



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 09:13 pm BST

PDB ID : 1LSP
Title : THE CRYSTAL STRUCTURE OF A BULGECIN-INHIBITED G-TYPE
LYSOZYME FROM THE EGG-WHITE OF THE AUSTRALIAN BLACK
SWAN. A COMPARISON OF THE BINDING OF BULGECIN TO THREE
MURAMIDASES
Authors : Karlsen, S.; Rao, Z.H.; Hough, E.; Isaacs, N.W.
Deposited on : 1995-02-09
Resolution : 2.45 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

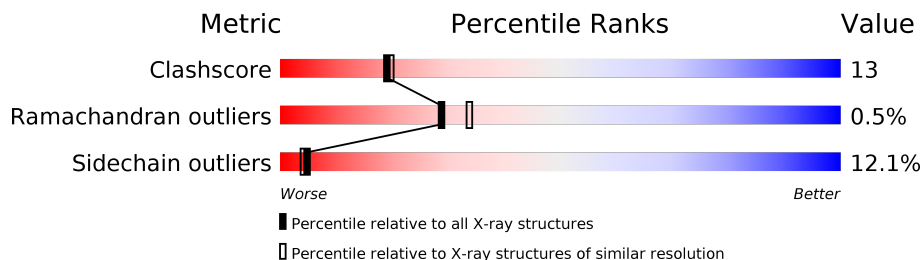
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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))
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)

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 on 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	185	

2 Entry composition [i](#)

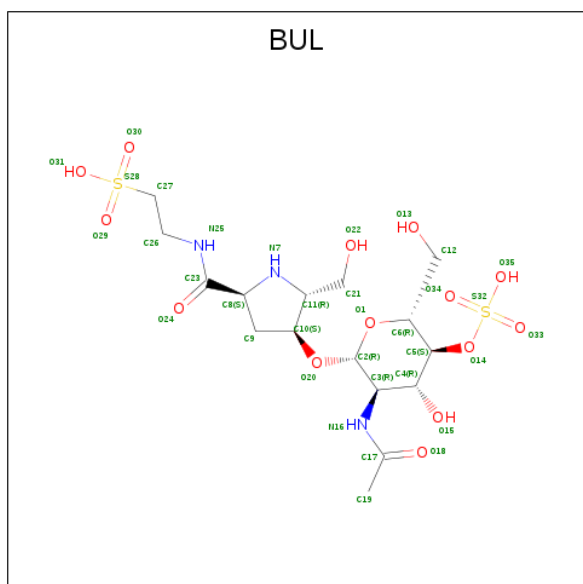
There are 3 unique types of molecules in this entry. The entry contains 1578 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 LYSOZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	185	1434	892	265	270	7	0	0	0

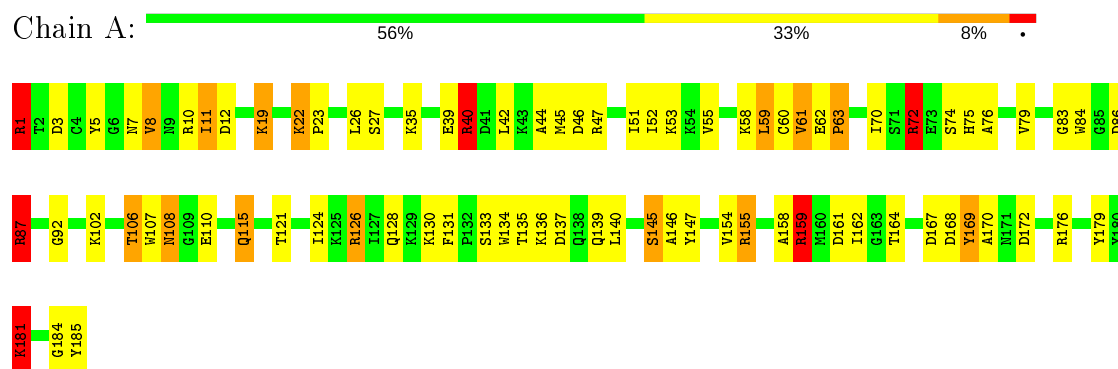
- Molecule 2 is BULGECIN A (three-letter code: BUL) (formula: C₁₆H₂₉N₃O₁₄S₂).



3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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. 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. 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: LYSOZYME



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	91.69Å 65.33Å 38.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.45 32.94 – 2.46	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.45) 78.9 (32.94-2.46)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.45Å)	Xtrriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.175 , (Not available) 0.354 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtrriage
Anisotropy	0.150	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 88.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.66	EDS
Total number of atoms	1578	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.28% 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: BUL

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	A	0.90	0/1461	2.23	56/1965 (2.8%)

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	A	0	6

There are no bond length outliers.

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	176	ARG	NE-CZ-NH1	-21.15	109.72	120.30
1	A	40	ARG	NE-CZ-NH2	-21.06	109.77	120.30
1	A	176	ARG	NE-CZ-NH2	18.34	129.47	120.30
1	A	155	ARG	NE-CZ-NH2	-12.54	114.03	120.30
1	A	72	ARG	NE-CZ-NH2	-12.41	114.09	120.30
1	A	168	ASP	CB-CG-OD2	-8.73	110.44	118.30
1	A	159	ARG	NE-CZ-NH1	-8.46	116.07	120.30
1	A	167	ASP	CB-CG-OD1	8.09	125.58	118.30
1	A	161	ASP	CB-CG-OD2	-8.04	111.07	118.30
1	A	40	ARG	NH1-CZ-NH2	7.99	128.19	119.40
1	A	72	ARG	NH1-CZ-NH2	7.82	128.00	119.40
1	A	3	ASP	CB-CG-OD2	-7.75	111.32	118.30
1	A	11	ILE	CA-C-O	7.74	136.35	120.10
1	A	42	LEU	CB-CG-CD2	-7.64	98.00	111.00
1	A	181	LYS	CB-CA-C	-7.48	95.44	110.40
1	A	155	ARG	CD-NE-CZ	-7.41	113.22	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	TYR	CB-CG-CD2	-7.40	116.56	121.00
1	A	181	LYS	N-CA-CB	7.39	123.90	110.60
1	A	79	VAL	N-CA-CB	-7.34	95.36	111.50
1	A	87	ARG	NE-CZ-NH2	-7.33	116.63	120.30
1	A	42	LEU	CB-CG-CD1	7.29	123.39	111.00
1	A	126	ARG	NE-CZ-NH2	7.20	123.90	120.30
1	A	12	ASP	CB-CG-OD1	6.84	124.46	118.30
1	A	86	ASP	CB-CG-OD1	-6.81	112.17	118.30
1	A	137	ASP	CB-CG-OD2	6.50	124.15	118.30
1	A	172	ASP	CB-CG-OD1	-6.41	112.53	118.30
1	A	146	ALA	CB-CA-C	6.32	119.58	110.10
1	A	161	ASP	CB-CG-OD1	6.23	123.91	118.30
1	A	76	ALA	CB-CA-C	6.09	119.23	110.10
1	A	145	SER	O-C-N	-6.07	112.99	122.70
1	A	136	LYS	CB-CA-C	6.04	122.48	110.40
1	A	158	ALA	CB-CA-C	-6.03	101.06	110.10
1	A	168	ASP	CB-CG-OD1	5.99	123.69	118.30
1	A	147	TYR	CB-CG-CD1	5.98	124.59	121.00
1	A	11	ILE	O-C-N	-5.86	113.32	122.70
1	A	115	GLN	CA-C-N	5.84	127.89	116.20
1	A	106	THR	N-CA-CB	-5.75	99.38	110.30
1	A	134	TRP	CA-CB-CG	5.63	124.41	113.70
1	A	79	VAL	CB-CA-C	5.60	122.04	111.40
1	A	44	ALA	N-CA-CB	-5.44	102.48	110.10
1	A	110	GLU	CG-CD-OE1	-5.42	107.45	118.30
1	A	135	THR	CA-CB-OG1	-5.42	97.61	109.00
1	A	184	GLY	N-CA-C	5.39	126.58	113.10
1	A	55	VAL	CA-CB-CG2	5.38	118.96	110.90
1	A	169	TYR	CB-CG-CD1	5.37	124.22	121.00
1	A	10	ARG	CD-NE-CZ	-5.31	116.16	123.60
1	A	155	ARG	NH1-CZ-NH2	5.24	125.16	119.40
1	A	39	GLU	OE1-CD-OE2	5.18	129.52	123.30
1	A	46	ASP	CB-CG-OD1	5.18	122.96	118.30
1	A	84	TRP	CA-CB-CG	-5.15	103.91	113.70
1	A	46	ASP	CB-CG-OD2	-5.15	113.67	118.30
1	A	53	LYS	CA-CB-CG	-5.14	102.10	113.40
1	A	59	LEU	CA-CB-CG	5.07	126.96	115.30
1	A	72	ARG	CA-CB-CG	5.06	124.54	113.40
1	A	61	VAL	CB-CA-C	5.03	120.95	111.40
1	A	86	ASP	CA-CB-CG	5.02	124.45	113.40

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	ARG	Sidechain
1	A	126	ARG	Sidechain
1	A	159	ARG	Sidechain
1	A	40	ARG	Sidechain
1	A	72	ARG	Sidechain
1	A	87	ARG	Sidechain

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	A	1434	0	1426	37	0
2	A	35	0	26	2	0
3	A	109	0	0	6	0
All	All	1578	0	1452	37	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 13.

All (37) 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:A:7:ASN:HB2	3:A:203:HOH:O	1.27	1.24
1:A:19:LYS:HB3	3:A:218:HOH:O	1.77	0.84
1:A:87:ARG:HB2	2:A:295:BUL:O29	1.93	0.68
1:A:159:ARG:HB3	1:A:162:ILE:HD12	1.76	0.65
1:A:130:LYS:HG2	1:A:131:PHE:CE2	2.33	0.64
1:A:130:LYS:HG2	1:A:131:PHE:CD2	2.32	0.64
1:A:5:TYR:O	1:A:140:LEU:HB2	1.98	0.63
1:A:35:LYS:HG2	1:A:179:TYR:HB2	1.80	0.63
1:A:145:SER:HB2	1:A:170:ALA:HB2	1.80	0.62
1:A:22:LYS:N	1:A:22:LYS:HD2	2.14	0.62
1:A:62:GLU:HG3	3:A:229:HOH:O	2.00	0.61
1:A:22:LYS:HE2	1:A:26:LEU:O	2.02	0.59
1:A:74:SER:O	1:A:75:HIS:HB2	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:ARG:NE	3:A:209:HOH:O	2.35	0.58
1:A:145:SER:HB2	1:A:170:ALA:CB	2.36	0.54
1:A:19:LYS:HD2	1:A:19:LYS:N	2.22	0.53
1:A:63:PRO:HB2	1:A:185:TYR:O	2.07	0.53
1:A:164:THR:HB	1:A:169:TYR:HB2	1.93	0.51
1:A:155:ARG:HB2	3:A:198:HOH:O	2.11	0.49
1:A:52:ILE:HD11	1:A:70:ILE:HD12	1.94	0.49
1:A:130:LYS:HE2	1:A:154:VAL:O	2.13	0.48
1:A:22:LYS:H	1:A:22:LYS:HD2	1.80	0.47
1:A:19:LYS:HD3	3:A:265:HOH:O	2.14	0.47
1:A:128:GLN:HG2	1:A:139:GLN:OE1	2.16	0.46
1:A:124:ILE:O	1:A:128:GLN:HG3	2.16	0.46
1:A:8:VAL:HG12	1:A:181:LYS:HD3	1.97	0.45
1:A:61:VAL:O	1:A:63:PRO:HD3	2.18	0.44
1:A:108:ASN:H	1:A:108:ASN:HD22	1.65	0.44
1:A:1:ARG:O	1:A:60:CYS:HA	2.18	0.43
1:A:1:ARG:HG2	1:A:1:ARG:HH11	1.84	0.43
1:A:52:ILE:CD1	1:A:70:ILE:HD12	2.49	0.42
1:A:45:MET:HB2	1:A:45:MET:HE2	1.90	0.42
1:A:87:ARG:NH1	2:A:295:BUL:O29	2.53	0.41
1:A:83:GLY:HA3	1:A:107:TRP:HB2	2.02	0.41
1:A:92:GLY:HA2	1:A:107:TRP:O	2.21	0.41
1:A:11:ILE:HD11	1:A:140:LEU:HD23	2.01	0.41
1:A:145:SER:CB	1:A:170:ALA:HB2	2.49	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	A	183/185 (99%)	174 (95%)	8 (4%)	1 (0%)	29 34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	63	PRO

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	A	149/149 (100%)	131 (88%)	18 (12%)	5 4

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	ARG
1	A	8	VAL
1	A	19	LYS
1	A	22	LYS
1	A	23	PRO
1	A	27	SER
1	A	47	ARG
1	A	51	ILE
1	A	58	LYS
1	A	59	LEU
1	A	72	ARG
1	A	102	LYS
1	A	106	THR
1	A	108	ASN
1	A	115	GLN
1	A	121	THR
1	A	133	SER
1	A	181	LYS

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

Mol	Chain	Res	Type
1	A	108	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	BUL	A	295	-	36,36,36	1.46	7 (19%)	41,53,53	3.45	21 (51%)

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	BUL	A	295	-	-	6/28/60/60	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	295	BUL	C8-N7	3.92	1.55	1.46
2	A	295	BUL	O1-C6	-3.17	1.36	1.44
2	A	295	BUL	C10-C11	2.94	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	295	BUL	C2-C3	-2.83	1.48	1.53
2	A	295	BUL	C11-N7	2.68	1.52	1.48
2	A	295	BUL	O20-C2	-2.38	1.35	1.41
2	A	295	BUL	O20-C10	-2.24	1.40	1.44

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	295	BUL	O15-C4-C3	-9.00	91.49	109.66
2	A	295	BUL	C9-C8-C23	7.04	121.70	111.19
2	A	295	BUL	C5-O14-S32	-6.58	106.15	118.88
2	A	295	BUL	O1-C6-C5	6.48	123.41	109.75
2	A	295	BUL	C23-C8-N7	-5.52	101.75	111.74
2	A	295	BUL	O35-S32-O33	5.08	126.16	108.49
2	A	295	BUL	C4-C3-N16	4.97	120.01	110.62
2	A	295	BUL	C2-O20-C10	4.95	122.98	115.33
2	A	295	BUL	O31-S28-C27	4.23	112.60	105.77
2	A	295	BUL	O34-S32-O33	-3.89	96.61	112.22
2	A	295	BUL	O31-S28-O29	3.67	120.24	111.27
2	A	295	BUL	O20-C2-O1	-3.66	100.45	110.67
2	A	295	BUL	C2-O1-C6	3.60	120.75	113.69
2	A	295	BUL	O15-C4-C5	-3.40	100.92	109.94
2	A	295	BUL	C9-C10-C11	3.24	108.41	103.80
2	A	295	BUL	O22-C21-C11	-2.85	104.17	111.09
2	A	295	BUL	O1-C2-C3	2.61	115.68	110.58
2	A	295	BUL	O30-S28-O29	-2.54	105.17	113.95
2	A	295	BUL	C12-C6-C5	2.52	120.66	113.33
2	A	295	BUL	O30-S28-C27	-2.46	103.96	106.92
2	A	295	BUL	O29-S28-C27	-2.34	104.10	106.92

There are no chirality outliers.

All (6) torsion outliers are listed below:

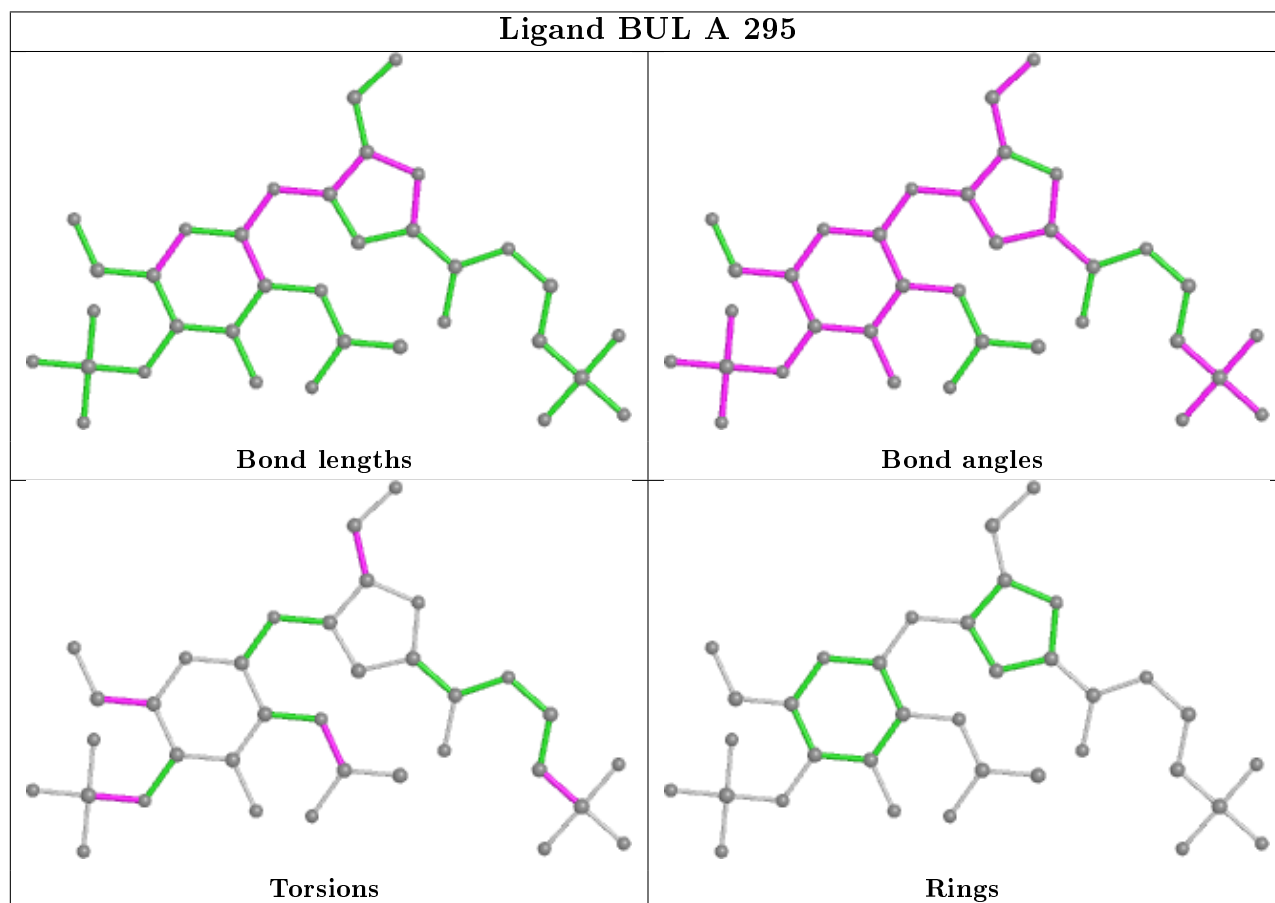
Mol	Chain	Res	Type	Atoms
2	A	295	BUL	N7-C11-C21-O22
2	A	295	BUL	C5-O14-S32-O35
2	A	295	BUL	O13-C12-C6-C5
2	A	295	BUL	C26-C27-S28-O29
2	A	295	BUL	C5-O14-S32-O34
2	A	295	BUL	O18-C17-N16-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	295	BUL	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 [\(i\)](#)

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

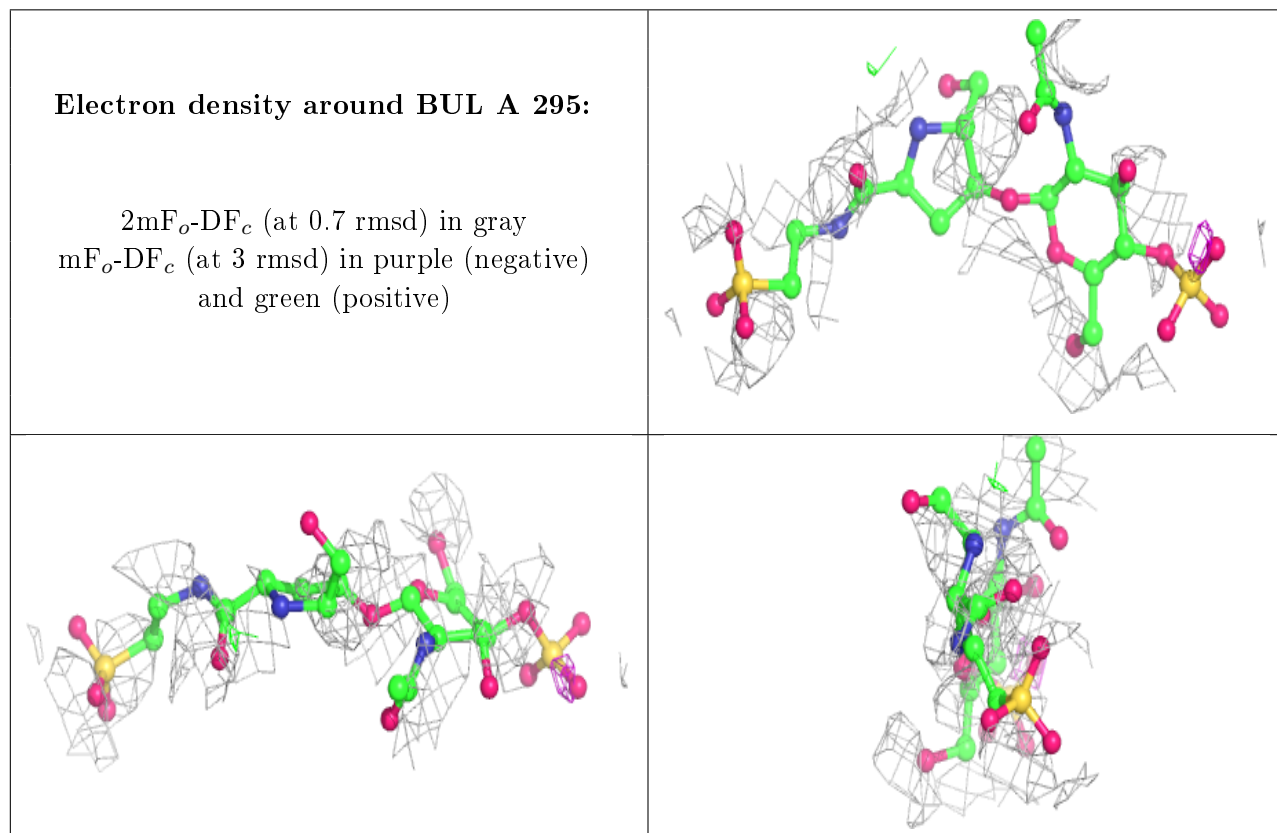
6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.