



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:04 PM UTC

PDB ID : 2Q8H / pdb_00002q8h
Title : Structure of pyruvate dehydrogenase kinase isoform 1 in complex with dichloroacetate (DCA)
Authors : Kato, M.; Li, J.; Chuang, J.L.; Chuang, D.T.
Deposited on : 2007-06-10
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

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)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

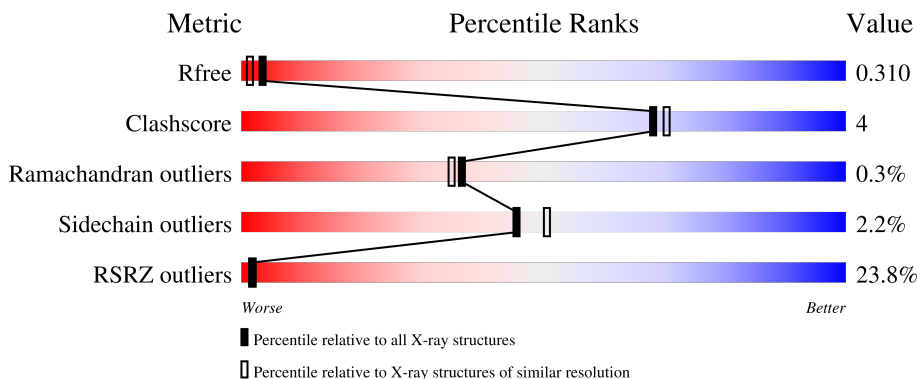
1 Overall quality at a glance

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))
R_{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (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 ≥ 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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	407	21% 82% 7% 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TF4	A	438	-	X	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3220 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.

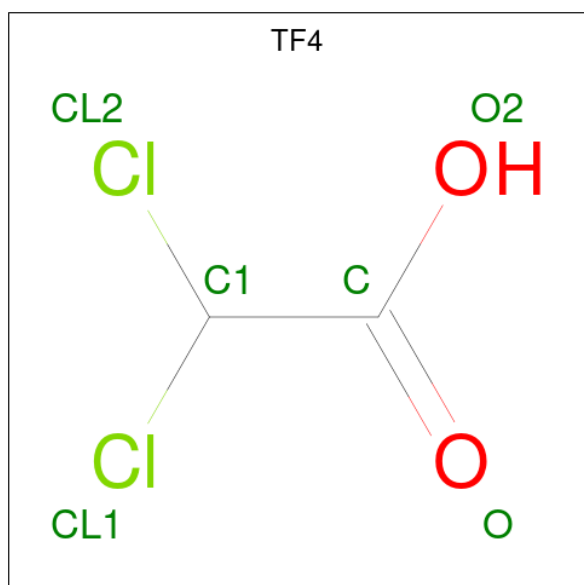
- Molecule 1 is a protein called [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	2	0
			2971	1906	506	544	15			

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

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

- Molecule 3 is DICHLORO-ACETIC ACID (CCD ID: TF4) (formula: C₂H₂Cl₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	Cl	O	0	0
			6	2	2	2		

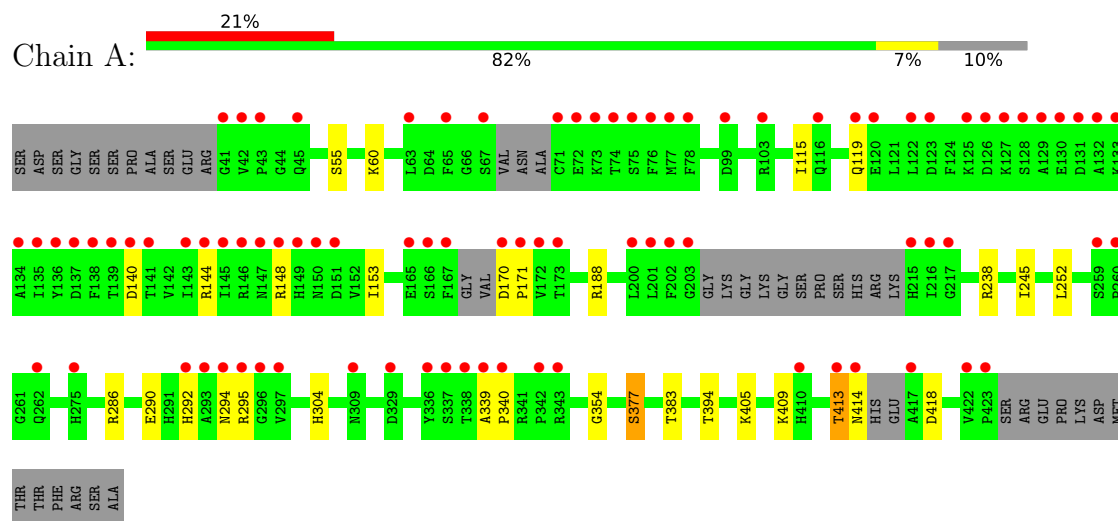
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	242	Total 242	O 242	0	0

3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

- Molecule 1: [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.32Å 98.32Å 110.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.8 (50.00-2.00) 96.9 (50.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.230 , 0.277 0.260 , 0.310	Depositor DCC
R_{free} test set	1802 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3220	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TF4, 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	0.83	1/3047 (0.0%)	0.97	0/4129

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	153	ILE	CA-CB	5.90	1.57	1.54

There are no bond angle outliers.

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	2971	0	2922	21	0
2	A	1	0	0	0	0
3	A	6	0	0	4	0
4	A	242	0	0	5	0
All	All	3220	0	2922	21	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 4.

All (21) 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:292:HIS:HA	1:A:295:ARG:HH11	1.50	0.77
1:A:292:HIS:HA	1:A:295:ARG:NH1	2.06	0.71
1:A:409:LYS:O	1:A:413:THR:HB	1.90	0.70
1:A:115:ILE:O	1:A:119:GLN:HG3	1.94	0.68
1:A:188:ARG:NH2	4:A:578:HOH:O	2.34	0.60
1:A:339:ALA:HB1	1:A:340:PRO:HD2	1.86	0.57
1:A:413:THR:O	1:A:414:ASN:HB2	2.04	0.57
1:A:377:SER:HB2	1:A:383:THR:OG1	2.07	0.55
1:A:286:ARG:O	1:A:290:GLU:HG3	2.07	0.54
1:A:405:LYS:HD2	1:A:409:LYS:HE3	1.90	0.53
1:A:304:HIS:HB2	4:A:634:HOH:O	2.09	0.52
1:A:188:ARG:NE	3:A:438:TF4:CL1	2.80	0.52
1:A:188:ARG:CD	3:A:438:TF4:CL1	2.97	0.50
1:A:354:GLY:HA3	4:A:541:HOH:O	2.13	0.49
1:A:188:ARG:HD3	3:A:438:TF4:O2	2.14	0.48
1:A:60:LYS:HD2	1:A:394:THR:HG22	1.99	0.45
1:A:144:ARG:O	1:A:148:ARG:HG2	2.19	0.43
1:A:294:ASN:ND2	4:A:659:HOH:O	2.51	0.43
1:A:170:ASP:OD1	1:A:171:PRO:HD2	2.20	0.41
1:A:188:ARG:HD3	3:A:438:TF4:CL1	2.58	0.41
1:A:188:ARG:NH2	4:A:646:HOH:O	2.54	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	357/407 (88%)	345 (97%)	11 (3%)	1 (0%)	36	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	245	ILE

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	327/360 (91%)	320 (98%)	7 (2%)	47 52

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	SER
1	A	140	ASP
1	A	238	ARG
1	A	252	LEU
1	A	377	SER
1	A	413	THR
1	A	418	ASP

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	215	HIS
1	A	291	HIS
1	A	304	HIS
1	A	410	HIS

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, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
3	TF4	A	438	-	5,5,5	1.57	1 (20%)	6,6,6	1.91	1 (16%)

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
3	TF4	A	438	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	438	TF4	O2-C	-2.01	1.24	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	438	TF4	CL2-C1-CL1	3.79	119.78	110.31

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	438	TF4	O-C-C1-CL2

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Mol	Chain	Res	Type	Atoms
3	A	438	TF4	O2-C-C1-CL2
3	A	438	TF4	O-C-C1-CL1
3	A	438	TF4	O2-C-C1-CL1

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	438	TF4	4	0

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 ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	365/407 (89%)	1.37	87 (23%) 2 2	19, 41, 58, 75	2 (0%)

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	136	TYR	7.9
1	A	132	ALA	6.7
1	A	293	ALA	5.6
1	A	65	PHE	5.5
1	A	172	VAL	5.3
1	A	77	MET	5.3
1	A	259	SER	5.1
1	A	134	ALA	5.1
1	A	43	PRO	4.8
1	A	129	ALA	4.7
1	A	74	THR	4.6
1	A	339	ALA	4.5
1	A	128	SER	4.4
1	A	42	VAL	4.3
1	A	133	LYS	4.3
1	A	173	THR	4.3
1	A	217	GLY	4.2
1	A	423	PRO	4.2
1	A	417	ALA	4.1
1	A	170	ASP	4.1
1	A	147	ASN	4.0
1	A	126	ASP	4.0
1	A	165	GLU	4.0
1	A	131	ASP	4.0
1	A	215	HIS	4.0
1	A	71	CYS	3.9
1	A	67	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	167	PHE	3.9
1	A	73	LYS	3.8
1	A	125	LYS	3.8
1	A	135	ILE	3.8
1	A	203	GLY	3.8
1	A	137	ASP	3.8
1	A	336	TYR	3.7
1	A	130	GLU	3.6
1	A	297	VAL	3.6
1	A	338	THR	3.5
1	A	422	VAL	3.5
1	A	340	PRO	3.4
1	A	150	ASN	3.3
1	A	144	ARG	3.3
1	A	143	ILE	3.2
1	A	216	ILE	3.2
1	A	166	SER	3.1
1	A	337	SER	3.1
1	A	202	PHE	3.1
1	A	123	ASP	3.1
1	A	141	THR	3.0
1	A	414	ASN	3.0
1	A	146	ARG	3.0
1	A	294	ASN	3.0
1	A	45	GLN	3.0
1	A	103	ARG	3.0
1	A	148	ARG	3.0
1	A	343	ARG	3.0
1	A	200	LEU	2.9
1	A	76	PHE	2.9
1	A	151	ASP	2.9
1	A	140	ASP	2.8
1	A	292	HIS	2.7
1	A	329	ASP	2.7
1	A	145	ILE	2.7
1	A	41	GLY	2.7
1	A	116	GLN	2.6
1	A	201	LEU	2.6
1	A	309	ASN	2.6
1	A	75	SER	2.6
1	A	127	LYS	2.6
1	A	72	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	262	GLN	2.5
1	A	138	PHE	2.5
1	A	139	THR	2.5
1	A	119	GLN	2.4
1	A	171	PRO	2.4
1	A	99	ASP	2.4
1	A	63	LEU	2.3
1	A	149	HIS	2.3
1	A	260	PRO	2.3
1	A	122	LEU	2.3
1	A	275[A]	HIS	2.2
1	A	78	PHE	2.2
1	A	410	HIS	2.2
1	A	120	GLU	2.1
1	A	342	PRO	2.1
1	A	413	THR	2.1
1	A	295	ARG	2.0
1	A	296	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	TF4	A	438	6/6	0.81	0.19	66,68,68,70	0
2	K	A	437	1/1	0.96	0.10	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.