



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:32 PM UTC

PDB ID : 3PHM / pdb_00003phm
Title : REDUCED (CU+) PEPTIDYLGLYCINE ALPHA-HYDROXYLATING
MONOOXYGENASE (PHM)
Authors : Prigge, S.T.; Amzel, L.M.
Deposited on : 1999-05-25
Resolution : 2.10 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)
Xtrriage (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

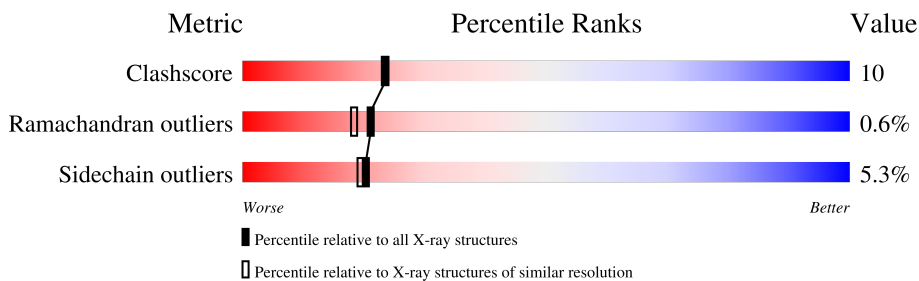
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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	310	 70% 27% .

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2622 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.

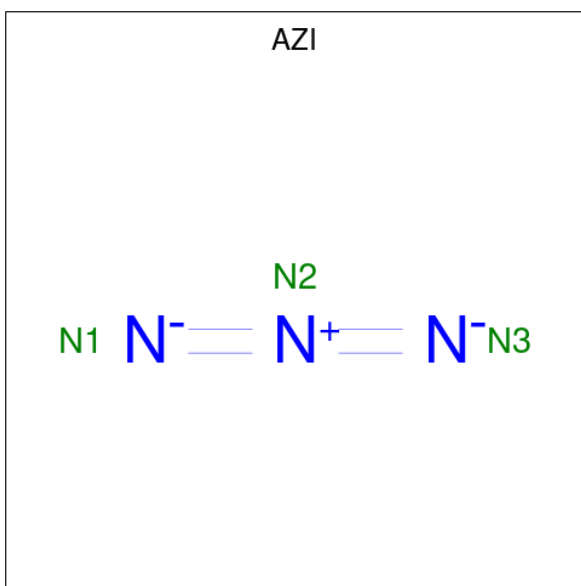
- Molecule 1 is a protein called PROTEIN (PEPTIDYLGLYCINE ALPHA-HYDROXYLATING MONOOXYGENASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	310	2418	1539	409	444	26	0	0	0

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cu	0	0
			2	2		

- Molecule 3 is AZIDE ION (CCD ID: AZI) (formula: N₃).

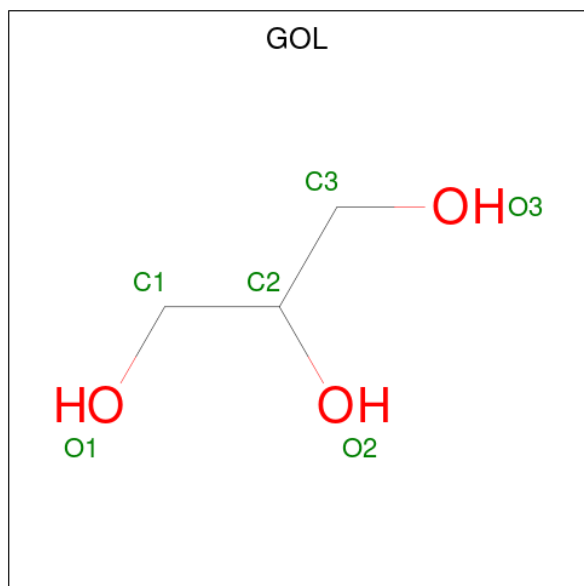


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	N	0	0
			3	3		

- Molecule 4 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ni 1 1	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0

- Molecule 6 is water.

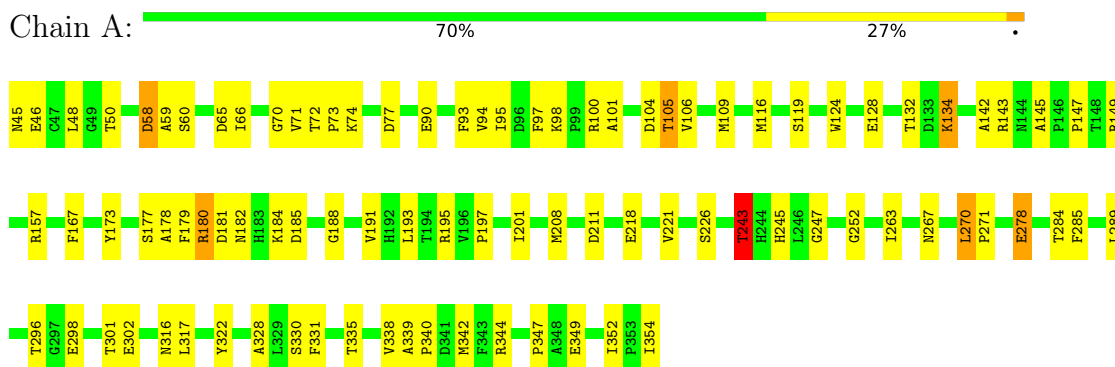
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	168	Total O 168 168	0	0

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. 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 (PEPTIDYLGLYCINE ALPHA-HYDROXYLATING MONOOXYGENASE)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.52Å 68.77Å 82.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.10	Depositor
% Data completeness (in resolution range)	89.0 (10.00-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.200 , 0.257	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2622	wwPDB-VP
Average B, all atoms (Å ²)	43.0	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: CU, NI, AZI, GOL

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	0.65	0/2486	1.12	21/3381 (0.6%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	ALA	N-CA-C	9.24	123.63	110.23
1	A	245	HIS	N-CA-C	9.03	123.39	112.38
1	A	263	ILE	N-CA-C	-8.26	103.82	111.67
1	A	50	THR	N-CA-C	7.31	121.30	112.38
1	A	330	SER	N-CA-C	7.00	121.57	112.89
1	A	267	ASN	N-CA-C	-6.98	99.54	109.24
1	A	48	LEU	N-CA-C	6.83	119.75	111.82
1	A	167	PHE	N-CA-C	-6.44	98.91	109.40
1	A	95	ILE	N-CA-C	6.43	119.07	112.90
1	A	143	ARG	N-CA-C	5.93	118.26	111.02
1	A	132	THR	N-CA-C	-5.82	104.85	111.14
1	A	181	ASP	N-CA-C	-5.54	106.22	112.87
1	A	106	VAL	N-CA-C	5.50	116.10	108.84
1	A	270	LEU	N-CA-C	-5.38	102.33	110.39
1	A	128	GLU	N-CA-C	-5.29	105.97	112.90
1	A	243	THR	N-CA-C	-5.16	100.89	108.79
1	A	105	THR	N-CA-C	5.16	118.04	111.69
1	A	211	ASP	N-CA-C	5.12	120.16	113.30
1	A	344	ARG	N-CA-C	-5.09	106.33	112.54
1	A	145	ALA	CA-C-N	5.01	125.54	120.38
1	A	145	ALA	C-N-CA	5.01	125.54	120.38

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	2418	0	2337	49	0
2	A	2	0	0	0	0
3	A	3	0	0	0	0
4	A	1	0	0	0	0
5	A	30	0	38	0	0
6	A	168	0	0	2	0
All	All	2622	0	2375	49	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 10.

All (49) 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:243:THR:HG21	1:A:247:GLY:HA3	1.47	0.94
1:A:296:THR:HG22	1:A:298:GLU:H	1.44	0.83
1:A:179:PHE:HZ	1:A:185:ASP:HB2	1.48	0.77
1:A:179:PHE:CZ	1:A:185:ASP:HB2	2.27	0.68
1:A:243:THR:CG2	1:A:247:GLY:HA3	2.24	0.67
1:A:301:THR:HG23	1:A:302:GLU:HG3	1.83	0.61
1:A:45:ASN:HB3	1:A:100:ARG:HB3	1.88	0.55
1:A:349:GLU:HA	1:A:352:ILE:HG12	1.89	0.54
1:A:101:ALA:HB2	1:A:109:MET:HE2	1.88	0.54
1:A:97:PHE:O	1:A:98:LYS:HD3	2.08	0.53
1:A:284:THR:HG22	1:A:285:PHE:N	2.23	0.53
1:A:72:THR:HG23	1:A:179:PHE:HD1	1.75	0.51
1:A:147:PRO:HD3	6:A:371:HOH:O	2.11	0.50
1:A:105:THR:HG21	1:A:179:PHE:HE2	1.76	0.50
1:A:98:LYS:NZ	6:A:450:HOH:O	2.37	0.48
1:A:177:SER:C	1:A:179:PHE:H	2.22	0.47
1:A:93:PHE:CE1	1:A:197:PRO:HA	2.49	0.47
1:A:218:GLU:HG2	1:A:221:VAL:CG2	2.45	0.47
1:A:252:GLY:HA3	1:A:317:LEU:HD21	1.96	0.46
1:A:94:VAL:HG13	1:A:191:VAL:CG1	2.46	0.45
1:A:142:ALA:HB1	1:A:271:PRO:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:ASP:CG	1:A:59:ALA:N	2.75	0.45
1:A:60:SER:O	1:A:195:ARG:NH1	2.49	0.45
1:A:66:ILE:O	1:A:188:GLY:HA3	2.16	0.45
1:A:180:ARG:C	1:A:182:ASN:N	2.75	0.44
1:A:338:VAL:C	1:A:340:PRO:HD3	2.42	0.44
1:A:74:LYS:HD3	1:A:74:LYS:HA	1.58	0.44
1:A:180:ARG:HA	1:A:180:ARG:HD2	1.50	0.44
1:A:70:GLY:CA	1:A:184:LYS:HB3	2.48	0.43
1:A:73:PRO:HD2	1:A:179:PHE:CD1	2.53	0.43
1:A:72:THR:HG23	1:A:179:PHE:CD1	2.53	0.43
1:A:101:ALA:HB2	1:A:109:MET:CE	2.48	0.43
1:A:208:MET:O	1:A:335:THR:HA	2.18	0.43
1:A:77:ASP:HA	1:A:173:TYR:O	2.18	0.43
1:A:180:ARG:C	1:A:182:ASN:H	2.25	0.43
1:A:119:SER:HB3	1:A:124:TRP:CD2	2.54	0.42
1:A:226:SER:HA	1:A:289:LEU:O	2.19	0.42
1:A:71:VAL:O	1:A:185:ASP:N	2.51	0.42
1:A:134:LYS:HE3	1:A:134:LYS:HA	2.01	0.42
1:A:191:VAL:HG12	1:A:193:LEU:HD22	2.01	0.41
1:A:339:ALA:N	1:A:340:PRO:HD3	2.35	0.41
1:A:45:ASN:CB	1:A:100:ARG:HB3	2.50	0.41
1:A:201:ILE:O	1:A:322:TYR:HA	2.21	0.41
1:A:208:MET:HB2	1:A:316:ASN:ND2	2.34	0.41
1:A:179:PHE:HZ	1:A:185:ASP:CB	2.28	0.41
1:A:339:ALA:HB3	1:A:342:MET:HE2	2.01	0.41
1:A:90:GLU:OE2	1:A:195:ARG:HD3	2.22	0.40
1:A:73:PRO:HD2	1:A:179:PHE:CG	2.56	0.40
1:A:278:GLU:CD	1:A:278:GLU:H	2.28	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	308/310 (99%)	294 (96%)	12 (4%)	2 (1%)	21 18

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	GLU
1	A	178	ALA

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	265/265 (100%)	251 (95%)	14 (5%)	20 19

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	ASP
1	A	65	ASP
1	A	104	ASP
1	A	116	MET
1	A	134	LYS
1	A	149	ARG
1	A	157	ARG
1	A	180	ARG
1	A	243	THR
1	A	270	LEU
1	A	278	GLU
1	A	331	PHE
1	A	347	PRO
1	A	354	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	136	ASN
1	A	222	ASN
1	A	316	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 [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	AZI	A	361	4	2,2,2	3.21	1 (50%)	0,1,1	-	-
5	GOL	A	362	4	5,5,5	0.34	0	5,5,5	0.26	0
5	GOL	A	704	-	5,5,5	0.48	0	5,5,5	0.36	0
5	GOL	A	701	-	5,5,5	0.47	0	5,5,5	0.23	0
5	GOL	A	703	-	5,5,5	0.47	0	5,5,5	0.23	0
5	GOL	A	702	-	5,5,5	0.56	0	5,5,5	0.32	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	A	362	4	-	1/4/4/4	-
5	GOL	A	704	-	-	0/4/4/4	-
5	GOL	A	701	-	-	0/4/4/4	-
5	GOL	A	703	-	-	1/4/4/4	-
5	GOL	A	702	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	361	AZI	N1-N2	-4.15	1.14	1.23

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	703	GOL	O1-C1-C2-O2
5	A	362	GOL	O2-C2-C3-O3

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.