



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 08:59 PM EDT

PDB ID : 7E1L / pdb_00007e1l
Title : Crystal structure of apo form PhlH
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Deposited on : 2021-02-01
Resolution : 2.40 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 Phenix2.0
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

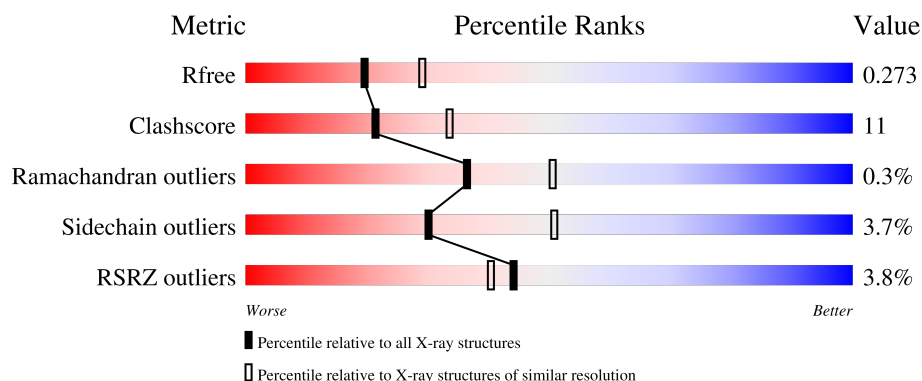
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

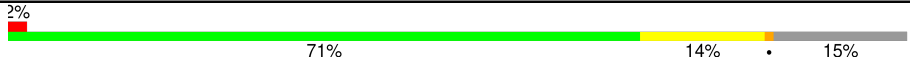
The reported resolution of this entry is 2.40 Å.

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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	234	
1	B	234	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3179 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 DUF1956 domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	199	Total	C	N	O	S	Se	0	2	0
			1530	969	279	277	2	3			
1	B	202	Total	C	N	O	S	Se	0	2	0
			1551	983	280	283	2	3			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MSE	-	initiating methionine	UNP Q4JIX5
A	-7	GLY	-	expression tag	UNP Q4JIX5
A	-6	HIS	-	expression tag	UNP Q4JIX5
A	-5	HIS	-	expression tag	UNP Q4JIX5
A	-4	HIS	-	expression tag	UNP Q4JIX5
A	-3	HIS	-	expression tag	UNP Q4JIX5
A	-2	HIS	-	expression tag	UNP Q4JIX5
A	-1	HIS	-	expression tag	UNP Q4JIX5
A	0	HIS	-	expression tag	UNP Q4JIX5
B	-8	MSE	-	initiating methionine	UNP Q4JIX5
B	-7	GLY	-	expression tag	UNP Q4JIX5
B	-6	HIS	-	expression tag	UNP Q4JIX5
B	-5	HIS	-	expression tag	UNP Q4JIX5
B	-4	HIS	-	expression tag	UNP Q4JIX5
B	-3	HIS	-	expression tag	UNP Q4JIX5
B	-2	HIS	-	expression tag	UNP Q4JIX5
B	-1	HIS	-	expression tag	UNP Q4JIX5
B	0	HIS	-	expression tag	UNP Q4JIX5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	44	Total	O	0	0
			44	44		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	54	Total	O	0	0
			54	54		

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	60.95Å 60.95Å 234.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 30.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.40) 99.9 (30.00-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.11 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.206 , 0.265 0.210 , 0.273	Depositor DCC
R_{free} test set	890 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	39.7	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3179	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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	1.20	5/1561 (0.3%)	1.23	1/2114 (0.0%)
1	B	1.16	4/1580 (0.3%)	1.23	0/2140
All	All	1.18	9/3141 (0.3%)	1.23	1/4254 (0.0%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	155	ILE	C-O	-7.24	1.15	1.24
1	B	204	HIS	CE1-NE2	6.36	1.39	1.32
1	A	162	HIS	CE1-NE2	6.01	1.38	1.32
1	A	219	THR	C-O	-5.61	1.17	1.24
1	A	204	HIS	CE1-NE2	5.57	1.38	1.32
1	B	76	HIS	C-O	5.54	1.30	1.24
1	A	25	ILE	C-O	-5.50	1.17	1.24
1	A	206	MSE	C-O	-5.20	1.18	1.24
1	B	172	VAL	C-O	-5.18	1.18	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	21	THR	CA-CB-OG1	-6.86	99.30	109.60

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	1530	0	1559	27	1
1	B	1551	0	1583	47	1
2	A	44	0	0	1	0
2	B	54	0	0	4	0
All	All	3179	0	3142	68	1

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 11.

All (68) 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:B:15:ARG:NH1	2:B:302:HOH:O	2.06	0.87
1:B:201:LEU:HG	1:B:205:MSE:CE	2.05	0.86
1:B:186:LEU:H	1:B:186:LEU:HD12	1.39	0.85
1:B:201:LEU:HG	1:B:205:MSE:HE2	1.61	0.82
1:B:184:GLN:NE2	1:B:184:GLN:HA	1.95	0.80
1:B:222:ASP:O	2:B:301:HOH:O	2.01	0.79
1:B:184:GLN:H	1:B:185:PRO:HD3	1.50	0.75
1:B:106:LEU:HD22	1:B:176:CYS:HB3	1.69	0.74
1:B:186:LEU:HD12	1:B:186:LEU:N	2.04	0.73
1:B:106:LEU:CD2	1:B:176:CYS:HB3	2.22	0.70
1:B:184:GLN:N	1:B:185:PRO:HD3	2.07	0.70
1:A:40:ASN:HD21	1:B:129:PRO:HB2	1.59	0.68
1:A:178[B]:PHE:HE2	1:A:186:LEU:HD22	1.60	0.67
1:B:184:GLN:N	1:B:185:PRO:CD	2.59	0.65
1:A:176:CYS:SG	1:A:205:MSE:HE2	2.39	0.63
1:A:178[A]:PHE:CE2	1:B:177:LEU:HB3	2.34	0.62
1:A:178[B]:PHE:CE2	1:A:186:LEU:HD22	2.34	0.62
1:A:186:LEU:HD11	1:A:194:LEU:HD22	1.81	0.60
1:A:35:GLU:OE1	1:A:35:GLU:HA	2.00	0.60
1:A:176:CYS:SG	1:A:205:MSE:CE	2.90	0.59
1:B:119:LEU:O	1:B:123:THR:HG23	2.03	0.59
1:A:40:ASN:ND2	1:B:129:PRO:HB2	2.19	0.58
1:A:186:LEU:C	1:A:186:LEU:HD12	2.30	0.57
1:A:41:THR:O	1:A:64:LYS:HE3	2.04	0.56
1:A:178[B]:PHE:CE2	1:A:186:LEU:CD2	2.90	0.55
1:B:137:LEU:HD21	1:B:142:PHE:CZ	2.44	0.52
1:B:125:GLU:CG	1:B:137:LEU:HD12	2.40	0.51
1:A:186:LEU:HD11	1:A:194:LEU:CD2	2.41	0.50
1:B:186:LEU:H	1:B:186:LEU:CD1	2.04	0.50
1:B:125:GLU:HG3	1:B:137:LEU:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:159:PRO:HD2	1:B:162:HIS:HB2	1.93	0.49
1:B:110:LEU:HD23	1:B:180:LEU:HD23	1.94	0.49
1:A:186:LEU:CD1	1:A:194:LEU:HD22	2.43	0.49
1:B:197:GLU:HG2	1:B:198:PRO:HD2	1.95	0.49
1:B:137:LEU:CD2	1:B:137:LEU:C	2.85	0.48
1:B:103:ILE:HD12	1:B:206:MSE:SE	2.64	0.48
1:B:106:LEU:O	1:B:106:LEU:HD23	2.14	0.48
1:B:130:SER:O	1:B:130:SER:OG	2.31	0.48
1:B:107:VAL:HG22	1:B:205:MSE:HE1	1.94	0.47
1:B:107:VAL:CG2	1:B:205:MSE:HE1	2.45	0.47
1:A:80:VAL:HA	1:A:83:GLU:HG2	1.96	0.47
1:B:106:LEU:HD23	1:B:106:LEU:C	2.40	0.46
1:A:204:HIS:ND1	1:B:216[A]:VAL:HG21	2.30	0.46
1:A:184:GLN:HA	1:A:184:GLN:OE1	2.15	0.46
1:B:35:GLU:HB2	1:B:36:GLN:HG3	1.98	0.46
1:B:141:SER:O	2:B:303:HOH:O	2.21	0.45
1:B:184:GLN:NE2	1:B:184:GLN:CA	2.73	0.44
1:A:86:VAL:HG21	1:A:105:VAL:HG11	1.99	0.43
1:A:100:ARG:NH2	1:A:203:ASP:OD1	2.51	0.43
1:B:122:LEU:HD23	1:B:122:LEU:HA	1.85	0.43
1:A:143:PRO:O	1:A:146:HIS:ND1	2.49	0.43
1:B:53[B]:ASN:OD1	1:B:56:ALA:N	2.49	0.42
1:A:179:LEU:HD13	1:A:201:LEU:HD21	2.02	0.42
1:A:183:HIS:O	1:A:187:LYS:N	2.51	0.42
1:B:34:ALA:HB1	1:B:120:LYS:HB2	2.02	0.42
1:B:177:LEU:HA	1:B:180:LEU:HD12	2.02	0.41
1:B:13:ALA:HB1	2:B:348:HOH:O	2.19	0.41
1:A:204:HIS:HD1	1:B:216[A]:VAL:HG21	1.85	0.41
1:B:124:ARG:NH1	1:B:183:HIS:HE1	2.18	0.41
1:B:164:THR:CG2	1:B:216[A]:VAL:HG13	2.50	0.41
1:B:186:LEU:N	1:B:186:LEU:CD1	2.73	0.41
1:A:111:HIS:O	2:A:301:HOH:O	2.22	0.41
1:A:188:GLN:O	1:A:188:GLN:HG2	2.21	0.41
1:A:103:ILE:HD12	1:A:206:MSE:SE	2.71	0.41
1:A:178[A]:PHE:CZ	1:B:177:LEU:HB3	2.56	0.41
1:B:124:ARG:HH12	1:B:183:HIS:HE1	1.69	0.40
1:B:26:LEU:HD13	1:B:26:LEU:C	2.46	0.40
1:B:201:LEU:CG	1:B:205:MSE:HE2	2.43	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96[B]:GLN:OE1	1:B:51:GLN:NE2[4_454]	1.96	0.24

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	197/234 (84%)	192 (98%)	5 (2%)	0	100	100
1	B	198/234 (85%)	192 (97%)	5 (2%)	1 (0%)	24	37
All	All	395/468 (84%)	384 (97%)	10 (2%)	1 (0%)	36	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	184	GLN

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	162/189 (86%)	160 (99%)	2 (1%)	63	81
1	B	166/189 (88%)	155 (93%)	11 (7%)	15	26
All	All	328/378 (87%)	315 (96%)	13 (4%)	30	47

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	LEU
1	A	177	LEU
1	B	111	HIS
1	B	121	VAL
1	B	128	SER
1	B	135	VAL
1	B	136	VAL
1	B	137	LEU
1	B	181	ILE
1	B	184	GLN
1	B	186	LEU
1	B	216[A]	VAL
1	B	216[B]	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	GLN
1	A	112	ASN
1	A	154	GLN
1	B	154	GLN
1	B	183	HIS
1	B	184	GLN
1	B	199	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	196/234 (83%)	-0.09	5 (2%) 57 53	23, 45, 96, 134	2 (1%)
1	B	199/234 (85%)	0.19	10 (5%) 34 30	19, 48, 113, 128	2 (1%)
All	All	395/468 (84%)	0.05	15 (3%) 44 40	19, 46, 107, 134	4 (1%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	135	VAL	4.1
1	B	196	LEU	3.9
1	B	136	VAL	3.6
1	A	143	PRO	3.6
1	B	129	PRO	3.2
1	B	186	LEU	2.7
1	A	190	VAL	2.6
1	B	127	LEU	2.5
1	B	142	PHE	2.5
1	A	144	LYS	2.5
1	B	130	SER	2.4
1	B	128	SER	2.3
1	A	186	LEU	2.2
1	A	178[A]	PHE	2.1
1	B	139	GLU	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.