



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2023 – 05:48 PM EDT

PDB ID : 2ISW  
Title : Structure of Giardia fructose-1,6-biphosphate aldolase in complex with phosphoglycolohydroxamate  
Authors : Galkin, A.; Herzberg, O.  
Deposited on : 2006-10-18  
Resolution : 1.75 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.

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) : 1.13  
EDS : 2.35  
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) : 2.35

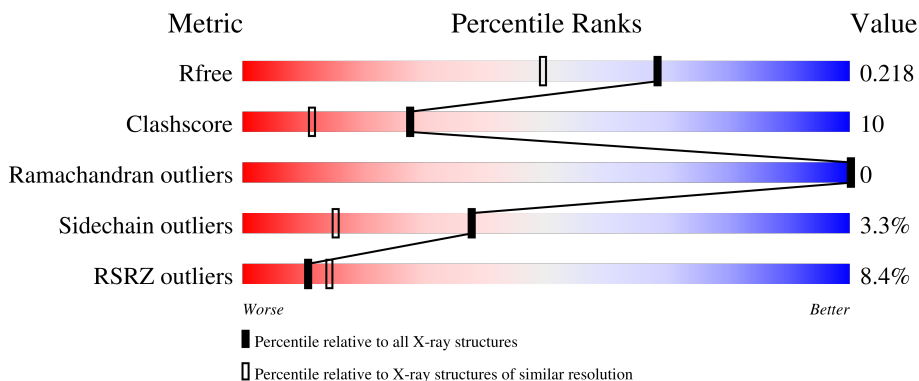
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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  $\geq 3$ , 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	323	 9% 79% 15% • 5%
1	B	323	 7% 70% 18% • 11%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4999 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.

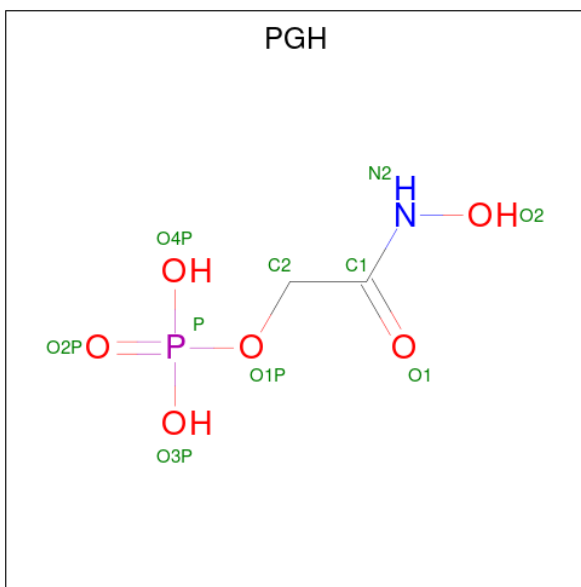
- Molecule 1 is a protein called Putative fructose-1,6-bisphosphate aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	307	2344	1488	404	435	17	0	0	0
1	B	288	2204	1401	378	408	17	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is PHOSPHOGLYCOLOHYDROXAMIC ACID (three-letter code: PGH) (formula: C<sub>2</sub>H<sub>6</sub>NO<sub>6</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	10	2	1	6	1	0	0

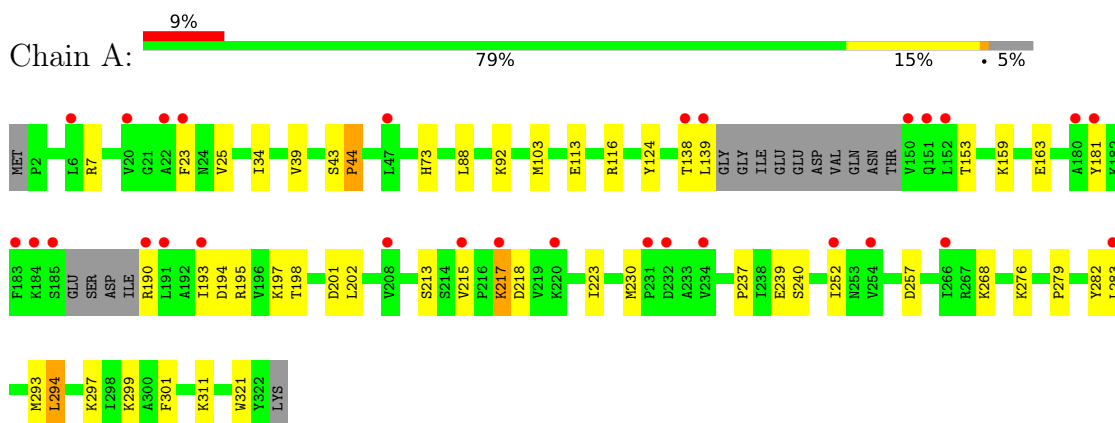
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	225	Total 225	O 225	0	0
4	B	215	Total 215	O 215	0	0

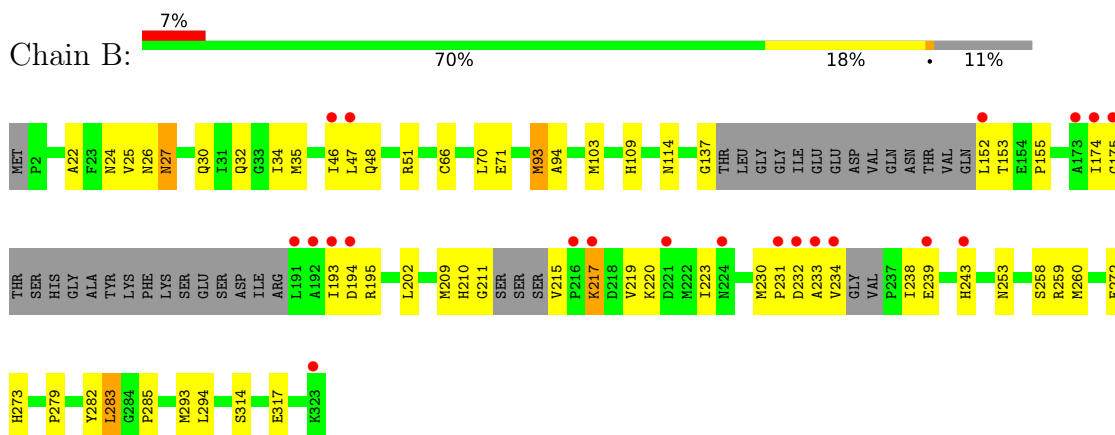
### 3 Residue-property plots [i](#)

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 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: Putative fructose-1,6-bisphosphate aldolase



- Molecule 1: Putative fructose-1,6-bisphosphate aldolase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.02Å 90.05Å 166.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.75 29.72 – 1.75	Depositor EDS
% Data completeness (in resolution range)	83.6 (30.00-1.75) 83.9 (29.72-1.75)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.69 (at 1.75Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.186 , 0.225 0.180 , 0.218	Depositor DCC
$R_{free}$ test set	2877 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.6	Xtrriage
Anisotropy	0.222	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 49.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.037 for -k,-h,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4999	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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: ZN, PGH

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	0.72	0/2386	0.84	1/3216 (0.0%)
1	B	0.77	0/2241	0.88	0/3015
All	All	0.74	0/4627	0.86	1/6231 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	PRO	CA-N-CD	-5.45	103.88	111.50

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	2344	0	2389	40	0
1	B	2204	0	2250	52	0
2	A	1	0	0	0	0
3	A	10	0	4	0	0
4	A	225	0	0	9	0
4	B	215	0	0	9	0
All	All	4999	0	4643	92	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 10.

All (92) 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:B:217:LYS:HA	1:B:217:LYS:HE3	1.49	0.93
1:B:32:GLN:HA	4:B:478:HOH:O	1.72	0.88
1:B:239:GLU:H	1:B:239:GLU:CD	1.78	0.86
1:A:276:LYS:HE2	4:A:452:HOH:O	1.75	0.86
1:A:190:ARG:HD2	4:A:473:HOH:O	1.74	0.85
1:A:268:LYS:HE2	4:A:490:HOH:O	1.81	0.81
1:B:71:GLU:HG3	4:B:475:HOH:O	1.82	0.79
1:B:93:MET:HE3	1:B:94:ALA:N	2.01	0.76
1:A:113:GLU:CD	1:A:116:ARG:HH21	1.93	0.72
1:B:215:VAL:HB	1:B:234:VAL:HG22	1.70	0.71
1:B:193:ILE:HD13	1:B:243:HIS:NE2	2.07	0.69
1:A:181:TYR:OH	1:A:230:MET:HG2	1.94	0.68
1:B:220:LYS:HZ2	1:B:230:MET:HB2	1.60	0.66
1:B:103:MET:CE	1:B:210:HIS:HE1	2.08	0.66
1:A:217:LYS:HA	1:A:217:LYS:HE3	1.78	0.66
1:B:259:ARG:CZ	4:B:393:HOH:O	2.42	0.66
1:A:299:LYS:HE3	4:A:505:HOH:O	1.98	0.64
1:B:272:GLU:HG2	1:B:273:HIS:CE1	2.34	0.63
1:A:213:SER:HB3	1:A:257:ASP:OD1	1.99	0.62
1:B:210:HIS:CD2	1:B:253:ASN:ND2	2.68	0.61
1:A:223:ILE:HG21	1:A:230:MET:CE	2.32	0.59
1:B:193:ILE:HG13	1:B:194:ASP:N	2.17	0.59
1:A:239:GLU:HG3	4:A:486:HOH:O	2.02	0.58
1:B:174:ILE:CG2	1:B:175:GLY:N	2.67	0.58
1:B:238:ILE:CG2	1:B:239:GLU:OE2	2.53	0.57
1:A:197:LYS:HE3	1:A:201:ASP:OD2	2.04	0.57
1:B:27:ASN:HD22	1:B:27:ASN:C	2.07	0.57
1:B:66:CYS:O	1:B:70:LEU:HD13	2.05	0.57
1:B:217:LYS:HA	1:B:217:LYS:CE	2.30	0.56
1:A:113:GLU:OE2	1:A:113:GLU:HA	2.06	0.56
1:B:153:THR:H	1:B:195:ARG:HH11	1.53	0.56
1:A:237:PRO:HG2	1:A:240:SER:OG	2.05	0.56
1:B:220:LYS:NZ	1:B:230:MET:HB2	2.21	0.55
1:B:233:ALA:O	1:B:234:VAL:C	2.43	0.55
1:B:239:GLU:CD	1:B:239:GLU:N	2.52	0.55
1:B:153:THR:H	1:B:195:ARG:NH1	2.05	0.55
1:B:174:ILE:HG22	1:B:175:GLY:N	2.22	0.55

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:LEU:CD1	4:A:445:HOH:O	2.55	0.54
1:B:137:GLY:HA3	4:B:536:HOH:O	2.09	0.53
1:A:116:ARG:HG2	1:A:116:ARG:HH11	1.74	0.52
1:B:259:ARG:NH1	4:B:393:HOH:O	2.44	0.51
1:B:238:ILE:HG22	1:B:239:GLU:OE2	2.10	0.51
1:B:137:GLY:C	4:B:482:HOH:O	2.49	0.51
1:A:92:LYS:HG2	1:A:124:TYR:CZ	2.46	0.50
1:B:109:HIS:HE1	4:B:348:HOH:O	1.93	0.50
1:A:159:LYS:O	1:A:163:GLU:HG3	2.12	0.49
1:B:26:ASN:HD22	1:B:30:GLN:HE22	1.60	0.49
1:B:223:ILE:HG21	1:B:230:MET:CE	2.42	0.49
1:B:26:ASN:H	1:B:30:GLN:NE2	2.10	0.49
1:A:239:GLU:HG3	4:A:484:HOH:O	2.14	0.48
1:B:26:ASN:H	1:B:30:GLN:HE21	1.62	0.48
1:B:152:LEU:HA	1:B:195:ARG:NH1	2.29	0.48
1:A:215:VAL:HG12	1:A:215:VAL:O	2.13	0.47
1:B:35:MET:HB2	4:B:478:HOH:O	2.14	0.47
1:A:213:SER:HB3	1:A:257:ASP:CG	2.34	0.47
1:A:193:ILE:HD12	1:A:194:ASP:N	2.29	0.47
1:A:293:MET:CE	1:A:294:LEU:HD13	2.45	0.47
1:B:24:ASN:HA	1:B:48:GLN:O	2.15	0.46
1:B:174:ILE:HG21	1:B:209:MET:CE	2.45	0.46
1:A:25:VAL:HG12	1:A:34:ILE:HD12	1.96	0.46
1:A:252:ILE:HD12	1:A:252:ILE:N	2.31	0.46
1:B:153:THR:N	1:B:195:ARG:NH1	2.64	0.45
1:A:198:THR:O	1:A:202:LEU:HD13	2.16	0.45
1:B:155:PRO:HB2	1:B:202:LEU:HD12	1.97	0.45
1:A:7:ARG:HD3	1:A:321:TRP:CE3	2.52	0.45
1:B:279:PRO:HA	1:B:282:TYR:CZ	2.51	0.44
1:A:193:ILE:HD12	1:A:193:ILE:C	2.38	0.44
1:B:210:HIS:O	1:B:211:GLY:C	2.56	0.44
1:A:153:THR:O	1:A:195:ARG:NH1	2.48	0.44
1:B:25:VAL:CG1	1:B:34:ILE:HD12	2.48	0.43
1:A:39:VAL:HG21	1:A:73:HIS:CE1	2.53	0.43
1:A:223:ILE:HG21	1:A:230:MET:HE3	1.99	0.43
1:A:197:LYS:O	1:A:197:LYS:HD2	2.18	0.43
1:B:25:VAL:CG1	1:B:34:ILE:CD1	2.97	0.43
1:B:51:ARG:HG3	4:B:385:HOH:O	2.17	0.43
1:B:174:ILE:HG21	1:B:209:MET:HE3	2.01	0.43
1:A:139:LEU:HD13	4:A:445:HOH:O	2.18	0.43
1:A:311:LYS:HE3	4:A:422:HOH:O	2.18	0.43

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:ARG:HG2	1:A:116:ARG:NH1	2.33	0.42
1:A:138:THR:O	1:A:139:LEU:HB2	2.19	0.42
1:B:103:MET:HE1	1:B:210:HIS:HE1	1.83	0.41
1:A:138:THR:O	1:A:139:LEU:CB	2.68	0.41
1:A:23:PHE:HB2	1:A:34:ILE:HD13	2.02	0.41
1:A:297:LYS:HG2	1:A:301:PHE:CZ	2.55	0.41
1:B:219:VAL:CG1	1:B:260:MET:HB3	2.51	0.41
1:B:258:SER:HA	1:B:293:MET:CE	2.51	0.41
1:B:314:SER:OG	1:B:317:GLU:HG3	2.21	0.41
1:A:88:LEU:HG	1:A:92:LYS:HE3	2.02	0.40
1:B:22:ALA:HA	1:B:46:ILE:HB	2.03	0.40
1:A:279:PRO:HA	1:A:282:TYR:CZ	2.55	0.40
1:B:282:TYR:CD1	1:B:283:LEU:HD13	2.57	0.40
1:B:230:MET:HA	1:B:231:PRO:HD3	1.98	0.40

There are no symmetry-related clashes.

## 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	301/323 (93%)	293 (97%)	8 (3%)	0	100 100
1	B	278/323 (86%)	270 (97%)	8 (3%)	0	100 100
All	All	579/646 (90%)	563 (97%)	16 (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	254/269 (94%)	247 (97%)	7 (3%)	43	20
1	B	238/269 (88%)	229 (96%)	9 (4%)	33	11
All	All	492/538 (91%)	476 (97%)	16 (3%)	38	15

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	SER
1	A	44	PRO
1	A	103	MET
1	A	217	LYS
1	A	218	ASP
1	A	283	LEU
1	A	294	LEU
1	B	27	ASN
1	B	47	LEU
1	B	93	MET
1	B	114	ASN
1	B	217	LYS
1	B	232	ASP
1	B	283	LEU
1	B	285	PRO
1	B	294	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	243	HIS
1	A	273	HIS
1	B	27	ASN
1	B	30	GLN
1	B	109	HIS
1	B	114	ASN
1	B	210	HIS
1	B	224	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	PGH	A	325	2	9,9,9	5.83	3 (33%)	10,12,12	3.80	3 (30%)

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	PGH	A	325	2	-	2/8/8/8	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	325	PGH	O1P-C2	14.75	1.53	1.43
3	A	325	PGH	C2-C1	8.73	1.68	1.51
3	A	325	PGH	O2-N2	2.30	1.45	1.40

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	325	PGH	O2-N2-C1	-7.53	108.67	119.79
3	A	325	PGH	O1-C1-N2	7.25	132.18	123.27
3	A	325	PGH	C2-C1-N2	-5.69	106.49	116.37

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	325	PGH	N2-C1-C2-O1P
3	A	325	PGH	O1-C1-C2-O1P

There are no ring outliers.

No monomer is involved in short contacts.

## 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	307/323 (95%)	0.36	29 (9%) <b>8</b> <b>11</b>	18, 28, 54, 78	0
1	B	288/323 (89%)	0.29	21 (7%) <b>15</b> <b>20</b>	16, 26, 62, 88	0
All	All	595/646 (92%)	0.33	50 (8%) <b>11</b> <b>14</b>	16, 27, 59, 88	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	175	GLY	9.3
1	B	233	ALA	8.7
1	B	232	ASP	8.6
1	B	152	LEU	8.4
1	B	234	VAL	8.3
1	B	191	LEU	8.3
1	A	183	PHE	7.3
1	A	150	VAL	6.8
1	B	192	ALA	6.2
1	A	184	LYS	5.9
1	A	185	SER	5.8
1	B	193	ILE	5.7
1	B	174	ILE	5.1
1	A	181	TYR	4.6
1	B	231	PRO	3.7
1	A	232	ASP	3.5
1	A	193	ILE	3.4
1	A	252	ILE	3.4
1	A	139	LEU	3.4
1	A	190	ARG	3.3
1	A	208	VAL	3.2
1	A	234	VAL	3.1
1	A	191	LEU	3.1
1	A	217	LYS	3.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	180	ALA	3.0
1	B	221	ASP	3.0
1	B	224	ASN	2.8
1	A	151	GLN	2.8
1	A	231	PRO	2.8
1	B	173	ALA	2.7
1	A	254	VAL	2.6
1	A	152	LEU	2.6
1	B	217	LYS	2.4
1	A	283	LEU	2.3
1	A	22	ALA	2.3
1	A	6	LEU	2.3
1	B	47	LEU	2.3
1	A	23	PHE	2.3
1	B	216	PRO	2.3
1	A	47	LEU	2.3
1	B	239	GLU	2.3
1	A	266	ILE	2.3
1	B	46	ILE	2.3
1	B	323	LYS	2.2
1	B	194	ASP	2.2
1	A	20	VAL	2.2
1	B	243	HIS	2.2
1	A	215	VAL	2.1
1	A	138	THR	2.1
1	A	220	LYS	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 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	PGH	A	325	10/10	0.97	0.09	36,49,58,59	0
2	ZN	A	326	1/1	0.99	0.16	56,56,56,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.