



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:50 PM UTC

PDB ID : 1DIN / pdb_00001din
Title : DIENELACTONE HYDROLASE AT 2.8 ANGSTROMS
Authors : Ollis, D.L.; Pathak, D.
Deposited on : 1996-03-14
Resolution : 1.80 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)
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

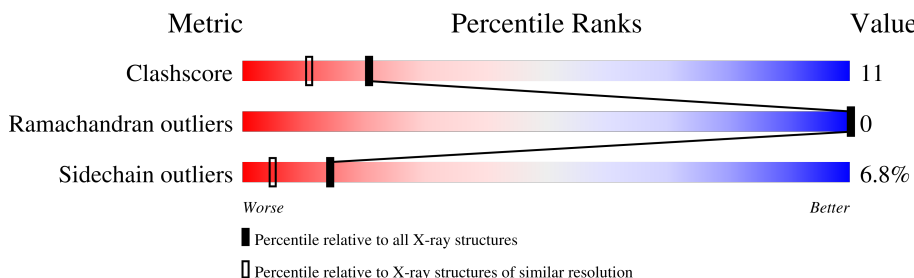
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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	237	 69% 23% 6% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2063 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 DIENELACTONE HYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	2	0
			1784	1138	307	332	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	CSD	CYS	microheterogeneity	PIR S02022

- Molecule 2 is water.

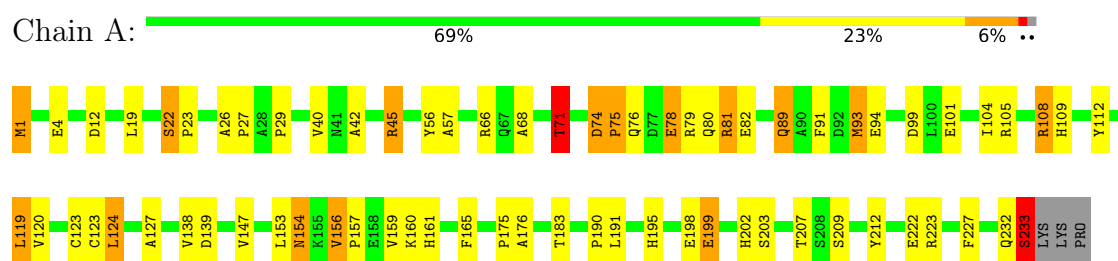
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	279	Total	O	0	0
			279	279		

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: DIENELACTONE HYDROLASE



4 Data and refinement statistics

Xtriage (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	48.90Å 71.45Å 78.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.80	Depositor
% Data completeness (in resolution range)	95.0 (10.00-1.80)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ, TNT	Depositor
R, R_{free}	0.150 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2063	wwPDB-VP
Average B, all atoms (Å ²)	23.0	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: CSD

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	2.41	4/1827 (0.2%)	2.12	51/2484 (2.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	233	SER	CA-C	67.51	2.94	1.52
1	A	233	SER	N-CA	61.79	2.63	1.46
1	A	4	GLU	CD-OE1	5.23	1.35	1.25
1	A	222	GLU	CD-OE1	5.05	1.34	1.25

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	232	GLN	CA-C-O	13.93	136.79	120.92
1	A	109	HIS	CA-CB-CG	-12.18	101.62	113.80
1	A	123[B]	CYS	CA-C-O	-10.48	105.53	120.51
1	A	124	LEU	N-CA-C	-9.39	101.04	111.28
1	A	74	ASP	CA-C-O	9.33	125.35	119.29
1	A	227	PHE	CA-CB-CG	9.03	122.83	113.80
1	A	232	GLN	CA-C-N	-8.84	105.78	121.70
1	A	232	GLN	C-N-CA	-8.84	105.78	121.70
1	A	202	HIS	CG-CD2-NE2	-8.22	98.97	107.20
1	A	232	GLN	N-CA-CB	8.09	122.06	109.69
1	A	202	HIS	CE1-NE2-CD2	7.96	116.96	109.00
1	A	108	ARG	NE-CZ-NH2	-7.94	112.06	119.20
1	A	199	GLU	N-CA-CB	-7.82	98.55	110.91
1	A	42	ALA	N-CA-C	7.62	119.22	111.07
1	A	108	ARG	CD-NE-CZ	7.23	134.52	124.40
1	A	233	SER	CB-CA-C	-7.16	96.50	110.10
1	A	139	ASP	CA-CB-CG	-6.94	105.66	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	93	MET	CG-SD-CE	-6.86	85.81	100.90
1	A	198	GLU	CA-C-N	-6.78	112.39	122.83
1	A	198	GLU	C-N-CA	-6.78	112.39	122.83
1	A	165	PHE	CA-CB-CG	-6.70	107.10	113.80
1	A	74	ASP	CA-CB-CG	-6.68	105.92	112.60
1	A	233	SER	N-CA-CB	-6.60	99.28	110.50
1	A	57	ALA	N-CA-C	-6.50	100.35	110.42
1	A	161	HIS	ND1-CE1-NE2	6.47	114.87	108.40
1	A	159	VAL	N-CA-CB	-6.27	103.86	110.82
1	A	156	VAL	CA-C-O	6.08	123.33	118.71
1	A	203	SER	CB-CA-C	-5.93	101.70	111.36
1	A	202	HIS	ND1-CG-CD2	5.87	111.97	106.10
1	A	190	PRO	N-CA-CB	5.84	109.32	103.48
1	A	195	HIS	ND1-CG-CD2	5.82	111.92	106.10
1	A	22	SER	N-CA-CB	5.82	117.89	110.04
1	A	176	ALA	CA-C-O	5.68	123.78	118.44
1	A	232	GLN	O-C-N	5.68	129.99	122.95
1	A	209	SER	CB-CA-C	-5.67	99.93	109.50
1	A	80	GLN	CA-CB-CG	-5.65	102.81	114.10
1	A	71	THR	N-CA-CB	5.56	118.14	109.97
1	A	82	GLU	CB-CG-CD	5.54	122.03	112.60
1	A	127	ALA	N-CA-C	-5.42	105.45	111.36
1	A	198	GLU	N-CA-C	5.40	120.28	111.37
1	A	81	ARG	CB-CA-C	-5.35	101.90	110.79
1	A	212	TYR	CA-C-O	-5.31	114.86	120.92
1	A	183	THR	CA-C-O	5.25	126.34	120.82
1	A	75	PRO	N-CA-CB	5.14	108.25	103.41
1	A	12	ASP	CA-C-N	-5.12	114.05	122.20
1	A	12	ASP	C-N-CA	-5.12	114.05	122.20
1	A	223	ARG	NE-CZ-NH2	-5.08	114.63	119.20
1	A	76	GLN	CB-CG-CD	-5.07	103.98	112.60
1	A	99	ASP	CA-CB-CG	5.06	117.66	112.60
1	A	147	VAL	CA-CB-CG2	-5.04	101.83	110.40
1	A	66	ARG	NE-CZ-NH2	5.03	123.72	119.20

There are no chirality outliers.

There are no planarity outliers.

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	1784	0	1724	39	0
2	A	279	0	0	8	0
All	All	2063	0	1724	39	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 (39) 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:91:PHE:HD2	1:A:93:MET:HE2	1.45	0.82
1:A:1:MET:HG3	1:A:40:VAL:O	1.84	0.78
1:A:175:PRO:HB3	2:A:485:HOH:O	1.85	0.76
1:A:68:ALA:O	1:A:71:THR:HG23	1.85	0.76
1:A:207:THR:HG23	2:A:471:HOH:O	1.87	0.74
1:A:1:MET:HB3	2:A:449:HOH:O	1.85	0.74
1:A:233:SER:CA	1:A:233:SER:N	2.63	0.62
1:A:78:GLU:HB3	1:A:79:ARG:HH11	1.65	0.60
1:A:93:MET:HE1	1:A:124:LEU:HD11	1.82	0.60
1:A:45:ARG:HH11	1:A:45:ARG:HG3	1.67	0.59
1:A:91:PHE:HD2	1:A:93:MET:CE	2.12	0.59
1:A:101:GLU:HG2	1:A:105:ARG:HH12	1.68	0.58
1:A:101:GLU:HG2	1:A:105:ARG:NH1	2.19	0.58
1:A:101:GLU:CG	1:A:105:ARG:HH12	2.17	0.58
1:A:1:MET:HG2	1:A:1:MET:O	1.98	0.58
1:A:91:PHE:CD2	1:A:93:MET:HE2	2.34	0.57
1:A:89:GLN:HG3	2:A:321:HOH:O	2.04	0.56
1:A:45:ARG:HB2	2:A:409:HOH:O	2.06	0.56
1:A:1:MET:HB2	2:A:306:HOH:O	2.06	0.55
1:A:79:ARG:N	1:A:79:ARG:HD2	2.23	0.53
1:A:156:VAL:N	1:A:157:PRO:HD2	2.23	0.53
1:A:27:PRO:HA	1:A:112:TYR:O	2.09	0.52
1:A:26:ALA:HB1	1:A:27:PRO:HA	1.91	0.51
1:A:45:ARG:O	1:A:45:ARG:NH1	2.44	0.51
1:A:93:MET:HE1	1:A:124:LEU:CD1	2.42	0.49
1:A:22:SER:HB2	1:A:23:PRO:HD2	1.94	0.49
1:A:93:MET:HE3	2:A:360:HOH:O	2.13	0.49
1:A:154:ASN:H	1:A:154:ASN:HD22	1.59	0.49
1:A:19:LEU:HD21	1:A:45:ARG:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:GLU:CD	1:A:105:ARG:HH12	2.22	0.47
1:A:91:PHE:CD2	1:A:93:MET:CE	2.97	0.46
1:A:119:LEU:HD13	1:A:120:VAL:N	2.33	0.43
1:A:160:LYS:C	1:A:191:LEU:HD13	2.44	0.43
1:A:74:ASP:OD1	1:A:75:PRO:HD2	2.19	0.43
1:A:29:PRO:HG2	1:A:56:TYR:CD1	2.55	0.42
1:A:81:ARG:HD3	2:A:478:HOH:O	2.19	0.42
1:A:154:ASN:H	1:A:154:ASN:ND2	2.18	0.41
1:A:104:ILE:HD13	1:A:138:VAL:HG13	2.03	0.40
1:A:233:SER:CA	1:A:233:SER:C	2.94	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	231/237 (98%)	225 (97%)	6 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	177/179 (99%)	165 (93%)	12 (7%)	14	5

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	45	ARG
1	A	71	THR
1	A	78	GLU
1	A	89	GLN
1	A	94	GLU
1	A	108	ARG
1	A	119	LEU
1	A	153	LEU
1	A	154	ASN
1	A	199	GLU
1	A	233	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	109	HIS
1	A	154	ASN
1	A	221	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue 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
1	CSD	A	123[A]	1	4,7,8	14.83	1 (25%)	1,8,10	12.64	1 (100%)

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	CSD	A	123[A]	1	-	1/2/6/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	123[A]	CSD	OD1-SG	-29.64	1.20	1.47

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	123[A]	CSD	OD1-SG-CB	-12.64	82.32	105.60

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	123[A]	CSD	CA-CB-SG-OD1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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 ⓘ

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.