



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:54 PM UTC

PDB ID : 7ASV / pdb_00007asv
Title : Crystal structure of tWHD2 of Rpc5 subunit of human RNA Polymerase III
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Deposited on : 2020-10-28
Resolution : 1.55 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

i

X-RAY DIFFRACTION

A.

the following graphic. The table shows the number of entries on which the scores are based.



Percentile relative to all X-ray structures

Percentile relative to X-ray structures of similar resolution

Whole archive
(#Entries)

Similar resolution
(#Entries, resolution range(Å))

Metric

Whole archive
(#Entries)

Similar resolution

 $(\# \text{Entries}, \text{resolution range}(\text{\AA}))$ R_{free}

180053

2145 (1.56-1.56)

Clashscore

190562

2189 (1.56-1.56)

Ramachandran outliers

187476

2153 (1.56-1.56)

Sidechain outliers

187428

2150 (1.56-1.56)

RSRZ outliers

180081

2146 (1.56-1.56)

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 $\leq 5\%$. 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.

Quality of chain

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5622 atoms, of which 2569 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 DNA-directed RNA polymerase III subunit RPC5.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	B	155	Total	C	H	N	O	S	Se	0	8	0
			2537	798	1276	221	233	5	4			
1	A	155	Total	C	H	N	O	S	Se	0	9	0
			2553	803	1287	222	231	5	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	555	PRO	SER	conflict	UNP Q9NVU0
A	555	PRO	SER	conflict	UNP Q9NVU0

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	H	O	0	0
			7	2	3	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	277	Total	O	0	0
			277	277		
3	A	241	Total	O	0	0
			241	241		

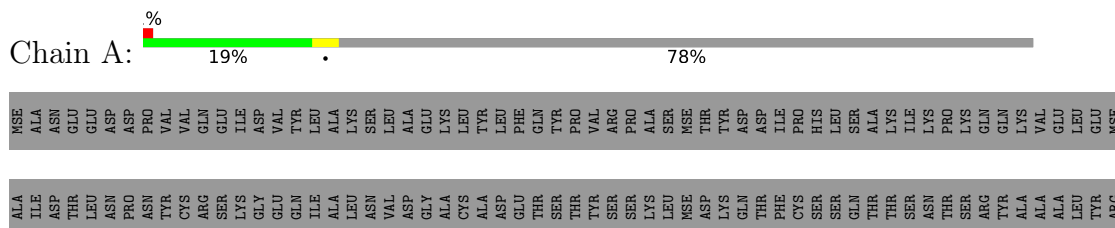
3 Residue-property plots

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: DNA-directed RNA polymerase III subunit RPC5



- Molecule 1: DNA-directed RNA polymerase III subunit RPC5





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	41.11Å 75.76Å 62.40Å 90.00° 103.57° 90.00°	Depositor
Resolution (Å)	30.33 – 1.55 30.33 – 1.55	Depositor EDS
% Data completeness (in resolution range)	96.1 (30.33-1.55) 99.1 (30.33-1.55)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.48Å)	Xtriage
Refinement program	PHENIX phenix-1.18.1-3865	Depositor
R, R_{free}	0.180 , 0.210 0.174 , 0.206	Depositor DCC
R_{free} test set	2918 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5622	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CME, ACT

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	0.47	0/1318	0.61	0/1771
1	B	0.53	1/1309 (0.1%)	0.63	0/1758
All	All	0.51	1/2627 (0.0%)	0.62	0/3529

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	667	MSE	SE-CE	-5.29	1.79	1.95

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	676	CME	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	1266	1287	1242	24	0
1	B	1261	1276	1235	11	0
2	A	4	3	3	0	0
2	B	4	3	3	0	0
3	A	241	0	0	5	0
3	B	277	0	0	1	1
All	All	3053	2569	2483	35	1

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 7.

All (35) 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:B:665[B]:ARG:NH2	1:B:686:ASP:OD2	2.09	0.84
1:A:688[B]:VAL:HG22	3:A:1038:HOH:O	1.82	0.79
1:A:556:THR:O	1:A:597:THR:HG21	1.84	0.77
1:B:656:ILE:HG21	1:B:667:MSE:HE1	1.74	0.69
1:B:656:ILE:CG2	1:B:667:MSE:HE1	2.23	0.68
1:A:554:ALA:CA	1:A:597:THR:HG22	2.27	0.65
1:B:673:THR:HG23	1:B:678:GLU:HA	1.78	0.64
1:B:663:VAL:HG11	1:B:667:MSE:HE2	1.83	0.61
1:A:554:ALA:C	1:A:597:THR:HG22	2.28	0.59
1:A:645:MSE:HE3	1:A:648:GLN:HB2	1.85	0.57
1:A:647:ASP:OD1	1:A:650:ARG:NH2	2.37	0.56
1:A:556:THR:H	1:A:597:THR:HG21	1.70	0.55
1:A:556:THR:H	1:A:597:THR:CG2	2.20	0.54
1:A:653:LEU:HD13	1:A:688[B]:VAL:HG12	1.90	0.54
1:A:649:HIS:HB3	1:A:688[B]:VAL:HG21	1.90	0.53
1:A:596:HIS:O	3:A:901:HOH:O	2.19	0.52
1:B:672:LEU:HB3	1:B:680:LEU:CD2	2.40	0.52
1:A:650:ARG:HG3	1:A:692:CYS:SG	2.50	0.51
1:A:645:MSE:HE1	1:A:648:GLN:HG2	1.94	0.49
1:B:708:SER:HB3	3:B:1098:HOH:O	2.14	0.47
1:A:653:LEU:C	1:A:653:LEU:HD23	2.40	0.47
1:A:691:ASP:OD1	3:A:902:HOH:O	2.20	0.47
1:A:662:ARG:HD2	1:A:699[B]:MSE:SE	2.65	0.46
1:A:644:ASP:C	1:A:644:ASP:OD2	2.59	0.45
1:B:683:GLN:H	1:B:683:GLN:CD	2.25	0.43
1:A:665:ARG:NH1	1:A:669:GLN:OE1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:ARG:NH2	1:A:686:ASP:OD1	2.51	0.43
1:A:684:GLU:O	1:A:688[B]:VAL:HG23	2.18	0.43
1:A:597:THR:O	1:A:600:SER:OG	2.25	0.42
1:B:656:ILE:HG23	1:B:667:MSE:HE1	1.99	0.42
1:A:597:THR:HB	3:A:918:HOH:O	2.19	0.42
1:B:605:ARG:HD2	1:B:605:ARG:C	2.45	0.41
1:A:676:CME:CB	1:A:680:LEU:HD11	2.50	0.41
1:B:656:ILE:HD13	1:B:667:MSE:HE1	2.01	0.41
1:A:554:ALA:N	3:A:918:HOH:O	2.54	0.40

All (1) 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:B:1001:HOH:O	3:B:1125:HOH:O[2_657]	2.17	0.03

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	161/708 (23%)	157 (98%)	4 (2%)	0	100	100
1	B	160/708 (23%)	157 (98%)	3 (2%)	0	100	100
All	All	321/1416 (23%)	314 (98%)	7 (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	A	144/600 (24%)	144 (100%)	0	100	100
1	B	144/600 (24%)	144 (100%)	0	100	100
All	All	288/1200 (24%)	288 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	669	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	CME	B	676	1	8,9,10	0.61	0	6,9,11	0.52	0
1	CME	A	676	1	8,9,10	0.75	0	6,9,11	0.88	0

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
1	CME	B	676	1	-	0/5/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CME	A	676	1	-	1/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	676	CME	CZ-CE-SD-SG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	676	CME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ACT	B	801	-	3,3,3	0.91	0	3,3,3	0.72	0
2	ACT	A	801	-	3,3,3	0.97	0	3,3,3	0.94	0

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 [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, 95th 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 ²)	Q<0.9
1	A	150/708 (21%)	-0.10	7 (4%) 36 44	13, 24, 54, 85	4 (2%)
1	B	150/708 (21%)	-0.31	3 (2%) 65 73	9, 22, 39, 60	4 (2%)
All	All	300/1416 (21%)	-0.20	10 (3%) 49 57	9, 23, 50, 85	8 (2%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	680	LEU	5.6
1	A	554	ALA	3.3
1	A	708	SER	3.2
1	B	708	SER	3.1
1	B	643	GLY	2.4
1	A	555	PRO	2.4
1	A	679	ASP	2.2
1	B	554	ALA	2.2
1	A	682	LYS	2.1
1	A	678	GLU	2.1

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CME	A	676	10/11	0.93	0.10	42,50,57,59	0
1	CME	B	676	10/11	0.98	0.07	18,27,48,49	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ACT	B	801	4/4	0.98	0.04	20,22,27,27	0
2	ACT	A	801	4/4	0.99	0.03	18,20,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.