



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:36 PM UTC

PDB ID : 1UOD / pdb_00001uod
Title : Crystal structure of the dihydroxyacetone kinase from E. coli in complex with dihydroxyacetone-phosphate
Authors : Siebold, C.; Garcia-Alles, L.F.; Luthi-Nyffeler, T.; Flukiger-Bruhwiller, K.; Burgi, H.-B.; Baumann, U.; Erni, B.
Deposited on : 2003-09-16
Resolution : 1.90 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 ⓘ 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

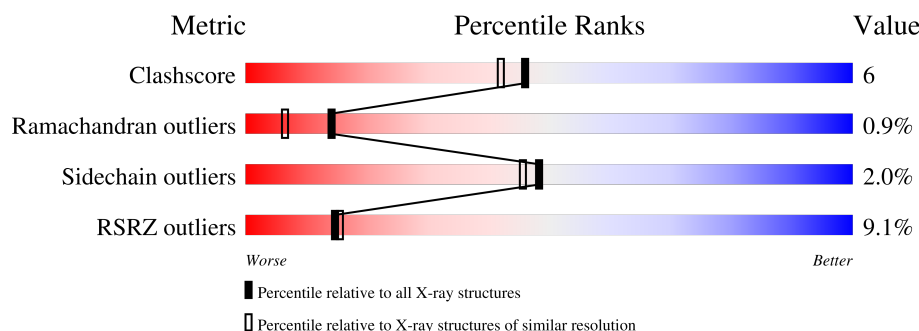
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (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 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 $\leq 5\%$. 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	366	9% 82% 9% 8%
1	B	366	7% 77% 13% 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	G3H	A	1369	X	-	-	-
2	G3H	B	1369	X	-	-	-

2 Entry composition [i](#)

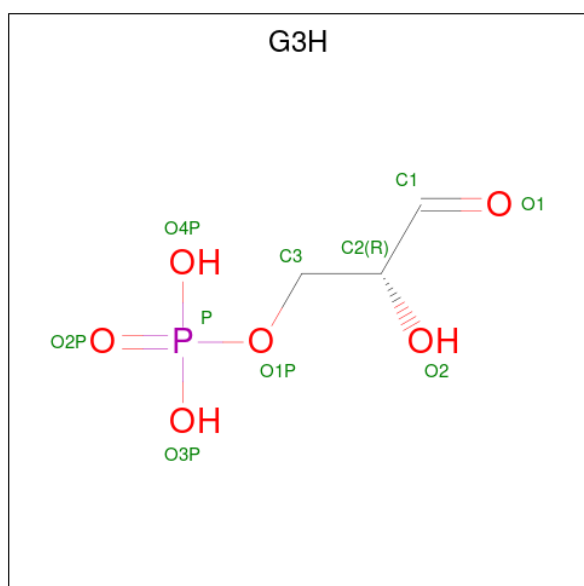
There are 4 unique types of molecules in this entry. The entry contains 5575 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DIHYDROXYACETONE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2534	1584	435	502	13			
1	B	336	Total	C	N	O	S	0	0	0
			2534	1584	435	502	13			

- Molecule 2 is GLYCERALDEHYDE-3-PHOSPHATE (CCD ID: G3H) (formula: $C_3H_7O_6P$).



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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

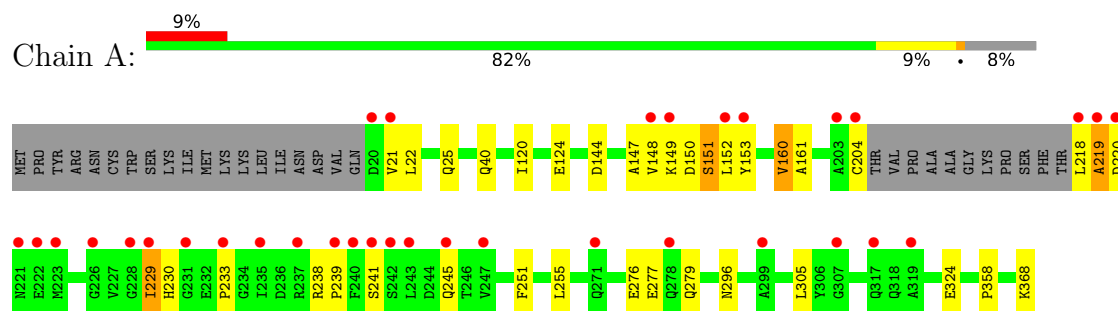
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	235	Total	O	0	0
			235	235		
4	B	242	Total	O	0	0
			242	242		

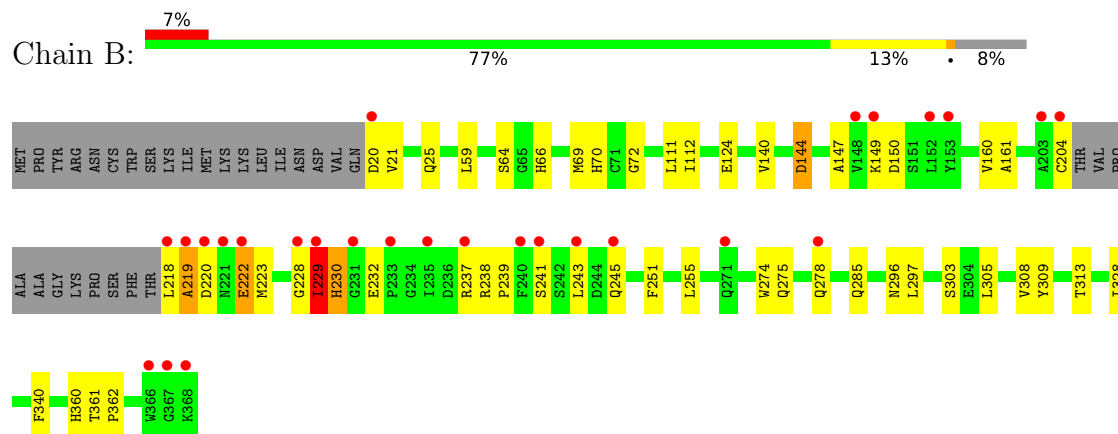
3 Residue-property plots

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: DIHYDROXYACETONE KINASE



• Molecule 1: DIHYDROXYACETONE KINASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	96.50Å 97.06Å 86.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.11 – 1.90 24.11 – 1.90	Depositor EDS
% Data completeness (in resolution range)	94.6 (24.11-1.90) 93.5 (24.11-1.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	19.84 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.167 , 0.206 (Not available) , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	13.8	Xtriage
Anisotropy	0.598	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5575	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.21 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0255e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: G3H, SO4

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	0.91	2/2579 (0.1%)	1.09	10/3503 (0.3%)
1	B	1.05	2/2579 (0.1%)	1.15	12/3503 (0.3%)
All	All	0.98	4/5158 (0.1%)	1.12	22/7006 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	229	ILE	C-N	29.07	1.74	1.33
1	A	229	ILE	C-N	18.45	1.59	1.33
1	B	230	HIS	N-CA	-8.05	1.37	1.46
1	A	230	HIS	N-CA	-6.73	1.38	1.46

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	229	ILE	CA-C-N	-13.95	100.59	122.49
1	B	229	ILE	C-N-CA	-13.95	100.59	122.49
1	A	245	GLN	OE1-CD-NE2	-9.86	112.74	122.60
1	B	245	GLN	OE1-CD-NE2	-9.77	112.83	122.60
1	B	230	HIS	N-CA-C	-9.30	100.31	112.41
1	A	229	ILE	CA-C-N	-8.00	109.93	122.49
1	A	229	ILE	C-N-CA	-8.00	109.93	122.49
1	B	147	ALA	N-CA-C	7.78	119.54	111.14
1	A	147	ALA	N-CA-C	7.26	119.27	111.36
1	A	230	HIS	N-CA-C	-7.05	103.24	112.41
1	B	144	ASP	N-CA-C	7.04	121.62	112.89
1	A	245	GLN	CG-CD-NE2	6.70	126.45	116.40
1	B	245	GLN	CG-CD-NE2	6.68	126.41	116.40
1	B	230	HIS	N-CA-CB	-6.64	100.24	111.20
1	A	144	ASP	N-CA-C	6.48	120.92	112.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	230	HIS	CA-CB-CG	6.44	120.24	113.80
1	A	230	HIS	CB-CA-C	-6.40	100.65	111.02
1	A	230	HIS	N-CA-CB	-5.83	101.58	111.20
1	A	161	ALA	N-CA-C	5.78	118.36	111.71
1	B	161	ALA	N-CA-C	5.57	119.18	112.38
1	B	64	SER	N-CA-C	-5.17	103.86	110.53
1	B	237	ARG	N-CA-C	-5.04	101.48	109.59

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	2534	0	2477	23	0
1	B	2534	0	2476	36	0
2	A	10	0	4	0	0
2	B	10	0	4	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	235	0	0	3	0
4	B	242	0	0	4	0
All	All	5575	0	4961	58	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 6.

All (58) 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:229:ILE:C	1:B:230:HIS:N	1.74	1.46
1:B:219:ALA:HB3	1:B:222:GLU:OE1	1.35	1.22
1:B:219:ALA:HB3	1:B:222:GLU:CD	1.77	1.07
1:B:229:ILE:C	1:B:230:HIS:CA	2.40	0.94
1:A:152:LEU:HD11	1:A:233:PRO:HD3	1.56	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:219:ALA:CB	1:B:222:GLU:CD	2.51	0.84
1:A:152:LEU:HD11	1:A:233:PRO:CD	2.11	0.81
1:B:66:HIS:CE1	1:B:229:ILE:HD13	2.17	0.78
1:A:152:LEU:CD1	1:A:233:PRO:HD3	2.19	0.71
1:A:22:LEU:HD21	4:A:2059:HOH:O	1.91	0.69
1:B:59:LEU:HD22	1:B:111:LEU:HD22	1.76	0.64
1:A:152:LEU:CD1	1:A:233:PRO:CD	2.77	0.63
1:B:296:ASN:HB2	1:B:305:LEU:HD11	1.82	0.62
1:B:229:ILE:C	1:B:229:ILE:HD12	2.25	0.61
1:B:20:ASP:HA	4:B:2001:HOH:O	2.01	0.61
1:A:21:VAL:O	1:A:25:GLN:HG3	2.02	0.59
1:B:72:GLY:O	1:B:362:PRO:HD2	2.02	0.59
1:B:238:ARG:HB2	1:B:239:PRO:HD2	1.85	0.59
1:B:218:LEU:O	1:B:219:ALA:HB2	2.04	0.57
1:B:21:VAL:O	1:B:25:GLN:HG3	2.06	0.56
1:A:151:SER:OG	1:A:152:LEU:N	2.38	0.56
1:A:218:LEU:O	1:A:219:ALA:HB2	2.06	0.55
1:A:238:ARG:HB2	1:A:239:PRO:HD2	1.88	0.55
1:B:229:ILE:HD11	1:B:230:HIS:CE1	2.45	0.51
1:A:148:VAL:O	1:A:148:VAL:HG23	2.12	0.49
1:B:223:MET:HE3	1:B:238:ARG:HD2	1.94	0.49
1:B:149:LYS:O	1:B:150:ASP:HB2	2.13	0.48
1:B:229:ILE:C	1:B:229:ILE:CD1	2.86	0.47
1:A:296:ASN:HB2	1:A:305:LEU:HD11	1.95	0.47
1:B:229:ILE:C	1:B:230:HIS:HA	2.34	0.47
1:A:324:GLU:OE1	4:A:2197:HOH:O	2.21	0.47
1:B:229:ILE:O	1:B:230:HIS:HA	2.15	0.47
1:B:361:THR:HB	1:B:362:PRO:CD	2.46	0.46
1:A:277:GLU:HG2	1:A:279:GLN:HE21	1.81	0.46
1:B:112:ILE:CD1	1:B:140:VAL:HB	2.45	0.45
1:B:230:HIS:N	1:B:232:GLU:OE2	2.50	0.45
1:B:251:PHE:CE2	1:B:255:LEU:HD11	2.52	0.45
1:B:124:GLU:HG2	1:B:274:TRP:CH2	2.52	0.45
1:B:228:GLY:HA2	4:B:2150:HOH:O	2.17	0.45
1:B:297:LEU:HG	1:B:340:PHE:HA	1.99	0.44
1:A:148:VAL:O	1:A:148:VAL:CG2	2.66	0.44
1:A:25:GLN:NE2	1:B:303:SER:HB2	2.33	0.43
1:A:251:PHE:CE2	1:A:255:LEU:HD11	2.54	0.43
1:B:243:LEU:HD11	1:B:308:VAL:CG2	2.49	0.43
1:A:149:LYS:O	1:A:150:ASP:HB2	2.19	0.43
1:A:358:PRO:HG3	1:A:368:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:MET:HA	1:B:70:HIS:HA	1.86	0.43
1:B:309:TYR:O	1:B:313:THR:HG23	2.19	0.43
1:A:153:TYR:HB3	4:A:2233:HOH:O	2.19	0.42
1:B:144:ASP:HB3	4:B:2143:HOH:O	2.19	0.42
1:A:120:ILE:O	1:A:124:GLU:HG3	2.20	0.42
1:B:309:TYR:CG	1:B:328:ILE:HD11	2.54	0.42
1:A:148:VAL:HG21	1:A:151:SER:HB2	2.03	0.41
1:B:218:LEU:O	1:B:219:ALA:CB	2.66	0.41
1:A:160:VAL:HG12	1:A:229:ILE:HD13	2.02	0.41
1:A:218:LEU:O	1:A:218:LEU:HG	2.21	0.41
1:B:219:ALA:O	1:B:220:ASP:HB2	2.20	0.40
1:B:360:HIS:HE1	4:B:2234:HOH:O	2.05	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	332/366 (91%)	323 (97%)	5 (2%)	4 (1%)	10	4
1	B	332/366 (91%)	323 (97%)	7 (2%)	2 (1%)	21	13
All	All	664/732 (91%)	646 (97%)	12 (2%)	6 (1%)	14	6

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	219	ALA
1	B	219	ALA
1	A	151	SER
1	A	220	ASP
1	A	160	VAL
1	B	160	VAL

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	271/298 (91%)	267 (98%)	4 (2%)	57	56
1	B	271/298 (91%)	264 (97%)	7 (3%)	40	35
All	All	542/596 (91%)	531 (98%)	11 (2%)	48	46

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	GLN
1	A	204	CYS
1	A	241	SER
1	A	276	GLU
1	B	204	CYS
1	B	222	GLU
1	B	229	ILE
1	B	241	SER
1	B	275	GLN
1	B	278	GLN
1	B	285	GLN

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	25	GLN
1	A	40	GLN
1	A	261	HIS
1	A	275	GLN
1	B	115	ASN
1	B	270	GLN
1	B	271	GLN
1	B	318	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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$
3	SO4	B	1370	-	4,4,4	0.27	0	6,6,6	0.42	0
3	SO4	A	1370	-	4,4,4	0.25	0	6,6,6	0.26	0
2	G3H	B	1369	1	8,9,9	2.42	2 (25%)	7,12,12	1.23	1 (14%)
2	G3H	A	1369	1	8,9,9	2.61	2 (25%)	7,12,12	1.09	1 (14%)

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	G3H	B	1369	1	1/1/2/3	3/7/8/8	-
2	G3H	A	1369	1	1/1/2/3	3/7/8/8	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1369	G3H	O1-C1	6.37	1.44	1.20
2	B	1369	G3H	O1-C1	6.01	1.42	1.20
2	A	1369	G3H	C3-C2	3.05	1.55	1.51
2	B	1369	G3H	C3-C2	2.51	1.55	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1369	G3H	O4P-P-O3P	2.21	116.08	107.80
2	B	1369	G3H	O1P-P-O2P	-2.20	100.49	106.44

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1369	G3H	C2
2	B	1369	G3H	C2

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1369	G3H	C3-O1P-P-O3P
2	A	1369	G3H	C3-O1P-P-O4P
2	B	1369	G3H	C3-O1P-P-O3P
2	B	1369	G3H	C3-O1P-P-O4P
2	A	1369	G3H	C3-O1P-P-O2P
2	B	1369	G3H	C3-O1P-P-O2P

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	229:ILE	C	230:HIS	N	1.74

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	336/366 (91%)	0.62	34 (10%) 12 13	5, 14, 36, 81	0
1	B	336/366 (91%)	0.55	27 (8%) 18 19	5, 13, 35, 82	0
All	All	672/732 (91%)	0.58	61 (9%) 15 15	5, 13, 36, 82	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	218	LEU	9.1
1	B	219	ALA	8.6
1	A	152	LEU	8.5
1	A	218	LEU	8.3
1	A	220	ASP	8.0
1	B	153	TYR	7.5
1	B	152	LEU	6.8
1	A	219	ALA	6.6
1	B	220	ASP	6.5
1	B	221	ASN	6.2
1	B	222	GLU	5.3
1	B	368	LYS	5.1
1	A	221	ASN	4.8
1	A	153	TYR	4.6
1	B	203	ALA	4.5
1	A	245	GLN	4.5
1	A	231	GLY	4.4
1	B	237	ARG	4.2
1	B	367	GLY	4.0
1	B	228	GLY	3.9
1	A	222	GLU	3.8
1	B	233	PRO	3.8
1	A	203	ALA	3.6
1	B	148	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	20	ASP	3.3
1	A	204	CYS	3.3
1	A	21	VAL	3.3
1	A	243	LEU	3.2
1	B	243	LEU	3.1
1	A	240	PHE	3.0
1	A	228	GLY	3.0
1	A	20	ASP	3.0
1	A	237	ARG	3.0
1	B	245	GLN	3.0
1	A	299	ALA	3.0
1	B	204	CYS	2.9
1	A	239	PRO	2.8
1	A	241	SER	2.7
1	A	148	VAL	2.7
1	A	149	LYS	2.7
1	A	319	ALA	2.7
1	A	229	ILE	2.6
1	B	149	LYS	2.6
1	B	231	GLY	2.5
1	B	235	ILE	2.5
1	B	241	SER	2.5
1	B	240	PHE	2.4
1	A	271	GLN	2.4
1	A	307	GLY	2.4
1	A	278	GLN	2.4
1	A	235	ILE	2.4
1	B	271	GLN	2.4
1	A	233	PRO	2.2
1	A	247	VAL	2.2
1	B	278	GLN	2.2
1	B	229	ILE	2.1
1	A	317	GLN	2.1
1	A	242	SER	2.1
1	A	226	GLY	2.1
1	B	366	TRP	2.0
1	A	223	MET	2.0

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 [i](#)

There are no oligosaccharides 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, 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	G3H	B	1369	10/10	0.84	0.14	17,23,43,46	0
2	G3H	A	1369	10/10	0.88	0.13	15,27,44,47	0
3	SO4	A	1370	5/5	0.96	0.09	23,27,34,38	0
3	SO4	B	1370	5/5	0.97	0.08	24,25,32,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.