



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 07:59 am BST

PDB ID : 4KRY  
Title : Structure of Aes from E. coli in covalent complex with PMS  
Authors : Schiefner, A.; Gerber, K.; Brosig, A.; Boos, W.  
Deposited on : 2013-05-17  
Resolution : 2.30 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](mailto: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.

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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

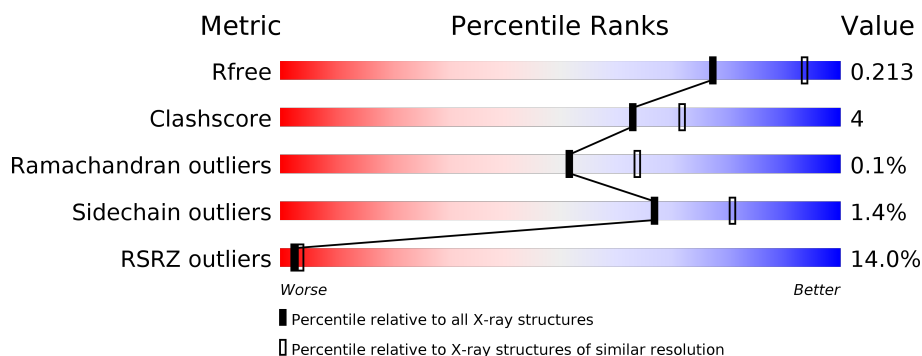
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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  $\geq 3$ , 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	333	<div> <div>12%</div> <div>87%</div> <div>9%</div> <div>5%</div> </div>
1	B	333	<div> <div>10%</div> <div>87%</div> <div>8%</div> <div>5%</div> </div>
1	C	333	<div> <div>18%</div> <div>84%</div> <div>11%</div> <div>5%</div> </div>
1	D	333	<div> <div>10%</div> <div>85%</div> <div>10%</div> <div>5%</div> </div>
1	E	333	<div> <div>9%</div> <div>88%</div> <div>11%</div> <div>•</div> </div>
1	F	333	<div> <div>22%</div> <div>89%</div> <div>7%</div> <div>5%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15961 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 esterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2537	1621	424	474	18			
1	B	318	Total	C	N	O	S	0	1	0
			2545	1626	427	474	18			
1	C	318	Total	C	N	O	S	0	2	0
			2554	1631	428	477	18			
1	D	318	Total	C	N	O	S	0	1	0
			2545	1626	427	474	18			
1	E	329	Total	C	N	O	S	0	3	0
			2660	1695	455	490	20			
1	F	318	Total	C	N	O	S	0	0	0
			2537	1621	424	474	18			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP P23872
A	-12	ARG	-	EXPRESSION TAG	UNP P23872
A	-11	GLY	-	EXPRESSION TAG	UNP P23872
A	-10	SER	-	EXPRESSION TAG	UNP P23872
A	-9	HIS	-	EXPRESSION TAG	UNP P23872
A	-8	HIS	-	EXPRESSION TAG	UNP P23872
A	-7	HIS	-	EXPRESSION TAG	UNP P23872
A	-6	HIS	-	EXPRESSION TAG	UNP P23872
A	-5	HIS	-	EXPRESSION TAG	UNP P23872
A	-4	HIS	-	EXPRESSION TAG	UNP P23872
A	-3	THR	-	EXPRESSION TAG	UNP P23872
A	-2	ASP	-	EXPRESSION TAG	UNP P23872
A	-1	PRO	-	EXPRESSION TAG	UNP P23872
A	0	ILE	-	EXPRESSION TAG	UNP P23872
B	-13	MET	-	EXPRESSION TAG	UNP P23872
B	-12	ARG	-	EXPRESSION TAG	UNP P23872
B	-11	GLY	-	EXPRESSION TAG	UNP P23872

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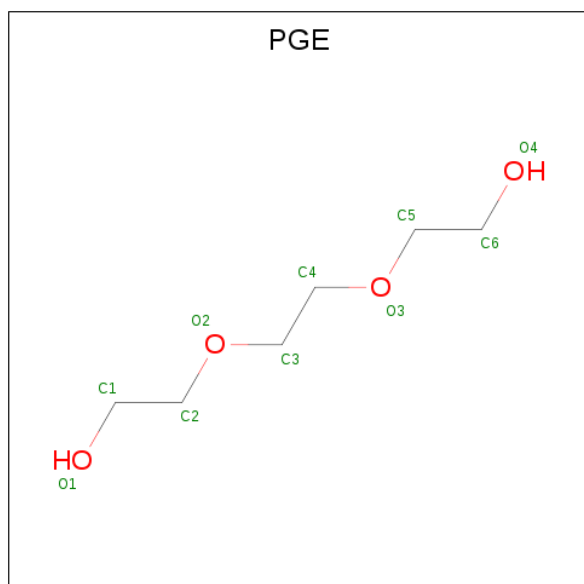
Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	SER	-	EXPRESSION TAG	UNP P23872
B	-9	HIS	-	EXPRESSION TAG	UNP P23872
B	-8	HIS	-	EXPRESSION TAG	UNP P23872
B	-7	HIS	-	EXPRESSION TAG	UNP P23872
B	-6	HIS	-	EXPRESSION TAG	UNP P23872
B	-5	HIS	-	EXPRESSION TAG	UNP P23872
B	-4	HIS	-	EXPRESSION TAG	UNP P23872
B	-3	THR	-	EXPRESSION TAG	UNP P23872
B	-2	ASP	-	EXPRESSION TAG	UNP P23872
B	-1	PRO	-	EXPRESSION TAG	UNP P23872
B	0	ILE	-	EXPRESSION TAG	UNP P23872
C	-13	MET	-	EXPRESSION TAG	UNP P23872
C	-12	ARG	-	EXPRESSION TAG	UNP P23872
C	-11	GLY	-	EXPRESSION TAG	UNP P23872
C	-10	SER	-	EXPRESSION TAG	UNP P23872
C	-9	HIS	-	EXPRESSION TAG	UNP P23872
C	-8	HIS	-	EXPRESSION TAG	UNP P23872
C	-7	HIS	-	EXPRESSION TAG	UNP P23872
C	-6	HIS	-	EXPRESSION TAG	UNP P23872
C	-5	HIS	-	EXPRESSION TAG	UNP P23872
C	-4	HIS	-	EXPRESSION TAG	UNP P23872
C	-3	THR	-	EXPRESSION TAG	UNP P23872
C	-2	ASP	-	EXPRESSION TAG	UNP P23872
C	-1	PRO	-	EXPRESSION TAG	UNP P23872
C	0	ILE	-	EXPRESSION TAG	UNP P23872
D	-13	MET	-	EXPRESSION TAG	UNP P23872
D	-12	ARG	-	EXPRESSION TAG	UNP P23872
D	-11	GLY	-	EXPRESSION TAG	UNP P23872
D	-10	SER	-	EXPRESSION TAG	UNP P23872
D	-9	HIS	-	EXPRESSION TAG	UNP P23872
D	-8	HIS	-	EXPRESSION TAG	UNP P23872
D	-7	HIS	-	EXPRESSION TAG	UNP P23872
D	-6	HIS	-	EXPRESSION TAG	UNP P23872
D	-5	HIS	-	EXPRESSION TAG	UNP P23872
D	-4	HIS	-	EXPRESSION TAG	UNP P23872
D	-3	THR	-	EXPRESSION TAG	UNP P23872
D	-2	ASP	-	EXPRESSION TAG	UNP P23872
D	-1	PRO	-	EXPRESSION TAG	UNP P23872
D	0	ILE	-	EXPRESSION TAG	UNP P23872
E	-13	MET	-	EXPRESSION TAG	UNP P23872
E	-12	ARG	-	EXPRESSION TAG	UNP P23872
E	-11	GLY	-	EXPRESSION TAG	UNP P23872

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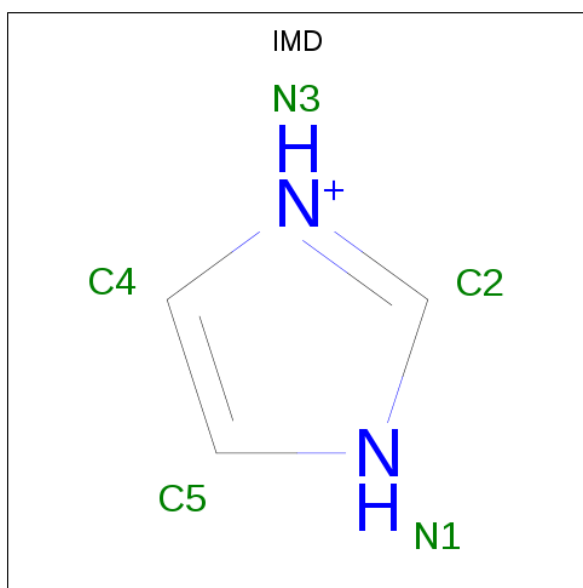
Chain	Residue	Modelled	Actual	Comment	Reference
E	-10	SER	-	EXPRESSION TAG	UNP P23872
E	-9	HIS	-	EXPRESSION TAG	UNP P23872
E	-8	HIS	-	EXPRESSION TAG	UNP P23872
E	-7	HIS	-	EXPRESSION TAG	UNP P23872
E	-6	HIS	-	EXPRESSION TAG	UNP P23872
E	-5	HIS	-	EXPRESSION TAG	UNP P23872
E	-4	HIS	-	EXPRESSION TAG	UNP P23872
E	-3	THR	-	EXPRESSION TAG	UNP P23872
E	-2	ASP	-	EXPRESSION TAG	UNP P23872
E	-1	PRO	-	EXPRESSION TAG	UNP P23872
E	0	ILE	-	EXPRESSION TAG	UNP P23872
F	-13	MET	-	EXPRESSION TAG	UNP P23872
F	-12	ARG	-	EXPRESSION TAG	UNP P23872
F	-11	GLY	-	EXPRESSION TAG	UNP P23872
F	-10	SER	-	EXPRESSION TAG	UNP P23872
F	-9	HIS	-	EXPRESSION TAG	UNP P23872
F	-8	HIS	-	EXPRESSION TAG	UNP P23872
F	-7	HIS	-	EXPRESSION TAG	UNP P23872
F	-6	HIS	-	EXPRESSION TAG	UNP P23872
F	-5	HIS	-	EXPRESSION TAG	UNP P23872
F	-4	HIS	-	EXPRESSION TAG	UNP P23872
F	-3	THR	-	EXPRESSION TAG	UNP P23872
F	-2	ASP	-	EXPRESSION TAG	UNP P23872
F	-1	PRO	-	EXPRESSION TAG	UNP P23872
F	0	ILE	-	EXPRESSION TAG	UNP P23872

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



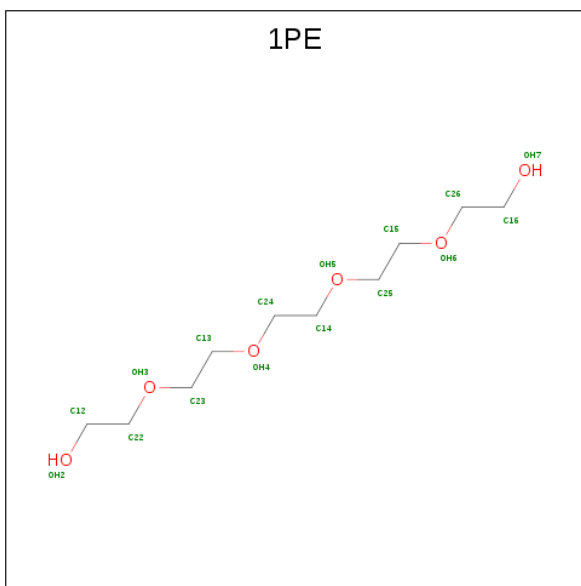
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	6	4		
2	A	1	Total	C	O	0	0
			10	6	4		
2	B	1	Total	C	O	0	0
			10	6	4		
2	C	1	Total	C	O	0	0
			10	6	4		
2	D	1	Total	C	O	0	0
			10	6	4		
2	D	1	Total	C	O	0	0
			10	6	4		
2	E	1	Total	C	O	0	0
			10	6	4		
2	F	1	Total	C	O	0	0
			10	6	4		

- Molecule 3 is IMIDAZOLE (three-letter code: IMD) (formula:  $C_3H_5N_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			5	3	2		
3	B	1	Total	C	N	0	0
			5	3	2		
3	D	1	Total	C	N	0	0
			5	3	2		
3	D	1	Total	C	N	0	0
			5	3	2		

- Molecule 4 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula:  $C_{10}H_{22}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			16	10	6		
4	E	1	Total	C	O	0	0
			16	10	6		

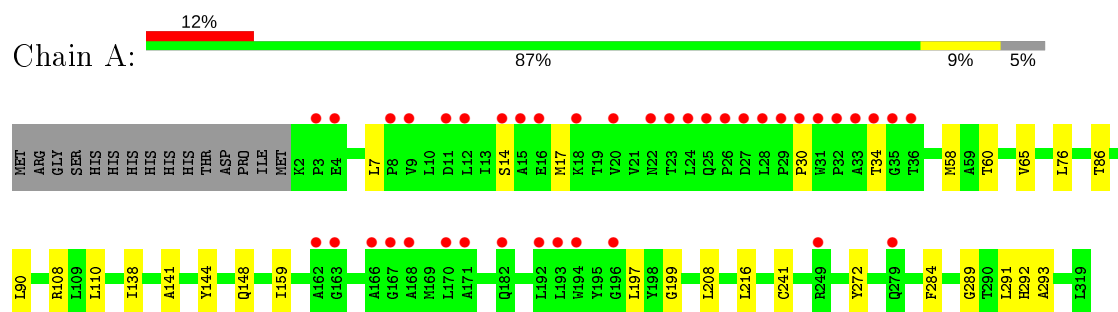
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	72	Total	O	0	0
			72	72		
5	B	82	Total	O	0	1
			83	83		
5	C	45	Total	O	0	0
			45	45		
5	D	98	Total	O	0	0
			98	98		
5	E	116	Total	O	0	1
			117	117		
5	F	36	Total	O	0	0
			36	36		

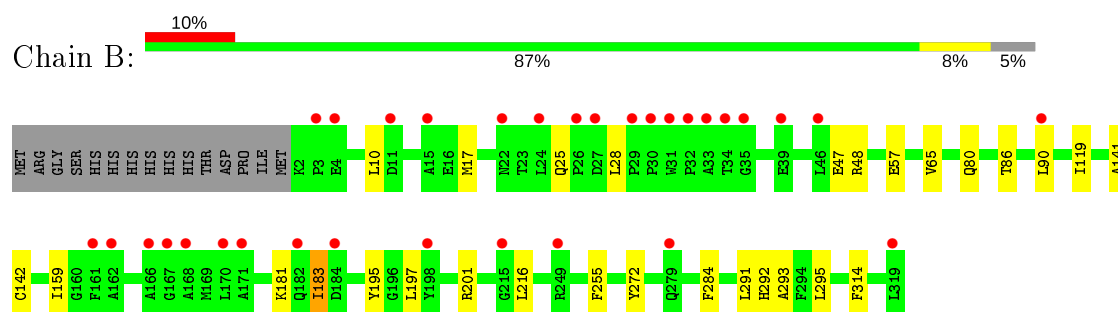
### 3 Residue-property plots [i](#)

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.

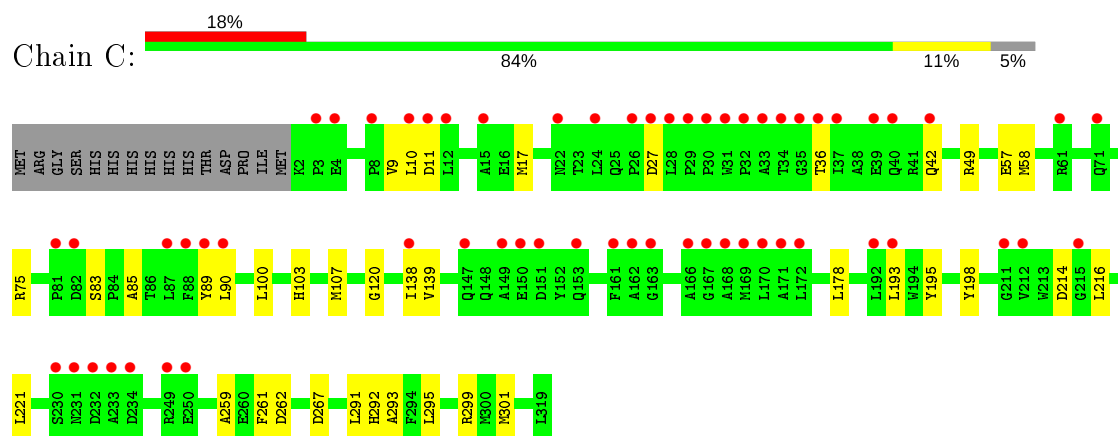
- Molecule 1: Acetyl esterase



- Molecule 1: Acetyl esterase

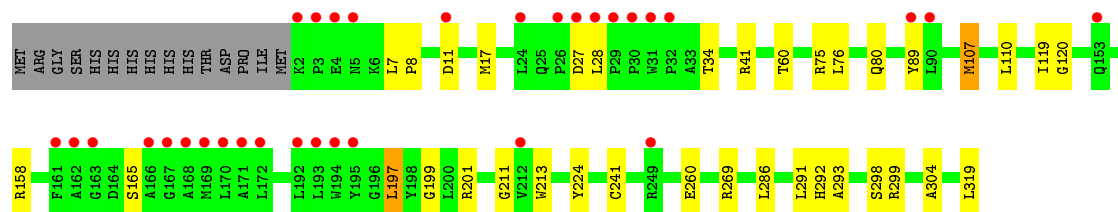
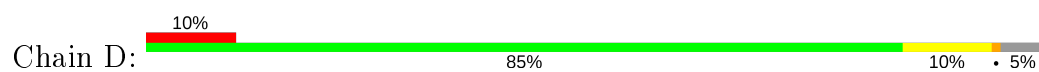


- Molecule 1: Acetyl esterase

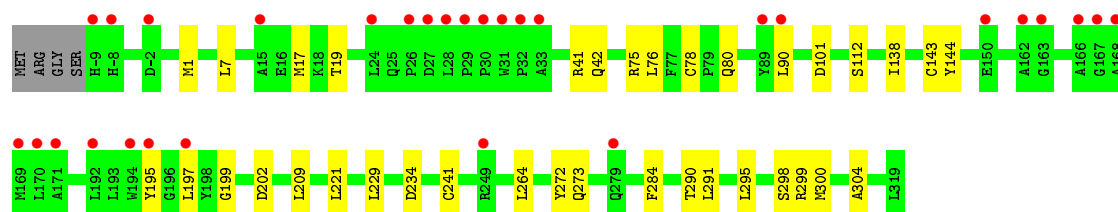
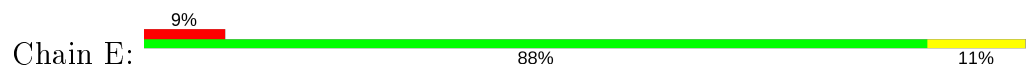


- Molecule 1: Acetyl esterase

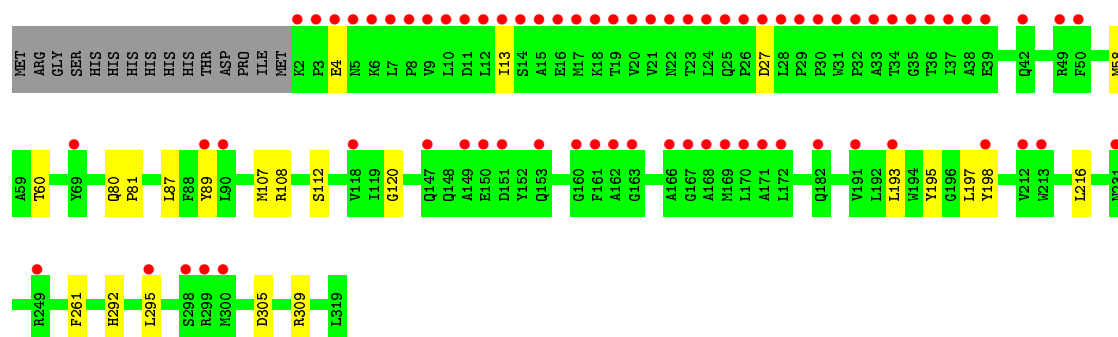
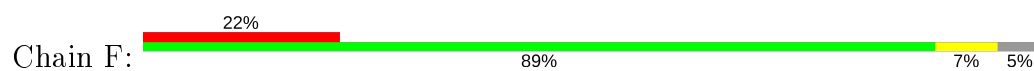




- Molecule 1: Acetyl esterase



- Molecule 1: Acetyl esterase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.40Å 111.40Å 282.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.37 – 2.30 29.35 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.37-2.30) 99.8 (29.35-2.30)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.40 (at 2.31Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.179 , 0.209 0.184 , 0.213	Depositor DCC
$R_{free}$ test set	7572 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.8	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 59.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.068 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	15961	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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: PGE, IPE, SEB, IMD

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	0.57	0/2586	0.70	0/3516
1	B	0.61	0/2597	0.76	1/3530 (0.0%)
1	C	0.49	0/2606	0.64	0/3542
1	D	0.68	0/2597	0.81	4/3530 (0.1%)
1	E	0.64	0/2719	0.79	5/3697 (0.1%)
1	F	0.50	0/2586	0.67	1/3516 (0.0%)
All	All	0.59	0/15691	0.73	11/21331 (0.1%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	41	ARG	NE-CZ-NH1	6.45	123.52	120.30
1	E	101	ASP	CB-CG-OD1	6.16	123.84	118.30
1	E	41	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	E	202	ASP	CB-CG-OD1	5.46	123.22	118.30
1	D	269	ARG	NE-CZ-NH1	5.42	123.01	120.30

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	2537	0	2450	19	0
1	B	2545	0	2463	20	0
1	C	2554	0	2468	26	0
1	D	2545	0	2463	23	0
1	E	2660	0	2563	25	0
1	F	2537	0	2450	19	0
2	A	20	0	28	1	0
2	B	10	0	14	1	0
2	C	10	0	14	2	0
2	D	20	0	28	3	0
2	E	10	0	14	1	0
2	F	10	0	14	2	0
3	A	5	0	5	0	0
3	B	5	0	5	0	0
3	D	10	0	10	0	0
4	D	16	0	22	0	0
4	E	16	0	22	2	0
5	A	72	0	0	0	0
5	B	83	0	0	0	0
5	C	45	0	0	0	0
5	D	98	0	0	3	0
5	E	117	0	0	2	0
5	F	36	0	0	0	0
All	All	15961	0	15033	131	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.

The worst 5 of 131 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:E:76:LEU:CD2	1:E:78[A]:CYS:SG	2.68	0.81
1:B:181:LYS:HE3	1:B:183:ILE:HD11	1.73	0.70
1:E:299[A]:ARG:HH11	1:E:299[A]:ARG:HG2	1.57	0.68
1:C:17:MET:HE3	1:C:291:LEU:H	1.59	0.67
1:F:197:LEU:HD12	2:F:401:PGE:H12	1.76	0.67

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	315/333 (95%)	306 (97%)	9 (3%)	0	100	100
1	B	316/333 (95%)	302 (96%)	14 (4%)	0	100	100
1	C	317/333 (95%)	302 (95%)	15 (5%)	0	100	100
1	D	316/333 (95%)	302 (96%)	14 (4%)	0	100	100
1	E	329/333 (99%)	317 (96%)	11 (3%)	1 (0%)	41	50
1	F	315/333 (95%)	303 (96%)	11 (4%)	1 (0%)	41	50
All	All	1908/1998 (96%)	1832 (96%)	74 (4%)	2 (0%)	51	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	1	MET
1	F	4	GLU

### 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	264/278 (95%)	263 (100%)	1 (0%)	91	96
1	B	265/278 (95%)	261 (98%)	4 (2%)	65	79
1	C	266/278 (96%)	258 (97%)	8 (3%)	41	57
1	D	265/278 (95%)	258 (97%)	7 (3%)	46	63
1	E	278/278 (100%)	277 (100%)	1 (0%)	91	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	264/278 (95%)	262 (99%)	2 (1%)	81	91
All	All	1602/1668 (96%)	1579 (99%)	23 (1%)	67	81

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	49	ARG
1	C	267	ASP
1	F	27	ASP
1	C	214	ASP
1	D	11	ASP

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

### 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	E	165	1	15,16,17	1.86	1 (6%)	15,21,23	0.71	0
1	SEB	B	165	1	15,16,17	2.41	1 (6%)	15,21,23	0.67	0
1	SEB	D	165	1	15,16,17	1.79	1 (6%)	15,21,23	0.90	1 (6%)
1	SEB	A	165	1	15,16,17	2.29	1 (6%)	15,21,23	1.08	1 (6%)
1	SEB	C	165	1	15,16,17	2.62	1 (6%)	15,21,23	0.90	0
1	SEB	F	165	1	15,16,17	2.67	1 (6%)	15,21,23	0.98	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	E	165	1	-	0/9/13/15	0/1/1/1
1	SEB	B	165	1	-	0/9/13/15	0/1/1/1
1	SEB	D	165	1	-	1/9/13/15	0/1/1/1
1	SEB	A	165	1	-	2/9/13/15	0/1/1/1
1	SEB	C	165	1	-	0/9/13/15	0/1/1/1
1	SEB	F	165	1	-	2/9/13/15	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	165	SEB	CE-SD	-10.02	1.68	1.78
1	C	165	SEB	CE-SD	-9.91	1.68	1.78
1	B	165	SEB	CE-SD	-9.07	1.69	1.78
1	A	165	SEB	CE-SD	-8.37	1.70	1.78
1	E	165	SEB	CE-SD	-6.66	1.71	1.78

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	165	SEB	OG-SD-CE	2.67	111.54	104.18
1	A	165	SEB	OD1-SD-CE	2.52	114.82	108.82
1	D	165	SEB	CB-OG-SD	2.12	123.78	119.23

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	F	165	SEB	SD-CE-CZ-CH2
1	F	165	SEB	SD-CE-CZ-CH1
1	A	165	SEB	SD-CE-CZ-CH1
1	A	165	SEB	SD-CE-CZ-CH2
1	D	165	SEB	CA-CB-OG-SD

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	165	SEB	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

14 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	$\# Z  > 2$
2	PGE	A	401	-	9,9,9	0.54	0	8,8,8	0.29	0
3	IMD	D	404	-	3,5,5	0.27	0	4,5,5	0.63	0
4	1PE	D	403	-	15,15,15	0.56	0	14,14,14	0.42	0
3	IMD	D	405	-	3,5,5	0.42	0	4,5,5	0.37	0
3	IMD	B	402	-	3,5,5	0.35	0	4,5,5	0.59	0
4	1PE	E	402	-	15,15,15	0.75	0	14,14,14	0.92	0
2	PGE	D	402	-	9,9,9	0.56	0	8,8,8	0.47	0
2	PGE	A	402	-	9,9,9	0.74	0	8,8,8	0.61	0
2	PGE	D	401	-	9,9,9	0.70	0	8,8,8	0.61	0
2	PGE	F	401	-	9,9,9	0.48	0	8,8,8	0.83	0
3	IMD	A	403	-	3,5,5	0.31	0	4,5,5	0.64	0
2	PGE	C	401	-	9,9,9	0.39	0	8,8,8	0.27	0
2	PGE	B	401	-	9,9,9	0.50	0	8,8,8	0.42	0
2	PGE	E	401	-	9,9,9	0.63	0	8,8,8	0.54	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
2	PGE	A	401	-	-	3/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	IMD	D	404	-	-	-	0/1/1/1
4	1PE	D	403	-	-	4/13/13/13	-
3	IMD	D	405	-	-	-	0/1/1/1
3	IMD	B	402	-	-	-	0/1/1/1
4	1PE	E	402	-	-	9/13/13/13	-
2	PGE	D	402	-	-	1/7/7/7	-
2	PGE	D	401	-	-	5/7/7/7	-
3	IMD	A	403	-	-	-	0/1/1/1
2	PGE	F	401	-	-	5/7/7/7	-
2	PGE	A	402	-	-	5/7/7/7	-
2	PGE	C	401	-	-	5/7/7/7	-
2	PGE	B	401	-	-	5/7/7/7	-
2	PGE	E	401	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	402	1PE	C14-C24-OH4-C13
2	B	401	PGE	O2-C3-C4-O3
2	E	401	PGE	O2-C3-C4-O3
2	B	401	PGE	O1-C1-C2-O2
4	D	403	1PE	OH2-C12-C22-OH3

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	PGE	1	0
4	E	402	1PE	2	0
2	D	402	PGE	2	0
2	D	401	PGE	1	0
2	F	401	PGE	2	0
2	C	401	PGE	2	0
2	B	401	PGE	1	0
2	E	401	PGE	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	317/333 (95%)	0.45	40 (12%) 3 5	25, 39, 88, 113	0
1	B	317/333 (95%)	0.33	32 (10%) 7 9	27, 37, 74, 115	0
1	C	317/333 (95%)	0.84	60 (18%) 1 1	32, 53, 95, 134	0
1	D	317/333 (95%)	0.36	32 (10%) 7 9	24, 31, 83, 128	0
1	E	328/333 (98%)	0.25	30 (9%) 9 12	24, 32, 52, 107	0
1	F	317/333 (95%)	1.05	73 (23%) 0 1	33, 50, 122, 144	0
All	All	1913/1998 (95%)	0.54	267 (13%) 2 4	24, 39, 91, 144	0

The worst 5 of 267 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	3	PRO	10.9
1	F	3	PRO	9.2
1	F	30	PRO	8.8
1	C	3	PRO	8.8
1	C	34	THR	8.6

### 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	SEB	D	165	16/17	0.94	0.15	26,32,35,35	0
1	SEB	C	165	16/17	0.94	0.17	41,59,67,68	0
1	SEB	F	165	16/17	0.94	0.16	39,54,64,64	0
1	SEB	E	165	16/17	0.95	0.15	28,36,38,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
1	SEB	A	165	16/17	0.96	0.17	33,44,48,48	0
1	SEB	B	165	16/17	0.97	0.14	33,43,48,49	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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	PGE	A	402	10/10	0.76	0.20	53,61,64,65	0
3	IMD	A	403	5/5	0.77	0.21	85,88,91,93	0
4	1PE	E	402	16/16	0.84	0.17	48,71,86,87	0
2	PGE	A	401	10/10	0.87	0.20	55,61,77,78	0
2	PGE	F	401	10/10	0.88	0.30	47,57,73,75	0
2	PGE	B	401	10/10	0.90	0.20	42,53,73,76	0
2	PGE	D	401	10/10	0.91	0.19	44,46,64,64	0
2	PGE	D	402	10/10	0.91	0.17	40,43,55,56	0
3	IMD	D	404	5/5	0.93	0.22	62,63,64,65	0
4	1PE	D	403	16/16	0.94	0.15	48,61,64,64	0
2	PGE	E	401	10/10	0.94	0.20	34,42,56,58	0
3	IMD	B	402	5/5	0.96	0.11	47,49,50,52	0
2	PGE	C	401	10/10	0.96	0.17	44,53,66,70	0
3	IMD	D	405	5/5	0.97	0.10	43,45,48,48	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.