



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 12:03 pm BST

PDB ID : 6YDV
Title : Crystal Structure of the Jmjc Domain of Human JMJD1B in complex with FM001511a from the DSPL fragment library
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Deposited on : 2020-03-21
Resolution : 2.07 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 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)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

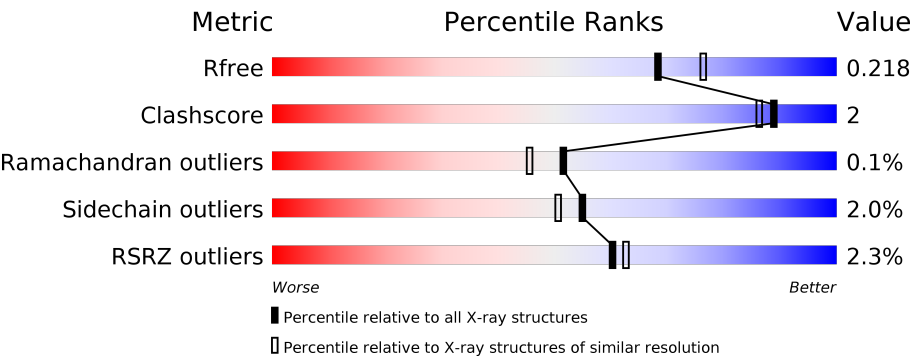
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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}	130704	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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 on 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.

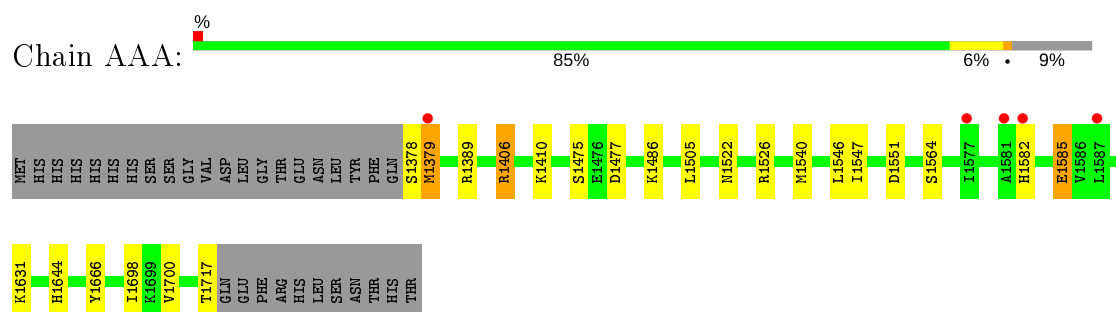
Mol	Chain	Length	Quality of chain
1	AAA	372	<div><div>%</div><div><div></div><div>85%</div><div>6%</div><div>9%</div></div></div>
1	BBB	372	<div><div>3%</div><div><div></div><div>87%</div><div>5%</div><div>8%</div></div></div>

ENTRY-COMPOSITION INFOmissingINFO

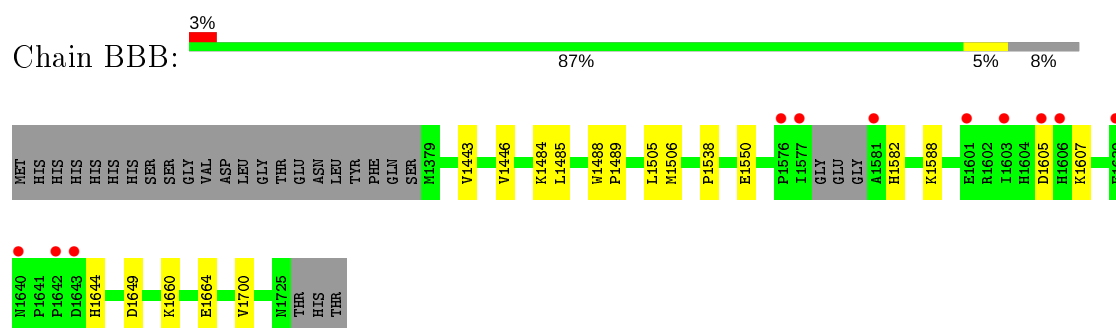
2 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: JMJD1B protein



• Molecule 1: JMJD1B protein



3 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.60 Å 93.79 Å 92.61 Å 90.00° 107.50° 90.00°	Depositor
Resolution (Å)	54.93 – 2.07 54.93 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.1 (54.93-2.07) 99.1 (54.93-2.07)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.07 Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.170 , 0.214 0.179 , 0.218	Depositor DCC
R_{free} test set	2774 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.619	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.036 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11507	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% 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.

4 Model quality

4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, ONQ, CL

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	AAA	0.67	0/2801	0.75	0/3803
1	BBB	0.68	0/2852	0.72	0/3869
All	All	0.67	0/5653	0.74	0/7672

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

4.2 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	AAA	2728	2639	2610	12	0
1	BBB	2778	2699	2668	9	0
2	AAA	15	12	0	1	0
3	AAA	4	0	0	0	0
3	BBB	1	0	0	0	0
4	AAA	1	0	0	0	0
4	BBB	1	0	0	0	0
5	AAA	336	0	0	2	1
5	BBB	293	0	0	1	1
All	All	6157	5350	5278	21	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 2.

All (21) 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:AAA:1582:HIS:CD2	1:AAA:1585:GLU:HG3	2.29	0.67
1:BBB:1644:HIS:NE2	1:BBB:1649:ASP:OD2	2.33	0.62
1:AAA:1389:ARG:HG3	2:AAA:1801:ONQ:O2	2.02	0.58
1:BBB:1443:VAL:HG21	1:BBB:1485:LEU:HD11	1.87	0.55
1:BBB:1505:LEU:HD22	1:BBB:1700:VAL:HG11	1.87	0.55
1:BBB:1488:TRP:HA	1:BBB:1489:PRO:C	2.29	0.52
1:AAA:1547:ILE:HA	1:AAA:1582:HIS:NE2	2.29	0.47
1:BBB:1506:MET:CE	1:BBB:1538:PRO:HG3	2.44	0.47
1:AAA:1475:SER:OG	1:AAA:1477:ASP:OD1	2.30	0.46
1:AAA:1522:ASN:O	1:AAA:1526:ARG:NH1	2.49	0.46
1:AAA:1406:ARG:HG3	5:AAA:1934:HOH:O	2.15	0.46
1:AAA:1631:LYS:HE2	1:AAA:1666:TYR:OH	2.18	0.44
1:AAA:1564:SER:HB3	5:AAA:1941:HOH:O	2.17	0.43
1:BBB:1506:MET:HE3	1:BBB:1538:PRO:HG3	2.00	0.42
1:AAA:1505:LEU:HD22	1:AAA:1700:VAL:HG11	2.02	0.41
1:BBB:1550:GLU:HG3	5:BBB:2042:HOH:O	2.20	0.41
1:AAA:1546:LEU:HB3	1:AAA:1551:ASP:HB3	2.03	0.41
1:AAA:1582:HIS:O	1:AAA:1582:HIS:CG	2.74	0.41
1:BBB:1446:VAL:HB	1:BBB:1484:LYS:HG2	2.03	0.40
1:BBB:1660:LYS:HE2	1:BBB:1664:GLU:OE2	2.22	0.40
1:AAA:1540:MET:HE2	1:AAA:1698:ILE:HG23	2.03	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)
5:AAA:2184:HOH:O	5:BBB:2176:HOH:O[2_657]	0.88	1.32

4.3 Torsion angles ⓘ

4.3.1 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	AAA	338/372 (91%)	328 (97%)	9 (3%)	1 (0%)	41	32
1	BBB	340/372 (91%)	323 (95%)	17 (5%)	0	100	100
All	All	678/744 (91%)	651 (96%)	26 (4%)	1 (0%)	51	45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	1379	MET

4.3.2 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	AAA	294/331 (89%)	286 (97%)	8 (3%)	44	39
1	BBB	300/331 (91%)	296 (99%)	4 (1%)	69	67
All	All	594/662 (90%)	582 (98%)	12 (2%)	55	51

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	1378	SER
1	AAA	1379	MET
1	AAA	1406	ARG
1	AAA	1410	LYS
1	AAA	1486	LYS
1	AAA	1585	GLU
1	AAA	1644	HIS
1	AAA	1717	THR
1	BBB	1582	HIS
1	BBB	1588	LYS
1	BBB	1605	ASP
1	BBB	1607	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

4.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

4.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

4.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 1 could not be matched to an existing wwPDB Chemical Component Dictionary definition at this stage and 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

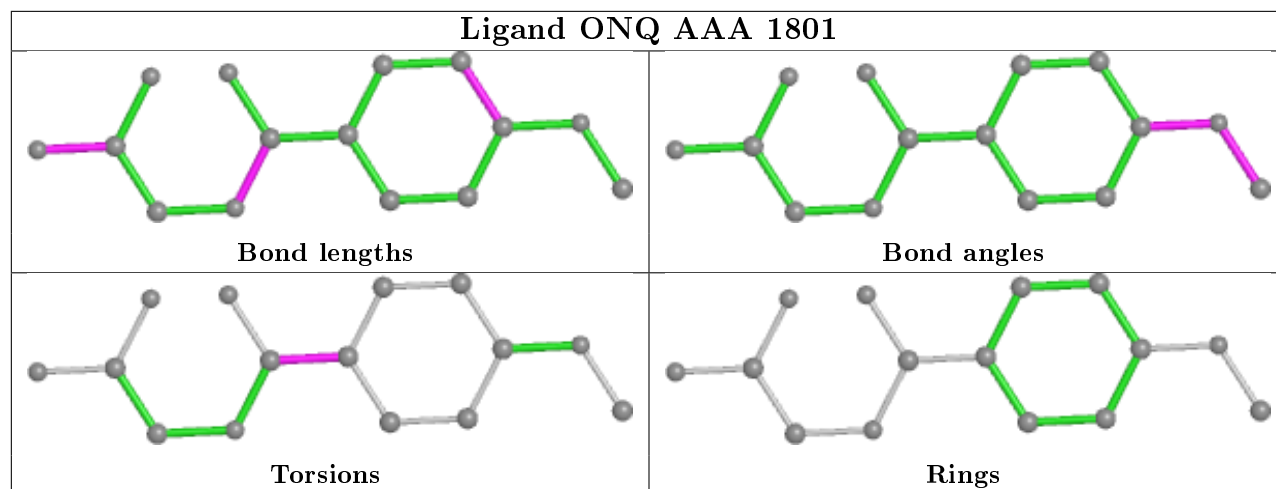
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data ⓘ

5.1 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	AAA	340/372 (91%)	-0.24	5 (1%) 73 75	21, 35, 74, 115	0
1	BBB	344/372 (92%)	-0.10	11 (3%) 47 50	24, 41, 83, 146	0
All	All	684/744 (91%)	-0.17	16 (2%) 60 63	21, 38, 79, 146	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	1577	ILE	5.6
1	AAA	1582	HIS	4.9
1	BBB	1581	ALA	4.6
1	AAA	1581	ALA	3.9
1	BBB	1643	ASP	3.4
1	BBB	1642	PRO	3.2
1	BBB	1605	ASP	3.1
1	BBB	1606	HIS	3.1
1	AAA	1577	ILE	2.9
1	AAA	1587	LEU	2.5
1	AAA	1379	MET	2.3
1	BBB	1640	ASN	2.2
1	BBB	1603	ILE	2.2
1	BBB	1576	PRO	2.2
1	BBB	1601	GLU	2.1
1	BBB	1639	GLU	2.0

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

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

5.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.4 Ligands [i](#)

LIGAND-RSR INFOmissingINFO

5.5 Other polymers [i](#)

There are no such residues in this entry.