



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 02:33 am BST

PDB ID : 6ISR  
Title : structure of lipase mutant with Cys-His-Asp catalytic triad  
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Deposited on : 2018-11-18  
Resolution : 2.60 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

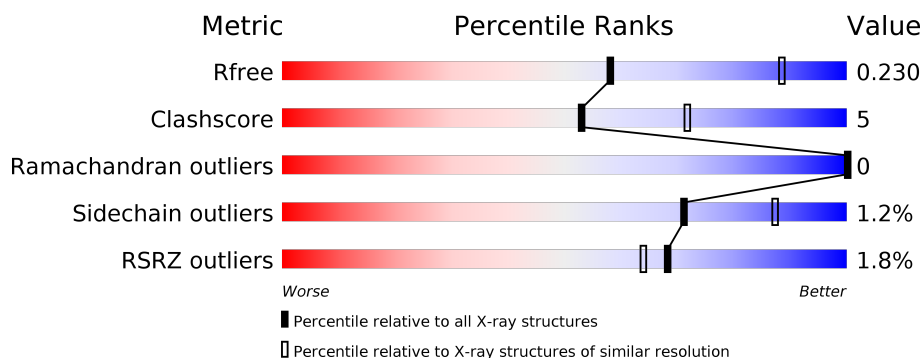
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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	321	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>13%</div> <div></div> </div> <div></div> </div>
1	B	321	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>12%</div> <div></div> </div> <div></div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4731 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 Lipase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	1	0
			2318	1467	389	451	11			
1	B	314	Total	C	N	O	S	0	0	0
			2307	1461	385	450	11			

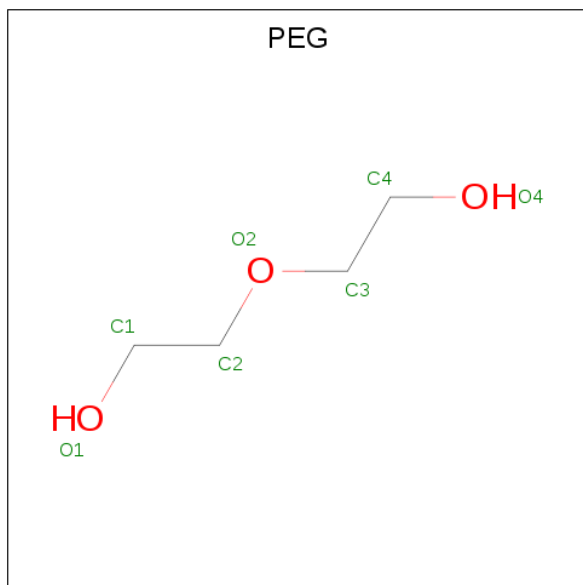
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P41365
A	-2	ALA	-	expression tag	UNP P41365
A	-1	MET	-	expression tag	UNP P41365
A	0	ALA	-	expression tag	UNP P41365
A	57	ALA	THR	engineered mutation	UNP P41365
A	89	THR	ALA	engineered mutation	UNP P41365
A	104	VAL	TRP	engineered mutation	UNP P41365
A	105	CYS	SER	engineered mutation	UNP P41365
A	149	GLY	VAL	engineered mutation	UNP P41365
A	281	TYR	ALA	engineered mutation	UNP P41365
A	282	TYR	ALA	engineered mutation	UNP P41365
B	-3	GLY	-	expression tag	UNP P41365
B	-2	ALA	-	expression tag	UNP P41365
B	-1	MET	-	expression tag	UNP P41365
B	0	ALA	-	expression tag	UNP P41365
B	57	ALA	THR	engineered mutation	UNP P41365
B	89	THR	ALA	engineered mutation	UNP P41365
B	104	VAL	TRP	engineered mutation	UNP P41365
B	105	CYS	SER	engineered mutation	UNP P41365
B	149	GLY	VAL	engineered mutation	UNP P41365
B	281	TYR	ALA	engineered mutation	UNP P41365
B	282	TYR	ALA	engineered mutation	UNP P41365

- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

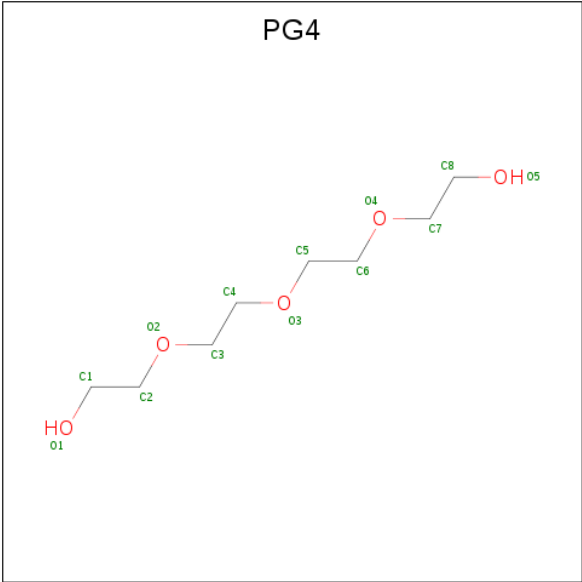
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Ni	0	0
			1	1		
2	A	1	Total	Ni	0	0
			1	1		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula:  $C_8H_{18}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	B	1	Total	C	O	0	0
			13	8	5		

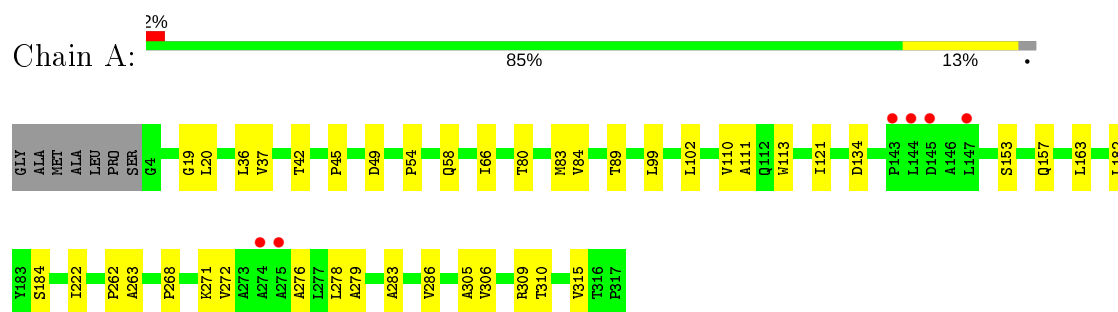
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	31	Total	O	0	0
			31	31		
5	B	26	Total	O	0	0
			26	26		

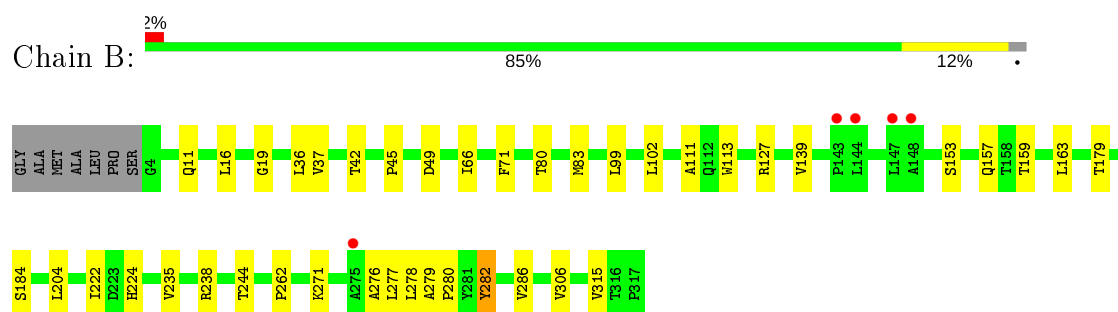
### 3 Residue-property plots [i](#)

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: Lipase B



#### • Molecule 1: Lipase B



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.29Å 44.56Å 132.95Å 90.00° 89.41° 90.00°	Depositor
Resolution (Å)	42.25 – 2.60 42.25 – 2.58	Depositor EDS
% Data completeness (in resolution range)	91.4 (42.25-2.60) 91.4 (42.25-2.58)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.40 (at 2.58Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.179 , 0.228 0.179 , 0.230	Depositor DCC
$R_{free}$ test set	876 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.2	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 28.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.447 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4731	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	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.*

<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: NI, PG4, PEG

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	0.40	0/2376	0.54	0/3260
1	B	0.43	0/2365	0.59	1/3245 (0.0%)
All	All	0.42	0/4741	0.57	1/6505 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	282	TYR	CB-CG-CD1	-5.38	117.77	121.00

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	2318	0	2288	25	0
1	B	2307	0	2274	24	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	7	0	10	2	0
3	B	14	0	20	3	0
4	A	13	0	18	1	0
4	B	13	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	31	0	0	0	0
5	B	26	0	0	0	0
All	All	4731	0	4628	50	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 5.

The worst 5 of 50 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:306:VAL:HA	1:A:315:VAL:HG23	1.65	0.77
1:A:309:ARG:NH2	1:A:310:THR:O	2.19	0.76
1:A:134:ASP:OD2	1:A:157:GLN:NE2	2.19	0.71
1:B:306:VAL:HA	1:B:315:VAL:HG23	1.72	0.70
1:B:244:THR:HA	3:B:402:PEG:H11	1.74	0.68

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	313/321 (98%)	299 (96%)	14 (4%)	0	100	100
1	B	312/321 (97%)	300 (96%)	12 (4%)	0	100	100
All	All	625/642 (97%)	599 (96%)	26 (4%)	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	254/257 (99%)	251 (99%)	3 (1%)	71	87
1	B	253/257 (98%)	250 (99%)	3 (1%)	71	87
All	All	507/514 (99%)	501 (99%)	6 (1%)	71	87

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	LEU
1	B	277	LEU
1	B	99	LEU
1	A	163	LEU
1	B	163	LEU

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

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	$\# Z  > 2$
3	PEG	B	402	-	6,6,6	0.45	0	5,5,5	0.32	0
4	PG4	A	403	-	12,12,12	0.48	0	11,11,11	0.37	0
3	PEG	A	402	-	6,6,6	0.52	0	5,5,5	0.30	0
3	PEG	B	403	-	6,6,6	0.48	0	5,5,5	0.26	0
4	PG4	B	404	-	12,12,12	0.50	0	11,11,11	0.42	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
3	PEG	B	402	-	-	3/4/4/4	-
4	PG4	A	403	-	-	8/10/10/10	-
3	PEG	A	402	-	-	1/4/4/4	-
3	PEG	B	403	-	-	0/4/4/4	-
4	PG4	B	404	-	-	6/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	404	PG4	O4-C7-C8-O5
4	B	404	PG4	O2-C3-C4-O3
3	B	402	PEG	O1-C1-C2-O2
4	A	403	PG4	C1-C2-O2-C3
3	B	402	PEG	C4-C3-O2-C2

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	402	PEG	3	0
4	A	403	PG4	1	0
3	A	402	PEG	2	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	314/321 (97%)	-0.51	6 (1%) 66 62	23, 36, 77, 108	1 (0%)
1	B	314/321 (97%)	-0.52	5 (1%) 72 68	24, 36, 80, 115	0
All	All	628/642 (97%)	-0.51	11 (1%) 68 64	23, 36, 79, 115	1 (0%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	143	PRO	3.6
1	B	148	ALA	3.6
1	A	143	PRO	3.0
1	B	147	LEU	2.9
1	A	275	ALA	2.9

### 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 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
3	PEG	A	402	7/7	0.87	0.18	56,56,58,58	0
4	PG4	A	403	13/13	0.90	0.21	58,58,61,61	0
3	PEG	B	403	7/7	0.90	0.17	60,62,63,64	0
4	PG4	B	404	13/13	0.90	0.18	56,57,59,59	0
3	PEG	B	402	7/7	0.94	0.14	60,61,61,61	0
2	NI	B	401	1/1	0.97	0.10	69,69,69,69	0
2	NI	A	401	1/1	0.97	0.07	70,70,70,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.