



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 12:05 AM BST

PDB ID : 3BD7  
Title : Glycogen Phosphorylase complex with 1(-D-glucopyranosyl) thymine  
Authors : Sovantzis, D.A.; Hadjiloi, T.; Hayes, J.M.; Zographos, S.E.; Chrysina, E.D.;  
Oikonomakos, N.G.  
Deposited on : 2007-11-14  
Resolution : 1.90 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 : 2.13.1  
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) : 2.13.1

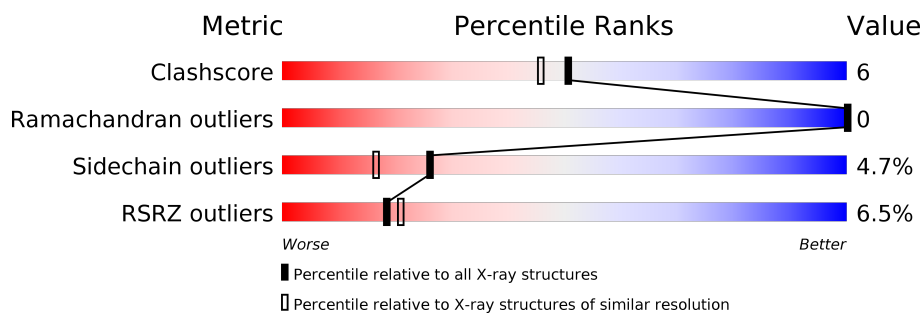
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	842	<div> <div>6%</div> <div>82%</div> <div>12%</div> <div>• •</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7005 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.

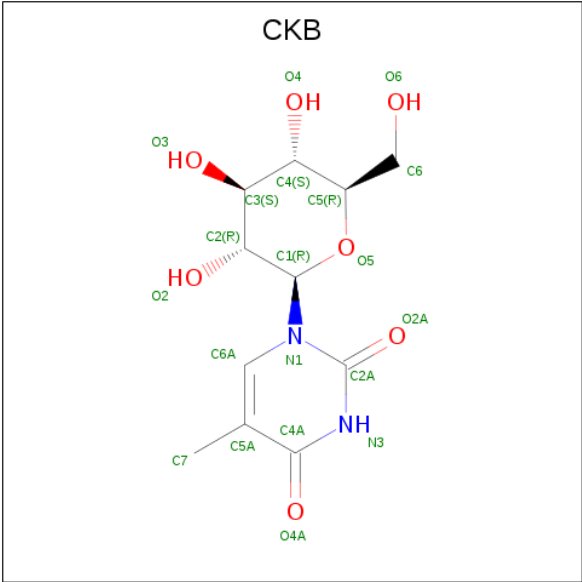
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	810	Total	C	N	O	S	0	0	0
			6589	4201	1160	1199	29			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula:  $C_8H_{10}NO_6P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is 1-beta-D-glucopyranosyl-5-methylpyrimidine-2,4(1H,3H)-dione (three-letter code: CKB) (formula:  $C_{11}H_{16}N_2O_7$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			20	11	2	7		
3	A	1	Total	C	N	O	0	0
			20	11	2	7		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	361	Total	O	0	0
			361	361		

### 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 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: Glycogen phosphorylase, muscle form



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	127.96 Å 127.96 Å 116.23 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.43 – 1.90 29.43 – 1.89	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.43-1.90) 98.6 (29.43-1.89)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 1.89 Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.185 , 0.205 0.179 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.6	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 55.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7005	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CKB, PLP

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	0.31	0/6736	0.58	0/9116

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 [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	6589	0	6533	75	0
2	A	15	0	7	0	0
3	A	40	0	5	0	0
4	A	361	0	0	11	0
All	All	7005	0	6545	75	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 6.

All (75) 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:708:PHE:HB3	1:A:710:ILE:HD11	1.54	0.90
1:A:708:PHE:HB3	1:A:710:ILE:CD1	2.13	0.79
1:A:138:ARG:O	1:A:138:ARG:HD3	1.85	0.77
1:A:455:VAL:H	1:A:459:HIS:HD2	1.35	0.75
1:A:433:GLU:OE1	1:A:437:LYS:HD2	1.89	0.73
1:A:678:ASN:HD22	1:A:679:MET:H	1.36	0.72
1:A:270:ASN:HB2	4:A:1317:HOH:O	1.89	0.71
1:A:549:LEU:HD12	1:A:557:ILE:HD13	1.72	0.68
1:A:235:ASN:HA	1:A:833:ARG:HG3	1.75	0.66
1:A:730:GLU:O	1:A:734:ARG:HG3	1.99	0.62
1:A:423:ASP:O	1:A:426:ARG:HG3	2.00	0.61
1:A:287:GLU:HG2	1:A:289:LYS:HG2	1.82	0.60
1:A:719:ASP:O	1:A:723:GLN:HG3	2.02	0.60
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.86	0.59
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.85	0.58
1:A:710:ILE:HD12	1:A:710:ILE:N	2.19	0.58
1:A:235:ASN:H	1:A:235:ASN:HD22	1.52	0.57
1:A:355:ASP:OD1	1:A:398:ARG:HD3	2.04	0.57
1:A:678:ASN:HD22	1:A:679:MET:N	2.03	0.55
1:A:282:ASN:HB2	4:A:1206:HOH:O	2.06	0.55
1:A:550:GLU:O	1:A:554:LYS:HD3	2.07	0.54
1:A:739:ARG:O	1:A:743:GLU:HG3	2.07	0.54
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.92	0.53
1:A:423:ASP:HB2	4:A:1222:HOH:O	2.09	0.53
1:A:678:ASN:ND2	1:A:679:MET:H	2.06	0.52
1:A:72:GLN:O	1:A:76:GLU:HG2	2.09	0.52
1:A:66:ARG:HG3	4:A:1341:HOH:O	2.08	0.51
1:A:341:HIS:HB2	1:A:342:PRO:HD3	1.93	0.51
1:A:65:GLY:O	1:A:69:ARG:HG2	2.11	0.51
1:A:568:LYS:HG3	1:A:574:LYS:HD3	1.92	0.51
1:A:678:ASN:HD22	1:A:678:ASN:N	2.09	0.51
1:A:236:ASN:CG	1:A:836:ALA:HB2	2.31	0.51
1:A:18:LEU:HD22	1:A:18:LEU:N	2.27	0.49
1:A:557:ILE:O	1:A:559:PRO:HD3	2.13	0.49
1:A:450:HIS:HD2	4:A:1254:HOH:O	1.95	0.48
1:A:181:ASP:HB3	1:A:184:ARG:NH2	2.28	0.48
1:A:510:GLU:HB2	4:A:1174:HOH:O	2.12	0.48
1:A:546:ALA:HA	1:A:557:ILE:HD11	1.96	0.48
1:A:706:GLU:H	1:A:706:GLU:CD	2.17	0.48
1:A:764:MET:HA	1:A:768:HIS:CE1	2.49	0.47
1:A:469:LYS:O	1:A:473:GLU:HG3	2.14	0.47
1:A:734:ARG:HD3	4:A:1331:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:LEU:HD23	1:A:147:MET:CE	2.44	0.47
1:A:831:ARG:O	1:A:833:ARG:NH1	2.48	0.46
1:A:325:ASN:HD21	1:A:327:ASP:HB2	1.79	0.46
1:A:434:GLY:O	1:A:435:ALA:C	2.53	0.46
1:A:727:ASN:OD1	1:A:729:GLN:HB3	2.15	0.46
1:A:235:ASN:N	1:A:235:ASN:HD22	2.11	0.46
1:A:450:HIS:HE1	4:A:1149:HOH:O	1.99	0.46
1:A:138:ARG:C	1:A:138:ARG:HD3	2.35	0.46
1:A:522:LEU:HD13	1:A:806:ALA:CB	2.45	0.45
1:A:536:LYS:HB3	1:A:536:LYS:NZ	2.31	0.45
1:A:556:HIS:CD2	1:A:556:HIS:N	2.84	0.44
1:A:13:ILE:HD11	1:A:16:ARG:HG3	1.99	0.44
1:A:20:GLY:HA3	4:A:1306:HOH:O	2.18	0.44
1:A:36:HIS:O	1:A:40:VAL:HA	2.17	0.44
1:A:463:LEU:CD2	1:A:467:ILE:HD11	2.48	0.44
1:A:494:LEU:C	1:A:494:LEU:HD23	2.37	0.44
1:A:67:TRP:HA	1:A:238:VAL:HB	1.99	0.44
1:A:648:TYR:HA	1:A:652:LEU:HD23	1.99	0.43
1:A:562:LEU:HD21	1:A:662:LEU:HB2	2.01	0.43
1:A:732:TYR:CZ	1:A:739:ARG:HG3	2.54	0.43
1:A:781:VAL:O	1:A:785:GLU:HG3	2.18	0.43
1:A:235:ASN:H	1:A:235:ASN:ND2	2.16	0.43
1:A:235:ASN:ND2	1:A:237:VAL:H	2.17	0.43
1:A:138:ARG:HB3	4:A:1130:HOH:O	2.17	0.43
1:A:795:ARG:O	1:A:799:ARG:HG3	2.19	0.42
1:A:689:ILE:O	1:A:689:ILE:HG23	2.18	0.42
1:A:69:ARG:HG3	4:A:1311:HOH:O	2.20	0.42
1:A:726:TYR:OH	1:A:774:PHE:HB2	2.20	0.42
1:A:678:ASN:N	1:A:678:ASN:ND2	2.66	0.42
1:A:456:ALA:C	1:A:481:ASN:HD21	2.24	0.41
1:A:713:MET:HB3	1:A:717:ASP:HB2	2.01	0.41
1:A:678:ASN:ND2	1:A:679:MET:N	2.67	0.41
1:A:423:ASP:O	1:A:427:ARG:HG3	2.22	0.40

There are no symmetry-related clashes.

## 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	804/842 (96%)	776 (96%)	28 (4%)	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	701/731 (96%)	668 (95%)	33 (5%)	26	16

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLU
1	A	90	TYR
1	A	104	LEU
1	A	115	LEU
1	A	138	ARG
1	A	211	GLN
1	A	234	ARG
1	A	235	ASN
1	A	325	ASN
1	A	400	LEU
1	A	433	GLU
1	A	444	LEU
1	A	510	GLU

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Mol	Chain	Res	Type
1	A	522	LEU
1	A	552	GLU
1	A	568	LYS
1	A	579	ASN
1	A	586	LEU
1	A	596	LYS
1	A	613	TYR
1	A	622	LEU
1	A	645	LEU
1	A	662	LEU
1	A	678	ASN
1	A	706	GLU
1	A	708	PHE
1	A	721	LEU
1	A	734	ARG
1	A	765	LEU
1	A	782	LYS
1	A	790	LEU
1	A	831	ARG
1	A	833	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	73	HIS
1	A	211	GLN
1	A	235	ASN
1	A	264	GLN
1	A	270	ASN
1	A	325	ASN
1	A	412	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	556	HIS
1	A	560	ASN
1	A	566	GLN
1	A	579	ASN
1	A	678	ASN
1	A	767	HIS

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Mol	Chain	Res	Type
1	A	832	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

3 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	CKB	A	940	-	16,21,21	2.24	5 (31%)	19,31,31	2.46	3 (15%)
2	PLP	A	999	1	15,15,16	1.53	4 (26%)	20,22,23	1.11	1 (5%)
3	CKB	A	998	-	16,21,21	2.28	3 (18%)	19,31,31	2.62	4 (21%)

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	CKB	A	940	-	-	0/2/26/26	0/2/2/2
2	PLP	A	999	1	-	1/6/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CKB	A	998	-	-	0/2/26/26	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	998	CKB	O5-C1	5.69	1.50	1.42
3	A	940	CKB	C4A-N3	4.99	1.41	1.33
3	A	940	CKB	C4A-C5A	4.82	1.51	1.41
3	A	998	CKB	C4A-C5A	4.68	1.51	1.41
3	A	998	CKB	C4A-N3	3.87	1.39	1.33
3	A	940	CKB	O5-C1	3.67	1.47	1.42
2	A	999	PLP	C4A-C4	3.00	1.57	1.51
2	A	999	PLP	C3-C2	-2.64	1.38	1.40
2	A	999	PLP	P-O3P	-2.61	1.44	1.54
2	A	999	PLP	P-O1P	-2.07	1.43	1.50
3	A	940	CKB	O5-C5	2.03	1.49	1.44
3	A	940	CKB	C4-C5	2.02	1.57	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	940	CKB	C4A-N3-C2A	9.50	123.16	115.14
3	A	998	CKB	C4A-N3-C2A	9.04	122.78	115.14
3	A	998	CKB	C6A-N1-C1	4.79	129.99	119.24
3	A	940	CKB	C6A-N1-C1	3.22	126.48	119.24
3	A	998	CKB	C3-C2-C1	-2.87	104.65	109.13
3	A	998	CKB	C5A-C6A-N1	-2.16	119.86	122.19
3	A	940	CKB	C3-C2-C1	-2.14	105.79	109.13
2	A	999	PLP	O3P-P-O1P	2.04	118.67	110.68

There are no chirality outliers.

All (1) torsion outliers are listed below:

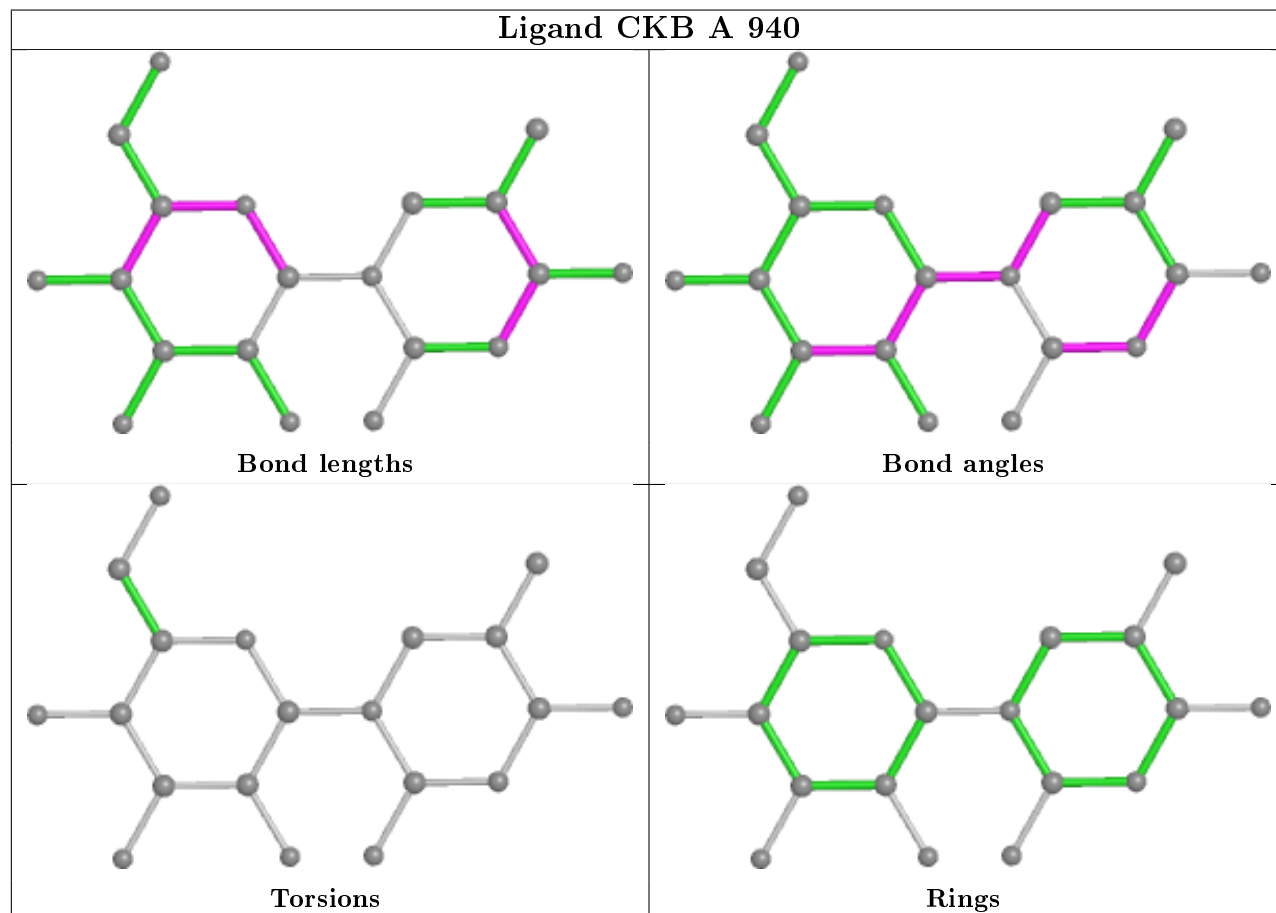
Mol	Chain	Res	Type	Atoms
2	A	999	PLP	C6-C5-C5A-O4P

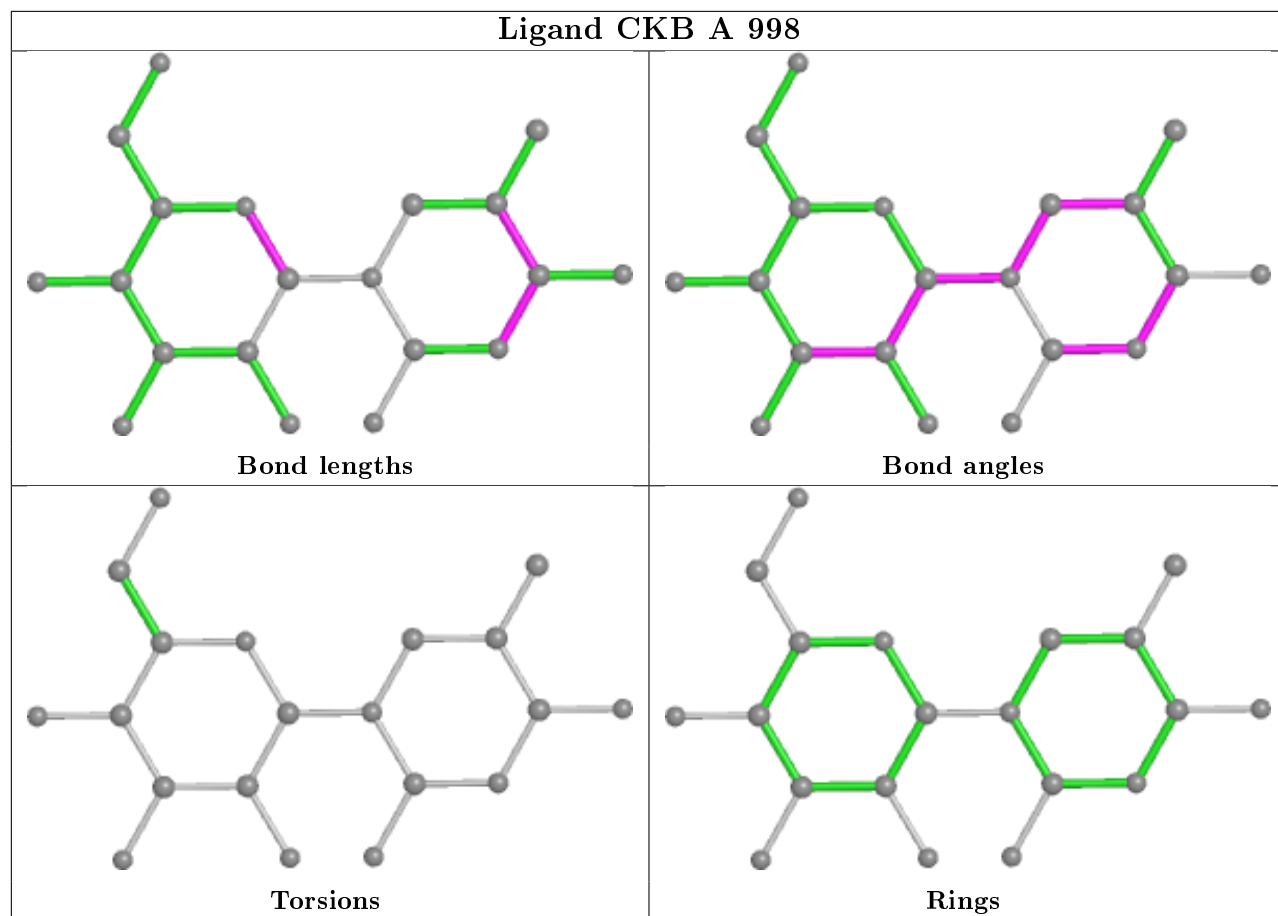
There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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	810/842 (96%)	0.26	53 (6%) 18 21	16, 26, 52, 84	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	324	THR	9.7
1	A	556	HIS	7.0
1	A	555	VAL	6.2
1	A	253	ASN	5.9
1	A	252	PHE	5.7
1	A	325	ASN	5.1
1	A	12	GLN	4.9
1	A	436	VAL	4.8
1	A	113	TYR	4.6
1	A	551	ARG	4.5
1	A	211	GLN	4.5
1	A	435	ALA	4.2
1	A	836	ALA	3.8
1	A	69	ARG	3.7
1	A	254	LEU	3.6
1	A	314	SER	3.5
1	A	358	ARG	3.3
1	A	554	LYS	3.3
1	A	835	PRO	3.2
1	A	13	ILE	3.1
1	A	753	LYS	3.1
1	A	21	VAL	3.0
1	A	832	GLN	3.0
1	A	583	VAL	2.9
1	A	831	ARG	2.8
1	A	510	GLU	2.8
1	A	532	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	22	GLU	2.8
1	A	833	ARG	2.7
1	A	580	CYS	2.7
1	A	547	ALA	2.7
1	A	426	ARG	2.6
1	A	434	GLY	2.5
1	A	171	CYS	2.4
1	A	605	ILE	2.4
1	A	683	LEU	2.3
1	A	723	GLN	2.3
1	A	577	LEU	2.3
1	A	337	LEU	2.2
1	A	444	LEU	2.2
1	A	552	GLU	2.2
1	A	626	ILE	2.2
1	A	581	LEU	2.2
1	A	433	GLU	2.1
1	A	77	LYS	2.1
1	A	344	LEU	2.1
1	A	345	ALA	2.1
1	A	492	LEU	2.1
1	A	768	HIS	2.1
1	A	346	ILE	2.1
1	A	752	PRO	2.1
1	A	87	LEU	2.0
1	A	18	LEU	2.0

## 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](#)

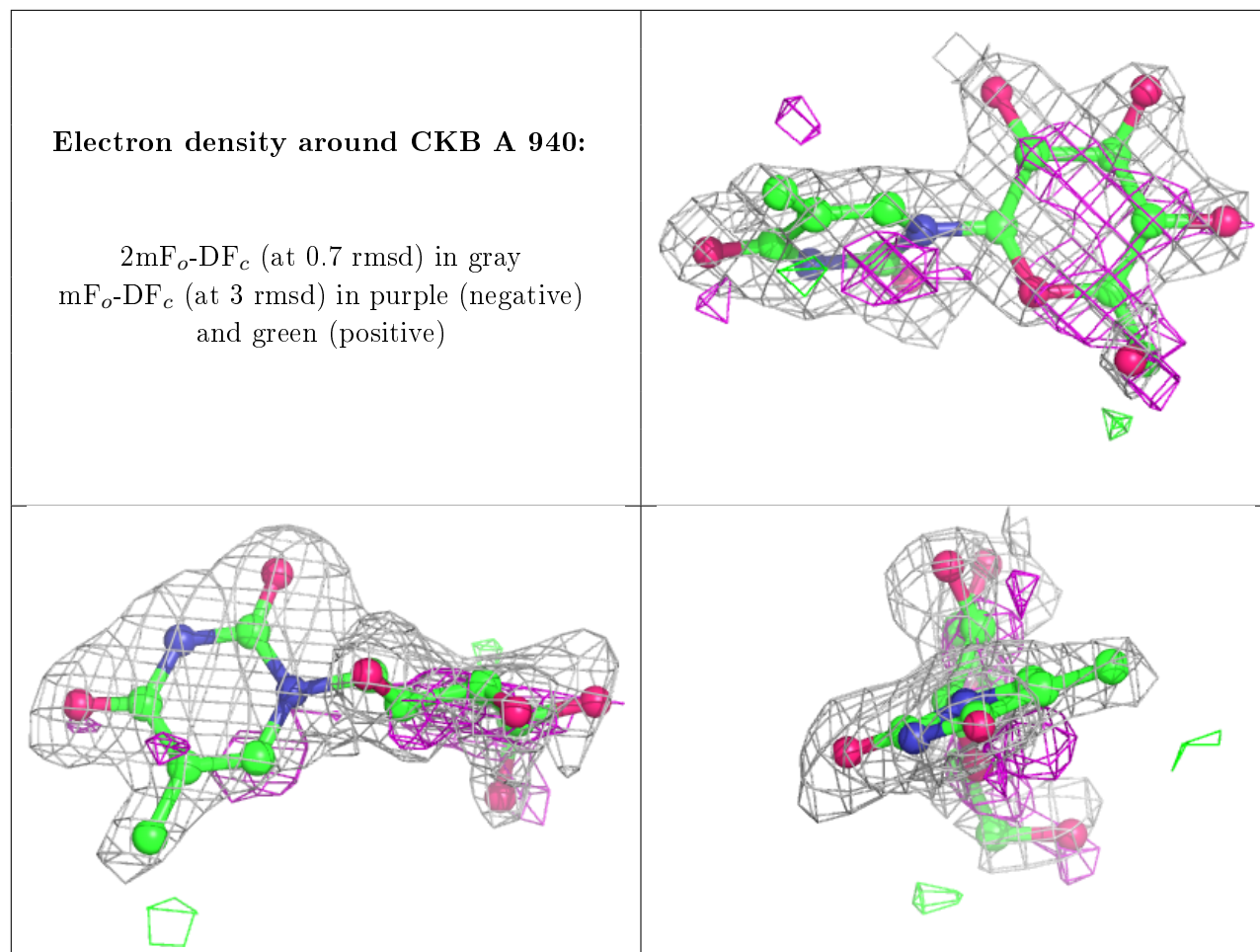
There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

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.

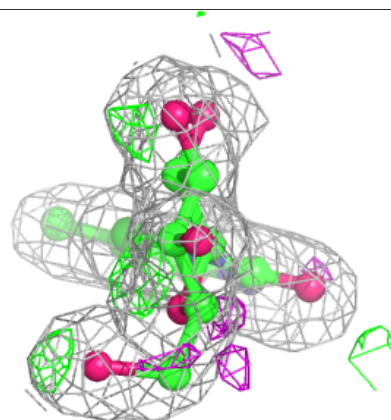
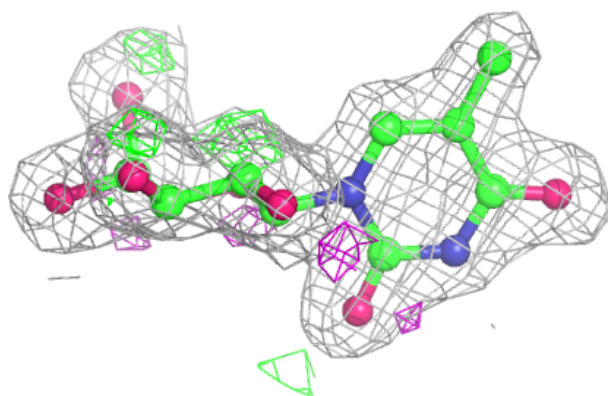
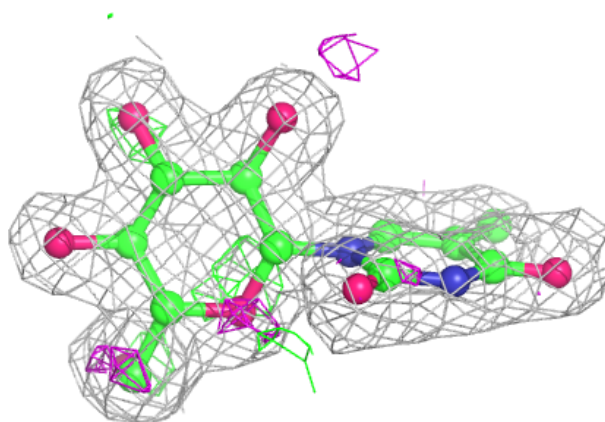
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CKB	A	940	20/20	0.73	0.34	35,42,47,47	0
3	CKB	A	998	20/20	0.94	0.11	15,16,19,20	0
2	PLP	A	999	15/16	0.99	0.09	14,17,19,20	0

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 CKB A 998:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers ⓘ

There are no such residues in this entry.