

wwPDB X-ray Structure Validation Summary Report (i)

Dec 17, 2023 – 03:05 PM EST

:	1QFE
:	THE STRUCTURE OF TYPE I 3-DEHYDROQUINATE DEHYDRATASE
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	1999-04-05
:	2.10 Å(reported)
	: : :

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

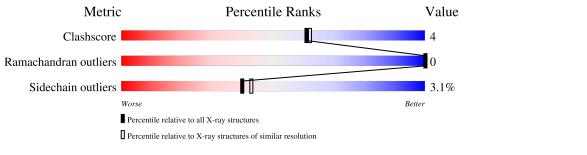
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	Similar resolution		
Metric	$(\# {\rm Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$		
Clashscore	141614	5710 (2.10-2.10)		
Ramachandran outliers	138981	5647 (2.10-2.10)		
Sidechain outliers	138945	5648 (2.10-2.10)		

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain	
1	А	252	85%	15%
1	В	252	84%	16%

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
2	DHS	А	301	Х	-	-	-
2	DHS	В	301	Х	-	-	-



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2 Entry composition (i)

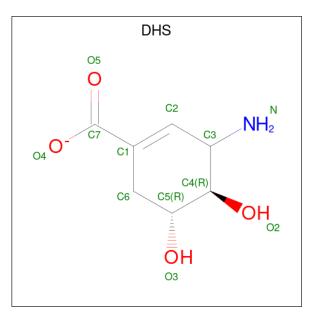
There are 3 unique types of molecules in this entry. The entry contains 4036 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (3-DEHYDROQUINATE DEHYDRATASE).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	252	Total	С	Ν	0	\mathbf{S}	0	1	0
	I A	202	1938	1221	336	367	14	0	1	U
1	D	252	Total	С	Ν	0	S	0	1	0
	D	2.02	1939	1222	335	368	14	0	1	U

• Molecule 2 is 3-AMINO-4,5-DIHYDROXY-CYCLOHEX-1-ENECARBOXYLATE (three-letter code: DHS) (formula: $C_7H_{10}NO_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total C O 11 7 4	0	0
2	В	1	Total C O 11 7 4	0	0

• Molecule 3 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	60	Total O 60 60	0	0
3	В	77	Total O 77 77	0	0

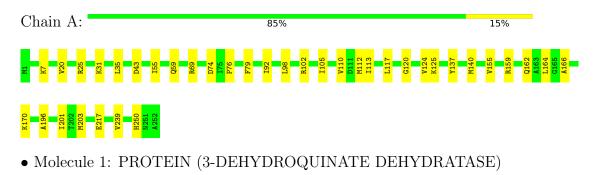


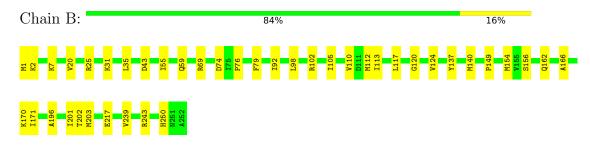
3 Residue-property plots (i)

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. 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: PROTEIN (3-DEHYDROQUINATE DEHYDRATASE)







4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	P 1 21 1	Depositor	
Cell constants	60.49Å 45.39 Å 85.47 Å	Depositor	
a, b, c, α , β , γ	90.00° 95.48° 90.00°	Depositor	
Resolution (Å)	12.00 - 2.10	Depositor	
% Data completeness	86.1 (12.00-2.10)	Depositor	
(in resolution range)	00.1 (12.00 2.10)	Depositor	
R_{merge}	0.10	Depositor	
R _{sym}	(Not available)	Depositor	
Refinement program	X-PLOR 3.1	Depositor	
R, R_{free}	0.199 , 0.247	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	4036	wwPDB-VP	
Average B, all atoms $(Å^2)$	22.0	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: DHS

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	А	0.47	0/1973	0.67	0/2672
1	В	0.48	0/1974	0.67	0/2673
All	All	0.47	0/3947	0.67	0/5345

There are no bond length outliers.

There are no bond angle outliers.

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	А	1938	0	1964	17	0
1	В	1939	0	1964	18	0
2	А	11	0	7	0	0
2	В	11	0	7	0	0
3	А	60	0	0	1	0
3	В	77	0	0	0	0
All	All	4036	0	3942	35	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.

The worst 5 of 35 close contacts within the same asymmetric unit are listed below, sorted by their



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:GLN:HE22	1:B:196:ALA:HA	1.66	0.60
1:A:162:GLN:HE22	1:A:196:ALA:HA	1.67	0.60
1:A:112:MET:HG2	1:A:137:TYR:HB2	1.84	0.57
1:B:217:GLU:OE2	1:B:250:HIS:HD2	1.87	0.57
1:A:217:GLU:OE2	1:A:250:HIS:HD2	1.88	0.56

clash magnitude.

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	Percer	ntiles
1	А	251/252~(100%)	247~(98%)	4(2%)	0	100	100
1	В	251/252~(100%)	246 (98%)	5 (2%)	0	100	100
All	All	502/504~(100%)	493 (98%)	9~(2%)	0	100	100

There are no Ramachandran outliers to report.

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	А	210/209~(100%)	204~(97%)	6 (3%)	42 46		
1	В	210/209~(100%)	203~(97%)	7 (3%)	38 40		

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Mol	Chain	Analysed Rotameric Out		Outliers	Percentiles
All	All	420/418~(100%)	407~(97%)	13 (3%)	40 43

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	59	GLN
1	В	69	ARG
1	В	243	ARG
1	В	156	SER
1	В	203	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	В	90	GLN
1	В	162	GLN
1	В	250	HIS
1	В	192	GLN
1	А	250	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are 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).

Mal	Type	Chain	Res Lin		Dec	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2		
2	DHS	А	301	1	11,11,12	1.01	0	$12,\!15,\!17$	1.82	3 (25%)		
2	DHS	В	301	1	11,11,12	1.06	0	12,15,17	1.81	5 (41%)		

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	DHS	А	301	1	1/1/4/6	1/4/17/20	0/1/1/1
2	DHS	В	301	1	1/1/4/6	0/4/17/20	0/1/1/1

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	А	301	DHS	O2-C4-C3	3.75	115.92	109.52
2	В	301	DHS	O2-C4-C3	3.35	115.23	109.52
2	А	301	DHS	C3-C4-C5	3.32	114.92	110.69
2	В	301	DHS	C3-C4-C5	3.24	114.81	110.69
2	В	301	DHS	O5-C7-C1	-2.32	117.59	121.59

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	А	301	DHS	C3
2	В	301	DHS	C3

All (1) torsion outliers are listed below:

Μ	ol	Chain	Res	Type	Atoms
4	2	А	301	DHS	C2-C1-C7-O5

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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

