



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 02:57 PM UTC

PDB ID : 1ZMB / pdb_00001zmb
Title : Crystal Structure of the Putative Acetylxyln Esterase from Clostridium acetobutylicum, Northeast Structural Genomics Target CaR6
Authors : Forouhar, F.; Vorobiev, S.M.; Abashidze, M.; Ciao, M.; Acton, T.B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2005-05-10
Resolution : 2.61 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 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

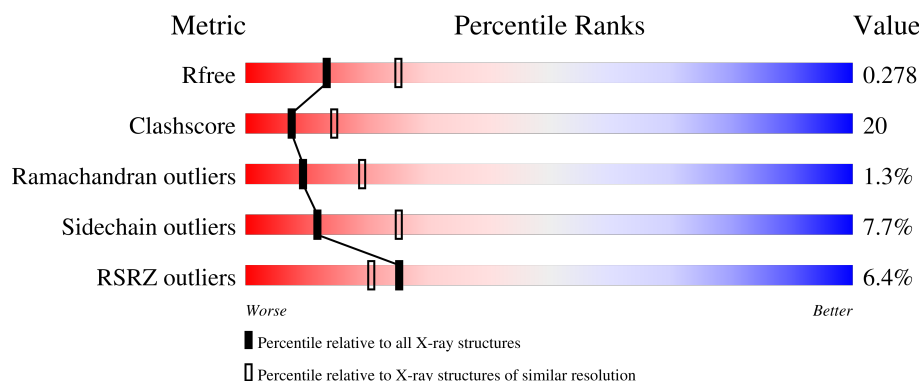
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	A	290	3% 66% 27% 5% ..
1	B	290	3% 65% 28%
1	C	290	10% 62% 31%
1	D	290	7% 64% 29%

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Mol	Chain	Length	Quality of chain
1	E	290	6% 62% 30% 5% ..
1	F	290	7% 63% 31% ...

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13791 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 Acetylxyln esterase related enzyme.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	Se	0	0	0
			2278	1457	381	426	4	10			
1	B	284	Total	C	N	O	S	Se	0	0	0
			2278	1457	381	426	4	10			
1	C	284	Total	C	N	O	S	Se	0	0	0
			2278	1457	381	426	4	10			
1	D	284	Total	C	N	O	S	Se	0	0	0
			2278	1457	381	426	4	10			
1	E	284	Total	C	N	O	S	Se	0	0	0
			2278	1457	381	426	4	10			
1	F	284	Total	C	N	O	S	Se	0	0	0
			2278	1457	381	426	4	10			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q97LM8
A	7	MSE	MET	modified residue	UNP Q97LM8
A	13	MSE	MET	modified residue	UNP Q97LM8
A	24	MSE	MET	modified residue	UNP Q97LM8
A	32	MSE	MET	modified residue	UNP Q97LM8
A	40	MSE	MET	modified residue	UNP Q97LM8
A	41	MSE	MET	modified residue	UNP Q97LM8
A	106	MSE	MET	modified residue	UNP Q97LM8
A	260	MSE	MET	modified residue	UNP Q97LM8
A	277	MSE	MET	modified residue	UNP Q97LM8
A	283	LEU	-	cloning artifact	UNP Q97LM8
A	284	GLU	-	cloning artifact	UNP Q97LM8
A	285	HIS	-	cloning artifact	UNP Q97LM8
A	286	HIS	-	cloning artifact	UNP Q97LM8
A	287	HIS	-	cloning artifact	UNP Q97LM8
A	288	HIS	-	cloning artifact	UNP Q97LM8
A	289	HIS	-	cloning artifact	UNP Q97LM8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	290	HIS	-	cloning artifact	UNP Q97LM8
B	1	MSE	MET	modified residue	UNP Q97LM8
B	7	MSE	MET	modified residue	UNP Q97LM8
B	13	MSE	MET	modified residue	UNP Q97LM8
B	24	MSE	MET	modified residue	UNP Q97LM8
B	32	MSE	MET	modified residue	UNP Q97LM8
B	40	MSE	MET	modified residue	UNP Q97LM8
B	41	MSE	MET	modified residue	UNP Q97LM8
B	106	MSE	MET	modified residue	UNP Q97LM8
B	260	MSE	MET	modified residue	UNP Q97LM8
B	277	MSE	MET	modified residue	UNP Q97LM8
B	283	LEU	-	cloning artifact	UNP Q97LM8
B	284	GLU	-	cloning artifact	UNP Q97LM8
B	285	HIS	-	cloning artifact	UNP Q97LM8
B	286	HIS	-	cloning artifact	UNP Q97LM8
B	287	HIS	-	cloning artifact	UNP Q97LM8
B	288	HIS	-	cloning artifact	UNP Q97LM8
B	289	HIS	-	cloning artifact	UNP Q97LM8
B	290	HIS	-	cloning artifact	UNP Q97LM8
C	1	MSE	MET	modified residue	UNP Q97LM8
C	7	MSE	MET	modified residue	UNP Q97LM8
C	13	MSE	MET	modified residue	UNP Q97LM8
C	24	MSE	MET	modified residue	UNP Q97LM8
C	32	MSE	MET	modified residue	UNP Q97LM8
C	40	MSE	MET	modified residue	UNP Q97LM8
C	41	MSE	MET	modified residue	UNP Q97LM8
C	106	MSE	MET	modified residue	UNP Q97LM8
C	260	MSE	MET	modified residue	UNP Q97LM8
C	277	MSE	MET	modified residue	UNP Q97LM8
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C	285	HIS	-	cloning artifact	UNP Q97LM8
C	286	HIS	-	cloning artifact	UNP Q97LM8
C	287	HIS	-	cloning artifact	UNP Q97LM8
C	288	HIS	-	cloning artifact	UNP Q97LM8
C	289	HIS	-	cloning artifact	UNP Q97LM8
C	290	HIS	-	cloning artifact	UNP Q97LM8
D	1	MSE	MET	modified residue	UNP Q97LM8
D	7	MSE	MET	modified residue	UNP Q97LM8
D	13	MSE	MET	modified residue	UNP Q97LM8
D	24	MSE	MET	modified residue	UNP Q97LM8
D	32	MSE	MET	modified residue	UNP Q97LM8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	40	MSE	MET	modified residue	UNP Q97LM8
D	41	MSE	MET	modified residue	UNP Q97LM8
D	106	MSE	MET	modified residue	UNP Q97LM8
D	260	MSE	MET	modified residue	UNP Q97LM8
D	277	MSE	MET	modified residue	UNP Q97LM8
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D	284	GLU	-	cloning artifact	UNP Q97LM8
D	285	HIS	-	cloning artifact	UNP Q97LM8
D	286	HIS	-	cloning artifact	UNP Q97LM8
D	287	HIS	-	cloning artifact	UNP Q97LM8
D	288	HIS	-	cloning artifact	UNP Q97LM8
D	289	HIS	-	cloning artifact	UNP Q97LM8
D	290	HIS	-	cloning artifact	UNP Q97LM8
E	1	MSE	MET	modified residue	UNP Q97LM8
E	7	MSE	MET	modified residue	UNP Q97LM8
E	13	MSE	MET	modified residue	UNP Q97LM8
E	24	MSE	MET	modified residue	UNP Q97LM8
E	32	MSE	MET	modified residue	UNP Q97LM8
E	40	MSE	MET	modified residue	UNP Q97LM8
E	41	MSE	MET	modified residue	UNP Q97LM8
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E	285	HIS	-	cloning artifact	UNP Q97LM8
E	286	HIS	-	cloning artifact	UNP Q97LM8
E	287	HIS	-	cloning artifact	UNP Q97LM8
E	288	HIS	-	cloning artifact	UNP Q97LM8
E	289	HIS	-	cloning artifact	UNP Q97LM8
E	290	HIS	-	cloning artifact	UNP Q97LM8
F	1	MSE	MET	modified residue	UNP Q97LM8
F	7	MSE	MET	modified residue	UNP Q97LM8
F	13	MSE	MET	modified residue	UNP Q97LM8
F	24	MSE	MET	modified residue	UNP Q97LM8
F	32	MSE	MET	modified residue	UNP Q97LM8
F	40	MSE	MET	modified residue	UNP Q97LM8
F	41	MSE	MET	modified residue	UNP Q97LM8
F	106	MSE	MET	modified residue	UNP Q97LM8
F	260	MSE	MET	modified residue	UNP Q97LM8
F	277	MSE	MET	modified residue	UNP Q97LM8
F	283	LEU	-	cloning artifact	UNP Q97LM8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	284	GLU	-	cloning artifact	UNP Q97LM8
F	285	HIS	-	cloning artifact	UNP Q97LM8
F	286	HIS	-	cloning artifact	UNP Q97LM8
F	287	HIS	-	cloning artifact	UNP Q97LM8
F	288	HIS	-	cloning artifact	UNP Q97LM8
F	289	HIS	-	cloning artifact	UNP Q97LM8
F	290	HIS	-	cloning artifact	UNP Q97LM8

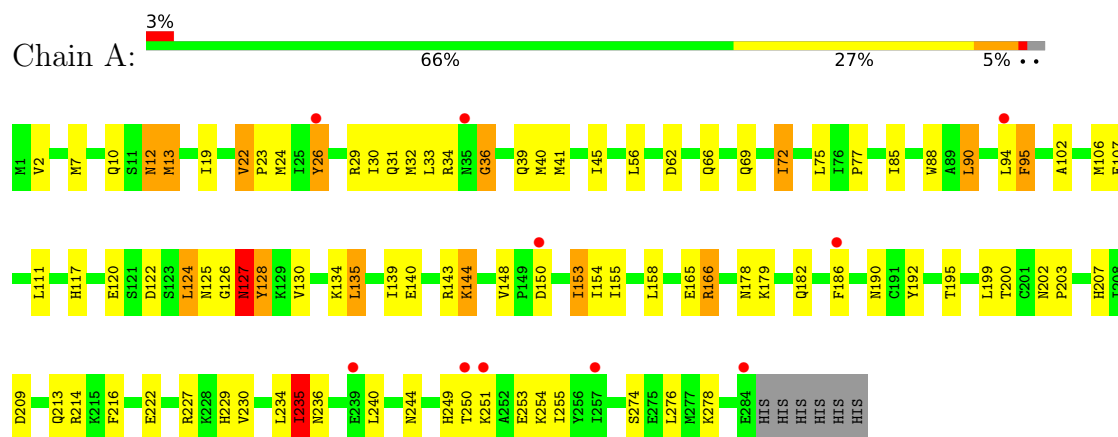
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	26	Total O 26 26	0	0
2	B	27	Total O 27 27	0	0
2	C	21	Total O 21 21	0	0
2	D	12	Total O 12 12	0	0
2	E	19	Total O 19 19	0	0
2	F	18	Total O 18 18	0	0

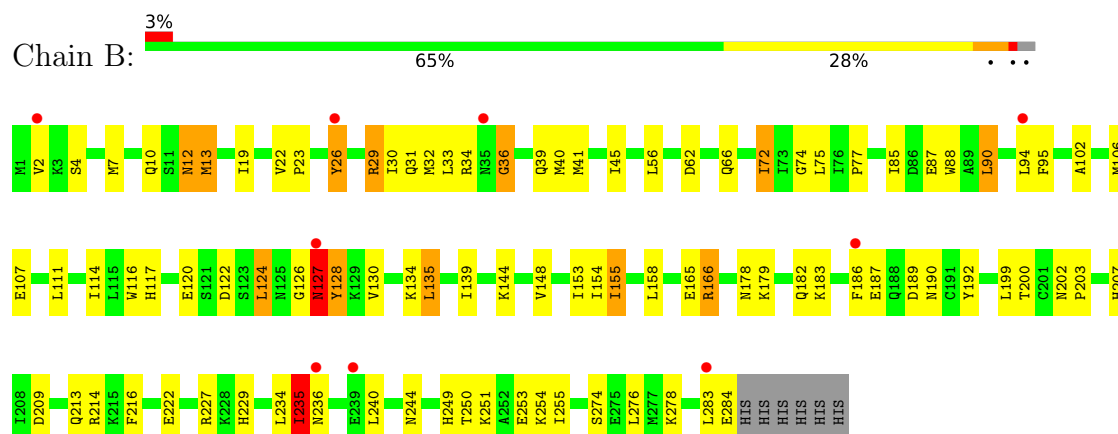
3 Residue-property plots [i](#)

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.

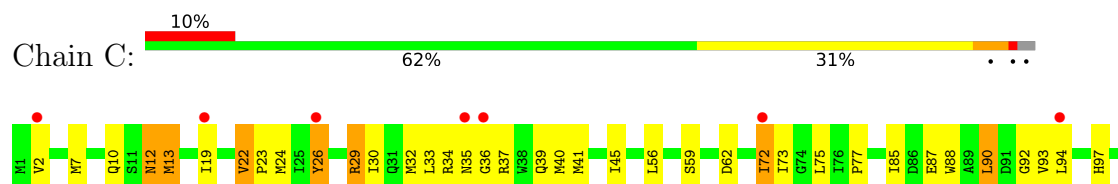
- Molecule 1: Acetylxylan esterase related enzyme

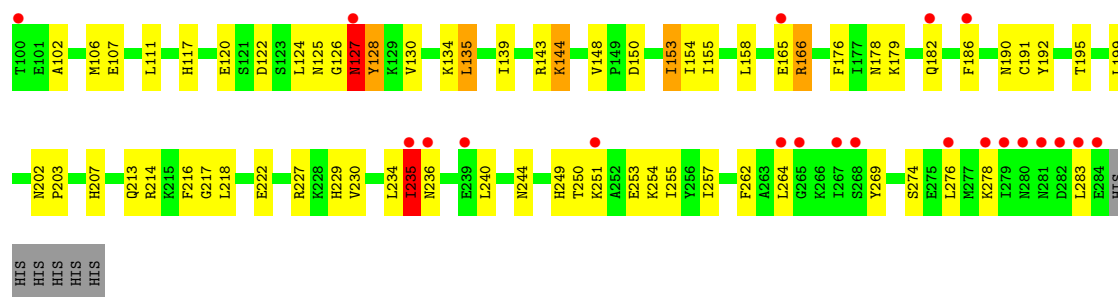


- Molecule 1: Acetylxylan esterase related enzyme

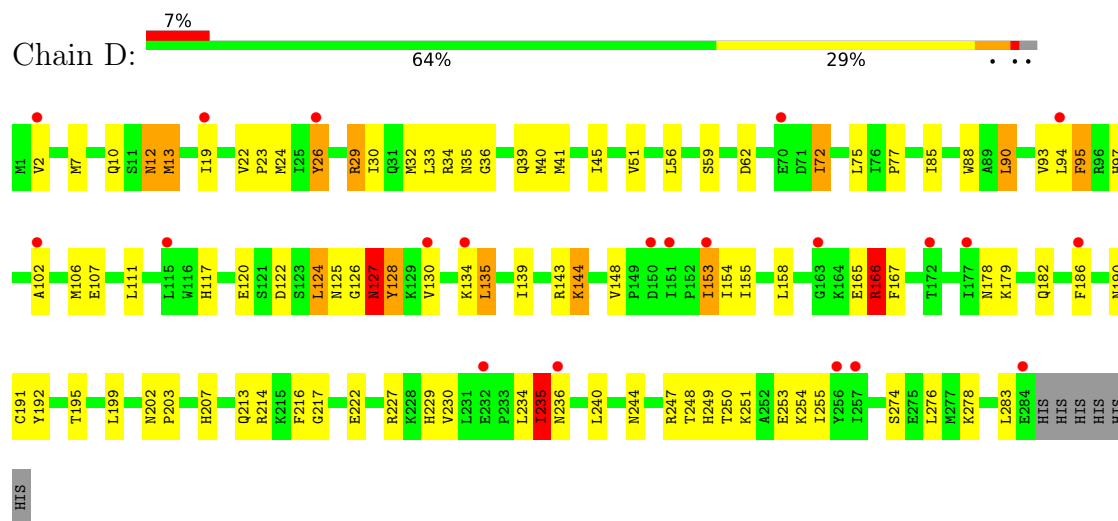


- Molecule 1: Acetylxylan esterase related enzyme

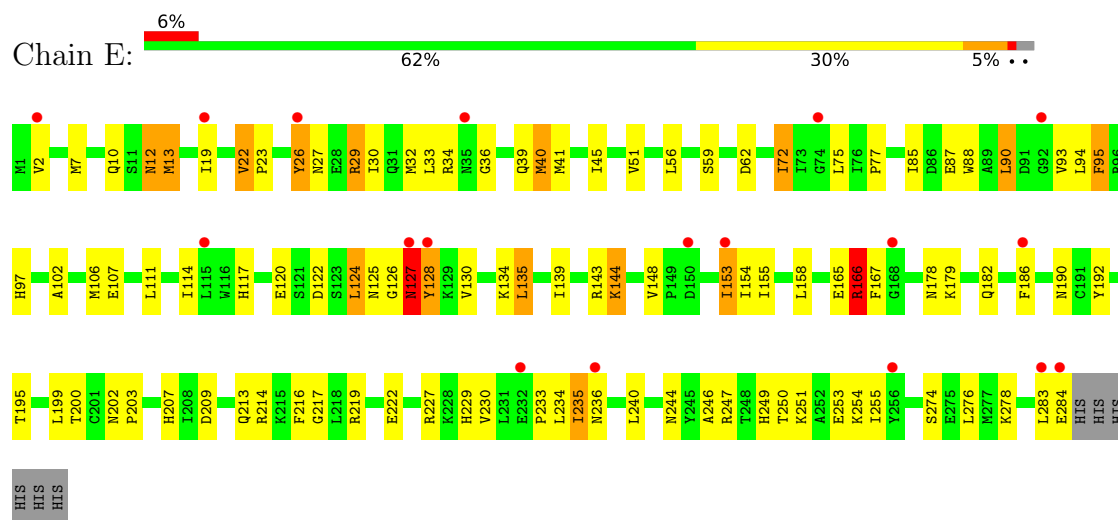




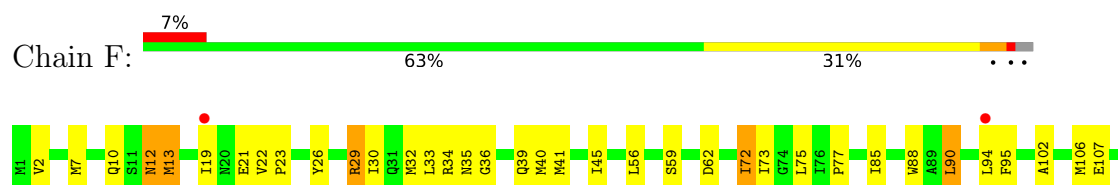
- Molecule 1: Acetylxylylan esterase related enzyme

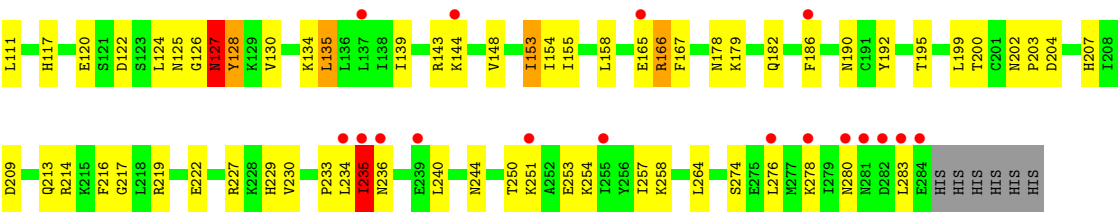


- Molecule 1: Acetylxylylan esterase related enzyme



- Molecule 1: Acetylxylylan esterase related enzyme





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.00Å 87.94Å 103.51Å 106.50° 100.22° 113.80°	Depositor
Resolution (Å)	29.31 – 2.61 29.31 – 2.61	Depositor EDS
% Data completeness (in resolution range)	82.9 (29.31-2.61) 92.9 (29.31-2.61)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.91 (at 2.61Å)	Xtriage
Refinement program	CNS 1.1, XTALVIEW	Depositor
R, R_{free}	0.243 , 0.269 0.255 , 0.278	Depositor DCC
R_{free} test set	11545 reflections (9.73%)	wwPDB-VP
Wilson B-factor (Å ²)	34.8	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.014 for -h,-k,h+k+l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	13791	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.52	0/2317	0.89	8/3105 (0.3%)
1	B	0.52	0/2317	0.89	8/3105 (0.3%)
1	C	0.51	0/2317	0.90	6/3105 (0.2%)
1	D	0.49	0/2317	0.88	7/3105 (0.2%)
1	E	0.47	0/2317	0.88	6/3105 (0.2%)
1	F	0.50	0/2317	0.90	7/3105 (0.2%)
All	All	0.50	0/13902	0.89	42/18630 (0.2%)

There are no bond length outliers.

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	128	TYR	N-CA-C	-9.29	101.95	113.38
1	B	128	TYR	N-CA-C	-9.22	102.04	113.38
1	C	128	TYR	N-CA-C	-9.22	102.04	113.38
1	E	128	TYR	N-CA-C	-9.16	102.11	113.38
1	A	128	TYR	N-CA-C	-9.06	102.24	113.38

There are no chirality outliers.

There are no planarity outliers.

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	2278	0	2245	88	0
1	B	2278	0	2245	95	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2278	0	2245	99	0
1	D	2278	0	2245	94	0
1	E	2278	0	2245	94	0
1	F	2278	0	2245	96	0
2	A	26	0	0	5	0
2	B	27	0	0	1	0
2	C	21	0	0	5	0
2	D	12	0	0	0	0
2	E	19	0	0	1	0
2	F	18	0	0	2	0
All	All	13791	0	13470	549	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 20.

The worst 5 of 549 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:182:GLN:HG2	1:F:186:PHE:CZ	1.39	1.55
1:F:182:GLN:CG	1:F:186:PHE:CZ	2.28	1.16
1:F:182:GLN:CG	1:F:186:PHE:HZ	1.63	1.11
1:A:106:MSE:HE1	1:A:111:LEU:HD22	1.41	1.01
1:B:106:MSE:HE1	1:B:111:LEU:HD22	1.39	1.01

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	282/290 (97%)	262 (93%)	17 (6%)	3 (1%)	11	23
1	B	282/290 (97%)	261 (93%)	18 (6%)	3 (1%)	11	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	282/290 (97%)	259 (92%)	19 (7%)	4 (1%)	9	17
1	D	282/290 (97%)	260 (92%)	18 (6%)	4 (1%)	9	17
1	E	282/290 (97%)	261 (93%)	17 (6%)	4 (1%)	9	17
1	F	282/290 (97%)	260 (92%)	18 (6%)	4 (1%)	9	17
All	All	1692/1740 (97%)	1563 (92%)	107 (6%)	22 (1%)	9	19

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	166	ARG
1	A	166	ARG
1	B	166	ARG
1	C	283	LEU
1	D	166	ARG

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	244/240 (102%)	224 (92%)	20 (8%)	10	22
1	B	244/240 (102%)	225 (92%)	19 (8%)	11	25
1	C	244/240 (102%)	225 (92%)	19 (8%)	11	25
1	D	244/240 (102%)	226 (93%)	18 (7%)	13	27
1	E	244/240 (102%)	224 (92%)	20 (8%)	10	22
1	F	244/240 (102%)	227 (93%)	17 (7%)	14	29
All	All	1464/1440 (102%)	1351 (92%)	113 (8%)	12	25

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	276	LEU
1	F	179	LYS

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Mol	Chain	Res	Type
1	D	165	GLU
1	F	166	ARG
1	F	39	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	147	ASN
1	F	182	GLN
1	C	97	HIS
1	C	39	GLN
1	F	188	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 [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	274/290 (94%)	0.18	10 (3%) 46 41	10, 25, 42, 60	0
1	B	274/290 (94%)	0.26	9 (3%) 49 44	10, 26, 40, 57	0
1	C	274/290 (94%)	0.69	28 (10%) 12 9	13, 34, 52, 76	0
1	D	274/290 (94%)	0.70	21 (7%) 19 15	18, 41, 52, 60	0
1	E	274/290 (94%)	0.72	18 (6%) 24 20	18, 38, 53, 64	0
1	F	274/290 (94%)	0.56	19 (6%) 23 19	17, 34, 51, 77	0
All	All	1644/1740 (94%)	0.52	105 (6%) 25 21	10, 33, 51, 77	0

The worst 5 of 105 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	283	LEU	6.4
1	D	186	PHE	6.3
1	C	283	LEU	6.3
1	F	284	GLU	4.5
1	F	137	LEU	4.2

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.