



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 09:40 AM UTC

PDB ID : 6IXL / pdb_00006ixl
Title : Crystal structure of isocitrate dehydrogenase from *Ostreococcus tauri*
Authors : Zhu, G.P.; Tang, W.G.; Wang, P.
Deposited on : 2018-12-11
Resolution : 1.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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

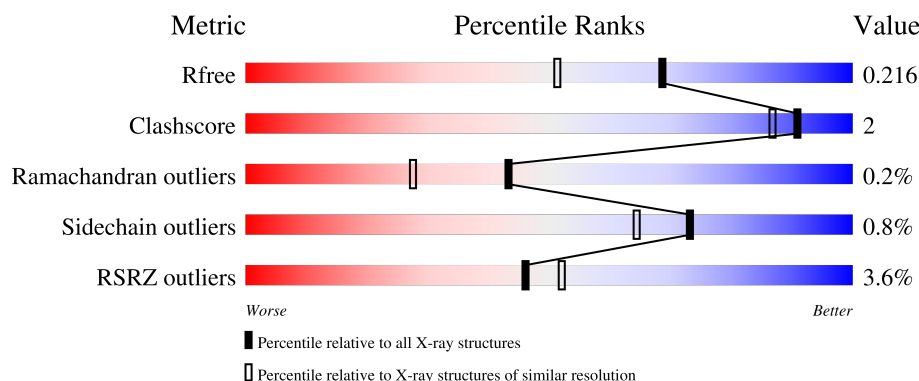
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	418	 93%
1	B	418	 92%
1	C	418	 92%
1	D	418	 91%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13686 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 Isocitrate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	1	0
			3165	1990	562	599	14			
1	B	405	Total	C	N	O	S	0	0	0
			3143	1978	552	599	14			
1	C	405	Total	C	N	O	S	0	1	0
			3168	1995	564	595	14			
1	D	404	Total	C	N	O	S	0	1	0
			3132	1976	546	596	14			

There are 32 discrepancies between the modelled and reference sequences:

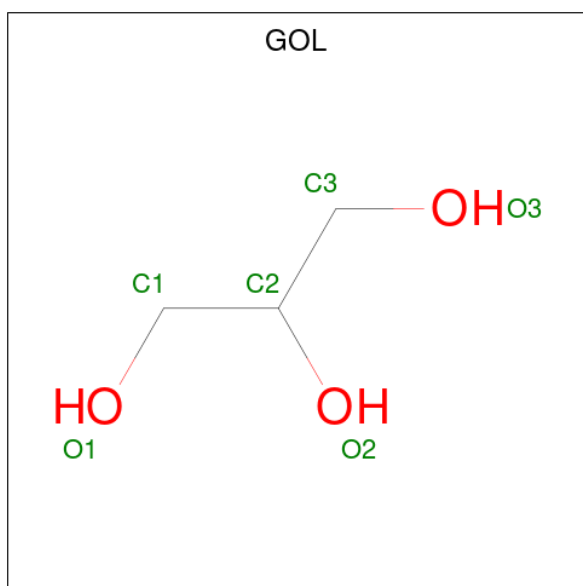
Chain	Residue	Modelled	Actual	Comment	Reference
A	12	GLY	-	expression tag	UNP A0A1Y5IEA9
A	13	HIS	-	expression tag	UNP A0A1Y5IEA9
A	14	HIS	-	expression tag	UNP A0A1Y5IEA9
A	15	HIS	-	expression tag	UNP A0A1Y5IEA9
A	16	HIS	-	expression tag	UNP A0A1Y5IEA9
A	17	HIS	-	expression tag	UNP A0A1Y5IEA9
A	18	HIS	-	expression tag	UNP A0A1Y5IEA9
A	19	HIS	-	expression tag	UNP A0A1Y5IEA9
B	12	GLY	-	expression tag	UNP A0A1Y5IEA9
B	13	HIS	-	expression tag	UNP A0A1Y5IEA9
B	14	HIS	-	expression tag	UNP A0A1Y5IEA9
B	15	HIS	-	expression tag	UNP A0A1Y5IEA9
B	16	HIS	-	expression tag	UNP A0A1Y5IEA9
B	17	HIS	-	expression tag	UNP A0A1Y5IEA9
B	18	HIS	-	expression tag	UNP A0A1Y5IEA9
B	19	HIS	-	expression tag	UNP A0A1Y5IEA9
C	12	GLY	-	expression tag	UNP A0A1Y5IEA9
C	13	HIS	-	expression tag	UNP A0A1Y5IEA9
C	14	HIS	-	expression tag	UNP A0A1Y5IEA9
C	15	HIS	-	expression tag	UNP A0A1Y5IEA9
C	16	HIS	-	expression tag	UNP A0A1Y5IEA9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	17	HIS	-	expression tag	UNP A0A1Y5IEA9
C	18	HIS	-	expression tag	UNP A0A1Y5IEA9
C	19	HIS	-	expression tag	UNP A0A1Y5IEA9
D	12	GLY	-	expression tag	UNP A0A1Y5IEA9
D	13	HIS	-	expression tag	UNP A0A1Y5IEA9
D	14	HIS	-	expression tag	UNP A0A1Y5IEA9
D	15	HIS	-	expression tag	UNP A0A1Y5IEA9
D	16	HIS	-	expression tag	UNP A0A1Y5IEA9
D	17	HIS	-	expression tag	UNP A0A1Y5IEA9
D	18	HIS	-	expression tag	UNP A0A1Y5IEA9
D	19	HIS	-	expression tag	UNP A0A1Y5IEA9

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

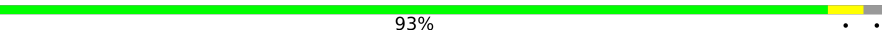
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	245	Total	O	0	0
			245	245		
4	B	213	Total	O	0	0
			213	213		
4	C	305	Total	O	0	0
			305	305		
4	D	254	Total	O	0	0
			254	254		

3 Residue-property plots

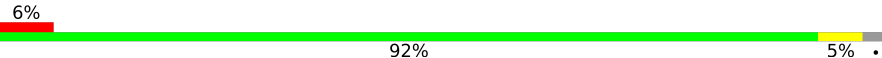
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

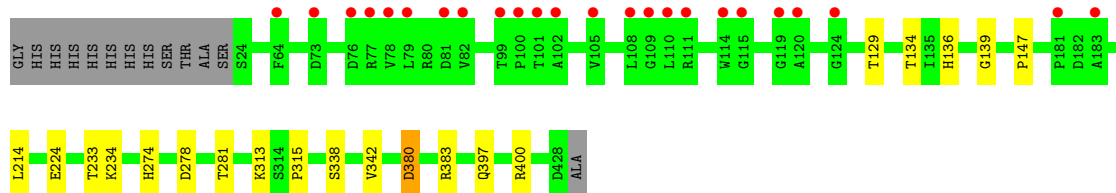
- Molecule 1: Isocitrate dehydrogenase

Chain A:  93%

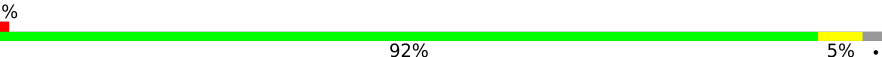


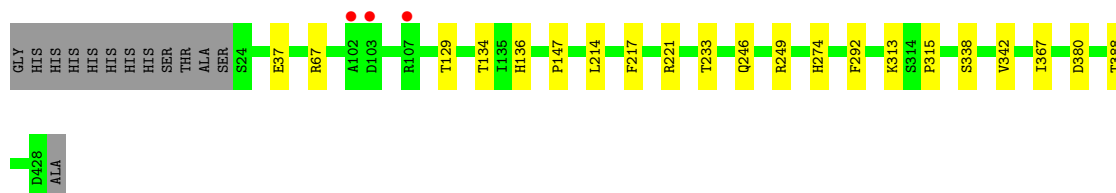
- Molecule 1: Isocitrate dehydrogenase

Chain B:  92% 5%



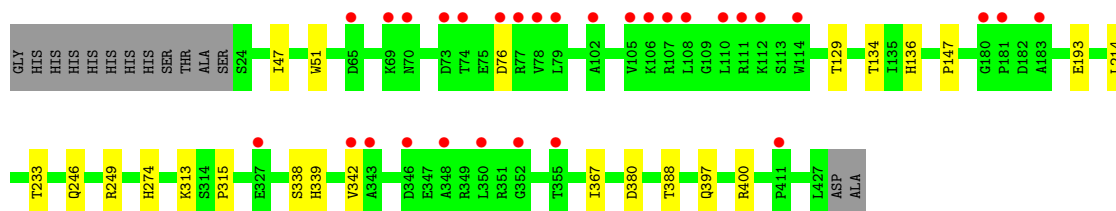
- Molecule 1: Isocitrate dehydrogenase

Chain C:  92% 5%



- Molecule 1: Isocitrate dehydrogenase

Chain D:  91% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.52Å 79.27Å 112.01Å 90.26° 102.32° 112.61°	Depositor
Resolution (Å)	20.00 – 1.75 20.00 – 1.75	Depositor EDS
% Data completeness (in resolution range)	96.4 (20.00-1.75) 96.4 (20.00-1.75)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 1.74Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.184 , 0.210 0.192 , 0.216	Depositor DCC
R_{free} test set	9913 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	17.6	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 34.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13686	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: GOL, 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	0.62	0/3235	0.81	0/4383
1	B	0.65	0/3210	0.84	0/4351
1	C	0.64	0/3238	0.81	0/4384
1	D	0.63	0/3202	0.82	0/4342
All	All	0.63	0/12885	0.82	0/17460

There are no bond length outliers.

There are no bond angle outliers.

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	3165	0	3067	9	0
1	B	3143	0	3029	10	0
1	C	3168	0	3087	12	0
1	D	3132	0	3015	11	0
2	A	6	0	8	1	0
2	B	12	0	16	0	0
2	C	12	0	16	2	0
2	D	6	0	8	1	0
3	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	245	0	0	2	0
4	B	213	0	0	0	0
4	C	305	0	0	0	0
4	D	254	0	0	1	0
All	All	13686	0	12246	42	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 2.

All (42) 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:397:GLN:OE1	1:B:400:ARG:NH2	2.21	0.74
1:D:397:GLN:OE1	1:D:400:ARG:NH2	2.30	0.64
1:C:233:THR:OG1	1:C:274:HIS:HE1	1.88	0.57
1:D:134:THR:OG1	1:D:136:HIS:HE1	1.89	0.56
1:B:134:THR:OG1	1:B:136:HIS:HE1	1.91	0.52
1:C:246:GLN:OE1	1:C:249:ARG:NH2	2.44	0.51
1:A:134:THR:OG1	1:A:136:HIS:HE1	1.95	0.50
1:B:233:THR:OG1	1:B:274:HIS:HE1	1.95	0.50
1:C:134:THR:OG1	1:C:136:HIS:HE1	1.95	0.49
1:D:129:THR:HB	1:D:214:LEU:HD13	1.95	0.48
1:D:233:THR:OG1	1:D:274:HIS:HE1	1.97	0.48
1:A:136:HIS:CE1	1:A:147:PRO:HA	2.50	0.47
1:A:367:ILE:HG23	1:A:388:THR:HB	1.97	0.47
1:C:367:ILE:HG23	1:C:388:THR:HB	1.96	0.47
1:D:193:GLU:HG2	4:D:829:HOH:O	2.15	0.47
1:B:139:GLY:HA3	1:B:400:ARG:HD3	1.95	0.47
1:B:278:ASP:O	1:B:281:THR:HG22	2.15	0.46
1:A:342:VAL:HA	2:A:501:GOL:H32	1.98	0.46
1:D:136:HIS:CE1	1:D:147:PRO:HA	2.52	0.44
1:B:129:THR:HB	1:B:214:LEU:HD13	1.98	0.44
1:C:129:THR:HB	1:C:214:LEU:HD13	2.00	0.43
1:C:292:PHE:HB3	2:C:502:GOL:C1	2.49	0.43
1:A:233:THR:OG1	1:A:274:HIS:HE1	2.00	0.43
1:D:367:ILE:HG23	1:D:388:THR:HB	2.01	0.43
1:D:246:GLN:OE1	1:D:249:ARG:NH2	2.52	0.43
1:D:339:HIS:HB2	2:D:501:GOL:H31	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:292:PHE:HB3	2:C:502:GOL:H12	2.00	0.42
1:C:136:HIS:CE1	1:C:147:PRO:HA	2.54	0.42
1:B:136:HIS:CE1	1:B:147:PRO:HA	2.55	0.42
1:B:380:ASP:OD1	1:B:383:ARG:HD3	2.20	0.42
1:A:215:ALA:HA	1:A:248:MET:HE3	2.02	0.42
1:C:217:PHE:CZ	1:C:221:ARG:HD3	2.55	0.41
1:B:315:PRO:O	1:B:338:SER:HB2	2.19	0.41
1:C:315:PRO:O	1:C:338:SER:HB2	2.20	0.41
1:C:37:GLU:HB3	1:C:67:ARG:HG2	2.03	0.41
1:A:149:LEU:O	1:A:293:GLY:HA2	2.21	0.41
1:C:233:THR:OG1	1:C:274:HIS:CE1	2.72	0.41
1:A:129:THR:HB	1:A:214:LEU:CD1	2.50	0.41
1:A:274:HIS:HD2	4:A:807:HOH:O	2.04	0.41
1:D:315:PRO:O	1:D:338:SER:HB2	2.20	0.41
4:A:634:HOH:O	1:B:234:LYS:HD3	2.20	0.40
1:D:47:ILE:HG23	1:D:51:TRP:CE3	2.57	0.40

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	404/418 (97%)	393 (97%)	10 (2%)	1 (0%)	43	27
1	B	403/418 (96%)	394 (98%)	8 (2%)	1 (0%)	43	27
1	C	404/418 (97%)	395 (98%)	8 (2%)	1 (0%)	43	27
1	D	403/418 (96%)	394 (98%)	8 (2%)	1 (0%)	43	27
All	All	1614/1672 (96%)	1576 (98%)	34 (2%)	4 (0%)	43	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	313	LYS
1	D	313	LYS
1	A	313	LYS
1	C	313	LYS

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	328/346 (95%)	326 (99%)	2 (1%)	78	71
1	B	324/346 (94%)	321 (99%)	3 (1%)	70	60
1	C	328/346 (95%)	326 (99%)	2 (1%)	78	71
1	D	321/346 (93%)	318 (99%)	3 (1%)	70	60
All	All	1301/1384 (94%)	1291 (99%)	10 (1%)	73	64

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	76	ASP
1	A	380	ASP
1	B	224	GLU
1	B	342	VAL
1	B	380	ASP
1	C	342	VAL
1	C	380	ASP
1	D	76	ASP
1	D	342	VAL
1	D	380	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	136	HIS
1	A	206	ASN
1	A	259	GLN

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Mol	Chain	Res	Type
1	A	274	HIS
1	A	371	ASN
1	B	136	HIS
1	B	212	HIS
1	B	274	HIS
1	C	136	HIS
1	C	165	ASN
1	C	212	HIS
1	C	274	HIS
1	C	378	ASN
1	D	136	HIS
1	D	212	HIS
1	D	274	HIS
1	D	286	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 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	D	502	-	4,4,4	0.53	0	6,6,6	0.26	0
2	GOL	C	502	-	5,5,5	0.27	0	5,5,5	0.52	0
3	SO4	A	503	-	4,4,4	0.44	0	6,6,6	0.20	0
2	GOL	D	501	-	5,5,5	0.23	0	5,5,5	0.38	0
2	GOL	B	502	-	5,5,5	0.15	0	5,5,5	0.33	0
3	SO4	B	503	-	4,4,4	0.46	0	6,6,6	0.32	0
2	GOL	B	501	-	5,5,5	0.21	0	5,5,5	0.66	0
3	SO4	A	502	-	4,4,4	0.38	0	6,6,6	0.31	0
2	GOL	A	501	-	5,5,5	0.32	0	5,5,5	0.72	0
2	GOL	C	501	-	5,5,5	0.33	0	5,5,5	0.74	0
3	SO4	C	503	-	4,4,4	0.43	0	6,6,6	0.22	0

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	GOL	C	502	-	-	2/4/4/4	-
2	GOL	D	501	-	-	2/4/4/4	-
2	GOL	B	502	-	-	0/4/4/4	-
2	GOL	B	501	-	-	1/4/4/4	-
2	GOL	A	501	-	-	4/4/4/4	-
2	GOL	C	501	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	C1-C2-C3-O3
2	C	501	GOL	O1-C1-C2-C3
2	D	501	GOL	O1-C1-C2-O2
2	D	501	GOL	O1-C1-C2-C3
2	C	501	GOL	O2-C2-C3-O3
2	A	501	GOL	O1-C1-C2-C3
2	C	501	GOL	C1-C2-C3-O3
2	C	502	GOL	C1-C2-C3-O3
2	A	501	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
2	C	501	GOL	O1-C1-C2-O2
2	C	502	GOL	O2-C2-C3-O3
2	A	501	GOL	O1-C1-C2-O2
2	B	501	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	502	GOL	2	0
2	D	501	GOL	1	0
2	A	501	GOL	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 ⓘ

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	405/418 (96%)	-0.15	2 (0%) 87 90	10, 18, 31, 47	1 (0%)
1	B	405/418 (96%)	0.14	24 (5%) 28 32	11, 19, 35, 51	0
1	C	405/418 (96%)	-0.31	3 (0%) 84 88	8, 15, 27, 51	1 (0%)
1	D	404/418 (96%)	0.22	30 (7%) 20 24	10, 18, 40, 63	1 (0%)
All	All	1619/1672 (96%)	-0.03	59 (3%) 46 52	8, 18, 35, 63	3 (0%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	108	LEU	5.0
1	B	114	TRP	4.3
1	D	110	LEU	4.3
1	D	108	LEU	3.9
1	B	110	LEU	3.8
1	B	78	VAL	3.5
1	D	114	TRP	3.5
1	B	109	GLY	3.4
1	D	105	VAL	3.3
1	B	120	ALA	3.3
1	D	111	ARG	3.2
1	B	105	VAL	3.2
1	D	74	THR	3.2
1	D	73	ASP	3.2
1	D	70	ASN	3.2
1	D	343	ALA	3.1
1	D	65	ASP	3.1
1	D	102	ALA	3.0
1	D	112	LYS	2.9
1	D	350	LEU	2.9
1	B	76	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	115	GLY	2.8
1	D	78	VAL	2.7
1	D	352	GLY	2.6
1	B	81	ASP	2.6
1	D	327	GLU	2.6
1	B	183	ALA	2.5
1	B	111	ARG	2.5
1	D	107	ARG	2.5
1	B	64	PHE	2.5
1	B	73	ASP	2.5
1	D	77	ARG	2.5
1	D	180	GLY	2.4
1	B	102	ALA	2.4
1	C	107	ARG	2.4
1	D	183	ALA	2.3
1	D	69	LYS	2.3
1	B	99	THR	2.3
1	B	181	PRO	2.2
1	D	348	ALA	2.2
1	A	428	ASP	2.2
1	C	103	ASP	2.2
1	B	100	PRO	2.2
1	D	181	PRO	2.2
1	C	102	ALA	2.2
1	B	119	GLY	2.2
1	A	24	SER	2.2
1	D	355	THR	2.1
1	D	411	PRO	2.1
1	B	79	LEU	2.1
1	D	79	LEU	2.1
1	B	77	ARG	2.1
1	B	101	THR	2.1
1	D	342	VAL	2.0
1	B	124	GLY	2.0
1	D	76	ASP	2.0
1	D	346	ASP	2.0
1	B	82	VAL	2.0
1	D	106	LYS	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	GOL	C	501	6/6	0.65	0.26	32,32,35,39	0
2	GOL	D	501	6/6	0.69	0.23	35,37,42,42	0
2	GOL	A	501	6/6	0.72	0.22	34,37,40,42	0
2	GOL	C	502	6/6	0.79	0.15	35,39,40,40	0
2	GOL	B	501	6/6	0.79	0.15	29,34,37,39	0
2	GOL	B	502	6/6	0.80	0.21	36,39,42,42	0
3	SO4	B	503	5/5	0.91	0.12	37,39,42,44	0
3	SO4	A	502	5/5	0.92	0.12	39,40,44,47	0
3	SO4	C	503	5/5	0.92	0.08	45,46,47,50	0
3	SO4	A	503	5/5	0.93	0.07	45,46,48,49	0
3	SO4	D	502	5/5	0.96	0.08	31,33,35,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.