



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:48 PM UTC

PDB ID : 1EDB / pdb_00001edb
Title : CRYSTALLOGRAPHIC AND FLUORESCENCE STUDIES OF THE INTERACTION OF HALOALKANE DEHALOGENASE WITH HALIDE IONS: STUDIES WITH HALIDE COMPOUNDS REVEAL A HALIDE BINDING SITE IN THE ACTIVE SITE
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Deposited on : 1993-05-13
Resolution : 2.01 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

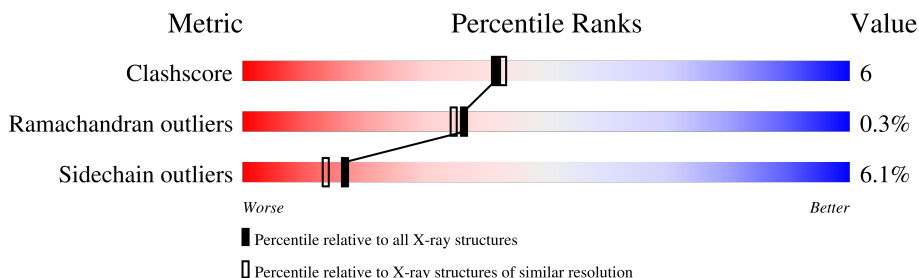
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	310	 70% 26% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2671 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 HALOALKANE DEHALOGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2479	1596	406	462	15			

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 3 is water.

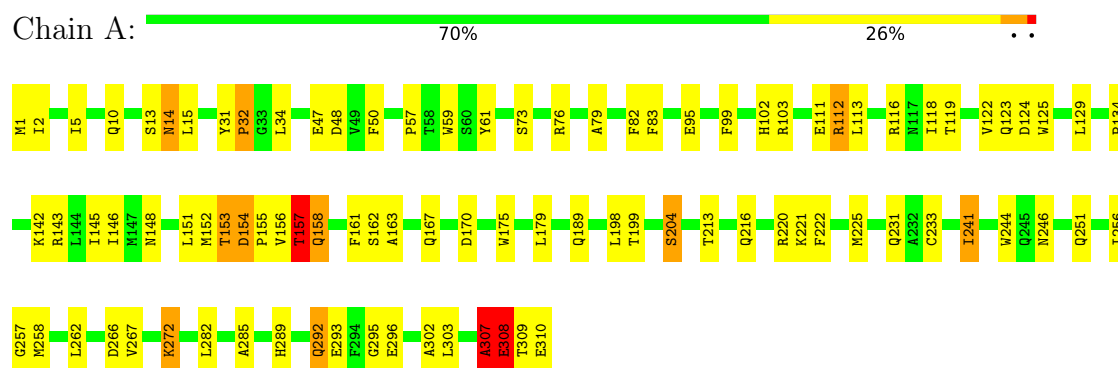
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	191	Total	O	0	0
			191	191		

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: HALOALKANE DEHALOGENASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	95.40 Å 72.90 Å 41.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.01	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-2.01)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.175 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2671	wwPDB-VP
Average B, all atoms (Å ²)	12.0	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: CL

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	0.91	0/2552	2.02	77/3470 (2.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	307	ALA	CB-CA-C	-11.85	85.85	109.67
1	A	308	GLU	CB-CA-C	9.79	128.04	110.72
1	A	216	GLN	N-CA-C	9.54	124.65	112.92
1	A	295	GLY	N-CA-C	9.27	124.64	112.77
1	A	308	GLU	CB-CG-CD	9.13	128.13	112.60
1	A	296	GLU	CA-C-O	8.09	129.37	120.63
1	A	307	ALA	CA-C-O	7.82	128.75	119.60
1	A	179	LEU	N-CA-C	7.73	120.83	111.40
1	A	285	ALA	N-CA-C	7.68	119.65	111.28
1	A	154	ASP	CA-CB-CG	-7.54	105.06	112.60
1	A	13	SER	CB-CA-C	-7.36	99.33	110.88
1	A	163	ALA	N-CA-C	7.34	119.28	111.28
1	A	154	ASP	N-CA-CB	7.30	118.21	109.74
1	A	267	VAL	CA-C-N	7.24	129.98	120.28
1	A	267	VAL	C-N-CA	7.24	129.98	120.28
1	A	129	LEU	CA-C-N	7.18	127.95	119.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129	LEU	C-N-CA	7.18	127.95	119.98
1	A	308	GLU	CA-C-N	7.16	135.22	121.54
1	A	308	GLU	C-N-CA	7.16	135.22	121.54
1	A	302	ALA	CA-C-O	-7.13	112.86	120.42
1	A	14	ASN	N-CA-C	7.06	120.84	112.93
1	A	118	ILE	N-CA-C	7.01	118.06	109.30
1	A	272	LYS	CA-C-O	6.65	127.62	120.10
1	A	231	GLN	N-CA-C	6.58	118.54	111.36
1	A	233	CYS	CA-C-O	6.54	127.90	120.90
1	A	272	LYS	O-C-N	-6.52	114.59	122.22
1	A	258	MET	N-CA-C	6.49	120.29	112.38
1	A	246	ASN	CA-CB-CG	6.41	119.01	112.60
1	A	59	TRP	CA-C-O	-6.36	114.50	121.31
1	A	119	THR	N-CA-C	-6.31	96.82	107.99
1	A	134	PRO	N-CA-CB	6.26	110.31	103.30
1	A	146	ILE	N-CA-C	6.22	116.81	108.11
1	A	157	THR	CB-CA-C	6.21	121.40	110.85
1	A	153	THR	O-C-N	-6.16	115.07	122.65
1	A	213	THR	N-CA-C	6.16	119.90	112.38
1	A	199	THR	N-CA-C	-6.16	100.81	110.36
1	A	256	ILE	N-CA-C	6.08	116.67	108.17
1	A	153	THR	N-CA-CB	-6.07	101.76	110.44
1	A	216	GLN	OE1-CD-NE2	-5.95	116.65	122.60
1	A	221	LYS	N-CA-C	5.94	119.71	112.23
1	A	102	HIS	CA-C-O	5.93	126.83	120.24
1	A	145	ILE	N-CA-C	-5.85	99.21	107.75
1	A	2	ILE	N-CA-C	-5.79	99.54	107.99
1	A	95	GLU	CA-C-N	5.75	129.05	120.31
1	A	95	GLU	C-N-CA	5.75	129.05	120.31
1	A	103	ARG	O-C-N	5.72	128.68	122.15
1	A	82	PHE	CA-C-O	-5.69	115.36	121.56
1	A	57	PRO	N-CA-C	-5.66	97.38	112.10
1	A	282	LEU	N-CA-C	-5.66	99.29	108.41
1	A	204	SER	CB-CA-C	5.63	121.48	110.67
1	A	61	TYR	CA-C-O	5.62	126.23	119.61
1	A	175	TRP	CA-CB-CG	5.60	124.23	113.60
1	A	50	PHE	CA-CB-CG	-5.59	108.21	113.80
1	A	241	ILE	CA-C-O	5.55	126.72	120.95
1	A	32	PRO	N-CA-C	5.55	119.21	110.50
1	A	303	LEU	N-CA-CB	5.53	118.25	110.12
1	A	10	GLN	CB-CG-CD	5.52	121.99	112.60
1	A	48	ASP	CA-CB-CG	5.49	118.09	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	156	VAL	N-CA-C	5.43	116.92	111.00
1	A	198	LEU	CA-C-O	-5.42	115.81	121.55
1	A	47	GLU	CB-CG-CD	5.37	121.73	112.60
1	A	257	GLY	N-CA-C	-5.37	100.45	113.18
1	A	293	GLU	CB-CA-C	5.37	121.65	110.32
1	A	244	TRP	CA-C-O	5.35	126.22	120.55
1	A	189	GLN	O-C-N	-5.27	116.39	122.09
1	A	76	ARG	N-CA-C	-5.26	101.11	109.96
1	A	167	GLN	CB-CA-C	-5.21	101.36	109.55
1	A	103	ARG	CB-CA-C	-5.19	102.03	110.85
1	A	79	ALA	O-C-N	5.18	125.42	121.27
1	A	285	ALA	CA-C-O	-5.18	115.06	120.55
1	A	83	PHE	N-CA-C	-5.17	102.73	110.23
1	A	158	GLN	CA-C-N	5.16	124.96	119.28
1	A	158	GLN	C-N-CA	5.16	124.96	119.28
1	A	122	VAL	N-CA-C	5.09	117.35	108.90
1	A	152	MET	O-C-N	-5.07	115.92	122.61
1	A	170	ASP	CA-CB-CG	5.04	117.64	112.60
1	A	111	GLU	CA-C-O	-5.02	115.53	120.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	307	ALA	Mainchain

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	2479	0	2379	31	0
2	A	1	0	0	0	0
3	A	191	0	0	5	0
All	All	2671	0	2379	31	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 (31) 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:GLN:HE21	1:A:292:GLN:H	1.09	0.93
1:A:225:MET:HE1	3:A:592:HOH:O	1.82	0.79
1:A:153:THR:HG21	1:A:158:GLN:HB2	1.68	0.75
1:A:142:LYS:HG2	1:A:143:ARG:HG3	1.69	0.74
1:A:112:ARG:HG3	1:A:112:ARG:HH11	1.54	0.71
1:A:124:ASP:OD1	1:A:289:HIS:NE2	2.26	0.66
1:A:220:ARG:HD3	3:A:470:HOH:O	1.97	0.64
1:A:99:PHE:HA	3:A:592:HOH:O	1.98	0.63
1:A:308:GLU:HB2	3:A:587:HOH:O	2.02	0.59
1:A:309:THR:O	1:A:309:THR:HG22	2.04	0.57
1:A:262:LEU:HD23	3:A:483:HOH:O	2.04	0.56
1:A:154:ASP:CG	1:A:157:THR:HG22	2.31	0.56
1:A:154:ASP:HB2	1:A:155:PRO:HD2	1.88	0.54
1:A:112:ARG:HH11	1:A:112:ARG:CG	2.21	0.54
1:A:292:GLN:H	1:A:292:GLN:NE2	1.92	0.53
1:A:309:THR:O	1:A:310:GLU:HG2	2.10	0.52
1:A:307:ALA:HB3	1:A:308:GLU:HG3	1.93	0.51
1:A:154:ASP:HB2	1:A:155:PRO:CD	2.45	0.47
1:A:251:GLN:HE22	1:A:309:THR:HB	1.82	0.45
1:A:151:LEU:HD13	1:A:241:ILE:HG13	1.99	0.45
1:A:292:GLN:HE21	1:A:292:GLN:N	1.93	0.43
1:A:112:ARG:CG	1:A:112:ARG:NH1	2.78	0.43
1:A:161:PHE:CD1	1:A:161:PHE:N	2.86	0.43
1:A:272:LYS:O	1:A:272:LYS:HG2	2.12	0.43
1:A:154:ASP:OD1	1:A:157:THR:HG22	2.20	0.42
1:A:31:TYR:N	1:A:32:PRO:CD	2.83	0.42
1:A:125:TRP:CH2	1:A:225:MET:CE	3.01	0.42
1:A:307:ALA:C	1:A:309:THR:H	2.26	0.42
1:A:251:GLN:NE2	1:A:309:THR:HB	2.36	0.41
1:A:154:ASP:OD2	1:A:157:THR:HG22	2.20	0.40
1:A:5:ILE:HG21	1:A:5:ILE:HD13	1.74	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	308/310 (99%)	291 (94%)	16 (5%)	1 (0%)	36	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	148	ASN

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	262/262 (100%)	246 (94%)	16 (6%)	17	14

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	14	ASN
1	A	15	LEU
1	A	34	LEU
1	A	73	SER
1	A	112	ARG
1	A	113	LEU
1	A	116	ARG
1	A	123	GLN
1	A	157	THR

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Mol	Chain	Res	Type
1	A	162	SER
1	A	204	SER
1	A	222	PHE
1	A	266	ASP
1	A	292	GLN
1	A	308	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	23	ASN
1	A	104	ASN
1	A	123	GLN
1	A	251	GLN
1	A	276	ASN
1	A	292	GLN
1	A	297	GLN
1	A	305	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 1 ligands modelled in this entry, 1 is 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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.