



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:28 AM UTC

PDB ID : 1DHP / pdb_00001dhp
Title : DIHYDRODIPICOLINATE SYNTHASE
Authors : Mirwaldt, C.; Korndorfer, I.; Huber, R.
Deposited on : 1995-02-09
Resolution : 2.30 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
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

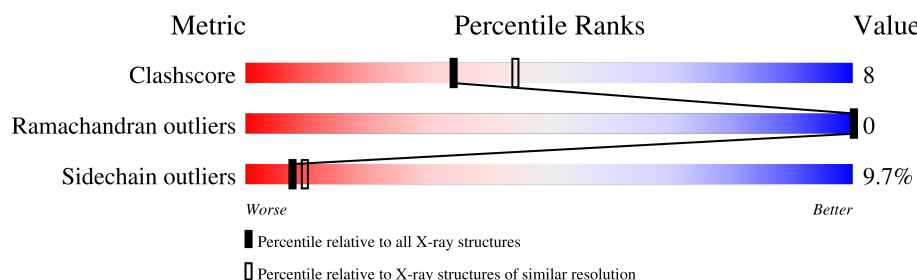
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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	292	78% 18% .
1	B	292	78% 20% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4726 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 DIHYDRODIPICOLINATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	0	0
			2190	1373	384	419	14			
1	B	292	Total	C	N	O	S	0	0	0
			2190	1373	384	419	14			

- Molecule 2 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	K	0	0
			1	1		
2	B	1	Total	K	0	0
			1	1		

- Molecule 3 is water.

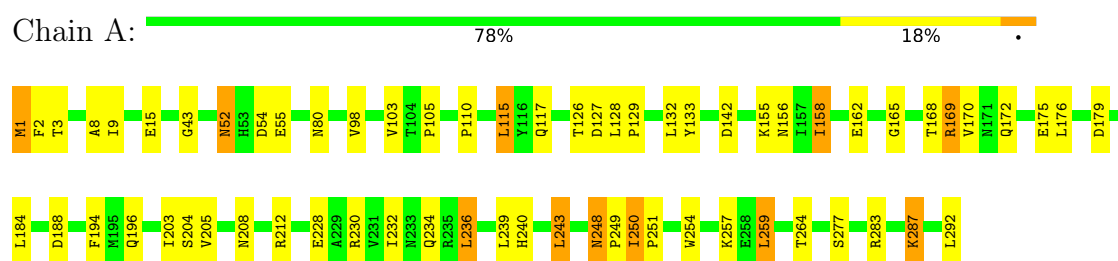
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	153	Total	O	0	0
			153	153		
3	B	191	Total	O	0	0
			191	191		

3 Residue-property plots

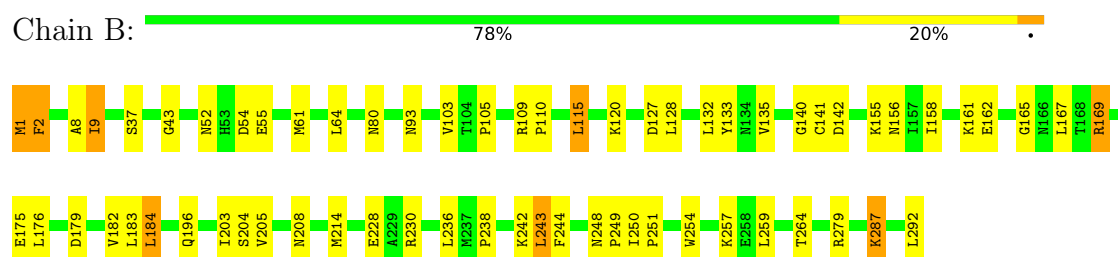
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: DIHYDRODIPICOLINATE SYNTHASE



• Molecule 1: DIHYDRODIPICOLINATE SYNTHASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	122.41 Å 122.41 Å 111.22 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.30)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.197 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4726	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.67	1/2225 (0.0%)	1.10	9/3022 (0.3%)
1	B	0.68	0/2225	1.13	14/3022 (0.5%)
All	All	0.67	1/4450 (0.0%)	1.11	23/6044 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	250	ILE	CA-CB	5.56	1.57	1.54

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	204	SER	N-CA-C	8.05	123.48	109.96
1	A	205	VAL	N-CA-C	-7.82	105.08	111.81
1	A	204	SER	N-CA-C	7.71	122.58	110.17
1	B	2	PHE	N-CA-C	-7.60	101.15	110.88
1	B	43	GLY	N-CA-C	-7.15	102.38	112.60
1	B	156	ASN	N-CA-C	7.15	120.11	111.82
1	B	158	ILE	N-CA-C	7.14	119.75	112.90
1	A	158	ILE	N-CA-C	6.94	121.00	113.43
1	A	43	GLY	N-CA-C	-6.85	102.81	112.60
1	B	165	GLY	N-CA-C	-6.55	106.65	115.36
1	B	9	ILE	N-CA-C	6.32	117.73	109.58
1	A	248	ASN	N-CA-C	-5.90	102.15	109.64
1	B	8	ALA	N-CA-C	-5.71	98.63	108.56
1	B	205	VAL	N-CA-C	-5.67	105.57	111.58
1	B	142	ASP	N-CA-C	5.65	117.61	108.34
1	A	203	ILE	N-CA-C	-5.62	98.34	106.88
1	A	8	ALA	N-CA-C	-5.61	97.43	107.98
1	A	127	ASP	N-CA-C	-5.49	106.58	113.72

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	ILE	N-CA-C	-5.29	98.84	106.88
1	A	165	GLY	N-CA-C	-5.17	108.11	115.30
1	B	161	LYS	N-CA-C	-5.14	99.41	108.20
1	B	37	SER	N-CA-C	5.07	116.88	111.36
1	B	167	LEU	N-CA-C	5.07	119.09	113.01

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	2190	0	2225	36	0
1	B	2190	0	2225	31	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	153	0	0	0	0
3	B	191	0	0	3	0
All	All	4726	0	4450	67	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 8.

All (67) 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:1:MET:SD	1:A:2:PHE:N	2.50	0.84
1:B:196:GLN:NE2	1:B:230:ARG:HH21	1.78	0.81
1:A:196:GLN:NE2	1:A:230:ARG:HH21	1.79	0.80
1:B:110:PRO:HG2	1:B:115:LEU:HD13	1.72	0.70
1:B:1:MET:SD	1:B:2:PHE:N	2.65	0.69
1:B:254:TRP:NE1	1:B:257:LYS:HZ3	1.90	0.68
1:A:254:TRP:CD1	1:A:257:LYS:HZ3	2.16	0.63
1:A:196:GLN:HE22	1:A:230:ARG:HH21	1.47	0.62
1:A:15:GLU:H	1:A:15:GLU:CD	2.08	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:PRO:HG2	1:A:115:LEU:HD13	1.82	0.61
1:A:172:GLN:O	1:A:176:LEU:HD13	2.01	0.61
1:B:254:TRP:NE1	1:B:257:LYS:NZ	2.48	0.61
1:A:254:TRP:NE1	1:A:257:LYS:HZ3	1.98	0.60
1:A:168:THR:O	1:A:172:GLN:HG3	2.02	0.60
1:B:287:LYS:HZ2	1:B:292:LEU:HB2	1.67	0.59
1:A:52:ASN:HD22	1:A:52:ASN:C	2.11	0.58
1:B:214:MET:HE1	3:B:327:HOH:O	2.01	0.58
1:B:196:GLN:HE22	1:B:230:ARG:HH21	1.52	0.58
1:A:52:ASN:ND2	1:A:55:GLU:H	2.03	0.57
1:A:129:PRO:HB3	1:A:158:ILE:HG12	1.85	0.56
1:B:103:VAL:HA	1:B:133:TYR:HB3	1.87	0.56
1:B:250:ILE:HB	1:B:251:PRO:HD3	1.88	0.56
1:A:9:ILE:HA	1:A:208:ASN:HD21	1.71	0.55
1:A:254:TRP:NE1	1:A:257:LYS:NZ	2.54	0.55
1:B:238:PRO:O	1:B:242:LYS:HG2	2.07	0.55
1:B:175:GLU:HG3	3:B:459:HOH:O	2.09	0.53
1:B:254:TRP:HE1	1:B:257:LYS:NZ	2.07	0.52
1:A:248:ASN:ND2	1:A:249:PRO:HA	2.24	0.51
1:A:98:VAL:O	1:A:129:PRO:HD2	2.11	0.51
1:A:250:ILE:HB	1:A:251:PRO:HD3	1.92	0.51
1:B:248:ASN:ND2	1:B:249:PRO:HA	2.27	0.50
1:B:287:LYS:HZ1	1:B:292:LEU:HB3	1.77	0.50
1:A:230:ARG:O	1:A:234:GLN:HG3	2.12	0.49
1:A:287:LYS:HD2	1:A:292:LEU:HB3	1.95	0.47
1:B:254:TRP:CD1	1:B:257:LYS:HZ3	2.33	0.47
1:A:1:MET:SD	1:A:2:PHE:CD2	3.09	0.46
1:B:52:ASN:ND2	1:B:55:GLU:H	2.14	0.46
1:B:287:LYS:NZ	1:B:292:LEU:HB3	2.30	0.46
1:B:287:LYS:NZ	1:B:292:LEU:CB	2.79	0.46
1:B:169:ARG:HD2	3:B:449:HOH:O	2.17	0.45
1:B:287:LYS:HZ2	1:B:292:LEU:CB	2.29	0.45
1:B:155:LYS:HB3	1:B:155:LYS:HE2	1.71	0.44
1:B:254:TRP:CE2	1:B:279:ARG:HG2	2.53	0.43
1:A:239:LEU:O	1:A:243:LEU:HB2	2.18	0.43
1:B:93:ASN:HA	1:B:128:LEU:HD21	2.00	0.43
1:A:52:ASN:C	1:A:52:ASN:ND2	2.77	0.43
1:A:257:LYS:HE2	1:A:257:LYS:HB3	1.89	0.43
1:A:142:ASP:OD1	1:A:169:ARG:NH2	2.52	0.42
1:B:242:LYS:C	1:B:244:PHE:H	2.27	0.42
1:A:52:ASN:HD21	1:A:54:ASP:HB2	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:ILE:HA	1:B:208:ASN:HD21	1.84	0.42
1:A:232:ILE:HG22	1:A:236:LEU:HD22	2.01	0.42
1:B:135:VAL:O	1:B:135:VAL:HG13	2.20	0.42
1:A:283:ARG:HG3	1:A:292:LEU:CD1	2.50	0.42
1:B:243:LEU:HD12	1:B:243:LEU:HA	1.79	0.42
1:A:196:GLN:HE21	1:A:196:GLN:HB2	1.66	0.42
1:A:52:ASN:HD22	1:A:54:ASP:N	2.18	0.41
1:A:188:ASP:HB3	1:A:240:HIS:ND1	2.35	0.41
1:A:170:VAL:HG22	1:A:194:PHE:CE2	2.55	0.41
1:B:254:TRP:CZ2	1:B:279:ARG:HG2	2.55	0.41
1:A:126:THR:HG23	1:A:156:ASN:HD21	1.86	0.41
1:A:254:TRP:HE1	1:A:257:LYS:NZ	2.18	0.41
1:B:182:VAL:HG12	1:B:184:LEU:HD22	2.02	0.41
1:A:259:LEU:HD12	1:A:259:LEU:HA	1.90	0.41
1:B:109:ARG:NH1	1:B:140:GLY:O	2.54	0.41
1:A:103:VAL:HA	1:A:133:TYR:HB3	2.04	0.40
1:A:239:LEU:HD12	1:A:239:LEU:HA	1.89	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	290/292 (99%)	282 (97%)	8 (3%)	0	100	100
1	B	290/292 (99%)	283 (98%)	7 (2%)	0	100	100
All	All	580/584 (99%)	565 (97%)	15 (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	238/238 (100%)	215 (90%)	23 (10%)	8	10
1	B	238/238 (100%)	215 (90%)	23 (10%)	8	10
All	All	476/476 (100%)	430 (90%)	46 (10%)	8	10

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	THR
1	A	52	ASN
1	A	80	ASN
1	A	105	PRO
1	A	115	LEU
1	A	117	GLN
1	A	128	LEU
1	A	132	LEU
1	A	155	LYS
1	A	162	GLU
1	A	169	ARG
1	A	175	GLU
1	A	179	ASP
1	A	184	LEU
1	A	212	ARG
1	A	228	GLU
1	A	236	LEU
1	A	243	LEU
1	A	259	LEU
1	A	264	THR
1	A	277	SER
1	A	287	LYS
1	B	1	MET
1	B	54	ASP
1	B	61	MET
1	B	64	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	80	ASN
1	B	105	PRO
1	B	115	LEU
1	B	120	LYS
1	B	127	ASP
1	B	132	LEU
1	B	141	CYS
1	B	162	GLU
1	B	169	ARG
1	B	176	LEU
1	B	179	ASP
1	B	183	LEU
1	B	184	LEU
1	B	228	GLU
1	B	236	LEU
1	B	243	LEU
1	B	259	LEU
1	B	264	THR
1	B	287	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	53	HIS
1	A	80	ASN
1	A	90	GLN
1	A	130	GLN
1	A	172	GLN
1	A	196	GLN
1	A	208	ASN
1	A	225	HIS
1	A	233	ASN
1	B	18	ASN
1	B	52	ASN
1	B	80	ASN
1	B	90	GLN
1	B	125	HIS
1	B	130	GLN
1	B	172	GLN
1	B	196	GLN
1	B	208	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

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.