



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 2, 2016 – 12:02 AM GMT

PDB ID : 9ICD  
Title : CATALYTIC MECHANISM OF NADP+-DEPENDENT ISOCITRATE DEHYDROGENASE: IMPLICATIONS FROM THE STRUCTURES OF MAGNESIUM-ISOCITRATE AND NADP+ COMPLEXES  
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Deposited on : 1991-07-29  
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](mailto: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.

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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

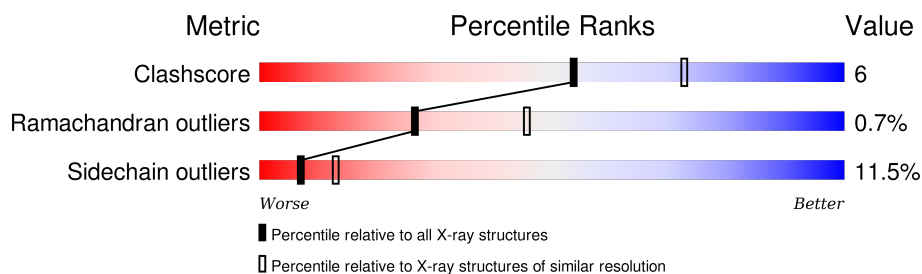
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	416	 73% 21% 5%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3275 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 ISOCITRATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	414	3147	2008	531	590	18	0	0	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	27	10	5	10	2	0	0

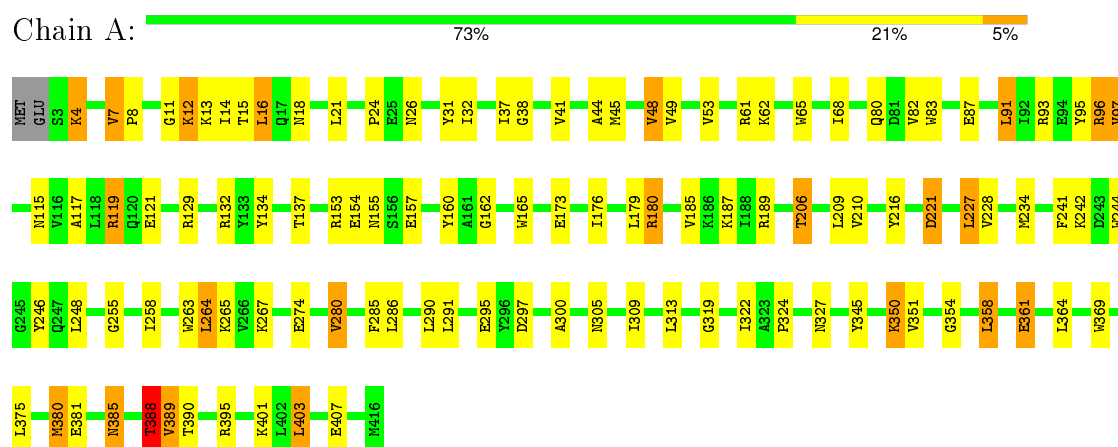
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	101	Total	O	0	0
			101	101		



Note EDS was not executed.

- Molecule 1: ISOCITRATE DEHYDROGENASE



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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, $R_{free}$	0.181 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3275	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	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: NAP

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	0.86	0/3208	1.54	45/4347 (1.0%)

There are no bond length outliers.

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	ARG	NE-CZ-NH2	12.84	126.72	120.30
1	A	61	ARG	NE-CZ-NH2	11.49	126.04	120.30
1	A	65	TRP	CD1-CG-CD2	9.46	113.87	106.30
1	A	129	ARG	NE-CZ-NH1	-9.17	115.72	120.30
1	A	165	TRP	CD1-CG-CD2	8.67	113.24	106.30
1	A	189	ARG	NE-CZ-NH2	8.30	124.45	120.30
1	A	180	ARG	NE-CZ-NH1	-7.88	116.36	120.30
1	A	369	TRP	CD1-CG-CD2	7.88	112.60	106.30
1	A	96	ARG	NE-CZ-NH2	7.72	124.16	120.30
1	A	244	TRP	CD1-CG-CD2	7.50	112.30	106.30
1	A	65	TRP	CE2-CD2-CG	-7.42	101.36	107.30
1	A	244	TRP	CG-CD2-CE3	7.34	140.51	133.90
1	A	380	MET	CG-SD-CE	-7.28	88.55	100.20
1	A	165	TRP	CE2-CD2-CG	-7.22	101.52	107.30
1	A	119	ARG	NE-CZ-NH1	-7.13	116.74	120.30
1	A	389	VAL	N-CA-CB	-7.08	95.93	111.50
1	A	132	ARG	NE-CZ-NH1	-6.91	116.85	120.30
1	A	244	TRP	CE2-CD2-CG	-6.81	101.85	107.30
1	A	83	TRP	CD1-CG-CD2	6.80	111.74	106.30
1	A	83	TRP	CE2-CD2-CG	-6.78	101.88	107.30
1	A	93	ARG	NE-CZ-NH2	6.69	123.65	120.30
1	A	388	THR	N-CA-CB	-6.67	97.63	110.30
1	A	369	TRP	CE2-CD2-CG	-6.45	102.14	107.30
1	A	180	ARG	NE-CZ-NH2	6.34	123.47	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	244	TRP	CB-CG-CD1	-6.28	118.84	127.00
1	A	31	TYR	CB-CG-CD1	-6.13	117.32	121.00
1	A	65	TRP	CG-CD1-NE1	-6.00	104.10	110.10
1	A	361	GLU	CA-CB-CG	6.00	126.60	113.40
1	A	263	TRP	CE2-CD2-CG	-5.94	102.55	107.30
1	A	390	THR	N-CA-CB	-5.92	99.05	110.30
1	A	274	GLU	CA-CB-CG	-5.88	100.47	113.40
1	A	165	TRP	CG-CD1-NE1	-5.86	104.24	110.10
1	A	263	TRP	CD1-CG-CD2	5.81	110.95	106.30
1	A	153	ARG	NE-CZ-NH1	-5.65	117.48	120.30
1	A	83	TRP	CG-CD1-NE1	-5.64	104.46	110.10
1	A	403	LEU	CA-CB-CG	5.58	128.14	115.30
1	A	244	TRP	CG-CD1-NE1	-5.51	104.59	110.10
1	A	216	TYR	CB-CG-CD1	-5.44	117.73	121.00
1	A	290	LEU	CA-CB-CG	5.38	127.66	115.30
1	A	83	TRP	CG-CD2-CE3	5.25	138.63	133.90
1	A	395	ARG	CB-CA-C	-5.21	99.97	110.40
1	A	189	ARG	NE-CZ-NH1	-5.21	117.70	120.30
1	A	319	GLY	CA-C-N	5.07	128.36	117.20
1	A	369	TRP	CG-CD1-NE1	-5.03	105.07	110.10
1	A	45	MET	CG-SD-CE	5.01	108.21	100.20

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	3147	0	3142	41	0
2	A	27	0	11	0	0
3	A	101	0	0	3	0
All	All	3275	0	3153	41	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 6.

All (41) 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:401:LYS:HE3	1:A:403:LEU:HD11	1.62	0.82
1:A:322:ILE:HG22	1:A:354:GLY:HA3	1.74	0.69
1:A:134:TYR:O	1:A:137:THR:HG23	1.96	0.64
1:A:16:LEU:HD23	1:A:96:ARG:HD2	1.79	0.63
1:A:345:TYR:CD2	1:A:350:LYS:HD2	2.37	0.60
1:A:324:PRO:HB3	1:A:358:LEU:HB3	1.83	0.60
1:A:206:THR:HB	1:A:241:PHE:CD2	2.37	0.59
1:A:117:ALA:O	1:A:121:GLU:HB2	2.02	0.59
1:A:162:GLY:HA2	3:A:490:HOH:O	2.02	0.59
1:A:280:VAL:HG22	1:A:285:PHE:HB2	1.87	0.55
1:A:305:ASN:O	1:A:309:ILE:HG12	2.07	0.54
1:A:26:ASN:HA	1:A:62:LYS:O	2.09	0.52
1:A:246:TYR:HD1	1:A:264:LEU:HD22	1.76	0.51
1:A:115:ASN:O	1:A:119:ARG:HG3	2.10	0.51
1:A:154:GLU:HA	1:A:209:LEU:HD13	1.93	0.50
1:A:14:ILE:HD12	1:A:97:VAL:HG13	1.94	0.50
1:A:388:THR:HG21	3:A:463:HOH:O	2.12	0.49
1:A:37:ILE:HB	1:A:351:VAL:HG21	1.95	0.49
1:A:44:ALA:O	1:A:48:VAL:HG13	2.13	0.48
1:A:11:GLY:HA2	1:A:26:ASN:O	2.14	0.47
1:A:87:GLU:O	1:A:91:LEU:HD22	2.16	0.46
1:A:176:ILE:O	1:A:180:ARG:HG3	2.16	0.46
1:A:206:THR:O	1:A:210:VAL:HG23	2.17	0.45
1:A:258:ILE:HD11	1:A:265:LYS:HG3	2.00	0.44
1:A:206:THR:HB	1:A:241:PHE:HD2	1.82	0.44
1:A:26:ASN:HB3	3:A:466:HOH:O	2.18	0.44
1:A:12:LYS:HB3	1:A:24:PRO:HG3	2.00	0.43
1:A:32:ILE:HG13	1:A:68:ILE:HG13	2.01	0.43
1:A:255:GLY:HA2	1:A:265:LYS:O	2.19	0.43
1:A:119:ARG:HD2	1:A:155:ASN:ND2	2.34	0.43
1:A:13:LYS:HG2	1:A:95:TYR:CE1	2.54	0.42
1:A:4:LYS:HB2	1:A:4:LYS:NZ	2.34	0.42
1:A:381:GLU:O	1:A:385:ASN:HB2	2.20	0.41
1:A:119:ARG:HD3	1:A:327:ASN:OD1	2.20	0.41
1:A:49:VAL:O	1:A:53:VAL:HG13	2.20	0.41
1:A:179:LEU:O	1:A:185:VAL:HG13	2.20	0.41
1:A:16:LEU:HD22	1:A:21:LEU:HD23	2.01	0.41
1:A:403:LEU:HB3	1:A:407:GLU:HB2	2.03	0.41
1:A:7:VAL:HA	1:A:8:PRO:HD3	1.90	0.41
1:A:38:GLY:HA2	1:A:41:VAL:HG22	2.02	0.40
1:A:227:LEU:HD12	1:A:300:ALA:HB3	2.03	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	412/416 (99%)	395 (96%)	14 (3%)	3 (1%)	26	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	221	ASP
1	A	297	ASP

### 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	323/338 (96%)	286 (88%)	37 (12%)	7	13

All (37) 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

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Mol	Chain	Res	Type
1	A	48	VAL
1	A	80	GLN
1	A	82	VAL
1	A	91	LEU
1	A	97	VAL
1	A	157	GLU
1	A	160	TYR
1	A	173	GLU
1	A	187	LYS
1	A	206	THR
1	A	221	ASP
1	A	227	LEU
1	A	228	VAL
1	A	234	MET
1	A	242	LYS
1	A	248	LEU
1	A	264	LEU
1	A	267	LYS
1	A	280	VAL
1	A	286	LEU
1	A	291	LEU
1	A	295	GLU
1	A	313	LEU
1	A	350	LYS
1	A	358	LEU
1	A	361	GLU
1	A	364	LEU
1	A	375	LEU
1	A	380	MET
1	A	385	ASN
1	A	388	THR
1	A	389	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	GLN
1	A	120	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

1 ligand 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$
2	NAP	A	417	-	24,29,52	1.46	4 (16%)	29,45,80	1.70	8 (27%)

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
2	NAP	A	417	-	-	0/11/31/67	0/3/3/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	417	NAP	P2B-O3X	2.27	1.62	1.54
2	A	417	NAP	PA-O5B	2.95	1.70	1.60
2	A	417	NAP	O4B-C1B	3.11	1.45	1.41
2	A	417	NAP	PA-O3	3.29	1.66	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	417	NAP	C3B-C2B-C1B	-3.26	96.42	102.73
2	A	417	NAP	O2B-C2B-C1B	-3.20	97.56	110.02
2	A	417	NAP	C1B-N9A-C4A	-2.38	123.35	126.94
2	A	417	NAP	O4B-C1B-N9A	2.13	112.56	108.10
2	A	417	NAP	O2A-PA-O1A	2.23	117.77	110.58
2	A	417	NAP	O4B-C4B-C5B	2.30	117.54	109.32
2	A	417	NAP	O2X-P2B-O1X	3.26	121.07	110.58
2	A	417	NAP	O5B-C5B-C4B	3.32	121.37	109.12

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 will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 6.3 Carbohydrates ⓘ

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

### 6.4 Ligands ⓘ

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

### 6.5 Other polymers ⓘ

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