



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 02:16 pm BST

PDB ID : 3M82
Title : Crystal structure of Acetyl xylan esterase (TM0077) from THERMOTOGA MARITIMA at 2.40 Å resolution (PMSF inhibitor complex structure)
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2010-03-17
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

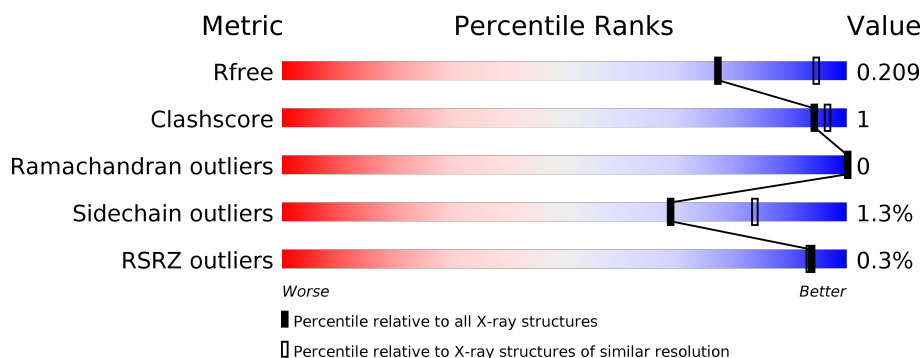
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 $\leq 5\%$. 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	337	 88% 7% 5%
1	B	337	 91% • 5%
1	C	337	 90% 6% 5%
1	D	337	 91% • 5%
1	E	337	 89% 6% 5%
1	F	337	 92% • 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 16721 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 Acetyl xylan esterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	2	0
			2620	1703	432	474	11			
1	B	321	Total	C	N	O	S	0	3	0
			2631	1709	437	474	11			
1	C	321	Total	C	N	O	S	0	1	0
			2611	1698	431	471	11			
1	D	321	Total	C	N	O	S	0	1	0
			2611	1698	431	471	11			
1	E	321	Total	C	N	O	S	0	4	0
			2635	1712	436	476	11			
1	F	321	Total	C	N	O	S	0	2	0
			2621	1704	432	474	11			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	leader sequence	UNP Q9WXT2
A	-10	GLY	-	leader sequence	UNP Q9WXT2
A	-9	SER	-	leader sequence	UNP Q9WXT2
A	-8	ASP	-	leader sequence	UNP Q9WXT2
A	-7	LYS	-	leader sequence	UNP Q9WXT2
A	-6	ILE	-	leader sequence	UNP Q9WXT2
A	-5	HIS	-	leader sequence	UNP Q9WXT2
A	-4	HIS	-	leader sequence	UNP Q9WXT2
A	-3	HIS	-	leader sequence	UNP Q9WXT2
A	-2	HIS	-	leader sequence	UNP Q9WXT2
A	-1	HIS	-	leader sequence	UNP Q9WXT2
A	0	HIS	-	leader sequence	UNP Q9WXT2
B	-11	MET	-	leader sequence	UNP Q9WXT2
B	-10	GLY	-	leader sequence	UNP Q9WXT2
B	-9	SER	-	leader sequence	UNP Q9WXT2
B	-8	ASP	-	leader sequence	UNP Q9WXT2
B	-7	LYS	-	leader sequence	UNP Q9WXT2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	ILE	-	leader sequence	UNP Q9WXT2
B	-5	HIS	-	leader sequence	UNP Q9WXT2
B	-4	HIS	-	leader sequence	UNP Q9WXT2
B	-3	HIS	-	leader sequence	UNP Q9WXT2
B	-2	HIS	-	leader sequence	UNP Q9WXT2
B	-1	HIS	-	leader sequence	UNP Q9WXT2
B	0	HIS	-	leader sequence	UNP Q9WXT2
C	-11	MET	-	leader sequence	UNP Q9WXT2
C	-10	GLY	-	leader sequence	UNP Q9WXT2
C	-9	SER	-	leader sequence	UNP Q9WXT2
C	-8	ASP	-	leader sequence	UNP Q9WXT2
C	-7	LYS	-	leader sequence	UNP Q9WXT2
C	-6	ILE	-	leader sequence	UNP Q9WXT2
C	-5	HIS	-	leader sequence	UNP Q9WXT2
C	-4	HIS	-	leader sequence	UNP Q9WXT2
C	-3	HIS	-	leader sequence	UNP Q9WXT2
C	-2	HIS	-	leader sequence	UNP Q9WXT2
C	-1	HIS	-	leader sequence	UNP Q9WXT2
C	0	HIS	-	leader sequence	UNP Q9WXT2
D	-11	MET	-	leader sequence	UNP Q9WXT2
D	-10	GLY	-	leader sequence	UNP Q9WXT2
D	-9	SER	-	leader sequence	UNP Q9WXT2
D	-8	ASP	-	leader sequence	UNP Q9WXT2
D	-7	LYS	-	leader sequence	UNP Q9WXT2
D	-6	ILE	-	leader sequence	UNP Q9WXT2
D	-5	HIS	-	leader sequence	UNP Q9WXT2
D	-4	HIS	-	leader sequence	UNP Q9WXT2
D	-3	HIS	-	leader sequence	UNP Q9WXT2
D	-2	HIS	-	leader sequence	UNP Q9WXT2
D	-1	HIS	-	leader sequence	UNP Q9WXT2
D	0	HIS	-	leader sequence	UNP Q9WXT2
E	-11	MET	-	leader sequence	UNP Q9WXT2
E	-10	GLY	-	leader sequence	UNP Q9WXT2
E	-9	SER	-	leader sequence	UNP Q9WXT2
E	-8	ASP	-	leader sequence	UNP Q9WXT2
E	-7	LYS	-	leader sequence	UNP Q9WXT2
E	-6	ILE	-	leader sequence	UNP Q9WXT2
E	-5	HIS	-	leader sequence	UNP Q9WXT2
E	-4	HIS	-	leader sequence	UNP Q9WXT2
E	-3	HIS	-	leader sequence	UNP Q9WXT2
E	-2	HIS	-	leader sequence	UNP Q9WXT2
E	-1	HIS	-	leader sequence	UNP Q9WXT2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	HIS	-	leader sequence	UNP Q9WXT2
F	-11	MET	-	leader sequence	UNP Q9WXT2
F	-10	GLY	-	leader sequence	UNP Q9WXT2
F	-9	SER	-	leader sequence	UNP Q9WXT2
F	-8	ASP	-	leader sequence	UNP Q9WXT2
F	-7	LYS	-	leader sequence	UNP Q9WXT2
F	-6	ILE	-	leader sequence	UNP Q9WXT2
F	-5	HIS	-	leader sequence	UNP Q9WXT2
F	-4	HIS	-	leader sequence	UNP Q9WXT2
F	-3	HIS	-	leader sequence	UNP Q9WXT2
F	-2	HIS	-	leader sequence	UNP Q9WXT2
F	-1	HIS	-	leader sequence	UNP Q9WXT2
F	0	HIS	-	leader sequence	UNP Q9WXT2

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	2	Total 2 Ca 2	0	0
2	E	1	Total 1 Ca 1	0	0
2	B	1	Total 1 Ca 1	0	0
2	C	1	Total 1 Ca 1	0	0
2	A	2	Total 2 Ca 2	0	0
2	F	1	Total 1 Ca 1	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	174	Total 174	O 174	0	0
5	B	163	Total 164	O 164	0	1
5	C	164	Total 165	O 165	0	1
5	D	161	Total 161	O 161	0	0
5	E	141	Total 141	O 141	0	0
5	F	143	Total 143	O 143	0	0

- Molecule 1: Acetyl xylan esterase



Chain F:

92%

• 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	103.57Å 104.50Å 221.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.97 – 2.40 48.95 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.97-2.40) 100.0 (48.95-2.40)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.2.0019, PHENIX	Depositor
R, R_{free}	0.160 , 0.208 0.164 , 0.209	Depositor DCC
R_{free} test set	4742 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.436	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.025 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16721	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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: CA, ACT, SEB, 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	0.78	0/2683	0.77	4/3637 (0.1%)
1	B	0.83	0/2694	0.78	2/3651 (0.1%)
1	C	0.82	0/2674	0.80	1/3625 (0.0%)
1	D	0.84	1/2674 (0.0%)	0.79	3/3625 (0.1%)
1	E	0.86	0/2698	0.75	1/3657 (0.0%)
1	F	0.86	1/2684 (0.0%)	0.77	1/3638 (0.0%)
All	All	0.83	2/16107 (0.0%)	0.78	12/21833 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	80	GLU	CG-CD	5.46	1.60	1.51
1	F	80	GLU	CG-CD	5.43	1.60	1.51

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	131	ASP	CB-CG-OD1	6.06	123.75	118.30
1	D	163	ASP	CB-CG-OD1	5.95	123.66	118.30
1	D	151	ASP	CB-CG-OD1	5.62	123.36	118.30
1	A	248	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	D	163	ASP	CB-CG-OD2	-5.32	113.52	118.30

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	2620	0	2517	8	0
1	B	2631	0	2531	7	0
1	C	2611	0	2512	7	0
1	D	2611	0	2512	4	0
1	E	2635	0	2529	10	0
1	F	2621	0	2519	5	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	2	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	4	0	3	0	0
3	B	4	0	3	1	0
3	E	4	0	3	1	0
4	A	8	0	12	2	0
4	B	4	0	6	0	0
4	C	4	0	6	0	0
4	E	4	0	6	0	0
4	F	4	0	6	1	0
5	A	174	0	0	1	0
5	B	164	0	0	1	0
5	C	165	0	0	0	0
5	D	161	0	0	0	0
5	E	141	0	0	0	0
5	F	143	0	0	1	0
All	All	16721	0	15165	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 1.

The worst 5 of 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)
1:F:185:ALA:HB1	4:F:417:EDO:H12	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:GLU:OE1	4:A:412:EDO:H12	1.99	0.61
1:B:142:PRO:HA	3:B:409:ACT:H1	1.84	0.58
1:E:93:ASN:HB3	1:E:123:GLY:HA3	1.85	0.57
1:E:64:TYR:OH	1:E:134:GLU:OE1	2.26	0.52

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	320/337 (95%)	309 (97%)	11 (3%)	0	100	100
1	B	321/337 (95%)	311 (97%)	10 (3%)	0	100	100
1	C	319/337 (95%)	309 (97%)	10 (3%)	0	100	100
1	D	319/337 (95%)	310 (97%)	9 (3%)	0	100	100
1	E	322/337 (96%)	311 (97%)	11 (3%)	0	100	100
1	F	320/337 (95%)	312 (98%)	8 (2%)	0	100	100
All	All	1921/2022 (95%)	1862 (97%)	59 (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	A	269/284 (95%)	263 (98%)	6 (2%)	52	71
1	B	270/284 (95%)	267 (99%)	3 (1%)	73	87
1	C	268/284 (94%)	262 (98%)	6 (2%)	52	71
1	D	268/284 (94%)	266 (99%)	2 (1%)	84	92
1	E	270/284 (95%)	269 (100%)	1 (0%)	91	96
1	F	269/284 (95%)	266 (99%)	3 (1%)	73	87
All	All	1614/1704 (95%)	1593 (99%)	21 (1%)	69	84

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	48	GLU
1	C	216	HIS
1	E	223	LEU
1	B	223	LEU
1	F	15	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	50	HIS
1	F	176	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	SEB	D	188	1	15,16,17	2.64	2 (13%)	15,21,23	1.09	1 (6%)
1	SEB	F	188	1	15,16,17	2.63	2 (13%)	15,21,23	1.37	1 (6%)
1	SEB	B	188	1	15,16,17	2.46	2 (13%)	15,21,23	1.51	2 (13%)
1	SEB	C	188	1	15,16,17	2.73	3 (20%)	15,21,23	1.15	2 (13%)
1	SEB	E	188	1	15,16,17	2.94	2 (13%)	15,21,23	1.21	2 (13%)
1	SEB	A	188	1	15,16,17	2.50	2 (13%)	15,21,23	1.01	1 (6%)

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	SEB	D	188	1	-	1/9/13/15	0/1/1/1
1	SEB	F	188	1	-	1/9/13/15	0/1/1/1
1	SEB	B	188	1	-	1/9/13/15	0/1/1/1
1	SEB	C	188	1	-	1/9/13/15	0/1/1/1
1	SEB	E	188	1	-	0/9/13/15	0/1/1/1
1	SEB	A	188	1	-	1/9/13/15	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	188	SEB	CE-SD	-9.81	1.68	1.78
1	C	188	SEB	CE-SD	-9.29	1.69	1.78
1	F	188	SEB	CE-SD	-8.79	1.69	1.78
1	D	188	SEB	CE-SD	-8.62	1.69	1.78
1	A	188	SEB	CE-SD	-8.23	1.70	1.78

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	188	SEB	CB-OG-SD	4.33	128.54	119.23
1	B	188	SEB	CB-OG-SD	4.08	127.99	119.23
1	C	188	SEB	OG-SD-CE	3.67	114.29	104.18
1	D	188	SEB	CB-OG-SD	3.13	125.95	119.23
1	E	188	SEB	OG-SD-CE	2.92	112.23	104.18

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	188	SEB	CB-OG-SD-OD2
1	D	188	SEB	CA-CB-OG-SD
1	F	188	SEB	CA-CB-OG-SD
1	B	188	SEB	CA-CB-OG-SD
1	A	188	SEB	CA-CB-OG-SD

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 17 ligands modelled in this entry, 8 are monoatomic - leaving 9 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	EDO	E	416	-	3,3,3	0.65	0	2,2,2	0.15	0
4	EDO	B	414	-	3,3,3	0.54	0	2,2,2	0.53	0
3	ACT	A	410	-	1,3,3	4.27	1 (100%)	0,3,3	0.00	-
4	EDO	C	415	-	3,3,3	0.49	0	2,2,2	0.31	0
3	ACT	B	409	-	1,3,3	2.53	1 (100%)	0,3,3	0.00	-
4	EDO	A	412	-	3,3,3	0.71	0	2,2,2	0.23	0
3	ACT	E	411	-	1,3,3	3.07	1 (100%)	0,3,3	0.00	-
4	EDO	F	417	-	3,3,3	0.54	0	2,2,2	0.09	0
4	EDO	A	413	-	3,3,3	0.48	0	2,2,2	0.20	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	A	412	-	-	1/1/1/1	-
4	EDO	B	414	-	-	1/1/1/1	-
4	EDO	C	415	-	-	1/1/1/1	-
4	EDO	E	416	-	-	0/1/1/1	-
4	EDO	F	417	-	-	1/1/1/1	-
4	EDO	A	413	-	-	0/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	410	ACT	CH3-C	4.27	1.54	1.48
3	E	411	ACT	CH3-C	3.07	1.52	1.48
3	B	409	ACT	CH3-C	2.53	1.52	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	412	EDO	O1-C1-C2-O2
4	B	414	EDO	O1-C1-C2-O2
4	C	415	EDO	O1-C1-C2-O2
4	F	417	EDO	O1-C1-C2-O2

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	409	ACT	1	0
4	A	412	EDO	1	0
3	E	411	ACT	1	0
4	F	417	EDO	1	0
4	A	413	EDO	1	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, 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	A	320/337 (94%)	-0.81	1 (0%) 94 93	15, 20, 37, 54	0
1	B	320/337 (94%)	-0.75	0 100 100	14, 20, 38, 55	0
1	C	320/337 (94%)	-0.79	1 (0%) 94 93	14, 20, 38, 54	0
1	D	320/337 (94%)	-0.84	1 (0%) 94 93	14, 20, 38, 55	0
1	E	320/337 (94%)	-0.87	1 (0%) 94 93	14, 21, 38, 54	0
1	F	320/337 (94%)	-0.81	1 (0%) 94 93	15, 21, 38, 54	0
All	All	1920/2022 (94%)	-0.81	5 (0%) 94 93	14, 20, 38, 55	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	PHE	2.8
1	D	3	PHE	2.6
1	F	3	PHE	2.6
1	E	3	PHE	2.4
1	C	3	PHE	2.1

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, 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
1	SEB	D	188	16/17	0.90	0.16	19,42,53,54	0
1	SEB	E	188	16/17	0.92	0.19	20,41,53,54	0
1	SEB	F	188	16/17	0.93	0.16	19,41,54,54	0
1	SEB	A	188	16/17	0.93	0.15	19,39,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	SEB	B	188	16/17	0.94	0.17	19,40,53,53	0
1	SEB	C	188	16/17	0.95	0.14	19,39,54,54	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, 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(\AA^2)	Q<0.9
2	CA	F	406	1/1	0.67	0.09	65,65,65,65	0
4	EDO	A	412	4/4	0.79	0.36	45,53,55,56	0
2	CA	B	408	1/1	0.80	0.08	64,64,64,64	0
2	CA	A	404	1/1	0.83	0.09	64,64,64,64	0
2	CA	D	405	1/1	0.84	0.12	65,65,65,65	0
2	CA	E	407	1/1	0.85	0.09	65,65,65,65	0
2	CA	C	403	1/1	0.91	0.12	60,60,60,60	0
3	ACT	A	410	4/4	0.94	0.14	23,25,28,28	0
3	ACT	E	411	4/4	0.95	0.13	34,34,37,37	0
4	EDO	E	416	4/4	0.96	0.12	25,25,32,34	0
4	EDO	B	414	4/4	0.97	0.14	20,25,28,32	0
4	EDO	F	417	4/4	0.97	0.12	24,32,36,38	0
4	EDO	C	415	4/4	0.97	0.13	23,24,28,30	0
3	ACT	B	409	4/4	0.98	0.09	18,19,19,20	0
4	EDO	A	413	4/4	0.98	0.09	21,24,24,31	0
2	CA	A	401	1/1	0.99	0.12	21,21,21,21	0
2	CA	D	402	1/1	0.99	0.08	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.