



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2CF5 / pdb\_00002cf5  
Title : Crystal Structures of the Arabidopsis Cinnamyl Alcohol Dehydrogenases, At-CAD5  
Authors : Youn, B.; Camacho, R.; Moinuddin, S.; Lee, C.; Davin, L.B.; Lewis, N.G.; Kang, C.  
Deposited on : 2006-02-16  
Resolution : 2.00 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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0  
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

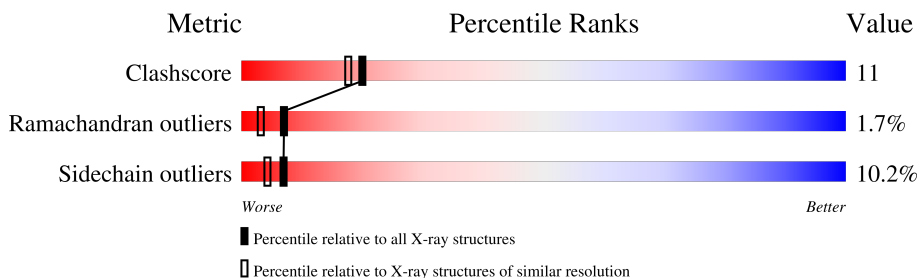
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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  $\geq 3$ , 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	357	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2866 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 CINNAMYL ALCOHOL DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	352	2665	1686	450	507	22	0	0	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	199	Total	O	0	0
			199	199		



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.22Å 54.22Å 312.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00	Depositor
% Data completeness (in resolution range)	98.2 (10.00-2.00)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.195 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2866	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	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:  
ZN

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	0.88	13/2715 (0.5%)	1.68	36/3674 (1.0%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	82	VAL	CA-CB	7.71	1.62	1.54
1	A	69	HIS	CD2-NE2	-7.02	1.30	1.37
1	A	256	HIS	CD2-NE2	-6.68	1.30	1.37
1	A	255	HIS	CD2-NE2	-6.59	1.30	1.37
1	A	52	HIS	CD2-NE2	-6.23	1.30	1.37
1	A	194	HIS	CD2-NE2	-6.08	1.31	1.37
1	A	48	HIS	CD2-NE2	-6.07	1.31	1.37
1	A	142	HIS	CD2-NE2	-5.99	1.31	1.37
1	A	206	HIS	CD2-NE2	-5.66	1.31	1.37
1	A	205	HIS	CD2-NE2	-5.46	1.31	1.37
1	A	174	HIS	CD2-NE2	-5.43	1.31	1.37
1	A	69	HIS	CG-ND1	-5.15	1.32	1.38
1	A	205	HIS	CG-ND1	-5.08	1.32	1.38

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	353	SER	N-CA-C	11.99	126.13	110.43
1	A	341	ASP	CA-CB-CG	8.76	121.36	112.60
1	A	151	GLU	N-CA-C	8.09	120.89	111.02
1	A	252	VAL	CA-C-N	7.31	126.95	119.56
1	A	252	VAL	C-N-CA	7.31	126.95	119.56
1	A	54	THR	CA-CB-OG1	-7.19	98.81	109.60
1	A	356	ASP	CA-CB-CG	7.13	119.73	112.60
1	A	266	LYS	CA-CB-CG	6.94	127.99	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	VAL	N-CA-C	6.75	118.31	108.58
1	A	182	LEU	N-CA-C	6.75	119.02	110.24
1	A	242	ALA	N-CA-C	6.39	124.42	110.80
1	A	17	ASP	CA-CB-CG	6.38	118.98	112.60
1	A	54	THR	CA-CB-CG2	6.33	121.26	110.50
1	A	126	ILE	N-CA-CB	-6.23	100.96	111.23
1	A	274	MET	CG-SD-CE	-5.95	87.81	100.90
1	A	343	ARG	CA-C-N	5.93	132.87	121.54
1	A	343	ARG	C-N-CA	5.93	132.87	121.54
1	A	194	HIS	CB-CG-CD2	-5.83	123.62	131.20
1	A	84	LYS	N-CA-C	-5.71	104.98	111.14
1	A	9	LYS	N-CA-C	5.56	118.79	109.95
1	A	110	LEU	N-CA-C	-5.53	103.81	110.44
1	A	89	ASP	CA-CB-CG	5.51	118.11	112.60
1	A	142	HIS	CB-CG-CD2	-5.33	124.28	131.20
1	A	327	MET	N-CA-C	5.29	118.84	112.38
1	A	86	THR	CA-CB-OG1	-5.27	101.69	109.60
1	A	205	HIS	CA-CB-CG	5.24	119.04	113.80
1	A	149	ILE	CA-C-N	5.23	125.23	119.89
1	A	149	ILE	C-N-CA	5.23	125.23	119.89
1	A	330	VAL	CB-CA-C	-5.22	104.43	112.05
1	A	48	HIS	CB-CG-CD2	-5.20	124.44	131.20
1	A	245	LEU	N-CA-C	5.18	118.05	109.46
1	A	170	SER	CA-C-N	5.17	124.79	119.05
1	A	170	SER	C-N-CA	5.17	124.79	119.05
1	A	69	HIS	CB-CG-CD2	-5.06	124.62	131.20
1	A	231	ILE	N-CA-C	-5.04	102.23	108.89
1	A	321	ILE	N-CA-CB	-5.04	107.24	112.28

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	2665	0	2666	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	0	0
3	A	199	0	0	1	0
All	All	2866	0	2666	61	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 (61) 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:156:GLU:HB3	1:A:347:VAL:HG11	1.67	0.76
1:A:309:MET:HE2	1:A:313:CYS:SG	2.26	0.75
1:A:278:ASN:HD22	1:A:278:ASN:H	1.36	0.71
1:A:274:MET:HE3	1:A:298:SER:HB3	1.71	0.70
1:A:189:LEU:HD12	1:A:216:LYS:HB3	1.80	0.63
1:A:172:LEU:HB3	1:A:203:MET:HE1	1.81	0.62
1:A:54:THR:HG22	1:A:55:LYS:HG3	1.83	0.61
1:A:278:ASN:H	1:A:278:ASN:ND2	2.01	0.59
1:A:58:LEU:H	1:A:58:LEU:HD13	1.67	0.59
1:A:53:GLN:HE21	1:A:58:LEU:HD21	1.66	0.59
1:A:21:ILE:HG23	1:A:331:ASN:ND2	2.20	0.56
1:A:43:CYS:SG	1:A:72:VAL:HG13	2.45	0.56
1:A:21:ILE:HG23	1:A:331:ASN:HD21	1.71	0.55
1:A:171:PRO:HG3	1:A:274:MET:HE1	1.90	0.54
1:A:56:ASN:ND2	1:A:61:SER:H	2.04	0.54
1:A:153:MET:SD	1:A:158:ALA:HB2	2.48	0.54
1:A:287:LEU:HA	1:A:290:LEU:HB3	1.90	0.53
1:A:267:LEU:HD23	1:A:291:GLY:O	2.09	0.53
1:A:327:MET:O	1:A:330:VAL:HG22	2.09	0.52
1:A:103:CYS:SG	1:A:105:PRO:HD2	2.51	0.51
1:A:38:ASN:HB3	1:A:77:GLU:HB3	1.93	0.50
1:A:198:LYS:HZ1	1:A:319:SER:H	1.61	0.49
1:A:66:VAL:H	1:A:132:GLN:NE2	2.10	0.49
1:A:65:MET:SD	1:A:122:ASN:ND2	2.86	0.49
1:A:220:ALA:HA	1:A:224:LEU:HD12	1.95	0.48
1:A:75:VAL:HG23	1:A:87:VAL:HA	1.95	0.48
1:A:62:ASN:H	1:A:122:ASN:HD21	1.59	0.48
1:A:324:VAL:HA	1:A:347:VAL:O	2.13	0.47
1:A:53:GLN:NE2	1:A:58:LEU:HD21	2.30	0.46
1:A:161:LEU:HG	1:A:309:MET:HE1	1.97	0.46
1:A:10:THR:HG21	1:A:138:ALA:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:LYS:HB2	1:A:229:TYR:OH	2.16	0.46
1:A:165:GLY:HA3	1:A:309:MET:HE3	1.98	0.45
1:A:71:VAL:CG2	1:A:134:GLY:HA3	2.47	0.45
1:A:274:MET:CE	1:A:298:SER:HB3	2.41	0.45
1:A:238:MET:HA	1:A:238:MET:HE2	1.98	0.45
1:A:189:LEU:HD11	1:A:220:ALA:HB2	1.99	0.45
1:A:158:ALA:HA	1:A:161:LEU:HD22	1.98	0.45
1:A:249:ILE:HD13	1:A:272:ILE:HB	1.99	0.44
1:A:187:LEU:HD23	1:A:250:ASP:OD1	2.17	0.44
1:A:158:ALA:O	1:A:162:LEU:HG	2.17	0.44
1:A:93:VAL:HG21	1:A:141:VAL:HG21	2.01	0.43
1:A:178:LYS:HG2	1:A:203:MET:HE2	2.00	0.43
1:A:56:ASN:O	1:A:58:LEU:HD22	2.18	0.43
1:A:8:ARG:CZ	1:A:8:ARG:HA	2.49	0.43
1:A:51:LEU:HD12	1:A:337:LEU:HD23	2.01	0.43
1:A:67:PRO:O	1:A:133:GLY:HA3	2.18	0.43
1:A:108:ARG:HB3	1:A:110:LEU:HD22	2.01	0.43
1:A:154:ALA:HB3	1:A:157:GLN:HB2	2.01	0.43
1:A:309:MET:SD	1:A:309:MET:C	3.02	0.43
1:A:336:ARG:HB3	1:A:341:ASP:HB3	2.01	0.42
1:A:137:LYS:HD2	1:A:350:VAL:HG12	2.01	0.42
1:A:220:ALA:HA	1:A:224:LEU:HB2	2.02	0.42
1:A:168:VAL:HG23	1:A:192:VAL:HG12	2.02	0.42
1:A:194:HIS:O	1:A:198:LYS:HG3	2.20	0.42
1:A:201:LYS:HA	1:A:201:LYS:HD2	1.91	0.41
1:A:350:VAL:C	1:A:352:GLY:H	2.29	0.41
1:A:11:THR:HG21	1:A:356:ASP:H	1.86	0.41
1:A:270:LYS:HG3	1:A:294:VAL:HB	2.02	0.40
1:A:304:LYS:HG3	1:A:305:GLU:N	2.36	0.40
1:A:18:PRO:HG2	3:A:2011:HOH:O	2.22	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	350/357 (98%)	309 (88%)	35 (10%)	6 (2%)	7 3

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	ASP
1	A	228	ASP
1	A	242	ALA
1	A	300	ILE
1	A	122	ASN
1	A	344	TYR

### 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	295/300 (98%)	265 (90%)	30 (10%)	7 4

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ARG
1	A	28	THR
1	A	51	LEU
1	A	54	THR
1	A	58	LEU
1	A	72	VAL
1	A	82	VAL
1	A	86	THR
1	A	109	ASP
1	A	110	LEU
1	A	111	GLU
1	A	122	ASN
1	A	147	VAL

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Mol	Chain	Res	Type
1	A	156	GLU
1	A	157	GLN
1	A	166	VAL
1	A	192	VAL
1	A	198	LYS
1	A	222	GLN
1	A	252	VAL
1	A	254	VAL
1	A	264	LEU
1	A	265	LEU
1	A	267	LEU
1	A	278	ASN
1	A	290	LEU
1	A	303	MET
1	A	314	LYS
1	A	322	ILE
1	A	354	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	53	GLN
1	A	56	ASN
1	A	62	ASN
1	A	122	ASN
1	A	129	GLN
1	A	132	GLN
1	A	206	HIS
1	A	214	ASN
1	A	255	HIS
1	A	278	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 2 ligands modelled in this entry, 2 are 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.