



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 07:48 PM GMT

PDB ID : 1TPC
Title : OFFSET OF A CATALYTIC LESION BY A BOUND WATER SOLUBLE
Authors : Zhang, Z.; Sugio, S.; Komives, E.A.; Liu, K.D.; Knowles, J.R.; Petsko, G.A.;
Ringe, D.
Deposited on : 1994-02-03
Resolution : 1.90 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>

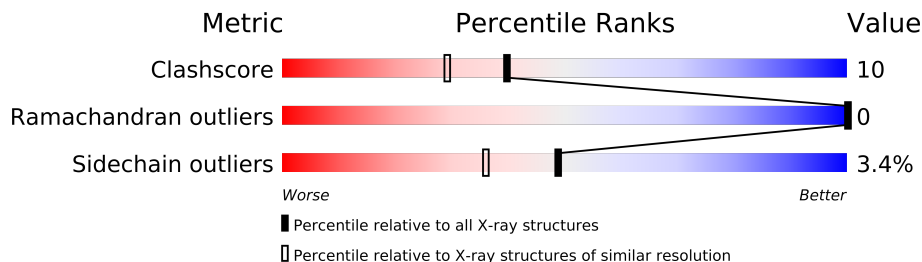
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
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 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	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (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 ≥ 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1	247	
1	2	247	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 3966 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.

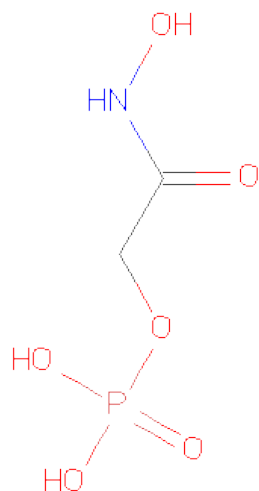
- Molecule 1 is a protein called TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	245	Total	C	N	O	S	0	0	0
			1856	1177	325	348	6			
1	2	245	Total	C	N	O	S	0	0	0
			1856	1177	325	348	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	96	PRO	SER	CONFLICT	UNP P00940
1	165	ASP	GLU	CONFLICT	UNP P00940
1	194	THR	SER	CONFLICT	UNP P00940
2	96	PRO	SER	CONFLICT	UNP P00940
2	165	ASP	GLU	CONFLICT	UNP P00940
2	194	THR	SER	CONFLICT	UNP P00940

- Molecule 2 is PHOSPHOGLYCOLOHYDROXAMICACID (three-letter code: PGH) (formula: C₂H₆NO₆P).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	1	116	Total	O	0	0
			116	116		
3	2	118	Total	O	0	0
			118	118		

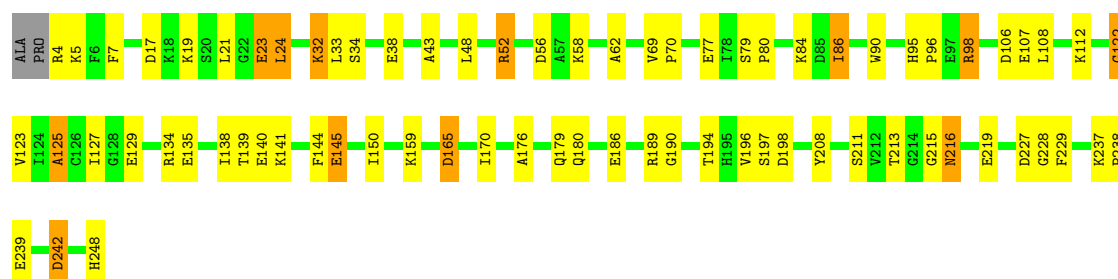
3 Residue-property plots

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.

Note EDS was not executed.

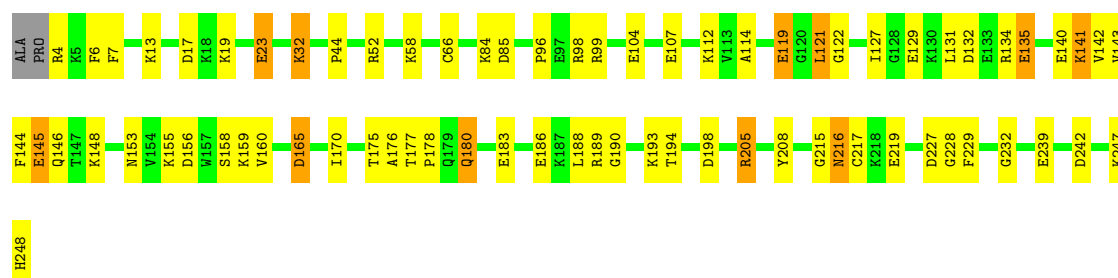
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain 1: 



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain 2: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	136.40Å 73.90Å 55.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.182 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3966	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1	1.10	7/1892 (0.4%)	1.70	29/2555 (1.1%)
1	2	1.12	12/1892 (0.6%)	1.81	35/2555 (1.4%)
All	All	1.11	19/3784 (0.5%)	1.75	64/5110 (1.3%)

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	1	0	1
1	2	0	1
All	All	0	2

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	145	GLU	CD-OE2	8.48	1.34	1.25
1	1	107	GLU	CD-OE2	7.26	1.33	1.25
1	1	219	GLU	CD-OE1	7.26	1.33	1.25
1	1	38	GLU	CD-OE2	6.95	1.33	1.25
1	2	186	GLU	CD-OE1	6.78	1.33	1.25
1	2	129	GLU	CD-OE1	6.60	1.32	1.25
1	2	23	GLU	CD-OE1	6.55	1.32	1.25
1	1	23	GLU	CD-OE1	6.46	1.32	1.25
1	1	135	GLU	CD-OE2	6.43	1.32	1.25
1	2	107	GLU	CD-OE2	6.43	1.32	1.25
1	2	145	GLU	CD-OE2	6.24	1.32	1.25
1	2	119	GLU	CD-OE1	6.04	1.32	1.25
1	2	183	GLU	CD-OE2	5.76	1.31	1.25
1	2	135	GLU	CD-OE2	5.66	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	140	GLU	CD-OE1	5.64	1.31	1.25
1	1	77	GLU	CD-OE1	5.47	1.31	1.25
1	2	239	GLU	CD-OE2	-5.40	1.19	1.25
1	2	104	GLU	CD-OE1	5.28	1.31	1.25
1	2	104	GLU	CD-OE2	-5.19	1.20	1.25

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	165	ASP	CB-CG-OD2	21.58	137.72	118.30
1	1	52	ARG	NE-CZ-NH2	-15.32	112.64	120.30
1	2	165	ASP	CB-CG-OD1	-14.14	105.57	118.30
1	2	52	ARG	NE-CZ-NH1	12.48	126.54	120.30
1	2	227	ASP	CB-CG-OD2	12.36	129.42	118.30
1	2	99	ARG	NE-CZ-NH2	11.29	125.94	120.30
1	1	56	ASP	CB-CG-OD1	10.86	128.07	118.30
1	2	189	ARG	NE-CZ-NH1	-10.62	114.99	120.30
1	2	215	GLY	C-N-CA	9.84	146.30	121.70
1	2	227	ASP	CB-CG-OD1	-9.24	109.99	118.30
1	2	216	ASN	CB-CA-C	-8.73	92.95	110.40
1	2	4	ARG	NE-CZ-NH2	-8.71	115.95	120.30
1	2	4	ARG	NE-CZ-NH1	8.57	124.59	120.30
1	1	134	ARG	NE-CZ-NH1	-8.37	116.11	120.30
1	1	165	ASP	CB-CG-OD2	8.35	125.81	118.30
1	1	216	ASN	CB-CA-C	-7.83	94.74	110.40
1	2	98	ARG	CD-NE-CZ	-7.65	112.89	123.60
1	1	106	ASP	CB-CG-OD2	-7.55	111.51	118.30
1	2	85	ASP	CB-CG-OD2	7.29	124.86	118.30
1	1	242	ASP	CB-CG-OD1	7.08	124.67	118.30
1	2	135	GLU	OE1-CD-OE2	6.93	131.61	123.30
1	2	216	ASN	CB-CG-OD1	6.68	134.96	121.60
1	2	216	ASN	OD1-CG-ND2	-6.65	106.60	121.90
1	1	189	ARG	NE-CZ-NH1	-6.62	116.99	120.30
1	1	125	ALA	N-CA-CB	-6.52	100.97	110.10
1	1	215	GLY	C-N-CA	6.49	137.93	121.70
1	2	99	ARG	NH1-CZ-NH2	-6.46	112.29	119.40
1	1	43	ALA	N-CA-CB	-6.35	101.21	110.10
1	1	84	LYS	CB-CA-C	-6.34	97.72	110.40
1	2	165	ASP	N-CA-CB	-6.31	99.24	110.60
1	1	216	ASN	CB-CG-ND2	6.13	131.41	116.70
1	2	232	GLY	CA-C-O	6.13	131.63	120.60
1	1	189	ARG	NE-CZ-NH2	6.11	123.35	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	98	ARG	NE-CZ-NH1	-6.08	117.26	120.30
1	2	205	ARG	CD-NE-CZ	5.96	131.94	123.60
1	1	129	GLU	OE1-CD-OE2	-5.92	116.19	123.30
1	1	145	GLU	CG-CD-OE1	5.89	130.09	118.30
1	1	4	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	2	239	GLU	CG-CD-OE1	-5.76	106.77	118.30
1	1	23	GLU	CG-CD-OE1	-5.70	106.89	118.30
1	1	122	GLY	N-CA-C	-5.65	98.98	113.10
1	2	160	VAL	CA-CB-CG1	5.59	119.28	110.90
1	1	227	ASP	CB-CG-OD2	5.55	123.30	118.30
1	2	17	ASP	CB-CG-OD1	5.52	123.27	118.30
1	1	52	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	1	186	GLU	CG-CD-OE1	-5.49	107.32	118.30
1	1	107	GLU	CG-CD-OE2	-5.46	107.37	118.30
1	1	216	ASN	CB-CG-OD1	-5.42	110.76	121.60
1	2	208	TYR	CB-CG-CD1	-5.36	117.78	121.00
1	1	77	GLU	OE1-CD-OE2	5.35	129.72	123.30
1	2	180	GLN	OE1-CD-NE2	5.33	134.17	121.90
1	2	144	PHE	CB-CG-CD2	-5.31	117.08	120.80
1	2	239	GLU	OE1-CD-OE2	5.30	129.66	123.30
1	2	242	ASP	CB-CG-OD2	5.29	123.06	118.30
1	2	121	LEU	CA-CB-CG	5.26	127.41	115.30
1	2	217	CYS	CA-CB-SG	5.25	123.46	114.00
1	2	135	GLU	CG-CD-OE2	-5.25	107.80	118.30
1	1	123	VAL	CG1-CB-CG2	-5.21	102.57	110.90
1	2	122	GLY	N-CA-C	-5.19	100.13	113.10
1	2	205	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	1	17	ASP	CB-CA-C	5.10	120.61	110.40
1	2	4	ARG	CD-NE-CZ	5.05	130.67	123.60
1	2	229	PHE	O-C-N	5.02	130.74	122.70
1	1	198	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	98	ARG	Sidechain
1	2	134	ARG	Sidechain

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	1	1856	0	1863	36	0
1	2	1856	0	1862	32	2
2	1	10	0	4	3	0
2	2	10	0	4	0	0
3	1	116	0	0	4	0
3	2	118	0	0	5	0
All	All	3966	0	3733	71	2

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 10.

All (71) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:1:32:LYS:H	1:1:32:LYS:HD3	1.00	1.08
1:2:58:LYS:HB3	3:2:487:HOH:O	1.63	0.97
1:1:32:LYS:N	1:1:32:LYS:HD3	1.80	0.95
1:1:32:LYS:H	1:1:32:LYS:CD	1.79	0.95
1:2:175:THR:HG21	1:2:216:ASN:ND2	1.93	0.83
1:2:159:LYS:HB2	3:2:453:HOH:O	1.86	0.75
2:1:250:PGH:N2	3:1:326:HOH:O	2.20	0.74
1:1:140:GLU:HG2	1:1:144:PHE:CE2	2.24	0.71
1:1:48:LEU:HB3	1:1:86:ILE:HD12	1.74	0.70
1:2:127:ILE:HD11	1:2:188:LEU:HD11	1.76	0.68
1:2:19:LYS:O	1:2:23:GLU:HG3	1.95	0.66
2:1:250:PGH:O2	3:1:326:HOH:O	2.12	0.65
1:2:176:ALA:HB1	1:2:180:GLN:HG3	1.79	0.64
1:2:156:ASP:O	3:2:453:HOH:O	2.14	0.64
1:2:141:LYS:NZ	1:2:145:GLU:OE1	2.29	0.64
2:1:250:PGH:C1	3:1:326:HOH:O	2.44	0.63
1:2:141:LYS:C	1:2:141:LYS:HD3	2.18	0.63
1:1:141:LYS:O	1:1:145:GLU:HG2	1.98	0.63
1:1:32:LYS:O	1:1:32:LYS:HG2	1.98	0.62
1:2:7:PHE:O	1:2:228:GLY:HA3	2.00	0.62
1:1:237:LYS:HB3	1:1:238:PRO:HD2	1.81	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:2:114:ALA:HB2	1:2:153:ASN:HB3	1.83	0.60
1:1:176:ALA:HB1	1:1:180:GLN:HG3	1.85	0.59
1:2:177:THR:H	1:2:180:GLN:HG2	1.66	0.59
1:1:213:THR:H	1:1:216:ASN:HB2	1.68	0.59
1:2:177:THR:H	1:2:180:GLN:CG	2.16	0.59
1:1:48:LEU:HB3	1:1:86:ILE:CD1	2.33	0.57
1:2:131:LEU:O	1:2:135:GLU:HG3	2.05	0.57
1:1:239:GLU:O	1:1:242:ASP:N	2.38	0.56
1:2:247:LYS:HE3	3:2:349:HOH:O	2.07	0.55
1:2:127:ILE:HD11	1:2:188:LEU:CD1	2.37	0.54
1:2:66:CYS:O	1:2:112:LYS:HD3	2.06	0.54
1:1:34:SER:HB2	1:1:248:HIS:NE2	2.22	0.54
1:2:32:LYS:NZ	3:2:415:HOH:O	2.40	0.54
1:1:96:PRO:HG2	1:1:170:ILE:CD1	2.38	0.53
1:1:7:PHE:O	1:1:228:GLY:HA3	2.08	0.53
1:1:211:SER:O	1:1:216:ASN:ND2	2.43	0.52
1:1:62:ALA:HB2	1:1:90:TRP:HB2	1.91	0.52
1:2:141:LYS:HD3	1:2:142:VAL:N	2.26	0.51
1:2:127:ILE:HD12	1:2:143:VAL:HB	1.93	0.51
1:1:208:TYR:O	1:1:229:PHE:HA	2.11	0.51
1:2:177:THR:N	1:2:180:GLN:HG2	2.28	0.49
1:2:190:GLY:O	1:2:194:THR:HG23	2.12	0.49
1:1:95:HIS:CG	1:1:96:PRO:HD2	2.47	0.49
1:2:96:PRO:HG2	1:2:170:ILE:HD11	1.95	0.48
1:1:19:LYS:O	1:1:23:GLU:HG3	2.13	0.48
1:2:193:LYS:HE2	1:2:198:ASP:OD1	2.14	0.47
1:1:122:GLY:HA2	1:1:159:LYS:HB3	1.97	0.47
1:2:142:VAL:O	1:2:146:GLN:HG3	2.15	0.47
1:2:247:LYS:C	1:2:248:HIS:HD2	2.19	0.46
1:1:69:VAL:HB	1:1:70:PRO:HD2	1.98	0.45
1:2:13:LYS:O	1:2:44:PRO:HG3	2.16	0.45
1:1:190:GLY:O	1:1:194:THR:HG23	2.17	0.45
1:1:52:ARG:NE	1:1:52:ARG:HA	2.32	0.45
1:1:79:SER:HB2	1:1:80:PRO:HD2	1.99	0.44
1:1:196:VAL:O	1:1:197:SER:HB3	2.16	0.44
1:1:24:LEU:C	1:1:24:LEU:HD23	2.38	0.44
1:1:108:LEU:HG	1:1:112:LYS:HE3	1.99	0.44
1:2:180:GLN:HE21	1:2:180:GLN:HB3	1.01	0.43
1:2:84:LYS:HG3	1:2:121:LEU:HD21	2.02	0.42
1:2:84:LYS:HD2	1:2:119:GLU:O	2.20	0.42
1:1:62:ALA:CB	1:1:90:TRP:HB2	2.49	0.42
1:1:5:LYS:NZ	3:1:521:HOH:O	2.34	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:1:138:ILE:O	1:1:139:THR:C	2.56	0.41
1:1:48:LEU:CB	1:1:86:ILE:HD12	2.48	0.41
1:2:6:PHE:CE1	1:2:228:GLY:HA2	2.55	0.41
1:1:33:LEU:O	1:1:34:SER:C	2.57	0.41
1:1:96:PRO:HG2	1:1:170:ILE:HD11	2.02	0.41
1:1:21:LEU:HD23	1:1:21:LEU:HA	1.83	0.40
1:2:178:PRO:HG2	1:2:219:GLU:HG2	2.04	0.40
1:1:125:ALA:HB1	1:1:150:ILE:HD13	2.04	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	Distance(Å)	Clash(Å)
1:2:19:LYS:NZ	1:2:194:THR:O[1_554]	1.56	0.64
1:2:132:ASP:OD2	1:2:155:LYS:NZ[3_546]	1.88	0.32

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	1	243/247 (98%)	235 (97%)	8 (3%)	0	100	100
1	2	243/247 (98%)	234 (96%)	9 (4%)	0	100	100
All	All	486/494 (98%)	469 (96%)	17 (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	1	191/192 (100%)	184 (96%)	7 (4%)	45	32
1	2	191/192 (100%)	185 (97%)	6 (3%)	52	41
All	All	382/384 (100%)	369 (97%)	13 (3%)	49	36

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	24	LEU
1	1	32	LYS
1	1	58	LYS
1	1	86	ILE
1	1	127	ILE
1	1	165	ASP
1	1	179	GLN
1	2	32	LYS
1	2	141	LYS
1	2	148	LYS
1	2	158	SER
1	2	165	ASP
1	2	205	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	111	GLN
1	1	179	GLN
1	2	53	GLN
1	2	111	GLN
1	2	115	HIS
1	2	179	GLN
1	2	180	GLN
1	2	216	ASN
1	2	248	HIS

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 ⓘ

2 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	PGH	1	250	-	9,9,9	2.96	4 (44%)	12,12,12	2.01	5 (41%)
2	PGH	2	250	-	9,9,9	2.87	2 (22%)	12,12,12	1.27	2 (16%)

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	PGH	1	250	-	-	0/8/8/8	0/0/0/0
2	PGH	2	250	-	-	0/8/8/8	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	250	PGH	P-O3P	6.68	1.79	1.54
2	1	250	PGH	P-O2P	6.15	1.71	1.51
2	1	250	PGH	P-O3P	4.89	1.72	1.54
2	2	250	PGH	P-O2P	4.23	1.65	1.51
2	1	250	PGH	P-O1P	2.49	1.68	1.60
2	1	250	PGH	P-O4P	2.26	1.63	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	250	PGH	O4P-P-O2P	-4.28	96.45	110.44
2	1	250	PGH	O3P-P-O1P	2.85	114.50	106.65
2	2	250	PGH	O4P-P-O1P	2.72	114.16	106.65
2	1	250	PGH	O1-C1-N2	2.43	126.40	123.47
2	1	250	PGH	O4P-P-O1P	2.13	112.52	106.65
2	1	250	PGH	O2-N2-C1	-2.10	116.45	119.57
2	2	250	PGH	O1P-P-O2P	2.06	112.74	106.71

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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.