



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1QST  
Title : CRYSTAL STRUCTURE OF TETRAHYMENA GCN5  
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Deposited on : 1999-06-23  
Resolution : 1.70 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

<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>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (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

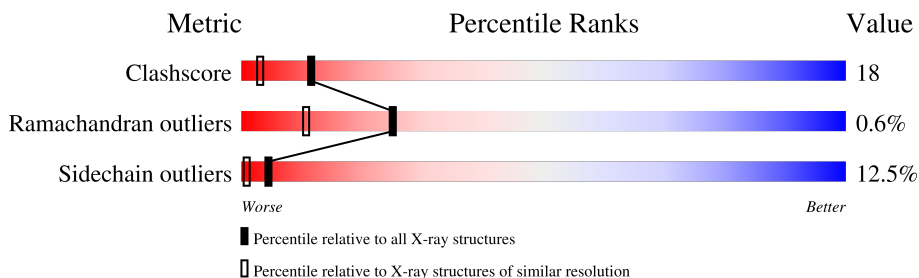
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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  $\geq 3$ , 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  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	160	 66% 26% 8%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1456 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 TGCN5 HISTONE ACETYL TRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	160	1345	871	232	233	9	0	0	0

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	15	8	2	4	1	0	0

- Molecule 3 is water.

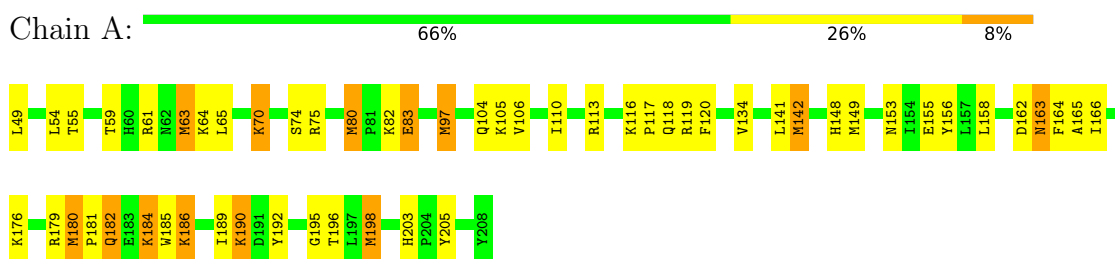
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	96	Total	O	0	0
			96	96		

### 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: TGCN5 HISTONE ACETYL TRANSFERASE



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.10Å 64.10Å 97.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 1.70	Depositor
% Data completeness (in resolution range)	99.1 (8.00-1.70)	Depositor
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.244 , 0.278	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	1456	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	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: EPE

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	0.51	6/1378 (0.4%)	0.63	0/1848

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	63	MET	SD-CE	5.35	2.07	1.77
1	A	142	MET	SD-CE	5.30	2.07	1.77
1	A	198	MET	SD-CE	5.26	2.07	1.77
1	A	80	MET	SD-CE	5.22	2.07	1.77
1	A	180	MET	SD-CE	5.14	2.06	1.77
1	A	97	MET	SD-CE	5.02	2.06	1.77

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	1345	0	1349	48	0
2	A	15	0	18	1	0
3	A	96	0	0	5	2
All	All	1456	0	1367	48	2

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 18.

All (48) 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:149:MET:SD	1:A:149:MET:CE	2.05	1.45
1:A:97:MET:CE	1:A:97:MET:SD	2.05	1.44
1:A:180:MET:CE	1:A:180:MET:SD	2.06	1.43
1:A:142:MET:SD	1:A:142:MET:CE	2.07	1.43
1:A:198:MET:CE	1:A:198:MET:SD	2.07	1.43
1:A:63:MET:CE	1:A:63:MET:SD	2.07	1.41
1:A:80:MET:CE	1:A:80:MET:SD	2.07	1.40
1:A:203:HIS:HD2	1:A:205:TYR:H	1.34	0.75
1:A:182:GLN:HB2	1:A:186:LYS:NZ	2.09	0.68
1:A:190:LYS:HD3	1:A:192:TYR:OH	1.94	0.66
1:A:110:ILE:HG13	1:A:141:LEU:HD21	1.83	0.61
1:A:63:MET:CE	1:A:63:MET:HB3	2.30	0.61
1:A:116:LYS:HB2	1:A:117:PRO:HD3	1.83	0.59
1:A:203:HIS:HE1	3:A:363:HOH:O	1.86	0.58
1:A:166:ILE:HD13	1:A:176:LYS:HZ1	1.68	0.58
1:A:182:GLN:HA	1:A:185:TRP:NE1	2.21	0.54
1:A:63:MET:CE	1:A:63:MET:CG	2.87	0.53
1:A:74:SER:OG	1:A:82:LYS:HD2	2.08	0.52
1:A:63:MET:HB3	1:A:63:MET:HE3	1.91	0.52
1:A:190:LYS:HD3	1:A:192:TYR:CZ	2.44	0.51
1:A:165:ALA:HB2	2:A:401:EPE:H71	1.92	0.51
1:A:180:MET:CE	1:A:180:MET:CG	2.89	0.51
1:A:181:PRO:O	1:A:184:LYS:HB2	2.12	0.49
1:A:142:MET:CE	1:A:142:MET:CG	2.91	0.49
1:A:166:ILE:HG23	1:A:176:LYS:HZ3	1.78	0.49
1:A:80:MET:CE	1:A:80:MET:CG	2.91	0.48
1:A:119:ARG:HH21	1:A:153:ASN:HB3	1.78	0.48
1:A:148:HIS:HE1	3:A:325:HOH:O	1.95	0.48
1:A:182:GLN:HB2	1:A:186:LYS:HZ2	1.77	0.48
1:A:198:MET:CE	1:A:198:MET:CG	2.89	0.48
1:A:54:LEU:HD21	1:A:65:LEU:CB	2.43	0.48
1:A:59:THR:O	1:A:63:MET:HG2	2.13	0.48
1:A:54:LEU:HD21	1:A:65:LEU:HB2	1.96	0.47
1:A:162:ASP:C	1:A:164:PHE:H	2.18	0.47
1:A:97:MET:CE	1:A:97:MET:CG	2.92	0.47
1:A:149:MET:CE	1:A:149:MET:CG	2.91	0.46
1:A:155:GLU:HG3	1:A:156:TYR:CD1	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:ASN:HA	1:A:166:ILE:HG13	1.98	0.46
1:A:158:LEU:HD11	1:A:180:MET:HE3	1.99	0.44
1:A:118:GLN:HB3	1:A:120:PHE:CE2	2.53	0.43
1:A:63:MET:CE	1:A:63:MET:CB	2.96	0.42
1:A:55:THR:HA	3:A:310:HOH:O	2.18	0.42
1:A:166:ILE:HD13	1:A:176:LYS:NZ	2.33	0.41
1:A:83:GLU:HB3	3:A:360:HOH:O	2.19	0.41
1:A:180:MET:HA	1:A:181:PRO:HD3	1.91	0.41
1:A:70:LYS:HE3	1:A:70:LYS:HB3	1.93	0.41
1:A:158:LEU:HD12	1:A:189:ILE:HD12	2.02	0.40
1:A:148:HIS:HD2	3:A:349:HOH:O	2.04	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:321:HOH:O	3:A:321:HOH:O[5_555]	2.08	0.12
3:A:344:HOH:O	3:A:364:HOH:O[5_555]	2.16	0.04

## 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	158/160 (99%)	150 (95%)	7 (4%)	1 (1%)	25 11

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	GLY



### 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	144/144 (100%)	126 (88%)	18 (12%)	<b>4</b> <b>1</b>

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	LEU
1	A	61	ARG
1	A	64	LYS
1	A	70	LYS
1	A	75	ARG
1	A	83	GLU
1	A	104	GLN
1	A	105	LYS
1	A	106	VAL
1	A	113	ARG
1	A	134	VAL
1	A	163	ASN
1	A	179	ARG
1	A	182	GLN
1	A	184	LYS
1	A	186	LYS
1	A	190	LYS
1	A	196	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	76	GLN
1	A	114	GLN
1	A	133	GLN
1	A	148	HIS
1	A	182	GLN
1	A	203	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](#)

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	EPE	A	401	-	15,15,15	1.90	3 (20%)	18,20,20	1.96	5 (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	EPE	A	401	-	-	2/9/19/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	EPE	O3S-S	5.28	1.66	1.47
2	A	401	EPE	C10-S	2.93	1.81	1.77
2	A	401	EPE	C3-N4	2.07	1.52	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	EPE	O2S-S-C10	5.38	113.39	106.92
2	A	401	EPE	O3S-S-O1S	-3.56	102.57	111.27
2	A	401	EPE	O1S-S-C10	-2.30	104.14	106.92
2	A	401	EPE	O2S-S-O1S	2.26	121.77	113.95
2	A	401	EPE	C2-C3-N4	2.13	115.02	110.64

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	EPE	N4-C7-C8-O8
2	A	401	EPE	C10-C9-N1-C6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	EPE	1	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 [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.