



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:51 PM GMT

PDB ID : 3EBP  
Title : Glycogen Phosphorylase b/ flavopiridol complex  
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Deposited on : 2008-08-28  
Resolution : 2.00 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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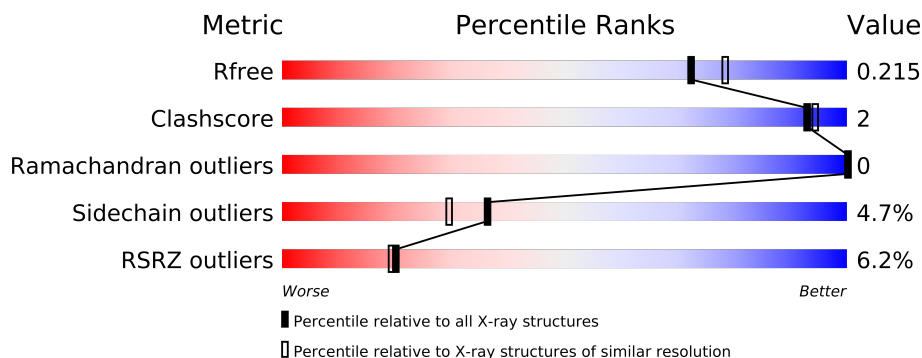
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

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))
$R_{free}$	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	842	

## 2 Entry composition i

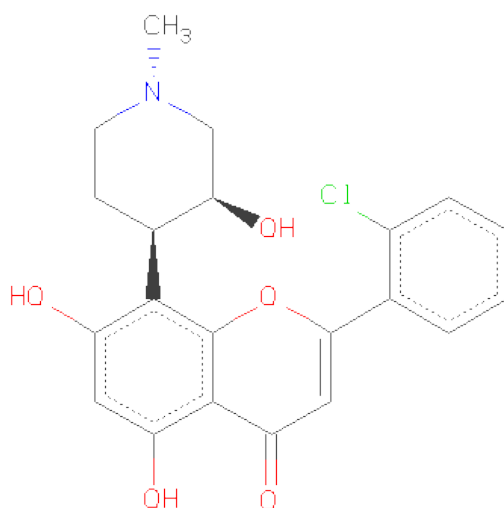
There are 3 unique types of molecules in this entry. The entry contains 6928 atoms, of which 0 are hydrogen and 0 are deuterium.

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
			Total	C	N	O	P	S			
1	A	810	6614	4214	1163	1206	1	30	0	3	0

- Molecule 2 is 2-(2-CHLORO-PHENYL)-5,7-DIHYDROXY-8-(3-HYDROXY-1-METHYL-PIPERIDIN-4-YL)-4H-BENZOPYRAN-4-ONE (three-letter code: CPB) (formula: C<sub>21</sub>H<sub>20</sub>ClNO<sub>5</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	28	21	1	1	5	0	0

- Molecule 3 is water.

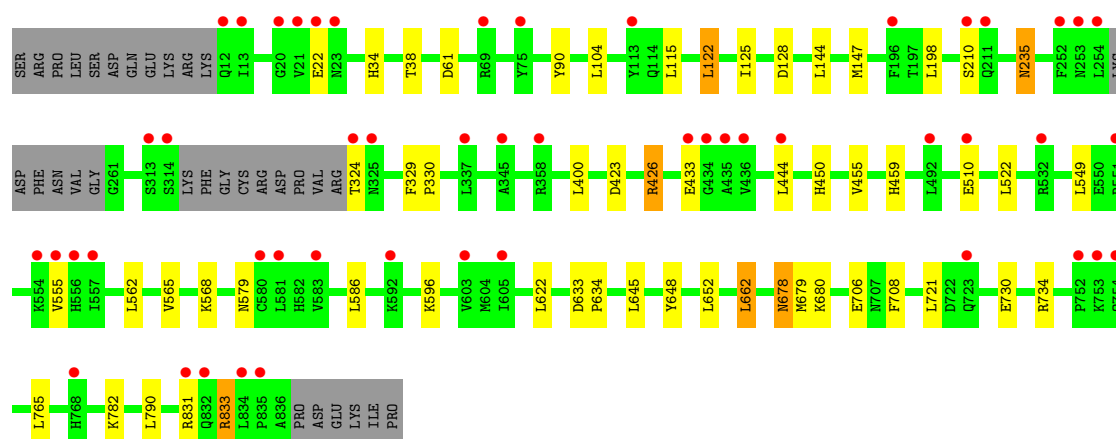
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	286	Total	O	0	0
			286	286		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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

Chain A: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	128.65Å 128.65Å 116.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.53 – 2.00 29.53 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (29.53-2.00) 98.6 (29.53-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.57 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.188 , 0.215 0.187 , 0.215	Depositor DCC
$R_{free}$ test set	3304 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.7	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 46.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 65052 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6928	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CPB, 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.37	0/6751	0.52	0/9136

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6614	0	6545	23	0
2	A	28	0	18	0	0
3	A	286	0	0	2	0
All	All	6928	0	6563	23	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (23) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:426:ARG:HH21	1:A:426:ARG:HG2	1.52	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:455:VAL:H	1:A:459:HIS:HD2	1.35	0.72
1:A:426:ARG:CG	1:A:426:ARG:HH21	2.04	0.71
1:A:730:GLU:O	1:A:734:ARG:HG3	1.91	0.70
1:A:678:ASN:HD22	1:A:679:MET:H	1.42	0.66
1:A:235:ASN:HA	1:A:833:ARG:HG3	1.86	0.57
1:A:122:LEU:HA	1:A:125:ILE:HD12	1.89	0.54
1:A:235:ASN:HD22	1:A:235:ASN:H	1.54	0.54
1:A:450:HIS:HE1	3:A:1044:HOH:O	1.91	0.52
1:A:34:HIS:HE1	1:A:61:ASP:OD1	1.93	0.52
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.95	0.49
1:A:549:LEU:HB3	1:A:555:VAL:HG23	1.94	0.49
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.95	0.48
1:A:678:ASN:HD22	1:A:679:MET:N	2.11	0.47
1:A:680:LLP:NZ	1:A:680:LLP:O3	2.44	0.47
1:A:426:ARG:NH2	1:A:426:ARG:CG	2.69	0.44
1:A:678:ASN:ND2	1:A:679:MET:H	2.13	0.43
1:A:562:LEU:HD21	1:A:662:LEU:HB2	2.00	0.42
1:A:144:LEU:HD23	1:A:147:MET:CE	2.51	0.41
1:A:648:TYR:HA	1:A:652:LEU:HD23	2.03	0.41
1:A:633:ASP:HA	1:A:634:PRO:HD3	1.94	0.41
1:A:450:HIS:HD2	3:A:1040:HOH:O	2.04	0.40
1:A:423:ASP:OD1	1:A:426:ARG:NH2	2.54	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	806/842 (96%)	786 (98%)	20 (2%)	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	703/730 (96%)	670 (95%)	33 (5%)	36 29

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	122	LEU
1	A	128	ASP
1	A	198	LEU
1	A	210	SER
1	A	235	ASN
1	A	324	THR
1	A	400	LEU
1	A	426	ARG
1	A	433	GLU
1	A	444	LEU
1	A	510	GLU
1	A	522	LEU
1	A	565	VAL
1	A	568	LYS
1	A	579	ASN
1	A	586	LEU
1	A	596	LYS
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	765	LEU
1	A	782	LYS
1	A	790	LEU

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Mol	Chain	Res	Type
1	A	831	ARG
1	A	833	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	235	ASN
1	A	270	ASN
1	A	412	ASN
1	A	450	HIS
1	A	459	HIS
1	A	481	ASN
1	A	484	ASN
1	A	566	GLN
1	A	579	ASN
1	A	678	ASN
1	A	832	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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	$\# Z  > 2$
1	LLP	A	680	1	24,24,25	4.26	5 (20%)	30,32,34	1.14	3 (10%)

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	-	0/15/17/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	680	LLP	O-C	19.27	1.24	1.11
1	A	680	LLP	O3-C3	-5.30	1.24	1.37
1	A	680	LLP	CA-C	3.09	1.54	1.48
1	A	680	LLP	C2-N1	2.57	1.38	1.33
1	A	680	LLP	C4'-NZ	-2.21	1.34	1.45

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	680	LLP	C6-C5-C4	3.16	120.50	118.10
1	A	680	LLP	OP4-P-OP1	-2.26	100.08	106.71
1	A	680	LLP	C5-C6-N1	-2.07	120.12	123.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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
2	CPB	A	940	-	31,31,31	1.28	4 (12%)	44,46,46	1.65	3 (6%)

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	CPB	A	940	-	-	1/8/21/21	0/2/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	940	CPB	C21-C2	-4.33	1.40	1.46
2	A	940	CPB	C7-C8	2.85	1.40	1.38
2	A	940	CPB	O1-C2	2.37	1.37	1.34
2	A	940	CPB	C8-C14	2.14	1.56	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	940	CPB	C3-C2-C21	-7.15	119.58	127.13
2	A	940	CPB	O1-C2-C21	4.94	120.02	113.52
2	A	940	CPB	C26-C21-C2	-2.20	118.05	120.39

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	940	CPB	O1-C2-C21-C22

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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%)	0.31	50 (6%) 20 19	18, 29, 47, 62	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	324	THR	8.3
1	A	253	ASN	7.8
1	A	556	HIS	7.4
1	A	555	VAL	5.8
1	A	254	LEU	5.6
1	A	435	ALA	5.2
1	A	252	PHE	5.2
1	A	436	VAL	4.8
1	A	211	GLN	4.4
1	A	21	VAL	3.8
1	A	20	GLY	3.7
1	A	69	ARG	3.6
1	A	113	TYR	3.6
1	A	551	ARG	3.4
1	A	314	SER	3.3
1	A	603	VAL	3.3
1	A	583	VAL	3.3
1	A	434	GLY	3.3
1	A	433	GLU	3.1
1	A	13	ILE	3.1
1	A	753	LYS	3.1
1	A	12	GLN	3.1
1	A	580	CYS	3.0
1	A	554	LYS	3.0
1	A	22	GLU	2.8
1	A	444	LEU	2.8
1	A	605	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	210	SER	2.7
1	A	752	PRO	2.7
1	A	23	ASN	2.7
1	A	532	ARG	2.7
1	A	581	LEU	2.7
1	A	325	ASN	2.7
1	A	557	ILE	2.7
1	A	835	PRO	2.6
1	A	723	GLN	2.6
1	A	75	TYR	2.6
1	A	510	GLU	2.5
1	A	358	ARG	2.4
1	A	832	GLN	2.4
1	A	834	LEU	2.4
1	A	831	ARG	2.3
1	A	492	LEU	2.3
1	A	754	GLN	2.2
1	A	768[A]	HIS	2.1
1	A	345	ALA	2.1
1	A	196	PHE	2.1
1	A	313	SER	2.1
1	A	592	LYS	2.0
1	A	337	LEU	2.0

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	LLP	A	680	24/25	0.11	-0.61	18,20,20,21	0

## 6.3 Carbohydrates ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CPB	A	940	28/28	0.14	1.56	30,33,36,38	0

## 6.5 Other polymers

There are no such residues in this entry.