



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:36 AM UTC

PDB ID : 4ICD / pdb_00004icd
Title : REGULATION OF ISOCITRATE DEHYDROGENASE BY PHOSPHORYLATION INVOLVES NO LONG-RANGE CONFORMATIONAL CHANGE IN THE FREE ENZYME
Authors : Hurley, J.H.; Dean, A.M.; Thorsness, P.E.; Koshlandjunior, D.E.; Stroud, R.M.
Deposited on : 1989-12-28
Resolution : 2.50 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

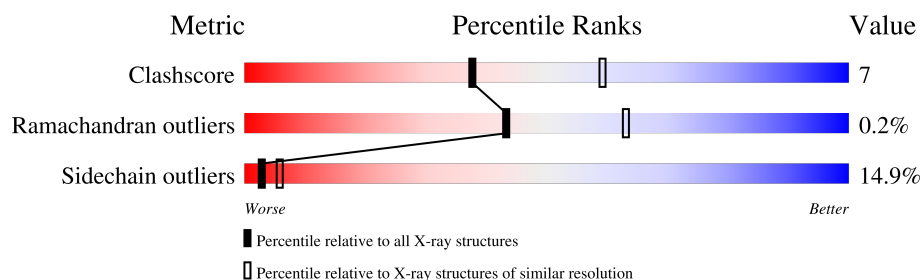
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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	416	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3293 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 PHOSPHORYLATED ISOCITRATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	P	S	0	0	0
			3150	2007	531	593	1	18			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	143	Total	O	0	0
			143	143		

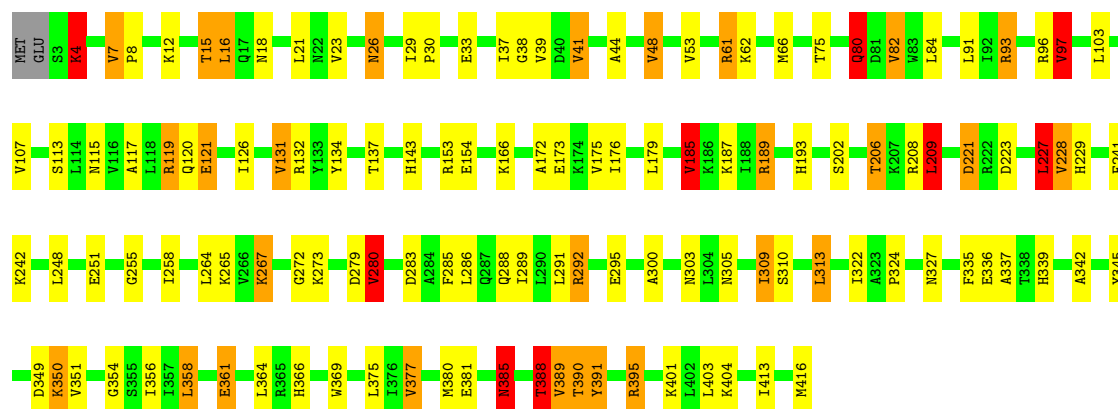
3 Residue-property plots

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: PHOSPHORYLATED ISOCITRATE DEHYDROGENASE

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.10Å 105.10Å 150.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.169 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3293	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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: SEP

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	1.04	16/3200 (0.5%)	1.75	47/4334 (1.1%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	131	VAL	CA-CB	7.98	1.64	1.54
1	A	193	HIS	CD2-NE2	-7.15	1.29	1.37
1	A	280	VAL	CA-CB	6.87	1.64	1.54
1	A	97	VAL	CA-CB	6.72	1.64	1.54
1	A	185	VAL	CA-CB	6.63	1.61	1.54
1	A	143	HIS	CD2-NE2	-6.59	1.30	1.37
1	A	228	VAL	CA-CB	6.36	1.62	1.54
1	A	82	VAL	CA-CB	6.00	1.60	1.53
1	A	229	HIS	CD2-NE2	-5.98	1.31	1.37
1	A	366	HIS	CD2-NE2	-5.98	1.31	1.37
1	A	377	VAL	CA-CB	5.87	1.62	1.54
1	A	41	VAL	CA-CB	5.85	1.62	1.54
1	A	339	HIS	CD2-NE2	-5.38	1.31	1.37
1	A	193	HIS	CG-ND1	-5.20	1.32	1.38
1	A	309	ILE	CA-CB	5.12	1.60	1.54
1	A	339	HIS	CG-ND1	-5.06	1.32	1.38

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	221	ASP	CA-CB-CG	11.52	124.12	112.60
1	A	389	VAL	N-CA-CB	-7.54	97.82	111.92
1	A	208	ARG	NE-CZ-NH2	7.41	125.87	119.20
1	A	26	ASN	OD1-CG-ND2	-7.19	115.41	122.60
1	A	390	THR	N-CA-CB	-7.00	100.35	110.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	ARG	NE-CZ-NH2	6.80	125.32	119.20
1	A	26	ASN	CB-CG-ND2	6.75	126.53	116.40
1	A	361	GLU	CA-CB-CG	6.48	127.07	114.10
1	A	4	LYS	CA-CB-CG	-6.37	101.37	114.10
1	A	153	ARG	NE-CZ-NH2	6.36	124.92	119.20
1	A	15	THR	CA-CB-OG1	-6.34	100.10	109.60
1	A	342	ALA	CA-C-N	6.28	125.97	119.56
1	A	342	ALA	C-N-CA	6.28	125.97	119.56
1	A	80	GLN	N-CA-C	6.28	120.50	112.34
1	A	388	THR	CA-CB-OG1	-6.28	100.19	109.60
1	A	336	GLU	N-CA-C	6.26	118.66	108.76
1	A	61	ARG	NE-CZ-NH2	6.02	124.62	119.20
1	A	221	ASP	CB-CA-C	-5.97	102.68	112.06
1	A	223	ASP	N-CA-C	5.93	120.24	112.89
1	A	366	HIS	CB-CG-CD2	-5.84	123.60	131.20
1	A	283	ASP	CA-CB-CG	5.83	118.42	112.60
1	A	120	GLN	N-CA-C	5.81	117.69	111.36
1	A	303	ASN	N-CA-C	5.71	117.19	110.97
1	A	395	ARG	CB-CA-C	-5.67	101.75	110.81
1	A	193	HIS	CB-CG-CD2	-5.56	123.97	131.20
1	A	279	ASP	CA-CB-CG	5.56	118.16	112.60
1	A	209	LEU	CD1-CG-CD2	5.51	122.93	110.80
1	A	335	PHE	CA-CB-CG	-5.42	108.38	113.80
1	A	388	THR	N-CA-CB	-5.40	100.52	110.56
1	A	391	TYR	N-CA-C	5.40	117.16	111.28
1	A	227	LEU	CA-C-N	-5.38	116.15	123.10
1	A	227	LEU	C-N-CA	-5.38	116.15	123.10
1	A	189	ARG	NE-CZ-NH2	5.36	124.03	119.20
1	A	33	GLU	CA-CB-CG	-5.32	103.46	114.10
1	A	309	ILE	CB-CA-C	-5.30	105.19	111.97
1	A	385	ASN	CA-CB-CG	-5.21	107.39	112.60
1	A	23	VAL	N-CA-C	5.18	113.00	107.76
1	A	395	ARG	CA-CB-CG	5.16	124.42	114.10
1	A	84	LEU	CA-C-N	5.15	125.06	119.76
1	A	84	LEU	C-N-CA	5.15	125.06	119.76
1	A	273	LYS	N-CA-C	5.14	117.75	110.50
1	A	337	ALA	N-CA-C	-5.13	102.26	109.96
1	A	388	THR	CA-C-O	5.11	127.39	121.11
1	A	313	LEU	N-CA-CB	-5.10	102.62	110.16
1	A	380	MET	CG-SD-CE	-5.10	89.69	100.90
1	A	132	ARG	CB-CG-CD	-5.08	99.61	111.30
1	A	388	THR	CB-CA-C	5.01	119.93	111.41

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	3150	0	3140	44	0
2	A	143	0	0	2	0
All	All	3293	0	3140	44	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 7.

All (44) 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:16:LEU:HD23	1:A:96:ARG:HD2	1.72	0.71
1:A:401:LYS:HE3	1:A:403:LEU:HD11	1.75	0.67
1:A:288:GLN:HE22	1:A:292:ARG:HD3	1.67	0.59
1:A:154:GLU:HA	1:A:209:LEU:HD13	1.83	0.59
1:A:305:ASN:O	1:A:309:ILE:HG12	2.02	0.58
1:A:4:LYS:HB2	1:A:4:LYS:NZ	2.19	0.58
1:A:267:LYS:HE2	1:A:272:GLY:HA2	1.86	0.57
1:A:134:TYR:O	1:A:137:THR:HG23	2.05	0.57
1:A:117:ALA:O	1:A:121:GLU:HB2	2.06	0.55
1:A:115:ASN:O	1:A:119:ARG:HG3	2.07	0.55
1:A:401:LYS:HE3	1:A:403:LEU:CD1	2.38	0.54
1:A:26:ASN:HA	1:A:62:LYS:O	2.07	0.54
1:A:258:ILE:HD11	1:A:265:LYS:HG3	1.89	0.54
1:A:206:THR:HB	1:A:241:PHE:CD2	2.43	0.53
1:A:37:ILE:HB	1:A:351:VAL:HG21	1.90	0.53
1:A:202:SER:O	1:A:206:THR:HG23	2.10	0.52
1:A:16:LEU:HD22	1:A:21:LEU:HD23	1.91	0.52
1:A:44:ALA:O	1:A:48:VAL:HG13	2.10	0.52
1:A:227:LEU:HD12	1:A:300:ALA:HB3	1.94	0.50
1:A:179:LEU:O	1:A:185:VAL:HG13	2.12	0.49
1:A:289:ILE:HD12	1:A:313:LEU:HD13	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:GLU:O	1:A:385:ASN:HB2	2.14	0.48
1:A:61:ARG:HH11	1:A:369:TRP:CD1	2.32	0.47
1:A:126:ILE:O	1:A:327:ASN:HA	2.16	0.46
1:A:280:VAL:HG22	1:A:285:PHE:HB2	1.97	0.46
1:A:30:PRO:HA	1:A:66:MET:O	2.17	0.45
1:A:413:ILE:O	1:A:416:MET:HB2	2.17	0.44
1:A:322:ILE:HG22	1:A:354:GLY:HA3	2.01	0.43
1:A:38:GLY:HA2	1:A:41:VAL:HG22	2.00	0.43
1:A:30:PRO:HD2	1:A:97:VAL:O	2.19	0.42
1:A:93:ARG:HD2	2:A:550:HOH:O	2.19	0.42
1:A:388:THR:HG21	2:A:471:HOH:O	2.20	0.42
1:A:29:ILE:HD12	1:A:97:VAL:HG22	2.02	0.42
1:A:358:LEU:HD12	1:A:358:LEU:HA	1.87	0.42
1:A:166:LYS:HE2	1:A:166:LYS:HB3	1.89	0.41
1:A:172:ALA:O	1:A:176:ILE:HG13	2.20	0.41
1:A:291:LEU:O	1:A:292:ARG:HG3	2.20	0.41
1:A:324:PRO:HB3	1:A:358:LEU:HB3	2.03	0.41
1:A:7:VAL:HA	1:A:8:PRO:HD3	1.89	0.41
1:A:255:GLY:HA2	1:A:265:LYS:O	2.19	0.41
1:A:349:ASP:O	1:A:404:LYS:HB3	2.22	0.40
1:A:345:TYR:CD2	1:A:350:LYS:HD2	2.56	0.40
1:A:75:THR:HB	1:A:80:GLN:HA	2.04	0.40
1:A:391:TYR:O	1:A:395:ARG:HG3	2.21	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	411/416 (99%)	397 (97%)	13 (3%)	1 (0%)	43 63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ASN

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	322/337 (96%)	274 (85%)	48 (15%)	3 6

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	7	VAL
1	A	12	LYS
1	A	15	THR
1	A	16	LEU
1	A	39	VAL
1	A	48	VAL
1	A	53	VAL
1	A	80	GLN
1	A	82	VAL
1	A	91	LEU
1	A	93	ARG
1	A	97	VAL
1	A	103	LEU
1	A	107	VAL
1	A	121	GLU
1	A	131	VAL
1	A	173	GLU
1	A	175	VAL
1	A	185	VAL
1	A	187	LYS
1	A	189	ARG
1	A	206	THR
1	A	209	LEU
1	A	221	ASP
1	A	227	LEU

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Mol	Chain	Res	Type
1	A	228	VAL
1	A	242	LYS
1	A	248	LEU
1	A	251	GLU
1	A	264	LEU
1	A	267	LYS
1	A	280	VAL
1	A	286	LEU
1	A	292	ARG
1	A	295	GLU
1	A	310	SER
1	A	350	LYS
1	A	356	ILE
1	A	358	LEU
1	A	361	GLU
1	A	364	LEU
1	A	375	LEU
1	A	377	VAL
1	A	385	ASN
1	A	388	THR
1	A	389	VAL
1	A	390	THR

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	80	GLN
1	A	143	HIS
1	A	287	GLN
1	A	288	GLN

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	SEP	A	113	1	8,9,10	1.11	1 (12%)	7,12,14	5.00	2 (28%)

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	SEP	A	113	1	-	3/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	113	SEP	P-O3P	-2.05	1.47	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	SEP	OG-CB-CA	-12.94	95.56	108.14
1	A	113	SEP	O3P-P-O1P	2.10	119.03	110.83

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	113	SEP	CB-OG-P-O3P
1	A	113	SEP	CB-OG-P-O1P
1	A	113	SEP	N-CA-CB-OG

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 [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.