Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 08:53 am BST

PDB ID	:	3TB2
Title	:	1-Cys peroxidoxin from Plasmodium Yoelli
Authors	:	Qiu, W.; Artz, J.D.; Vedadi, M.; Sharma, S.; Houston, S.; Lew, J.; Wasney, G.; Amani, M.; Xu, X.; Bray, J.; Sundstrom, M.; Arrowsmith, C.; Edwards, A.; Hui, R.; Bochkarev, A.; Structural Genomics Consortium (SGC)
Deposited on	:	2011-08-04
Resolution	:	2.30 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:

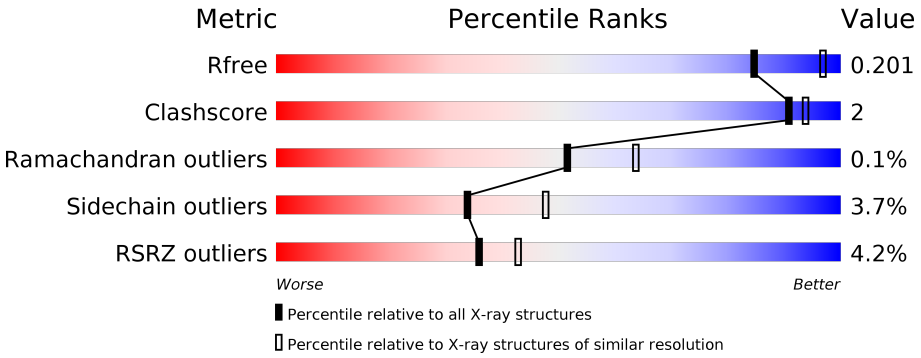
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	220	3% 95% 5%
1	B	220	8% 89% 10%
1	C	220	3% 93% 7%
1	D	220	3% 93% 7%

2 Entry composition

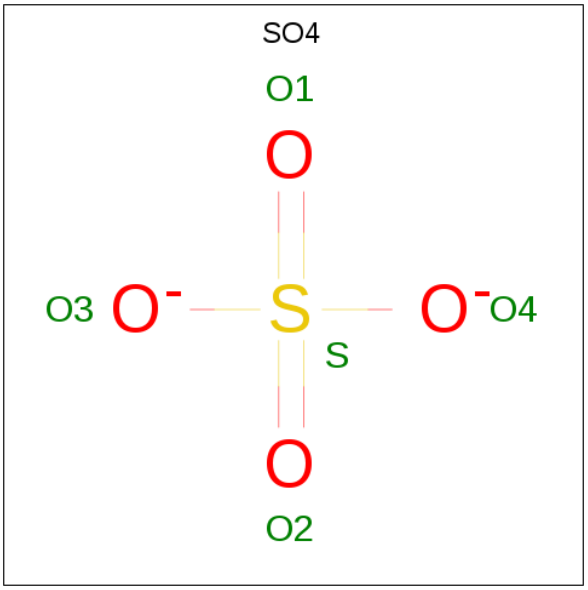
There are 5 unique types of molecules in this entry. The entry contains 7866 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 1-Cys peroxiredoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1771	1140	289	331	11			
1	B	219	Total	C	N	O	S	0	0	0
			1771	1140	289	331	11			
1	C	220	Total	C	N	O	S	0	1	0
			1786	1150	292	332	12			
1	D	219	Total	C	N	O	S	0	1	0
			1778	1145	291	331	11			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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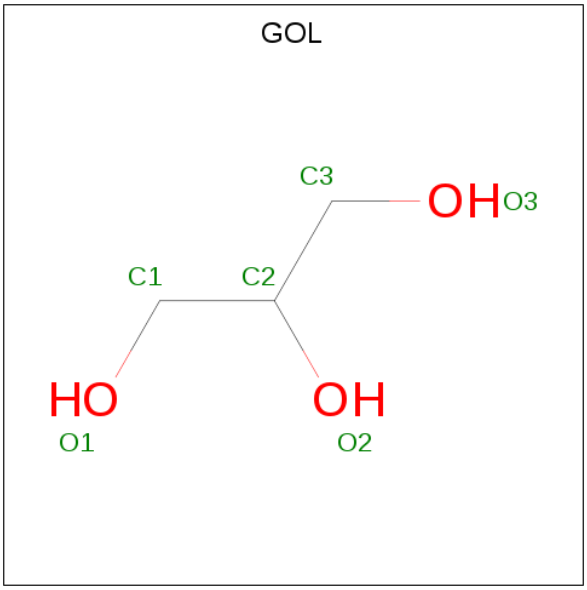
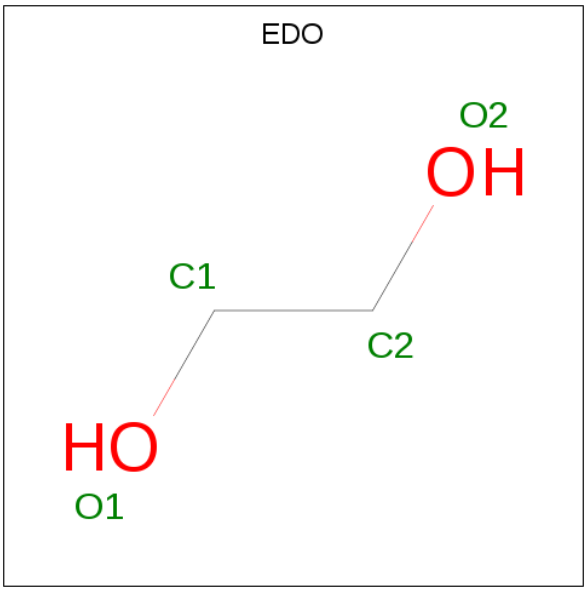
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O S 5 4 1	0	0
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 5 is water.

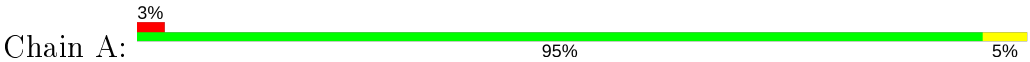
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	164	Total O 164 164	0	0
5	B	138	Total O 138 138	0	0
5	C	173	Total O 173 173	0	0
5	D	152	Total O 152 152	0	0

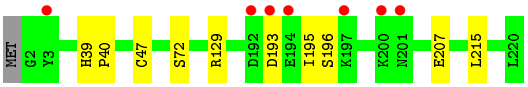
3 Residue-property plots (i)

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: 1-Cys peroxiredoxin

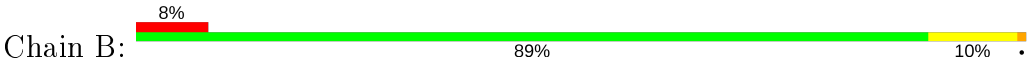
Chain A:





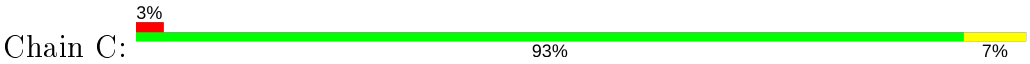
- Molecule 1: 1-Cys peroxiredoxin

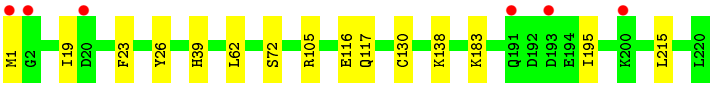
Chain B:



- Molecule 1: 1-Cys peroxiredoxin

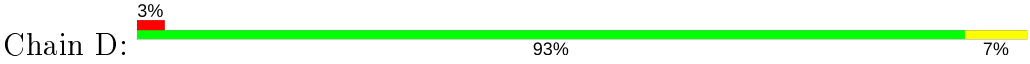
Chain C:

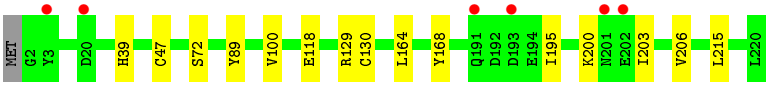




- Molecule 1: 1-Cys peroxiredoxin

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	90.39Å 156.84Å 178.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	78.42 – 2.30 19.97 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (78.42-2.30) 99.8 (19.97-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.32 (at 2.30Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.166 , 0.203 0.164 , 0.201	Depositor DCC
R_{free} test set	2858 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	36.0	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 51.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.015 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.024 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7866	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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: GOL, CSD, EDO, 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	0.49	0/1806	0.66	0/2443
1	B	0.50	0/1806	0.67	0/2443
1	C	0.49	0/1825	0.70	0/2468
1	D	0.46	0/1817	0.65	0/2458
All	All	0.48	0/7254	0.67	0/9812

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

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	1771	0	1771	3	0
1	B	1771	0	1771	10	0
1	C	1786	0	1790	7	0
1	D	1778	0	1778	5	0
2	A	10	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	0	8	0	0
3	C	6	0	8	0	0
3	D	6	0	8	1	0
4	A	24	0	36	0	0
4	B	12	0	18	3	0
4	C	24	0	36	2	0
4	D	24	0	36	1	0
5	A	164	0	0	0	0
5	B	138	0	0	0	0
5	C	173	0	0	0	0
5	D	152	0	0	0	0
All	All	7866	0	7268	25	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 (25) 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:153:ASN:HD21	4:B:224:EDO:H12	1.24	0.98
1:B:19:ILE:HG13	1:B:20:ASP:N	1.97	0.77
1:C:183:LYS:H	4:C:228:EDO:H12	1.68	0.59
1:B:206:VAL:HB	1:B:215:LEU:HD23	1.86	0.56
1:D:206:VAL:HB	1:D:215:LEU:HD23	1.87	0.56
1:B:17:SER:O	1:B:19:ILE:HG23	2.08	0.54
1:B:39:HIS:HB2	1:B:47:CSD:OD1	2.09	0.53
4:B:224:EDO:H11	4:D:227:EDO:H11	1.91	0.52
1:C:116:GLU:HG2	1:C:117:GLN:HG2	1.94	0.49
1:C:26:TYR:CE1	1:C:138:LYS:HG2	2.50	0.47
1:B:153:ASN:ND2	4:B:224:EDO:H12	2.09	0.45
1:B:40:PRO:HD2	1:B:47:CSD:OD1	2.16	0.45
1:C:39:HIS:CE1	1:C:72:SER:HB3	2.52	0.45
1:C:19:ILE:HD11	1:C:23:PHE:HB2	1.98	0.45
1:C:183:LYS:H	4:C:228:EDO:C1	2.29	0.44
1:B:188:PRO:HD3	3:D:222:GOL:H11	2.00	0.44
1:D:47:CSD:OD1	1:D:129:ARG:NH1	2.48	0.44
1:B:164:LEU:O	1:B:168:TYR:HB2	2.19	0.42
1:A:40:PRO:HD2	1:A:47:CSD:OD1	2.21	0.41
1:D:39:HIS:CE1	1:D:72:SER:HB3	2.56	0.41
1:A:39:HIS:CE1	1:A:72:SER:HB3	2.56	0.41
1:A:47:CSD:OD1	1:A:129:ARG:NH1	2.49	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:TYR:CZ	1:C:138:LYS:HG2	2.56	0.40
1:B:215:LEU:HD21	1:D:89:TYR:CD1	2.56	0.40
1:D:164:LEU:O	1:D:168:TYR:HB2	2.21	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	216/220 (98%)	211 (98%)	5 (2%)	0	100 100
1	B	216/220 (98%)	211 (98%)	4 (2%)	1 (0%)	29 35
1	C	218/220 (99%)	213 (98%)	5 (2%)	0	100 100
1	D	217/220 (99%)	211 (97%)	6 (3%)	0	100 100
All	All	867/880 (98%)	846 (98%)	20 (2%)	1 (0%)	51 64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	18	GLY

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	198/199 (100%)	193 (98%)	5 (2%)	47	65
1	B	198/199 (100%)	186 (94%)	12 (6%)	18	25
1	C	200/199 (100%)	194 (97%)	6 (3%)	41	57
1	D	199/199 (100%)	193 (97%)	6 (3%)	41	57
All	All	795/796 (100%)	766 (96%)	29 (4%)	34	49

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	193	ASP
1	A	195	ILE
1	A	196	SER
1	A	207	GLU
1	A	215	LEU
1	B	19	ILE
1	B	20	ASP
1	B	32	SER
1	B	62	LEU
1	B	130	CYS
1	B	138	LYS
1	B	170	THR
1	B	192	ASP
1	B	193	ASP
1	B	195	ILE
1	B	202	GLU
1	B	203	ILE
1	C	1	MET
1	C	62	LEU
1	C	105	ARG
1	C	130	CYS
1	C	195	ILE
1	C	215	LEU
1	D	100	VAL
1	D	118	GLU
1	D	130	CYS
1	D	195	ILE
1	D	200	LYS
1	D	203	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	HIS
1	A	58	HIS
1	D	177	ASN
1	D	191	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

4 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	CSD	B	47	1	3,7,8	0.56	0	1,8,10	1.95	0
1	CSD	A	47	1	3,7,8	0.50	0	1,8,10	2.36	1 (100%)
1	CSD	D	47	1	3,7,8	0.58	0	1,8,10	0.15	0
1	CSD	C	47	1	3,7,8	0.65	0	1,8,10	0.96	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
1	CSD	B	47	1	-	0/2/6/8	-
1	CSD	A	47	1	-	0/2/6/8	-
1	CSD	D	47	1	-	1/2/6/8	-
1	CSD	C	47	1	-	1/2/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	47	CSD	OD1-SG-CB	-2.36	101.04	105.54

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	47	CSD	CA-CB-SG-OD1
1	C	47	CSD	CA-CB-SG-OD1

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	47	CSD	2	0
1	A	47	CSD	2	0
1	D	47	CSD	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

30 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	GOL	B	222	-	5,5,5	0.96	0	5,5,5	0.79	0
3	GOL	D	222	-	5,5,5	0.78	0	5,5,5	1.12	0
3	GOL	C	222	-	5,5,5	0.89	0	5,5,5	1.08	0
4	EDO	D	225	-	3,3,3	0.47	0	2,2,2	0.41	0
4	EDO	A	224	-	3,3,3	0.43	0	2,2,2	0.28	0
2	SO4	A	222	-	4,4,4	0.29	0	6,6,6	0.08	0
4	EDO	C	224	-	3,3,3	0.42	0	2,2,2	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	EDO	D	223	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	A	229	-	3,3,3	0.50	0	2,2,2	0.28	0
2	SO4	B	221	-	4,4,4	0.18	0	6,6,6	0.07	0
3	GOL	A	223	-	5,5,5	0.55	0	5,5,5	0.95	0
4	EDO	A	227	-	3,3,3	0.46	0	2,2,2	0.29	0
4	EDO	B	223	-	3,3,3	0.44	0	2,2,2	0.44	0
4	EDO	D	226	-	3,3,3	0.42	0	2,2,2	0.34	0
4	EDO	A	226	-	3,3,3	0.45	0	2,2,2	0.39	0
4	EDO	D	224	-	3,3,3	0.47	0	2,2,2	0.37	0
4	EDO	C	225	-	3,3,3	0.44	0	2,2,2	0.31	0
4	EDO	A	225	-	3,3,3	0.53	0	2,2,2	0.23	0
4	EDO	B	225	-	3,3,3	0.57	0	2,2,2	0.12	0
2	SO4	D	221	-	4,4,4	0.23	0	6,6,6	0.11	0
4	EDO	C	228	-	3,3,3	0.53	0	2,2,2	0.16	0
2	SO4	C	221	-	4,4,4	0.24	0	6,6,6	0.14	0
2	SO4	A	221	-	4,4,4	0.26	0	6,6,6	0.14	0
4	EDO	C	227	-	3,3,3	0.42	0	2,2,2	0.61	0
4	EDO	C	226	-	3,3,3	0.49	0	2,2,2	0.34	0
4	EDO	C	223	-	3,3,3	0.51	0	2,2,2	0.17	0
4	EDO	D	227	-	3,3,3	0.41	0	2,2,2	0.44	0
4	EDO	B	224	-	3,3,3	0.63	0	2,2,2	0.45	0
4	EDO	A	228	-	3,3,3	0.45	0	2,2,2	0.39	0
4	EDO	D	228	-	3,3,3	0.48	0	2,2,2	0.27	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
3	GOL	B	222	-	-	2/4/4/4	-
3	GOL	D	222	-	-	3/4/4/4	-
3	GOL	C	222	-	-	2/4/4/4	-
4	EDO	D	225	-	-	0/1/1/1	-
4	EDO	A	224	-	-	1/1/1/1	-
4	EDO	C	224	-	-	0/1/1/1	-
4	EDO	D	223	-	-	0/1/1/1	-
4	EDO	A	229	-	-	1/1/1/1	-
3	GOL	A	223	-	-	0/4/4/4	-
4	EDO	A	227	-	-	0/1/1/1	-
4	EDO	B	223	-	-	0/1/1/1	-
4	EDO	A	226	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	D	224	-	-	1/1/1/1	-
4	EDO	C	225	-	-	0/1/1/1	-
4	EDO	A	225	-	-	1/1/1/1	-
4	EDO	B	225	-	-	1/1/1/1	-
4	EDO	C	228	-	-	1/1/1/1	-
4	EDO	D	226	-	-	0/1/1/1	-
4	EDO	C	227	-	-	0/1/1/1	-
4	EDO	C	226	-	-	0/1/1/1	-
4	EDO	C	223	-	-	0/1/1/1	-
4	EDO	D	227	-	-	1/1/1/1	-
4	EDO	B	224	-	-	1/1/1/1	-
4	EDO	A	228	-	-	1/1/1/1	-
4	EDO	D	228	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	222	GOL	C1-C2-C3-O3
3	C	222	GOL	O1-C1-C2-C3
3	D	222	GOL	O1-C1-C2-C3
4	D	224	EDO	O1-C1-C2-O2
4	A	225	EDO	O1-C1-C2-O2
4	D	227	EDO	O1-C1-C2-O2
3	B	222	GOL	O2-C2-C3-O3
3	C	222	GOL	O1-C1-C2-O2
3	D	222	GOL	O1-C1-C2-O2
4	A	228	EDO	O1-C1-C2-O2
4	B	225	EDO	O1-C1-C2-O2
4	B	224	EDO	O1-C1-C2-O2
3	D	222	GOL	O2-C2-C3-O3
4	A	224	EDO	O1-C1-C2-O2
4	A	229	EDO	O1-C1-C2-O2
4	C	228	EDO	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	222	GOL	1	0
4	C	228	EDO	2	0
4	D	227	EDO	1	0
4	B	224	EDO	3	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, 95^{th} 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	218/220 (99%)	-0.31	7 (3%)	47	54	25, 34, 74, 91	0
1	B	218/220 (99%)	-0.08	18 (8%)	11	15	28, 42, 87, 104	0
1	C	219/220 (99%)	-0.33	6 (2%)	54	62	25, 35, 68, 86	0
1	D	218/220 (99%)	-0.27	6 (2%)	53	60	28, 39, 74, 95	0
All	All	873/880 (99%)	-0.25	37 (4%)	36	43	25, 37, 75, 104	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	MET	7.0
1	B	201	ASN	4.3
1	B	20	ASP	4.1
1	C	2	GLY	3.6
1	A	200	LYS	3.6
1	B	191	GLN	3.6
1	B	2	GLY	3.5
1	C	200	LYS	3.4
1	B	181	GLY	3.3
1	A	192	ASP	3.3
1	B	18	GLY	3.2
1	D	193	ASP	3.1
1	A	197	LYS	3.0
1	B	198	HIS	3.0
1	C	20	ASP	2.9
1	C	193	ASP	2.9
1	A	193	ASP	2.8
1	B	94	LYS	2.8
1	B	192	ASP	2.7
1	D	20	ASP	2.7
1	D	3	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	31	ASN	2.7
1	B	202	GLU	2.7
1	B	200	LYS	2.6
1	C	191	GLN	2.6
1	A	201	ASN	2.6
1	D	202	GLU	2.6
1	B	199	PHE	2.5
1	A	194	GLU	2.5
1	A	3	TYR	2.2
1	D	191	GLN	2.2
1	B	59	GLU	2.2
1	B	4	HIS	2.1
1	B	197	LYS	2.1
1	D	201	ASN	2.1
1	B	19	ILE	2.0
1	B	193	ASP	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, 95^{th} 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	CSD	B	47	8/9	0.96	0.09	34,36,41,42	0
1	CSD	A	47	8/9	0.97	0.08	29,31,35,36	0
1	CSD	D	47	8/9	0.97	0.09	33,35,39,39	0
1	CSD	C	47	8/9	0.99	0.07	26,29,33,35	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, 95^{th} 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
4	EDO	C	228	4/4	0.75	0.23	63,63,65,71	0
4	EDO	B	225	4/4	0.77	0.40	86,86,87,91	0
2	SO4	B	221	5/5	0.77	0.24	148,152,153,153	0
4	EDO	D	224	4/4	0.84	0.15	69,70,70,78	0
4	EDO	D	228	4/4	0.84	0.20	79,79,79,86	0
4	EDO	B	224	4/4	0.85	0.25	41,43,44,48	0
4	EDO	A	226	4/4	0.87	0.32	79,79,79,86	0
4	EDO	C	226	4/4	0.88	0.19	68,68,69,77	0
4	EDO	A	227	4/4	0.88	0.24	74,75,76,80	0
4	EDO	A	225	4/4	0.88	0.19	69,72,74,75	0
4	EDO	B	223	4/4	0.89	0.28	61,61,62,71	0
3	GOL	D	222	6/6	0.89	0.16	47,50,51,51	0
4	EDO	A	229	4/4	0.89	0.31	73,75,76,77	0
4	EDO	C	227	4/4	0.90	0.29	70,70,71,75	0
4	EDO	C	225	4/4	0.91	0.20	55,56,58,65	0
4	EDO	D	225	4/4	0.92	0.23	69,71,73,74	0
3	GOL	A	223	6/6	0.93	0.14	42,46,47,48	0
3	GOL	C	222	6/6	0.93	0.15	42,44,45,46	0
2	SO4	A	222	5/5	0.93	0.23	90,94,96,96	0
4	EDO	A	228	4/4	0.93	0.18	59,59,60,64	0
2	SO4	C	221	5/5	0.93	0.27	89,93,94,94	0
2	SO4	D	221	5/5	0.95	0.19	101,106,106,107	0
4	EDO	D	223	4/4	0.95	0.19	59,61,63,63	0
4	EDO	C	223	4/4	0.96	0.15	40,41,46,47	0
3	GOL	B	222	6/6	0.96	0.10	41,43,43,45	0
4	EDO	D	226	4/4	0.96	0.14	62,64,65,68	0
4	EDO	A	224	4/4	0.96	0.11	38,39,43,46	0
4	EDO	D	227	4/4	0.97	0.18	56,57,59,63	0
2	SO4	A	221	5/5	0.97	0.18	64,68,70,71	0
4	EDO	C	224	4/4	0.99	0.07	39,41,42,46	0

6.5 Other polymers (i)

There are no such residues in this entry.