



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Sep 11, 2017 – 04:11 PM EDT

PDB ID : 5WCB
EMDB ID: : EMD-8796
Title : Katanin hexamer in the ring conformation
Authors : Zehr, E.A.; Szyk, A.; Piszczek, G.; Szczesna, E.; Zuo, X.; Roll-Mecak, A.
Deposited on : unknown
Resolution : 6.00 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

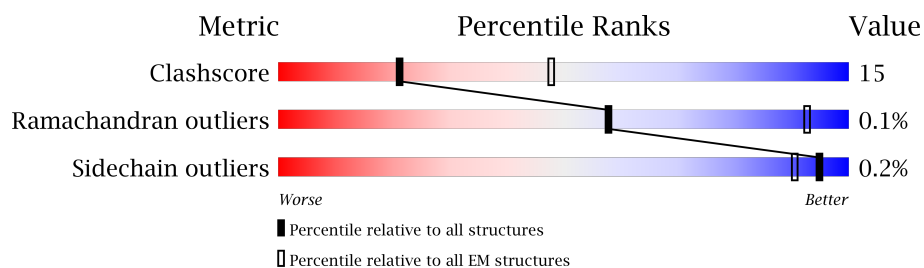
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.00 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)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	472	49% 9% 41%
1	B	472	43% 16% 41%
1	C	472	45% 14% 41%
1	D	472	46% 12% 41%
1	E	472	45% 14% 41%
1	F	472	44% 14% 41%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11395 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Meiotic spindle formation protein mei-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	277	Total	C	N	O	S	0	0
			1877	1185	327	358	7		
1	B	277	Total	C	N	O	S	0	0
			1877	1185	327	358	7		
1	C	277	Total	C	N	O	S	0	0
			1871	1182	324	358	7		
1	D	277	Total	C	N	O	S	0	0
			1867	1181	321	358	7		
1	E	277	Total	C	N	O	S	0	0
			1871	1182	324	358	7		
1	F	277	Total	C	N	O	S	0	0
			1877	1185	327	358	7		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	293	GLN	GLU	engineered mutation	UNP P34808
B	293	GLN	GLU	engineered mutation	UNP P34808
C	293	GLN	GLU	engineered mutation	UNP P34808
D	293	GLN	GLU	engineered mutation	UNP P34808
E	293	GLN	GLU	engineered mutation	UNP P34808
F	293	GLN	GLU	engineered mutation	UNP P34808

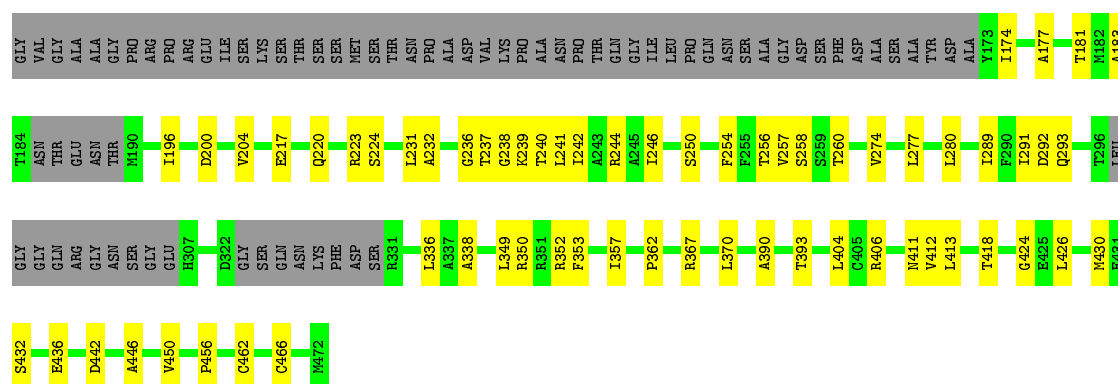
- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



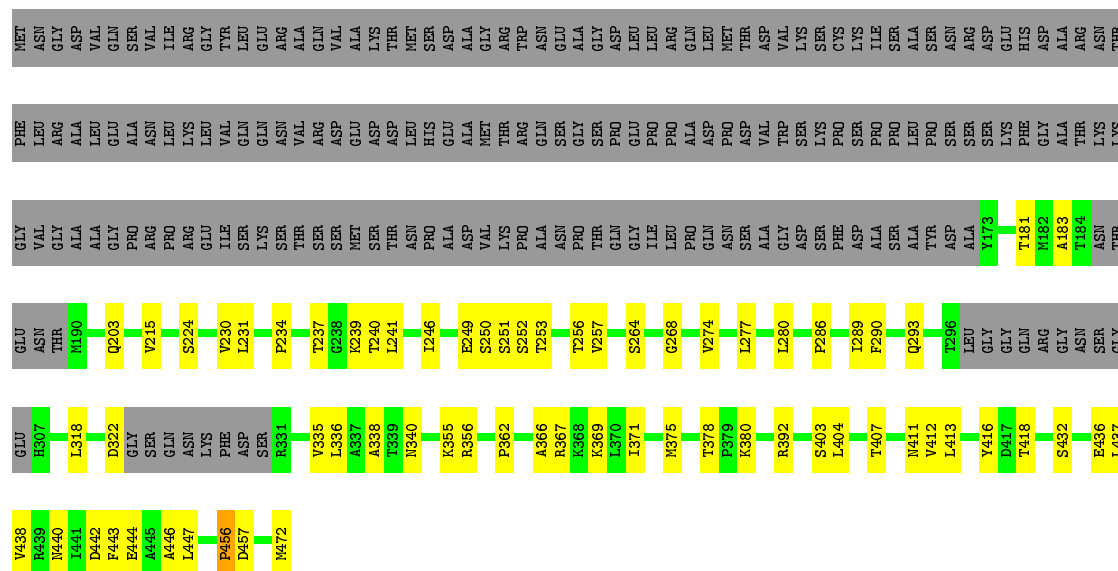
Mol	Chain	Residues	Atoms					AltConf
2	B	1	Total 31	C 10	N 5	O 13	P 3	0
2	C	1	Total 31	C 10	N 5	O 13	P 3	0
2	D	1	Total 31	C 10	N 5	O 13	P 3	0
2	E	1	Total 31	C 10	N 5	O 13	P 3	0
2	F	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 1: Meiotic spindle formation protein mei-1





- Molecule 1: Meiotic spindle formation protein mei-1



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	16185	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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: ATP

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.32	0/1904	0.58	2/2604 (0.1%)
1	B	0.34	0/1904	0.56	1/2604 (0.0%)
1	C	0.35	0/1898	0.59	2/2597 (0.1%)
1	D	0.36	0/1894	0.59	1/2592 (0.0%)
1	E	0.36	0/1898	0.61	2/2597 (0.1%)
1	F	0.33	0/1904	0.57	1/2604 (0.0%)
All	All	0.34	0/11402	0.58	9/15598 (0.1%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	456	PRO	CA-N-CD	-8.80	99.19	111.50
1	E	456	PRO	CA-N-CD	-8.71	99.31	111.50
1	D	456	PRO	CA-N-CD	-8.70	99.32	111.50
1	B	456	PRO	CA-N-CD	-8.66	99.37	111.50
1	F	456	PRO	CA-N-CD	-8.59	99.48	111.50

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	1877	0	1649	48	0
1	B	1877	0	1650	54	0
1	C	1871	0	1639	54	0
1	D	1867	0	1632	61	0
1	E	1871	0	1639	66	0
1	F	1877	0	1650	60	0
2	B	31	0	12	5	0
2	C	31	0	12	5	0
2	D	31	0	12	4	0
2	E	31	0	12	3	0
2	F	31	0	12	3	0
All	All	11395	0	9919	318	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 15.

The worst 5 of 318 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:318:LEU:CD2	1:A:352:ARG:NH1	1.70	1.50
1:E:411:ASN:ND2	1:E:442:ASP:HA	1.34	1.42
1:A:318:LEU:HD22	1:A:352:ARG:NH1	1.25	1.39
1:C:453:SER:OG	1:D:350:ARG:CB	1.91	1.18
1:A:318:LEU:HD23	1:A:352:ARG:NH1	1.55	1.17

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 PDB entries followed by that with respect to all EM entries.

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	269/472 (57%)	243 (90%)	25 (9%)	1 (0%)	38	77
1	B	269/472 (57%)	244 (91%)	25 (9%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	269/472 (57%)	222 (82%)	47 (18%)	0	100	100
1	D	269/472 (57%)	237 (88%)	32 (12%)	0	100	100
1	E	269/472 (57%)	225 (84%)	44 (16%)	0	100	100
1	F	269/472 (57%)	241 (90%)	28 (10%)	0	100	100
All	All	1614/2832 (57%)	1412 (88%)	201 (12%)	1 (0%)	58	89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	321	MET

5.3.2 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 PDB entries followed by that with respect to all EM entries.

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	157/395 (40%)	157 (100%)	0	100	100
1	B	157/395 (40%)	157 (100%)	0	100	100
1	C	156/395 (40%)	156 (100%)	0	100	100
1	D	155/395 (39%)	154 (99%)	1 (1%)	89	94
1	E	156/395 (40%)	155 (99%)	1 (1%)	89	94
1	F	157/395 (40%)	157 (100%)	0	100	100
All	All	938/2370 (40%)	936 (100%)	2 (0%)	95	97

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

Mol	Chain	Res	Type
1	D	357	ILE
1	E	352	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	411	ASN
1	D	411	ASN
1	E	411	ASN
1	F	203	GLN
1	F	411	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	ATP	B	501	-	27,33,33	0.92	1 (3%)	25,52,52	1.75	3 (12%)
2	ATP	C	501	-	27,33,33	0.95	2 (7%)	25,52,52	1.92	3 (12%)
2	ATP	D	501	-	27,33,33	0.89	1 (3%)	25,52,52	1.80	2 (8%)
2	ATP	E	501	-	27,33,33	0.89	1 (3%)	25,52,52	1.79	2 (8%)
2	ATP	F	501	-	27,33,33	0.92	1 (3%)	25,52,52	1.75	2 (8%)

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	ATP	B	501	-	-	0/18/38/38	0/3/3/3
2	ATP	C	501	-	-	0/18/38/38	0/3/3/3
2	ATP	D	501	-	-	0/18/38/38	0/3/3/3
2	ATP	E	501	-	-	0/18/38/38	0/3/3/3
2	ATP	F	501	-	-	0/18/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	ATP	O4'-C1'	2.11	1.44	1.41
2	C	501	ATP	C5-C4	2.77	1.46	1.40
2	D	501	ATP	C5-C4	2.79	1.46	1.40
2	E	501	ATP	C5-C4	2.79	1.46	1.40
2	F	501	ATP	C5-C4	2.80	1.46	1.40

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	501	ATP	N3-C2-N1	-7.03	122.73	128.86
2	D	501	ATP	N3-C2-N1	-7.00	122.77	128.86
2	B	501	ATP	N3-C2-N1	-6.88	122.87	128.86
2	F	501	ATP	N3-C2-N1	-6.86	122.89	128.86
2	C	501	ATP	N3-C2-N1	-6.82	122.92	128.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	ATP	5	0
2	C	501	ATP	5	0
2	D	501	ATP	4	0
2	E	501	ATP	3	0
2	F	501	ATP	3	0

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.