



wwPDB X-ray Structure Validation Summary Report ⓘ

May 17, 2020 – 05:40 am BST

PDB ID : 6IE7
Title : Crystal structure of ADCP1 tandem Agenet domain 1-2 in complex with H3K9me2
Authors : Zhao, S.; Zhang, B.; Li, H.
Deposited on : 2018-09-13
Resolution : 2.70 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 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
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

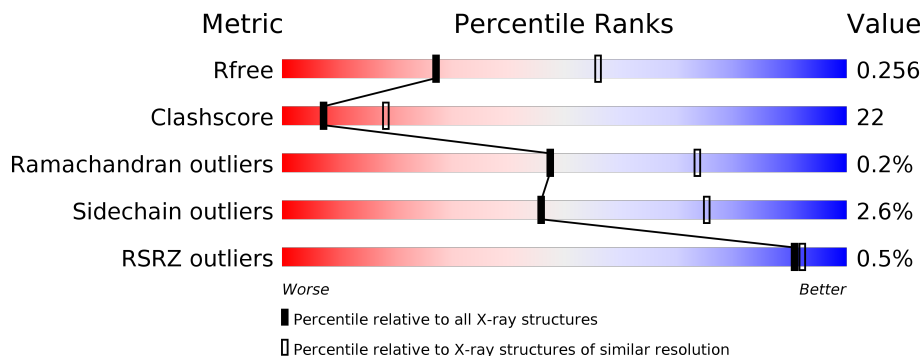
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	A	152	 57% 30% 13%
1	B	152	 53% 32% 14%
1	C	152	 50% 34% 16%
1	D	152	 49% 39% 12%
2	E	11	 18% 64% 9% 9%
2	F	11	 27% 64% 9%

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Mol	Chain	Length	Quality of chain
2	G	11	 64% 36%
2	H	11	 73% 27%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4727 atoms, of which 16 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 Agenet domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	133	1094	708	179	204	3	0	0	0
1	B	131	1075	697	176	198	4	0	0	0
1	C	128	1052	681	173	195	3	0	0	0
1	D	134	1099	708	180	207	4	0	0	0

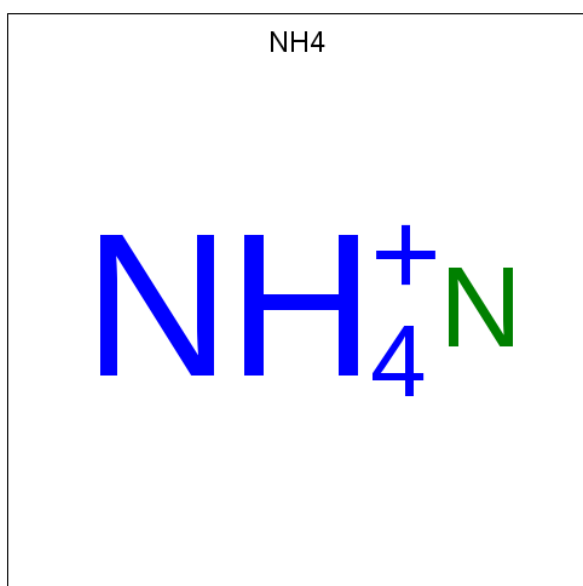
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q500V5
A	-3	PRO	-	expression tag	UNP Q500V5
A	-2	LEU	-	expression tag	UNP Q500V5
A	-1	GLY	-	expression tag	UNP Q500V5
A	0	SER	-	expression tag	UNP Q500V5
B	-4	GLY	-	expression tag	UNP Q500V5
B	-3	PRO	-	expression tag	UNP Q500V5
B	-2	LEU	-	expression tag	UNP Q500V5
B	-1	GLY	-	expression tag	UNP Q500V5
B	0	SER	-	expression tag	UNP Q500V5
C	-4	GLY	-	expression tag	UNP Q500V5
C	-3	PRO	-	expression tag	UNP Q500V5
C	-2	LEU	-	expression tag	UNP Q500V5
C	-1	GLY	-	expression tag	UNP Q500V5
C	0	SER	-	expression tag	UNP Q500V5
D	-4	GLY	-	expression tag	UNP Q500V5
D	-3	PRO	-	expression tag	UNP Q500V5
D	-2	LEU	-	expression tag	UNP Q500V5
D	-1	GLY	-	expression tag	UNP Q500V5
D	0	SER	-	expression tag	UNP Q500V5

- Molecule 2 is a protein called H3K9me2 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	10	Total 81	C 48	N 19	O 14	0	0	0
2	F	10	Total 81	C 48	N 19	O 14	0	0	0
2	G	11	Total 88	C 52	N 20	O 16	0	0	0
2	H	11	Total 88	C 52	N 20	O 16	0	0	0

- Molecule 3 is AMMONIUM ION (three-letter code: NH4) (formula: H₄N).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	H	N		
3	A	1	Total 5	H 4	N 1	0	0
3	B	1	Total 5	H 4	N 1	0	0
3	C	1	Total 5	H 4	N 1	0	0
3	D	1	Total 5	H 4	N 1	0	0

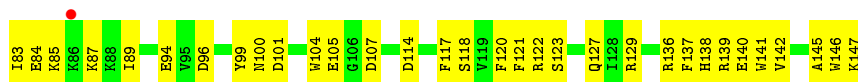
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	13	Total 13	O 13	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	9	Total O 9 9	0	0
4	F	3	Total O 3 3	0	0
4	C	10	Total O 10 10	0	0
4	D	14	Total O 14 14	0	0



- Molecule 2: H3K9me2 peptide



- Molecule 2: H3K9me2 peptide



- Molecule 2: H3K9me2 peptide



- Molecule 2: H3K9me2 peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	41.47Å 111.34Å 68.14Å 90.00° 90.63° 90.00°	Depositor
Resolution (Å)	33.91 – 2.70 33.91 – 2.70	Depositor EDS
% Data completeness (in resolution range)	88.9 (33.91-2.70) 88.9 (33.91-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.01 (at 2.68Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.190 , 0.256 0.193 , 0.256	Depositor DCC
R_{free} test set	811 reflections (5.35%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtrriage
Anisotropy	0.563	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 24.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.165 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4727	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.80% 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: NH4, MLY

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	0.48	0/1123	0.66	0/1510
1	B	0.45	0/1104	0.62	0/1486
1	C	0.48	0/1081	0.64	0/1454
1	D	0.44	0/1128	0.60	0/1516
2	E	0.51	0/69	0.81	0/90
2	F	0.48	0/69	0.71	0/90
2	G	0.44	0/76	0.64	0/100
2	H	0.38	0/76	0.64	0/100
All	All	0.46	0/4726	0.64	0/6346

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 [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	1094	0	1068	50	0
1	B	1075	0	1051	46	0
1	C	1052	0	1023	61	0
1	D	1099	0	1070	52	0
2	E	81	0	93	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	81	0	94	10	0
2	G	88	0	100	4	0
2	H	88	0	100	4	0
3	A	1	4	0	0	0
3	B	1	4	0	0	0
3	C	1	4	0	0	0
3	D	1	4	0	0	0
4	A	13	0	0	1	0
4	B	9	0	0	1	0
4	C	10	0	0	1	0
4	D	14	0	0	3	0
4	F	3	0	0	0	0
All	All	4711	16	4599	207	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 22.

The worst 5 of 207 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:34:ILE:HD11	1:A:50:GLU:HB2	1.30	1.08
1:D:53:THR:HG21	1:D:101:ASP:HB3	1.42	1.02
1:C:53:THR:HG21	1:C:101:ASP:HB3	1.38	1.00
1:A:53:THR:CG2	1:A:101:ASP:HB3	1.94	0.97
1:A:10:LYS:NZ	4:A:301:HOH:O	1.90	0.95

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	127/152 (84%)	123 (97%)	4 (3%)	0	100	100
1	B	125/152 (82%)	120 (96%)	4 (3%)	1 (1%)	19	43
1	C	122/152 (80%)	119 (98%)	3 (2%)	0	100	100
1	D	130/152 (86%)	125 (96%)	5 (4%)	0	100	100
2	E	7/11 (64%)	7 (100%)	0	0	100	100
2	F	7/11 (64%)	7 (100%)	0	0	100	100
2	G	8/11 (73%)	8 (100%)	0	0	100	100
2	H	8/11 (73%)	8 (100%)	0	0	100	100
All	All	534/652 (82%)	517 (97%)	16 (3%)	1 (0%)	47	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	6	PRO

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	119/136 (88%)	117 (98%)	2 (2%)	60	84
1	B	117/136 (86%)	116 (99%)	1 (1%)	78	92
1	C	114/136 (84%)	110 (96%)	4 (4%)	36	65
1	D	120/136 (88%)	117 (98%)	3 (2%)	47	76
2	E	7/8 (88%)	6 (86%)	1 (14%)	3	8
2	F	7/8 (88%)	7 (100%)	0	100	100
2	G	8/8 (100%)	7 (88%)	1 (12%)	4	10
2	H	8/8 (100%)	7 (88%)	1 (12%)	4	10
All	All	500/576 (87%)	487 (97%)	13 (3%)	46	75

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	72	GLN
1	C	109	THR
1	D	107	ASP
1	C	20	ASP
1	D	81	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	127	GLN
1	C	72	GLN
1	C	127	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](#)

4 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	$\# Z > 2$
2	MLY	E	9	2	9,10,11	0.65	0	6,11,13	0.62	0
2	MLY	F	9	2	9,10,11	0.54	0	6,11,13	1.14	0
2	MLY	G	9	2	9,10,11	0.58	0	6,11,13	0.96	0
2	MLY	H	9	2	9,10,11	0.55	0	6,11,13	1.23	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
2	MLY	E	9	2	-	1/8/9/11	-
2	MLY	F	9	2	-	4/8/9/11	-
2	MLY	G	9	2	-	0/8/9/11	-
2	MLY	H	9	2	-	1/8/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	9	MLY	O-C-CA-CB
2	F	9	MLY	CG-CD-CE-NZ
2	F	9	MLY	CA-CB-CG-CD
2	E	9	MLY	CD-CE-NZ-CH2
2	F	9	MLY	CE-CD-CG-CB

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	9	MLY	1	0
2	F	9	MLY	1	0
2	H	9	MLY	3	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are modelled with single atom - 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.

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	133/152 (87%)	-0.31	1 (0%) 86 87	24, 41, 66, 78	0
1	B	131/152 (86%)	-0.31	0 100 100	25, 43, 63, 70	0
1	C	128/152 (84%)	-0.25	0 100 100	25, 44, 68, 80	0
1	D	134/152 (88%)	-0.22	2 (1%) 73 76	26, 46, 74, 91	0
2	E	9/11 (81%)	-0.14	0 100 100	31, 36, 46, 50	0
2	F	9/11 (81%)	0.09	0 100 100	37, 44, 51, 54	0
2	G	10/11 (90%)	-0.22	0 100 100	37, 45, 56, 58	0
2	H	10/11 (90%)	-0.38	0 100 100	36, 42, 51, 54	0
All	All	564/652 (86%)	-0.27	3 (0%) 91 92	24, 44, 66, 91	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	86	LYS	2.5
1	D	10	LYS	2.3
1	A	37	PRO	2.3

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
2	MLY	E	9	11/12	0.97	0.16	31,36,45,49	0
2	MLY	F	9	11/12	0.97	0.14	25,31,43,45	0
2	MLY	G	9	11/12	0.97	0.15	28,31,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MLY	H	9	11/12	0.97	0.22	32,35,42,46	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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(\AA^2)	Q<0.9
3	NH4	C	201	1/1	0.87	0.24	45,54,54,54	0
3	NH4	B	201	1/1	0.92	0.27	39,47,47,47	0
3	NH4	A	201	1/1	0.92	0.28	35,42,42,42	0
3	NH4	D	201	1/1	0.96	0.30	40,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.