



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 28, 2025 – 07:01 PM EDT

PDB ID : 3H2T / pdb\_00003h2t  
Title : Crystal structure of gene product 6, baseplate protein of bacteriophage T4  
Authors : Aksyuk, A.A.; Leiman, P.G.; Shneider, M.M.; Mesyanzhinov, V.V.; Rossmann, M.G.  
Deposited on : 2009-04-14  
Resolution : 3.20 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.

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	:	4-5-2 with Phenix2.0rc1
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

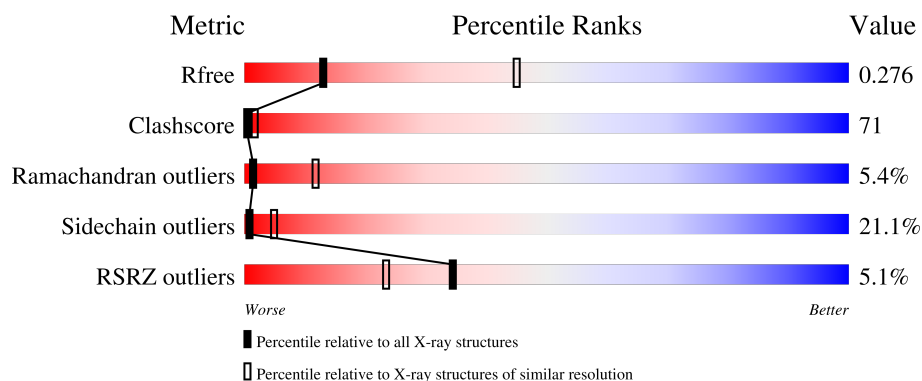
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	164625	1370 (3.20-3.20)
Clashscore	180529	1497 (3.20-3.20)
Ramachandran outliers	177936	1479 (3.20-3.20)
Sidechain outliers	177891	1478 (3.20-3.20)
RSRZ outliers	164620	1371 (3.20-3.20)

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  $\leq 5\%$ . 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	335	<div> <div>5%</div> <div>30%</div> <div>49%</div> <div>15%</div> <div>• •</div> </div>
1	B	335	<div> <div>5%</div> <div>33%</div> <div>40%</div> <div>19%</div> <div>• •</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5251 atoms, of which 2 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 Baseplate structural protein Gp6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	0	0
			2622	1667	424	528	3			
1	B	324	Total	C	N	O	S	0	0	0
			2608	1658	422	525	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	661	LEU	-	expression tag	UNP P19060
A	662	GLU	-	expression tag	UNP P19060
A	663	HIS	-	expression tag	UNP P19060
A	664	HIS	-	expression tag	UNP P19060
A	665	HIS	-	expression tag	UNP P19060
A	666	HIS	-	expression tag	UNP P19060
A	667	HIS	-	expression tag	UNP P19060
A	668	HIS	-	expression tag	UNP P19060
B	661	LEU	-	expression tag	UNP P19060
B	662	GLU	-	expression tag	UNP P19060
B	663	HIS	-	expression tag	UNP P19060
B	664	HIS	-	expression tag	UNP P19060
B	665	HIS	-	expression tag	UNP P19060
B	666	HIS	-	expression tag	UNP P19060
B	667	HIS	-	expression tag	UNP P19060
B	668	HIS	-	expression tag	UNP P19060

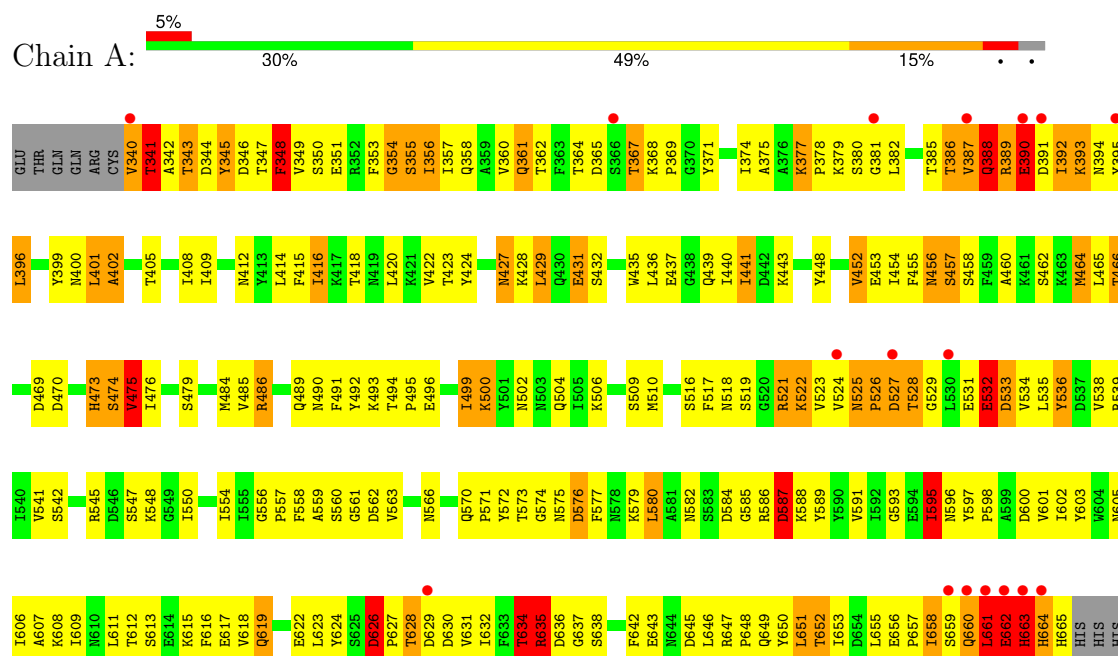
- Molecule 2 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	8	Total	O		0	0
			8	8			
2	B	11	Total	H	O	0	0
			13	2	11		

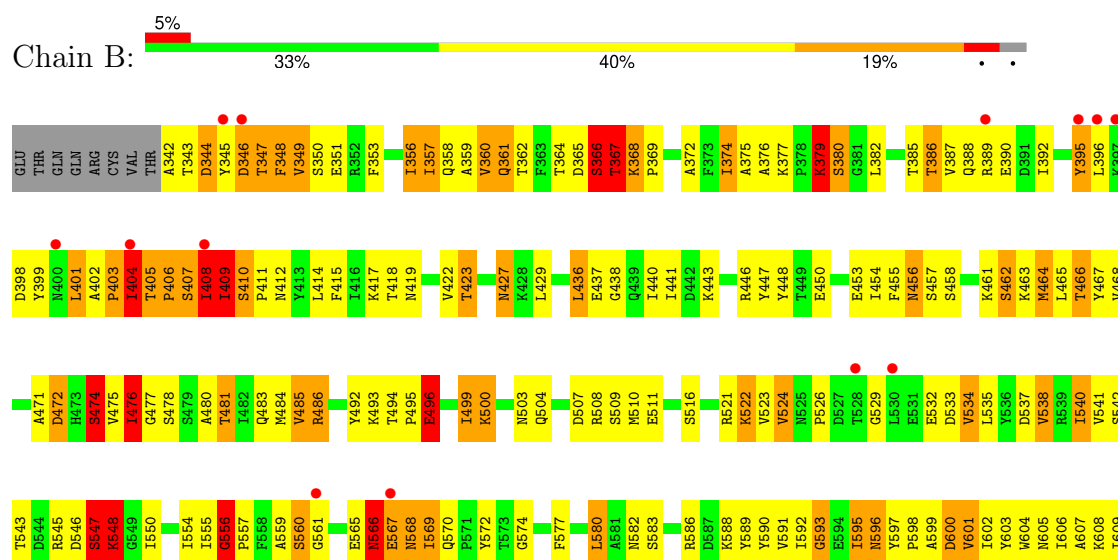
### 3 Residue-property plots

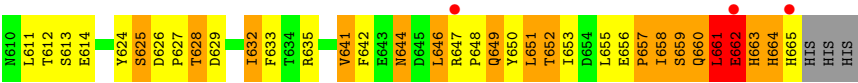
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Baseplate structural protein Gp6



#### • Molecule 1: Baseplate structural protein Gp6





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.77Å 94.58Å 136.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.86 – 3.20 44.86 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (44.86-3.20) 99.6 (44.86-3.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.57 (at 3.19Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.230 , 0.322 0.272 , 0.276	Depositor DCC
$R_{free}$ test set	853 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	80.9	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 88.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	5251	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% of the height of the origin peak. No significant pseudotranslation is detected.*

<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	0.67	0/2677	1.25	42/3637 (1.2%)
1	B	0.73	3/2663 (0.1%)	1.29	42/3617 (1.2%)
All	All	0.70	3/5340 (0.1%)	1.27	84/7254 (1.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	409	ILE	CA-CB	-9.64	1.48	1.55
1	B	476	ILE	CA-CB	-6.12	1.45	1.54
1	B	408	ILE	CA-CB	-5.83	1.47	1.54

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	389	ARG	CB-CA-C	-21.79	71.19	111.06
1	B	548	LYS	N-CA-C	17.48	137.85	113.56
1	B	405	THR	C-N-CD	-16.64	56.78	125.00
1	A	646	LEU	N-CA-CB	-14.18	89.50	110.49
1	B	534	VAL	N-CA-CB	-12.80	90.11	111.23

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	2622	0	2546	399	28
1	B	2608	0	2530	351	16
2	A	8	0	0	3	0
2	B	11	2	0	5	0
All	All	5249	2	5076	731	28

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 71.

The worst 5 of 731 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:559:ALA:C	1:A:561:GLY:HA3	1.49	1.37
1:A:661:LEU:HD13	1:A:662:GLU:N	1.06	1.36
1:A:385:THR:CG2	1:A:389:ARG:N	1.88	1.36
1:B:661:LEU:C	1:B:661:LEU:HD13	1.48	1.32
1:A:525:ASN:CB	1:A:526:PRO:HD2	1.59	1.31

The worst 5 of 28 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)
1:A:381:GLY:CA	1:A:527:ASP:CG[4_455]	0.41	1.79
1:A:663:HIS:C	1:B:662:GLU:OE1[3_554]	0.57	1.63
1:A:381:GLY:C	1:A:527:ASP:OD2[4_455]	0.68	1.52
1:A:663:HIS:O	1:B:662:GLU:CD[3_554]	0.68	1.52
1:A:663:HIS:CB	1:B:662:GLU:OE2[3_554]	0.89	1.31

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	324/335 (97%)	260 (80%)	48 (15%)	16 (5%)	2	14
1	B	322/335 (96%)	261 (81%)	42 (13%)	19 (6%)	1	10
All	All	646/670 (96%)	521 (81%)	90 (14%)	35 (5%)	1	12

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	348	PHE
1	A	354	GLY
1	A	392	ILE
1	A	393	LYS
1	A	526	PRO

### 5.3.2 Protein sidechains ⓘ

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	295/304 (97%)	236 (80%)	59 (20%)	1	5
1	B	293/304 (96%)	228 (78%)	65 (22%)	1	4
All	All	588/608 (97%)	464 (79%)	124 (21%)	1	5

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	662	GLU
1	B	596	ASN
1	B	386	THR
1	B	595	ILE
1	B	651	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	394	ASN

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Mol	Chain	Res	Type
1	B	489	GLN
1	B	663	HIS
1	B	427	ASN
1	B	490	ASN

### 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](#)

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	326/335 (97%)	0.31	17 (5%) 34 23	20, 84, 154, 227	0
1	B	324/335 (96%)	0.33	16 (4%) 36 25	25, 84, 151, 276	0
All	All	650/670 (97%)	0.32	33 (5%) 34 23	20, 84, 154, 276	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	567	GLU	5.4
1	A	390	GLU	5.4
1	B	395	TYR	4.8
1	A	659	SER	4.7
1	B	530	LEU	4.6

### 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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.