



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 07:20 PM GMT

PDB ID : 1B57
Title : CLASS II FRUCTOSE-1,6-BISPHOSPHATEALDOLASE IN COMPLEX
WITH PHOSPHOGLYCOLOHYDROXAMATE
Authors : Hall, D.R.; Hunter, W.N.
Deposited on : 1999-01-12
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
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

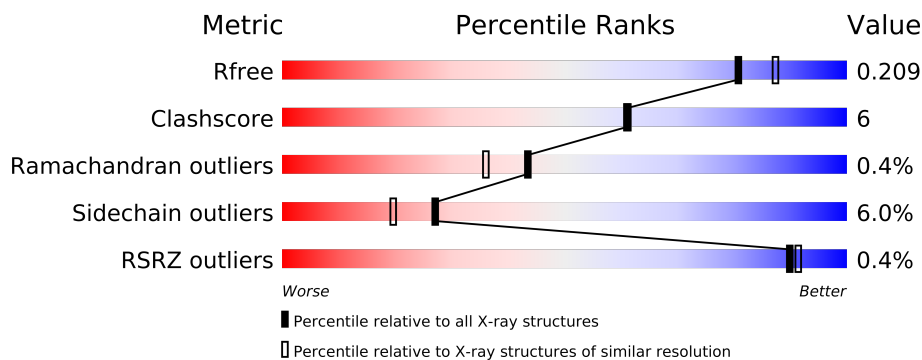
The following versions of software and data (see [references](#)) were used in the production of this report:

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 ≥ 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	358	
1	B	358	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5503 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 PROTEIN (FRUCTOSE-BISPHOSPHATEALDOLASE II).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	0	0	0
			2624	1665	440	509	10			
1	B	346	Total	C	N	O	S	0	0	0
			2624	1665	440	509	10			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Zn	0	0
			3	3		
2	A	4	Total	Zn	0	0
			4	4		

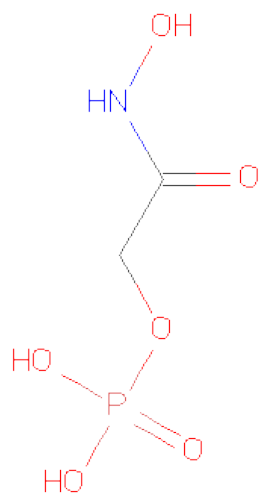
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Na	0	0
			1	1		
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is PHOSPHOGLYCOLOHYDROXAMICACID (three-letter code: PGH) (formula: C₂H₆NO₆P).



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

- Molecule 6 is water.

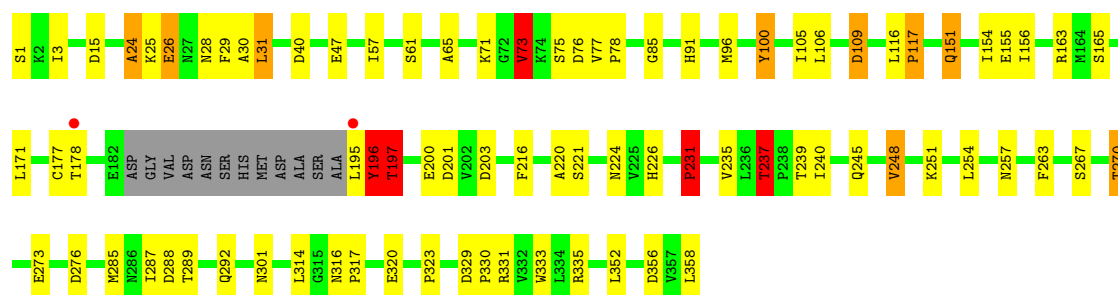
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	113	Total	O	0	0
			113	113		
6	B	112	Total	O	0	0
			112	112		

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.

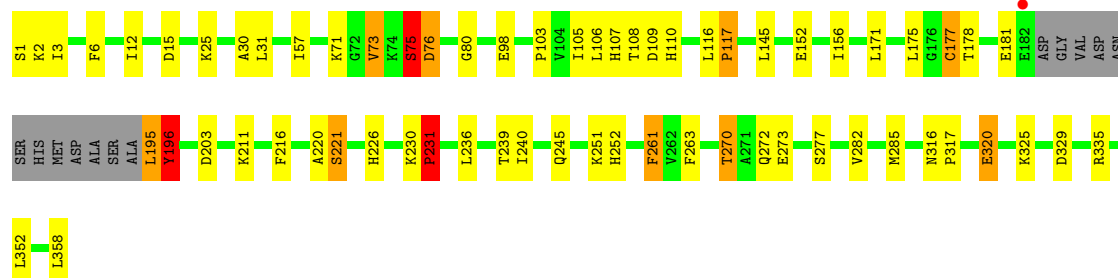
• Molecule 1: PROTEIN (FRUCTOSE-BISPHOSPHATEALDOLASE II)

Chain A: 



• Molecule 1: PROTEIN (FRUCTOSE-BISPHOSPHATEALDOLASE II)

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	78.24Å 78.24Å 289.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.00 67.76 – 2.00	Depositor EDS
% Data completeness (in resolution range)	78.5 (30.00-2.00) 76.3 (67.76-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.00Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.192 , 0.230 0.172 , 0.209	Depositor DCC
R_{free} test set	2691 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.2	EDS
Estimated twinning fraction	0.039 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 55402 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5503	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: NA, ZN, PGH, CL

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	0.65	0/2683	1.33	23/3648 (0.6%)
1	B	0.65	0/2683	1.35	15/3648 (0.4%)
All	All	0.65	0/5366	1.34	38/7296 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	18
1	B	0	13
All	All	0	31

There are no bond length outliers.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	196	TYR	CB-CG-CD2	8.90	126.34	121.00
1	A	331	ARG	NE-CZ-NH1	-8.63	115.98	120.30
1	B	15	ASP	CB-CG-OD1	8.11	125.60	118.30
1	A	163	ARG	NE-CZ-NH2	-8.09	116.26	120.30
1	B	75	SER	N-CA-CB	7.92	122.38	110.50
1	A	26	GLU	CB-CA-C	7.06	124.52	110.40
1	A	196	TYR	CB-CG-CD2	6.59	124.95	121.00
1	B	15	ASP	CB-CG-OD2	-6.55	112.41	118.30
1	B	108	THR	CA-CB-CG2	-6.55	103.23	112.40
1	A	73	VAL	CB-CA-C	-6.53	98.99	111.40
1	A	40	ASP	CB-CG-OD1	6.39	124.05	118.30
1	A	15	ASP	CB-CG-OD1	6.34	124.01	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	237	THR	N-CA-CB	-6.30	98.33	110.30
1	B	31	LEU	CA-CB-CG	6.28	129.74	115.30
1	A	73	VAL	N-CA-CB	6.26	125.27	111.50
1	A	329	ASP	CB-CG-OD1	6.25	123.93	118.30
1	B	329	ASP	CB-CG-OD1	6.15	123.84	118.30
1	A	335	ARG	CD-NE-CZ	6.01	132.02	123.60
1	A	237	THR	CA-CB-CG2	5.93	120.70	112.40
1	A	231	PRO	N-CA-C	5.87	127.37	112.10
1	B	107	HIS	N-CA-CB	-5.83	100.10	110.60
1	A	109	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	B	320	GLU	CB-CA-C	-5.70	99.00	110.40
1	A	197	THR	CA-CB-CG2	-5.58	104.59	112.40
1	A	26	GLU	CA-CB-CG	5.51	125.52	113.40
1	A	201	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	31	LEU	CA-CB-CG	5.46	127.85	115.30
1	A	73	VAL	CG1-CB-CG2	5.44	119.61	110.90
1	A	276	ASP	CB-CG-OD2	-5.42	113.42	118.30
1	A	100	TYR	CG-CD1-CE1	-5.42	116.96	121.30
1	B	335	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	B	76	ASP	CB-CG-OD1	5.29	123.06	118.30
1	A	356	ASP	CB-CG-OD1	5.27	123.05	118.30
1	B	181	GLU	CA-CB-CG	5.25	124.95	113.40
1	B	181	GLU	OE1-CD-OE2	-5.23	117.02	123.30
1	B	221	SER	N-CA-CB	5.19	118.28	110.50
1	B	196	TYR	CB-CA-C	-5.17	100.06	110.40
1	A	195	LEU	CA-C-N	5.15	128.53	117.20

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	117	PRO	Mainchain
1	A	151	GLN	Mainchain
1	A	156	ILE	Mainchain
1	A	165	SER	Mainchain
1	A	177	CYS	Mainchain
1	A	197	THR	Mainchain
1	A	220	ALA	Mainchain
1	A	24	ALA	Mainchain
1	A	248	VAL	Mainchain
1	A	25	LYS	Mainchain
1	A	267	SER	Mainchain

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Mol	Chain	Res	Type	Group
1	A	301	ASN	Mainchain
1	A	320	GLU	Mainchain
1	A	333	TRP	Mainchain
1	A	47	GLU	Mainchain
1	A	61	SER	Mainchain
1	A	73	VAL	Mainchain
1	A	96	MET	Mainchain
1	B	1	SER	Mainchain
1	B	117	PRO	Mainchain
1	B	175	LEU	Mainchain
1	B	195	LEU	Mainchain
1	B	196	TYR	Mainchain
1	B	220	ALA	Mainchain
1	B	231	PRO	Mainchain
1	B	25	LYS	Mainchain
1	B	261	PHE	Mainchain
1	B	285	MET	Mainchain
1	B	320	GLU	Mainchain
1	B	6	PHE	Mainchain
1	B	98	GLU	Mainchain

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	2624	0	2520	30	0
1	B	2624	0	2520	32	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	1	0
5	A	10	0	3	1	0
5	B	10	0	3	1	0
6	A	113	0	0	1	0
6	B	112	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5503	0	5046	60	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 6.

All (60) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:270:THR:HG22	1:A:273:GLU:H	1.28	0.98
1:B:270:THR:HG22	1:B:273:GLU:H	1.26	0.97
1:B:12:ILE:HD11	1:B:103:PRO:HB2	1.59	0.84
1:A:77:VAL:HB	1:A:78:PRO:HD2	1.62	0.80
1:B:203:ASP:OD2	1:B:251:LYS:NZ	2.18	0.73
1:B:251:LYS:NZ	1:B:252:HIS:NE2	2.37	0.70
1:B:203:ASP:CG	1:B:251:LYS:HZ2	1.95	0.70
1:A:316:ASN:HB2	1:A:317:PRO:CD	2.21	0.70
1:B:270:THR:HG23	1:B:272:GLN:H	1.58	0.68
1:A:316:ASN:HB2	1:A:317:PRO:HD2	1.81	0.62
1:B:203:ASP:OD1	1:B:251:LYS:NZ	2.32	0.61
1:A:100:TYR:CE1	1:B:73:VAL:HG13	2.40	0.56
1:B:270:THR:HB	1:B:273:GLU:OE1	2.05	0.56
1:A:178:THR:HG21	1:A:226:HIS:CE1	2.41	0.56
1:B:30:ALA:HB3	1:B:352:LEU:HD22	1.90	0.53
1:A:65:ALA:O	1:A:85:GLY:HA3	2.09	0.53
1:A:285:MET:CE	1:A:287:ILE:HD11	2.39	0.52
1:A:24:ALA:HB1	1:A:29:PHE:O	2.11	0.51
1:B:270:THR:CG2	1:B:272:GLN:H	2.23	0.51
1:B:116:LEU:N	1:B:117:PRO:CD	2.74	0.50
1:B:178:THR:HG21	1:B:226:HIS:CE1	2.47	0.49
1:B:277:SER:HB3	1:B:282:VAL:HG21	1.93	0.49
1:B:195:LEU:O	1:B:196:TYR:HD1	1.96	0.48
1:B:251:LYS:HG2	1:B:252:HIS:CD2	2.48	0.48
1:A:196:TYR:N	1:A:196:TYR:CD1	2.82	0.48
1:B:316:ASN:HB2	1:B:317:PRO:CD	2.44	0.47
1:B:230:LYS:HA	1:B:231:PRO:HD3	1.74	0.47
1:A:91:HIS:CE1	6:A:437:HOH:O	2.67	0.47
1:A:203:ASP:OD1	1:A:251:LYS:NZ	2.47	0.47
1:B:177:CYS:HB3	6:B:393:HOH:O	2.13	0.47
1:A:316:ASN:CB	1:A:317:PRO:CD	2.89	0.46
1:B:203:ASP:CG	1:B:251:LYS:NZ	2.62	0.46
1:A:237:THR:HG22	1:A:240:ILE:HG12	1.97	0.46
1:A:30:ALA:HB3	1:A:352:LEU:HD22	1.97	0.45
1:B:75:SER:OG	1:B:80:GLY:HA3	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:196:TYR:N	1:A:196:TYR:HD1	2.14	0.45
1:A:116:LEU:N	1:A:117:PRO:CD	2.79	0.45
1:A:1:SER:HB3	4:A:365:CL:CL	2.54	0.45
1:A:314:LEU:HD23	1:A:323:PRO:HA	1.99	0.45
1:A:109:ASP:OD2	5:A:359:PGH:O2	2.34	0.44
1:A:248:VAL:HG12	1:A:254:LEU:HD12	1.98	0.44
1:B:245:GLN:HG2	1:B:261:PHE:HE2	1.83	0.44
1:A:171:LEU:O	1:A:216:PHE:HA	2.18	0.44
1:B:57:ILE:HG12	1:B:105:ILE:HB	2.00	0.43
1:A:57:ILE:HG12	1:A:105:ILE:HB	2.00	0.43
1:A:245:GLN:CD	1:A:257:ASN:HA	2.37	0.43
1:B:3:ILE:HB	1:B:358:LEU:HA	2.01	0.42
1:B:251:LYS:HG2	1:B:252:HIS:NE2	2.34	0.42
1:A:151:GLN:O	1:A:155:GLU:HG3	2.20	0.42
1:B:171:LEU:O	1:B:216:PHE:HA	2.18	0.42
1:B:240:ILE:HG23	6:B:407:HOH:O	2.19	0.42
1:A:200:GLU:H	1:A:200:GLU:CD	2.24	0.42
1:B:236:LEU:HD12	1:B:273:GLU:HB3	2.02	0.41
1:A:289:THR:OG1	1:B:325:LYS:NZ	2.52	0.41
1:A:3:ILE:HB	1:A:358:LEU:HA	2.02	0.41
1:B:109:ASP:OD2	5:B:359:PGH:O2	2.38	0.41
1:A:288:ASP:O	1:A:292:GLN:HG3	2.21	0.41
1:B:145:LEU:CD1	1:B:156:ILE:HB	2.51	0.41
1:A:203:ASP:CG	1:A:251:LYS:HZ2	2.23	0.40
1:B:178:THR:HG21	1:B:226:HIS:ND1	2.35	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	342/358 (96%)	328 (96%)	13 (4%)	1 (0%)	50	44
1	B	342/358 (96%)	332 (97%)	8 (2%)	2 (1%)	33	24
All	All	684/716 (96%)	660 (96%)	21 (3%)	3 (0%)	43	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	231	PRO
1	B	231	PRO
1	B	110	HIS

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	276/296 (93%)	256 (93%)	20 (7%)	21	13
1	B	276/296 (93%)	263 (95%)	13 (5%)	36	29
All	All	552/592 (93%)	519 (94%)	33 (6%)	27	20

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

Mol	Chain	Res	Type
1	A	26	GLU
1	A	28	ASN
1	A	31	LEU
1	A	71	LYS
1	A	73	VAL
1	A	75	SER
1	A	76	ASP
1	A	106	LEU
1	A	154	ILE
1	A	196	TYR
1	A	197	THR
1	A	221	SER
1	A	224	ASN
1	A	231	PRO
1	A	235	VAL
1	A	237	THR
1	A	239	THR
1	A	263	PHE
1	A	270	THR
1	A	330	PRO
1	B	2	LYS

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Mol	Chain	Res	Type
1	B	71	LYS
1	B	73	VAL
1	B	75	SER
1	B	76	ASP
1	B	106	LEU
1	B	152	GLU
1	B	177	CYS
1	B	211	LYS
1	B	221	SER
1	B	239	THR
1	B	263	PHE
1	B	270	THR

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

Mol	Chain	Res	Type
1	A	18	GLN
1	A	62	ASN
1	A	79	GLN
1	A	95	GLN
1	B	18	GLN
1	B	62	ASN
1	B	79	GLN
1	B	272	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 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
5	PGH	A	359	3,2	9,9,9	1.59	2 (22%)	12,12,12	2.14	3 (25%)
5	PGH	B	359	3,2	9,9,9	2.31	2 (22%)	12,12,12	3.28	5 (41%)

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
5	PGH	A	359	3,2	-	0/8/8/8	0/0/0/0
5	PGH	B	359	3,2	-	0/8/8/8	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	359	PGH	C1-N2	6.02	1.38	1.32
5	A	359	PGH	C1-N2	3.19	1.35	1.32
5	A	359	PGH	O1P-C2	-2.30	1.41	1.43
5	B	359	PGH	O1P-C2	-2.10	1.41	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	359	PGH	O2-N2-C1	-9.46	105.56	119.57
5	A	359	PGH	O2-N2-C1	-4.37	113.10	119.57
5	A	359	PGH	O1-C1-N2	-3.98	118.67	123.47
5	B	359	PGH	O1-C1-N2	-3.32	119.47	123.47
5	A	359	PGH	O1P-C2-C1	2.90	114.97	110.20
5	B	359	PGH	C2-C1-N2	-2.66	111.62	116.31
5	B	359	PGH	O1P-C2-C1	2.36	114.09	110.20
5	B	359	PGH	O3P-P-O2P	2.12	117.37	110.44

There are no chirality outliers.

There are no torsion outliers.

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, 95th 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 ²)	Q<0.9
1	A	346/358 (96%)	-0.57	2 (0%) 86 88	12, 24, 48, 68	0
1	B	346/358 (96%)	-0.53	1 (0%) 91 93	11, 23, 48, 68	0
All	All	692/716 (96%)	-0.55	3 (0%) 90 91	11, 24, 48, 68	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	195	LEU	4.2
1	B	182	GLU	3.0
1	A	178	THR	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

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, 95th 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(\AA^2)	Q<0.9
5	PGH	A	359	10/10	0.09	0.71	18,20,21,22	0
2	ZN	B	360	1/1	0.09	0.46	17,17,17,17	0
3	NA	B	364	1/1	0.09	0.25	21,21,21,21	0
2	ZN	A	360	1/1	0.10	-0.12	18,18,18,18	0
5	PGH	B	359	10/10	0.08	-0.43	14,16,17,20	0
3	NA	A	364	1/1	0.07	-0.80	22,22,22,22	0
2	ZN	A	361	1/1	0.05	-1.10	30,30,30,30	0
2	ZN	B	361	1/1	0.06	-1.24	28,28,28,28	0
4	CL	A	365	1/1	0.09	-1.38	22,22,22,22	0
2	ZN	A	362	1/1	0.05	-2.08	49,49,49,49	0
2	ZN	B	362	1/1	0.05	-2.28	47,47,47,47	0
2	ZN	A	363	1/1	0.07	-2.73	28,28,28,28	0

6.5 Other polymers ⓘ

There are no such residues in this entry.