



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 07:23 pm BST

PDB ID : 2IU4
Title : Dihydroxyacetone kinase operon co-activator Dha-DhaQ
Authors : Srinivas, A.; Christen, S.; Baumann, U.; Erni, B.
Deposited on : 2006-05-27
Resolution : 1.96 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 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 : 2.11
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) : 2.11

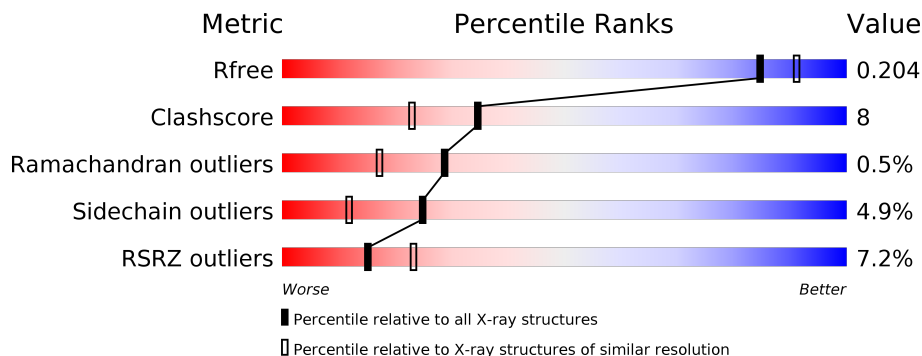
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 1.96 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 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	336	 7% 81% 15% ..
1	B	336	 7% 82% 14% ..

2 Entry composition [i](#)

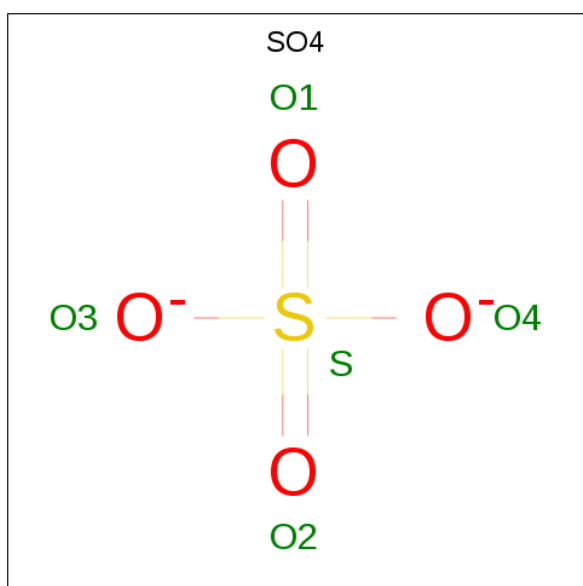
There are 3 unique types of molecules in this entry. The entry contains 5483 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	A	325	Total 2536	C 1632	N 419	O 476	S 9	0	0	0
1	B	331	Total 2589	C 1666	N 426	O 488	S 9	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

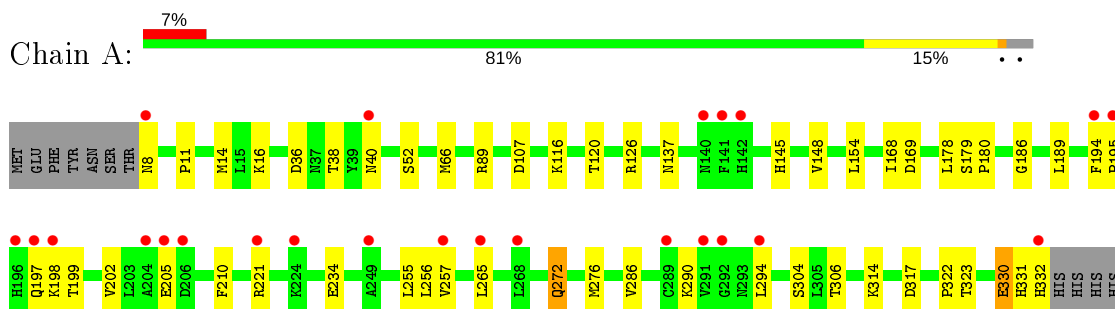
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	167	Total 167	O 167	0	0
3	B	171	Total 171	O 171	0	0

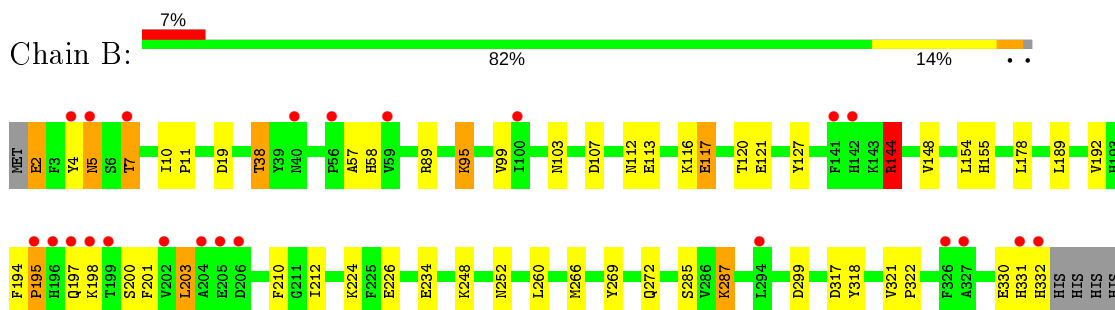
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	99.90Å 99.90Å 188.57Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.96 35.63 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-1.96) 99.0 (35.63-1.96)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.27 (at 1.95Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.181 , 0.209 0.181 , 0.204	Depositor DCC
R_{free} test set	1585 reflections (2.02%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtrriage
Anisotropy	0.117	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5483	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HIQ, 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	0.45	0/2574	0.72	0/3484
1	B	0.44	0/2629	0.73	2/3559 (0.1%)
All	All	0.44	0/5203	0.72	2/7043 (0.0%)

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	1	0
1	B	0	1
All	All	1	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	144	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	B	144	ARG	NE-CZ-NH1	5.84	123.22	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	38	THR	CB

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	2	GLU	Peptide

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	2536	0	2547	42	0
1	B	2589	0	2589	47	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
3	A	167	0	0	4	0
3	B	171	0	0	7	1
All	All	5483	0	5136	85	1

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 8.

All (85) 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:A:290:LYS:NZ	1:A:330:GLU:OE2	1.62	1.30
1:A:255:LEU:HD23	1:A:276:MET:CE	1.62	1.30
1:A:332:HIS:HA	3:A:2163:HOH:O	1.12	1.26
1:A:255:LEU:HD23	1:A:276:MET:HE2	1.28	1.10
1:A:255:LEU:CD2	1:A:276:MET:CE	2.35	1.05
1:A:255:LEU:CD2	1:A:276:MET:HE1	1.92	1.00
1:A:36:ASP:OD1	1:A:38:THR:HG22	1.70	0.92
1:A:255:LEU:CD2	1:A:276:MET:HE2	2.01	0.83
1:A:255:LEU:HD22	1:A:276:MET:HE1	1.63	0.80
1:B:58:HIS:HD1	1:B:155:HIS:HE1	1.33	0.77
1:B:5:ASN:CG	3:B:2001:HOH:O	2.26	0.74
1:A:255:LEU:HD23	1:A:276:MET:HE1	1.52	0.73
1:B:58:HIS:ND1	1:B:155:HIS:HE1	1.89	0.70
1:A:179:SER:HB3	1:A:180:PRO:HD3	1.75	0.69
1:B:113:GLU:O	1:B:117:GLU:HG3	1.92	0.69
1:B:7:THR:HA	3:B:2002:HOH:O	1.91	0.69
1:B:2:GLU:HG3	1:B:2:GLU:O	1.92	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:LYS:O	1:B:120:THR:HG23	1.95	0.65
1:A:276:MET:CE	1:A:286:VAL:HG11	2.27	0.65
1:A:52:SER:OG	1:B:266:MET:CE	2.44	0.64
1:A:210:PHE:CE2	1:A:234:GLU:HG2	2.35	0.61
1:B:7:THR:CA	3:B:2002:HOH:O	2.48	0.60
1:A:194:PHE:HB3	1:A:195:PRO:HD2	1.83	0.60
1:B:194:PHE:HB2	1:B:198:LYS:HG3	1.84	0.60
1:B:5:ASN:ND2	3:B:2001:HOH:O	2.35	0.60
1:A:126:ARG:HG3	1:A:168:ILE:HG13	1.85	0.59
1:A:52:SER:OG	1:B:266:MET:HE1	2.05	0.57
1:A:66:MET:HG3	1:A:323:THR:HG21	1.85	0.57
1:B:103:ASN:O	1:B:144:ARG:HD3	2.04	0.57
1:B:113:GLU:O	1:B:117:GLU:CG	2.53	0.56
1:A:332:HIS:CA	3:A:2163:HOH:O	1.98	0.55
1:A:154:LEU:HD23	1:A:178:LEU:HD23	1.89	0.54
1:B:89:ARG:HD2	3:B:2061:HOH:O	2.08	0.53
1:A:11:PRO:HG3	1:A:52:SER:OG	2.09	0.53
1:B:112:ASN:O	1:B:116:LYS:HG3	2.08	0.52
1:A:89:ARG:HD3	3:A:2048:HOH:O	2.08	0.52
1:B:117:GLU:O	1:B:121:GLU:HG3	2.10	0.52
1:B:5:ASN:HD22	1:B:11:PRO:HB3	1.75	0.52
1:A:16:LYS:NZ	3:A:2004:HOH:O	2.43	0.52
1:A:276:MET:HE1	1:A:286:VAL:HG11	1.92	0.51
1:A:52:SER:OG	1:B:266:MET:HE2	2.11	0.50
1:A:290:LYS:HE3	1:A:294:LEU:HD22	1.93	0.50
1:A:322:PRO:HB3	1:A:331:HIS:CD2	2.46	0.50
1:B:322:PRO:HG3	1:B:331:HIS:CG	2.45	0.50
1:A:137:ASN:OD1	1:A:145:HIS:HE1	1.95	0.50
1:B:4:TYR:OH	1:B:299:ASP:CG	2.50	0.49
1:B:5:ASN:HD22	1:B:11:PRO:CB	2.25	0.49
1:B:5:ASN:HB3	1:B:11:PRO:HB3	1.95	0.49
1:A:272:GLN:HE21	1:A:272:GLN:HB3	1.28	0.48
1:B:201:PHE:HE1	1:B:203:LEU:HG	1.78	0.48
1:B:212:ILE:HD11	1:B:260:LEU:HD11	1.96	0.48
1:A:194:PHE:HB3	1:A:195:PRO:CD	2.43	0.47
1:B:210:PHE:CE2	1:B:234:GLU:HG2	2.49	0.47
1:B:212:ILE:CD1	1:B:260:LEU:HD11	2.44	0.47
1:A:257:VAL:HG21	1:A:272:GLN:HG3	1.96	0.47
1:B:154:LEU:HD23	1:B:178:LEU:HD23	1.97	0.47
1:B:192:VAL:HB	1:B:200:SER:HB3	1.97	0.47
1:B:38:THR:CG2	3:B:2021:HOH:O	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ARG:NH1	1:A:169:ASP:OD1	2.47	0.45
1:A:186:GLY:HA2	1:A:304:SER:HA	1.99	0.45
1:B:226:GLU:HA	1:B:226:GLU:OE1	2.16	0.45
1:A:276:MET:HE3	1:A:286:VAL:HG11	1.98	0.44
1:B:10:ILE:HG23	1:B:11:PRO:HD2	1.99	0.44
1:A:314:LYS:HE3	1:A:317:ASP:HB2	2.00	0.44
1:B:252:ASN:HD22	1:B:285:SER:HB2	1.82	0.44
1:A:126:ARG:HG3	1:A:168:ILE:CG1	2.48	0.44
1:B:318:TYR:O	1:B:321:VAL:HG22	2.18	0.44
1:A:14:MET:HG3	1:B:269:TYR:HB2	2.00	0.43
1:B:194:PHE:HB2	1:B:198:LYS:CG	2.47	0.43
1:A:116:LYS:O	1:A:120:THR:HG23	2.19	0.43
1:B:287:LYS:HA	1:B:287:LYS:HD2	1.75	0.43
1:B:317:ASP:O	1:B:321:VAL:HG13	2.18	0.43
1:B:57:ALA:HA	1:B:58:HIS:HA	1.72	0.43
1:A:198:LYS:HG3	1:A:199:THR:N	2.34	0.43
1:B:38:THR:HG22	3:B:2021:HOH:O	2.19	0.43
1:A:265:LEU:HD12	1:A:265:LEU:HA	1.86	0.42
1:B:95:LYS:HB3	1:B:95:LYS:HE3	1.74	0.42
1:A:256:LEU:HB2	1:A:306:THR:HB	2.02	0.42
1:B:321:VAL:HA	1:B:322:PRO:HD3	1.90	0.41
1:B:195:PRO:O	1:B:198:LYS:HG2	2.21	0.41
1:A:179:SER:N	1:A:180:PRO:CD	2.84	0.41
1:B:58:HIS:HD1	1:B:155:HIS:CE1	2.24	0.41
1:B:99:VAL:O	1:B:127:TYR:HA	2.21	0.41
1:B:212:ILE:H	1:B:212:ILE:HG13	1.71	0.40
1:B:58:HIS:ND1	1:B:155:HIS:CE1	2.80	0.40

All (1) 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	Interatomic distance (Å)	Clash overlap (Å)
3:B:2006:HOH:O	3:B:2125:HOH:O[4_455]	1.30	0.90

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	322/336 (96%)	311 (97%)	10 (3%)	1 (0%)	41	30
1	B	328/336 (98%)	314 (96%)	12 (4%)	2 (1%)	25	14
All	All	650/672 (97%)	625 (96%)	22 (3%)	3 (0%)	29	17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	195	PRO
1	A	148	VAL
1	B	148	VAL

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	273/284 (96%)	263 (96%)	10 (4%)	34	22
1	B	279/284 (98%)	262 (94%)	17 (6%)	18	7
All	All	552/568 (97%)	525 (95%)	27 (5%)	25	12

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	40	ASN
1	A	107	ASP
1	A	189	LEU
1	A	197	GLN
1	A	202	VAL
1	A	205	GLU
1	A	221	ARG
1	A	272	GLN

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Mol	Chain	Res	Type
1	A	330	GLU
1	B	5	ASN
1	B	7	THR
1	B	19	ASP
1	B	38	THR
1	B	95	LYS
1	B	107	ASP
1	B	117	GLU
1	B	144	ARG
1	B	189	LEU
1	B	197	GLN
1	B	203	LEU
1	B	224	LYS
1	B	248	LYS
1	B	272	GLN
1	B	287	LYS
1	B	330	GLU
1	B	332	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	112	ASN
1	A	145	HIS
1	A	331	HIS
1	B	112	ASN
1	B	155	HIS
1	B	196	HIS
1	B	252	ASN
1	B	272	GLN
1	B	331	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues 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
1	HIQ	A	215	1	10,16,17	1.07	1 (10%)	7,22,24	1.09	0
1	HIQ	B	215	1	10,16,17	0.90	0	7,22,24	1.53	2 (28%)

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
1	HIQ	A	215	1	-	2/11/18/20	0/1/1/1
1	HIQ	B	215	1	-	2/11/18/20	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	215	HIQ	CD2-CG	2.39	1.39	1.36

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	215	HIQ	O2-C2-C1	-2.69	102.24	107.63
1	B	215	HIQ	CB-CA-C	-2.36	107.05	111.47

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	215	HIQ	O-C-CA-CB
1	A	215	HIQ	CA-CB-CG-ND1
1	B	215	HIQ	O-C-CA-CB
1	B	215	HIQ	CA-CB-CG-ND1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
2	SO4	A	1370	-	4,4,4	0.15	0	6,6,6	0.67	0
2	SO4	B	1370	-	4,4,4	0.16	0	6,6,6	0.64	0
2	SO4	B	1373	-	4,4,4	0.39	0	6,6,6	0.57	0
2	SO4	A	1373	-	4,4,4	0.56	0	6,6,6	0.72	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 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	324/336 (96%)	0.36	24 (7%) 14 22	22, 28, 38, 52	0
1	B	330/336 (98%)	0.43	23 (6%) 16 24	23, 28, 40, 55	0
All	All	654/672 (97%)	0.39	47 (7%) 15 23	22, 28, 40, 55	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	GLN	6.8
1	B	7	THR	6.0
1	B	196	HIS	5.4
1	B	142	HIS	5.2
1	A	196	HIS	5.1
1	B	198	LYS	5.1
1	B	202	VAL	4.9
1	A	141	PHE	4.9
1	A	205	GLU	4.7
1	B	5	ASN	4.4
1	A	140	ASN	4.3
1	B	205	GLU	4.1
1	A	198	LYS	4.1
1	B	4	TYR	4.1
1	B	197	GLN	4.0
1	B	332	HIS	4.0
1	A	142	HIS	3.7
1	A	195	PRO	3.3
1	A	206	ASP	3.2
1	A	294	LEU	3.2
1	A	332	HIS	3.2
1	B	141	PHE	3.2
1	A	291	VAL	3.2
1	B	331	HIS	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	195	PRO	2.9
1	A	204	ALA	2.9
1	B	199	THR	2.9
1	B	294	LEU	2.8
1	A	40	ASN	2.6
1	A	8	ASN	2.6
1	A	224	LYS	2.6
1	A	265	LEU	2.6
1	B	206	ASP	2.6
1	A	289	CYS	2.5
1	A	268	LEU	2.5
1	B	326	PHE	2.3
1	B	59	VAL	2.2
1	B	40	ASN	2.2
1	A	249	ALA	2.2
1	A	221	ARG	2.1
1	A	257	VAL	2.1
1	B	204	ALA	2.1
1	B	327	ALA	2.1
1	A	292	GLY	2.1
1	B	56	PRO	2.1
1	B	100	ILE	2.1
1	A	194	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	HIQ	B	215	16/17	0.95	0.10	25,30,33,35	0
1	HIQ	A	215	16/17	0.96	0.09	24,28,31,33	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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(\AA^2)	Q<0.9
2	SO4	A	1373	5/5	0.62	0.38	32,41,45,52	0
2	SO4	B	1373	5/5	0.64	0.36	41,45,50,54	0
2	SO4	A	1370	5/5	0.99	0.11	23,24,24,25	0
2	SO4	B	1370	5/5	0.99	0.12	20,21,25,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.