



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:12 PM UTC

PDB ID : 1T4V / pdb_00001t4v
Title : Crystal Structure Analysis of a novel Oxyguanidine bound to Thrombin
Authors : Spurlino, J.
Deposited on : 2004-04-30
Resolution : 2.00 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

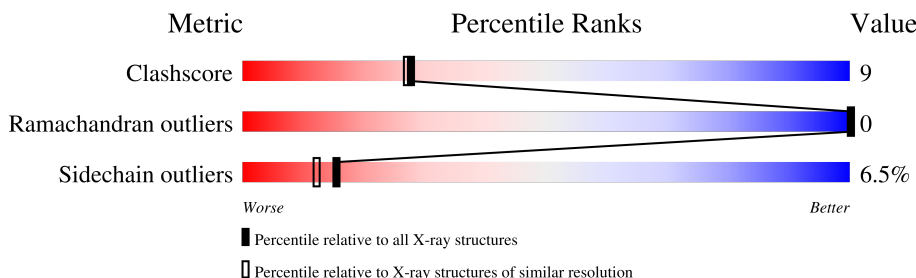
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	L	26	 85% 12% •
2	H	259	 76% 17% • •
3	I	11	 73% 18% 9%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3214 atoms, of which 746 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 Prothrombin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	L	26	Total	C	H	N	O	S	9	0	0
			265	134	50	35	45	1			

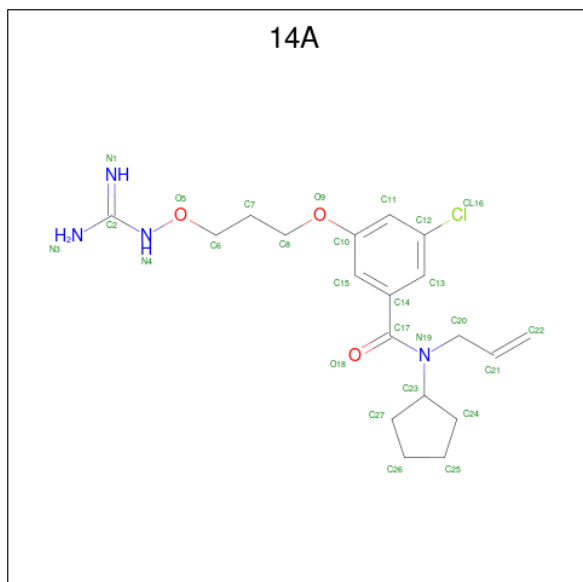
- Molecule 2 is a protein called Prothrombin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	249	Total	C	H	N	O	S	18	0	0
			2473	1285	461	354	359	14			

- Molecule 3 is a protein called Hirudin IIIA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	I	11	Total	C	H	N	O	S	13	0	0
			119	64	15	12	27	1			

- Molecule 4 is N-ALLYL-5-AMIDINOAMINOXY-PROPYLOXY-3-CHLORO-N-CYCLOPENTYLBENZAMIDE (CCD ID: 14A) (formula: C₁₉H₂₇ClN₄O₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	H	1	Total	C	Cl	N	O	0	0
			27	19	1	4	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	10	Total	H	O	0	0
			30	20	10		
5	H	100	Total	H	O	0	0
			300	200	100		

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. 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.

Note EDS was not executed.

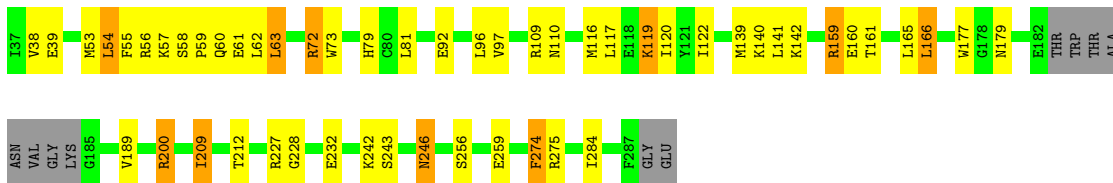
- Molecule 1: Prothrombin

Chain L:  85% 12%



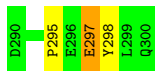
- Molecule 2: Prothrombin

Chain H:  76% 17%



- Molecule 3: Hirudin IIIA

Chain I:  73% 18% 9%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	70.97Å 71.75Å 72.82Å 90.00° 100.52° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.210 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3214	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TYS, 14A

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	L	0.55	0/217	0.80	0/287
2	H	0.69	1/2064 (0.0%)	0.87	0/2789
3	I	0.50	0/88	0.56	0/115
All	All	0.67	1/2369 (0.0%)	0.86	0/3191

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	L	0	1
2	H	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	209	ILE	CA-CB	6.33	1.61	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	200	ARG	Sidechain
2	H	274	PHE	Sidechain
1	L	32	TYR	Sidechain

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	L	215	50	211	2	0
2	H	2012	461	1983	37	1
3	I	104	15	82	2	0
4	H	27	0	26	3	0
5	H	100	200	0	2	1
5	L	10	20	0	0	0
All	All	2468	746	2302	41	1

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 9.

All (41) 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)
2:H:259:GLU:HG2	4:H:1411:14A:H222	1.67	0.77
2:H:81:LEU:HD13	2:H:120:ILE:HD13	1.72	0.71
2:H:56:ARG:O	2:H:60:GLN:HA	1.91	0.69
2:H:57:LYS:O	2:H:60:GLN:HG2	1.96	0.65
2:H:117:LEU:HD13	2:H:139:MET:HE2	1.79	0.64
2:H:179:ASN:ND2	2:H:232:GLU:HB3	2.19	0.58
2:H:72:ARG:NH2	2:H:140:LYS:HD3	2.20	0.57
1:L:32:TYR:HE2	2:H:242:LYS:O	1.87	0.56
2:H:56:ARG:HB2	2:H:63:LEU:HD13	1.89	0.54
2:H:53:MET:HB2	2:H:177:TRP:CZ3	2.43	0.54
2:H:73:TRP:CH2	2:H:140:LYS:HE3	2.43	0.53
2:H:200:ARG:NH1	2:H:212:THR:O	2.41	0.53
2:H:59:PRO:O	2:H:61:GLU:HG2	2.10	0.52
2:H:161:THR:HG22	2:H:165:LEU:HD12	1.93	0.51
2:H:159:ARG:HA	2:H:274:PHE:CZ	2.47	0.49
3:I:295:PRO:CB	3:I:297:GLU:HG3	2.44	0.48
3:I:295:PRO:HB2	3:I:297:GLU:HG3	1.95	0.48
2:H:72:ARG:HH21	2:H:140:LYS:HD3	1.78	0.48
2:H:92:GLU:OE2	2:H:119:LYS:HD3	2.14	0.47
2:H:97:VAL:HG21	2:H:141:LEU:HD21	1.95	0.47
2:H:38:VAL:O	2:H:228:GLY:HA2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:81:LEU:HD13	2:H:120:ILE:HG21	1.97	0.47
2:H:109:ARG:O	2:H:110:ASN:HB2	2.15	0.47
2:H:209:ILE:HD12	4:H:1411:14A:H262	1.97	0.47
2:H:55:PHE:CZ	2:H:60:GLN:HB3	2.50	0.46
2:H:243:SER:HB3	2:H:246:ASN:ND2	2.31	0.46
2:H:97:VAL:HG13	2:H:117:LEU:HD21	1.98	0.45
2:H:259:GLU:N	5:H:443:HOH:O	2.50	0.45
2:H:166:LEU:HD23	2:H:166:LEU:HA	1.80	0.44
2:H:39:GLU:HG3	2:H:227:ARG:HB2	1.99	0.44
2:H:117:LEU:CD1	2:H:139:MET:HE2	2.47	0.44
2:H:275:ARG:HE	2:H:275:ARG:HB3	1.64	0.43
1:L:26:ARG:O	1:L:30:GLU:HG3	2.18	0.43
2:H:79:HIS:CE1	2:H:256:SER:O	2.71	0.43
2:H:246:ASN:C	2:H:246:ASN:HD22	2.25	0.43
4:H:1411:14A:C13	4:H:1411:14A:H23	2.47	0.43
2:H:79:HIS:HE1	2:H:256:SER:O	2.01	0.43
2:H:116:MET:HE2	5:H:430:HOH:O	2.20	0.42
2:H:53:MET:HG3	2:H:62:LEU:HD12	2.01	0.41
2:H:54:LEU:HD12	2:H:97:VAL:HG12	2.03	0.40
2:H:58:SER:HA	2:H:59:PRO:C	2.47	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:109:ARG:HH12	5:H:348:HOH:H1[2_555]	1.31	0.29

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	L	5/26 (19%)	5 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	4/259 (2%)	4 (100%)	0	0	100	100
All	All	9/285 (3%)	9 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

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	L	24/24 (100%)	23 (96%)	1 (4%)	26	25
2	H	197/225 (88%)	184 (93%)	13 (7%)	15	12
3	I	10/10 (100%)	9 (90%)	1 (10%)	7	4
All	All	231/259 (89%)	216 (94%)	15 (6%)	15	12

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	28	LEU
2	H	54	LEU
2	H	63	LEU
2	H	72	ARG
2	H	96	LEU
2	H	119	LYS
2	H	122	ILE
2	H	142	LYS
2	H	159	ARG
2	H	160	GLU
2	H	166	LEU
2	H	189	VAL
2	H	246	ASN
2	H	284	ILE
3	I	297	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such

sidechains are listed below:

Mol	Chain	Res	Type
2	H	110	ASN
2	H	179	ASN
2	H	246	ASN
2	H	286	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue 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	$\# Z > 2$
3	TYS	I	298	3	15,16,17	1.71	4 (26%)	15,22,24	0.36	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
3	TYS	I	298	3	-	0/10/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	298	TYS	O2-S	3.49	1.60	1.45
3	I	298	TYS	O1-S	3.42	1.60	1.45
3	I	298	TYS	O3-S	3.21	1.70	1.50
3	I	298	TYS	OH-CZ	-2.78	1.38	1.42

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	$\# Z > 2$
4	14A	H	1411	-	27,28,28	1.23	4 (14%)	31,36,36	1.51	6 (19%)

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	14A	H	1411	-	-	1/22/31/31	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1411	14A	O5-N4	-2.95	1.34	1.40
4	H	1411	14A	C20-N19	2.66	1.50	1.46
4	H	1411	14A	C11-C12	2.40	1.42	1.38
4	H	1411	14A	C13-C14	-2.02	1.36	1.39

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	1411	14A	C23-N19-C17	-3.75	111.89	123.21
4	H	1411	14A	C14-C17-N19	3.60	125.83	118.72
4	H	1411	14A	O18-C17-C14	-2.78	114.77	120.29
4	H	1411	14A	C25-C24-C23	2.69	110.66	104.61
4	H	1411	14A	C21-C20-N19	2.20	118.89	113.73
4	H	1411	14A	C26-C27-C23	2.11	109.35	104.61

There are no chirality outliers.

All (1) torsion outliers are listed below:

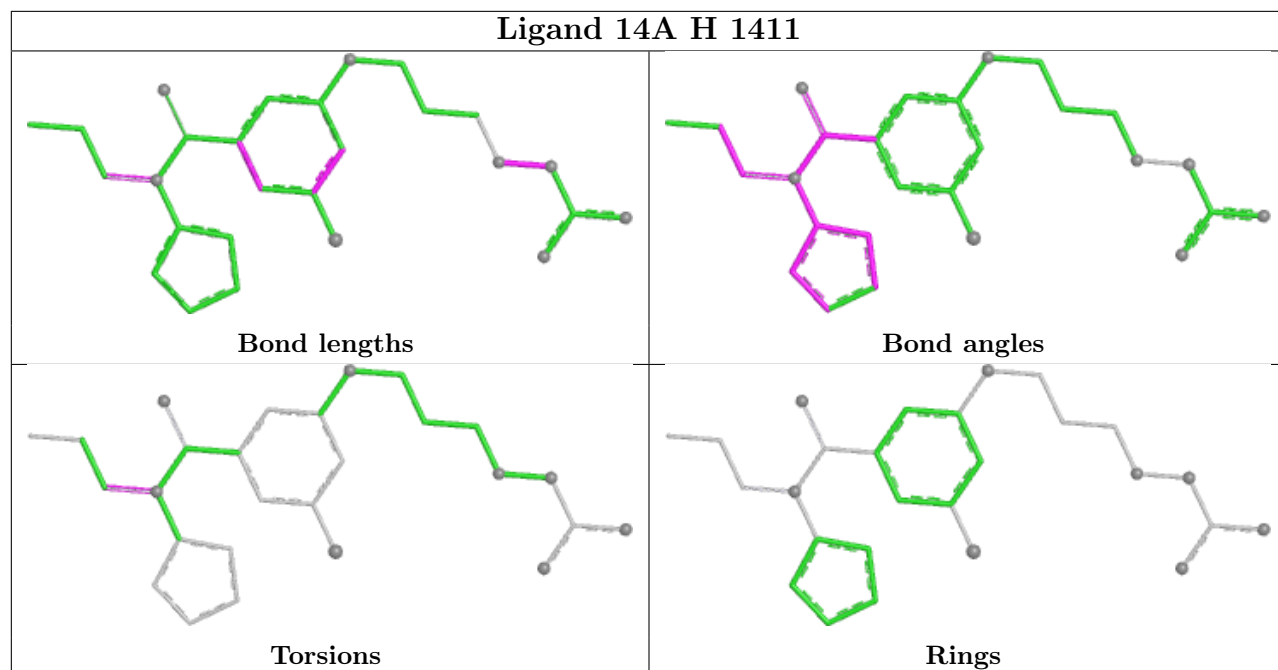
Mol	Chain	Res	Type	Atoms
4	H	1411	14A	C21-C20-N19-C17

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	1411	14A	3	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.