



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 02:26 am BST

PDB ID : 6I9V  
Title : Crystal structure of the halohydrin dehalogenase HheG T123G mutant  
Authors : Kluenemann, T.; Blankenfeldt, W.; Schallmeyer, A.  
Deposited on : 2018-11-26  
Resolution : 2.80 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](mailto: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.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

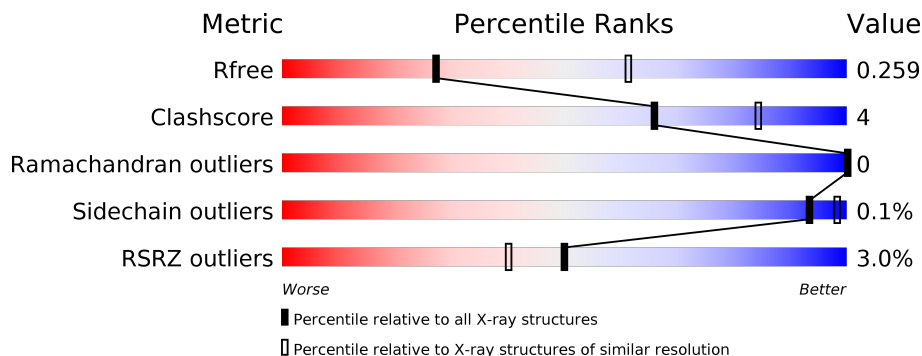
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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.



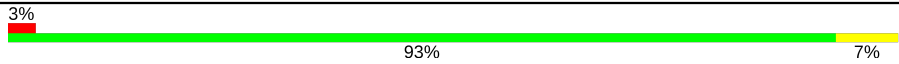
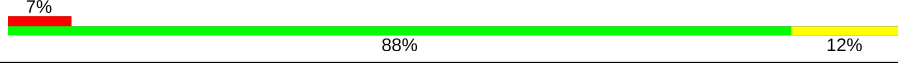
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 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	258	
1	B	258	
1	C	258	
1	D	258	
1	E	258	
1	F	258	

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Mol	Chain	Length	Quality of chain
1	G	258	 3% 93% 7%
1	H	258	 7% 88% 12%

## 2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 30005 atoms, of which 14831 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 Putative oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	257	3732	1175	1844	336	362	15	0	2	0
1	B	255	3730	1173	1848	336	359	14	0	2	0
1	C	257	3747	1178	1855	337	362	15	0	2	0
1	D	258	3776	1187	1873	339	361	16	0	3	0
1	E	257	3747	1178	1855	337	362	15	0	2	0
1	F	255	3727	1172	1847	335	358	15	0	2	0
1	G	257	3747	1178	1855	337	362	15	0	2	0
1	H	257	3750	1178	1854	340	364	14	0	2	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	GLY	THR	engineered mutation	UNP M5A5Y8
B	123	GLY	THR	engineered mutation	UNP M5A5Y8
C	123	GLY	THR	engineered mutation	UNP M5A5Y8
D	123	GLY	THR	engineered mutation	UNP M5A5Y8
E	123	GLY	THR	engineered mutation	UNP M5A5Y8
F	123	GLY	THR	engineered mutation	UNP M5A5Y8
G	123	GLY	THR	engineered mutation	UNP M5A5Y8
H	123	GLY	THR	engineered mutation	UNP M5A5Y8

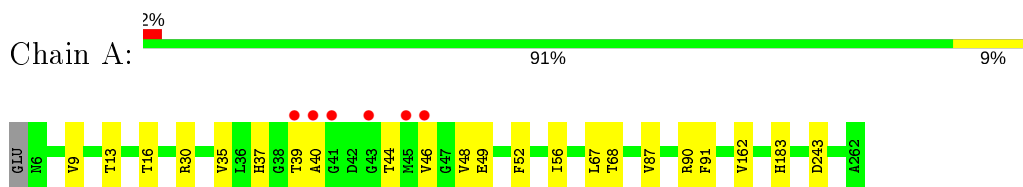
- Molecule 2 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
2	A	5	Total O 5 5	0	0
2	B	4	Total O 4 4	0	0
2	C	5	Total O 5 5	0	0
2	D	9	Total O 9 9	0	0
2	E	12	Total O 12 12	0	0
2	F	7	Total O 7 7	0	0
2	G	4	Total O 4 4	0	0
2	H	3	Total O 3 3	0	0

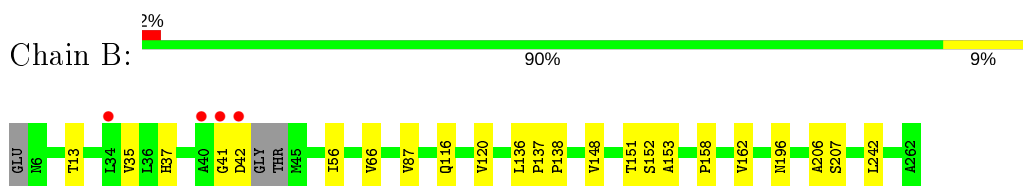
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

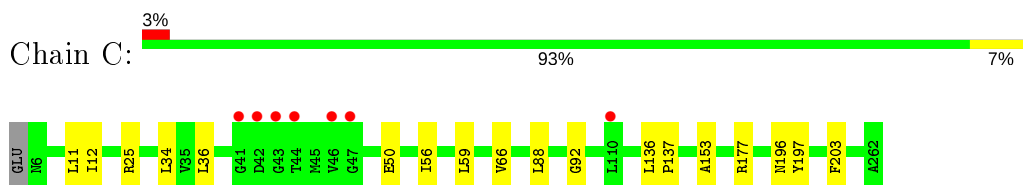
- Molecule 1: Putative oxidoreductase



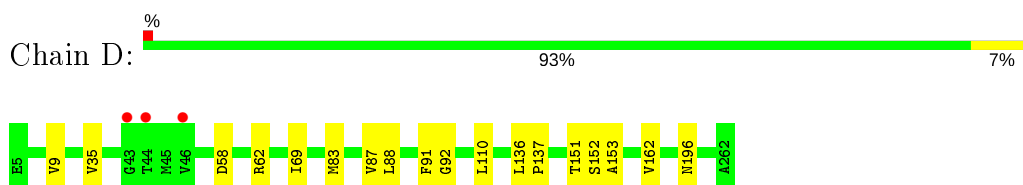
- Molecule 1: Putative oxidoreductase



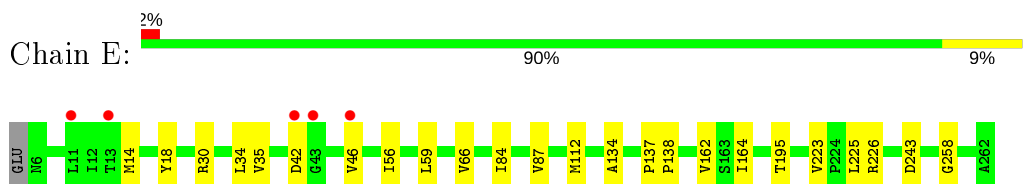
- Molecule 1: Putative oxidoreductase



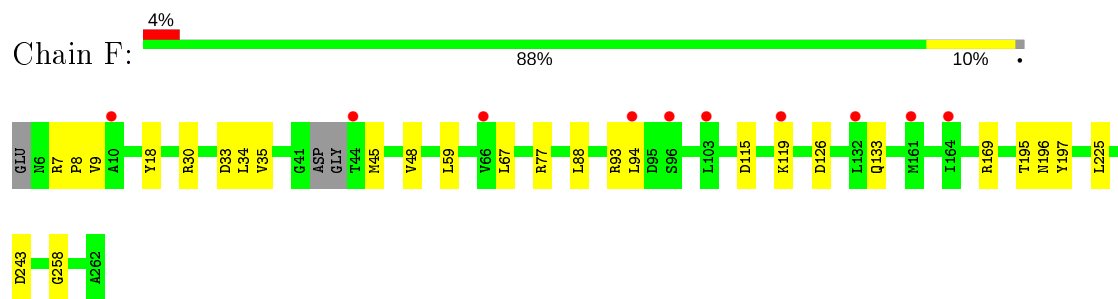
- Molecule 1: Putative oxidoreductase



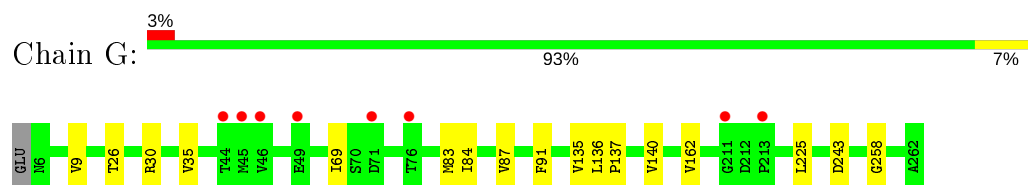
- Molecule 1: Putative oxidoreductase



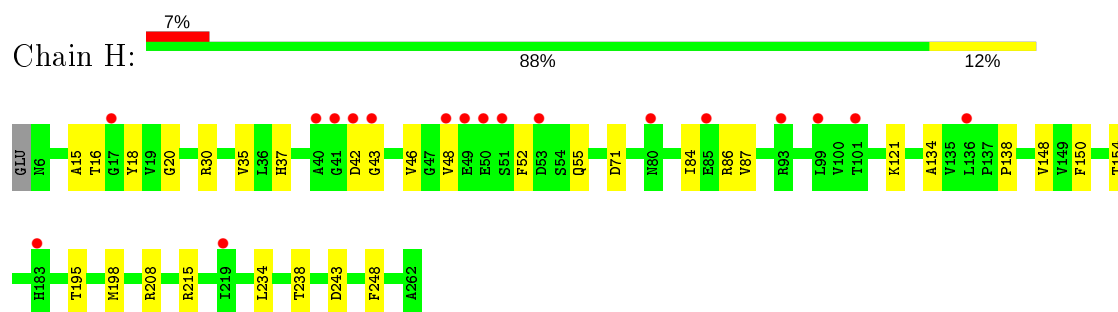
- Molecule 1: Putative oxidoreductase



- Molecule 1: Putative oxidoreductase



- Molecule 1: Putative oxidoreductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.03Å 141.32Å 172.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	172.52 – 2.80 172.53 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (172.52-2.80) 99.7 (172.53-2.80)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.54 (at 2.82Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.222 , 0.259 0.222 , 0.259	Depositor DCC
$R_{free}$ test set	3078 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.1	Xtrriage
Anisotropy	0.611	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 48.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	30005	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.62 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.6739e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

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	0.25	0/1925	0.43	0/2608
1	B	0.25	0/1918	0.43	0/2595
1	C	0.25	0/1929	0.43	0/2612
1	D	0.25	0/1943	0.44	0/2629
1	E	0.25	0/1929	0.44	0/2612
1	F	0.25	0/1916	0.43	0/2593
1	G	0.25	0/1929	0.43	0/2612
1	H	0.25	0/1933	0.44	0/2617
All	All	0.25	0/15422	0.43	0/20878

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	A	1888	1844	1844	16	0
1	B	1882	1848	1848	15	0
1	C	1892	1855	1855	10	0
1	D	1903	1873	1875	11	0
1	E	1892	1855	1855	17	0
1	F	1880	1847	1847	20	0
1	G	1892	1855	1855	12	0
1	H	1896	1854	1854	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	5	0	0	0	0
2	B	4	0	0	0	0
2	C	5	0	0	0	0
2	D	9	0	0	0	0
2	E	12	0	0	0	0
2	F	7	0	0	2	0
2	G	4	0	0	0	0
2	H	3	0	0	1	0
All	All	15174	14831	14833	120	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 120 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:G:35:VAL:HG11	1:G:87:VAL:HG22	1.51	0.91
1:E:35:VAL:HG11	1:E:87:VAL:HG12	1.53	0.90
1:A:35:VAL:HG11	1:A:87:VAL:HG22	1.60	0.82
1:F:7:ARG:NH1	1:F:33:ASP:OD1	2.17	0.76
1:H:84:ILE:HD11	1:H:138:PRO:HG3	1.66	0.75

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	257/258 (100%)	238 (93%)	19 (7%)	0	100 100
1	B	253/258 (98%)	243 (96%)	10 (4%)	0	100 100
1	C	257/258 (100%)	242 (94%)	15 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	259/258 (100%)	241 (93%)	18 (7%)	0	100	100
1	E	257/258 (100%)	243 (95%)	14 (5%)	0	100	100
1	F	253/258 (98%)	238 (94%)	15 (6%)	0	100	100
1	G	257/258 (100%)	246 (96%)	11 (4%)	0	100	100
1	H	257/258 (100%)	244 (95%)	13 (5%)	0	100	100
All	All	2050/2064 (99%)	1935 (94%)	115 (6%)	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	A	192/196 (98%)	192 (100%)	0	100	100
1	B	192/196 (98%)	192 (100%)	0	100	100
1	C	193/196 (98%)	193 (100%)	0	100	100
1	D	194/196 (99%)	194 (100%)	0	100	100
1	E	193/196 (98%)	193 (100%)	0	100	100
1	F	192/196 (98%)	192 (100%)	0	100	100
1	G	193/196 (98%)	193 (100%)	0	100	100
1	H	193/196 (98%)	192 (100%)	1 (0%)	88	96
All	All	1542/1568 (98%)	1541 (100%)	1 (0%)	93	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	248	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	257/258 (99%)	0.28	6 (2%) 60 51	29, 57, 116, 203	0
1	B	255/258 (98%)	0.27	4 (1%) 72 66	38, 60, 112, 189	0
1	C	257/258 (99%)	0.27	7 (2%) 54 44	43, 65, 112, 193	0
1	D	258/258 (100%)	0.13	3 (1%) 79 73	28, 42, 97, 168	0
1	E	257/258 (99%)	0.28	5 (1%) 66 59	35, 53, 99, 140	0
1	F	255/258 (98%)	0.52	10 (3%) 39 29	50, 72, 111, 164	0
1	G	257/258 (99%)	0.32	8 (3%) 49 39	35, 65, 122, 167	0
1	H	257/258 (99%)	0.64	18 (7%) 16 9	53, 96, 158, 201	0
All	All	2053/2064 (99%)	0.34	61 (2%) 50 40	28, 63, 123, 203	0

The worst 5 of 61 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	44	THR	6.6
1	D	44	THR	6.4
1	A	40	ALA	6.1
1	G	46	VAL	6.0
1	C	43	GLY	5.0

### 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 carbohydrates in this entry.

## 6.4 Ligands

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.