



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 06:18 am BST

PDB ID : 3G9T
Title : Crystal structure of EstE5, was soaked by p-nitrophenyl butyrate for 5sec
Authors : Hwang, K.Y.; Nam, K.H.
Deposited on : 2009-02-14
Resolution : 1.96 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 ⓘ symbol.

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

MolProbity : 4.02b-467
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

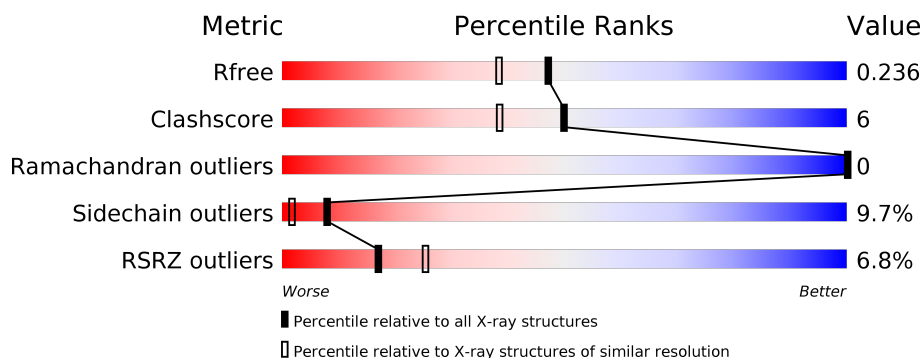
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	322	<div> <div>6%</div> <div>75%</div> <div>14%</div> <div>9%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2320 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 Esterase/lipase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	294	2221	1413	390	404	14	0	0	0

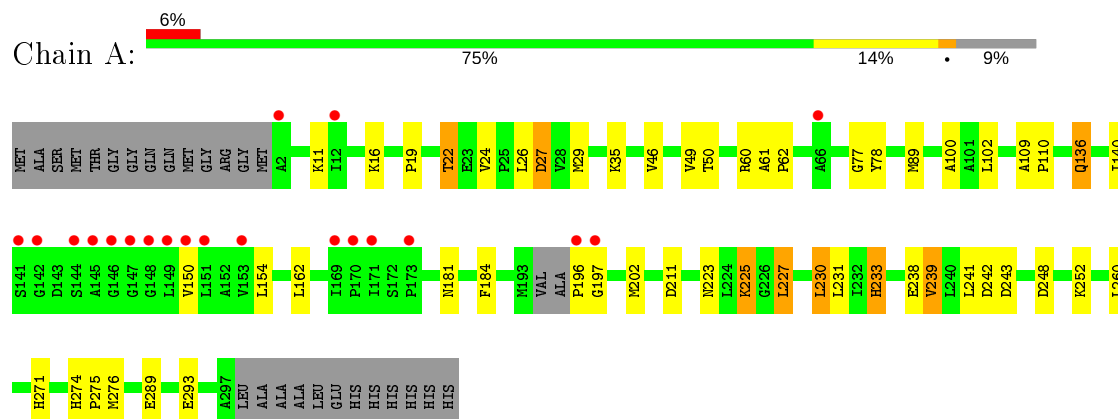
There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	INITIATING METHIONINE	UNP Q0GMU2
A	-11	ALA	-	EXPRESSION TAG	UNP Q0GMU2
A	-10	SER	-	EXPRESSION TAG	UNP Q0GMU2
A	-9	MET	-	EXPRESSION TAG	UNP Q0GMU2
A	-8	THR	-	EXPRESSION TAG	UNP Q0GMU2
A	-7	GLY	-	EXPRESSION TAG	UNP Q0GMU2
A	-6	GLY	-	EXPRESSION TAG	UNP Q0GMU2
A	-5	GLN	-	EXPRESSION TAG	UNP Q0GMU2
A	-4	GLN	-	EXPRESSION TAG	UNP Q0GMU2
A	-3	MET	-	EXPRESSION TAG	UNP Q0GMU2
A	-2	GLY	-	EXPRESSION TAG	UNP Q0GMU2
A	-1	ARG	-	EXPRESSION TAG	UNP Q0GMU2
A	0	GLY	-	EXPRESSION TAG	UNP Q0GMU2
A	298	LEU	-	EXPRESSION TAG	UNP Q0GMU2
A	299	ALA	-	EXPRESSION TAG	UNP Q0GMU2
A	300	ALA	-	EXPRESSION TAG	UNP Q0GMU2
A	301	ALA	-	EXPRESSION TAG	UNP Q0GMU2
A	302	LEU	-	EXPRESSION TAG	UNP Q0GMU2
A	303	GLU	-	EXPRESSION TAG	UNP Q0GMU2
A	304	HIS	-	EXPRESSION TAG	UNP Q0GMU2
A	305	HIS	-	EXPRESSION TAG	UNP Q0GMU2
A	306	HIS	-	EXPRESSION TAG	UNP Q0GMU2
A	307	HIS	-	EXPRESSION TAG	UNP Q0GMU2
A	308	HIS	-	EXPRESSION TAG	UNP Q0GMU2
A	309	HIS	-	EXPRESSION TAG	UNP Q0GMU2

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	99	Total	O	0	0
			99	99		

- Molecule 1: Esterase/lipase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	61.24Å 61.24Å 148.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.59 – 1.96 32.59 – 1.96	Depositor EDS
% Data completeness (in resolution range)	98.4 (32.59-1.96) 98.4 (32.59-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.88 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.193 , 0.230 0.196 , 0.236	Depositor DCC
R_{free} test set	1065 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2320	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.20% 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

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	0.84	0/2274	0.81	3/3085 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	230	LEU	CA-CB-CG	5.40	127.72	115.30
1	A	211	ASP	CB-CG-OD1	5.31	123.08	118.30
1	A	202	MET	CG-SD-CE	5.21	108.54	100.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	196	PRO	Peptide

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	2221	0	2228	26	0
2	A	99	0	0	5	0
All	All	2320	0	2228	26	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 6.

All (26) 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:A:27:ASP:HB2	2:A:359:HOH:O	1.74	0.88
1:A:223:ASN:HD21	1:A:225:LYS:HB2	1.49	0.78
1:A:136:GLN:H	1:A:136:GLN:HE21	1.33	0.75
1:A:197:GLY:HA2	2:A:362:HOH:O	1.89	0.73
1:A:271:HIS:HD1	1:A:271:HIS:H	1.43	0.66
1:A:289:GLU:O	1:A:293:GLU:HG3	1.96	0.66
1:A:238:GLU:HB2	2:A:340:HOH:O	1.96	0.65
1:A:248:ASP:O	1:A:252:LYS:HG2	2.03	0.57
1:A:89:MET:HE2	2:A:341:HOH:O	2.04	0.56
1:A:136:GLN:H	1:A:136:GLN:NE2	2.01	0.55
1:A:24:VAL:O	1:A:29:MET:HE3	2.11	0.50
1:A:233:HIS:HD2	1:A:271:HIS:NE2	2.08	0.49
1:A:154:LEU:HD13	1:A:227:LEU:HD13	1.94	0.49
1:A:60:ARG:HG2	1:A:100:ALA:HB2	1.96	0.48
1:A:184:PHE:CD2	1:A:239:VAL:HG13	2.48	0.47
1:A:77:GLY:O	1:A:78:TYR:HB2	2.16	0.46
1:A:24:VAL:O	1:A:29:MET:CE	2.64	0.45
1:A:274:HIS:CG	1:A:275:PRO:HD3	2.53	0.44
1:A:60:ARG:HG2	1:A:100:ALA:CB	2.47	0.44
1:A:140:ILE:HG22	1:A:150:VAL:HG22	2.00	0.44
1:A:197:GLY:CA	2:A:362:HOH:O	2.57	0.43
1:A:154:LEU:CD1	1:A:227:LEU:HD13	2.49	0.43
1:A:19:PRO:O	1:A:22:THR:HG23	2.18	0.43
1:A:61:ALA:HB1	1:A:62:PRO:HD2	2.01	0.42
1:A:181:ASN:HB3	1:A:242:ASP:HB2	2.02	0.41
1:A:109:ALA:HB1	1:A:110:PRO:HA	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	290/322 (90%)	283 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	227/246 (92%)	205 (90%)	22 (10%)	8	2

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	16	LYS
1	A	22	THR
1	A	26	LEU
1	A	27	ASP
1	A	35	LYS
1	A	46	VAL
1	A	49	VAL
1	A	50	THR
1	A	102	LEU
1	A	136	GLN
1	A	162	LEU
1	A	225	LYS

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Mol	Chain	Res	Type
1	A	227	LEU
1	A	230	LEU
1	A	231	LEU
1	A	233	HIS
1	A	239	VAL
1	A	241	LEU
1	A	243	ASP
1	A	260	LEU
1	A	276	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	GLN
1	A	136	GLN
1	A	181	ASN
1	A	223	ASN
1	A	233	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

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	A	294/322 (91%)	0.23	20 (6%)	17 25	25, 32, 42, 58	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	196	PRO	3.0
1	A	2	ALA	3.0
1	A	66	ALA	2.7
1	A	150	VAL	2.6
1	A	142	GLY	2.5
1	A	151	LEU	2.4
1	A	148	GLY	2.2
1	A	173	PRO	2.2
1	A	147	GLY	2.2
1	A	197	GLY	2.2
1	A	141	SER	2.2
1	A	170	PRO	2.2
1	A	171	ILE	2.2
1	A	153	VAL	2.2
1	A	144	SER	2.1
1	A	145	ALA	2.1
1	A	146	GLY	2.0
1	A	149	LEU	2.0
1	A	12	ILE	2.0
1	A	169	ILE	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 [i](#)

There are no carbohydrates 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.