



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2B2U / pdb_00002b2u
Title : Tandem chromodomains of human CHD1 complexed with Histone H3 Tail containing trimethyllysine 4 and dimethylarginine 2
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Deposited on : 2005-09-19
Resolution : 2.95 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

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

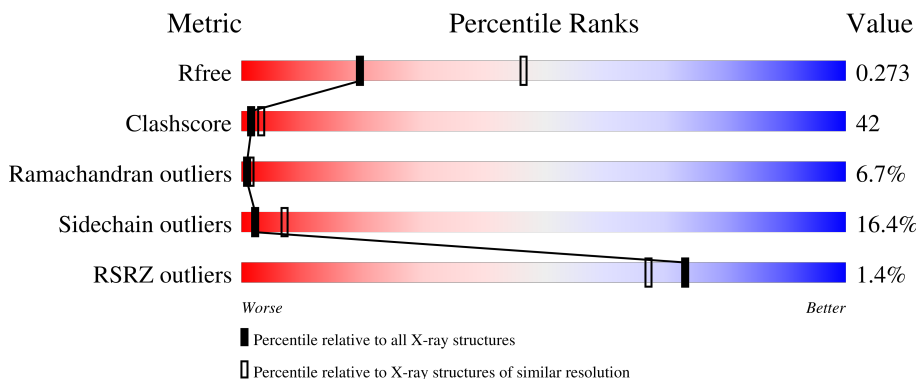
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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 $\leq 5\%$. 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	187	 % 39% 41% 12% • 7%
1	B	187	 % 37% 34% 17% • 8%
2	C	115	 3% 30% 25% 18% • 24%
3	D	16	 6% 12% 12% 69%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3568 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 Chromodomain-helicase-DNA-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	173	1429	902	245	275	7	0	0	0
1	B	172	1402	884	238	273	7	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP O14646
A	2	LYS	-	cloning artifact	UNP O14646
A	3	LYS	-	cloning artifact	UNP O14646
A	4	HIS	-	expression tag	UNP O14646
A	5	HIS	-	expression tag	UNP O14646
A	6	HIS	-	expression tag	UNP O14646
A	7	HIS	-	expression tag	UNP O14646
A	8	HIS	-	expression tag	UNP O14646
A	9	HIS	-	expression tag	UNP O14646
A	186	LYS	-	cloning artifact	UNP O14646
A	187	LYS	-	cloning artifact	UNP O14646
B	1	MET	-	cloning artifact	UNP O14646
B	2	LYS	-	cloning artifact	UNP O14646
B	3	LYS	-	cloning artifact	UNP O14646
B	4	HIS	-	expression tag	UNP O14646
B	5	HIS	-	expression tag	UNP O14646
B	6	HIS	-	expression tag	UNP O14646
B	7	HIS	-	expression tag	UNP O14646
B	8	HIS	-	expression tag	UNP O14646
B	9	HIS	-	expression tag	UNP O14646
B	186	LYS	-	cloning artifact	UNP O14646
B	187	LYS	-	cloning artifact	UNP O14646

- Molecule 2 is a protein called Chromodomain-helicase-DNA-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	87	691	432	123	133	3	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	cloning artifact	UNP O14646
C	2	LYS	-	cloning artifact	UNP O14646
C	3	LYS	-	cloning artifact	UNP O14646
C	4	HIS	-	expression tag	UNP O14646
C	5	HIS	-	expression tag	UNP O14646
C	6	HIS	-	expression tag	UNP O14646
C	7	HIS	-	expression tag	UNP O14646
C	8	HIS	-	expression tag	UNP O14646
C	9	HIS	-	expression tag	UNP O14646

- Molecule 3 is a protein called Histone H3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	D	5	46	29	10	7	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	2	DA2	ARG	modified residue	UNP P68431
D	4	M3L	LYS	modified residue	UNP P68431
D	16	TYR	-	SEE REMARK 999	UNP P68431

Chain D:  6% 12% 12% 69%

A1	R2	T3	K4	Q5	THR	ALA	ARG	LYS	SER	THR	GLY	GLY	LYS	ALA	TYR
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4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	111.98Å 54.75Å 100.27Å 90.00° 112.32° 90.00°	Depositor
Resolution (Å)	20.00 – 2.95 20.00 – 2.95	Depositor EDS
% Data completeness (in resolution range)	92.4 (20.00-2.95) 93.9 (20.00-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.95Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.238 , 0.290 0.235 , 0.273	Depositor DCC
R_{free} test set	814 reflections (7.17%)	wwPDB-VP
Wilson B-factor (Å ²)	47.2	Xtrriage
Anisotropy	0.377	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3568	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: M3L, DA2

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	0.60	0/1464	1.18	18/1969 (0.9%)
1	B	0.61	0/1435	1.29	26/1934 (1.3%)
2	C	0.70	0/705	1.40	15/949 (1.6%)
3	D	0.57	0/19	0.85	0/23
All	All	0.62	0/3623	1.27	59/4875 (1.2%)

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	B	0	1
3	D	0	1
All	All	0	2

There are no bond length outliers.

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	84	ASN	CB-CA-C	-16.33	85.71	111.51
1	B	47	ALA	N-CA-C	14.86	129.31	111.33
2	C	14	GLU	N-CA-C	10.88	133.97	110.80
2	C	53	LYS	N-CA-C	-10.55	93.55	110.32
1	A	110	PRO	N-CA-C	-9.02	102.58	113.86

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	182	TYR	Peptide
3	D	4	M3L	Peptide

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	1429	0	1362	111	0
1	B	1402	0	1311	113	0
2	C	691	0	655	69	0
3	D	46	0	56	8	0
All	All	3568	0	3384	293	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 42.

The worst 5 of 293 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)
3:D:2:DA2:HCD1	3:D:2:DA2:C1	1.58	1.34
3:D:2:DA2:CD	3:D:2:DA2:HC11	1.47	1.33
1:B:181:GLU:O	1:B:183:PHE:HB3	1.19	1.25
1:B:181:GLU:O	1:B:183:PHE:CB	1.89	1.21
1:A:136:ILE:HD13	1:A:136:ILE:H	1.12	1.09

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	169/187 (90%)	145 (86%)	18 (11%)	6 (4%)	2	6
1	B	166/187 (89%)	130 (78%)	21 (13%)	15 (9%)	0	1
2	C	85/115 (74%)	70 (82%)	8 (9%)	7 (8%)	0	1
3	D	1/16 (6%)	0	1 (100%)	0	100	100
All	All	421/505 (83%)	345 (82%)	48 (11%)	28 (7%)	1	1

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	13	PHE
1	B	49	PHE
1	B	170	LEU
1	B	171	ILE
1	B	181	GLU

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	150/164 (92%)	132 (88%)	18 (12%)	5	14
1	B	145/164 (88%)	118 (81%)	27 (19%)	1	4
2	C	69/101 (68%)	54 (78%)	15 (22%)	1	2
3	D	2/9 (22%)	2 (100%)	0	100	100
All	All	366/438 (84%)	306 (84%)	60 (16%)	2	7

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	89	LYS
2	C	81	LYS
1	B	126	LEU
2	C	80	LEU
2	C	97	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	119	GLN
2	C	46	ASN
1	B	129	GLN
2	C	69	HIS
1	B	156	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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
3	M3L	D	4	3	10,11,12	1.09	0	9,14,16	0.67	0
3	DA2	D	2	3	10,12,13	1.01	0	8,14,16	1.32	1 (12%)

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
3	M3L	D	4	3	-	4/9/10/12	-
3	DA2	D	2	3	-	6/12/13/15	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	D	2	DA2	CB-CG-CD	-3.10	103.11	112.07

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	2	DA2	N-CA-CB-CG
3	D	2	DA2	C-CA-CB-CG
3	D	2	DA2	O-C-CA-CB
3	D	4	M3L	O-C-CA-CB
3	D	4	M3L	CG-CD-CE-NZ

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	4	M3L	2	0
3	D	2	DA2	6	0

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, 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	173/187 (92%)	-0.14	1 (0%) 85 82	11, 35, 61, 73	0
1	B	172/187 (91%)	0.11	2 (1%) 76 71	14, 47, 67, 78	0
2	C	87/115 (75%)	0.10	3 (3%) 48 41	22, 42, 68, 80	0
3	D	3/16 (18%)	1.10	0 100 100	8, 8, 25, 33	0
All	All	435/505 (86%)	0.01	6 (1%) 73 67	8, 42, 66, 80	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	62	ILE	2.7
2	C	55	PRO	2.5
2	C	54	GLU	2.4
1	B	136	ILE	2.1
1	B	137	ILE	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
3	DA2	D	2	13/14	0.84	0.11	2,13,22,31	0
3	M3L	D	4	12/13	0.92	0.11	14,25,32,38	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.