

Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 11:50 AM EDT

PDB ID : 2QRP

Title: Glycogen Phosphorylase b in complex with (1R)-3'-(2-naphthyl)-spiro[1,5-an

hydro-D-glucitol-1,5'-isoxazoline

Authors: Gizilis, G.; Alexacou, K.M.; Chrysina, E.D.; Zographos, S.E.; Leonidas, D.D.;

Oikonomakos, N.G.

Deposited on : 2007-07-28

Resolution : 1.86 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 (i) 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 (1)) 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)

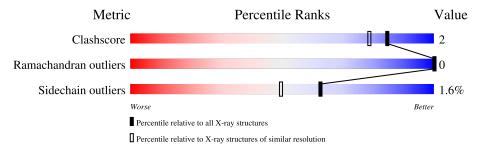
Validation Pipeline (wwPDB-VP) : 2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.86 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar \ resolution} \\ (\#{\rm Entries, \ resolution \ range(\AA)}) \end{array}$
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	A	842	90%	6%	•

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	S06	A	998	X	-	-	-



2 Entry composition (i)

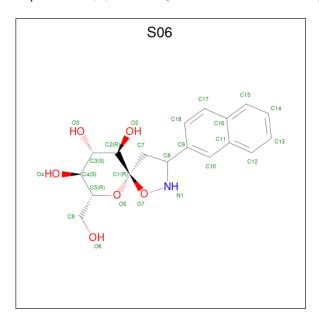
There are 4 unique types of molecules in this entry. The entry contains 7578 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycogen phosphorylase, muscle form.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	A	811	Total 6624	C 4217	N 1172	O 1204	P 1	S 30	0	3	0

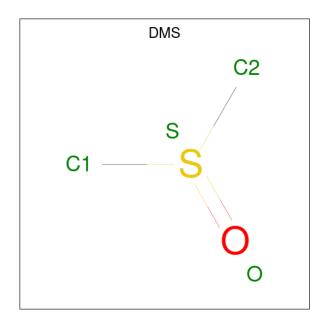
• Molecule 2 is (3S,5R,7R,8S,9S,10R)-7-(hydroxymethyl)-3-(2-naphthyl)-1,6-dioxa-2-azaspiro[4.5]decane-8,9,10-triol (three-letter code: S06) (formula: $C_{18}H_{21}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	Λ	1	Total	С	N	О	0	0
2 A	1	25	18	1	6	0		

• Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).





Mol	Chain	Residues	A	ton	ns		ZeroOcc	AltConf									
3	Λ	1	Total	С	О	S	0	0									
3	A	1	4	2	1	1	0	0									
3	A	1	Total	С	О	S	0	0									
J	Λ	1	4	2	1	1	U	U									
3	A	1	Total	С	О	S	0	0									
	71	1	4	2	1	1	0	U									
3	A	1	Total	С	Ο	S	0	0									
	11	1	4	2	1	1	Ü	U									
3	A	1	Total	С	Ο	S	0	0									
		_	4	2	1	1		Ů									
3	A	1	Total	С	0	S	0	0									
			4	2	1	1											
3	A	1	Total	С	0	S	0	0									
			4	2	1	1											
3	A	A	A	A	A	A	A	A	A	A	1	Total	С	0	S	0	0
			4	2	1	1											
3	A	1	Total	С	O 1	S	0	0									
			4	$\frac{2}{C}$	$\frac{1}{O}$	1 S											
3	A	1	Total 4	2	1	3 1	0	0									
			Total	$\frac{Z}{C}$	O	$\frac{1}{S}$											
3	A	1	4	2	1	1	0	0									
			Total	$\frac{2}{C}$	O	S											
3	A	1	4	2	1	1	0	0									
	_		Total	$\frac{2}{C}$	O	S											
3	A	1	4	2	1	1	0	0									
	3 A	-	Total	\overline{C}	0	S	_	0									
3		A 1	4	2	1	$\tilde{1}$	0										
	<u> </u>	I	<u> </u>				$\frac{\perp}{ntinued\ on\ r}$	ort mage									

Continued on next page...



 $Continued\ from\ previous\ page...$

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

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	869	Total O 869 869	0	0

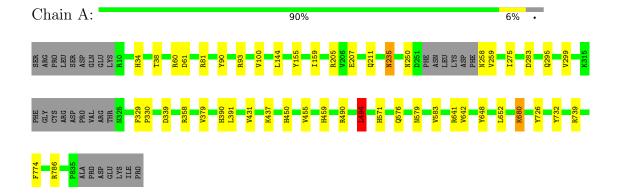


3 Residue-property plots (i)

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: Glycogen phosphorylase, muscle form





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 43 21 2	Depositor	
Cell constants	126.02Å 126.02Å 114.88Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	30.00 - 1.86	Depositor	
% Data completeness	99.9 (30.00-1.86)	Depositor	
(in resolution range)	33.3 (80.00 1.00)		
R_{merge}	(Not available)	Depositor	
R_{sym}	0.05	Depositor	
Refinement program	REFMAC 5.2.0019	Depositor	
R, R_{free}	0.194 , 0.219	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	7578	wwPDB-VP	
Average B, all atoms (Å ²)	21.0	wwPDB-VP	



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: S06, DMS, LLP

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).

Mal	Chain	Bond	lengths	Bond angles		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.35	0/6764	0.49	1/9149 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	494	LEU	CA-CB-CG	6.82	130.97	115.30

There are no chirality outliers.

There are no planarity outliers.

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	6624	0	6563	31	1
2	A	25	0	20	0	0
3	A	60	0	90	1	0
4	A	869	0	0	5	1
All	All	7578	0	6673	31	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 2.

All (31) close contacts within the same asymmetric unit are listed below, sorted by their clash



magnitude.

Atom-1	Atom-2	Interatomic	Clash
		$\operatorname{distance} (\mathrm{\AA})$	overlap (Å)
1:A:490:ARG:HA	1:A:494:LEU:HG	1.38	1.01
1:A:100:VAL:HG21	1:A:494:LEU:HD22	1.54	0.90
1:A:258:ASN:O	4:A:1482:HOH:O	2.07	0.71
1:A:455:VAL:H	1:A:459:HIS:HD2	1.41	0.68
1:A:93[B]:ARG:NH2	4:A:1355:HOH:O	2.30	0.65
1:A:159:ILE:CG1	1:A:299:VAL:CG2	2.78	0.62
1:A:159:ILE:HG13	1:A:299:VAL:CG2	2.31	0.61
1:A:81:ARG:NH1	1:A:155:TYR:OH	2.36	0.59
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.86	0.58
1:A:450:HIS:HD2	4:A:1072:HOH:O	1.91	0.53
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.92	0.53
1:A:205:ARG:NH2	1:A:207:GLU:OE2	2.39	0.53
1:A:283:ASP:O	1:A:571:HIS:NE2	2.42	0.51
1:A:235:ASN:H	1:A:235:ASN:HD22	1.56	0.51
1:A:450:HIS:HE1	4:A:1062:HOH:O	1.94	0.51
1:A:680:LLP:O3	1:A:680:LLP:NZ	2.44	0.51
1:A:726:TYR:OH	1:A:774:PHE:HB2	2.12	0.50
1:A:159:ILE:HG12	1:A:299:VAL:HG22	1.94	0.49
1:A:583:VAL:HG11	1:A:642:VAL:HG21	1.95	0.48
1:A:431:VAL:HG11	1:A:437:LYS:HE2	1.96	0.48
1:A:159:ILE:CG1	1:A:299:VAL:HG22	2.43	0.48
1:A:100:VAL:CG2	1:A:494:LEU:HD22	2.36	0.47
1:A:648:TYR:HA	1:A:652:LEU:HD23	1.98	0.45
1:A:211:GLN:O	1:A:358:ARG:NH1	2.50	0.44
1:A:159:ILE:HG13	1:A:299:VAL:HG21	2.01	0.43
1:A:275:ILE:O	1:A:295:GLN:HG2	2.19	0.43
1:A:786:ARG:NH2	4:A:1849:HOH:O	2.52	0.42
1:A:732:TYR:CZ	1:A:739:ARG:HG3	2.53	0.42
1:A:329:PHE:HB3	1:A:330:PRO:HD3	2.01	0.41
1:A:786:ARG:NH2	3:A:939:DMS:O	2.53	0.41
1:A:390:HIS:CD2	1:A:391:LEU:N	2.88	0.41

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	$egin{array}{ll} ext{Interatomic} \ ext{distance} \ (ext{\AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:A:259:VAL:CG1	4:A:1229:HOH:O[7_556]	2.18	0.02



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	807/842 (96%)	784 (97%)	23 (3%)	0	100 100

There are no Ramachandran outliers to report.

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	704/730 (96%)	693 (98%)	11 (2%)	62 49

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	ARG
1	A	90	TYR
1	A	144	LEU
1	A	235	ASN
1	A	250	ASN
1	A	339	ASP
1	A	379	VAL
1	A	494	LEU
1	A	576	GLN
1	A	579	ASN
1	A	641	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:



Mol	Chain	Res	Type
1	A	34	HIS
1	A	72	GLN
1	A	106	ASN
1	A	167	ASN
1	A	235	ASN
1	A	284	ASN
1	A	325	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	566	GLN
1	A	576	GLN
1	A	579	ASN
1	A	767	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	Dec	Link	Bo	ond leng	$ ag{ths}$	B	ond ang	eles
IVIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	LLP	A	680	1	23,24,25	1.69	3 (13%)	25,32,34	1.32	4 (16%)

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
1	LLP	A	680	1	-	2/16/17/19	0/1/1/1



All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
1	A	680	LLP	O3-C3	-5.50	1.24	1.37
1	A	680	LLP	C2-N1	2.72	1.39	1.33
1	A	680	LLP	C4-C4'	2.62	1.51	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	680	LLP	CE-NZ-C4'	-2.62	110.85	118.90
1	A	680	LLP	C4-C4'-NZ	-2.62	112.29	124.31
1	A	680	LLP	C5-C6-N1	-2.45	119.74	123.82
1	A	680	LLP	OP4-P-OP1	-2.28	100.07	106.47

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	680	LLP	C4-C5-C5'-OP4
1	A	680	LLP	C6-C5-C5'-OP4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	680	LLP	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

16 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	Во	Bond lengths			ond ang	les
WIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DMS	A	940	_	3,3,3	2.64	1 (33%)	3,3,3	0.45	0
3	DMS	A	939	-	3,3,3	2.61	1 (33%)	3,3,3	0.60	0
3	DMS	A	947	-	3,3,3	2.68	1 (33%)	3,3,3	0.56	0
3	DMS	A	931	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
3	DMS	A	948	-	3,3,3	2.68	1 (33%)	3,3,3	0.50	0
3	DMS	A	946	-	3,3,3	2.60	1 (33%)	3,3,3	0.47	0
3	DMS	A	942	-	3,3,3	2.67	1 (33%)	3,3,3	0.47	0
3	DMS	A	938	-	3,3,3	2.66	1 (33%)	3,3,3	0.46	0
3	DMS	A	936	-	3,3,3	2.57	1 (33%)	3,3,3	0.45	0
3	DMS	A	953	-	3,3,3	2.65	1 (33%)	3,3,3	0.51	0
3	DMS	A	945	-	3,3,3	2.65	1 (33%)	3,3,3	0.58	0
3	DMS	A	959	-	3,3,3	2.67	1 (33%)	3,3,3	0.50	0
3	DMS	A	934	-	3,3,3	2.66	1 (33%)	3,3,3	0.43	0
3	DMS	A	972	-	3,3,3	2.63	1 (33%)	3,3,3	0.51	0
3	DMS	A	937	-	3,3,3	2.65	1 (33%)	3,3,3	0.54	0
2	S06	A	998	-	26,28,28	2.13	2 (7%)	35,42,42	1.56	1 (2%)

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	S06	A	998	-	1/1/6/7	2/6/40/40	0/4/4/4

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
2	A	998	S06	C9-C8	-7.99	1.40	1.52
2	A	998	S06	C8-N1	-5.92	1.33	1.46
3	A	947	DMS	O-S	4.50	1.80	1.50
3	A	948	DMS	O-S	4.49	1.80	1.50
3	A	959	DMS	O-S	4.48	1.80	1.50
3	A	934	DMS	O-S	4.48	1.80	1.50
3	A	942	DMS	O-S	4.47	1.80	1.50
3	A	938	DMS	O-S	4.47	1.80	1.50

Continued on next page...



$\alpha \cdots$	· ·	•	
Continued	trom	mromonie	maaa
-	110116	DICULUUS	Duuc
	.,	1	1

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
3	A	931	DMS	O-S	4.47	1.80	1.50
3	A	953	DMS	O-S	4.47	1.80	1.50
3	A	945	DMS	O-S	4.45	1.80	1.50
3	A	937	DMS	O-S	4.44	1.80	1.50
3	A	940	DMS	O-S	4.43	1.80	1.50
3	A	972	DMS	O-S	4.40	1.80	1.50
3	A	939	DMS	O-S	4.38	1.79	1.50
3	A	946	DMS	O-S	4.35	1.79	1.50
3	A	936	DMS	O-S	4.30	1.79	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
2	A	998	S06	C9-C8-N1	8.17	124.49	112.22

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	998	S06	C8

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	998	S06	C7-C8-C9-C10
2	A	998	S06	C7-C8-C9-C18

There are no ring outliers.

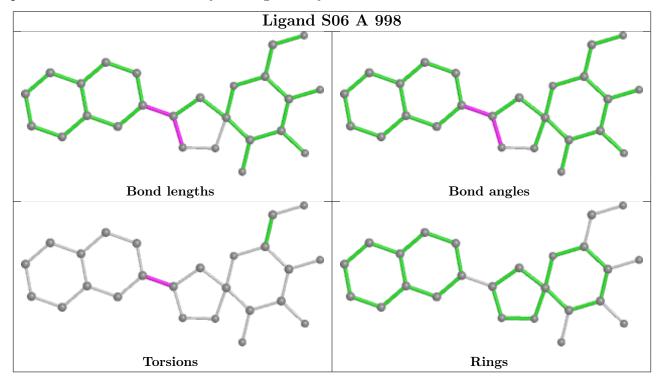
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	939	DMS	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 then 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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

