



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 3, 2023 – 10:05 AM EDT

PDB ID : 8TFG  
Title : 1.88A CRYSTAL STRUCTURE OF MYCOBACTERIUM TUBERCULOSIS  
TOPOISOMERASE I  
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Deposited on : 2023-07-11  
Resolution : 1.88 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](mailto: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>.

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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 : 2.34  
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) : 2.34

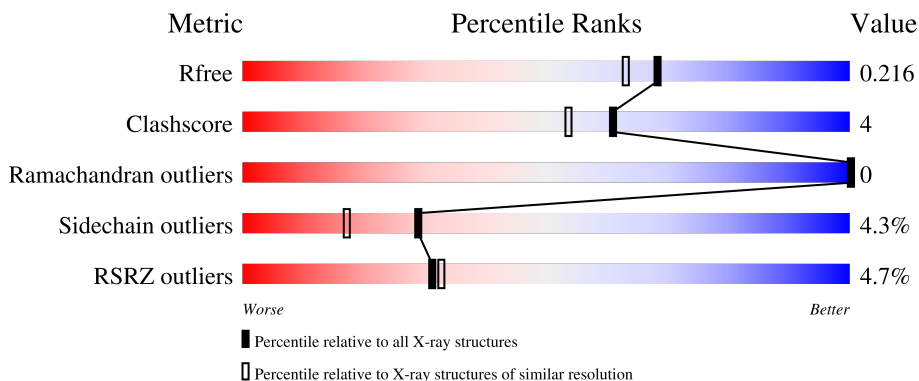
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.88 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	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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  $\geq 3$ , 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	688	

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
3	ACT	A	813	-	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5875 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 DNA topoisomerase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	688	5428	3403	971	1045	9	0	11	0

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



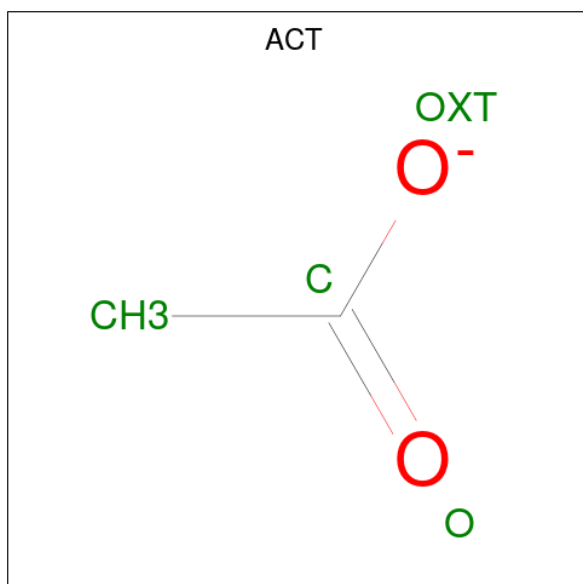
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	4	2	2	0	0
2	A	1	4	2	2	0	0
2	A	1	4	2	2	0	0
2	A	1	4	2	2	0	0
2	A	1	4	2	2	0	0

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

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

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

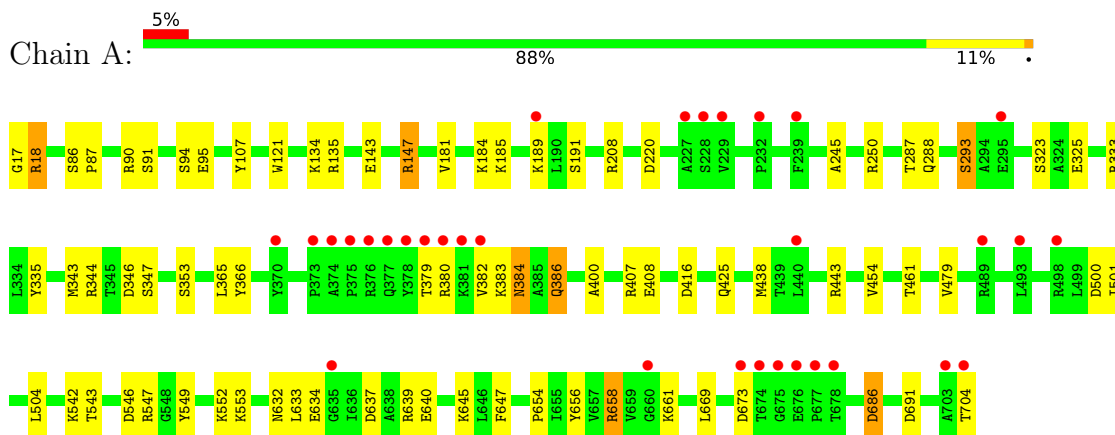
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	373	Total	O	0	2
			375	375		

### 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 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: DNA topoisomerase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.37Å 92.88Å 139.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.49 – 1.88 49.49 – 1.88	Depositor EDS
% Data completeness (in resolution range)	98.7 (49.49-1.88) 98.7 (49.49-1.88)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.42 (at 1.88Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.178 , 0.217 0.176 , 0.216	Depositor DCC
$R_{free}$ test set	3362 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.2	Xtrriage
Anisotropy	0.200	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 37.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5875	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: ACT, 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	0.70	2/5550 (0.0%)	0.79	3/7538 (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	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	549	TYR	CE2-CZ	5.26	1.45	1.38
1	A	335	TYR	CD2-CE2	5.04	1.47	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	ARG	CB-CG-CD	-5.51	97.28	111.60
1	A	691	ASP	CB-CG-OD1	5.32	123.09	118.30
1	A	220	ASP	CB-CG-OD2	-5.01	113.79	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	250	ARG	Sidechain



## 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	5428	0	5393	46	0
2	A	44	0	66	10	0
3	A	28	0	21	4	0
4	A	375	0	0	6	0
All	All	5875	0	5480	49	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 4.

All (49) 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:656:TYR:CE1	1:A:658:ARG:HD3	2.19	0.78
1:A:656:TYR:HE1	1:A:658:ARG:HD3	1.50	0.76
1:A:121:TRP:CZ2	2:A:803:EDO:H21	2.27	0.70
1:A:353:SER:HA	3:A:816:ACT:H2	1.76	0.67
1:A:425:GLN:HG2	4:A:1144:HOH:O	1.95	0.66
1:A:408:GLU:HG3	4:A:909:HOH:O	1.95	0.65
1:A:552:LYS:NZ	2:A:810:EDO:H22	2.11	0.65
1:A:143:GLU:OE2	1:A:147:ARG:NH1	2.32	0.62
1:A:325:GLU:OE2	1:A:542:LYS:HE2	2.02	0.60
1:A:686:ASP:N	1:A:686:ASP:OD1	2.34	0.59
1:A:87:PRO:O	1:A:90:ARG:HG3	2.04	0.58
1:A:347:SER:HB2	1:A:382:VAL:HG21	1.84	0.58
1:A:333:ARG:HA	2:A:809:EDO:H11	1.87	0.56
1:A:400:ALA:HB1	2:A:808:EDO:H11	1.87	0.56
1:A:346:ASP:OD1	1:A:382:VAL:HG13	2.06	0.56
1:A:637:ASP:HB3	1:A:640:GLU:OE2	2.07	0.55
2:A:811:EDO:H22	4:A:1230:HOH:O	2.07	0.54
1:A:552:LYS:HZ3	2:A:810:EDO:H22	1.74	0.52
1:A:293:SER:HB2	1:A:443:ARG:HB3	1.93	0.51
1:A:542:LYS:NZ	1:A:546:ASP:OD2	2.42	0.50
1:A:91:SER:O	1:A:95:GLU:HG3	2.12	0.50
1:A:17:GLY:N	1:A:18:ARG:HH11	2.10	0.50
1:A:365[A]:LEU:HD23	1:A:366:TYR:CZ	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:TYR:CZ	1:A:134:LYS:HD2	2.46	0.49
1:A:384:ASN:HD22	1:A:386:GLN:H	1.59	0.49
1:A:245:ALA:HB3	1:A:454:VAL:HB	1.94	0.49
1:A:634:GLU:HA	1:A:634:GLU:OE1	2.13	0.49
1:A:181:VAL:HG22	1:A:633:LEU:HD11	1.95	0.47
2:A:809:EDO:H22	4:A:1067:HOH:O	2.14	0.47
1:A:501:ILE:O	3:A:818:ACT:H3	2.15	0.47
1:A:344:ARG:O	2:A:806:EDO:H22	2.15	0.47
1:A:384:ASN:HD21	1:A:386:GLN:HB2	1.78	0.47
1:A:384:ASN:ND2	1:A:386:GLN:HB2	2.31	0.46
1:A:501:ILE:HG21	1:A:504:LEU:HG	1.97	0.46
1:A:632:ASN:OD1	1:A:634:GLU:HB2	2.16	0.46
1:A:400:ALA:CB	2:A:808:EDO:H11	2.45	0.45
1:A:543[A]:THR:HG23	1:A:547:ARG:NE	2.32	0.45
3:A:813:ACT:H1	4:A:1245:HOH:O	2.17	0.45
1:A:479:VAL:CG2	3:A:813:ACT:H2	2.47	0.44
1:A:407:ARG:HB2	4:A:909:HOH:O	2.17	0.44
1:A:658:ARG:HB3	1:A:658:ARG:NH1	2.32	0.44
1:A:288:GLN:NE2	1:A:500:ASP:OD1	2.49	0.43
1:A:504:LEU:HD23	1:A:504:LEU:HA	1.90	0.42
1:A:661:LYS:H	1:A:661:LYS:HG2	1.59	0.41
1:A:323:SER:HA	2:A:810:EDO:H21	2.01	0.41
1:A:438:MET:HB2	1:A:461:THR:OG1	2.21	0.41
1:A:637:ASP:OD2	1:A:640:GLU:HG3	2.20	0.41
1:A:184:LYS:HD3	1:A:185:LYS:HE2	2.03	0.40
1:A:645:LYS:HE2	1:A:654:PRO:HB3	2.04	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	697/688 (101%)	684 (98%)	13 (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	571/563 (101%)	546 (96%)	25 (4%)	28	16

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ARG
1	A	86	SER
1	A	94	SER
1	A	135	ARG
1	A	147	ARG
1	A	189	LYS
1	A	191	SER
1	A	287[A]	THR
1	A	287[B]	THR
1	A	293	SER
1	A	343	MET
1	A	379	THR
1	A	380	ARG
1	A	383	LYS
1	A	384	ASN
1	A	386	GLN
1	A	416	ASP
1	A	553	LYS
1	A	639	ARG
1	A	647	PHE
1	A	658	ARG
1	A	669	LEU
1	A	673	ASP

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Mol	Chain	Res	Type
1	A	686	ASP
1	A	704	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	384	ASN

### 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](#)

18 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	EDO	A	806	-	3,3,3	0.90	0	2,2,2	0.50	0
2	EDO	A	804	-	3,3,3	0.57	0	2,2,2	0.29	0
2	EDO	A	809	-	3,3,3	0.39	0	2,2,2	0.88	0
3	ACT	A	817	-	3,3,3	1.80	1 (33%)	3,3,3	1.22	0
3	ACT	A	815	-	3,3,3	1.03	0	3,3,3	2.04	2 (66%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	ACT	A	812	-	3,3,3	1.76	1 (33%)	3,3,3	0.92	0
2	EDO	A	811	-	3,3,3	0.87	0	2,2,2	0.76	0
2	EDO	A	805	-	3,3,3	0.76	0	2,2,2	0.21	0
3	ACT	A	813	-	3,3,3	0.54	0	3,3,3	1.70	1 (33%)
2	EDO	A	810	-	3,3,3	0.75	0	2,2,2	0.67	0
3	ACT	A	818	-	3,3,3	1.39	1 (33%)	3,3,3	1.37	0
2	EDO	A	801	-	3,3,3	0.56	0	2,2,2	0.43	0
2	EDO	A	807	-	3,3,3	0.67	0	2,2,2	0.36	0
3	ACT	A	814	-	3,3,3	1.68	1 (33%)	3,3,3	1.36	0
3	ACT	A	816	-	3,3,3	1.53	1 (33%)	3,3,3	1.18	0
2	EDO	A	803	-	3,3,3	0.68	0	2,2,2	1.13	0
2	EDO	A	802	-	3,3,3	0.61	0	2,2,2	0.70	0
2	EDO	A	808	-	3,3,3	0.45	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
2	EDO	A	806	-	-	0/1/1/1	-
2	EDO	A	804	-	-	0/1/1/1	-
2	EDO	A	809	-	-	1/1/1/1	-
2	EDO	A	811	-	-	1/1/1/1	-
2	EDO	A	805	-	-	0/1/1/1	-
2	EDO	A	810	-	-	0/1/1/1	-
2	EDO	A	801	-	-	1/1/1/1	-
2	EDO	A	807	-	-	1/1/1/1	-
2	EDO	A	803	-	-	1/1/1/1	-
2	EDO	A	802	-	-	0/1/1/1	-
2	EDO	A	808	-	-	1/1/1/1	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	814	ACT	CH3-C	2.67	1.60	1.49
3	A	817	ACT	CH3-C	2.67	1.60	1.49
3	A	812	ACT	CH3-C	2.66	1.60	1.49
3	A	816	ACT	CH3-C	2.28	1.58	1.49
3	A	818	ACT	CH3-C	2.11	1.58	1.49

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	815	ACT	O-C-CH3	-2.75	111.62	122.33
3	A	813	ACT	O-C-CH3	-2.16	113.92	122.33
3	A	815	ACT	OXT-C-O	2.05	129.61	122.05

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	811	EDO	O1-C1-C2-O2
2	A	803	EDO	O1-C1-C2-O2
2	A	808	EDO	O1-C1-C2-O2
2	A	809	EDO	O1-C1-C2-O2
2	A	807	EDO	O1-C1-C2-O2
2	A	801	EDO	O1-C1-C2-O2

There are no ring outliers.

9 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	806	EDO	1	0
2	A	809	EDO	2	0
2	A	811	EDO	1	0
3	A	813	ACT	2	0
2	A	810	EDO	3	0
3	A	818	ACT	1	0
3	A	816	ACT	1	0
2	A	803	EDO	1	0
2	A	808	EDO	2	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	688/688 (100%)	0.21	32 (4%) 31 33	22, 38, 73, 112	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	704	THR	5.1
1	A	379	THR	5.1
1	A	229	VAL	4.9
1	A	374	ALA	4.4
1	A	382	VAL	4.3
1	A	674	THR	4.1
1	A	375	PRO	3.6
1	A	675	GLY	3.5
1	A	232	PRO	3.4
1	A	380	ARG	3.3
1	A	228	SER	3.3
1	A	377	GLN	3.3
1	A	381	LYS	3.2
1	A	676	GLU	3.2
1	A	378	TYR	3.1
1	A	703	ALA	3.1
1	A	493	LEU	3.0
1	A	295[A]	GLU	2.6
1	A	635	GLY	2.6
1	A	660	GLY	2.6
1	A	189	LYS	2.5
1	A	677	PRO	2.5
1	A	678	THR	2.5
1	A	373	PRO	2.4
1	A	673	ASP	2.3
1	A	227	ALA	2.3
1	A	370	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	239	PHE	2.3
1	A	376	ARG	2.2
1	A	489	ARG	2.0
1	A	440	LEU	2.0
1	A	498	ARG	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no monosaccharides 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	EDO	A	811	4/4	0.64	0.23	42,46,50,52	0
3	ACT	A	816	4/4	0.64	0.29	56,70,72,78	0
3	ACT	A	817	4/4	0.65	0.24	48,57,58,61	0
3	ACT	A	814	4/4	0.81	0.16	37,41,46,52	0
2	EDO	A	810	4/4	0.82	0.25	39,45,51,61	0
3	ACT	A	818	4/4	0.84	0.32	71,76,77,80	0
2	EDO	A	807	4/4	0.88	0.34	44,48,51,53	0
2	EDO	A	808	4/4	0.89	0.26	51,56,60,62	0
2	EDO	A	803	4/4	0.89	0.18	40,41,41,45	0
3	ACT	A	815	4/4	0.89	0.16	37,39,42,49	0
3	ACT	A	812	4/4	0.91	0.18	31,38,43,45	0
3	ACT	A	813	4/4	0.93	0.15	45,46,47,48	0
2	EDO	A	801	4/4	0.94	0.13	33,35,39,42	0
2	EDO	A	809	4/4	0.95	0.29	40,43,43,52	0
2	EDO	A	805	4/4	0.95	0.15	39,40,41,52	0
2	EDO	A	804	4/4	0.97	0.10	31,32,34,36	0
2	EDO	A	802	4/4	0.97	0.11	30,31,36,40	0
2	EDO	A	806	4/4	0.97	0.12	30,35,42,46	0



## 6.5 Other polymers [i](#)

There are no such residues in this entry.