



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:55 PM GMT

PDB ID : 1D7K
Title : CRYSTAL STRUCTURE OF HUMAN ORNITHINE DECARBOXYLASE
AT 2.1 ANGSTROMS RESOLUTION
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Deposited on : 1999-10-18
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

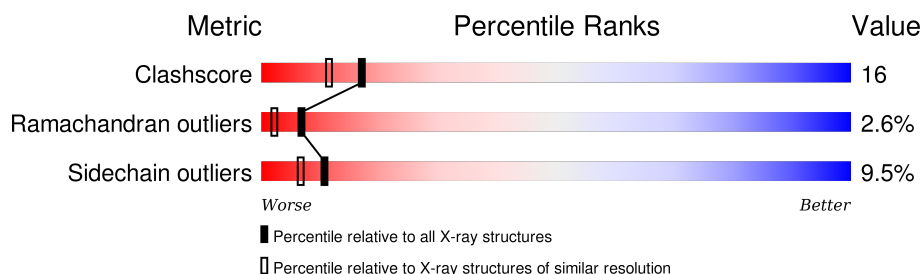
1 Overall quality at a glance

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	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	421	 63% 24% 8% . .
1	B	421	 55% 32% 7% . .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6824 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 HUMAN ORNITHINE DECARBOXYLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	412	Total	C	N	O	P	S	0	0	0
			3242	2073	537	610	1	21			
1	B	407	Total	C	N	O	P	S	0	0	0
			3181	2037	531	591	1	21			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	349	ARG	LYS	CONFLICT	UNP P11926
A	415	GLN	GLU	CONFLICT	UNP P11926
B	349	ARG	LYS	CONFLICT	UNP P11926
B	415	GLN	GLU	CONFLICT	UNP P11926

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	219	Total	O	0	0
			219	219		
2	B	182	Total	O	0	0
			182	182		

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.68 Å 107.45 Å 139.71 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.50 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (30.50-2.10)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.212 , 0.288	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6824	wwPDB-VP
Average B, all atoms (Å ²)	26.0	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: LLP

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	0.80	0/3291	1.78	57/4458 (1.3%)
1	B	0.78	0/3226	1.84	76/4367 (1.7%)
All	All	0.79	0/6517	1.81	133/8825 (1.5%)

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	24
1	B	0	15
All	All	0	39

There are no bond length outliers.

The worst 5 of 133 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	61	ARG	CD-NE-CZ	34.11	171.35	123.60
1	B	35	ASP	CB-CG-OD1	17.21	133.79	118.30
1	A	61	ARG	NE-CZ-NH1	16.90	128.75	120.30
1	B	61	ARG	NE-CZ-NH1	13.85	127.23	120.30
1	A	425	PHE	CB-CG-CD1	13.07	129.95	120.80

There are no chirality outliers.

5 of 39 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	16	GLU	Peptide

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Mol	Chain	Res	Type	Group
1	A	26	GLN	Peptide
1	A	29	ASN	Mainchain
1	A	35	ASP	Peptide
1	A	7	GLU	Peptide

5.2 Too-close contacts

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	3242	0	3186	104	0
1	B	3181	0	3135	112	0
2	A	219	0	0	9	0
2	B	182	0	0	10	0
All	All	6824	0	6321	208	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 16.

The worst 5 of 208 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:426:PRO:CB	1:A:427:PRO:HD3	1.77	1.13
1:A:426:PRO:HB2	1:A:427:PRO:HD3	1.18	1.11
1:A:79:THR:HG23	1:A:417:MET:HE2	1.29	1.11
1:A:15:ASP:O	1:A:16:GLU:O	1.71	1.06
1:B:173:THR:HB	1:B:175:ARG:HD3	1.43	1.01

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	407/421 (97%)	371 (91%)	23 (6%)	13 (3%)	5	1
1	B	402/421 (96%)	362 (90%)	32 (8%)	8 (2%)	9	4
All	All	809/842 (96%)	733 (91%)	55 (7%)	21 (3%)	7	2

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	GLU
1	A	160	SER
1	A	312	GLN
1	A	344	PRO
1	A	360	CYS

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	348/358 (97%)	315 (90%)	33 (10%)	11	7
1	B	337/358 (94%)	305 (90%)	32 (10%)	11	7
All	All	685/716 (96%)	620 (90%)	65 (10%)	11	7

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	353	SER
1	B	28	ILE
1	B	398	ASN
1	A	369	ARG
1	B	10	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	125	ASN
1	B	419	GLN
1	B	188	ASN
1	A	385	ASN
1	B	146	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are 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$
1	LLP	A	69	1	23,24,25	1.21	3 (13%)	28,32,34	2.53	11 (39%)
1	LLP	B	69	1	23,24,25	1.22	2 (8%)	28,32,34	2.36	14 (50%)

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
1	LLP	A	69	1	-	0/15/17/19	0/1/1/1
1	LLP	B	69	1	-	0/15/17/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	69	LLP	P-OP3	-2.56	1.45	1.54
1	B	69	LLP	P-OP3	-2.44	1.45	1.54
1	B	69	LLP	CB-CA	-2.23	1.51	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	69	LLP	C2'-C2	2.09	1.54	1.50
1	A	69	LLP	C3-C2	2.18	1.42	1.40

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	LLP	O-C-CA	-4.36	114.13	125.49
1	B	69	LLP	C5'-C5-C4	-3.77	115.12	121.47
1	B	69	LLP	C3-C2-N1	-3.71	115.49	120.61
1	A	69	LLP	C5'-C5-C4	-3.50	115.58	121.47
1	A	69	LLP	C5-C6-N1	-3.13	118.42	123.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	69	LLP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates 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](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.