



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 02:02 AM UTC

PDB ID : 1PHZ / pdb_00001phz
Title : STRUCTURE OF PHOSPHORYLATED PHENYLALANINE HYDROXY-
LASE
Authors : Kobe, B.; Jennings, I.G.; House, C.M.; Michell, B.J.; Cotton, R.G.; Kemp,
B.E.
Deposited on : 1998-11-11
Resolution : 2.20 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
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

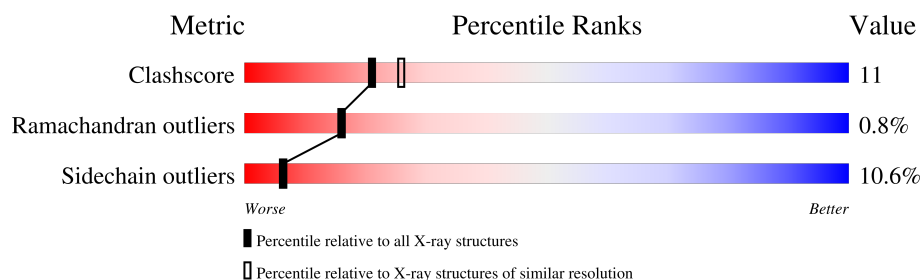
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	429	 68% 21% • 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3467 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 PROTEIN (PHENYLALANINE HYDROXYLASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	0	0	0
			3285	2103	556	617	9			

- Molecule 2 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	181	Total	O	0	0
			181	181		

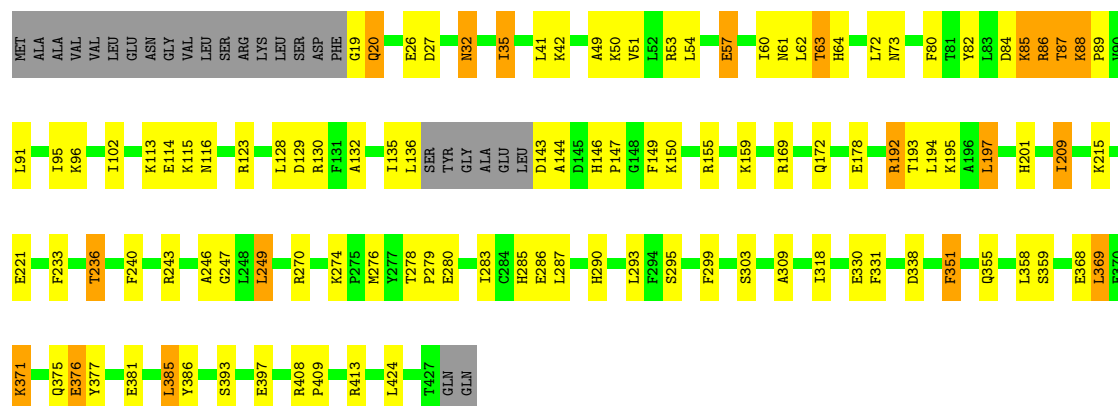
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

• Molecule 1: PROTEIN (PHENYLALANINE HYDROXYLASE)

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	56.78Å 56.78Å 302.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.00 – 2.20	Depositor
% Data completeness (in resolution range)	94.3 (99.00-2.20)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.223 , 0.297	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3467	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

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: FE

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	0.35	0/3369	0.83	4/4562 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	318	ILE	N-CA-C	-6.98	103.67	110.72
1	A	369	LEU	N-CA-C	5.74	118.28	111.33
1	A	287	LEU	N-CA-C	5.54	117.40	111.36
1	A	338	ASP	N-CA-C	-5.19	106.95	113.28

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	3285	0	3199	71	0
2	A	1	0	0	0	0
3	A	181	0	0	6	0
All	All	3467	0	3199	71	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 11.

All (71) 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:20:GLN:HE22	1:A:376:GLU:HG2	0.96	1.12
1:A:20:GLN:NE2	1:A:376:GLU:HG2	1.79	0.97
1:A:20:GLN:HE22	1:A:376:GLU:CG	1.86	0.84
1:A:135:ILE:HG13	1:A:246:ALA:HB3	1.62	0.81
1:A:197:LEU:HD21	1:A:355:GLN:HG3	1.67	0.76
1:A:368:GLU:HB3	1:A:371:LYS:HE3	1.69	0.75
1:A:41:LEU:HD22	1:A:51:VAL:HG21	1.70	0.72
1:A:233:PHE:O	1:A:236:THR:HG22	1.90	0.69
1:A:84:ASP:OD1	1:A:86:ARG:HB2	1.95	0.66
1:A:146:HIS:CD2	1:A:147:PRO:HD2	2.30	0.66
1:A:19:GLY:O	1:A:20:GLN:HG3	1.95	0.66
1:A:146:HIS:CD2	1:A:279:PRO:HG3	2.30	0.65
1:A:64:HIS:HB3	1:A:82:TYR:O	1.98	0.64
1:A:35:ILE:HG21	1:A:91:LEU:HD11	1.79	0.64
1:A:49:ALA:O	1:A:53:ARG:HB2	2.00	0.60
1:A:201:HIS:CD2	1:A:358:LEU:HD12	2.37	0.59
1:A:270:ARG:HB3	1:A:278:THR:CG2	2.34	0.58
1:A:146:HIS:HD2	1:A:147:PRO:HD2	1.68	0.57
1:A:278:THR:HB	1:A:280:GLU:O	2.04	0.57
1:A:385:LEU:HD12	1:A:386:TYR:N	2.19	0.56
1:A:32:ASN:O	1:A:84:ASP:HB2	2.05	0.56
1:A:147:PRO:HG3	1:A:274:LYS:HE3	1.88	0.56
1:A:129:ASP:OD1	1:A:243:ARG:NH1	2.39	0.56
1:A:135:ILE:HD12	1:A:247:GLY:H	1.70	0.56
1:A:375:GLN:HE21	1:A:376:GLU:H	1.54	0.56
1:A:375:GLN:HE21	1:A:376:GLU:N	2.04	0.55
1:A:193:THR:HB	1:A:351:PHE:CD2	2.41	0.54
1:A:194:LEU:HG	1:A:351:PHE:HD2	1.72	0.54
1:A:285:HIS:HD2	1:A:286:GLU:OE1	1.90	0.53
1:A:87:THR:O	1:A:91:LEU:HG	2.10	0.52
1:A:72:LEU:HD23	1:A:73:ASN:ND2	2.24	0.52
1:A:149:PHE:CD2	1:A:150:LYS:HE3	2.45	0.52
1:A:123:ARG:HD2	3:A:543:HOH:O	2.10	0.51
1:A:26:GLU:HB3	3:A:667:HOH:O	2.12	0.50
1:A:61:ASN:C	1:A:63:THR:H	2.19	0.50
1:A:194:LEU:HG	1:A:351:PHE:CD2	2.46	0.50
1:A:169:ARG:H	1:A:172:GLN:NE2	2.09	0.50
1:A:135:ILE:CD1	1:A:247:GLY:H	2.25	0.49
1:A:280:GLU:HB2	3:A:647:HOH:O	2.13	0.49
1:A:293:LEU:O	1:A:299:PHE:HB3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:LEU:HG	3:A:580:HOH:O	2.13	0.48
1:A:20:GLN:OE1	1:A:377:TYR:O	2.32	0.47
1:A:53:ARG:O	1:A:57:GLU:HB3	2.16	0.46
1:A:385:LEU:HD12	1:A:385:LEU:C	2.40	0.46
1:A:135:ILE:HD13	1:A:249:LEU:CD1	2.46	0.46
1:A:393:SER:O	1:A:397:GLU:HG2	2.16	0.46
1:A:192:ARG:HG3	1:A:221:GLU:OE2	2.15	0.46
1:A:51:VAL:O	1:A:54:LEU:HB3	2.16	0.45
1:A:115:LYS:O	1:A:116:ASN:HB2	2.17	0.45
1:A:270:ARG:HB3	1:A:278:THR:HG22	1.98	0.45
1:A:285:HIS:HE1	1:A:330:GLU:OE2	2.00	0.45
1:A:144:ALA:HA	1:A:149:PHE:CD2	2.52	0.44
1:A:376:GLU:HA	3:A:559:HOH:O	2.17	0.44
1:A:60:ILE:HG12	1:A:87:THR:CG2	2.47	0.44
1:A:35:ILE:HG21	1:A:91:LEU:CD1	2.47	0.44
1:A:286:GLU:O	1:A:290:HIS:HB2	2.19	0.43
1:A:143:ASP:O	1:A:149:PHE:HB2	2.19	0.43
1:A:155:ARG:CB	1:A:155:ARG:HH11	2.32	0.43
1:A:330:GLU:HG3	1:A:331:PHE:CE2	2.54	0.42
1:A:276:MET:HB3	1:A:351:PHE:HE1	1.84	0.42
1:A:91:LEU:O	1:A:95:ILE:HG13	2.19	0.42
1:A:35:ILE:HD11	1:A:85:LYS:HE3	2.01	0.42
1:A:72:LEU:HD23	1:A:73:ASN:HD21	1.84	0.42
1:A:80:PHE:HA	1:A:123:ARG:NH2	2.35	0.42
1:A:88:LYS:N	1:A:89:PRO:CD	2.82	0.41
1:A:129:ASP:OD1	1:A:243:ARG:NH2	2.51	0.41
1:A:309:ALA:HB2	3:A:544:HOH:O	2.20	0.41
1:A:135:ILE:HG22	1:A:136:LEU:N	2.35	0.41
1:A:135:ILE:HD12	1:A:247:GLY:C	2.46	0.41
1:A:209:ILE:HG21	1:A:295:SER:HB2	2.03	0.41
1:A:128:LEU:O	1:A:132:ALA:HB2	2.20	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	399/429 (93%)	377 (94%)	19 (5%)	3 (1%)	16	16

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	62	LEU
1	A	409	PRO

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	357/378 (94%)	319 (89%)	38 (11%)	6	6

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ASP
1	A	32	ASN
1	A	35	ILE
1	A	42	LYS
1	A	50	LYS
1	A	57	GLU
1	A	63	THR
1	A	85	LYS
1	A	86	ARG
1	A	87	THR
1	A	88	LYS
1	A	96	LYS
1	A	102	ILE
1	A	113	LYS
1	A	114	GLU
1	A	130	ARG

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Mol	Chain	Res	Type
1	A	159	LYS
1	A	178	GLU
1	A	192	ARG
1	A	195	LYS
1	A	197	LEU
1	A	209	ILE
1	A	215	LYS
1	A	236	THR
1	A	240	PHE
1	A	249	LEU
1	A	283	ILE
1	A	303	SER
1	A	351	PHE
1	A	359	SER
1	A	369	LEU
1	A	371	LYS
1	A	376	GLU
1	A	381	GLU
1	A	385	LEU
1	A	408	ARG
1	A	413	ARG
1	A	424	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	73	ASN
1	A	134	GLN
1	A	146	HIS
1	A	172	GLN
1	A	235	GLN
1	A	285	HIS
1	A	375	GLN
1	A	383	GLN
1	A	426	ASN

5.3.3 RNA ⓘ

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.