Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:58 pm BST

PDB ID	:	6ILB
Title	:	Native crystal structure of fructuronate-tagaturonate epimerase UxaE from Cohnella laeviribosi
Authors	:	Choi, M.Y.; Kang, L.W.; Ho, T.H.; Nguyen, D.Q.; Lee, I.H.; Lee, J.H.; Park, Y.S.; Park, H.J.
Deposited on	:	2018-10-17
Resolution	:	2.51 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:

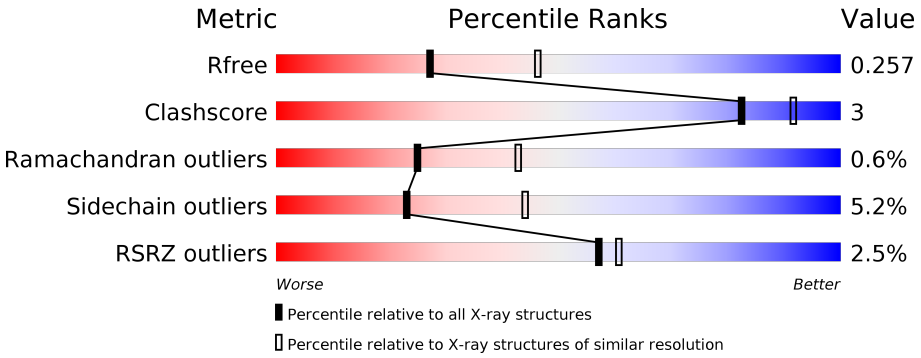
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.51 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	489	3% 87% 13%
1	D	489	2% 90% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7834 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.

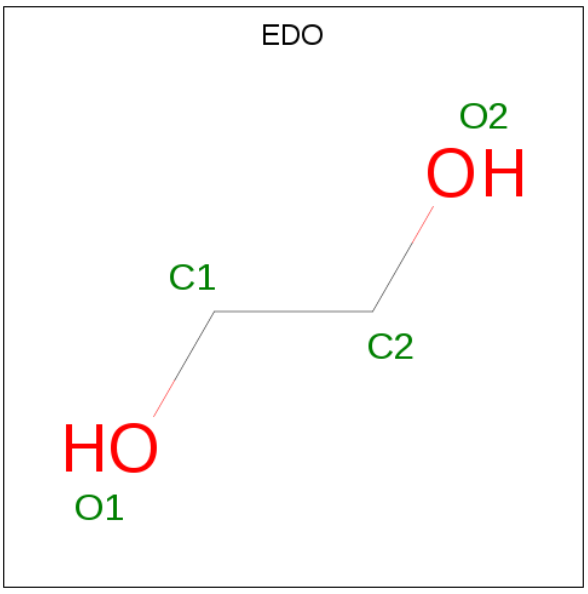
- Molecule 1 is a protein called Fructuronate-tagaturonate epimerase UxaE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	489	Total	C	N	O	P	S	0	0	0
			3892	2457	684	739	1	11			
1	D	489	Total	C	N	O	P	S	0	0	0
			3892	2457	684	739	1	11			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

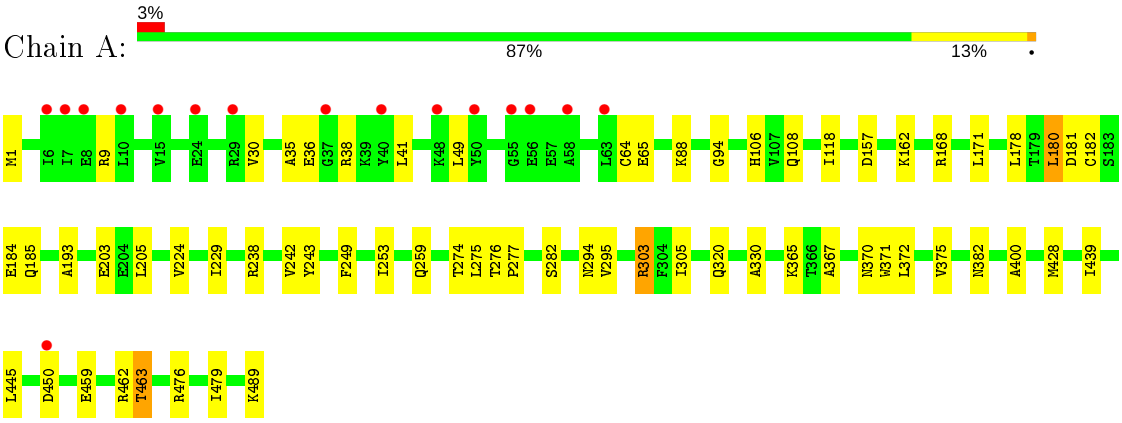
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	21	Total O 21 21	0	0
4	D	19	Total O 19 19	0	0

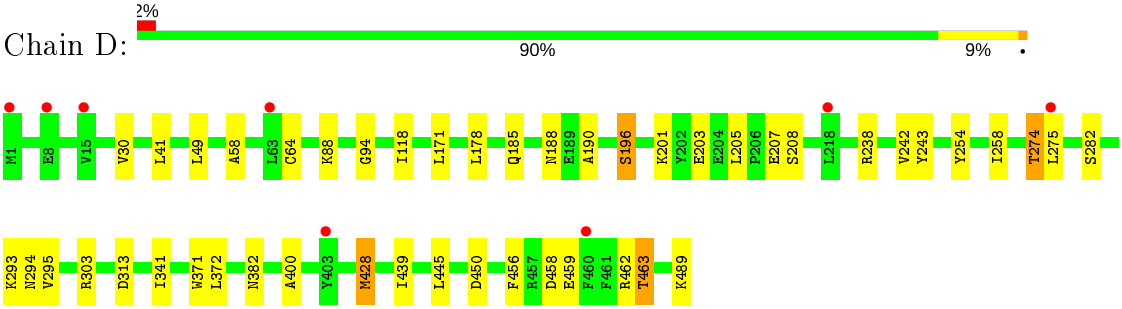
3 Residue-property plots (i)

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: Fructuronate-tagaturonate epimerase UxaE



- Molecule 1: Fructuronate-tagaturonate epimerase UxaE



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	51.82Å 73.47Å 74.67Å 98.14° 110.16° 90.12°	Depositor
Resolution (Å)	48.57 – 2.51 39.39 – 2.51	Depositor EDS
% Data completeness (in resolution range)	94.8 (48.57-2.51) 94.8 (39.39-2.51)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.04 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.189 , 0.259 0.192 , 0.257	Depositor DCC
R_{free} test set	1681 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	56.7	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 24.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.469 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7834	wwPDB-VP
Average B, all atoms (Å^2)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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: MN, EDO, SEP

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	0.63	0/3961	0.82	2/5344 (0.0%)
1	D	0.62	0/3961	0.81	1/5344 (0.0%)
All	All	0.62	0/7922	0.82	3/10688 (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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	313	ASP	CB-CG-OD1	5.63	123.37	118.30
1	A	462	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	168	ARG	NE-CZ-NH1	5.25	122.92	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	35	ALA	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	3892	0	3804	24	0
1	D	3892	0	3804	15	0
2	A	1	0	0	0	0
2	D	1	0	0	0	0
3	A	4	0	6	0	0
3	D	4	0	6	0	0
4	A	21	0	0	0	0
4	D	19	0	0	0	0
All	All	7834	0	7620	39	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 3.

All (39) 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:D:372:LEU:HD22	1:D:428:MET:CE	2.15	0.76
1:A:370:ASN:HD21	1:A:479:ILE:HD11	1.53	0.73
1:D:372:LEU:HD22	1:D:428:MET:HE3	1.75	0.66
1:D:459:GLU:O	1:D:463:THR:HG22	1.98	0.63
1:A:171:LEU:HD21	1:A:178:LEU:HD11	1.82	0.62
1:A:224:VAL:HG21	1:A:229:ILE:HD12	1.84	0.59
1:A:30:VAL:HG21	1:A:49:LEU:HD21	1.86	0.58
1:A:305:ILE:HD13	1:A:320:GLN:HG2	1.87	0.54
1:A:459:GLU:O	1:A:463:THR:HG22	2.09	0.53
1:A:224:VAL:HG12	1:A:330:ALA:HB1	1.91	0.52
1:A:243:TYR:CE2	1:A:282:SER:HB3	2.45	0.52
1:A:157:ASP:OD2	1:A:365:LYS:NZ	2.39	0.52
1:A:94:GLY:HA2	1:A:118:ILE:HB	1.91	0.51
1:D:243:TYR:CE2	1:D:282:SER:HB3	2.45	0.51
1:A:375:VAL:HB	1:A:428:MET:HE2	1.94	0.50
1:D:400:ALA:HB1	1:D:439:ILE:HG23	1.95	0.49
1:A:238:ARG:O	1:A:242:VAL:HG23	2.14	0.47
1:D:171:LEU:HD21	1:D:178:LEU:HD11	1.97	0.46
1:D:188:ASN:HD21	1:D:274:THR:HA	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:94:GLY:HA2	1:D:118:ILE:HB	1.97	0.46
1:A:106:HIS:HE1	1:A:370:ASN:ND2	2.14	0.45
1:D:458:ASP:O	1:D:462:ARG:HB2	2.16	0.45
1:D:178:LEU:HD12	1:D:258:ILE:CD1	2.45	0.45
1:A:400:ALA:HB1	1:A:439:ILE:HG23	1.99	0.45
1:A:375:VAL:CG1	1:A:428:MET:HE2	2.47	0.44
1:A:180:LEU:HD13	1:A:182:CYS:SG	2.57	0.44
1:D:238:ARG:O	1:D:242:VAL:HG23	2.17	0.44
1:A:277:PRO:HA	1:A:303:ARG:HB3	1.99	0.43
1:D:30:VAL:HG21	1:D:49:LEU:HD21	1.99	0.43
1:A:372:LEU:HD22	1:A:428:MET:CE	2.48	0.43
1:A:41:LEU:HB2	1:A:64:CYS:HB2	2.01	0.43
1:A:372:LEU:HD22	1:A:428:MET:HE3	2.00	0.42
1:D:341:ILE:N	1:D:341:ILE:HD12	2.34	0.42
1:D:254:TYR:CG	1:D:295:VAL:HG13	2.55	0.41
1:A:274:THR:HG23	1:A:276:THR:O	2.20	0.41
1:A:108:GLN:HB3	1:A:476:ARG:HD3	2.03	0.41
1:A:249:PHE:CE1	1:A:253:ILE:HD11	2.56	0.40
1:D:41:LEU:HB2	1:D:64:CYS:HB2	2.02	0.40
1:A:162:LYS:CG	1:A:181:ASP:HB3	2.51	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	486/489 (99%)	463 (95%)	20 (4%)	3 (1%)	25	43
1	D	486/489 (99%)	466 (96%)	17 (4%)	3 (1%)	25	43
All	All	972/978 (99%)	929 (96%)	37 (4%)	6 (1%)	25	43

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	58	ALA
1	D	190	ALA
1	A	36	GLU
1	A	193	ALA
1	D	196	SER
1	A	367	ALA

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	401/402 (100%)	380 (95%)	21 (5%)	23 44
1	D	401/402 (100%)	380 (95%)	21 (5%)	23 44
All	All	802/804 (100%)	760 (95%)	42 (5%)	23 44

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	9	ARG
1	A	38	ARG
1	A	65	GLU
1	A	88	LYS
1	A	180	LEU
1	A	184	GLU
1	A	185	GLN
1	A	203	GLU
1	A	205	LEU
1	A	259	GLN
1	A	275	LEU
1	A	294	ASN
1	A	295	VAL
1	A	303	ARG
1	A	371	TRP
1	A	382	ASN
1	A	445	LEU

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Mol	Chain	Res	Type
1	A	450	ASP
1	A	463	THR
1	A	489	LYS
1	D	88	LYS
1	D	185	GLN
1	D	196	SER
1	D	201	LYS
1	D	203	GLU
1	D	205	LEU
1	D	207	GLU
1	D	208	SER
1	D	274	THR
1	D	275	LEU
1	D	293	LYS
1	D	294	ASN
1	D	303	ARG
1	D	371	TRP
1	D	382	ASN
1	D	428	MET
1	D	445	LEU
1	D	450	ASP
1	D	456	PHE
1	D	463	THR
1	D	489	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	106	HIS
1	A	136	GLN
1	A	192	GLN
1	A	370	ASN
1	A	382	ASN
1	D	89	GLN
1	D	106	HIS
1	D	136	GLN
1	D	185	GLN
1	D	188	ASN
1	D	370	ASN
1	D	382	ASN
1	D	411	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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	SEP	D	345	1	8,9,10	0.46	0	8,12,14	1.50	2 (25%)
1	SEP	A	345	1	8,9,10	0.68	0	8,12,14	1.33	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	SEP	D	345	1	-	1/5/8/10	-
1	SEP	A	345	1	-	2/5/8/10	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	345	SEP	P-OG-CB	2.66	125.62	118.30
1	D	345	SEP	O3P-P-O2P	2.03	115.38	107.64

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	345	SEP	CB-OG-P-O3P
1	A	345	SEP	CB-OG-P-O1P

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Mol	Chain	Res	Type	Atoms
1	A	345	SEP	CB-OG-P-O3P

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)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	EDO	D	502	-	3,3,3	0.58	0	2,2,2	0.22	0
3	EDO	A	502	-	3,3,3	0.34	0	2,2,2	0.69	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	EDO	D	502	-	-	1/1/1/1	-
3	EDO	A	502	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	502	EDO	O1-C1-C2-O2

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, 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	488/489 (99%)	0.14	16 (3%) 46 50	38, 59, 93, 131	0
1	D	488/489 (99%)	0.06	8 (1%) 72 74	39, 59, 93, 124	0
All	All	976/978 (99%)	0.10	24 (2%) 57 61	38, 59, 93, 131	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	450	ASP	6.1
1	A	15	VAL	4.5
1	D	1	MET	4.4
1	A	6	ILE	3.9
1	A	63	LEU	3.7
1	A	55	GLY	3.2
1	D	275	LEU	3.2
1	A	50	TYR	3.0
1	D	15	VAL	2.8
1	A	10	LEU	2.7
1	A	29	ARG	2.7
1	A	37	GLY	2.5
1	A	7	ILE	2.5
1	D	460	PHE	2.4
1	A	58	ALA	2.4
1	D	8	GLU	2.4
1	D	63	LEU	2.3
1	A	8	GLU	2.3
1	D	403	TYR	2.1
1	A	40	TYR	2.1
1	A	56	GLU	2.1
1	A	24	GLU	2.1
1	D	218	LEU	2.1
1	A	48	LYS	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	SEP	D	345	10/11	0.96	0.12	45,50,62,64	0
1	SEP	A	345	10/11	0.98	0.10	47,51,61,62	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
3	EDO	D	502	4/4	0.83	0.16	61,61,63,78	0
3	EDO	A	502	4/4	0.92	0.20	60,64,66,80	0
2	MN	D	501	1/1	0.95	0.13	64,64,64,64	0
2	MN	A	501	1/1	0.95	0.12	64,64,64,64	0

6.5 Other polymers (i)

There are no such residues in this entry.