



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 2, 2025 – 07:17 pm BST

PDB ID : 9QDV / pdb_00009qdv
Title : Crystal structure of the polyester hydrolase Leipzig 7 (PHL7) mut3 variant expressed in E. coli (E_PHL7mut3)
Authors : Useini, A.; Strater, N.; Striedner, G.; Sonnendecker, C.
Deposited on : 2025-03-07
Resolution : 0.89 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 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 Phenix2.0rc1
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

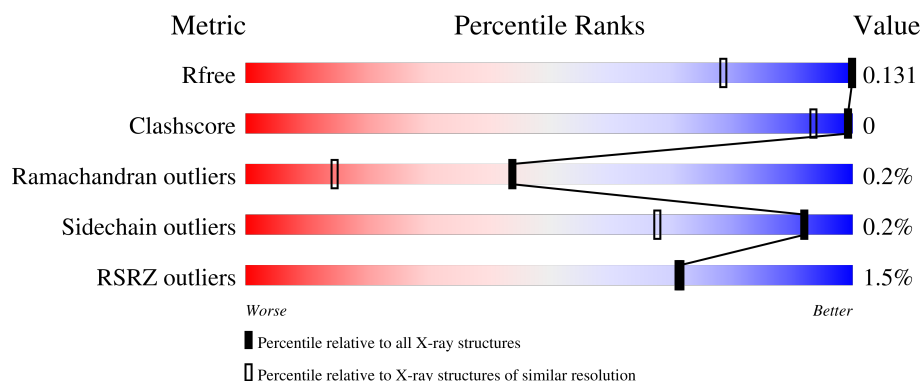
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

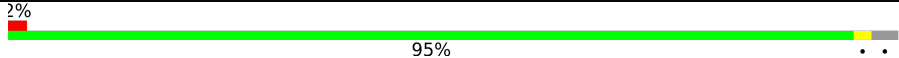
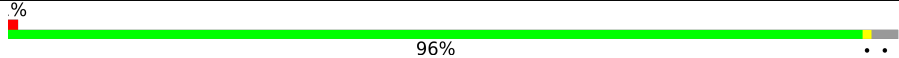
The reported resolution of this entry is 0.89 Å.

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}	164625	1232 (1.00-0.80)
Clashscore	180529	1367 (1.00-0.80)
Ramachandran outliers	177936	1294 (1.00-0.80)
Sidechain outliers	177891	1295 (1.00-0.80)
RSRZ outliers	164620	1231 (1.00-0.80)

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	267	
1	B	267	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9151 atoms, of which 4095 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 Polyester Hydrolase Leipzig 7 (PHL-7), catalysis-deficient S131A mutant.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	259	Total	C	H	N	O	S	0	24	0
			4104	1299	2026	363	409	7			
1	B	259	Total	C	H	N	O	S	0	32	0
			4192	1322	2069	375	419	7			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	131	SER	ALA	engineered mutation	UNP A0AA82WPD4
A	175	GLU	GLN	engineered mutation	UNP A0AA82WPD4
A	210	THR	LEU	engineered mutation	UNP A0AA82WPD4
A	233	LYS	ASP	engineered mutation	UNP A0AA82WPD4
A	260	LEU	-	expression tag	UNP A0AA82WPD4
A	261	GLU	-	expression tag	UNP A0AA82WPD4
A	262	HIS	-	expression tag	UNP A0AA82WPD4
A	263	HIS	-	expression tag	UNP A0AA82WPD4
A	264	HIS	-	expression tag	UNP A0AA82WPD4
A	265	HIS	-	expression tag	UNP A0AA82WPD4
A	266	HIS	-	expression tag	UNP A0AA82WPD4
A	267	HIS	-	expression tag	UNP A0AA82WPD4
B	131	SER	ALA	engineered mutation	UNP A0AA82WPD4
B	175	GLU	GLN	engineered mutation	UNP A0AA82WPD4
B	210	THR	LEU	engineered mutation	UNP A0AA82WPD4
B	233	LYS	ASP	engineered mutation	UNP A0AA82WPD4
B	260	LEU	-	expression tag	UNP A0AA82WPD4
B	261	GLU	-	expression tag	UNP A0AA82WPD4
B	262	HIS	-	expression tag	UNP A0AA82WPD4
B	263	HIS	-	expression tag	UNP A0AA82WPD4
B	264	HIS	-	expression tag	UNP A0AA82WPD4
B	265	HIS	-	expression tag	UNP A0AA82WPD4
B	266	HIS	-	expression tag	UNP A0AA82WPD4
B	267	HIS	-	expression tag	UNP A0AA82WPD4

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	462	Total 476	O 476	0	21
2	B	378	Total 379	O 379	0	8

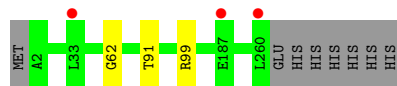
3 Residue-property plots [i](#)

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: Polyester Hydrolase Leipzig 7 (PHL-7), catalysis-deficient S131A mutant



- Molecule 1: Polyester Hydrolase Leipzig 7 (PHL-7), catalysis-deficient S131A mutant



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	150.44Å 43.90Å 100.12Å 90.00° 130.87° 90.00°	Depositor
Resolution (Å)	32.93 – 0.89 32.93 – 0.89	Depositor EDS
% Data completeness (in resolution range)	80.2 (32.93-0.89) 80.2 (32.93-0.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 0.89Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.119 , 0.131 0.119 , 0.131	Depositor DCC
R_{free} test set	2940 reflections (0.79%)	wwPDB-VP
Wilson B-factor (Å ²)	8.6	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.007 for -h-2*k,-k,l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	9151	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.70% 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	0.48	0/2211	0.67	0/3012
1	B	0.43	0/2272	0.61	0/3094
All	All	0.46	0/4483	0.64	0/6106

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	2
1	B	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	87	ILE	Peptide
1	A	99	ARG	Sidechain
1	B	99	ARG	Sidechain

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	2078	2026	1954	2	0
1	B	2123	2069	1977	0	0
2	A	476	0	0	0	0
2	B	379	0	0	0	0
All	All	5056	4095	3931	2	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 0.

All (2) 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:83:VAL:HG11	1:A:120[B]:ILE:HD11	1.99	0.44
1:A:110:LEU:HB3	1:A:120[B]:ILE:CD1	2.52	0.40

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	281/267 (105%)	276 (98%)	5 (2%)	0	100	100
1	B	291/267 (109%)	285 (98%)	4 (1%)	2 (1%)	19	3
All	All	572/534 (107%)	561 (98%)	9 (2%)	2 (0%)	44	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	62[A]	GLY
1	B	62[B]	GLY

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	233/218 (107%)	233 (100%)	0	100	100
1	B	238/218 (109%)	237 (100%)	1 (0%)	89	67
All	All	471/436 (108%)	470 (100%)	1 (0%)	92	68

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	91	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	A	239	GLN
1	B	95	GLN
1	B	213	ASN

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

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 [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	259/267 (97%)	-0.59	5 (1%)	66 66	4, 8, 15, 28	14 (5%)
1	B	259/267 (97%)	-0.39	3 (1%)	76 76	4, 10, 20, 34	22 (8%)
All	All	518/534 (97%)	-0.49	8 (1%)	71 71	4, 9, 17, 34	36 (6%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260[A]	LEU	4.6
1	B	33	LEU	3.5
1	B	260	LEU	3.3
1	A	63[A]	PHE	3.2
1	A	33	LEU	2.6
1	A	111	ARG	2.3
1	B	187[A]	GLU	2.2
1	A	2	ALA	2.1

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.