



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7Y8U / pdb_00007y8u
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.

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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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

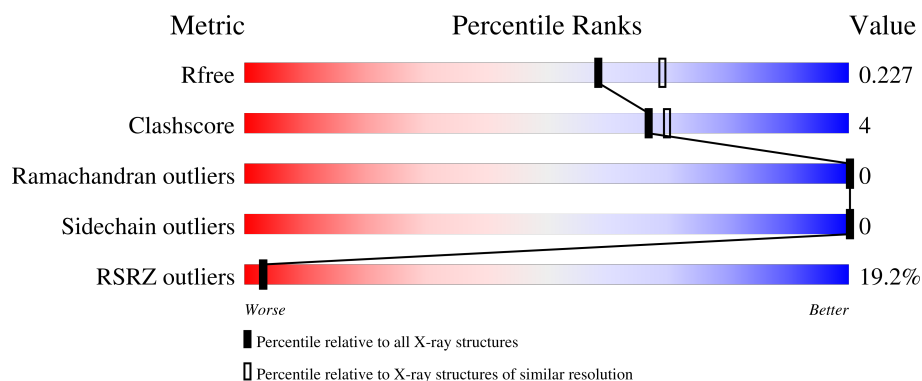
1 Overall quality at a glance

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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 $\leq 5\%$. 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	E	395	21% 82% 12% 6%
2	F	366	15% 86% 8% 5%

2 Entry composition

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 (CCD ID: PO4) (formula: O₄P).



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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

4 Data and refinement statistics

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 41.92 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (41.92-2.10) 99.4 (41.92-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.35 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.203 , 0.227 0.203 , 0.227	Depositor DCC
R_{free} test set	3524 reflections (4.68%)	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 , 56.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	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.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0.07	0/3088	0.22	0/4161
2	F	0.09	0/2955	0.23	0/3989
All	All	0.08	0/6043	0.22	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	18	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	44	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 (44) 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:246:MET:HE2	2:F:300:TYR:HB3	1.83	0.60
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:270:ILE:HG23	1:E:285:VAL:HG22	1.99	0.45
2:F:242:LEU:HD22	2:F:246:MET:HE3	1.97	0.45
1:E:25:GLU:OE2	1:E:145:TYR:OH	2.35	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:159:ILE:HA	2:F:162:MET:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	53	ASN
1	E	95	GLN
1	E	121	GLN
1	E	172	ASN
1	E	231	HIS
1	E	291	GLN
2	F	3	ASN
2	F	23	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 oligosaccharides 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	F	406	-	4,4,4	0.97	0	6,6,6	0.45	0
4	EDO	F	408	-	3,3,3	0.44	0	2,2,2	0.36	0
3	PO4	F	403	-	4,4,4	0.95	0	6,6,6	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	F	412	-	3,3,3	0.41	0	2,2,2	0.38	0
3	PO4	F	401	-	4,4,4	0.99	0	6,6,6	0.49	0
3	PO4	F	405	-	4,4,4	0.95	0	6,6,6	0.46	0
4	EDO	F	415	-	3,3,3	0.44	0	2,2,2	0.31	0
4	EDO	F	414	-	3,3,3	0.43	0	2,2,2	0.37	0
3	PO4	F	402	-	4,4,4	0.94	0	6,6,6	0.46	0
3	PO4	E	403	-	4,4,4	0.96	0	6,6,6	0.46	0
3	PO4	F	404	-	4,4,4	0.97	0	6,6,6	0.45	0
3	PO4	E	401	-	4,4,4	0.96	0	6,6,6	0.48	0
3	PO4	E	404	-	4,4,4	0.96	0	6,6,6	0.47	0
4	EDO	F	407	-	3,3,3	0.43	0	2,2,2	0.37	0
3	PO4	E	402	-	4,4,4	0.95	0	6,6,6	0.44	0
4	EDO	F	410	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	F	411	-	3,3,3	0.44	0	2,2,2	0.35	0
4	EDO	F	413	-	3,3,3	0.42	0	2,2,2	0.36	0
4	EDO	F	409	-	3,3,3	0.43	0	2,2,2	0.41	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	407	-	-	1/1/1/1	-
4	EDO	F	412	-	-	0/1/1/1	-
4	EDO	F	410	-	-	0/1/1/1	-
4	EDO	F	415	-	-	0/1/1/1	-
4	EDO	F	411	-	-	0/1/1/1	-
4	EDO	F	414	-	-	0/1/1/1	-
4	EDO	F	413	-	-	0/1/1/1	-
4	EDO	F	409	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	409	EDO	O1-C1-C2-O2
4	F	407	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, 95th 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%)	1.29	82 (22%)	2 2	37, 69, 133, 169	0
2	F	347/366 (94%)	0.78	56 (16%)	4 5	26, 50, 104, 146	5 (1%)
All	All	718/761 (94%)	1.04	138 (19%)	3 3	26, 59, 126, 169	5 (0%)

All (138) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	256	TYR	10.6
1	E	197	PHE	9.6
2	F	2	LEU	9.4
1	E	292	LEU	8.5
2	F	145	ILE	8.2
1	E	212	ILE	6.3
1	E	378	VAL	6.2
2	F	212	VAL	6.2
2	F	214	VAL	6.2
2	F	215	ASN	6.0
2	F	221	LYS	5.9
1	E	22	SER	5.8
1	E	216	PHE	5.6
2	F	211	LYS	5.5
2	F	48	TYR	5.5
1	E	211	ASP	5.1
1	E	253	HIS	5.1
1	E	251	TYR	5.0
1	E	217	SER	4.9
2	F	306	TRP	4.8
1	E	21	ALA	4.7
1	E	200	TYR	4.5
1	E	286	LEU	4.5
1	E	194	ILE	4.5

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Mol	Chain	Res	Type	RSRZ
2	F	258	VAL	4.5
1	E	23	GLY	4.4
2	F	47	THR	4.3
2	F	147	LYS	4.3
1	E	262	LEU	4.3
2	F	210	HIS	4.2
2	F	209	THR	4.2
1	E	214	THR	4.2
2	F	364	VAL	4.1
1	E	144	LYS	4.0
1	E	199	TYR	4.0
1	E	364	TYR	3.9
1	E	26	PHE	3.8
1	E	263	VAL	3.8
1	E	189	ILE	3.8
1	E	205	ILE	3.8
1	E	195	LYS	3.7
1	E	94	TYR	3.6
1	E	206	ASN	3.6
1	E	257	PHE	3.6
1	E	297	THR	3.5
1	E	128	SER	3.5
1	E	82	PHE	3.5
2	F	254	LEU	3.5
1	E	377	ILE	3.4
2	F	259	SER	3.4
1	E	27	THR	3.3
2	F	275	VAL	3.3
1	E	222	ILE	3.3
1	E	296	LEU	3.3
1	E	269	HIS	3.2
2	F	45	GLY	3.2
1	E	223	LEU	3.2
2	F	49	HIS	3.2
2	F	3	ASN	3.2
1	E	294	THR	3.1
2	F	148	GLU	3.1
1	E	260	LEU	3.1
1	E	250	LYS	3.1
1	E	308	PHE	3.0
1	E	252	GLY	3.0
1	E	24	MET	3.0

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Mol	Chain	Res	Type	RSRZ
2	F	349	LEU	3.0
1	E	90	ILE	3.0
1	E	201	ILE	3.0
2	F	150	HIS	3.0
2	F	309	MET	3.0
1	E	264	ASP	2.9
1	E	126	SER	2.9
2	F	213	ASN	2.9
1	E	255	VAL	2.9
1	E	68	HIS	2.9
1	E	298	LYS	2.8
1	E	221	SER	2.8
2	F	255	GLU	2.8
1	E	30	LYS	2.8
1	E	158	LYS	2.8
2	F	30	GLU	2.7
2	F	299	THR	2.7
1	E	270	ILE	2.7
1	E	285	VAL	2.7
2	F	289	GLN	2.6
2	F	320[A]	HIS	2.6
1	E	127	ASP	2.6
1	E	129	HIS	2.6
2	F	50	ASN	2.6
1	E	256	LEU	2.6
1	E	300	GLN	2.6
2	F	149	ARG	2.6
2	F	43	ILE	2.6
2	F	205	TYR	2.6
2	F	133	GLY	2.6
2	F	206	GLY	2.6
1	E	141	ALA	2.6
2	F	46	LEU	2.6
2	F	292	MET	2.5
2	F	44	GLY	2.5
1	E	301	HIS	2.5
2	F	157	GLU	2.5
2	F	225	LEU	2.5
1	E	134	ARG	2.5
1	E	229	PHE	2.5
1	E	25	GLU	2.4
1	E	20	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	290	ASN	2.4
1	E	299	ILE	2.4
1	E	293	SER	2.4
2	F	282	ARG	2.4
1	E	196	ASP	2.4
1	E	117	ILE	2.4
2	F	252	GLN	2.3
1	E	247	TYR	2.3
1	E	198	ASN	2.3
1	E	284	THR	2.3
2	F	188	ASN	2.3
1	E	342	HIS	2.2
1	E	376	SER	2.2
1	E	215	ASP	2.2
2	F	257	ASP	2.2
2	F	357	GLU	2.2
2	F	15	ASN	2.2
2	F	223	MET	2.2
2	F	294	GLU	2.1
2	F	4	LYS	2.1
1	E	213	ARG	2.1
2	F	5	SER	2.1
2	F	295	HIS	2.1
1	E	49	SER	2.1
2	F	253	GLN	2.1
2	F	9	LYS	2.1
1	E	85	LYS	2.0
1	E	208	GLY	2.0
1	E	271	SER	2.0
1	E	-2	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides 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, 95th 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	PO4	F	405	5/5	0.64	0.16	66,86,117,118	0
3	PO4	F	406	5/5	0.71	0.13	68,99,116,119	0
4	EDO	F	415	4/4	0.72	0.28	58,65,67,73	0
4	EDO	F	407	4/4	0.73	0.25	60,66,73,77	0
3	PO4	E	403	5/5	0.73	0.14	80,86,98,100	0
4	EDO	F	411	4/4	0.75	0.21	54,60,67,75	0
4	EDO	F	408	4/4	0.78	0.25	52,52,55,62	0
3	PO4	F	404	5/5	0.80	0.12	67,88,94,101	0
3	PO4	E	404	5/5	0.81	0.14	67,82,98,99	0
4	EDO	F	410	4/4	0.83	0.18	60,64,68,72	0
4	EDO	F	414	4/4	0.85	0.19	68,71,71,72	0
3	PO4	F	403	5/5	0.86	0.14	56,68,81,104	0
4	EDO	F	413	4/4	0.89	0.22	47,65,68,73	0
4	EDO	F	412	4/4	0.90	0.17	48,55,60,63	0
3	PO4	E	402	5/5	0.90	0.12	51,64,83,97	0
3	PO4	F	402	5/5	0.93	0.13	47,56,60,69	0
4	EDO	F	409	4/4	0.93	0.11	47,48,51,62	0
3	PO4	E	401	5/5	0.96	0.07	53,66,68,72	0
3	PO4	F	401	5/5	0.97	0.08	44,48,54,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.