wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 08:51 PM EDT

PDB ID	:	6TIW / pdb_00006tiw
EMDB ID	:	EMD-10421
Title	:	Human kinesin-5 motor domain in the GSK state bound to microtubules (Conformation 2)
Authors	:	Pena, A.; Sweeney, A.; Cook, A.D.; Moores, C.A.; Topf, M.
Deposited on	:	2019-11-22
Resolution	:	3.80 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the ⓘ 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 ⓘ) were used in the production of this report:

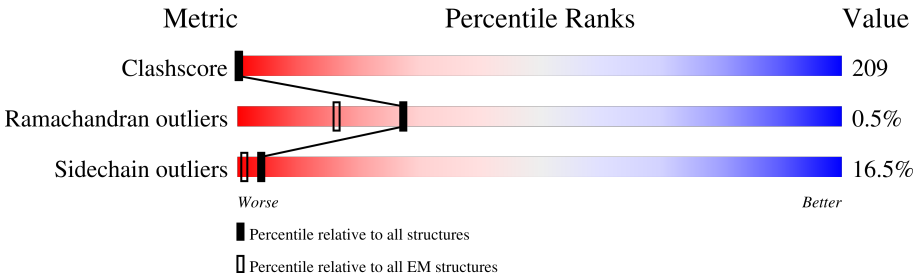
EMDB validation analysis	:	0.0.1.dev117
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	FAILED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

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 3.80 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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%

Mol	Chain	Length	Quality of chain
1	K	391	16% 58% 10% • 15%
2	B	429	10% 72% 15% •
3	A	438	8% 75% 14% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MZK	K	501	-	-	X	-
5	G2P	A	501	-	-	X	-
5	G2P	B	501	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9491 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 Kinesin-like protein KIF11.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	K	334	Total	C	N	O	S	0	0
			2607	1630	466	501	10		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-21	MET	-	initiating methionine	UNP P52732
K	-20	HIS	-	expression tag	UNP P52732
K	-19	HIS	-	expression tag	UNP P52732
K	-18	HIS	-	expression tag	UNP P52732
K	-17	HIS	-	expression tag	UNP P52732
K	-16	HIS	-	expression tag	UNP P52732
K	-15	HIS	-	expression tag	UNP P52732
K	-14	SER	-	expression tag	UNP P52732
K	-13	SER	-	expression tag	UNP P52732
K	-12	GLY	-	expression tag	UNP P52732
K	-11	VAL	-	expression tag	UNP P52732
K	-10	ASP	-	expression tag	UNP P52732
K	-9	LEU	-	expression tag	UNP P52732
K	-8	GLY	-	expression tag	UNP P52732
K	-7	THR	-	expression tag	UNP P52732
K	-6	GLU	-	expression tag	UNP P52732
K	-5	ASN	-	expression tag	UNP P52732
K	-4	LEU	-	expression tag	UNP P52732
K	-3	TYR	-	expression tag	UNP P52732
K	-2	PHE	-	expression tag	UNP P52732
K	-1	GLN	-	expression tag	UNP P52732
K	0	SER	-	expression tag	UNP P52732

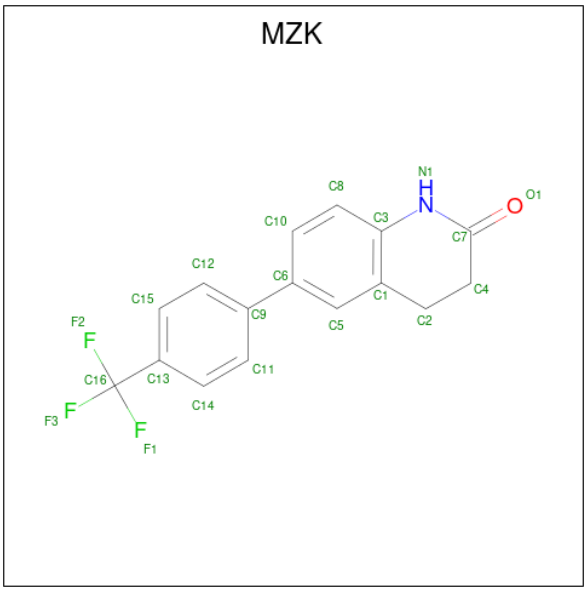
- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	429	Total	C	N	O	S	0	0
			3372	2117	578	651	26		

- Molecule 3 is a protein called Tubulin alpha-1B chain.

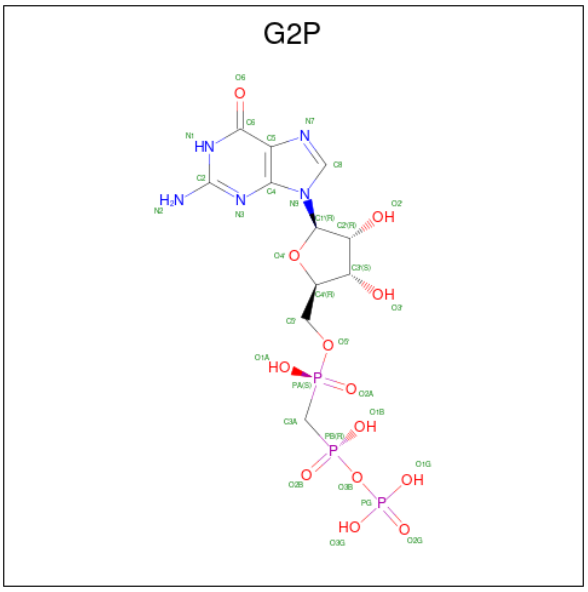
Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	438	Total	C	N	O	S	0	0
			3425	2167	582	654	22		

- Molecule 4 is 6-[4-(trifluoromethyl)phenyl]-3,4-dihydro-1 {H}-quinolin-2-one (CCD ID: MZK) (formula: $C_{16}H_{12}F_3NO$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
4	K	1	Total	C	F	N	O	0
			21	16	3	1	1	

- Molecule 5 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: G2P) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
5	B	1	Total	C	N	O	P	0
			32	11	5	13	3	
5	A	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

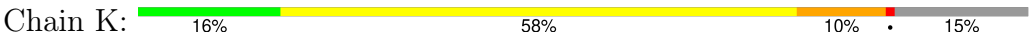
Mol	Chain	Residues	Atoms		AltConf
6	B	1	Total	Mg	0
			1	1	
6	A	1	Total	Mg	0
			1	1	

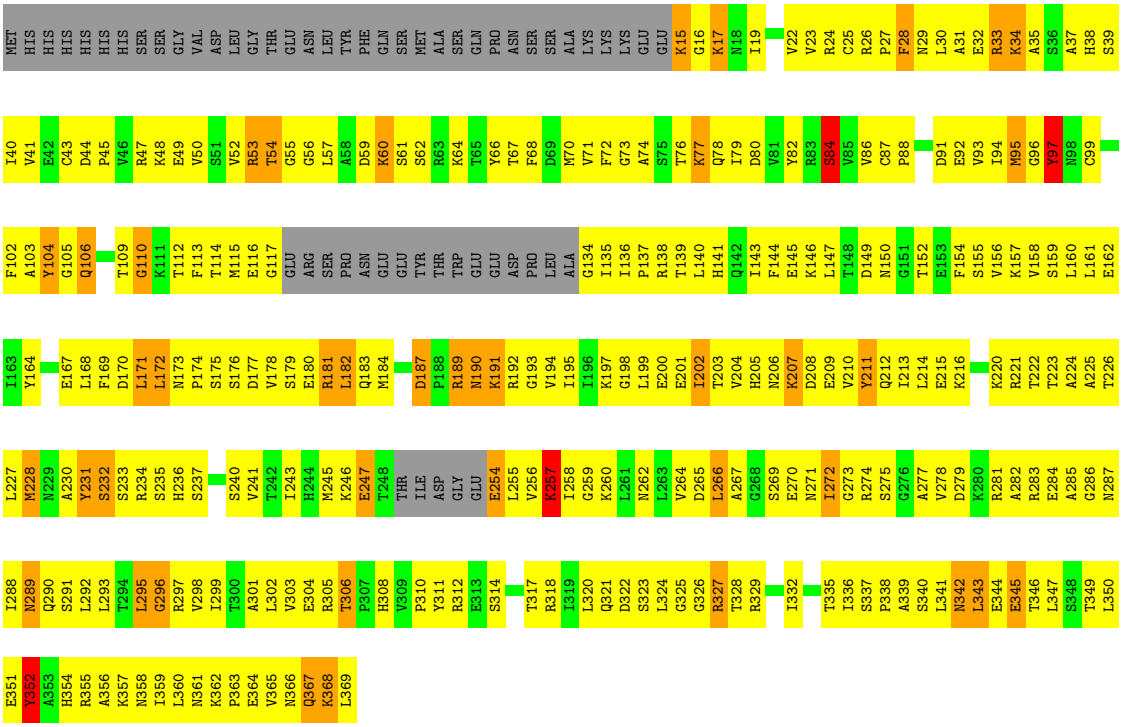
3 Residue-property plots (i)

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. 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: Kinesin-like protein KIF11

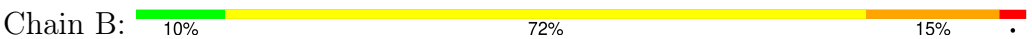
Chain K:

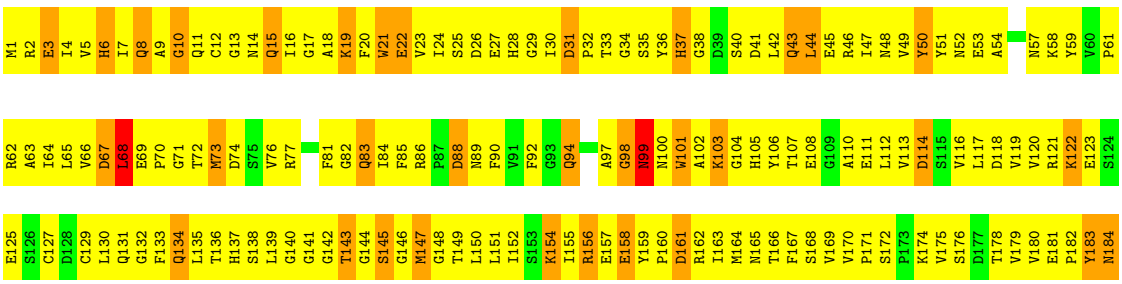


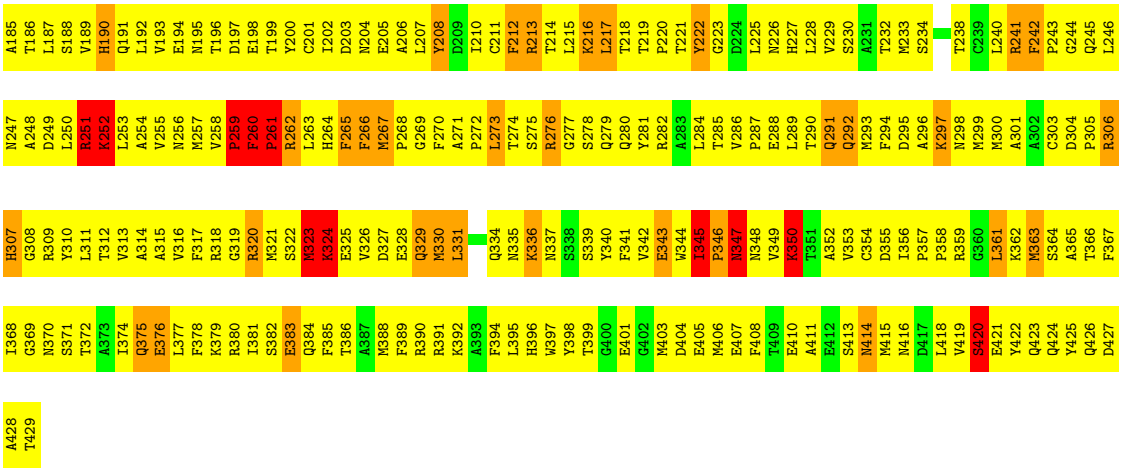


- Molecule 2: Tubulin beta chain

Chain B:

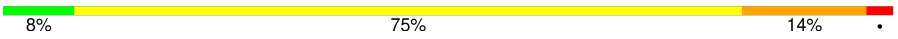






• Molecule 3: Tubulin alpha-1B chain

Chain A:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=-25.7°, rise=8.9 Å, axial sym=C1	Depositor
Number of segments used	507219	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	45	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G2P, MG, MZK

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	K	1.68	13/2640 (0.5%)	1.27	18/3557 (0.5%)
2	B	1.20	5/3447 (0.1%)	1.57	40/4669 (0.9%)
3	A	1.23	12/3503 (0.3%)	1.41	41/4754 (0.9%)
All	All	1.36	30/9590 (0.3%)	1.44	99/12980 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	K	0	5
2	B	0	10
3	A	1	18
All	All	1	33

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	84	SER	CB-OG	-56.93	0.68	1.42
2	B	324	LYS	CE-NZ	25.12	2.11	1.49
1	K	254	GLU	CB-CG	-24.02	1.06	1.52
3	A	221	ARG	CB-CG	19.21	2.04	1.52
3	A	221	ARG	CG-CD	16.02	1.92	1.51

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	251	ARG	NE-CZ-NH2	35.87	138.24	120.30
2	B	251	ARG	NH1-CZ-NH2	-24.10	92.89	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	10	GLY	O-C-N	-19.90	90.86	122.70
3	A	403	ALA	O-C-N	-17.81	94.20	122.70
2	B	260	PHE	CB-CG-CD2	-15.53	109.93	120.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	221	ARG	CA

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	K	106	GLN	Sidechain
1	K	110	GLY	Peptide
1	K	296	GLY	Mainchain
1	K	352	TYR	Sidechain
1	K	53	ARG	Mainchain

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	K	2607	0	2670	967	0
2	B	3372	0	3253	1554	0
3	A	3425	0	3334	1601	0
4	K	21	0	0	14	0
5	A	32	0	14	18	0
5	B	32	0	14	20	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
All	All	9491	0	9285	3916	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 209.

The worst 5 of 3916 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)
2:B:324:LYS:CD	2:B:324:LYS:CE	1.85	1.55
3:A:221:ARG:CA	3:A:221:ARG:CB	1.85	1.51
1:K:181:ARG:HH21	1:K:197:LYS:CG	1.19	1.51
3:A:221:ARG:CD	3:A:221:ARG:CG	1.92	1.47
1:K:95:MET:CE	1:K:97:TYR:HB2	1.45	1.43

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	K	328/391 (84%)	322 (98%)	6 (2%)	0	100	100
2	B	427/429 (100%)	421 (99%)	4 (1%)	2 (0%)	25	58
3	A	436/438 (100%)	422 (97%)	10 (2%)	4 (1%)	14	45
All	All	1191/1258 (95%)	1165 (98%)	20 (2%)	6 (0%)	27	58

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	261	PRO
3	A	179	THR
3	A	100	ALA
3	A	405	VAL
3	A	406	HIS

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 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	K	292/343 (85%)	255 (87%)	37 (13%)	3 19
2	B	369/369 (100%)	299 (81%)	70 (19%)	1 8
3	A	369/369 (100%)	306 (83%)	63 (17%)	1 11
All	All	1030/1081 (95%)	860 (84%)	170 (16%)	4 12

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	84	ARG
3	A	254	GLU
3	A	96	LYS
3	A	179	THR
3	A	309	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	414	ASN
3	A	88	HIS
3	A	342	GLN
2	B	424	GLN
3	A	15	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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	G2P	B	501	6	25,34,34	1.24	3 (12%)	32,54,54	2.24	6 (18%)
4	MZK	K	501	-	23,23,23	0.93	1 (4%)	34,34,34	0.76	0
5	G2P	A	501	6	25,34,34	1.10	1 (4%)	32,54,54	2.10	4 (12%)

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	G2P	B	501	6	-	4/15/38/38	0/3/3/3
4	MZK	K	501	-	-	0/10/19/19	0/3/3/3
5	G2P	A	501	6	-	7/15/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	501	MZK	C7-N1	3.11	1.38	1.35
5	B	501	G2P	C6-N1	3.08	1.38	1.33
5	A	501	G2P	C6-N1	3.05	1.38	1.33
5	B	501	G2P	PA-O1A	-2.37	1.50	1.56
5	B	501	G2P	PB-O1B	-2.31	1.50	1.56

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	501	G2P	C5-C6-N1	-8.31	112.31	123.42
5	B	501	G2P	C5-C6-N1	-8.20	112.46	123.42
5	B	501	G2P	C2-N1-C6	6.53	125.04	115.96
5	A	501	G2P	C2-N1-C6	6.49	124.99	115.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	501	G2P	N3-C2-N1	-3.19	123.15	127.21

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	G2P	PB-C3A-PA-O1A
5	B	501	G2P	PB-C3A-PA-O2A
5	B	501	G2P	PB-C3A-PA-O5'
5	A	501	G2P	PB-O3B-PG-O1G
5	A	501	G2P	PB-C3A-PA-O1A

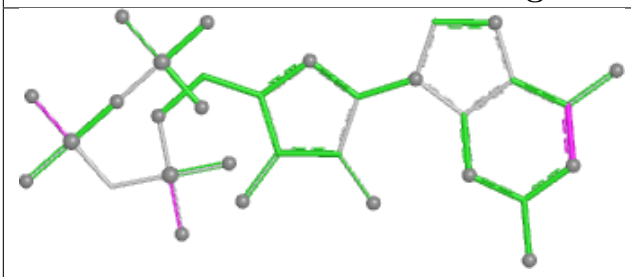
There are no ring outliers.

3 monomers are involved in 52 short contacts:

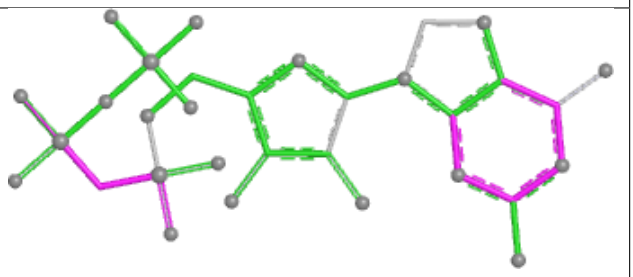
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	501	G2P	20	0
4	K	501	MZK	14	0
5	A	501	G2P	18	0

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 then 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.

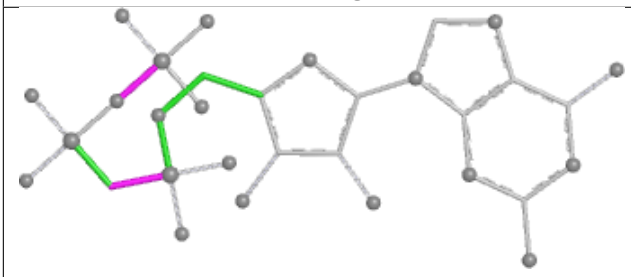
Ligand G2P B 501



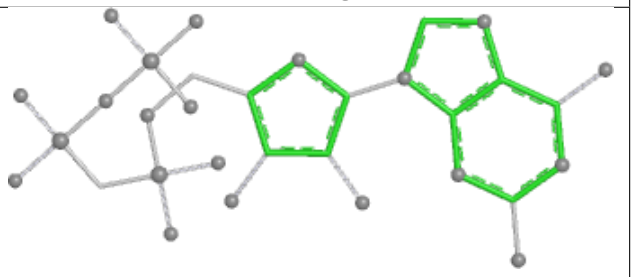
Bond lengths



Bond angles

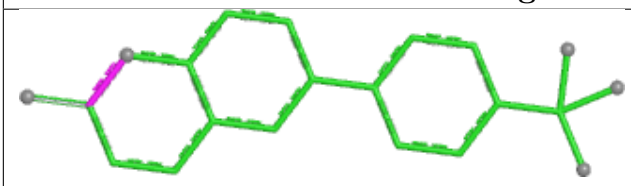


Torsions

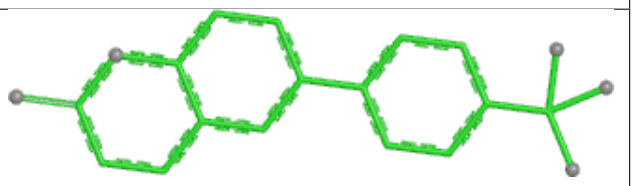


Rings

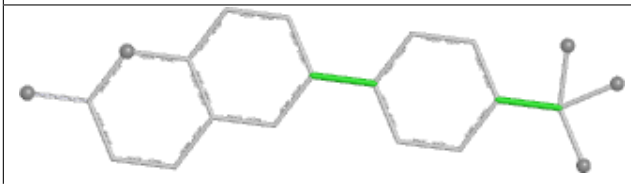
Ligand MZK K 501



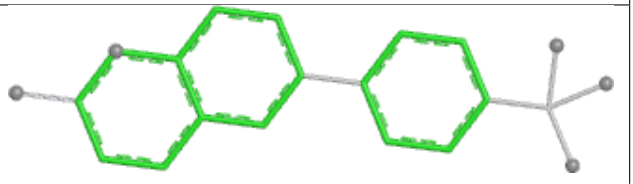
Bond lengths



Bond angles

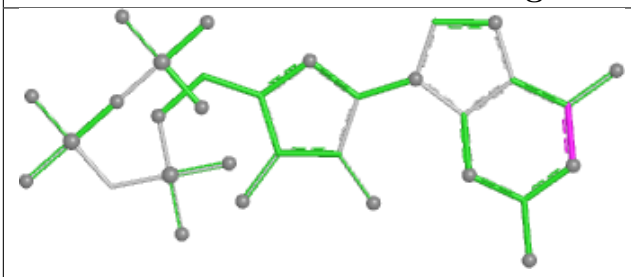


Torsions

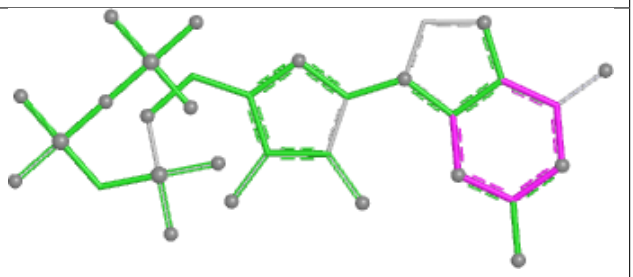


Rings

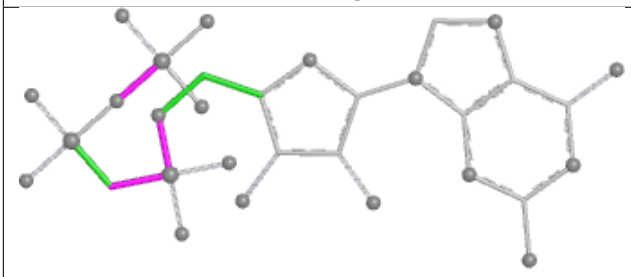
Ligand G2P A 501



Bond lengths



Bond angles



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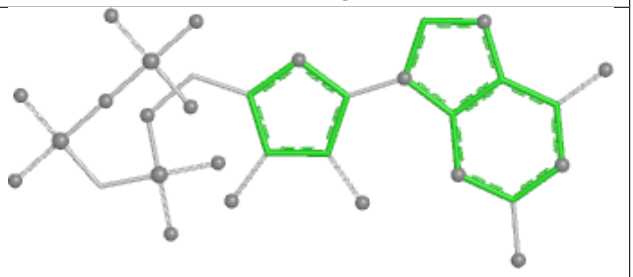

Rings

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-10421. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution

This section was not generated.

7.2 Volume estimate versus contour level

This section was not generated.

7.3 Rotationally averaged power spectrum

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.