



wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 09:59 pm BST

PDB ID : 6TA3 / pdb_00006ta3
EMDB ID : EMD-10421
Title : Human kinesin-5 motor domain in the GSK-1 state bound to microtubules (Conformation 1)
Authors : Pena, A.; Sweeney, A.; Cook, A.D.; Moores, C.A.; Topf, M.
Deposited on : 2019-10-29
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 : 1.8.4, CSD as541be (2020)
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

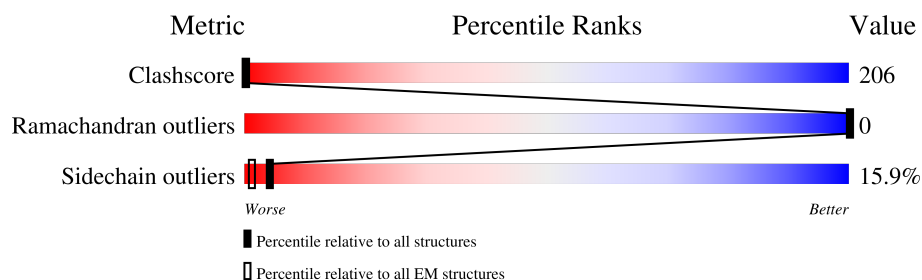
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

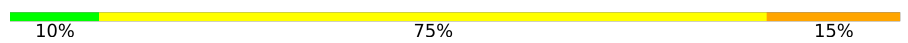
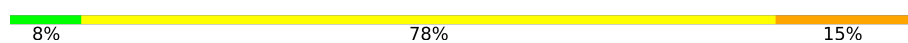
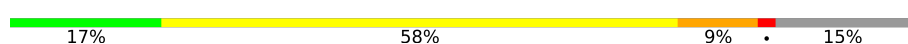
The reported resolution of this entry is 3.80 Å.

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	B	429	
2	A	438	
3	K	391	

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	G2P	A	501	-	-	X	-
4	G2P	B	501	-	-	X	-

2 Entry composition

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 Tubulin beta chain.

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

- Molecule 2 is a protein called Tubulin alpha-1B chain.

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

- Molecule 3 is a protein called Kinesin-like protein KIF11.

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

There are 22 discrepancies between the modelled and reference sequences:

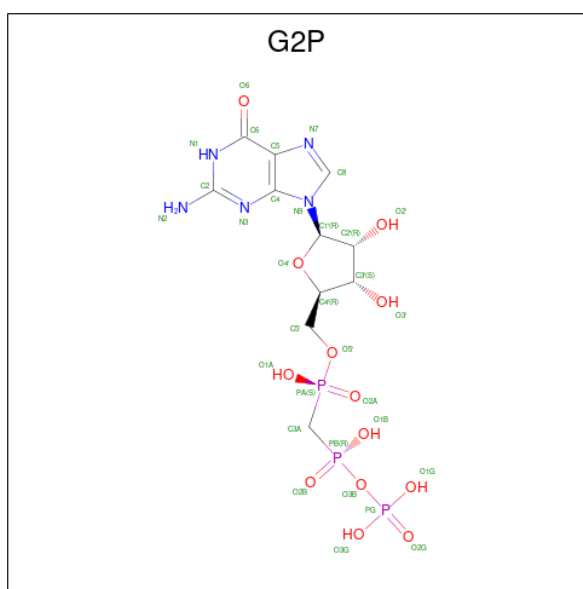
Chain	Residue	Modelled	Actual	Comment	Reference
K	-21	MET	-	initiating methionine	UNP P52732
K	-20	HIS	-	expression tag	UNP P52732
K	-19	HIS	-	expression tag	UNP P52732
K	-18	HIS	-	expression tag	UNP P52732
K	-17	HIS	-	expression tag	UNP P52732
K	-16	HIS	-	expression tag	UNP P52732
K	-15	HIS	-	expression 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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 4 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: G2P) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



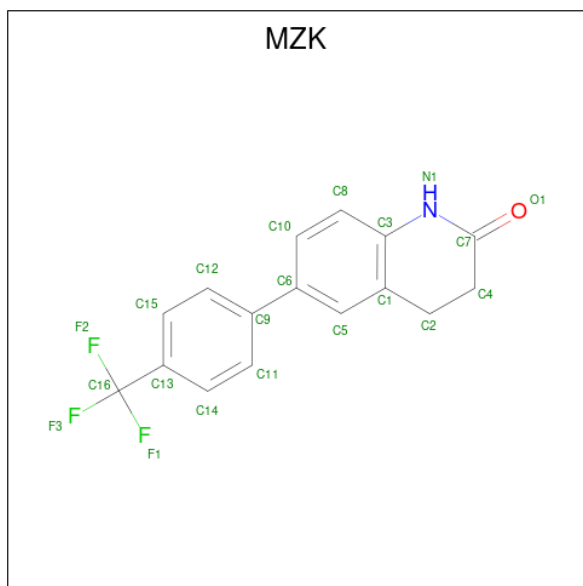
Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total	C	N	O	P	0
			32	11	5	13	3	
4	A	1	Total	C	N	O	P	0
			32	11	5	13	3	

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 6 is 6-[4-(trifluoromethyl)phenyl]-3,4-dihydro-1 {H}-quinolin-2-one (CCD ID:

MZK) (formula: C₁₆H₁₂F₃NO) (labeled as "Ligand of Interest" by depositor).

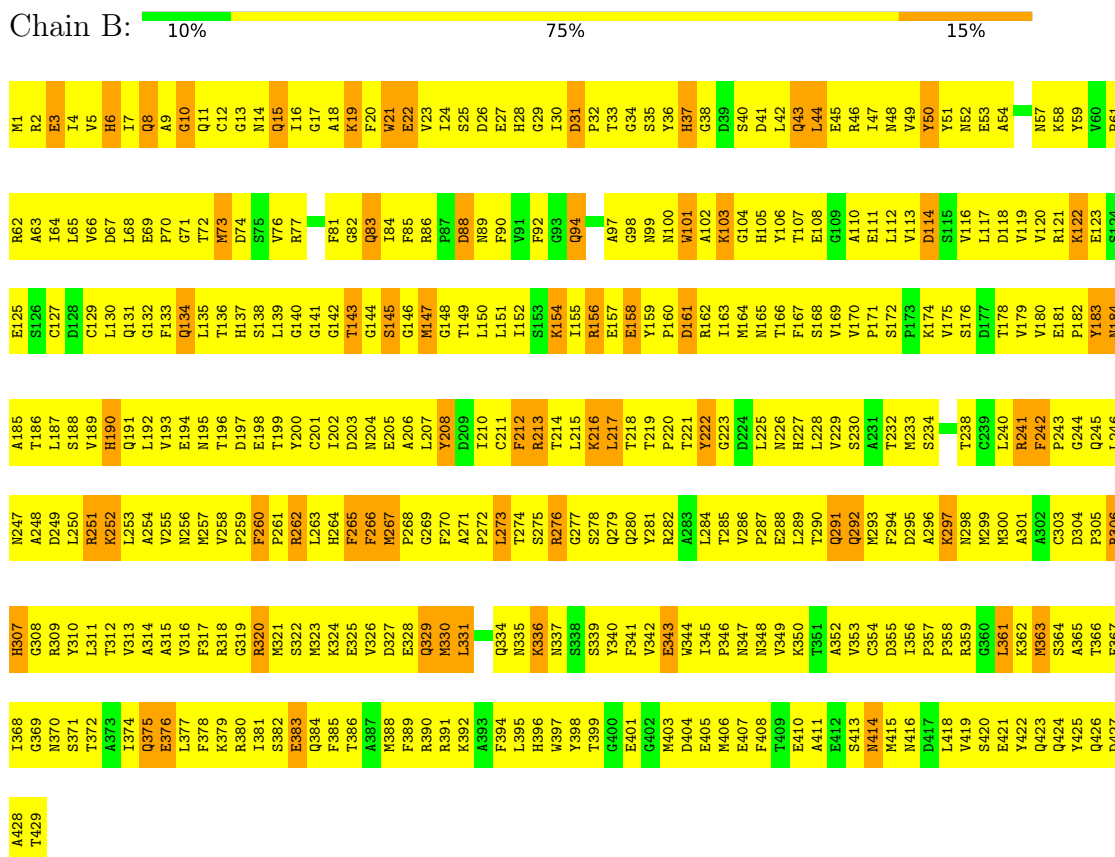


Mol	Chain	Residues	Atoms					AltConf
			Total	C	F	N	O	
6	K	1	21	16	3	1	1	0

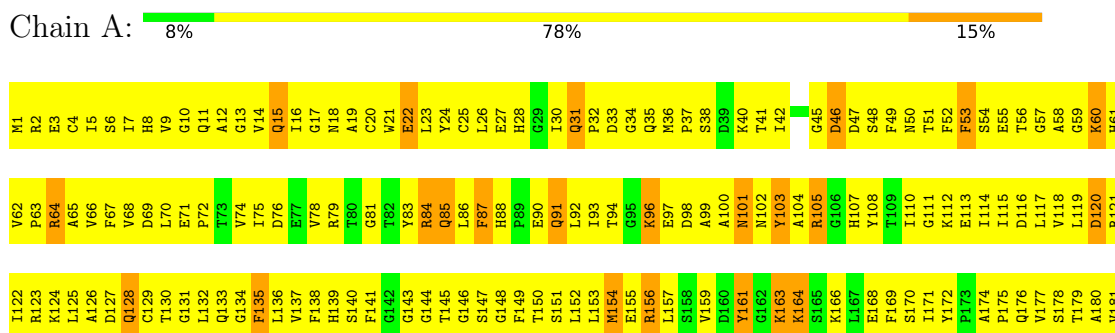
3 Residue-property plots

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: Tubulin beta chain



- Molecule 2: Tubulin alpha-1B chain



V182	L242	M302	V362	E423
E183	R243	V303	V363	D424
P184	F244	K304	P364	M425
Y185	D245	C305	A426	A426
N186	G246	D306	D367	A427
S187	A247	P307	L368	L428
I188	L248	R308	A369	E429
L189	L249	H309	K370	K430
T190	V250	K311	V371	D431
H191	D251	K312	Q372	Y432
H192	L252	Y312	K373	E433
T193	T253	M313	A374	E434
L194	E254	A314	V375	V435
L195	F255	C315	C376	G436
E196	Q256	C316	K377	V437
H197	T257	L317	L378	D438
S198	N258	L318	S379	
D199	L259	Y319	N380	
C200	V260	R320	T381	
A201	P261	G321	T382	
F202	Y262	D322	A383	
M203	P263	V323	K384	
V204	R264	V324	A385	
D205	I265	P325	E386	
N206	H266	K326	A387	
E207	F267	D327	W388	
A208	P268	V328	A389	
I209	L269	N329	K390	
Y210	A270	A330	L391	
D211	T271	A331	D392	
L212	Y272	I332	H393	
C213	A273	A333	K394	
R214	T274	T334	F395	
R215	V275	I335	D396	
N216	I276	K336	L397	
L217	T277	T337	M398	
D218	A278	K338	Y399	
I219	E279	R339	A400	
E220	K280	S340	K401	
R221	A281	I341	A402	
P222	Y282	Q342	A403	
T223	H283	F343	F404	
Y224	E284	V344	V405	
T225	Q285	D345	H406	
N226	L286	W346	W407	
L227	S287	P347	Y408	
N228	V288	P348	V409	
R229	A289	T349	Q410	
L230	E290	G350	E411	
I231	I291	F351	G412	
S232	T292	K352	M413	
Q233	R293	V353	E414	
I234	A294	G354	E415	
V235	C295	I355	G416	
S236	F296	N356	E417	
S237	E297	Y357	F418	
I238	P298	Q358	S419	
T239	A299	P359	E420	
A240	N300	P360	A421	
S241	Q301	T361	R422	

• Molecule 3: Kinesin-like protein KIF11

Chain K: 17% 58% 9% 15%

MET	Y102	L143	L227	T288	A353
HIS	A103	Y164	M228	N289	H354
HIS	Y104	E167	N229	Q290	R355
HIS	G105	L168	A230	S291	A356
HIS	Q106	F169	S231	K357	N358
HIS	T109	D170	S232	L292	L359
SER	G110	L171	S233	L293	L360
SER	K111	L172	R234	R297	N361
GLY	T112	M173	S235	V298	K362
VAL	F113	P174	H236	I299	P363
ASP	T114	S175	S237	T300	E364
LEU	M115	S176	S240	A301	V365
GLY	E116	D177	V241	L302	V366
THR	G117	V178	T242	V303	Q367
GLU	GLU	S179	I243	E304	K368
ASN	ARG	E180	H244	T306	L369
ASN	P181	L182	M245	P307	
PHE	ASN	Q183	K246	H308	
GLN	GLU	M184	E247	V309	
GLN	TRP	D187	T248	P310	
GLN	GLU	P188	ILE	Y311	
GLN	GLU	A189	ASP	R312	
GLN	GLU	N190	GLY	E313	
GLN	GLU	K191	GLU	S314	
GLN	GLU	G192	E254	T317	
GLN	GLU	G193	L255	R318	
GLN	GLU	V194	V256	L319	
GLN	GLU	I195	K257	L320	
GLN	GLU	L196	L258	Q321	
GLN	GLU	L197	G259	D322	
GLN	GLU	G198	L260	S323	
GLN	GLU	L199	L261	L324	
GLN	GLU	E200	N262	G325	
GLN	GLU	R138	L263	G326	
GLN	GLU	T139	L264	R327	
GLN	GLU	L140	D265	T328	
GLN	GLU	H141	L266	R329	
GLN	GLU	I143	A267	I332	
GLN	GLU	F144	S269	T335	
GLN	GLU	K145	E270	L336	
GLN	GLU	L146	N271	S337	
GLN	GLU	L147	I272	P338	
GLN	GLU	T148	G273	A339	
GLN	GLU	D149	R274	S340	
GLN	GLU	N150	S275	L341	
GLN	GLU	G151	G276	N342	
GLN	GLU	T152	A277	L343	
GLN	GLU	E153	V278	E344	
GLN	GLU	F154	D279	E345	
GLN	GLU	S155	K280	T346	
GLN	GLU	V156	R281	L347	
GLN	GLU	V157	A282	R283	
GLN	GLU	K157	R283	S348	
GLN	GLU	N158	E284	T349	
GLN	GLU	S159	A285	L350	
GLN	GLU	L160	G286	E351	
GLN	GLU	L161	A224	Y352	
GLN	GLU	L162	T225		
GLN	GLU	T226			
GLN	GLU	T227			
GLN	GLU	T228			
GLN	GLU	T229			
GLN	GLU	T230			
GLN	GLU	T231			
GLN	GLU	T232			
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GLN	GLU	T282			
GLN	GLU	T283			
GLN	GLU	T284			
GLN	GLU	T285			
GLN	GLU	T286			
GLN	GLU	T287			

4 Experimental information

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 ($e^-/\text{\AA}^2$)	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 [i](#)

5.1 Standard geometry [i](#)

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

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	B	1.06	0/3447	1.21	3/4669 (0.1%)
2	A	1.04	0/3503	1.14	1/4754 (0.0%)
3	K	1.67	11/2640 (0.4%)	1.26	18/3557 (0.5%)
All	All	1.25	11/9590 (0.1%)	1.20	22/12980 (0.2%)

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	B	0	1
2	A	0	3
3	K	0	6
All	All	0	10

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	84	SER	CB-OG	-56.93	0.68	1.42
3	K	254	GLU	CB-CG	-24.02	1.06	1.52
3	K	247	GLU	CB-CG	-13.94	1.25	1.52
3	K	247	GLU	CD-OE1	-11.45	1.13	1.25
3	K	257	LYS	CB-CG	-10.64	1.23	1.52

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	10	GLY	O-C-N	-19.90	90.86	122.70
1	B	10	GLY	CA-C-N	14.42	148.93	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	254	GLU	CA-CB-CG	11.92	139.62	113.40
3	K	84	SER	CA-CB-OG	10.40	139.29	111.20
3	K	257	LYS	CA-CB-CG	9.90	135.18	113.40

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	399	TYR	Sidechain
2	A	402	ARG	Mainchain
2	A	415	GLU	Sidechain
1	B	15	GLN	Peptide
3	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	B	3372	0	3243	1485	0
2	A	3425	0	3330	1589	0
3	K	2607	0	2670	964	0
4	A	32	0	14	31	0
4	B	32	0	14	19	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	K	21	0	0	0	0
All	All	9491	0	9271	3868	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 206.

The worst 5 of 3868 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:A:427:ALA:HB2	3:K:57:LEU:CD2	1.27	1.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:427:ALA:CB	3:K:57:LEU:CD2	1.84	1.55
3:K:181:ARG:HH21	3:K:197:LYS:CG	1.19	1.51
2:A:409:VAL:HG21	3:K:293:LEU:CG	1.46	1.44
3:K:95:MET:CE	3:K:97:TYR:HB2	1.45	1.43

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 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 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	B	427/429 (100%)	426 (100%)	1 (0%)	0	100	100
2	A	436/438 (100%)	434 (100%)	2 (0%)	0	100	100
3	K	328/391 (84%)	322 (98%)	6 (2%)	0	100	100
All	All	1191/1258 (95%)	1182 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	B	369/369 (100%)	303 (82%)	66 (18%)	1	9
2	A	369/369 (100%)	307 (83%)	62 (17%)	1	12
3	K	292/343 (85%)	256 (88%)	36 (12%)	4	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1030/1081 (95%)	866 (84%)	164 (16%)	4 13

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	346	TRP
3	K	181	ARG
2	A	394	LYS
3	K	28	PHE
3	K	207	LYS

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	A	176	GLN
2	A	300	ASN
3	K	342	ASN
2	A	186	ASN
2	A	233	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
4	G2P	A	501	5	27,34,34	1.11	1 (3%)	33,54,54	1.99	5 (15%)
4	G2P	B	501	1,5	27,34,34	1.19	3 (11%)	33,54,54	2.13	7 (21%)
6	MZK	K	501	-	23,23,23	1.37	1 (4%)	34,34,34	1.15	3 (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
4	G2P	A	501	5	-	7/15/38/38	0/3/3/3
4	G2P	B	501	1,5	-	4/15/38/38	0/3/3/3
6	MZK	K	501	-	-	0/10/19/19	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	K	501	MZK	C7-N1	3.84	1.39	1.35
4	B	501	G2P	C6-N1	3.01	1.38	1.33
4	A	501	G2P	C6-N1	2.99	1.38	1.33
4	B	501	G2P	PA-O1A	-2.46	1.50	1.56
4	B	501	G2P	PB-O1B	-2.40	1.50	1.56

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	G2P	C5-C6-N1	-8.13	112.31	123.43
4	B	501	G2P	C5-C6-N1	-8.02	112.46	123.43
4	B	501	G2P	C2-N1-C6	5.73	125.04	115.93
4	A	501	G2P	C2-N1-C6	5.70	124.99	115.93
4	B	501	G2P	O1B-PB-C3A	3.17	119.55	106.58

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

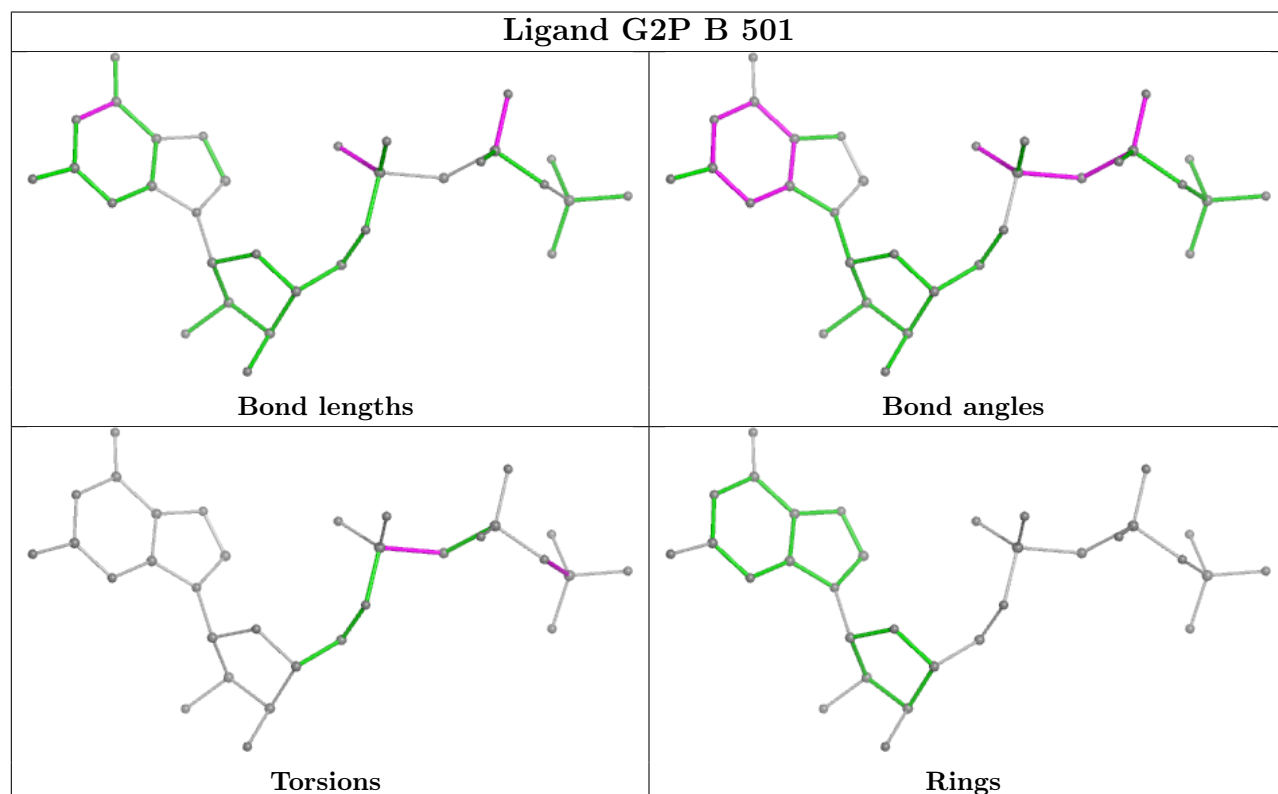
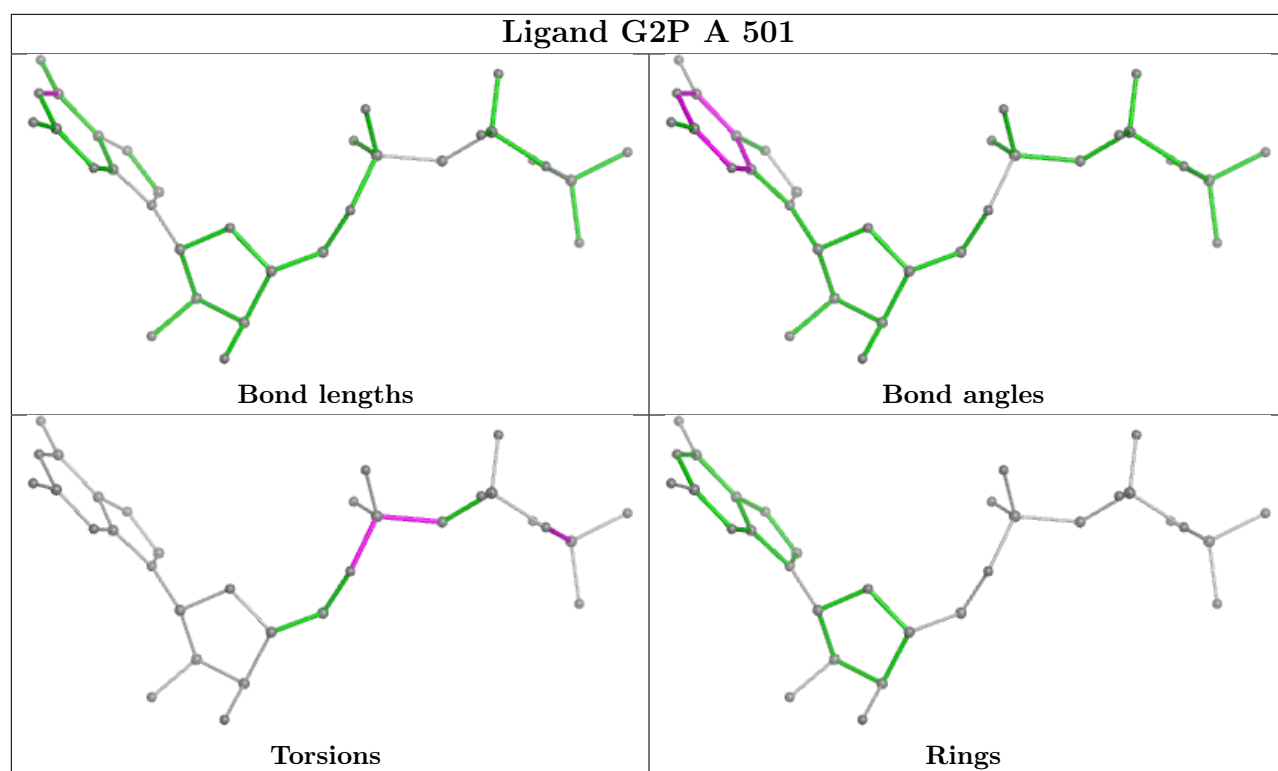
Mol	Chain	Res	Type	Atoms
4	B	501	G2P	PB-C3A-PA-O1A
4	B	501	G2P	PB-C3A-PA-O2A
4	B	501	G2P	PB-C3A-PA-O5'
4	A	501	G2P	PB-O3B-PG-O1G
4	A	501	G2P	PB-C3A-PA-O1A

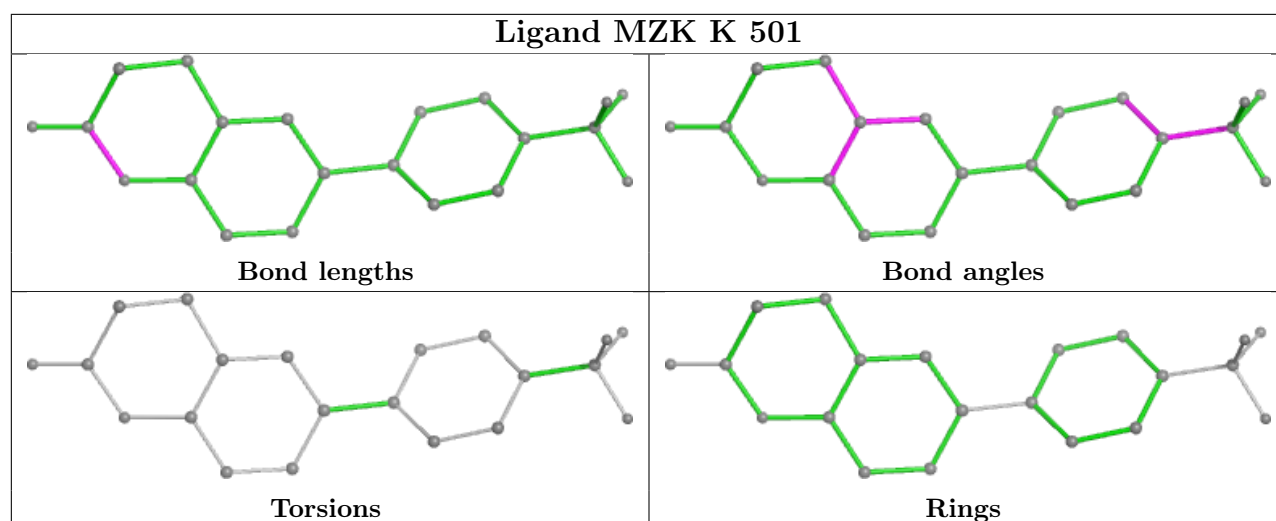
There are no ring outliers.

2 monomers are involved in 50 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	G2P	31	0
4	B	501	G2P	19	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 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.





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

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

9 Map-model fit

This section was not generated.