B-C6	-3.49	1.19	1.30
3	AAA	601	NAG	C1-C2	3.48	1.57	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	AAA	603	NAG	C1-O5-C5	4.39	118.08	112.19
3	AAA	603	NAG	C2-N2-C7	4.30	128.66	122.90
3	AAA	603	NAG	C3-C4-C5	-4.05	102.89	110.23
3	AAA	601	NAG	O5-C1-C2	3.10	116.08	111.29
3	AAA	601	NAG	C2-N2-C7	3.07	127.02	122.90
3	AAA	602	NAG	C4-C3-C2	-2.91	106.75	111.02
3	AAA	602	NAG	C1-C2-N2	2.78	114.82	110.43
3	AAA	602	NAG	C3-C4-C5	-2.77	105.21	110.23
3	AAA	603	NAG	O3-C3-C2	2.18	113.94	109.40
3	AAA	601	NAG	O7-C7-N2	2.16	125.79	121.98

There are no chirality outliers.

All (8) torsion outliers are listed below:

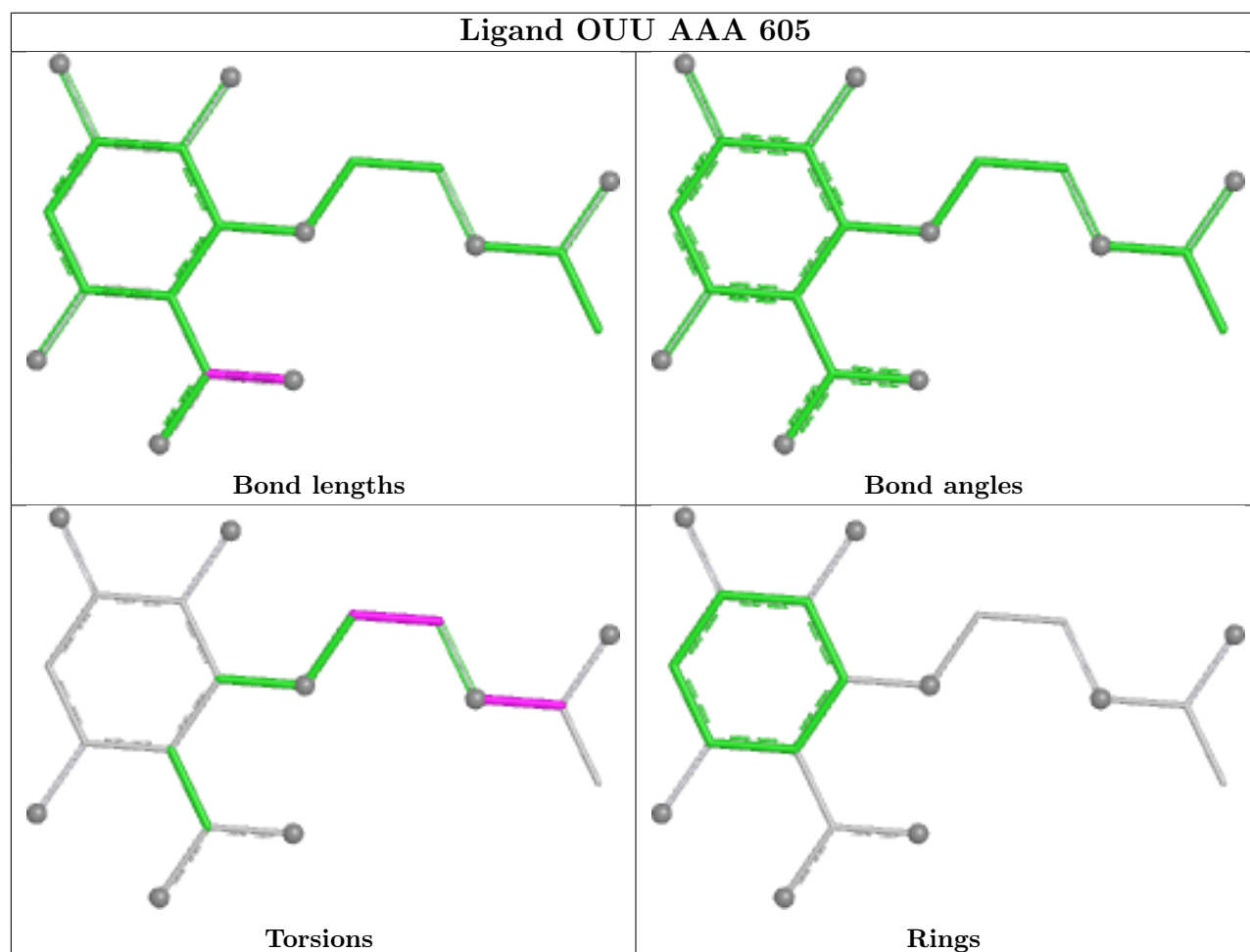
Mol	Chain	Res	Type	Atoms
5	AAA	605	OUU	C12-C11-N10-C9
5	AAA	605	OUU	O13-C11-N10-C9
3	AAA	603	NAG	O5-C5-C6-O6
3	AAA	603	NAG	C4-C5-C6-O6
3	AAA	603	NAG	C8-C7-N2-C2
3	AAA	603	NAG	O7-C7-N2-C2
5	AAA	605	OUU	O4-C8-C9-N10
4	AAA	604	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	AAA	605	OUU	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 ⓘ

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	384/385 (99%)	0.40	17 (4%) 39 45	20, 35, 61, 87	0
2	BBB	73/74 (98%)	0.48	1 (1%) 73 79	24, 37, 59, 81	0
All	All	457/459 (99%)	0.42	18 (3%) 43 50	20, 35, 61, 87	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	386	PHE	4.1
1	AAA	160	PHE	3.7
1	AAA	258	PHE	3.5
1	AAA	242	LEU	3.4
1	AAA	197	LEU	3.2
1	AAA	165	TYR	2.9
1	AAA	428	ARG	2.9
1	AAA	440	THR	2.5
1	AAA	235	ILE	2.4
1	AAA	426	SER	2.4
2	BBB	72	LEU	2.3
1	AAA	252	LEU	2.3
1	AAA	543	ILE	2.1
1	AAA	272	ARG	2.1
1	AAA	275	THR	2.1
1	AAA	173	LEU	2.1
1	AAA	233	ALA	2.1
1	AAA	425	GLY	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

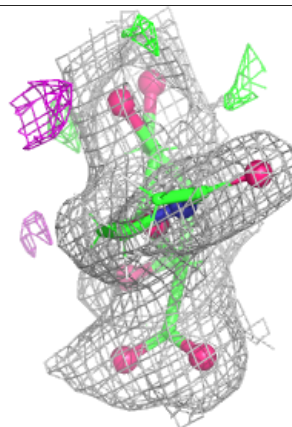
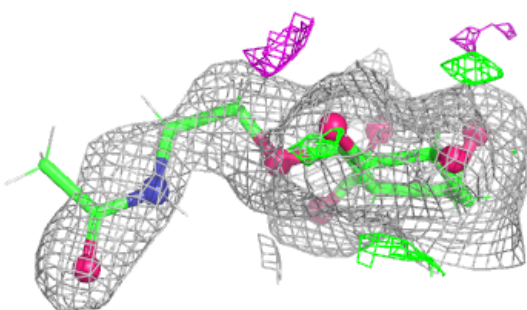
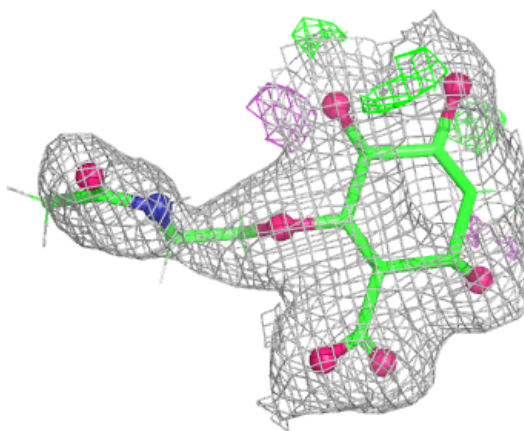
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	AAA	602	14/15	0.60	0.14	67,82,89,93	3
3	NAG	AAA	601	14/15	0.64	0.14	63,79,85,88	3
3	NAG	AAA	603	14/15	0.73	0.13	56,64,69,72	3
4	EDO	AAA	604	4/4	0.92	0.14	27,36,39,40	1
5	OUU	AAA	605	19/19	0.94	0.10	29,34,63,65	3

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 OUU AAA 605:

$2mF_o-DF_c$ (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.