



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2024 – 01:02 PM EDT

PDB ID : 1JIM
Title : STEREOSPECIFIC REACTION OF 3-METHOXY-4-CHLORO-7-AMINO
ISOCOUMARIN WITH CRYSTALLINE PORCINE PANCREATIC ELAS-
TASE
Authors : Meyer, E.
Deposited on : 1993-03-19
Resolution : 2.31 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

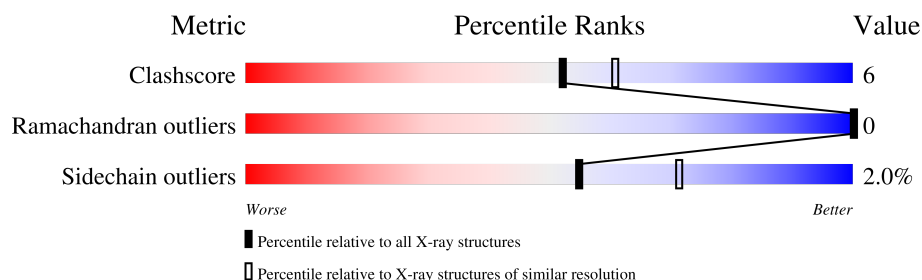
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)

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	A	240	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1978 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 PORCINE PANCREATIC ELASTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	240	1822	1135	330	347	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

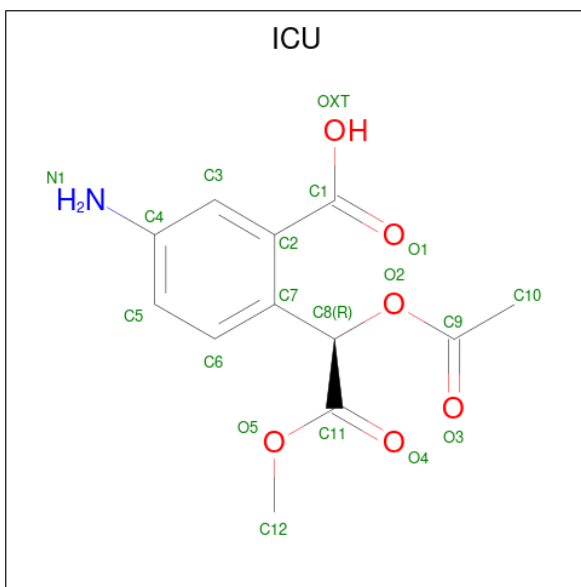
Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ASN	ASP	conflict	UNP P00772

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is METHYL(2-ACETOXY-2-(2-CARBOXY-4-AMINO-PHENYL))ACETATE (three-letter code: ICU) (formula: C₁₂H₁₃NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	12	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	133	Total	O	0	0
			133	133		

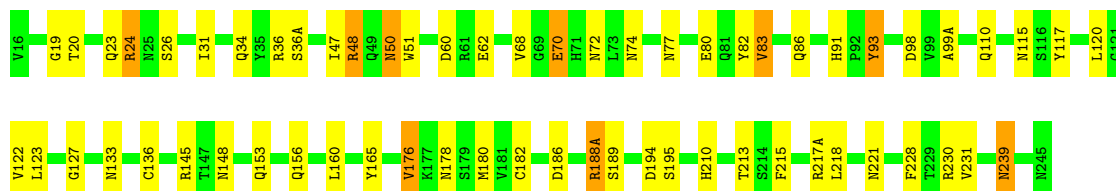
3 Residue-property plots [i](#)

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: PORCINE PANCREATIC ELASTASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.40Å 58.10Å 75.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.31	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.31)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	EREF	Depositor
R, R_{free}	0.153 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1978	wwPDB-VP
Average B, all atoms (Å ²)	14.0	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: SO4, ICU

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	1.18	0/1862	1.85	25/2543 (1.0%)

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	24

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	ARG	NE-CZ-NH2	-32.08	104.26	120.30
1	A	230	ARG	NE-CZ-NH1	23.39	131.99	120.30
1	A	230	ARG	CD-NE-CZ	17.30	147.82	123.60
1	A	217(A)	ARG	NE-CZ-NH1	-13.27	113.66	120.30
1	A	188(A)	ARG	NE-CZ-NH2	-10.45	115.08	120.30
1	A	24	ARG	NE-CZ-NH2	7.55	124.08	120.30
1	A	70	GLU	OE1-CD-OE2	-7.40	114.42	123.30
1	A	230	ARG	CG-CD-NE	-7.10	96.89	111.80
1	A	213	THR	CA-CB-CG2	6.43	121.41	112.40
1	A	188(A)	ARG	NH1-CZ-NH2	6.21	126.23	119.40
1	A	145	ARG	NE-CZ-NH2	6.19	123.39	120.30
1	A	82	TYR	CB-CG-CD1	-6.07	117.36	121.00
1	A	195	SER	CB-CA-C	-6.03	98.65	110.10
1	A	160	LEU	N-CA-CB	-5.91	98.58	110.40
1	A	117	TYR	CB-CG-CD1	-5.72	117.57	121.00
1	A	218	LEU	CB-CA-C	-5.50	99.75	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	194	ASP	CB-CG-OD2	5.44	123.19	118.30
1	A	24	ARG	CG-CD-NE	-5.36	100.54	111.80
1	A	83	VAL	CG1-CB-CG2	-5.36	102.33	110.90
1	A	165	TYR	CB-CG-CD1	-5.26	117.84	121.00
1	A	239	ASN	O-C-N	5.16	130.95	122.70
1	A	24	ARG	CB-CA-C	-5.13	100.14	110.40
1	A	122	VAL	CA-CB-CG1	5.05	118.48	110.90
1	A	120	LEU	CB-CG-CD1	-5.05	102.41	111.00
1	A	136	CYS	CA-CB-SG	5.05	123.08	114.00

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	115	ASN	Sidechain
1	A	133	ASN	Mainchain
1	A	148	ASN	Sidechain
1	A	153	GLN	Sidechain
1	A	178	ASN	Sidechain
1	A	180	MET	Mainchain
1	A	186	ASP	Sidechain
1	A	189	SER	Mainchain
1	A	210	HIS	Mainchain
1	A	221	ASN	Mainchain
1	A	239	ASN	Sidechain
1	A	24	ARG	Mainchain
1	A	34	GLN	Sidechain
1	A	36	ARG	Mainchain
1	A	36(A)	SER	Mainchain
1	A	60	ASP	Sidechain
1	A	62	GLU	Sidechain
1	A	70	GLU	Sidechain
1	A	74	ASN	Sidechain
1	A	80	GLU	Peptide
1	A	86	GLN	Sidechain
1	A	93	TYR	Sidechain
1	A	98	ASP	Sidechain
1	A	99(A)	ALA	Mainchain

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	A	1822	0	1758	20	4
2	A	5	0	0	1	0
3	A	18	0	12	2	0
4	A	133	0	0	2	6
All	All	1978	0	1770	20	6

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 6.

All (20) 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:19:GLY:HA3	4:A:635:HOH:O	1.71	0.88
1:A:72:ASN:H	1:A:77:ASN:HD21	1.23	0.84
1:A:156:GLN:HB3	4:A:635:HOH:O	1.85	0.76
1:A:83:VAL:HG13	1:A:110:GLN:HG2	1.74	0.69
1:A:48:ARG:HB2	1:A:51:TRP:HB2	1.84	0.59
1:A:50:ASN:HD22	1:A:50:ASN:H	1.53	0.56
1:A:123:LEU:HD22	1:A:231:VAL:HG11	1.88	0.56
1:A:83:VAL:CG1	1:A:110:GLN:HG2	2.36	0.53
1:A:91:HIS:HD2	1:A:93:TYR:H	1.54	0.53
1:A:31:ILE:HG22	1:A:68:VAL:HG12	1.90	0.52
1:A:215:PHE:HB3	3:A:251:ICU:H123	1.91	0.51
1:A:72:ASN:N	1:A:77:ASN:HD21	2.01	0.48
1:A:72:ASN:H	1:A:77:ASN:ND2	2.02	0.47
1:A:47:ILE:O	1:A:48:ARG:HD2	2.15	0.46
1:A:127:GLY:HA2	2:A:419:SO4:O2	2.18	0.44
1:A:176:VAL:HG21	1:A:182:CYS:SG	2.58	0.43
1:A:50:ASN:HD22	1:A:50:ASN:N	2.14	0.43
1:A:228:PHE:CD1	1:A:228:PHE:N	2.87	0.41
1:A:23:GLN:HB2	1:A:26:SER:OG	2.21	0.41
1:A:215:PHE:CB	3:A:251:ICU:H123	2.51	0.41

All (6) 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)
1:A:20:THR:N	4:A:633:HOH:O[4_466]	1.28	0.92
1:A:19:GLY:C	4:A:633:HOH:O[4_466]	1.43	0.77
4:A:559:HOH:O	4:A:634:HOH:O[3_546]	1.44	0.76
4:A:636:HOH:O	4:A:644:HOH:O[3_556]	1.65	0.55
1:A:19:GLY:O	4:A:633:HOH:O[4_466]	1.73	0.47
1:A:20:THR:CA	4:A:633:HOH:O[4_466]	1.75	0.45

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	A	238/240 (99%)	226 (95%)	12 (5%)	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	A	198/198 (100%)	194 (98%)	4 (2%)	55	71

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ARG
1	A	50	ASN
1	A	176	VAL

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Mol	Chain	Res	Type
1	A	188(A)	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	49	GLN
1	A	50	ASN
1	A	75	GLN
1	A	77	ASN
1	A	91	HIS
1	A	153	GLN
1	A	204	ASN
1	A	239	ASN
1	A	240	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 monosaccharides 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
3	ICU	A	251	1	18,18,19	1.45	5 (27%)	21,24,26	1.56	4 (19%)
2	SO4	A	419	-	4,4,4	0.16	0	6,6,6	0.43	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	ICU	A	251	1	-	4/16/16/18	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	251	ICU	C3-C2	-2.60	1.36	1.40
3	A	251	ICU	C2-C7	2.47	1.43	1.40
3	A	251	ICU	C2-C1	-2.34	1.41	1.47
3	A	251	ICU	C6-C5	-2.10	1.34	1.38
3	A	251	ICU	O2-C8	2.09	1.48	1.44

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	251	ICU	C8-O2-C9	3.35	120.47	115.69
3	A	251	ICU	O2-C9-C10	3.17	116.91	111.09
3	A	251	ICU	O4-C11-C8	-2.88	118.50	124.62
3	A	251	ICU	C6-C7-C8	-2.57	116.51	120.96

There are no chirality outliers.

All (4) torsion outliers are listed below:

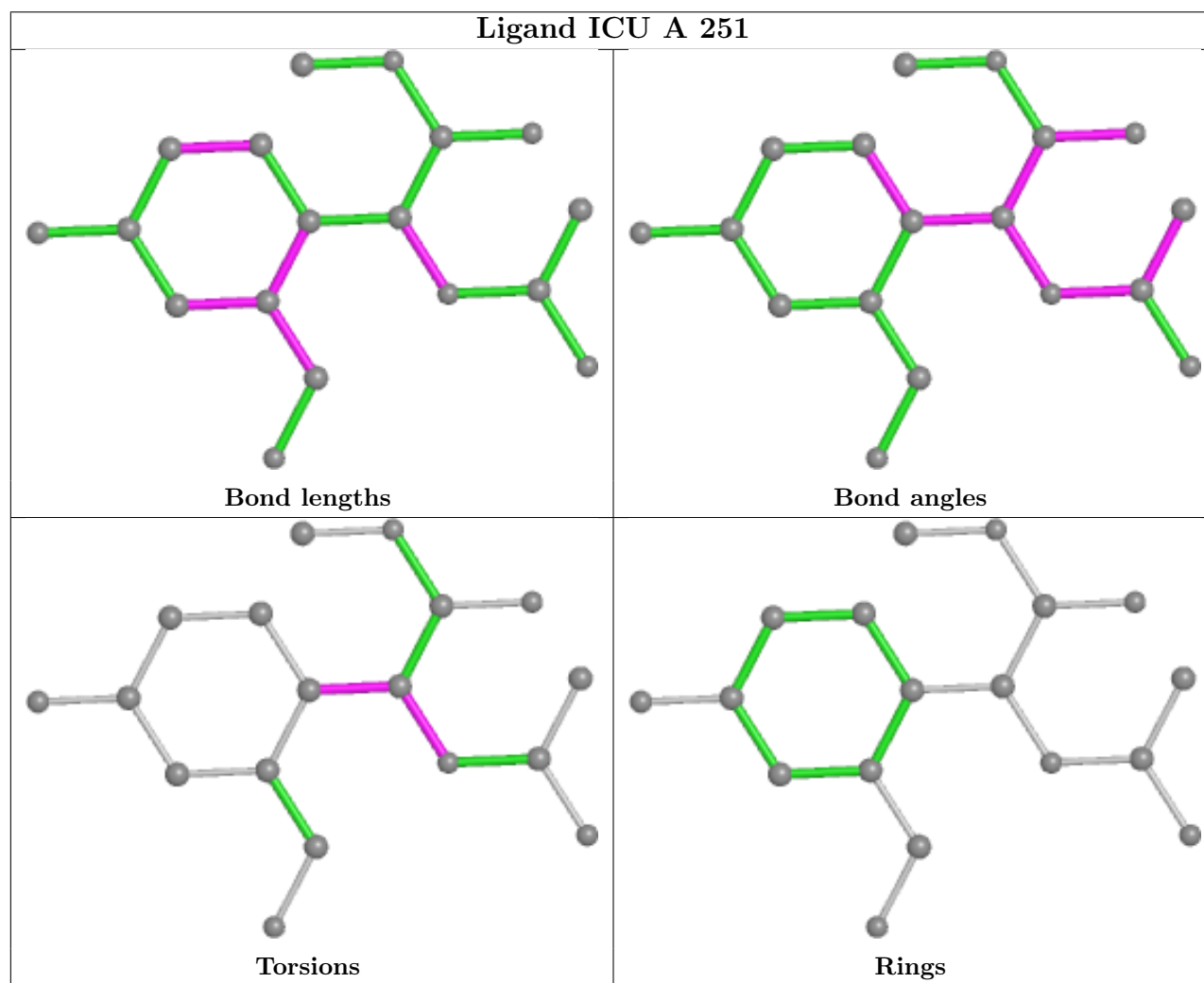
Mol	Chain	Res	Type	Atoms
3	A	251	ICU	C2-C7-C8-C11
3	A	251	ICU	C7-C8-O2-C9
3	A	251	ICU	C11-C8-O2-C9
3	A	251	ICU	C6-C7-C8-C11

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	251	ICU	2	0
2	A	419	SO4	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 [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.