



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:29 PM UTC

PDB ID : 7OU6 / pdb_00007ou6
Title : Human O-GlcNAc hydrolase in complex with DNJNAc-thiazolidines
Authors : Males, A.; Davies, G.J.; Gonzalez-Cuesta, M.; Mellet, C.O.; Fernandez, J.M.G.; Sidhu, P.; Ashmus, R.; Busmann, J.; Vocadlo, D.J.; Foster, L.
Deposited on : 2021-06-11
Resolution : 2.41 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

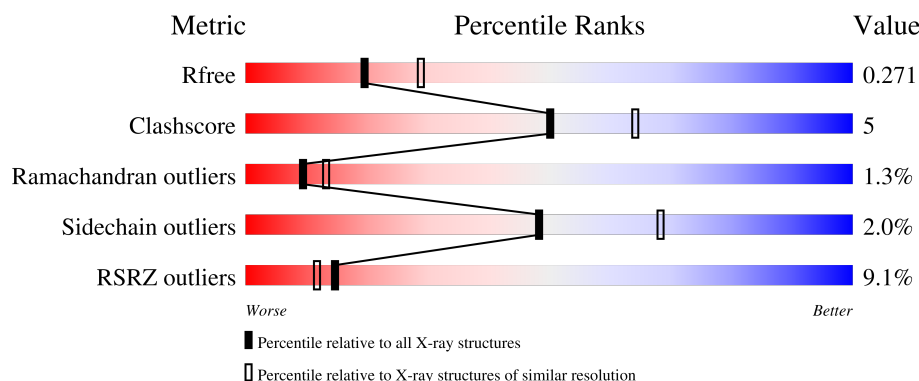
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	916	6% 39% 7% 53%
1	BBB	916	3% 41% 6% 52%

2 Entry composition [i](#)

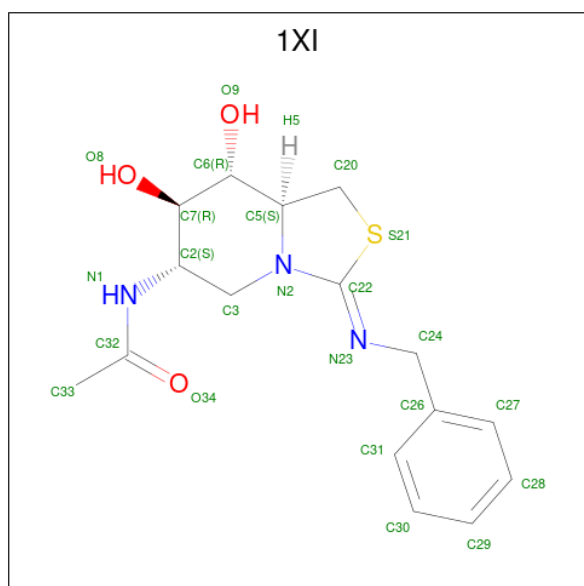
There are 3 unique types of molecules in this entry. The entry contains 13220 atoms, of which 6452 are hydrogens and 0 are deuteriums.

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 Protein O-GlcNAcase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	430	Total	C	H	N	O	S	152	0	0
			6372	2131	3098	531	592	20			
1	BBB	436	Total	C	H	N	O	S	127	0	0
			6742	2236	3312	549	621	24			

- Molecule 2 is {N}-(3 {Z},6 {S},7 {R},8 {R},8 {a} {S})-7,8-bis(oxidanyl)-3-(phenylmethyl)imino-1,5,6,7,8,8 {a}-hexahydro-[1,3]thiazolo[3,4-a]pyridin-6-yl]ethanamide (CCD ID: 1XI) (formula: C₁₆H₂₁N₃O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	AAA	1	Total	C	H	N	O	S	2	0
			44	16	21	3	3	1		
2	BBB	1	Total	C	H	N	O	S	2	0
			44	16	21	3	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	8	Total 8	O 8	0	0
3	BBB	10	Total 10	O 10	0	0

Chain BBB:



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	101.29Å 101.29Å 284.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.28 – 2.41 58.28 – 2.41	Depositor EDS
% Data completeness (in resolution range)	99.9 (58.28-2.41) 99.9 (58.28-2.41)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.221 , 0.271 0.219 , 0.271	Depositor DCC
R_{free} test set	1735 reflections (2.68%)	wwPDB-VP
Wilson B-factor (Å ²)	78.3	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 70.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13220	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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: 1XI

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	1.07	0/3365	1.49	2/4589 (0.0%)
1	BBB	1.05	2/3525 (0.1%)	1.48	4/4795 (0.1%)
All	All	1.06	2/6890 (0.0%)	1.48	6/9384 (0.1%)

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	BBB	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	271	ILE	N-CA	5.23	1.51	1.46
1	BBB	539	VAL	N-CA	5.02	1.50	1.46

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	394	PRO	N-CA-C	-5.51	102.44	111.21
1	AAA	686	ALA	CA-C-N	5.33	125.86	119.94
1	AAA	686	ALA	C-N-CA	5.33	125.86	119.94
1	BBB	635	THR	CA-CB-OG1	-5.11	101.94	109.60
1	BBB	314	PRO	N-CA-CB	-5.07	97.92	103.25
1	BBB	394	PRO	CA-C-O	-5.07	115.68	121.56

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	BBB	100	ASP	Peptide

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	3274	3098	2955	45	0
1	BBB	3430	3312	3226	36	0
2	AAA	23	21	0	1	0
2	BBB	23	21	0	0	0
3	AAA	8	0	0	0	0
3	BBB	10	0	0	0	0
All	All	6768	6452	6181	68	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 5.

All (68) 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:693:LEU:HB3	1:AAA:694:PRO:CD	2.20	0.71
1:AAA:689:PHE:CD2	1:BBB:651:MET:HE1	2.28	0.69
1:AAA:651:MET:HE1	1:BBB:689:PHE:CE2	2.27	0.69
1:AAA:693:LEU:HB3	1:AAA:694:PRO:HD3	1.80	0.63
1:AAA:241:LEU:O	1:AAA:273:ARG:NH1	2.32	0.61
1:AAA:651:MET:HE1	1:BBB:689:PHE:CD2	2.36	0.61
1:AAA:693:LEU:O	1:AAA:694:PRO:C	2.47	0.58
1:AAA:626:THR:O	1:AAA:630:ASN:ND2	2.38	0.57
1:AAA:142:ASP:OD1	1:BBB:547:LEU:HA	2.06	0.55
1:AAA:686:ALA:HB1	1:BBB:650:ILE:HD12	1.88	0.54
1:BBB:248:LEU:HA	1:BBB:276:VAL:O	2.08	0.54
1:BBB:293:LEU:O	1:BBB:323:VAL:HG11	2.08	0.54
1:AAA:268:SER:O	1:AAA:272:LYS:N	2.36	0.54
1:AAA:220:CYS:HB3	1:AAA:250:THR:OG1	2.07	0.53
1:AAA:284:ASN:HB2	1:AAA:290:ARG:O	2.08	0.53
1:BBB:196:VAL:HG13	1:BBB:241:LEU:HA	1.90	0.53
1:AAA:67:GLY:HA2	1:AAA:96:ALA:O	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:693:LEU:CB	1:AAA:694:PRO:CD	2.87	0.52
1:BBB:96:ALA:N	1:BBB:97:PRO:HD3	2.24	0.52
1:BBB:101:TYR:CE2	1:BBB:102:LYS:HE3	2.45	0.51
1:AAA:104:ARG:NH2	1:AAA:105:MET:HE1	2.27	0.50
1:AAA:606:GLU:O	1:AAA:610:ARG:HB2	2.12	0.50
1:AAA:60:PHE:CD2	1:AAA:332:TYR:CE1	2.99	0.49
1:AAA:94:LEU:HD11	1:AAA:136:ALA:HB2	1.95	0.49
1:BBB:67:GLY:HA2	1:BBB:96:ALA:O	2.12	0.49
1:BBB:662:GLY:O	1:BBB:663:CYS:SG	2.68	0.49
1:BBB:650:ILE:HG22	1:BBB:651:MET:HE2	1.96	0.48
1:BBB:75:MET:SD	1:BBB:122:LEU:HD22	2.53	0.48
1:BBB:169:PHE:O	1:BBB:212:PHE:HA	2.14	0.47
1:AAA:563:ASP:HA	1:AAA:572:GLY:HA3	1.96	0.47
1:BBB:192:ALA:O	1:BBB:196:VAL:HG23	2.15	0.46
1:AAA:625:PHE:HD1	1:AAA:644:VAL:HG12	1.79	0.46
1:AAA:263:SER:O	1:AAA:267:VAL:HG12	2.16	0.46
1:AAA:624:MET:HE2	1:AAA:624:MET:HB3	1.86	0.46
1:AAA:684:GLY:CA	1:BBB:290:ARG:HD3	2.46	0.46
1:AAA:684:GLY:N	1:BBB:290:ARG:HD3	2.30	0.46
1:AAA:62:CYS:SG	1:AAA:90:LEU:CD2	3.04	0.45
1:AAA:125:ALA:O	1:AAA:129:TYR:HD2	1.99	0.45
1:BBB:65:VAL:HG23	1:BBB:94:LEU:HG	1.99	0.45
1:AAA:304:ILE:N	1:AAA:305:PRO:CD	2.80	0.45
1:BBB:102:LYS:NZ	1:BBB:110:MET:O	2.49	0.45
1:AAA:385:THR:HG22	1:AAA:555:LEU:HD22	1.97	0.44
1:BBB:302:GLU:O	1:BBB:305:PRO:HD2	2.17	0.44
1:AAA:96:ALA:N	1:AAA:97:PRO:HD3	2.32	0.44
1:AAA:103:HIS:O	1:AAA:103:HIS:CG	2.70	0.44
1:AAA:102:LYS:HE2	1:AAA:109:GLU:HB3	1.99	0.44
1:BBB:304:ILE:HB	1:BBB:305:PRO:HD3	2.00	0.43
1:AAA:554:THR:O	1:AAA:557:ASP:HB2	2.18	0.43
1:AAA:544:GLU:CG	1:BBB:144:THR:HG21	2.49	0.43
1:BBB:135:TYR:O	1:BBB:169:PHE:HA	2.18	0.43
1:AAA:248:LEU:HA	1:AAA:276:VAL:O	2.18	0.43
1:AAA:286:TYR:HA	1:BBB:645:TRP:CZ3	2.53	0.43
1:BBB:267:VAL:O	1:BBB:271:ILE:HG12	2.19	0.42
1:AAA:686:ALA:HB1	1:BBB:650:ILE:CD1	2.49	0.42
1:BBB:567:LEU:HB3	1:BBB:568:PRO:HD2	2.01	0.42
1:BBB:285:ASP:OD1	1:BBB:285:ASP:N	2.52	0.42
1:BBB:264:ILE:HG13	1:BBB:303:LEU:HD22	2.02	0.42
1:BBB:225:TYR:HA	1:BBB:226:PRO:HA	1.89	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:250:THR:HA	1:AAA:278:TRP:O	2.19	0.42
1:AAA:295:PRO:HD3	1:AAA:380:LEU:HD22	2.02	0.41
1:AAA:260:PRO:O	1:AAA:263:SER:OG	2.38	0.41
1:AAA:249:TRP:O	1:AAA:277:ILE:HA	2.20	0.41
1:AAA:544:GLU:HG2	1:BBB:144:THR:HG21	2.03	0.41
1:AAA:689:PHE:CE2	1:BBB:651:MET:HE1	2.55	0.41
1:AAA:67:GLY:O	2:AAA:1001:1XI:O8	2.39	0.40
1:AAA:629:SER:OG	1:BBB:105:MET:HE2	2.20	0.40
1:BBB:200:ASN:O	1:BBB:204:GLN:HG3	2.21	0.40
1:BBB:151:VAL:HG12	1:BBB:155:LYS:HE3	2.02	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	420/916 (46%)	372 (89%)	41 (10%)	7 (2%)	7	9
1	BBB	424/916 (46%)	396 (93%)	24 (6%)	4 (1%)	14	20
All	All	844/1832 (46%)	768 (91%)	65 (8%)	11 (1%)	9	13

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	587	ALA
1	AAA	693	LEU
1	AAA	189	SER
1	AAA	588	ASN
1	BBB	101	TYR
1	BBB	591	VAL
1	BBB	112	SER
1	AAA	691	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	BBB	314	PRO
1	AAA	573	PRO
1	AAA	314	PRO

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	306/797 (38%)	300 (98%)	6 (2%)	48	68
1	BBB	348/797 (44%)	341 (98%)	7 (2%)	48	68
All	All	654/1594 (41%)	641 (98%)	13 (2%)	48	68

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	301	THR
1	AAA	547	LEU
1	AAA	561	LEU
1	AAA	573	PRO
1	AAA	631	CYS
1	AAA	640	MET
1	BBB	119	LEU
1	BBB	152	SER
1	BBB	191	PHE
1	BBB	198	ILE
1	BBB	222	THR
1	BBB	278	TRP
1	BBB	314	PRO

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

5.3.3 RNA ⓘ

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](#)

2 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	$\# Z > 2$
2	1XI	AAA	1001	-	23,25,25	0.75	2 (8%)	22,35,35	0.75	1 (4%)
2	1XI	BBB	1001	-	23,25,25	0.87	1 (4%)	22,35,35	0.97	2 (9%)

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	1XI	AAA	1001	-	-	1/9/38/38	0/3/3/3
2	1XI	BBB	1001	-	-	3/9/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	1001	1XI	C22-N23	2.35	1.30	1.26
2	AAA	1001	1XI	C22-N23	2.11	1.29	1.26
2	AAA	1001	1XI	C3-N2	-2.10	1.44	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	BBB	1001	1XI	C7-C6-C5	-2.46	107.21	111.37
2	BBB	1001	1XI	C6-C7-C2	2.41	114.55	111.02
2	AAA	1001	1XI	C6-C7-C2	2.35	114.47	111.02

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	1001	1XI	C3-C2-N1-C32
2	BBB	1001	1XI	C3-C2-N1-C32
2	BBB	1001	1XI	N2-C22-N23-C24
2	BBB	1001	1XI	C7-C2-N1-C32

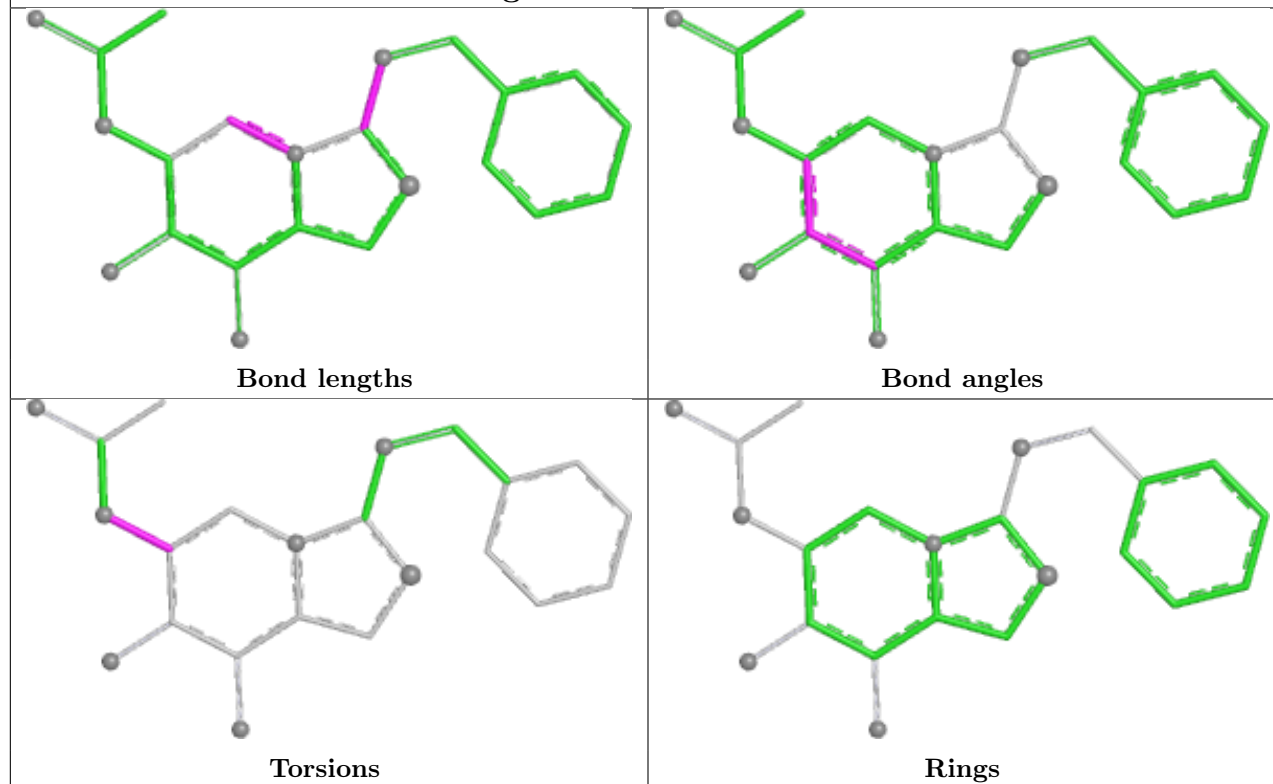
There are no ring outliers.

1 monomer is involved in 1 short contact:

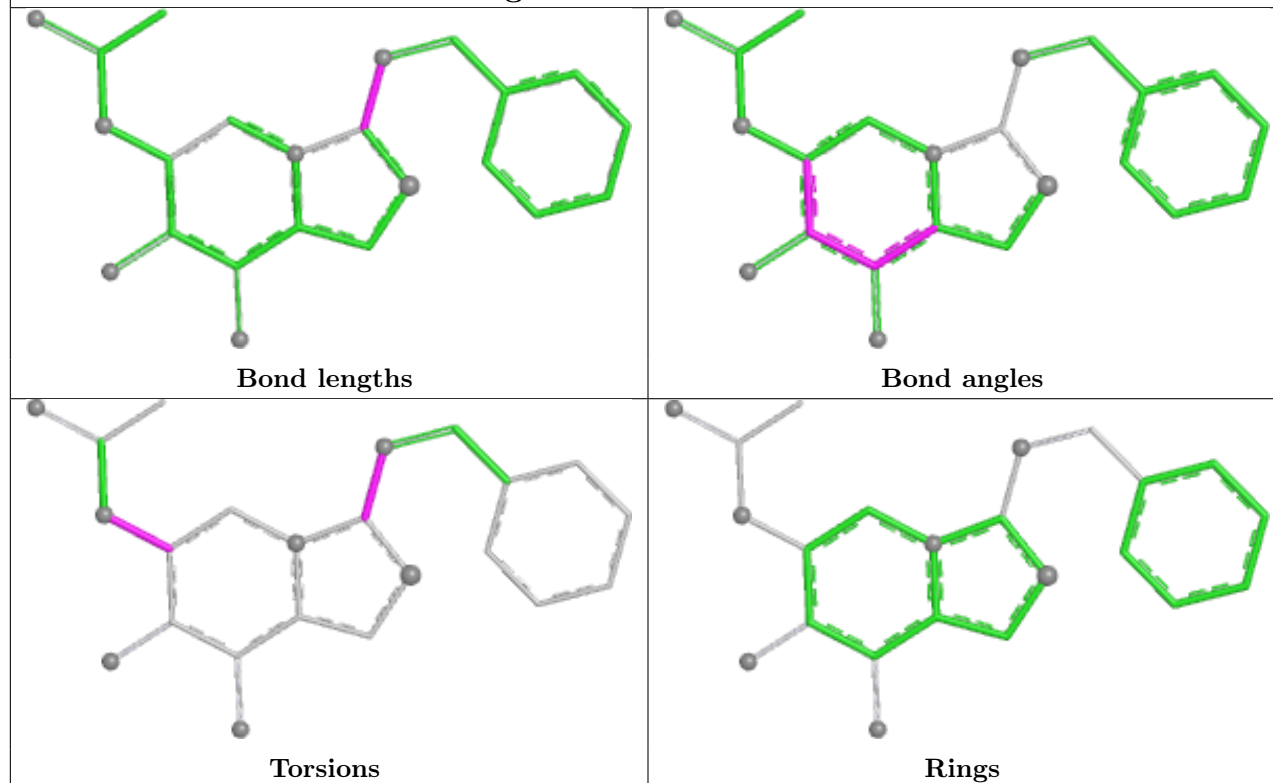
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	1001	1XI	1	0

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.

Ligand 1XI AAA 1001



Ligand 1XI BBB 1001



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	AAA	430/916 (46%)	0.75	53 (12%) 8 6	58, 91, 127, 192	0
1	BBB	436/916 (47%)	0.30	26 (5%) 27 24	51, 78, 120, 152	0
All	All	866/1832 (47%)	0.52	79 (9%) 15 12	51, 85, 125, 192	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	681	PHE	6.0
1	AAA	538	PHE	5.9
1	BBB	602	GLU	5.2
1	AAA	259	ILE	4.8
1	AAA	591	VAL	4.8
1	AAA	663	CYS	4.6
1	BBB	603	LYS	4.5
1	AAA	59	ARG	4.4
1	AAA	335	ASN	4.4
1	AAA	278	TRP	4.4
1	AAA	198	ILE	4.1
1	AAA	605	GLU	4.0
1	BBB	679	TRP	3.9
1	AAA	589	SER	3.7
1	AAA	604	ILE	3.6
1	AAA	681	PHE	3.6
1	BBB	682	ARG	3.5
1	AAA	690	GLN	3.5
1	AAA	271	ILE	3.4
1	AAA	543	ASN	3.4
1	AAA	547	LEU	3.4
1	AAA	603	LYS	3.4
1	AAA	336	MET	3.3
1	AAA	299	ARG	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AAA	325	ILE	3.2
1	BBB	270	ILE	3.2
1	BBB	677	GLU	3.0
1	BBB	264	ILE	3.0
1	AAA	373	LEU	3.0
1	BBB	543	ASN	3.0
1	BBB	591	VAL	2.9
1	BBB	395	HIS	2.9
1	AAA	280	ASN	2.9
1	BBB	678	PRO	2.9
1	BBB	336	MET	2.8
1	AAA	254	VAL	2.8
1	AAA	542	PRO	2.8
1	AAA	377	GLN	2.8
1	AAA	658	VAL	2.7
1	AAA	395	HIS	2.7
1	AAA	223	PHE	2.7
1	AAA	235	ARG	2.6
1	BBB	693	LEU	2.6
1	BBB	59	ARG	2.6
1	AAA	694	PRO	2.6
1	AAA	274	ALA	2.4
1	AAA	590	SER	2.4
1	BBB	592	VAL	2.3
1	AAA	611	ALA	2.3
1	BBB	581	GLU	2.3
1	AAA	539	VAL	2.3
1	AAA	321	ASN	2.3
1	AAA	303	LEU	2.2
1	BBB	605	GLU	2.2
1	AAA	657	PHE	2.2
1	AAA	300	SER	2.2
1	BBB	271	ILE	2.2
1	BBB	538	PHE	2.2
1	BBB	604	ILE	2.2
1	AAA	551	GLU	2.2
1	BBB	184	ASP	2.2
1	AAA	230	GLN	2.1
1	BBB	545	LYS	2.1
1	AAA	212	PHE	2.1
1	AAA	621	VAL	2.1
1	BBB	658	VAL	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	AAA	324	ALA	2.1
1	AAA	186	GLU	2.1
1	AAA	615	GLU	2.1
1	AAA	189	SER	2.1
1	AAA	179	ASN	2.1
1	AAA	545	LYS	2.1
1	AAA	178	HIS	2.1
1	BBB	663	CYS	2.0
1	AAA	261	VAL	2.0
1	AAA	570	GLU	2.0
1	BBB	171	LEU	2.0
1	AAA	295	PRO	2.0
1	AAA	622	MET	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](#)

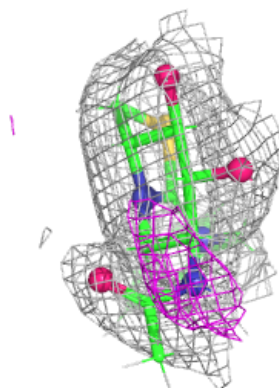
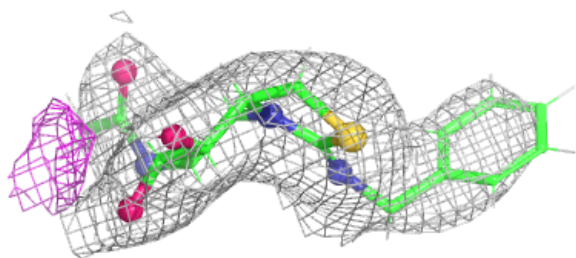
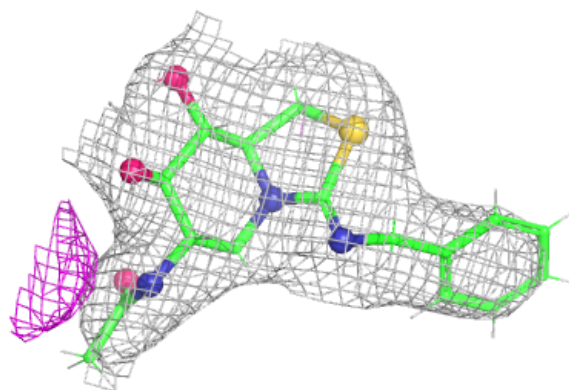
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	1XI	AAA	1001	23/23	0.96	0.10	63,75,124,130	2
2	1XI	BBB	1001	23/23	0.98	0.09	57,65,110,114	2

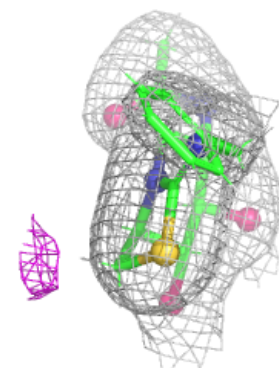
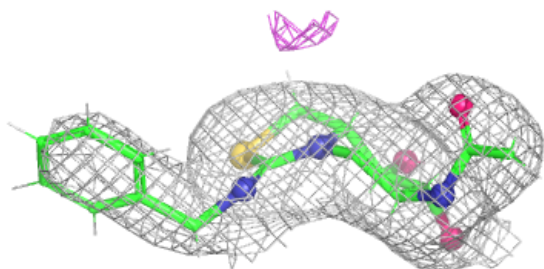
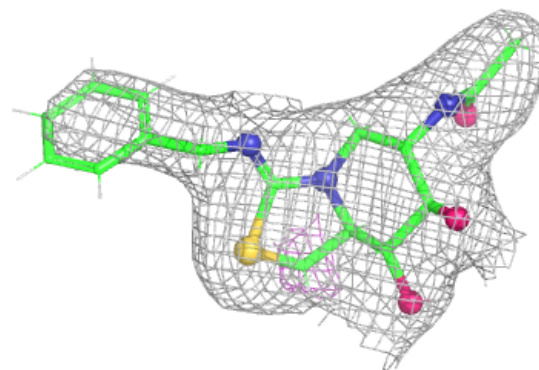
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 1XI AAA 1001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around 1XI BBB 1001:**

$2mF_o-DF_c$ (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.