



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:25 PM GMT

PDB ID : 4OUI  
Title : Structure of Vibrio cholerae chitin de-N-acetylase in complex with TRI-ACETYLCHITOTRIOSE (CTO)  
Authors : Albesa-Jove, D.; Andres, E.; Biarnes, X.; Planas, A.; Guerin, M.E.  
Deposited on : 2014-02-17  
Resolution : 2.17 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

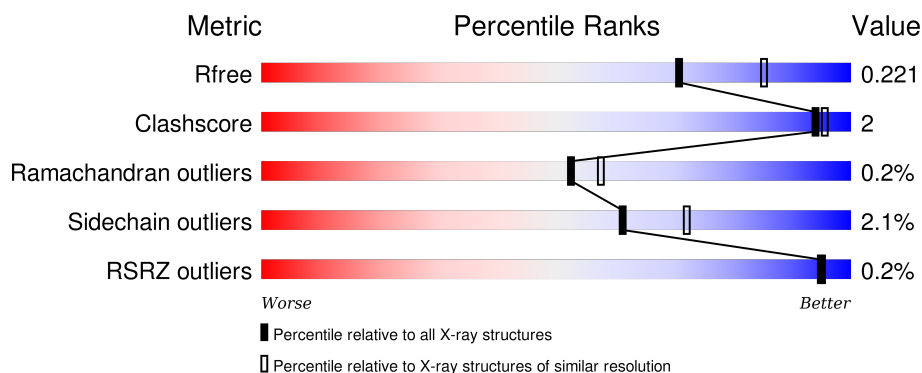
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 2.17 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))
$R_{free}$	91344	5130 (2.20-2.16)
Clashscore	102246	5965 (2.20-2.16)
Ramachandran outliers	100387	5863 (2.20-2.16)
Sidechain outliers	100360	5864 (2.20-2.16)
RSRZ outliers	91569	5142 (2.20-2.16)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	419	 93%
1	B	419	 91% 5%

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
4	CTO	A	503	-	-	-	X
4	CTO	B	503	-	-	-	X
5	EDO	A	504	-	-	-	X
5	EDO	A	505	-	-	-	X
5	EDO	A	506	-	-	-	X
5	EDO	B	504	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7179 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 Deacetylase DA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	404	Total	C	N	O	S	0	1	1
			3168	2012	533	613	10			
1	B	404	Total	C	N	O	S	0	3	1
			3178	2017	539	612	10			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	EXPRESSION TAG	UNP M7M1G8
A	39	SER	ASP	ENGINEERED MUTATION	UNP M7M1G8
A	432	GLU	-	EXPRESSION TAG	UNP M7M1G8
A	433	LEU	-	EXPRESSION TAG	UNP M7M1G8
A	434	ARG	-	EXPRESSION TAG	UNP M7M1G8
A	435	ARG	-	EXPRESSION TAG	UNP M7M1G8
A	436	GLN	-	EXPRESSION TAG	UNP M7M1G8
A	437	TRP	-	EXPRESSION TAG	UNP M7M1G8
A	438	SER	-	EXPRESSION TAG	UNP M7M1G8
A	439	HIS	-	EXPRESSION TAG	UNP M7M1G8
A	440	PRO	-	EXPRESSION TAG	UNP M7M1G8
A	441	GLN	-	EXPRESSION TAG	UNP M7M1G8
A	442	PHE	-	EXPRESSION TAG	UNP M7M1G8
A	443	GLU	-	EXPRESSION TAG	UNP M7M1G8
A	444	LYS	-	EXPRESSION TAG	UNP M7M1G8
B	26	MET	-	EXPRESSION TAG	UNP M7M1G8
B	39	SER	ASP	ENGINEERED MUTATION	UNP M7M1G8
B	432	GLU	-	EXPRESSION TAG	UNP M7M1G8
B	433	LEU	-	EXPRESSION TAG	UNP M7M1G8
B	434	ARG	-	EXPRESSION TAG	UNP M7M1G8
B	435	ARG	-	EXPRESSION TAG	UNP M7M1G8
B	436	GLN	-	EXPRESSION TAG	UNP M7M1G8
B	437	TRP	-	EXPRESSION TAG	UNP M7M1G8
B	438	SER	-	EXPRESSION TAG	UNP M7M1G8
B	439	HIS	-	EXPRESSION TAG	UNP M7M1G8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	440	PRO	-	EXPRESSION TAG	UNP M7M1G8
B	441	GLN	-	EXPRESSION TAG	UNP M7M1G8
B	442	PHE	-	EXPRESSION TAG	UNP M7M1G8
B	443	GLU	-	EXPRESSION TAG	UNP M7M1G8
B	444	LYS	-	EXPRESSION TAG	UNP M7M1G8

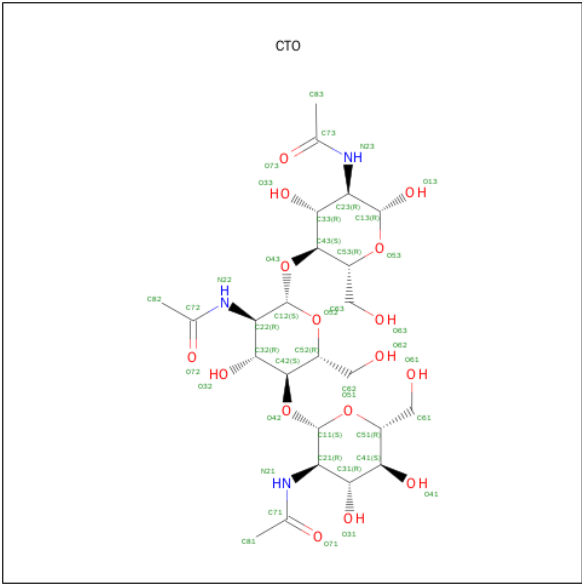
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is SUGAR (TRIACETYLCHITOTRIOSE) (three-letter code: CTO) (formula: C<sub>24</sub>H<sub>41</sub>N<sub>3</sub>O<sub>16</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			43	24	3	16		
4	B	1	Total	C	N	O	0	0
			43	24	3	16		

- Molecule 5 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
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	391	Total	O	0	4
			395	395		
6	B	326	Total	O	0	2
			328	328		

### 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 errors 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.

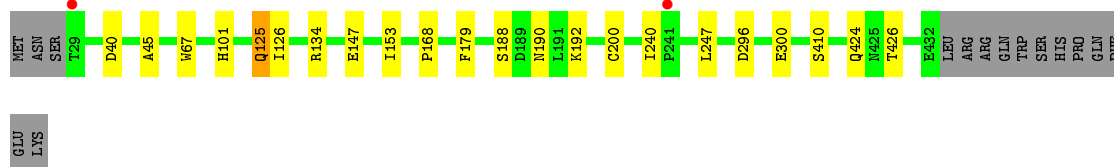
- Molecule 1: Deacetylase DA1

Chain A:  93%



- Molecule 1: Deacetylase DA1

Chain B:  91% 5%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.10Å 98.94Å 154.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	83.32 – 2.17 83.32 – 2.17	Depositor EDS
% Data completeness (in resolution range)	99.1 (83.32-2.17) 99.0 (83.32-2.17)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 2.16Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.161 , 0.214 0.172 , 0.221	Depositor DCC
$R_{free}$ test set	2670 reflections (5.38%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.6	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 47.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 52318 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7179	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, CTO, MG, 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	0.53	0/3264	0.60	0/4466
1	B	0.51	0/3274	0.59	0/4480
All	All	0.52	0/6538	0.59	0/8946

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	3168	0	2993	14	0
1	B	3178	0	2999	8	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	43	0	41	8	0
4	B	43	0	41	0	0
5	A	16	0	24	0	0
5	B	4	0	6	0	0
6	A	395	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	328	0	0	3	0
All	All	7179	0	6104	22	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 (22) 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:238:TRP:HD1	4:A:503:CTO:H23	1.59	0.65
1:B:125:GLN:NE2	6:B:915:HOH:O	2.29	0.64
1:A:431:LEU:HB3	1:A:432:GLU:HB2	1.89	0.54
1:B:125:GLN:HG2	6:B:746:HOH:O	2.10	0.51
1:A:238:TRP:CD1	4:A:503:CTO:H23	2.44	0.50
1:A:125:GLN:HG2	6:A:967:HOH:O	2.13	0.48
1:A:273:ASN:HD21	4:A:503:CTO:H832	1.80	0.47
1:B:147:GLU:HG2	1:B:153:ILE:CG2	2.45	0.46
1:A:147:GLU:HG2	1:A:153:ILE:CG2	2.46	0.45
1:B:126:ILE:HD11	1:B:192:LYS:HG3	1.99	0.45
1:A:237:ASN:HB2	4:A:503:CTO:H831	2.00	0.44
1:A:238:TRP:CD1	4:A:503:CTO:H43	2.53	0.44
1:B:45:ALA:HB2	1:B:300:GLU:HB2	1.99	0.43
1:A:273:ASN:H	1:A:273:ASN:ND2	2.16	0.43
1:B:424:GLN:OE1	6:B:836:HOH:O	2.22	0.42
1:A:237:ASN:HB2	4:A:503:CTO:O73	2.19	0.42
1:A:273:ASN:HD21	4:A:503:CTO:C83	2.33	0.41
1:B:410[A]:SER:OG	1:B:426:THR:O	2.36	0.41
1:A:271:PRO:HD2	4:A:503:CTO:HOD	1.85	0.41
1:A:251:VAL:HB	1:A:252:PRO:HD3	2.03	0.41
1:A:195:GLU:O	6:A:892:HOH:O	2.22	0.41
1:B:101:HIS:CE1	1:B:168:PRO:HB3	2.57	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	403/419 (96%)	393 (98%)	10 (2%)	0	100	100
1	B	405/419 (97%)	396 (98%)	7 (2%)	2 (0%)	34	33
All	All	808/838 (96%)	789 (98%)	17 (2%)	2 (0%)	52	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	40	ASP
1	B	190	ASN

### 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	341/358 (95%)	336 (98%)	5 (2%)	72	82
1	B	341/358 (95%)	331 (97%)	10 (3%)	50	59
All	All	682/716 (95%)	667 (98%)	15 (2%)	61	70

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	TRP
1	A	125	GLN
1	A	179	PHE
1	A	259	LYS
1	A	296	ASP
1	B	67	TRP
1	B	125	GLN
1	B	134[A]	ARG
1	B	134[B]	ARG
1	B	179	PHE
1	B	188	SER

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Mol	Chain	Res	Type
1	B	200	CYS
1	B	240	ILE
1	B	247	LEU
1	B	296	ASP

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

Mol	Chain	Res	Type
1	A	354	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 for Mogul analysis.

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$
4	CTO	A	503	2	45,45,45	1.71	7 (15%)	55,65,65	1.51	12 (21%)
5	EDO	A	504	-	3,3,3	0.57	0	2,2,2	0.30	0
5	EDO	A	505	-	3,3,3	0.53	0	2,2,2	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	EDO	A	506	-	3,3,3	0.65	0	2,2,2	0.12	0
5	EDO	A	507	-	3,3,3	0.56	0	2,2,2	0.47	0
4	CTO	B	503	2	45,45,45	1.63	7 (15%)	55,65,65	1.69	10 (18%)
5	EDO	B	504	-	3,3,3	0.52	0	2,2,2	0.25	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
4	CTO	A	503	2	-	0/26/86/86	0/3/3/3
5	EDO	A	504	-	-	0/1/1/1	0/0/0/0
5	EDO	A	505	-	-	0/1/1/1	0/0/0/0
5	EDO	A	506	-	-	0/1/1/1	0/0/0/0
5	EDO	A	507	-	-	0/1/1/1	0/0/0/0
4	CTO	B	503	2	-	0/26/86/86	0/3/3/3
5	EDO	B	504	-	-	0/1/1/1	0/0/0/0

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	CTO	C13-C23	-6.03	1.45	1.53
4	B	503	CTO	C13-C23	-3.87	1.48	1.53
4	B	503	CTO	C41-C51	-2.79	1.47	1.53
4	A	503	CTO	C41-C51	-2.01	1.48	1.53
4	B	503	CTO	C83-C73	2.62	1.55	1.50
4	A	503	CTO	C82-C72	2.67	1.55	1.50
4	A	503	CTO	C73-N23	2.79	1.45	1.34
4	B	503	CTO	C73-N23	3.02	1.45	1.34
4	B	503	CTO	C71-N21	3.22	1.46	1.34
4	A	503	CTO	C83-C73	3.34	1.57	1.50
4	A	503	CTO	C71-N21	3.42	1.47	1.34
4	B	503	CTO	C82-C72	3.46	1.57	1.50
4	A	503	CTO	C72-N22	4.83	1.52	1.34
4	B	503	CTO	C72-N22	5.46	1.55	1.34

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	503	CTO	C13-O53-C53	-5.23	103.80	113.47
4	B	503	CTO	O72-C72-C82	-4.83	113.19	122.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	CTO	C12-O43-C43	-3.55	108.74	118.01
4	B	503	CTO	C12-O43-C43	-3.27	109.45	118.01
4	B	503	CTO	O42-C42-C52	-3.16	101.01	109.32
4	A	503	CTO	O72-C72-C82	-3.12	116.34	122.06
4	A	503	CTO	O31-C31-C21	-2.44	104.68	109.66
4	B	503	CTO	O43-C12-O52	-2.42	104.55	110.68
4	A	503	CTO	O73-C73-N23	-2.31	117.15	121.86
4	A	503	CTO	C13-O53-C53	-2.16	109.47	113.47
4	A	503	CTO	O42-C42-C52	-2.10	103.81	109.32
4	A	503	CTO	C22-N22-C72	2.01	128.27	123.10
4	A	503	CTO	C32-C22-N22	2.02	114.84	110.66
4	B	503	CTO	O32-C32-C42	2.06	114.76	109.87
4	A	503	CTO	C83-C73-N23	2.21	120.34	116.11
4	A	503	CTO	O43-C43-C33	2.24	112.94	107.17
4	B	503	CTO	O52-C12-C22	2.30	115.78	110.78
4	A	503	CTO	O42-C42-C32	2.44	113.46	107.17
4	B	503	CTO	C22-N22-C72	2.72	130.09	123.10
4	B	503	CTO	O42-C42-C32	3.10	115.17	107.17
4	B	503	CTO	C82-C72-N22	3.34	122.50	116.11
4	A	503	CTO	C82-C72-N22	3.42	122.66	116.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	CTO	8	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	404/419 (96%)	-0.57	0 100 100	10, 19, 37, 62	0
1	B	404/419 (96%)	-0.54	2 (0%) 91 92	12, 21, 41, 66	0
All	All	808/838 (96%)	-0.56	2 (0%) 95 95	10, 20, 39, 66	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	241	PRO	2.5
1	B	29	THR	2.2

### 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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	EDO	A	504	4/4	0.84	0.27	30.05	45,45,47,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	EDO	B	504	4/4	0.97	0.15	6.88	17,28,44,45	0
4	CTO	A	503	43/43	0.82	0.26	5.75	25,42,59,65	0
5	EDO	A	506	4/4	0.87	0.16	4.92	39,43,44,49	0
5	EDO	A	505	4/4	0.89	0.14	3.47	35,37,50,58	0
4	CTO	B	503	43/43	0.91	0.14	2.10	20,30,44,54	0
3	MG	B	502	1/1	0.96	0.07	-0.70	15,15,15,15	0
2	ZN	A	501	1/1	0.99	0.04	-4.47	30,30,30,30	0
2	ZN	B	501	1/1	0.99	0.06	-4.86	23,23,23,23	0
3	MG	A	502	1/1	0.98	0.04	-7.63	14,14,14,14	0
5	EDO	A	507	4/4	0.92	0.27	-	22,38,39,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.