wwPDB X-ray Structure Validation Summary Report (i)

Mar 9, 2026 – 02:10 PM UTC

PDB ID	:	5D6W / pdb_00005d6w
Title	:	Crystal structure of double tudor domain of human lysine demethylase KDM4A
Authors	:	Wang, F.; Su, Z.; Denu, J.M.; Phillips Jr., G.N.; Enzyme Discovery for Natural Product Biosynthesis (NatPro)
Deposited on	:	2015-08-13
Resolution	:	1.99 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 (i) 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 (1)) were used in the production of this report:

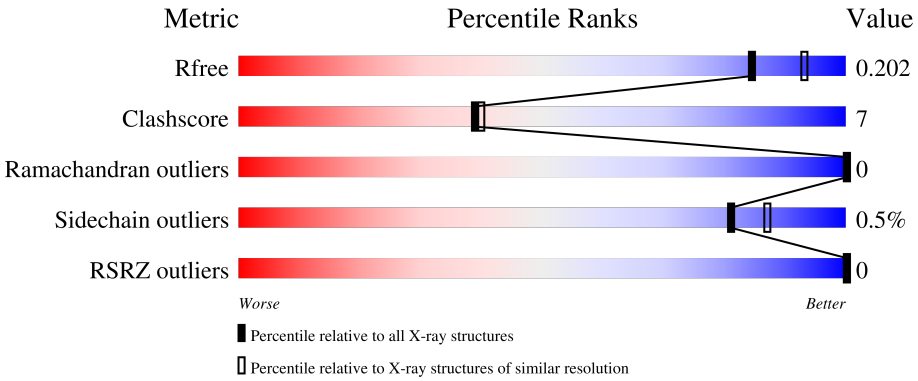
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 <=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	121	81% 14% 5%
1	B	121	81% 13% • 5%
1	C	121	84% 11% 5%
1	D	121	87% 8% 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4350 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.

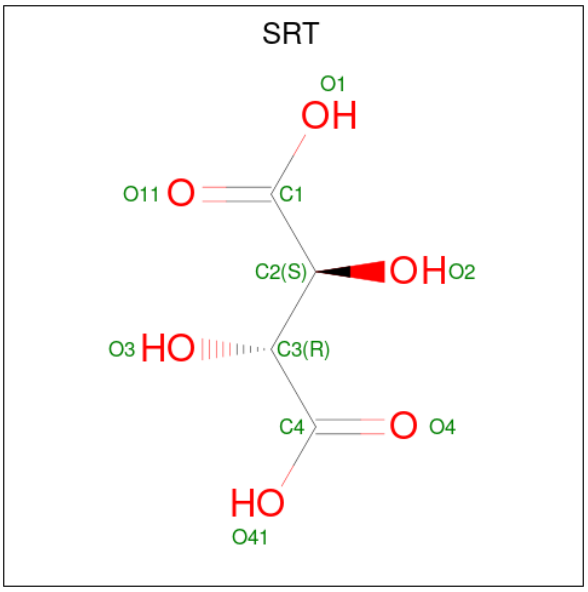
- Molecule 1 is a protein called Lysine-specific demethylase 4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	115	Total	C	N	O	S	0	2	0
			945	596	154	192	3			
1	B	115	Total	C	N	O	S	0	3	0
			956	602	158	193	3			
1	C	115	Total	C	N	O	S	0	1	0
			936	591	153	189	3			
1	D	115	Total	C	N	O	S	0	3	0
			958	603	161	191	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	891	GLY	-	expression tag	UNP O75164
A	892	SER	-	expression tag	UNP O75164
A	893	HIS	-	expression tag	UNP O75164
A	894	MET	-	expression tag	UNP O75164
B	891	GLY	-	expression tag	UNP O75164
B	892	SER	-	expression tag	UNP O75164
B	893	HIS	-	expression tag	UNP O75164
B	894	MET	-	expression tag	UNP O75164
C	891	GLY	-	expression tag	UNP O75164
C	892	SER	-	expression tag	UNP O75164
C	893	HIS	-	expression tag	UNP O75164
C	894	MET	-	expression tag	UNP O75164
D	891	GLY	-	expression tag	UNP O75164
D	892	SER	-	expression tag	UNP O75164
D	893	HIS	-	expression tag	UNP O75164
D	894	MET	-	expression tag	UNP O75164

- Molecule 2 is S,R MESO-TARTARIC ACID (CCD ID: SRT) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 10 4 6	0	0
2	B	1	Total C O 10 4 6	0	0
2	C	1	Total C O 10 4 6	0	0
2	D	1	Total C O 10 4 6	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	122	Total O 122 122	0	0
3	B	130	Total O 130 130	0	0
3	C	135	Total O 135 135	0	0
3	D	128	Total O 128 128	0	0

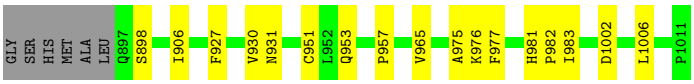
3 Residue-property plots (i)

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 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: Lysine-specific demethylase 4A

Chain A:





- Molecule 1: Lysine-specific demethylase 4A

Chain B:





- Molecule 1: Lysine-specific demethylase 4A

Chain C:





- Molecule 1: Lysine-specific demethylase 4A

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	190.64Å 190.64Å 116.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.08 – 1.99 36.08 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.08-1.99) 95.3 (36.08-1.99)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.19 (at 2.00Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.168 , 0.196 0.173 , 0.202	Depositor DCC
R_{free} test set	2026 reflections (3.65%)	wwPDB-VP
Wilson B-factor (Å^2)	32.0	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 45.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.429 for -1/3*h+1/3*k+4/3*l,-k,2/3*h+1/3*k+1/3*l 0.458 for -2/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+4/3*l,-1/3*h+1/3*k+1/3*l 0.448 for -h,1/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+1/3*l	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	4350	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SRT

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	0.42	0/967	0.75	0/1312
1	B	0.43	0/978	0.75	0/1326
1	C	0.44	0/958	0.74	0/1300
1	D	0.43	0/980	0.73	0/1328
All	All	0.43	0/3883	0.74	0/5266

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

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	945	0	878	15	0
1	B	956	0	890	14	0
1	C	936	0	873	12	0
1	D	958	0	897	8	0
2	A	10	0	4	1	0
2	B	10	0	4	1	0
2	C	10	0	4	0	0
2	D	10	0	4	1	0
3	A	122	0	0	10	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	130	0	0	6	4
3	C	135	0	0	4	0
3	D	128	0	0	6	2
All	All	4350	0	3554	50	4

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.

The worst 5 of 50 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:976:LYS:O	3:A:1201:HOH:O	2.05	0.73
1:D:985:MET:HE3	1:D:997:VAL:HG12	1.72	0.69
1:C:976:LYS:HD2	3:C:1205:HOH:O	1.94	0.67
1:D:913[B]:ARG:NH1	3:D:1205:HOH:O	2.29	0.66
1:A:975:ALA:HB1	3:A:1201:HOH:O	1.95	0.65

All (4) 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:1207:HOH:O	3:D:1220:HOH:O[8_455]	2.06	0.14
3:A:1271:HOH:O	3:B:1219:HOH:O[5_554]	2.14	0.06
3:B:1292:HOH:O	3:D:1211:HOH:O[16_554]	2.17	0.03
3:A:1211:HOH:O	3:B:1299:HOH:O[15_444]	2.19	0.01

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	115/121 (95%)	113 (98%)	2 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	116/121 (96%)	114 (98%)	2 (2%)	0	100	100
1	C	114/121 (94%)	112 (98%)	2 (2%)	0	100	100
1	D	116/121 (96%)	115 (99%)	1 (1%)	0	100	100
All	All	461/484 (95%)	454 (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	105/107 (98%)	104 (99%)	1 (1%)	68	75
1	B	106/107 (99%)	105 (99%)	1 (1%)	70	78
1	C	104/107 (97%)	104 (100%)	0	100	100
1	D	106/107 (99%)	106 (100%)	0	100	100
All	All	421/428 (98%)	419 (100%)	2 (0%)	81	87

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	965	VAL
1	B	941	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	916	GLN
1	A	987	GLN
1	B	916	GLN
1	C	916	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)

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)

4 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	SRT	D	1101	-	9,9,9	1.08	0	12,12,12	1.50	4 (33%)
2	SRT	A	1101	-	9,9,9	1.10	0	12,12,12	1.49	4 (33%)
2	SRT	C	1101	-	9,9,9	1.14	0	12,12,12	1.59	4 (33%)
2	SRT	B	1101	-	9,9,9	1.09	0	12,12,12	1.45	4 (33%)

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	SRT	D	1101	-	-	4/12/12/12	-
2	SRT	A	1101	-	-	6/12/12/12	-
2	SRT	C	1101	-	-	5/12/12/12	-
2	SRT	B	1101	-	-	6/12/12/12	-

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1101	SRT	O1-C1-C2	2.96	121.53	113.31
2	C	1101	SRT	O1-C1-C2	2.85	121.22	113.31
2	A	1101	SRT	O41-C4-C3	2.60	120.53	113.31
2	C	1101	SRT	O41-C4-C3	2.59	120.51	113.31
2	B	1101	SRT	O1-C1-C2	2.56	120.43	113.31

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	SRT	O1-C1-C2-O2
2	A	1101	SRT	O11-C1-C2-O2
2	B	1101	SRT	O1-C1-C2-O2
2	B	1101	SRT	O11-C1-C2-O2
2	C	1101	SRT	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1101	SRT	1	0
2	A	1101	SRT	1	0
2	B	1101	SRT	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

6.1 Protein, DNA and RNA chains

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	115/121 (95%)	-1.21	0	100	100	21, 36, 56, 72	2 (1%)
1	B	115/121 (95%)	-1.21	0	100	100	20, 36, 55, 71	3 (2%)
1	C	115/121 (95%)	-1.24	0	100	100	22, 38, 59, 68	1 (0%)
1	D	115/121 (95%)	-1.18	0	100	100	18, 36, 57, 64	3 (2%)
All	All	460/484 (95%)	-1.21	0	100	100	18, 37, 58, 72	9 (1%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

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
2	SRT	B	1101	10/10	0.98	0.05	60,79,90,91	0
2	SRT	D	1101	10/10	0.98	0.05	57,77,83,85	0
2	SRT	C	1101	10/10	0.99	0.04	57,76,81,83	0
2	SRT	A	1101	10/10	0.99	0.05	62,76,85,89	0

6.5 Other polymers (i)

There are no such residues in this entry.