Full wwPDB X-ray Structure Validation Report (i)

Apr 28, 2024 – 01:22 pm BST

PDB ID	:	1GVF
Title	:	Structure of tagatose-1,6-bisphosphate aldolase
Authors	:	Hall, D.R.; Hunter, W.N.
Deposited on	:	2002-02-11
Resolution	:	1.45 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

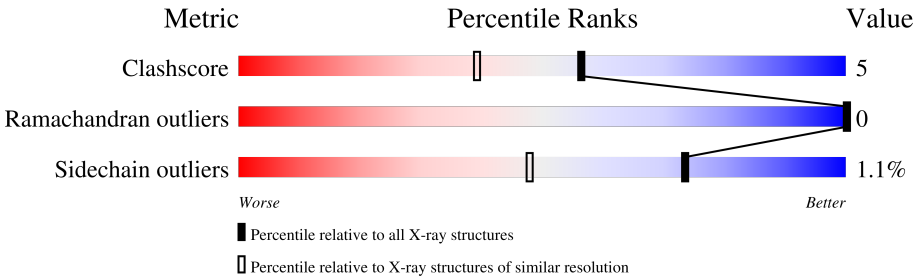
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)

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 >=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 <=5%

Mol	Chain	Length	Quality of chain
1	A	286	86% 8% • 5%
1	B	286	86% 8% • •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PGH	B	287	-	X	-	-
5	EDO	B	1294	-	X	X	-

2 Entry composition

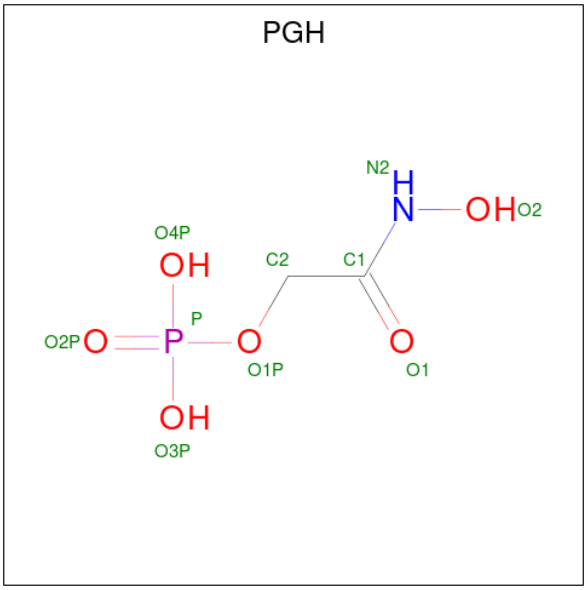
There are 6 unique types of molecules in this entry. The entry contains 4997 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 TAGATOSE-BISPHOSPHATE ALDOLASE AGAY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	7	0
			2115	1339	368	397	11			
1	B	275	Total	C	N	O	S	0	8	0
			2144	1359	380	394	11			

- Molecule 2 is PHOSPHOGLYCOLOHYDROXAMIC ACID (three-letter code: PGH) (formula: $C_2H_6NO_6P$).



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

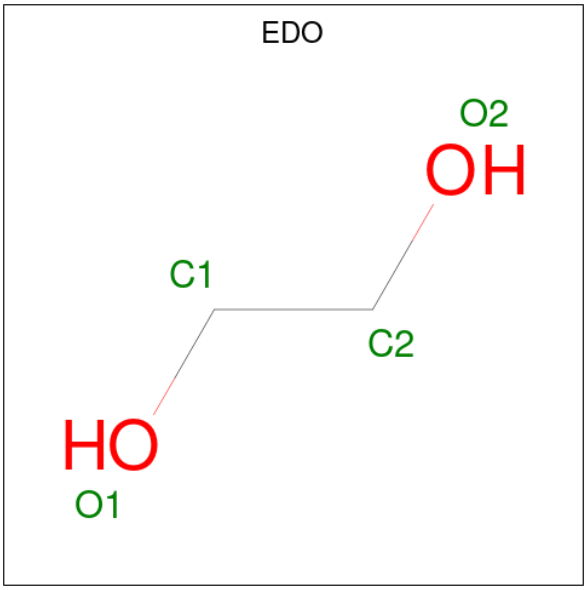
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

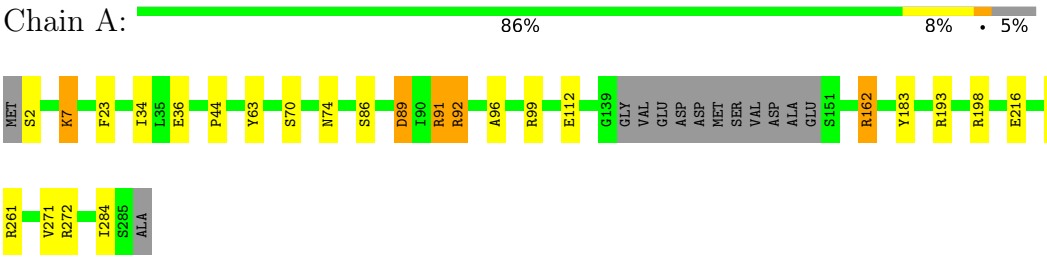
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	353	Total O 353 353	0	2
6	B	305	Total O 305 305	0	1

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. 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. 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.

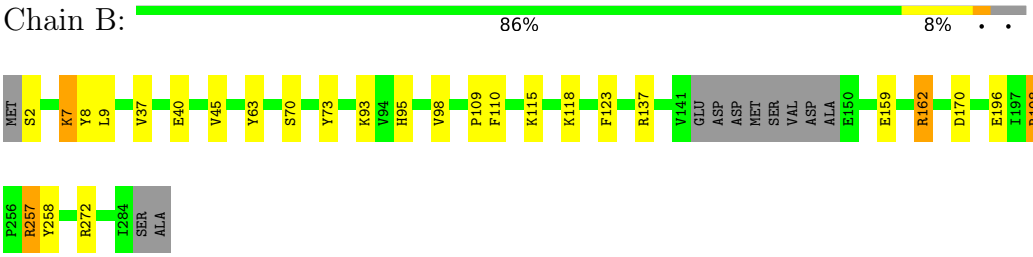
• Molecule 1: TAGATOSE-BISPHOSPHATE ALDOLASE AGAY

Chain A:



• Molecule 1: TAGATOSE-BISPHOSPHATE ALDOLASE AGAY

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	72.65Å 100.46Å 206.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.45 29.72 – 2.17	Depositor EDS
% Data completeness (in resolution range)	93.4 (10.00-1.45) 91.5 (29.72-2.17)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.91 (at 2.18Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.127 , 0.173 0.276 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	16.9	Xtriage
Anisotropy	0.296	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 43.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	4997	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.96% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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, EDO

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	0.62	0/2188	1.16	18/2970 (0.6%)
1	B	0.61	0/2216	1.39	24/3005 (0.8%)
All	All	0.61	0/4404	1.28	42/5975 (0.7%)

There are no bond length outliers.

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	257	ARG	CD-NE-CZ	15.08	144.72	123.60
1	B	198[A]	ARG	CD-NE-CZ	11.82	140.15	123.60
1	B	198[B]	ARG	CD-NE-CZ	11.82	140.15	123.60
1	B	198[A]	ARG	NE-CZ-NH1	10.15	125.38	120.30
1	B	198[B]	ARG	NE-CZ-NH1	10.15	125.38	120.30
1	B	137	ARG	NE-CZ-NH2	-9.91	115.34	120.30
1	B	220	ARG	NE-CZ-NH2	-9.78	115.41	120.30
1	B	272[A]	ARG	NE-CZ-NH1	9.60	125.10	120.30
1	B	272[B]	ARG	NE-CZ-NH1	9.60	125.10	120.30
1	A	92	ARG	CD-NE-CZ	8.00	134.81	123.60
1	B	220	ARG	NH1-CZ-NH2	7.58	127.74	119.40
1	A	220	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	B	220	ARG	NE-CZ-NH1	-6.90	116.85	120.30
1	A	261	ARG	NE-CZ-NH2	-6.85	116.88	120.30
1	A	261	ARG	NE-CZ-NH1	6.79	123.70	120.30
1	B	198[A]	ARG	NE-CZ-NH2	-6.72	116.94	120.30
1	B	198[B]	ARG	NE-CZ-NH2	-6.72	116.94	120.30
1	A	198	ARG	NE-CZ-NH2	6.70	123.65	120.30
1	A	89	ASP	CB-CG-OD1	6.55	124.19	118.30
1	A	99	ARG	NE-CZ-NH2	6.41	123.51	120.30
1	A	63	TYR	CB-CG-CD1	6.02	124.61	121.00
1	B	162[A]	ARG	NE-CZ-NH2	-5.75	117.43	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	162[B]	ARG	NE-CZ-NH2	-5.75	117.43	120.30
1	B	73	TYR	CB-CG-CD1	-5.73	117.56	121.00
1	B	272[A]	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	B	272[B]	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	B	162[A]	ARG	CD-NE-CZ	5.68	131.55	123.60
1	B	162[B]	ARG	CD-NE-CZ	5.68	131.55	123.60
1	A	220	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	92	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	B	73	TYR	CG-CD1-CE1	-5.53	116.87	121.30
1	A	162	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	63	TYR	CB-CG-CD2	5.35	124.21	121.00
1	A	183	TYR	CB-CG-CD2	-5.32	117.81	121.00
1	B	196	GLU	OE1-CD-OE2	-5.32	116.92	123.30
1	A	63	TYR	CB-CG-CD2	-5.30	117.82	121.00
1	A	7	LYS	CA-CB-CG	5.29	125.05	113.40
1	A	259	TYR	CB-CG-CD2	5.26	124.16	121.00
1	B	8	TYR	CB-CG-CD1	5.21	124.13	121.00
1	A	91[A]	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	91[B]	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	272	ARG	NE-CZ-NH2	-5.19	117.71	120.30

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	2115	0	2084	18	0
1	B	2144	0	2139	23	0
2	A	10	0	3	0	0
2	B	10	0	3	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	24	0	36	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	32	0	48	12	0
6	A	353	0	0	4	0
6	B	305	0	0	9	0
All	All	4997	0	4313	43	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 5.

All (43) 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)
5:B:1294:EDO:C2	5:B:1294:EDO:C1	2.41	0.98
1:A:7:LYS:HG2	6:B:2151:HOH:O	1.87	0.75
1:A:193:ARG:HB2	5:A:1291:EDO:H11	1.71	0.73
1:A:7:LYS:HD3	6:B:2010:HOH:O	1.88	0.73
5:B:1294:EDO:H22	6:B:2140:HOH:O	1.95	0.67
1:A:112:GLU:HG2	6:A:2187:HOH:O	1.96	0.65
1:A:2:SER:N	1:A:70:SER:HG	1.97	0.62
1:A:284:ILE:HG22	5:A:1294:EDO:H21	1.82	0.62
1:B:2:SER:N	1:B:70:SER:HG	1.99	0.60
1:A:2:SER:N	5:A:1289:EDO:HO1	1.99	0.60
1:A:74:ASN:OD1	5:B:1292:EDO:H22	2.04	0.58
1:A:96:ALA:O	5:A:1293:EDO:H11	2.05	0.56
1:B:2:SER:N	5:B:1289:EDO:HO1	2.04	0.56
1:B:115:LYS:HA	5:B:1294:EDO:H11	1.88	0.55
1:B:37:VAL:O	1:B:40:GLU:HG3	2.07	0.55
1:B:255:ASP:HB3	1:B:258:TYR:CD2	2.43	0.54
1:B:7[B]:LYS:HD3	1:B:170:ASP:OD1	2.08	0.53
1:B:95:HIS:CE1	5:B:1292:EDO:H11	2.43	0.52
1:B:115:LYS:HB2	5:B:1294:EDO:H11	1.90	0.52
1:B:109:PRO:HB2	6:B:2137:HOH:O	2.10	0.52
1:B:115:LYS:CA	5:B:1294:EDO:H11	2.39	0.52
6:A:2014:HOH:O	1:B:7[A]:LYS:HE3	2.10	0.52
1:B:198[B]:ARG:HD2	6:B:2209:HOH:O	2.09	0.51
1:A:162:ARG:HD2	6:A:2221:HOH:O	2.10	0.51
1:A:36:GLU:OE2	5:A:1292:EDO:H11	2.11	0.50
1:B:115:LYS:CB	5:B:1294:EDO:H11	2.43	0.49
1:B:45:VAL:H	5:B:1288:EDO:H22	1.77	0.48
1:B:7[B]:LYS:HE3	6:B:2183:HOH:O	2.14	0.48
1:B:118:LYS:HD3	5:B:1294:EDO:C2	2.44	0.47
1:B:93:LYS:O	1:B:98[B]:VAL:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91[B]:ARG:NH1	6:A:2147:HOH:O	2.49	0.44
1:A:36:GLU:OE2	5:A:1292:EDO:H22	2.17	0.44
1:B:110:PHE:CE1	1:B:159:GLU:HG2	2.53	0.44
1:B:220:ARG:NH2	6:B:2236:HOH:O	2.49	0.44
1:A:23:PHE:CG	1:A:34[B]:ILE:HD12	2.53	0.44
1:A:34[B]:ILE:HD13	1:A:271:VAL:CG2	2.48	0.44
1:A:89:ASP:OD1	1:A:92:ARG:NH2	2.51	0.43
1:B:7[A]:LYS:NZ	6:B:2007:HOH:O	2.51	0.42
1:B:9:LEU:HD12	6:B:2027:HOH:O	2.17	0.42
1:B:123:PHE:HB2	5:B:1295:EDO:H11	2.02	0.41
1:A:34[B]:ILE:HD13	1:A:271:VAL:HG21	2.03	0.41
1:A:44:PRO:HB3	5:A:1294:EDO:H11	2.01	0.41

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	276/286 (96%)	270 (98%)	6 (2%)	0	100	100
1	B	279/286 (98%)	273 (98%)	6 (2%)	0	100	100
All	All	555/572 (97%)	543 (98%)	12 (2%)	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	229/237 (97%)	227 (99%)	2 (1%)	78 57
1	B	231/237 (98%)	226 (98%)	5 (2%)	52 18
All	All	460/474 (97%)	453 (98%)	7 (2%)	73 35

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	SER
1	A	216	GLU
1	B	7[A]	LYS
1	B	7[B]	LYS
1	B	162[A]	ARG
1	B	162[B]	ARG
1	B	257	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS
1	B	56	HIS
1	B	127	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)

Of 20 ligands modelled in this entry, 4 are monoatomic - leaving 16 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	EDO	A	1291	-	3,3,3	0.60	0	2,2,2	0.83	0
5	EDO	A	1290	-	3,3,3	0.65	0	2,2,2	0.26	0
5	EDO	B	1288	-	3,3,3	0.73	0	2,2,2	0.46	0
5	EDO	B	1291	-	3,3,3	0.75	0	2,2,2	0.48	0
5	EDO	A	1293	-	3,3,3	0.78	0	2,2,2	0.64	0
5	EDO	B	1293	-	3,3,3	0.66	0	2,2,2	0.08	0
5	EDO	A	1289	-	3,3,3	0.80	0	2,2,2	1.11	0
5	EDO	B	1290	-	3,3,3	0.32	0	2,2,2	0.36	0
5	EDO	B	1292	-	3,3,3	0.67	0	2,2,2	0.29	0
5	EDO	A	1294	-	3,3,3	0.64	0	2,2,2	0.53	0
5	EDO	B	1289	-	3,3,3	0.59	0	2,2,2	0.68	0
5	EDO	A	1292	-	3,3,3	0.72	0	2,2,2	0.28	0
5	EDO	B	1294	-	3,3,3	7.74	1 (33%)	2,2,2	3.54	2 (100%)
2	PGH	A	287	4,3	9,9,9	5.84	3 (33%)	10,12,12	3.84	3 (30%)
5	EDO	B	1295	-	3,3,3	0.56	0	2,2,2	0.26	0
2	PGH	B	287	4,3	9,9,9	3.64	5 (55%)	10,12,12	2.66	5 (50%)

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	EDO	A	1291	-	-	1/1/1/1	-
5	EDO	A	1290	-	-	1/1/1/1	-
5	EDO	B	1288	-	-	0/1/1/1	-
5	EDO	B	1291	-	-	0/1/1/1	-
5	EDO	A	1293	-	-	1/1/1/1	-
5	EDO	B	1293	-	-	1/1/1/1	-
5	EDO	A	1289	-	-	0/1/1/1	-
5	EDO	B	1290	-	-	1/1/1/1	-
5	EDO	B	1292	-	-	1/1/1/1	-
5	EDO	A	1294	-	-	0/1/1/1	-
5	EDO	B	1289	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	1292	-	-	1/1/1/1	-
5	EDO	B	1294	-	-	1/1/1/1	-
2	PGH	A	287	4,3	-	4/8/8/8	-
5	EDO	B	1295	-	-	1/1/1/1	-
2	PGH	B	287	4,3	-	3/8/8/8	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	287	PGH	O1P-C2	14.41	1.53	1.43
5	B	1294	EDO	C2-C1	13.40	2.41	1.48
2	A	287	PGH	C2-C1	9.35	1.70	1.51
2	B	287	PGH	C2-C1	6.99	1.65	1.51
2	B	287	PGH	C1-N2	6.44	1.39	1.32
2	B	287	PGH	P-O3P	-3.36	1.41	1.54
2	B	287	PGH	O2-N2	2.71	1.46	1.40
2	B	287	PGH	P-O2P	-2.29	1.43	1.50
2	A	287	PGH	C1-N2	-2.03	1.30	1.32

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	287	PGH	O2-N2-C1	-7.40	108.86	119.79
2	A	287	PGH	O1-C1-N2	6.78	131.59	123.27
2	A	287	PGH	C2-C1-N2	-6.33	105.38	116.37
2	B	287	PGH	C2-C1-N2	-5.16	107.41	116.37
2	B	287	PGH	O1-C1-C2	4.63	132.63	119.61
5	B	1294	EDO	O2-C2-C1	-3.62	85.85	111.91
5	B	1294	EDO	O1-C1-C2	-3.45	87.08	111.91
2	B	287	PGH	O1-C1-N2	-3.34	119.17	123.27
2	B	287	PGH	O4P-P-O3P	2.29	116.37	107.64
2	B	287	PGH	O2-N2-C1	-2.03	116.80	119.79

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	287	PGH	C2-O1P-P-O2P
2	A	287	PGH	C2-O1P-P-O3P
2	A	287	PGH	C2-O1P-P-O4P
2	B	287	PGH	C2-O1P-P-O3P

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Mol	Chain	Res	Type	Atoms
5	A	1293	EDO	O1-C1-C2-O2
5	B	1290	EDO	O1-C1-C2-O2
5	B	1294	EDO	O1-C1-C2-O2
5	B	1295	EDO	O1-C1-C2-O2
5	A	1292	EDO	O1-C1-C2-O2
5	B	1292	EDO	O1-C1-C2-O2
2	B	287	PGH	C2-O1P-P-O4P
5	B	1293	EDO	O1-C1-C2-O2
2	B	287	PGH	O1-C1-C2-O1P
2	A	287	PGH	O1-C1-C2-O1P
5	A	1291	EDO	O1-C1-C2-O2
5	A	1290	EDO	O1-C1-C2-O2

There are no ring outliers.

10 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1291	EDO	1	0
5	B	1288	EDO	1	0
5	A	1293	EDO	1	0
5	A	1289	EDO	1	0
5	B	1292	EDO	2	0
5	A	1294	EDO	2	0
5	B	1289	EDO	1	0
5	A	1292	EDO	2	0
5	B	1294	EDO	7	0
5	B	1295	EDO	1	0

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.