



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:06 PM UTC

PDB ID : 2AEX / pdb_00002aex
Title : The 1.58Å Crystal Structure of Human Coproporphyrinogen Oxidase Reveals the Structural Basis of Hereditary Coproporphyrria
Authors : Lee, D.S.; Flachsova, E.; Bodnarova, M.; Demeler, B.; Martasek, P.; Raman, C.S.
Deposited on : 2005-07-24
Resolution : 1.58 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) : 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

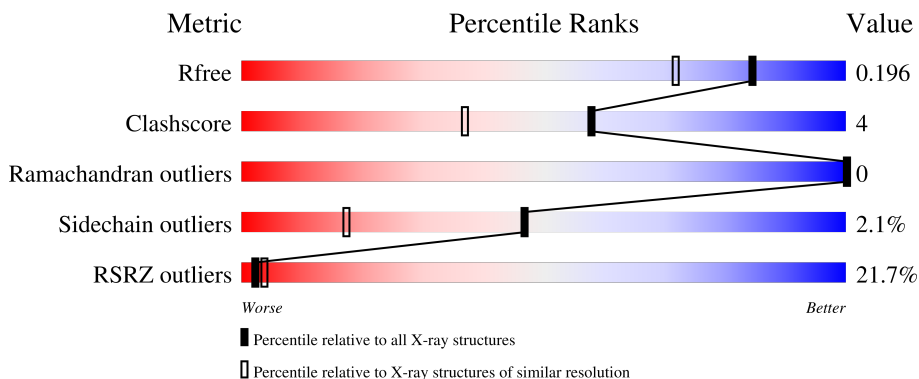
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	346	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3198 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.

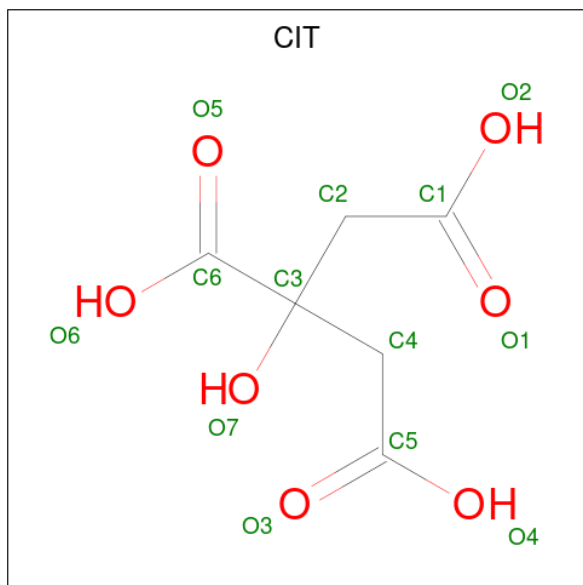
- Molecule 1 is a protein called Coproporphyrinogen III oxidase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	336	2822	1776	505	524	17	0	15	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	109	GLY	-	cloning artifact	UNP P36551
A	110	SER	-	cloning artifact	UNP P36551

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	13	6	7	0	0

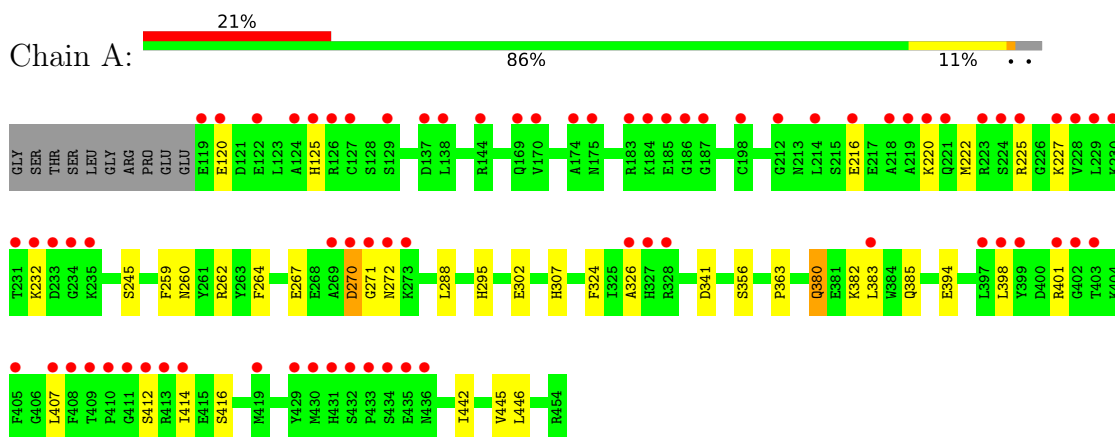
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	363	Total 363	O 363	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 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: Coproporphyrinogen III oxidase, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 3	Depositor
Cell constants a, b, c, α , β , γ	112.74Å 112.74Å 112.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.31 – 1.58 31.31 – 1.58	Depositor EDS
% Data completeness (in resolution range)	99.5 (31.31-1.58) 99.5 (31.31-1.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 1.58Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.186 , 0.208 0.197 , 0.196	Depositor DCC
R_{free} test set	3270 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	0.019 for l,-k,h	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3198	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CIT

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	0.64	0/2893	0.77	0/3902

There are no bond length outliers.

There are no bond angle outliers.

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	2822	0	2717	25	0
2	A	13	0	5	0	0
3	A	363	0	0	3	0
All	All	3198	0	2722	25	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 4.

All (25) 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:341[A]:ASP:OD2	3:A:730:HOH:O	1.86	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:GLU:O	1:A:220:LYS:HG2	1.88	0.74
1:A:270[A]:ASP:OD1	1:A:272:ASN:HB2	1.89	0.72
1:A:225:ARG:HD2	1:A:227:LYS:HE2	1.72	0.69
1:A:412:SER:HB3	1:A:416[A]:SER:OG	1.96	0.65
1:A:382:LYS:NZ	1:A:385:GLN:HE22	1.98	0.61
1:A:270[A]:ASP:OD2	1:A:271:GLY:N	2.35	0.59
1:A:324:PHE:CE2	1:A:326:ALA:HA	2.41	0.56
1:A:307:HIS:HE1	1:A:356:SER:OG	1.88	0.56
1:A:227:LYS:N	1:A:227:LYS:HD2	2.21	0.55
1:A:307:HIS:HD2	3:A:513:HOH:O	1.90	0.53
1:A:270[A]:ASP:CG	1:A:271:GLY:N	2.67	0.51
1:A:295:HIS:HE1	1:A:363:PRO:O	1.94	0.51
1:A:302:GLU:HG3	3:A:704:HOH:O	2.11	0.50
1:A:120:GLU:OE1	1:A:125:HIS:ND1	2.37	0.47
1:A:380:GLN:H	1:A:380:GLN:HE21	1.63	0.46
1:A:394:GLU:HG2	1:A:398[B]:LEU:HD23	1.98	0.45
1:A:245:SER:HB3	1:A:259:PHE:CE2	2.52	0.45
1:A:288:LEU:HD22	1:A:445[B]:VAL:HG21	2.01	0.43
1:A:382:LYS:HZ2	1:A:385:GLN:HE22	1.63	0.42
1:A:222:MET:HE1	1:A:264:PHE:CZ	2.55	0.42
1:A:380:GLN:H	1:A:380:GLN:NE2	2.17	0.42
1:A:260:ASN:ND2	1:A:262[A]:ARG:NH2	2.68	0.42
1:A:442:ILE:O	1:A:446:LEU:HG	2.21	0.41
1:A:232:LYS:NZ	1:A:267:GLU:OE1	2.39	0.41

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	349/346 (101%)	341 (98%)	8 (2%)	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	305/298 (102%)	297 (97%)	8 (3%)	40 11

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	270[A]	ASP
1	A	270[B]	ASP
1	A	380	GLN
1	A	383[A]	LEU
1	A	383[B]	LEU
1	A	401	ARG
1	A	407	LEU
1	A	414	ILE

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	195	GLN
1	A	213	ASN
1	A	260	ASN
1	A	272	ASN
1	A	274	GLN
1	A	295	HIS
1	A	307	HIS
1	A	327	HIS
1	A	380	GLN
1	A	385	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](#)

1 ligand is modelled in this entry.

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
2	CIT	A	500	-	12,12,12	1.44	3 (25%)	17,17,17	1.24	2 (11%)

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
2	CIT	A	500	-	-	0/16/16/16	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	CIT	C3-C6	-2.52	1.50	1.53
2	A	500	CIT	O7-C3	2.06	1.47	1.43
2	A	500	CIT	O4-C5	-2.01	1.24	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	CIT	O6-C6-C3	2.75	118.41	113.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500	CIT	C2-C3-C6	-2.28	104.99	110.03

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 [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	336/346 (97%)	1.17	73 (21%) 2 4	12, 27, 61, 68	15 (4%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	397	LEU	10.7
1	A	398[A]	LEU	10.0
1	A	429	TYR	8.4
1	A	186	GLY	6.8
1	A	431	HIS	5.9
1	A	271	GLY	5.9
1	A	401	ARG	5.3
1	A	231	THR	5.3
1	A	187	GLY	4.7
1	A	408	PHE	4.7
1	A	270[A]	ASP	4.5
1	A	224	SER	4.5
1	A	185	GLU	4.4
1	A	269	ALA	4.4
1	A	227	LYS	4.3
1	A	214	LEU	4.2
1	A	119	GLU	4.1
1	A	399	TYR	4.0
1	A	412	SER	3.9
1	A	272	ASN	3.9
1	A	403	THR	3.6
1	A	405	PHE	3.6
1	A	414	ILE	3.5
1	A	436	ASN	3.5
1	A	225	ARG	3.5
1	A	402	GLY	3.4
1	A	419	MET	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	228	VAL	3.3
1	A	409	THR	3.3
1	A	407	LEU	3.3
1	A	411	GLY	3.3
1	A	216	GLU	3.3
1	A	183	ARG	3.2
1	A	184	LYS	3.2
1	A	174	ALA	3.1
1	A	144	ARG	3.1
1	A	410	PRO	3.0
1	A	327	HIS	3.0
1	A	198	CYS	3.0
1	A	137	ASP	2.8
1	A	138	LEU	2.8
1	A	170	VAL	2.7
1	A	235	LYS	2.7
1	A	233	ASP	2.7
1	A	383[A]	LEU	2.7
1	A	435	GLU	2.7
1	A	175	ASN	2.6
1	A	232	LYS	2.5
1	A	430	MET	2.5
1	A	122	GLU	2.5
1	A	129	SER	2.5
1	A	220	LYS	2.5
1	A	229	LEU	2.5
1	A	218	ALA	2.4
1	A	434	SER	2.4
1	A	169[A]	GLN	2.4
1	A	433	PRO	2.4
1	A	328	ARG	2.4
1	A	127	CYS	2.3
1	A	234	GLY	2.3
1	A	219	ALA	2.3
1	A	126	ARG	2.2
1	A	223	ARG	2.2
1	A	432	SER	2.2
1	A	413	ARG	2.2
1	A	212	GLY	2.1
1	A	326	ALA	2.1
1	A	125	HIS	2.1
1	A	120	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	124	ALA	2.1
1	A	273	LYS	2.0
1	A	221	GLN	2.0
1	A	230	LYS	2.0

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](#)

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, 95th 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(Å ²)	Q<0.9
2	CIT	A	500	13/13	0.80	0.14	28,33,38,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.