Full wwPDB X-ray Structure Validation Report (i)

Oct 4, 2022 – 06:12 PM JST

PDB ID	:	7Y8U
Title	:	Crystal structure of AlbEF homolog from Quasibacillus thermotolerans
Authors	:	Ishida, K.; Nakamura, A.; Kojima, S.
Deposited on	:	2022-06-24
Resolution	:	2.10 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 (i) 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 (1)) were used in the production of this report:

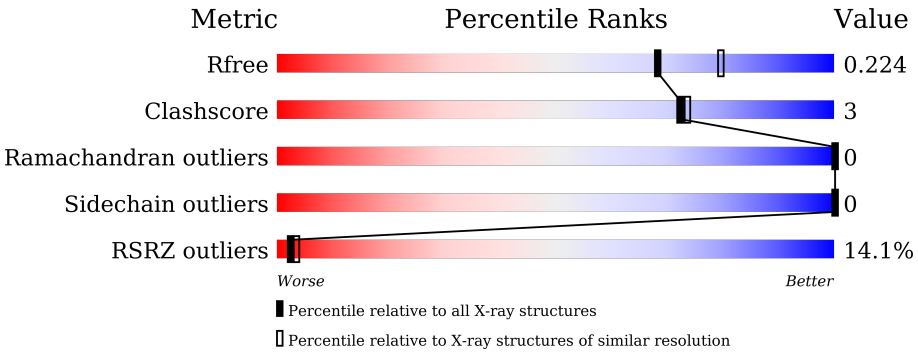
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	E	395	19% 81% 13% 6%
2	F	366	7% 88% 7% 5%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6167 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 AlbE homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	371	Total	C	N	O	S	0	0	0
			3027	1942	506	568	11			

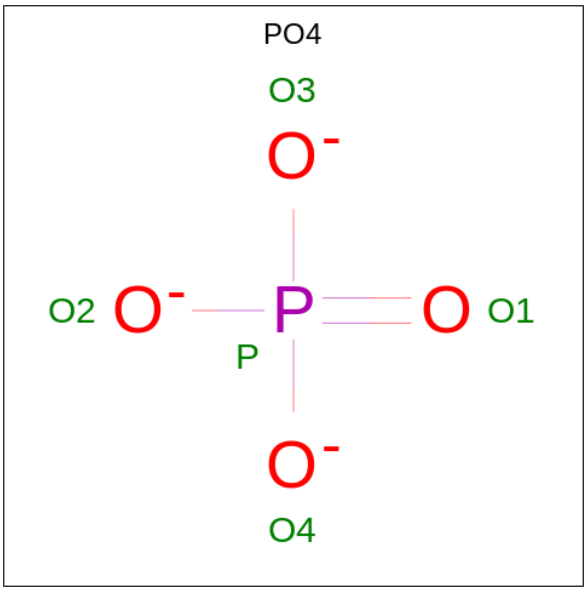
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-13	MET	-	initiating methionine	UNP A0A837GIQ1
E	-12	GLY	-	expression tag	UNP A0A837GIQ1
E	-11	SER	-	expression tag	UNP A0A837GIQ1
E	-10	SER	-	expression tag	UNP A0A837GIQ1
E	-9	HIS	-	expression tag	UNP A0A837GIQ1
E	-8	HIS	-	expression tag	UNP A0A837GIQ1
E	-7	HIS	-	expression tag	UNP A0A837GIQ1
E	-6	HIS	-	expression tag	UNP A0A837GIQ1
E	-5	HIS	-	expression tag	UNP A0A837GIQ1
E	-4	HIS	-	expression tag	UNP A0A837GIQ1
E	-3	SER	-	expression tag	UNP A0A837GIQ1
E	-2	GLN	-	expression tag	UNP A0A837GIQ1
E	-1	ASP	-	expression tag	UNP A0A837GIQ1
E	0	PRO	-	expression tag	UNP A0A837GIQ1

- Molecule 2 is a protein called AlbF homolog.

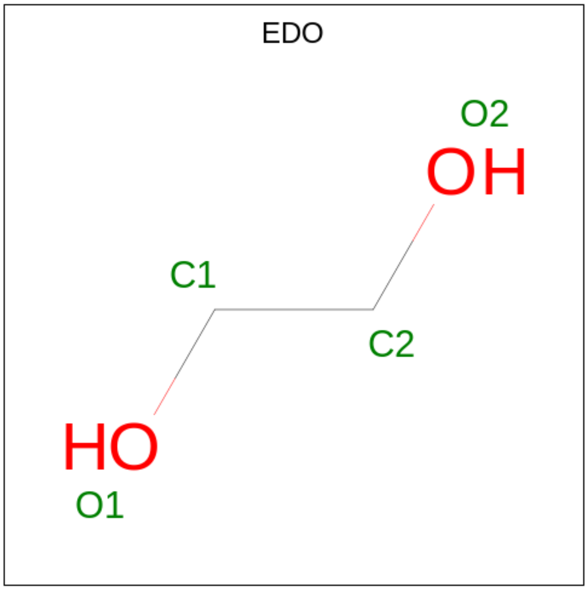
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	347	Total	C	N	O	S	0	4	0
			2885	1850	484	540	11			

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0
3	F	1	Total O P 5 4 1	0	0
3	F	1	Total O P 5 4 1	0	0
3	F	1	Total O P 5 4 1	0	0
3	F	1	Total O P 5 4 1	0	0
3	F	1	Total O P 5 4 1	0	0
3	F	1	Total O P 5 4 1	0	0

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



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

- Molecule 5 is water.

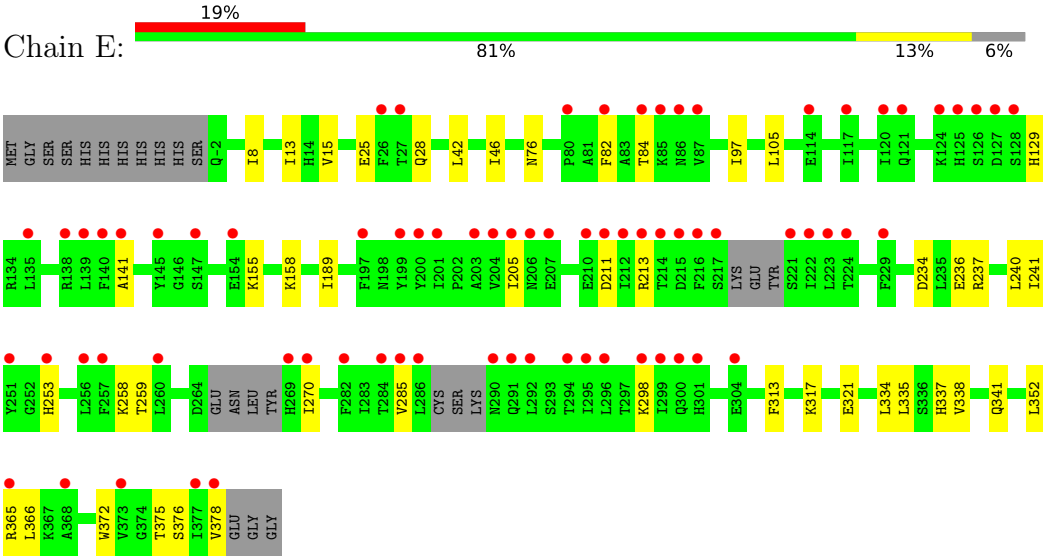
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	60	Total O 60 60	0	0
5	F	109	Total O 109 109	0	0

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.

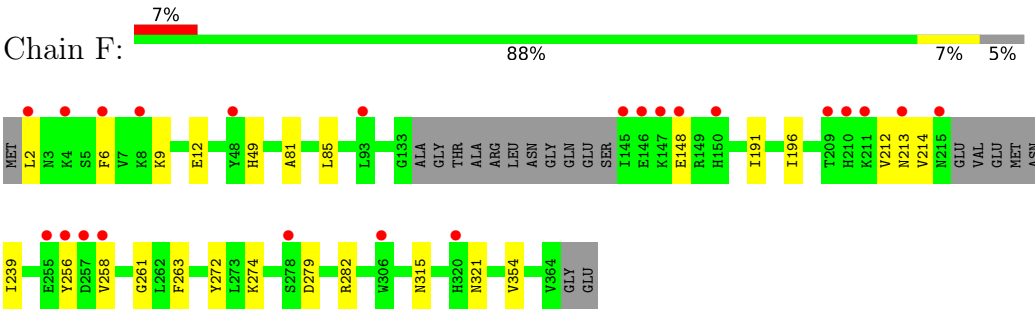
• Molecule 1: AlbE homolog

Chain E:



• Molecule 2: AlbF homolog

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	136.93Å 136.93Å 118.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.92 – 2.10 44.82 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (41.92-2.10) 99.5 (44.82-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.35 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.203 , 0.227 0.202 , 0.224	Depositor DCC
R_{free} test set	3524 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å^2)	41.1	Xtriage
Anisotropy	0.452	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 52.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6167	wwPDB-VP
Average B, all atoms (Å^2)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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: PO4, 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	E	0.24	0/3088	0.42	0/4161
2	F	0.25	0/2955	0.43	0/3989
All	All	0.24	0/6043	0.43	0/8150

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	E	3027	0	3010	28	0
2	F	2885	0	2856	15	0
3	E	20	0	0	0	0
3	F	30	0	0	0	0
4	F	36	0	54	2	0
5	E	60	0	0	0	0
5	F	109	0	0	0	0
All	All	6167	0	5920	41	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 (41) 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)
2:F:81:ALA:H	4:F:411:EDO:H12	1.48	0.79
1:E:246:GLY:HA2	1:E:250:LYS:HB3	1.70	0.74
2:F:234:LEU:HD12	4:F:407:EDO:H21	1.74	0.70
1:E:189:ILE:HD13	1:E:338:VAL:HG21	1.77	0.67
2:F:258:VAL:HG12	2:F:279:ASP:HB3	1.75	0.66
1:E:236:GLU:HA	1:E:240:LEU:HB2	1.77	0.65
1:E:236:GLU:OE2	1:E:365:ARG:NH1	2.29	0.65
1:E:213:ARG:HD3	1:E:378:VAL:HG22	1.81	0.61
2:F:256:TYR:CD2	2:F:282:ARG:HB3	2.37	0.59
1:E:8:ILE:HG13	1:E:189:ILE:HG13	1.84	0.58
1:E:25:GLU:HB3	1:E:28:GLN:HG2	1.87	0.57
2:F:49:HIS:NE2	2:F:213:ASN:O	2.32	0.56
1:E:46:ILE:HD13	1:E:97:ILE:HG12	1.89	0.55
1:E:84:THR:HA	2:F:2:LEU:HD13	1.88	0.55
1:E:13:ILE:HD12	1:E:76:ASN:HB3	1.90	0.54
2:F:239:ILE:HG21	2:F:354:VAL:HG21	1.89	0.54
1:E:337:HIS:CE1	1:E:341:GLN:HG3	2.44	0.52
1:E:82:PHE:HB3	2:F:6:PHE:HB2	1.91	0.52
1:E:211:ASP:HB2	1:E:376:SER:HA	1.93	0.51
1:E:321:GLU:HG3	1:E:352:LEU:HD22	1.93	0.50
1:E:241:ILE:HG12	1:E:366:LEU:HD21	1.92	0.50
2:F:263:PHE:HB3	2:F:272:TYR:HB2	1.93	0.49
1:E:259:THR:HG23	1:E:298:LYS:HE3	1.94	0.49
2:F:315:ASN:HB3	2:F:321:ASN:HB3	1.96	0.48
1:E:189:ILE:HD11	1:E:334:LEU:HD21	1.96	0.47
2:F:212:VAL:HG12	2:F:214:VAL:HG23	1.97	0.47
1:E:15:VAL:HG11	1:E:335:LEU:HD22	1.97	0.46
2:F:261:GLY:N	2:F:274:LYS:O	2.43	0.46
1:E:372:TRP:HE1	1:E:375:THR:HG1	1.62	0.45
1:E:270:ILE:HG23	1:E:285:VAL:HG22	1.99	0.45
1:E:141:ALA:HB3	1:E:205:ILE:HD12	1.98	0.45
2:F:85:LEU:HD21	2:F:148:GLU:HG3	1.99	0.44
1:E:129:HIS:O	1:E:133:ILE:HG12	2.18	0.44
2:F:191:ILE:HG23	2:F:196:ILE:HD13	1.99	0.44
1:E:313:PHE:CE2	1:E:317:LYS:HD2	2.54	0.43
1:E:42:LEU:HD23	1:E:105:LEU:HD21	2.00	0.43
1:E:253:HIS:HB2	1:E:258:LYS:HD2	2.00	0.43
2:F:9:LYS:O	2:F:12:GLU:HG2	2.20	0.41
1:E:234:ASP:OD1	1:E:237:ARG:NH1	2.48	0.41
1:E:240:LEU:HD13	1:E:362:ASP:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:155:LYS:HA	1:E:158:LYS:HE2	2.02	0.41

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	E	363/395 (92%)	352 (97%)	11 (3%)	0	100	100
2	F	345/366 (94%)	334 (97%)	11 (3%)	0	100	100
All	All	708/761 (93%)	686 (97%)	22 (3%)	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	E	341/362 (94%)	341 (100%)	0	100	100
2	F	322/332 (97%)	322 (100%)	0	100	100
All	All	663/694 (96%)	663 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

19 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	PO4	E	402	-	4,4,4	0.91	0	6,6,6	0.41	0
3	PO4	F	405	-	4,4,4	0.91	0	6,6,6	0.43	0
4	EDO	F	415	-	3,3,3	0.47	0	2,2,2	0.26	0
3	PO4	F	404	-	4,4,4	0.92	0	6,6,6	0.42	0
3	PO4	E	401	-	4,4,4	0.91	0	6,6,6	0.44	0
3	PO4	F	401	-	4,4,4	0.94	0	6,6,6	0.46	0
4	EDO	F	408	-	3,3,3	0.47	0	2,2,2	0.31	0
4	EDO	F	409	-	3,3,3	0.46	0	2,2,2	0.36	0
4	EDO	F	407	-	3,3,3	0.46	0	2,2,2	0.32	0
3	PO4	F	406	-	4,4,4	0.92	0	6,6,6	0.42	0
3	PO4	E	404	-	4,4,4	0.92	0	6,6,6	0.44	0
3	PO4	F	403	-	4,4,4	0.90	0	6,6,6	0.46	0
3	PO4	F	402	-	4,4,4	0.90	0	6,6,6	0.43	0
4	EDO	F	412	-	3,3,3	0.44	0	2,2,2	0.34	0
4	EDO	F	414	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	F	410	-	3,3,3	0.46	0	2,2,2	0.33	0
3	PO4	E	403	-	4,4,4	0.91	0	6,6,6	0.43	0
4	EDO	F	413	-	3,3,3	0.46	0	2,2,2	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	EDO	F	411	-	3,3,3	0.47	0	2,2,2	0.31	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	EDO	F	408	-	-	0/1/1/1	-
4	EDO	F	414	-	-	0/1/1/1	-
4	EDO	F	410	-	-	0/1/1/1	-
4	EDO	F	409	-	-	1/1/1/1	-
4	EDO	F	415	-	-	0/1/1/1	-
4	EDO	F	407	-	-	0/1/1/1	-
4	EDO	F	413	-	-	0/1/1/1	-
4	EDO	F	412	-	-	0/1/1/1	-
4	EDO	F	411	-	-	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
4	F	409	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	407	EDO	1	0
4	F	411	EDO	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, 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	E	371/395 (93%)	1.28	77 (20%) 1 0	37, 69, 133, 169	0
2	F	347/366 (94%)	0.71	24 (6%) 16 21	28, 51, 106, 146	1 (0%)
All	All	718/761 (94%)	1.00	101 (14%) 2 3	28, 59, 126, 169	1 (0%)

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	292	LEU	11.8
1	E	205	ILE	10.3
1	E	216	PHE	9.4
2	F	256	TYR	9.3
1	E	212	ILE	9.3
1	E	222	ILE	8.7
2	F	2	LEU	8.3
1	E	127	ASP	8.2
2	F	147	LYS	6.7
1	E	214	THR	6.5
1	E	206	ASN	6.5
2	F	145	ILE	6.4
1	E	223	LEU	6.3
1	E	377	ILE	6.3
1	E	215	ASP	5.7
1	E	378	VAL	5.7
1	E	221	SER	5.6
1	E	141	ALA	5.6
1	E	128	SER	5.6
1	E	213	ARG	5.5
1	E	204	VAL	5.4
1	E	197	PHE	5.4
1	E	27	THR	5.3
1	E	364	TYR	4.9

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Mol	Chain	Res	Type	RSRZ
2	F	257	ASP	4.9
1	E	200	TYR	4.8
1	E	203	ALA	4.8
1	E	124	LYS	4.7
1	E	286	LEU	4.6
1	E	211	ASP	4.6
1	E	290	ASN	4.5
1	E	285	VAL	4.2
2	F	258	VAL	4.2
1	E	256	LEU	4.1
1	E	121	GLN	4.0
1	E	126	SER	4.0
2	F	146	GLU	4.0
1	E	138	ARG	3.9
1	E	253	HIS	3.9
1	E	85	LYS	3.8
2	F	306	TRP	3.8
1	E	140	PHE	3.7
1	E	217	SER	3.7
1	E	139	LEU	3.6
1	E	368	ALA	3.6
1	E	201	ILE	3.5
1	E	117	ILE	3.4
1	E	199	TYR	3.3
1	E	125	HIS	3.2
1	E	295	ILE	3.2
2	F	8	LYS	3.2
1	E	269	HIS	3.1
2	F	215	ASN	3.1
1	E	294	THR	3.1
1	E	260	LEU	3.1
1	E	82	PHE	3.1
1	E	373	VAL	3.1
1	E	26	PHE	3.0
1	E	284	THR	3.0
2	F	48	TYR	3.0
1	E	154	GLU	2.9
1	E	120	ILE	2.9
1	E	251	TYR	2.9
1	E	147	SER	2.9
1	E	291	GLN	2.8
2	F	148	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	270	ILE	2.8
1	E	130	SER	2.8
2	F	221	LYS	2.8
1	E	298	LYS	2.7
1	E	135	LEU	2.7
2	F	150	HIS	2.7
1	E	304	GLU	2.6
2	F	255	GLU	2.6
1	E	86	ASN	2.6
1	E	257	PHE	2.6
2	F	6	PHE	2.6
1	E	87	VAL	2.5
2	F	320[A]	HIS	2.5
2	F	211	LYS	2.5
2	F	210	HIS	2.5
1	E	365	ARG	2.5
1	E	114	GLU	2.5
1	E	282	PHE	2.4
1	E	300	GLN	2.3
1	E	301	HIS	2.3
2	F	278	SER	2.3
2	F	209	THR	2.2
1	E	80	PRO	2.2
1	E	224	THR	2.2
2	F	93	LEU	2.2
1	E	229	PHE	2.2
1	E	207	GLU	2.2
1	E	210	GLU	2.2
1	E	299	ILE	2.1
1	E	296	LEU	2.1
1	E	145	TYR	2.1
2	F	4	LYS	2.1
2	F	213	ASN	2.0
1	E	84	THR	2.0
1	E	131	GLY	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^{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	F	407	4/4	0.58	0.34	60,66,73,77	0
4	EDO	F	411	4/4	0.65	0.25	54,60,67,75	0
4	EDO	F	415	4/4	0.65	0.33	58,65,67,73	0
4	EDO	F	410	4/4	0.70	0.20	60,64,68,72	0
4	EDO	F	408	4/4	0.71	0.25	52,52,55,62	0
3	PO4	F	405	5/5	0.79	0.29	66,86,117,118	0
4	EDO	F	414	4/4	0.80	0.24	68,71,71,72	0
4	EDO	F	413	4/4	0.86	0.25	47,65,68,73	0
3	PO4	F	406	5/5	0.87	0.24	68,99,116,119	0
3	PO4	F	403	5/5	0.88	0.18	56,68,81,104	0
3	PO4	F	404	5/5	0.90	0.16	67,88,94,101	0
3	PO4	E	403	5/5	0.91	0.24	80,86,98,100	0
4	EDO	F	412	4/4	0.92	0.21	48,55,60,63	0
3	PO4	E	402	5/5	0.93	0.15	51,64,83,97	0
4	EDO	F	409	4/4	0.93	0.17	47,48,51,62	0
3	PO4	E	404	5/5	0.95	0.31	67,82,98,99	0
3	PO4	F	402	5/5	0.96	0.13	47,56,60,69	0
3	PO4	E	401	5/5	0.98	0.16	53,66,68,72	0
3	PO4	F	401	5/5	0.99	0.14	44,48,54,56	0

6.5 Other polymers (i)

There are no such residues in this entry.