



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:56 am BST

PDB ID : 6FJD  
Title : Human KIBRA C2 domain mutant C771A in complex with phosphatidylinositol 4,5-bisphosphate  
Authors : Crennell, S.J.; Posner, M.G.; Bagby, S.  
Deposited on : 2018-01-22  
Resolution : 2.90 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](mailto: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.

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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

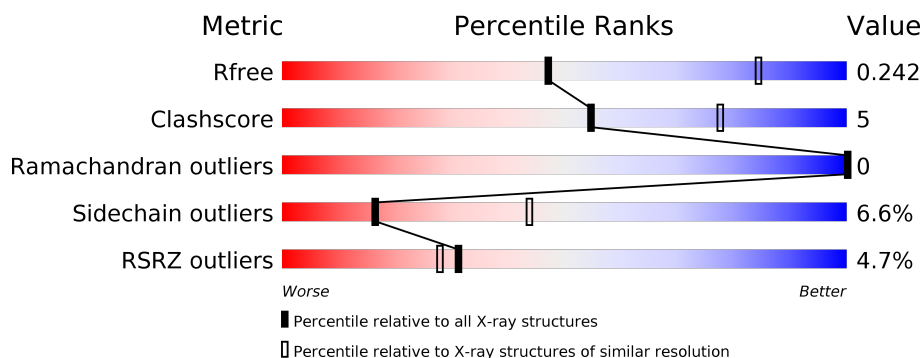
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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  $\geq 3$ , 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	A	140	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 81%; height: 10px; background-color: green;"></div> <div style="width: 10%; height: 10px; background-color: yellow;"></div> <div style="width: 8%; height: 10px; background-color: orange;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div>
1	B	140	<div> <div style="width: 7%; height: 10px; background-color: red;"></div> <div style="width: 75%; height: 10px; background-color: green;"></div> <div style="width: 13%; height: 10px; background-color: yellow;"></div> <div style="width: 10%; height: 10px; background-color: orange;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> </div>

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
4	PBU	A	809	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4317 atoms, of which 2133 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 KIBRA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	129	Total	C	H	N	O	S	0	1	0
			2072	645	1041	185	196	5			
1	B	126	Total	C	H	N	O	S	0	0	0
			1993	624	1000	173	191	5			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	646	MET	-	initiating methionine	UNP Q8IX03
A	647	ARG	-	expression tag	UNP Q8IX03
A	648	GLY	-	expression tag	UNP Q8IX03
A	649	SER	-	expression tag	UNP Q8IX03
A	650	HIS	-	expression tag	UNP Q8IX03
A	651	HIS	-	expression tag	UNP Q8IX03
A	652	HIS	-	expression tag	UNP Q8IX03
A	653	HIS	-	expression tag	UNP Q8IX03
A	654	HIS	-	expression tag	UNP Q8IX03
A	655	HIS	-	expression tag	UNP Q8IX03
A	656	GLY	-	expression tag	UNP Q8IX03
A	657	SER	-	expression tag	UNP Q8IX03
A	771	ALA	CYS	engineered mutation	UNP Q8IX03
B	646	MET	-	initiating methionine	UNP Q8IX03
B	647	ARG	-	expression tag	UNP Q8IX03
B	648	GLY	-	expression tag	UNP Q8IX03
B	649	SER	-	expression tag	UNP Q8IX03
B	650	HIS	-	expression tag	UNP Q8IX03
B	651	HIS	-	expression tag	UNP Q8IX03
B	652	HIS	-	expression tag	UNP Q8IX03
B	653	HIS	-	expression tag	UNP Q8IX03
B	654	HIS	-	expression tag	UNP Q8IX03
B	655	HIS	-	expression tag	UNP Q8IX03
B	656	GLY	-	expression tag	UNP Q8IX03
B	657	SER	-	expression tag	UNP Q8IX03

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Chain	Residue	Modelled	Actual	Comment	Reference
B	771	ALA	CYS	engineered mutation	UNP Q8IX03

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



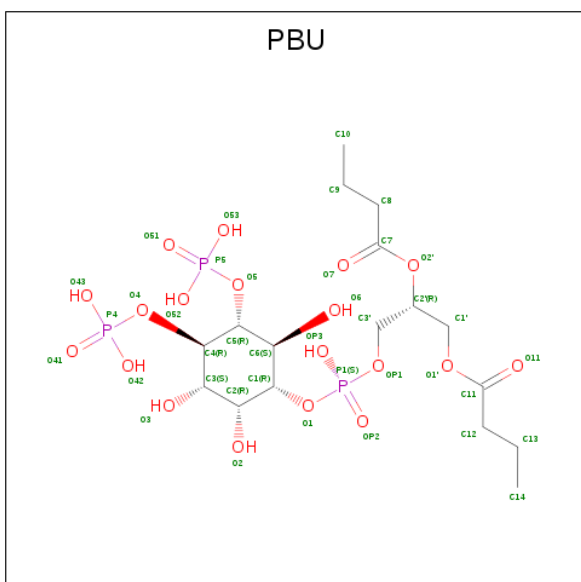
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	A	1	Total	C	H	O	0	0
			14	3	8	3		
2	B	1	Total	C	H	O	0	0
			14	3	8	3		
2	B	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



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

- Molecule 4 is (2R)-3-[[[(R)-HYDROXY{[(1R,2R,3S,4R,5R,6S)-2,3,6-TRIHYDROXY-4,5-BIS(PHOSPHONOOXY)CYCLOHEXYL]OXY}PHOSPHORYL]OXY}PROPANE-1,2-DIYL DIBUTANOATE (three-letter code: PBU) (formula: C<sub>17</sub>H<sub>33</sub>O<sub>19</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	O	P	0	0
			67	17	28	19	3		

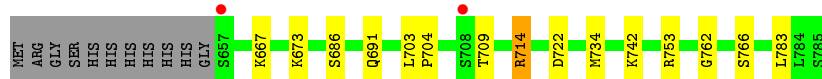
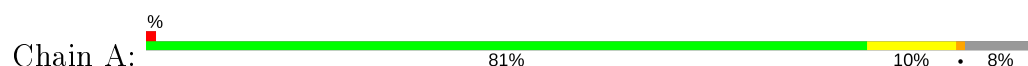
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	31	Total	O	0	0
			31	31		
5	B	22	Total	O	0	0
			22	22		

### 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: Protein KIBRA



#### • Molecule 1: Protein KIBRA





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.40 Å 83.40 Å 208.25 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.47 – 2.90 29.47 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (29.47-2.90) 99.5 (29.47-2.90)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 2.90 Å)	Xtriage
Refinement program	PHENIX (1.12rc0_2797: ???)	Depositor
R, $R_{free}$	0.203 , 0.242 0.203 , 0.242	Depositor DCC
$R_{free}$ test set	506 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.5	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4317	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PBU, GOL, SO4

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	0.46	0/1046	0.63	0/1415
1	B	0.44	0/1006	0.63	0/1361
All	All	0.45	0/2052	0.63	0/2776

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	1031	1041	1039	10	0
1	B	993	1000	1001	10	1
2	A	36	48	48	2	0
2	B	12	16	16	0	0
3	A	10	0	0	1	0
3	B	10	0	0	0	0
4	A	39	28	28	0	1
5	A	31	0	0	5	1
5	B	22	0	0	2	0
All	All	2184	2133	2132	22	2

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 (22) 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:667:LYS:NZ	5:A:901:HOH:O	1.98	0.95
1:A:753[B]:ARG:NH1	5:A:902:HOH:O	2.00	0.94
1:B:714:ARG:NH1	1:B:757:GLU:OE2	2.04	0.90
1:A:714:ARG:NH2	5:A:903:HOH:O	2.06	0.88
1:A:686:SER:OG	1:A:722:ASP:OD1	1.97	0.82
2:A:805:GOL:O1	2:A:805:GOL:O3	2.09	0.67
1:A:686:SER:HG	1:A:722:ASP:CG	2.02	0.58
1:A:673:LYS:NZ	5:A:904:HOH:O	2.41	0.53
1:B:745:ARG:HD3	5:B:903:HOH:O	2.10	0.51
1:B:745:ARG:NH1	5:B:903:HOH:O	2.39	0.49
1:B:697:ASN:OD1	1:B:714:ARG:HD3	2.14	0.47
2:A:805:GOL:HO3	2:A:805:GOL:HO1	1.53	0.45
1:B:665:ALA:HA	1:B:777:SER:O	2.18	0.44
1:B:674:GLN:HG2	1:B:733:SER:HA	1.99	0.44
1:A:753[A]:ARG:NH1	5:A:907:HOH:O	2.51	0.43
1:A:667:LYS:HD2	3:A:807:SO4:O4	2.18	0.43
1:B:775:GLU:HA	1:B:775:GLU:OE1	2.19	0.42
1:B:736:TYR:HB3	1:B:737:PRO:HD3	2.02	0.42
1:B:752:ASP:HB2	1:B:756:LEU:HB3	2.01	0.41
1:A:703:LEU:HA	1:A:704:PRO:C	2.40	0.40
1:A:762:GLY:HA2	1:A:783:LEU:HD22	2.02	0.40
1:B:689:LEU:O	1:B:689:LEU:HG	2.21	0.40

All (2) 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)
5:A:904:HOH:O	5:A:904:HOH:O[8_555]	1.85	0.35
1:B:776:ARG:HH12	4:A:809:PBU:OP3[6_555]	1.50	0.10

## 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	128/140 (91%)	121 (94%)	7 (6%)	0	100	100
1	B	122/140 (87%)	111 (91%)	11 (9%)	0	100	100
All	All	250/280 (89%)	232 (93%)	18 (7%)	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	116/124 (94%)	110 (95%)	6 (5%)	23	55
1	B	112/124 (90%)	103 (92%)	9 (8%)	12	33
All	All	228/248 (92%)	213 (93%)	15 (7%)	16	44

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

Mol	Chain	Res	Type
1	A	691	GLN
1	A	709	THR
1	A	714	ARG
1	A	734	MET
1	A	742	LYS
1	A	766	SER
1	B	670	GLU
1	B	689	LEU
1	B	690	GLN
1	B	691	GLN
1	B	714	ARG
1	B	733	SER
1	B	734	MET
1	B	751	THR
1	B	766	SER

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

Mol	Chain	Res	Type
1	B	764	GLN

### 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](#)

13 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	GOL	A	801	-	5,5,5	0.88	0	5,5,5	1.04	0
3	SO4	A	808	-	4,4,4	0.30	0	6,6,6	0.49	0
2	GOL	A	805	-	5,5,5	0.81	0	5,5,5	1.00	0
2	GOL	A	802	-	5,5,5	1.23	1 (20%)	5,5,5	0.71	0
2	GOL	B	802	-	5,5,5	0.86	0	5,5,5	1.05	0
3	SO4	A	807	-	4,4,4	0.09	0	6,6,6	0.26	0
2	GOL	A	806	-	5,5,5	1.55	1 (20%)	5,5,5	0.88	0
2	GOL	B	801	-	5,5,5	0.82	0	5,5,5	1.03	0
3	SO4	B	803	-	4,4,4	0.16	0	6,6,6	0.15	0
2	GOL	A	803	-	5,5,5	1.27	1 (20%)	5,5,5	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	B	804	-	4,4,4	0.15	0	6,6,6	0.20	0
2	GOL	A	804	-	5,5,5	0.91	0	5,5,5	1.01	0
4	PBU	A	809	-	39,39,39	1.50	5 (12%)	53,57,57	1.39	7 (13%)

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	GOL	A	801	-	-	2/4/4/4	-
2	GOL	A	805	-	-	0/4/4/4	-
2	GOL	A	802	-	-	4/4/4/4	-
2	GOL	B	802	-	-	0/4/4/4	-
2	GOL	A	806	-	-	0/4/4/4	-
2	GOL	B	801	-	-	1/4/4/4	-
2	GOL	A	803	-	-	2/4/4/4	-
2	GOL	A	804	-	-	3/4/4/4	-
4	PBU	A	809	-	-	11/36/60/60	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	809	PBU	P5-O5	4.43	1.67	1.59
4	A	809	PBU	P4-O4	4.11	1.67	1.59
4	A	809	PBU	O1'-C11	2.98	1.42	1.33
2	A	806	GOL	C1-C2	2.97	1.63	1.51
4	A	809	PBU	O2'-C2'	-2.17	1.41	1.46
4	A	809	PBU	O2'-C7	2.16	1.40	1.34
2	A	802	GOL	C3-C2	2.05	1.60	1.51
2	A	803	GOL	C3-C2	2.03	1.60	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	809	PBU	O2'-C7-C8	4.83	121.91	111.50
4	A	809	PBU	C2-C3-C4	3.88	118.54	109.68
4	A	809	PBU	C3-C2-C1	3.17	116.92	109.68
4	A	809	PBU	C6-C1-C2	3.15	115.39	110.85
4	A	809	PBU	O1'-C11-C12	2.96	121.20	111.91
4	A	809	PBU	O2'-C7-O7	-2.53	117.59	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	A	809	PBU	C3-C4-C5	2.13	116.54	111.66

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	GOL	C1-C2-C3-O3
2	A	801	GOL	O2-C2-C3-O3
2	A	802	GOL	O1-C1-C2-C3
2	A	803	GOL	O1-C1-C2-C3
4	A	809	PBU	C4-O4-P4-O41
2	A	802	GOL	O1-C1-C2-O2
4	A	809	PBU	C3'-OP1-P1-O1
2	A	804	GOL	C1-C2-C3-O3
2	A	803	GOL	O1-C1-C2-O2
4	A	809	PBU	C7-C8-C9-C10
4	A	809	PBU	C11-C12-C13-C14
2	B	801	GOL	C1-C2-C3-O3
2	A	804	GOL	O2-C2-C3-O3
4	A	809	PBU	C12-C11-O1'-C1'
2	A	802	GOL	O2-C2-C3-O3
4	A	809	PBU	O11-C11-O1'-C1'
4	A	809	PBU	C3'-OP1-P1-OP3
4	A	809	PBU	O1'-C1'-C2'-C3'
4	A	809	PBU	O1'-C1'-C2'-O2'
4	A	809	PBU	C5-O5-P5-O51
4	A	809	PBU	C5-O5-P5-O53
2	A	802	GOL	C1-C2-C3-O3
2	A	804	GOL	O1-C1-C2-O2

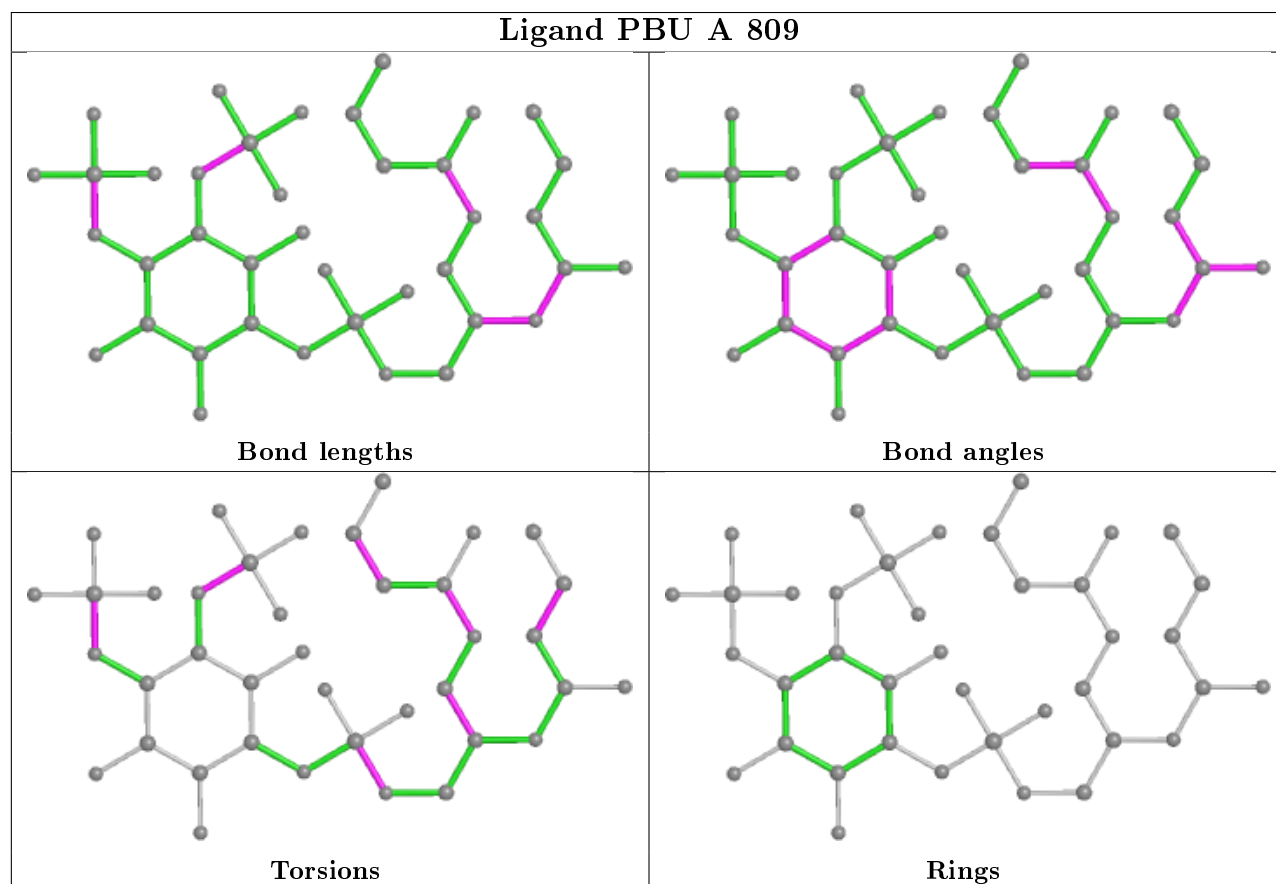
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	805	GOL	2	0
3	A	807	SO4	1	0
4	A	809	PBU	0	1

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	129/140 (92%)	-0.32	2 (1%) 72 71	16, 24, 63, 83	0
1	B	126/140 (90%)	-0.03	10 (7%) 12 10	14, 28, 80, 100	0
All	All	255/280 (91%)	-0.18	12 (4%) 31 28	14, 25, 74, 100	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	752	ASP	5.9
1	B	708	SER	4.2
1	B	751	THR	4.2
1	B	693	ASP	4.0
1	B	756	LEU	3.6
1	A	708	SER	3.5
1	A	657	SER	3.1
1	B	690	GLN	2.9
1	B	707	GLU	2.7
1	B	775	GLU	2.4
1	B	692	GLN	2.1
1	B	773	SER	2.1

### 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 carbohydrates in this entry.

## 6.4 Ligands ⓘ

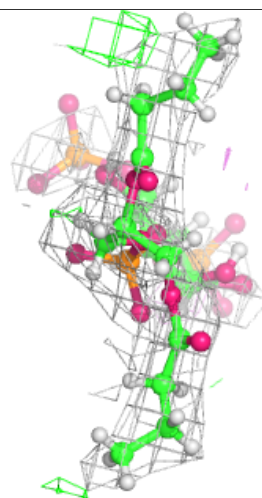
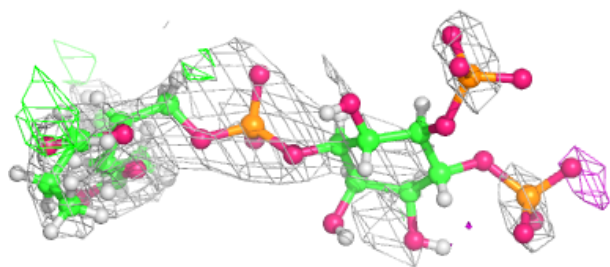
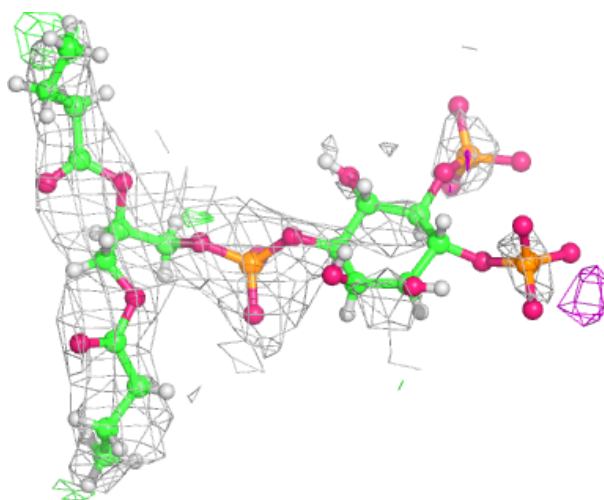
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	PBU	A	809	39/39	0.54	0.46	38,81,131,149	0
3	SO4	A	808	5/5	0.80	0.29	62,71,74,106	0
2	GOL	A	806	6/6	0.84	0.32	22,41,75,75	0
3	SO4	B	804	5/5	0.84	0.22	75,85,106,123	0
2	GOL	A	805	6/6	0.84	0.34	23,58,70,73	0
3	SO4	A	807	5/5	0.86	0.19	52,65,86,132	0
2	GOL	B	802	6/6	0.87	0.35	43,83,103,103	0
2	GOL	A	801	6/6	0.90	0.27	32,50,76,76	0
2	GOL	A	804	6/6	0.91	0.22	31,46,68,82	0
2	GOL	A	803	6/6	0.92	0.17	26,43,65,65	0
2	GOL	A	802	6/6	0.92	0.20	26,33,55,67	0
2	GOL	B	801	6/6	0.97	0.16	32,40,52,63	0
3	SO4	B	803	5/5	0.97	0.12	18,21,45,47	0

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 PBU A 809:**

$2mF_o-DF_c$  (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.