



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Aug 20, 2017 – 07:10 PM EDT

PDB ID : 4CK6
EMDB ID: : EMD-2533
Title : Pseudo-atomic model of microtubule-bound human kinesin-5 motor domain in the ADP.AIFx state, based on cryo-electron microscopy experiment.
Authors : Goulet, A.; Major, J.; Jun, Y.; Gross, S.; Rosenfeld, S.; Moores, C.
Deposited on : unknown
Resolution : 9.20 Å(reported)
Based on PDB ID : 1JFF, 3HQD

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

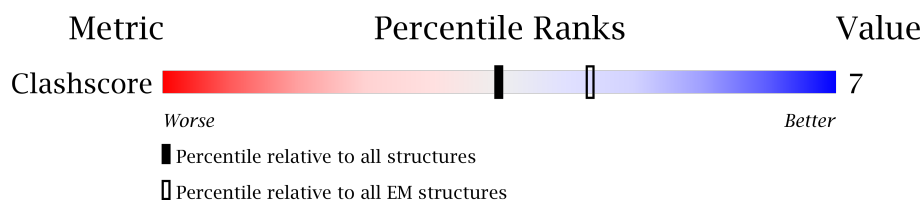
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY



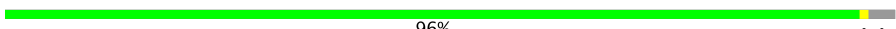
The reported resolution of this entry is 9.20 Å.

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

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	452	 90% • 9%
2	B	445	 94% • •
3	C	373	 96% • •

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 1354 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 TUBULIN ALPHA-1D CHAIN.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	412	Total C 412 412	0	412

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ILE	VAL	conflict	UNP Q2HJ86
A	114	ILE	LEU	conflict	UNP Q2HJ86
A	136	SER	LEU	conflict	UNP Q2HJ86
A	137	VAL	ILE	conflict	UNP Q2HJ86
A	265	GLY	ILE	conflict	UNP Q2HJ86
A	358	GLU	ASP	conflict	UNP Q2HJ86
A	437	VAL	MET	conflict	UNP Q2HJ86
A	450	GLU	ASP	conflict	UNP Q2HJ86

- Molecule 2 is a protein called TUBULIN BETA-2B CHAIN.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	B	426	Total C 426 426	0	426

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	55	ALA	THR	conflict	UNP Q6B856
B	170	VAL	MET	conflict	UNP Q6B856
B	296	ALA	SER	conflict	UNP Q6B856
B	316	VAL	ILE	conflict	UNP Q6B856

- Molecule 3 is a protein called KINESIN-LIKE PROTEIN KIF11.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	C	361	Total C 361 361	0	361

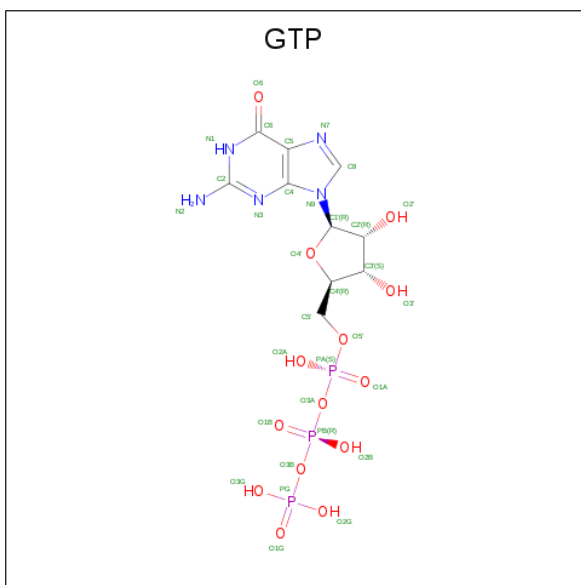
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	25	VAL	CYS	conflict	UNP P52732
C	43	SER	CYS	conflict	UNP P52732
C	87	ALA	CYS	conflict	UNP P52732
C	99	ALA	CYS	conflict	UNP P52732
C	126	CYS	THR	engineered mutation	UNP P52732
C	368	HIS	-	expression tag	UNP P52732
C	369	HIS	-	expression tag	UNP P52732
C	370	HIS	-	expression tag	UNP P52732
C	371	HIS	-	expression tag	UNP P52732
C	372	HIS	-	expression tag	UNP P52732
C	373	HIS	-	expression tag	UNP P52732

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

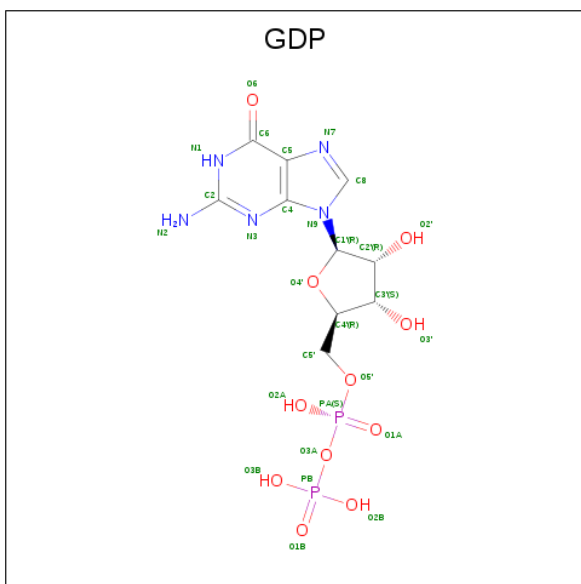
Mol	Chain	Residues	Atoms	AltConf
4	A	1	Total Mg 1 1	0
4	C	1	Total Mg 1 1	0

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



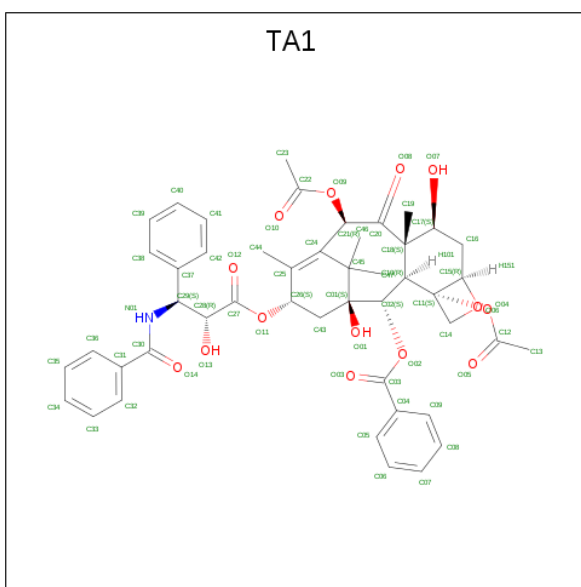
Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{11}\text{P}_2$).



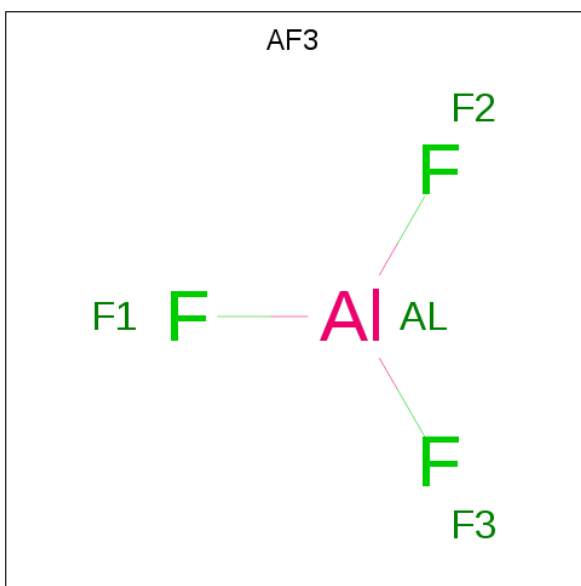
Mol	Chain	Residues	Atoms					AltConf
6	B	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 7 is TAXOL (three-letter code: TA1) (formula: $C_{47}H_{51}NO_{14}$).



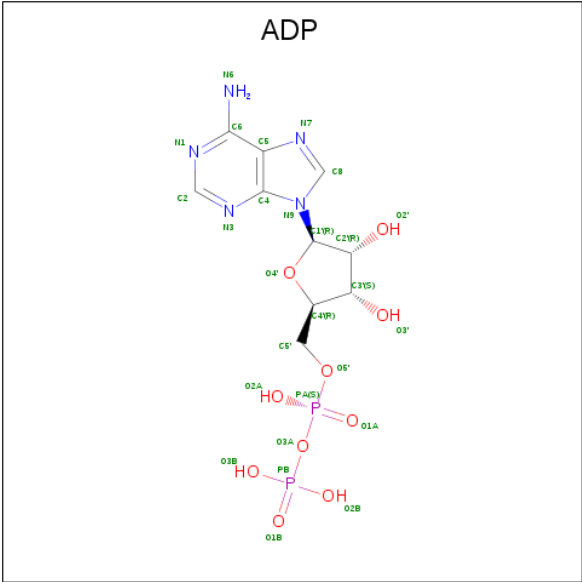
Mol	Chain	Residues	Atoms				AltConf
7	B	1	Total	C	N	O	0
			62	47	1	14	

- Molecule 8 is ALUMINUM FLUORIDE (three-letter code: AF3) (formula: AlF_3).



Mol	Chain	Residues	Atoms			AltConf
8	C	1	Total	Al	F	0
			4	1	3	

- Molecule 9 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$).



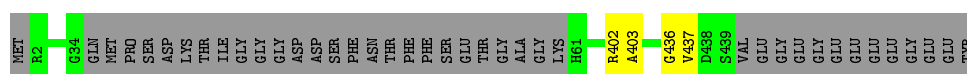
Mol	Chain	Residues	Atoms					AltConf
9	C	1	Total	C	N	O	P	0
			27	10	5	10	2	

3 Residue-property plots

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. 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. 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.

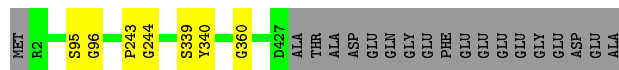
- Molecule 1: TUBULIN ALPHA-1D CHAIN

Chain A: 



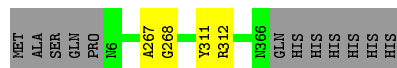
- Molecule 2: TUBULIN BETA-2B CHAIN

Chain B: 



- Molecule 3: KINESIN-LIKE PROTEIN KIF11

Chain C: 



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of particles used	10692	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	FREALIGN	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	18	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	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: GDP, MG, TA1, ADP, GTP, AF3

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	412	0	0	2	0
2	B	426	0	0	4	0
3	C	361	0	0	2	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	32	0	12	0	0
6	B	28	0	12	0	0
7	B	62	0	51	3	0
8	C	4	0	0	0	0
9	C	27	0	12	0	0
All	All	1354	0	87	10	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 7.

The worst 5 of 10 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:436:GLY:CA	1:A:437:VAL:CA	2.46	0.94
2:B:243:PRO:CA	2:B:244:GLY:CA	2.55	0.84
3:C:267:ALA:CA	3:C:268:GLY:CA	2.67	0.71
2:B:95:SER:CA	2:B:96:GLY:CA	2.75	0.65
7:B:1211:TA1:H463	7:B:1211:TA1:H261	1.80	0.63

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 for Mogul analysis.

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$
5	GTP	A	1209	4	27,34,34	1.49	3 (11%)	27,54,54	2.14	4 (14%)
6	GDP	B	1210	-	25,30,30	2.62	8 (32%)	26,47,47	3.66	9 (34%)
7	TA1	B	1211	-	68,68,68	1.97	20 (29%)	105,105,105	1.33	9 (8%)
8	AF3	C	1206	9,4	0,3,3	0.00	-	0,3,3	0.00	-
9	ADP	C	1207	8,4	25,29,29	1.29	4 (16%)	24,45,45	1.46	4 (16%)

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
5	GTP	A	1209	4	-	0/18/38/38	0/3/3/3
6	GDP	B	1210	-	-	0/12/32/32	0/3/3/3
7	TA1	B	1211	-	-	0/41/127/127	0/5/7/7
8	AF3	C	1206	9,4	-	0/0/0/0	0/0/0/0
9	ADP	C	1207	8,4	-	0/12/32/32	0/3/3/3

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	1211	TA1	C08-C07	-5.16	1.25	1.38
6	B	1210	GDP	PB-O2B	-3.55	1.40	1.54
9	C	1207	ADP	PB-O3A	-2.37	1.56	1.60
7	B	1211	TA1	C04-C03	-2.31	1.44	1.49
9	C	1207	ADP	O4'-C1'	-2.26	1.38	1.41

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1210	GDP	C6-C5-C4	-11.47	109.43	120.84
5	A	1209	GTP	C5-C6-N1	-7.10	113.38	123.48
6	B	1210	GDP	N2-C2-N1	-5.98	107.69	117.24
6	B	1210	GDP	C4-C5-N7	-4.99	104.59	109.41
6	B	1210	GDP	N3-C2-N1	-4.92	120.28	127.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	1211	TA1	3	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.