



wwPDB EM Validation Summary Report ⓘ

Jul 20, 2024 – 10:20 am BST

PDB ID : 8QV2
EMDB ID : EMD-18665
Title : Structure of the native γ -Tubulin Ring Complex (γ TuRC) capping microtubule minus ends at the spindle pole body
Authors : Dendooven, T.; Yatskevich, S.; Burt, A.; Bellini, D.; Kilmartin, J.; Barford, D.
Deposited on : 2023-10-17
Resolution : 9.20 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:

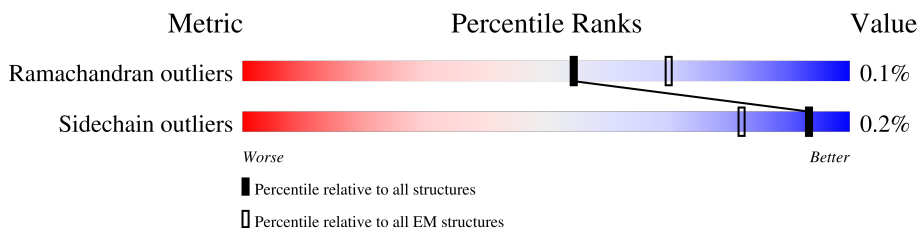
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

1 Overall quality at a glance i

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.



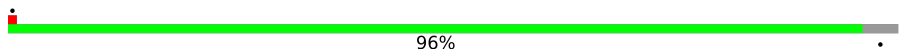
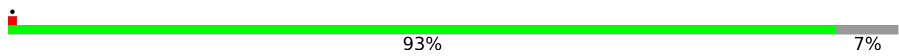
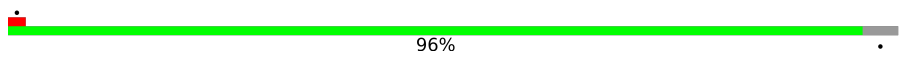
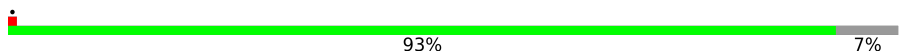
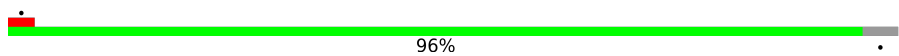







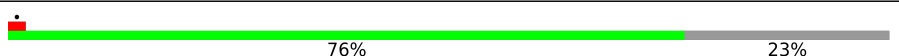
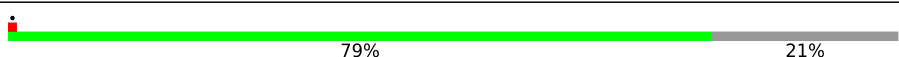
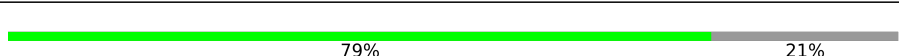

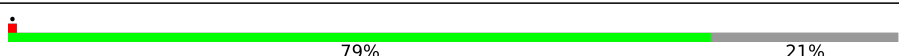
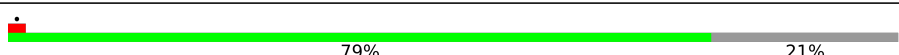
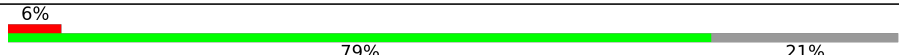
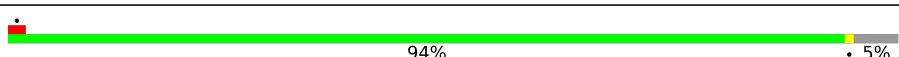
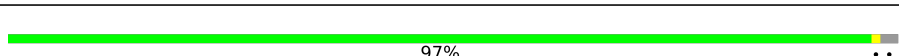
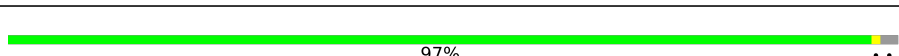
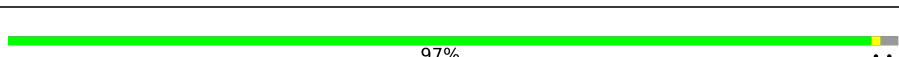
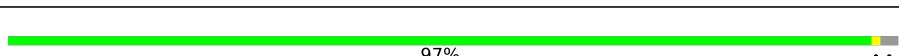
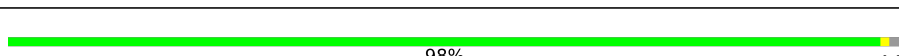
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	a	473	<div style="display: flex; align-items: center;"> <div style="width: 15%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 78%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">15% 93% 7%</p>
1	b	473	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 94%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 4%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 96% .</p>
1	c	473	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 91%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 93% 7%</p>
1	d	473	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 94%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 4%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 96% .</p>
1	e	473	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 91%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 93% 7%</p>
1	f	473	<div style="display: flex; align-items: center;"> <div style="width: 94%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 4%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 96% .</p>
1	g	473	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 91%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 93% 7%</p>
1	h	473	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 94%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 4%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 96% .</p>
1	i	473	<div style="display: flex; align-items: center;"> <div style="width: 93%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 7%; height: 10px; background-color: grey; margin-right: 5px;"></div> </div> <p style="text-align: center;">. 93% 7%</p>

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Mol	Chain	Length	Quality of chain
1	j	473	 96%
1	k	473	 93% 7%
1	l	473	 96%
1	m	473	 93% 7%
1	n	473	 96%
2	C	823	 84% 16% 5%
2	E	823	 85% 15%
2	G	823	 85% 15%
2	I	823	 85% 15%
2	K	823	 85% 15%
2	M	823	 85% 15%
2	O	823	 85% 15%
3	D	846	 76% 23%
3	F	846	 79% 21%
3	H	846	 79% 21%
3	J	846	 79% 21%
3	L	846	 79% 21%
3	N	846	 79% 21%
3	P	846	 79% 21% 6%
4	Ab	447	 94% 5%
4	Ac	447	 97% ..
4	Ad	447	 97% ..
4	Ae	447	 97% ..
4	Af	447	 97% ..
4	Ag	447	 98% ..

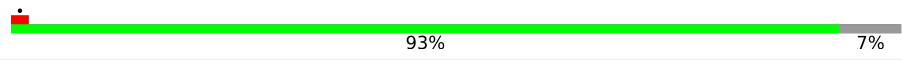
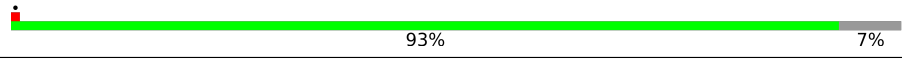
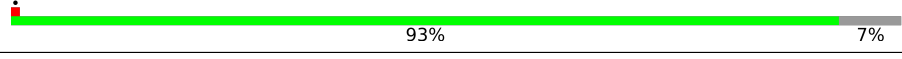
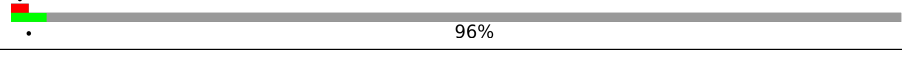
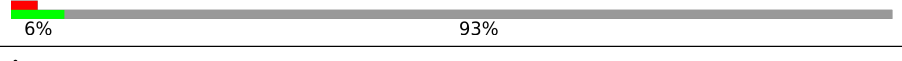
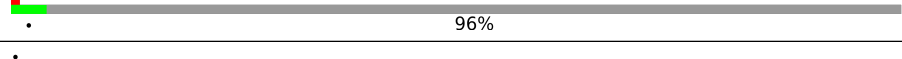
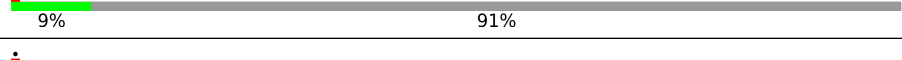
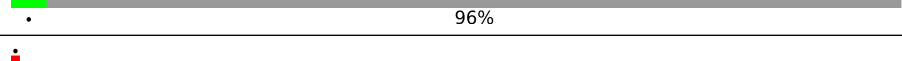
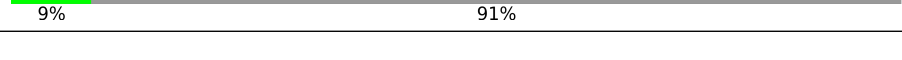
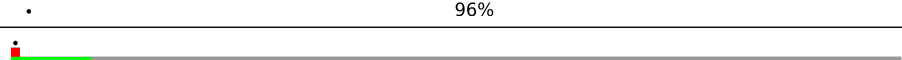
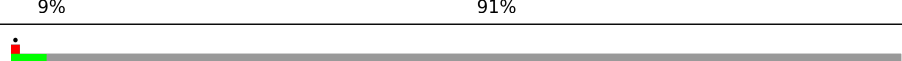
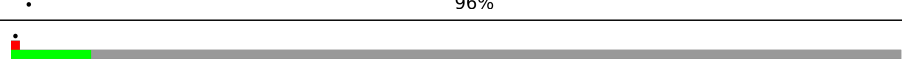
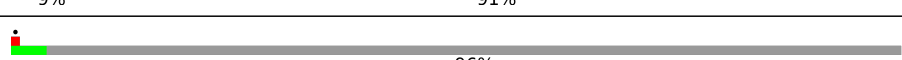
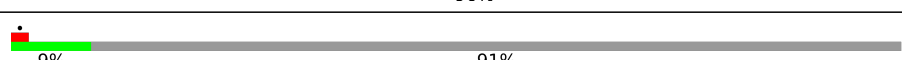
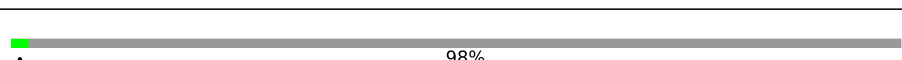
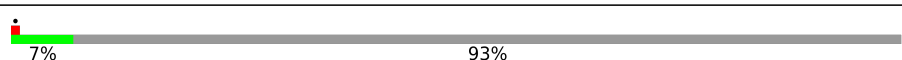
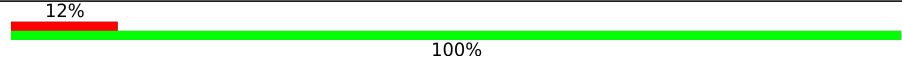

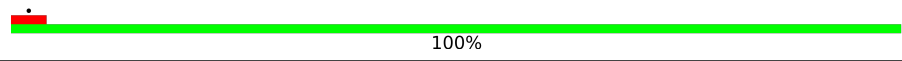

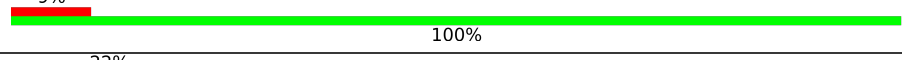

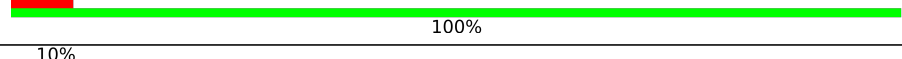


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Mol	Chain	Length	Quality of chain
4	Ah	447	97%
4	Ai	447	98%
4	Aj	447	98%
4	Ak	447	97%
4	Al	447	98%
4	Am	447	98%
4	An	447	98%
4	Ao	447	98%
4	Ap	447	98%
4	Aq	447	97%
4	Ar	447	98%
5	Bb	457	90% 9%
5	Bc	457	93% 7%
5	Bd	457	93% 7%
5	Be	457	93% 7%
5	Bf	457	93% 7%
5	Bg	457	93% 7%
5	Bh	457	93% 7%
5	Bi	457	93% 7%
5	Bj	457	93% 7%
5	Bk	457	93% 7%
5	Bl	457	93% 7%
5	Bm	457	93% 7%
5	Bn	457	93% 7%
5	Bo	457	93% 7%

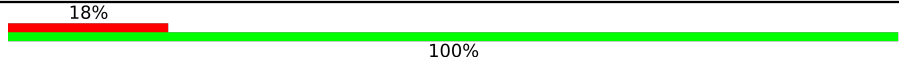
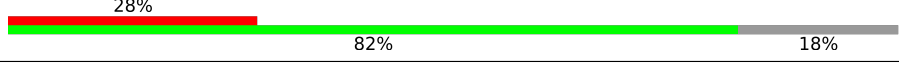
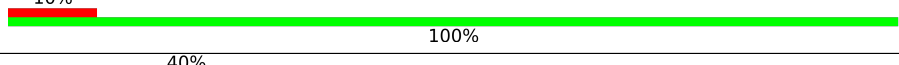


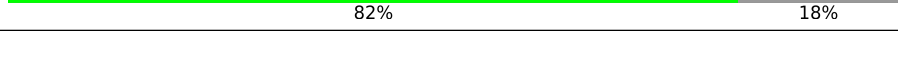
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Mol	Chain	Length	Quality of chain
5	Bp	457	
5	Bq	457	
5	Br	457	
6	Sa	944	
6	Sb	944	
6	Sc	944	
6	Sd	944	
6	Se	944	
6	Sf	944	
6	Sg	944	
6	Sh	944	
6	Si	944	
6	Sj	944	
6	Sk	944	
6	Sl	944	
6	Sm	944	
6	Sn	944	
7	Ua	67	
7	Ub	67	
7	Uc	67	
7	Ud	67	
7	Ue	67	
7	Uf	67	
7	Ug	67	
7	Uh	67	

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Mol	Chain	Length	Quality of chain
7	Ui	67	 18% 100%
7	Uj	67	 28% 82% 18%
7	Uk	67	 10% 100%
7	Ul	67	 40% 82% 18%
7	Um	67	 42% 100%
7	Un	67	 58% 82% 18%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 255200 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 gamma chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	b	453	Total 3545	C 2217	N 599	O 712	S 17	0	0
1	c	441	Total 3448	C 2158	N 585	O 689	S 16	0	0
1	d	453	Total 3545	C 2217	N 599	O 712	S 17	0	0
1	e	439	Total 3433	C 2149	N 581	O 687	S 16	0	0
1	f	453	Total 3545	C 2217	N 599	O 712	S 17	0	0
1	g	441	Total 3448	C 2158	N 585	O 689	S 16	0	0
1	h	453	Total 3545	C 2217	N 599	O 712	S 17	0	0
1	i	439	Total 3433	C 2149	N 581	O 687	S 16	0	0
1	j	453	Total 3545	C 2217	N 599	O 712	S 17	0	0
1	k	441	Total 3448	C 2158	N 585	O 689	S 16	0	0
1	l	453	Total 3545	C 2217	N 599	O 712	S 17	0	0
1	m	439	Total 3433	C 2149	N 581	O 687	S 16	0	0
1	n	453	Total 3545	C 2217	N 599	O 712	S 17	0	0
1	a	440	Total 3441	C 2153	N 584	O 688	S 16	0	0

- Molecule 2 is a protein called Spindle pole body component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	693	Total 5778	C 3716	N 974	O 1059	S 29	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	G	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	I	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	K	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	M	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		
2	O	701	Total	C	N	O	S	0	0
			5847	3760	985	1073	29		

- Molecule 3 is a protein called Spindle pole body component.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	651	Total	C	N	O	S	0	0
			5390	3494	886	994	16		
3	F	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	H	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	J	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	L	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	N	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		
3	P	672	Total	C	N	O	S	0	0
			5557	3595	918	1028	16		

- Molecule 4 is a protein called Tubulin alpha-1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ad	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ac	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Af	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		
4	Ae	440	Total	C	N	O	S	0	0
			3438	2167	585	667	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	Ah	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Ag	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Aj	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Ai	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Al	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Ak	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	An	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Am	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Ab	423	Total 3312	C 2089	N 563	O 641	S 19	0	0
4	Ap	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Ao	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Ar	440	Total 3438	C 2167	N 585	O 667	S 19	0	0
4	Aq	440	Total 3438	C 2167	N 585	O 667	S 19	0	0

- Molecule 5 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	Bd	427	Total 3343	C 2098	N 571	O 653	S 21	0	0
5	Bc	427	Total 3343	C 2098	N 571	O 653	S 21	0	0
5	Bf	427	Total 3343	C 2098	N 571	O 653	S 21	0	0
5	Be	427	Total 3343	C 2098	N 571	O 653	S 21	0	0
5	Bh	427	Total 3343	C 2098	N 571	O 653	S 21	0	0
5	Bg	427	Total 3343	C 2098	N 571	O 653	S 21	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	Bj	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bi	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bl	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bk	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bn	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bm	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bb	414	Total	C	N	O	S	0	0
			3247	2038	554	634	21		
5	Bp	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bo	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Br	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		
5	Bq	427	Total	C	N	O	S	0	0
			3343	2098	571	653	21		

- Molecule 6 is a protein called Spindle pole body component 110.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Sc	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sd	85	Total	C	N	O	S	0	0
			714	439	130	144	1		
6	Se	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sf	86	Total	C	N	O	S	0	0
			723	444	131	147	1		
6	Sg	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sh	85	Total	C	N	O	S	0	0
			714	439	130	144	1		
6	Si	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sj	86	Total	C	N	O	S	0	0
			723	444	131	147	1		

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Mol	Chain	Residues	Atoms				AltConf	Trace	
6	Sk	42	Total	C	N	O	0	0	
			352	215	61	76			
6	Sl	85	Total	C	N	O	S	0	0
			714	439	130	144	1		
6	Sa	42	Total	C	N	O		0	0
			352	215	61	76			
6	Sb	62	Total	C	N	O		0	0
			517	318	91	108			
6	Sm	20	Total	C	N	O		0	0
			171	107	31	33			
6	Sn	64	Total	C	N	O	S	0	0
			545	337	102	105	1		

- Molecule 7 is a protein called Unknow protein.

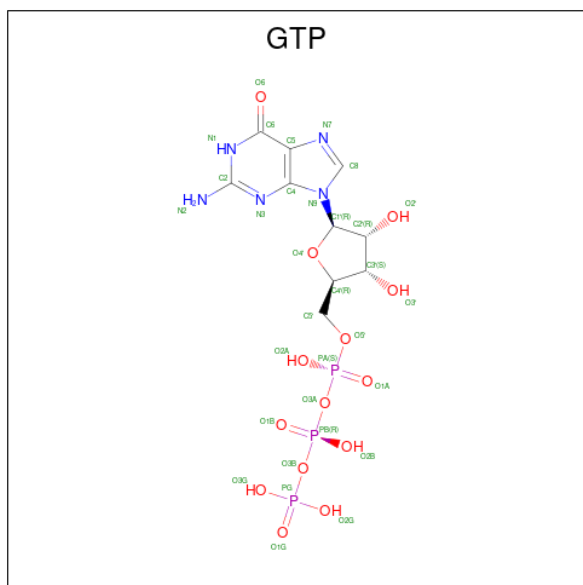
Mol	Chain	Residues	Atoms				AltConf	Trace
7	Ue	67	Total	C	N	O	0	0
			335	201	67	67		
7	Uf	55	Total	C	N	O	0	0
			275	165	55	55		
7	Ui	67	Total	C	N	O	0	0
			335	201	67	67		
7	Uj	55	Total	C	N	O	0	0
			275	165	55	55		
7	Um	67	Total	C	N	O	0	0
			335	201	67	67		
7	Un	55	Total	C	N	O	0	0
			275	165	55	55		
7	Ua	67	Total	C	N	O	0	0
			335	201	67	67		
7	Ub	55	Total	C	N	O	0	0
			275	165	55	55		
7	Ug	67	Total	C	N	O	0	0
			335	201	67	67		
7	Uh	55	Total	C	N	O	0	0
			275	165	55	55		
7	Uk	67	Total	C	N	O	0	0
			335	201	67	67		
7	Ul	55	Total	C	N	O	0	0
			275	165	55	55		
7	Uc	67	Total	C	N	O	0	0
			335	201	67	67		

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Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	Ud	55	275	165	55	55	0	0

- Molecule 8 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



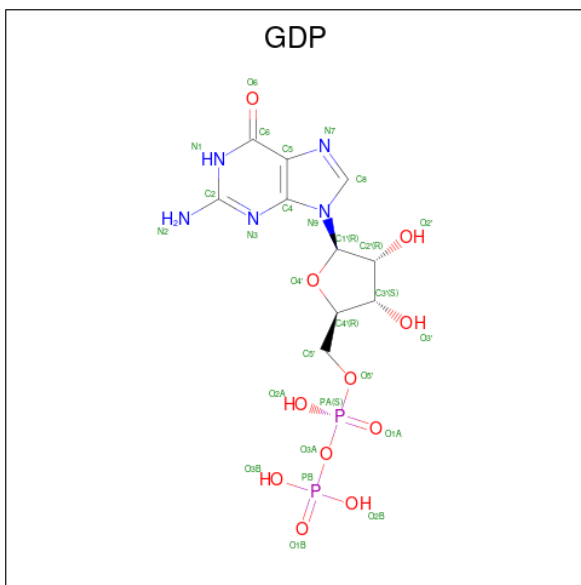
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
8	b	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	c	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	d	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	e	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	f	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	g	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	h	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	i	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	j	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	k	1	Total	C	N	O	P	0
			32	10	5	14	3	

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Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
8	l	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	m	1	Total	C	N	O	P	0
			32	10	5	14	3	
8	n	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



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

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		AltConf
			Total	O	
10	Ue	1	Total	O	0
			1	1	
10	Ui	1	Total	O	0
			1	1	
10	Um	1	Total	O	0
			1	1	
10	Ua	1	Total	O	0
			1	1	
10	Ug	1	Total	O	0
			1	1	

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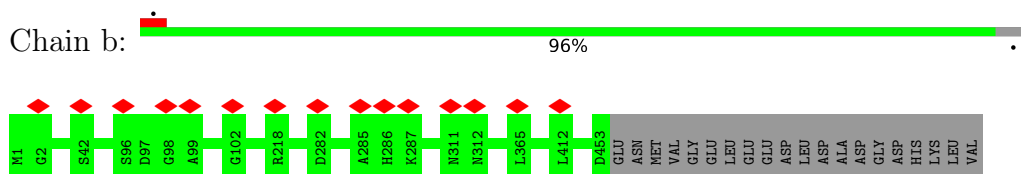
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Mol	Chain	Residues	Atoms		AltConf
10	Uk	1	Total	O	0
			1	1	
10	Uc	1	Total	O	0
			1	1	

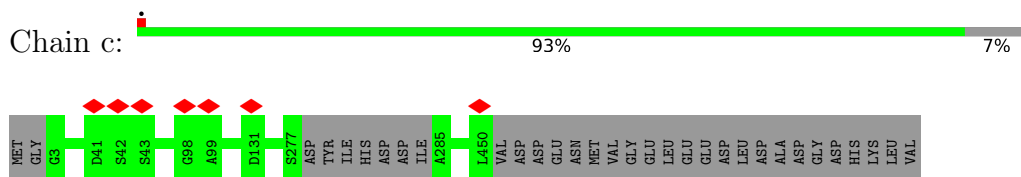
3 Residue-property plots [i](#)

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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

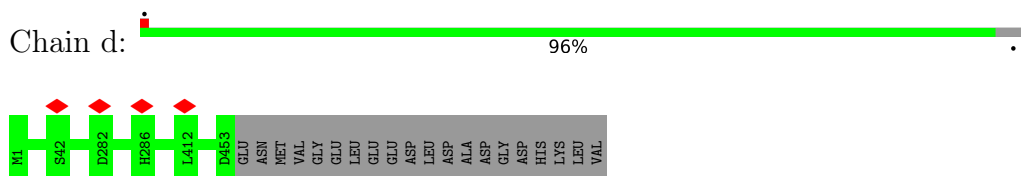
- Molecule 1: Tubulin gamma chain



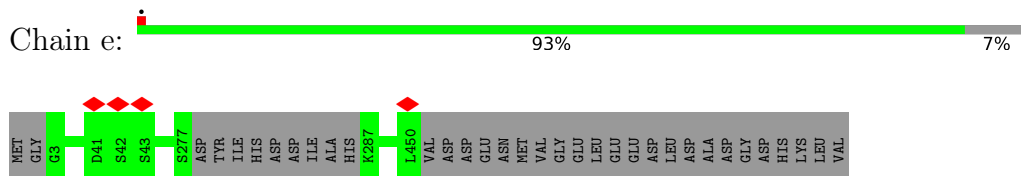
- Molecule 1: Tubulin gamma chain



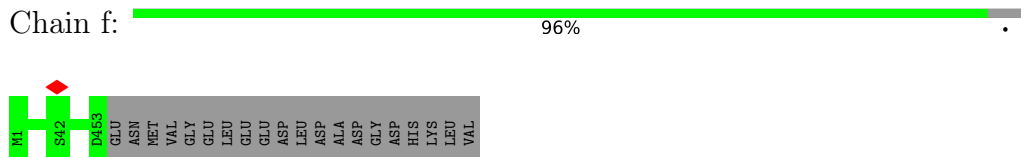
- Molecule 1: Tubulin gamma chain



- Molecule 1: Tubulin gamma chain



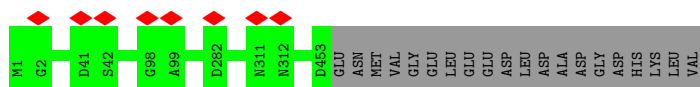
- Molecule 1: Tubulin gamma chain



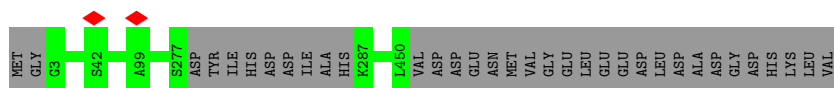
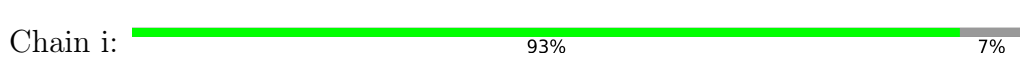
• Molecule 1: Tubulin gamma chain



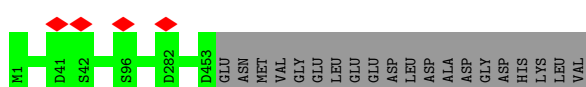
• Molecule 1: Tubulin gamma chain



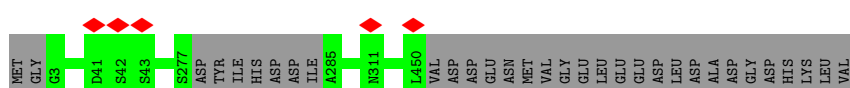
• Molecule 1: Tubulin gamma chain



• Molecule 1: Tubulin gamma chain



• Molecule 1: Tubulin gamma chain



• Molecule 1: Tubulin gamma chain

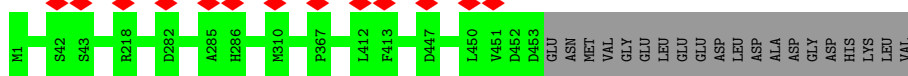


• Molecule 1: Tubulin gamma chain

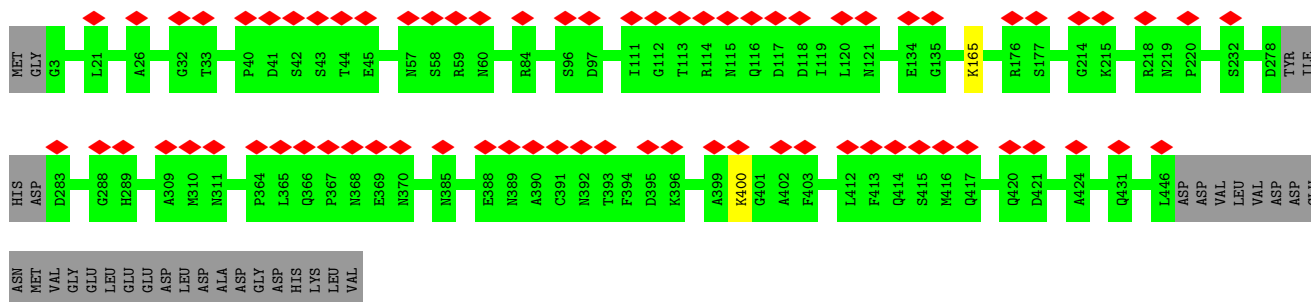




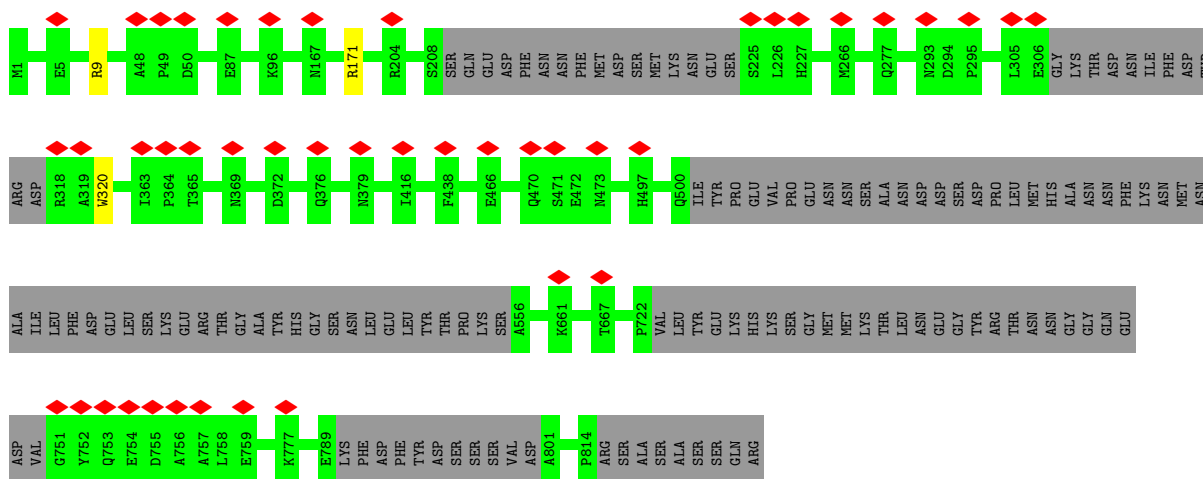
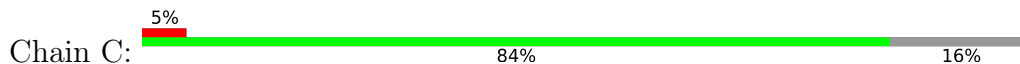
• Molecule 1: Tubulin gamma chain



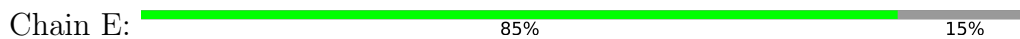
• Molecule 1: Tubulin gamma chain

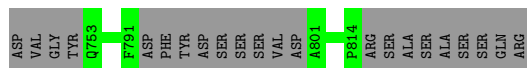
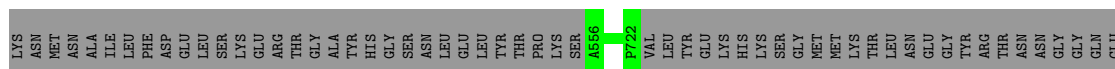


• Molecule 2: Spindle pole body component

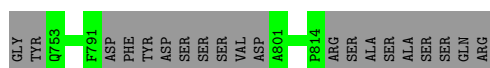
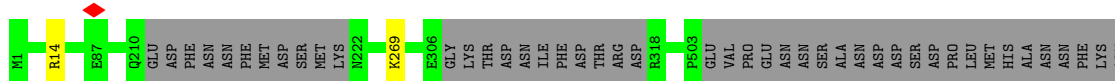


• Molecule 2: Spindle pole body component

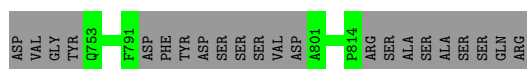
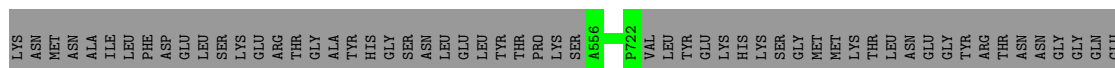
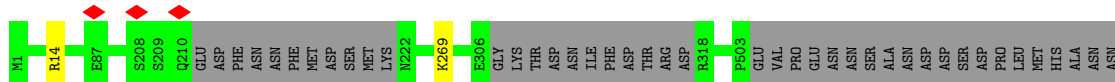
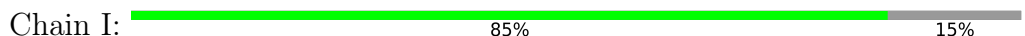




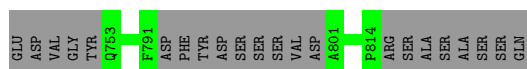
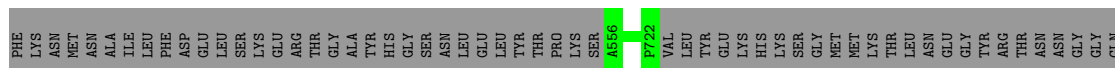
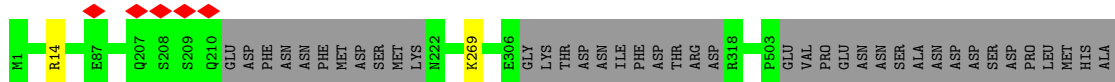
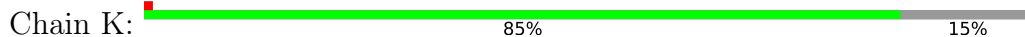
• Molecule 2: Spindle pole body component




• Molecule 2: Spindle pole body component

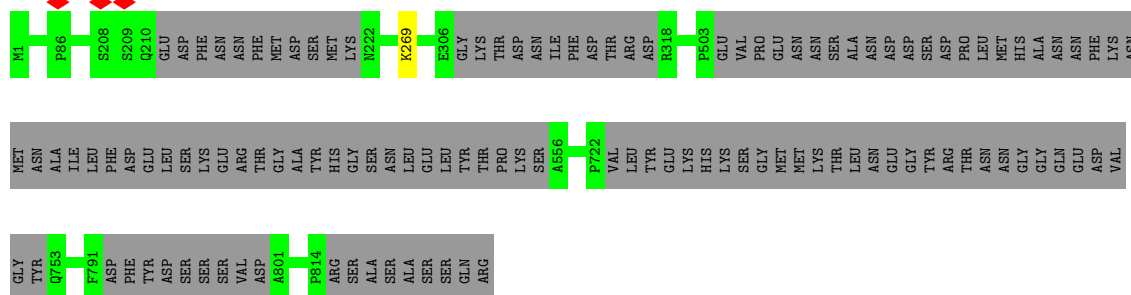


• Molecule 2: Spindle pole body component




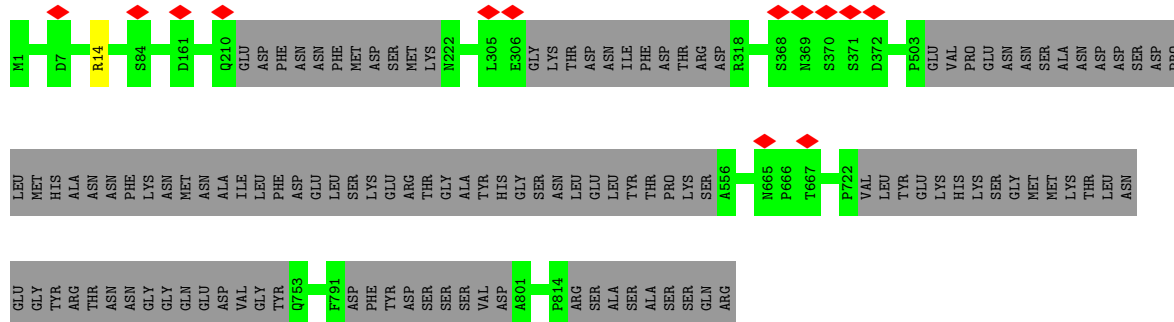
• Molecule 2: Spindle pole body component

Chain M:  85% 15%



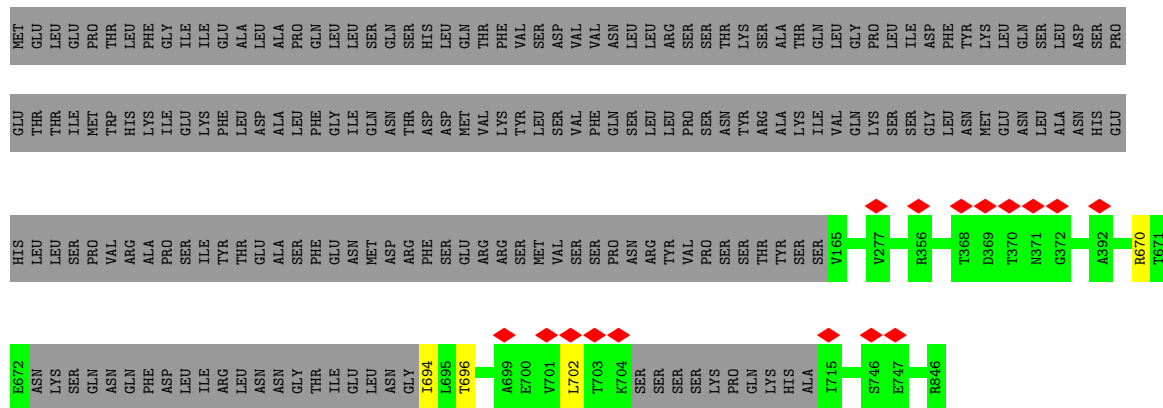
• Molecule 2: Spindle pole body component

Chain O:  85% 15%




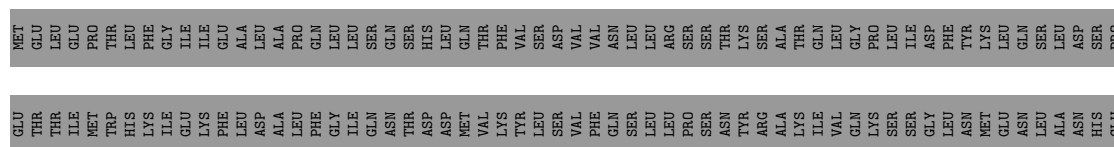
• Molecule 3: Spindle pole body component

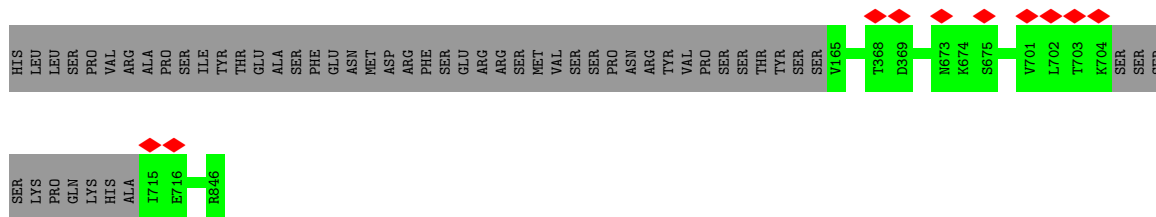
Chain D:  76% 23%



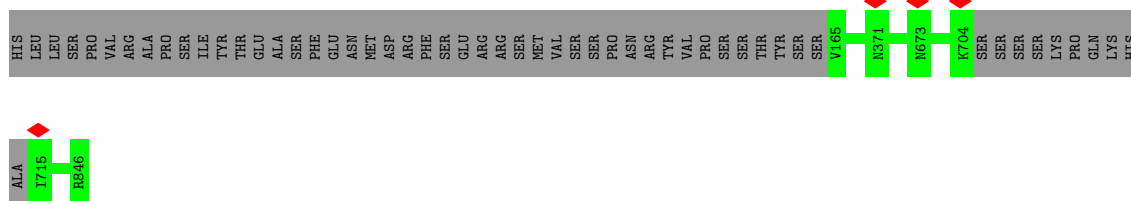
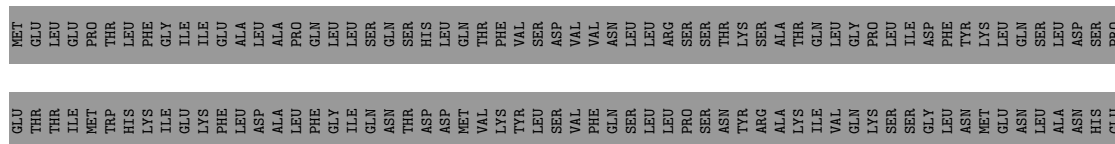
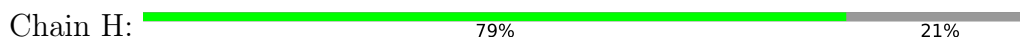
• Molecule 3: Spindle pole body component

Chain F:  79% 21%

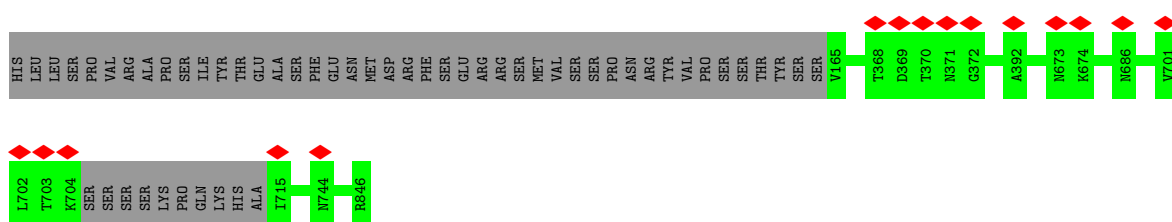
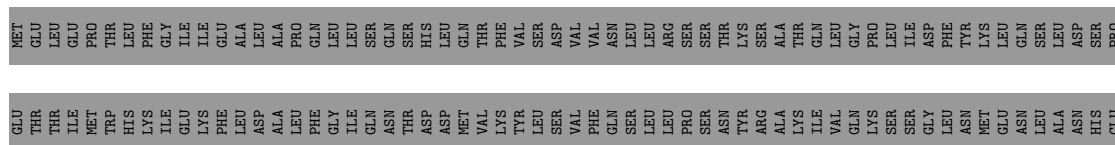
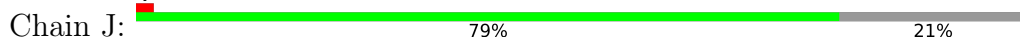




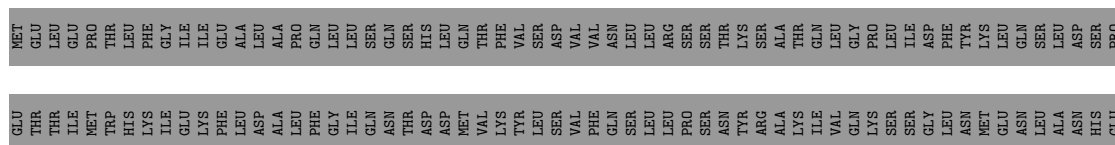
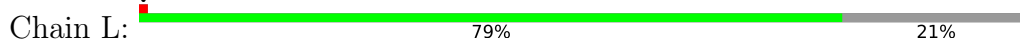
● Molecule 3: Spindle pole body component



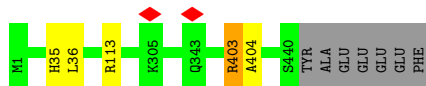
● Molecule 3: Spindle pole body component



● Molecule 3: Spindle pole body component



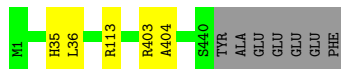
• Molecule 4: Tubulin alpha-1 chain



• Molecule 4: Tubulin alpha-1 chain



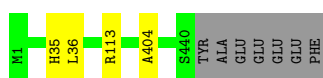
• Molecule 4: Tubulin alpha-1 chain



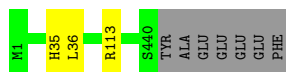
• Molecule 4: Tubulin alpha-1 chain



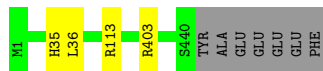
• Molecule 4: Tubulin alpha-1 chain



• Molecule 4: Tubulin alpha-1 chain



• Molecule 4: Tubulin alpha-1 chain



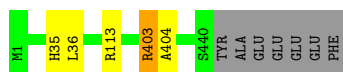
• Molecule 4: Tubulin alpha-1 chain

Chain Al:  98%



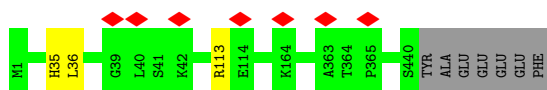
• Molecule 4: Tubulin alpha-1 chain

Chain Ak:  97%



• Molecule 4: Tubulin alpha-1 chain

Chain An:  98%



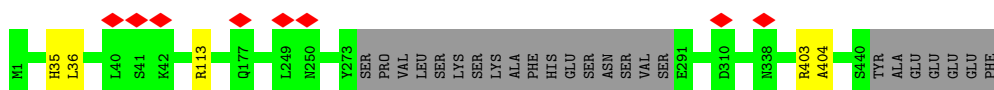
• Molecule 4: Tubulin alpha-1 chain

Chain Am:  98%



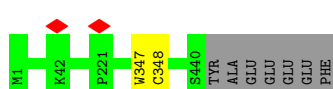
• Molecule 4: Tubulin alpha-1 chain

Chain Ab:  94% 5%



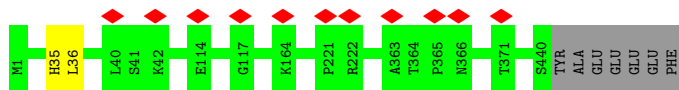
• Molecule 4: Tubulin alpha-1 chain

Chain Ap:  98%

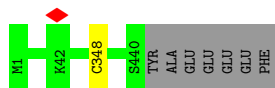


• Molecule 4: Tubulin alpha-1 chain

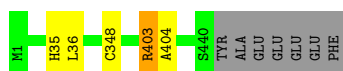
Chain Ao:  98%



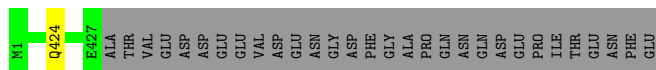
• Molecule 4: Tubulin alpha-1 chain



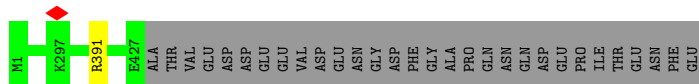
• Molecule 4: Tubulin alpha-1 chain



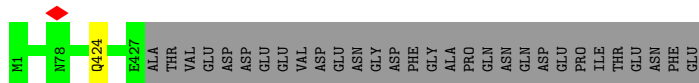
• Molecule 5: Tubulin beta chain



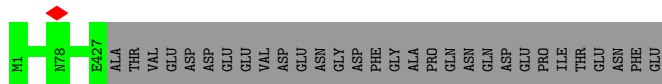
• Molecule 5: Tubulin beta chain



• Molecule 5: Tubulin beta chain

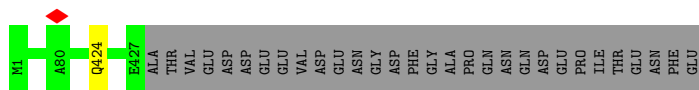


• Molecule 5: Tubulin beta chain

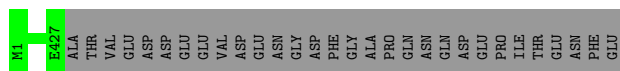


• Molecule 5: Tubulin beta chain

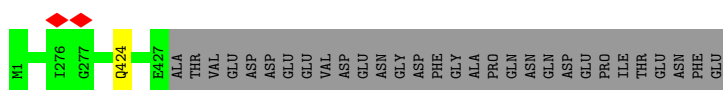




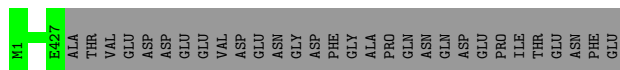
• Molecule 5: Tubulin beta chain



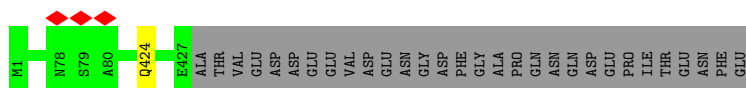
• Molecule 5: Tubulin beta chain



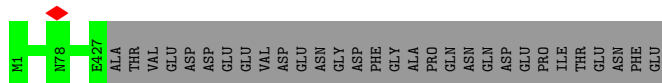
• Molecule 5: Tubulin beta chain



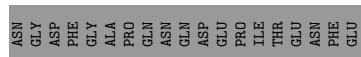
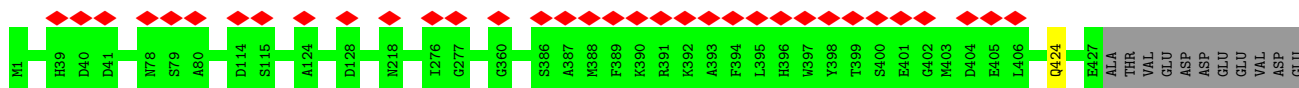
• Molecule 5: Tubulin beta chain



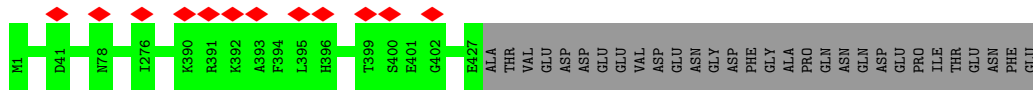
• Molecule 5: Tubulin beta chain



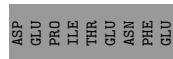
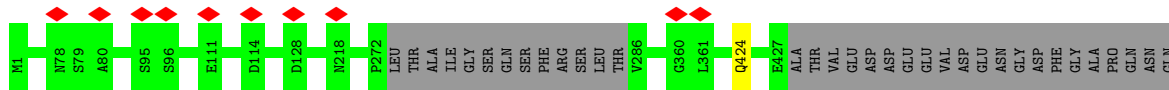
• Molecule 5: Tubulin beta chain



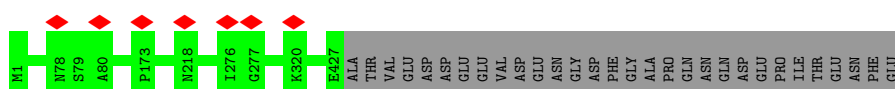
• Molecule 5: Tubulin beta chain



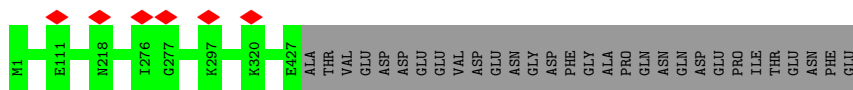
• Molecule 5: Tubulin beta chain



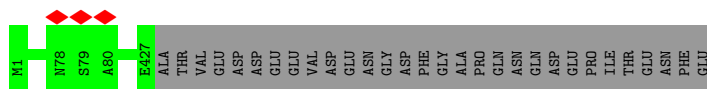
• Molecule 5: Tubulin beta chain



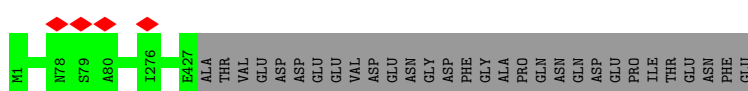
• Molecule 5: Tubulin beta chain



• Molecule 5: Tubulin beta chain



• Molecule 5: Tubulin beta chain



• Molecule 6: Spindle pole body component 110

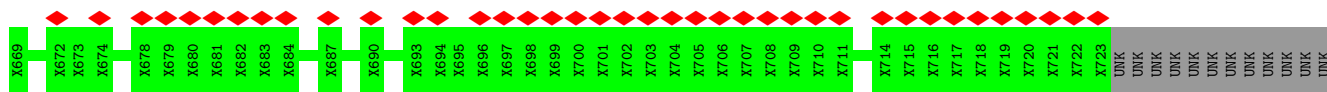


Table with 15 rows of amino acid residues, including GLU, SER, ILE, THR, ASP, MET, VAL, ARG, LYS, PHE, LEU, ASN, ALA, GLY, and THR.

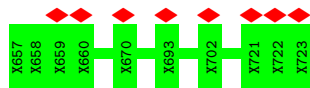
Molecule 6: Spindle pole body component 110



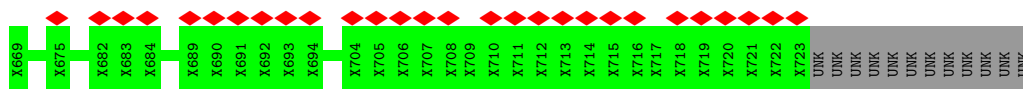
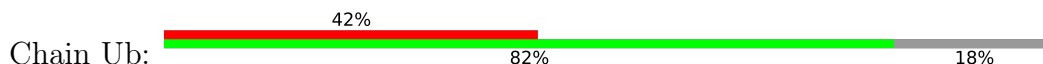
Table with 15 rows of amino acid residues, including MET, ASP, GLU, ILE, THR, SER, VAL, ARG, LYS, PHE, LEU, ASN, ALA, GLY, and THR. A central bar contains residue numbers: Q122, R146, M180, D181, M184, D195, L196, K197, M198, R199, L200, Q201, A202, L203, E204, K205, E206. Red diamonds are placed above the bar, corresponding to specific residues in the table below.



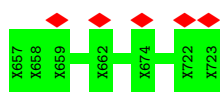
• Molecule 7: Unkown protein



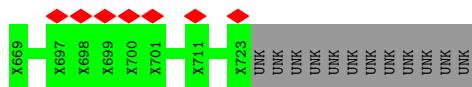
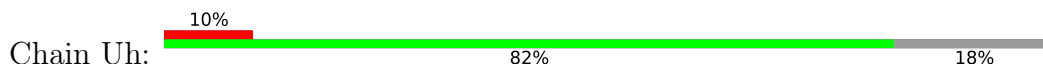
• Molecule 7: Unkown protein



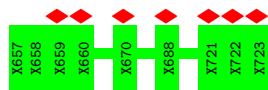
• Molecule 7: Unkown protein



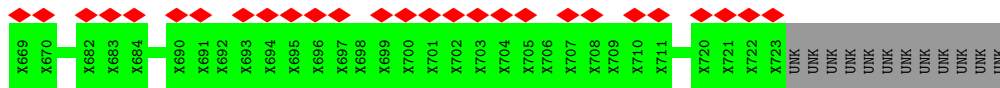
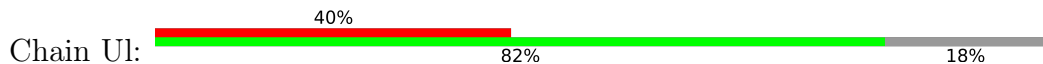
• Molecule 7: Unkown protein



• Molecule 7: Unkown protein

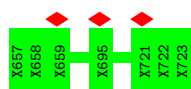


• Molecule 7: Unkown protein




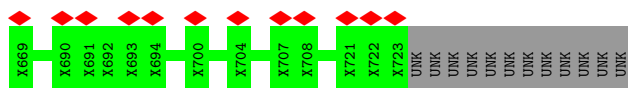
• Molecule 7: Unkown protein

Chain Uc:  100%



• Molecule 7: Unkown protein

Chain Ud:  18% 82% 18%



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	7910	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 ($e^-/\text{\AA}^2$)	123	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.814	Depositor
Minimum map value	-0.437	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.243	Depositor
Map size (Å)	554.39996, 554.39996, 554.39996	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	3.2999997, 3.2999997, 3.2999997	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: GTP, GDP

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	0.24	0/3513	0.41	0/4769
1	b	0.24	0/3620	0.40	0/4917
1	c	0.24	0/3520	0.40	0/4779
1	d	0.24	0/3620	0.40	0/4917
1	e	0.24	0/3504	0.40	0/4757
1	f	0.24	0/3620	0.40	0/4917
1	g	0.24	0/3520	0.40	0/4779
1	h	0.24	0/3620	0.40	0/4917
1	i	0.24	0/3504	0.40	0/4757
1	j	0.24	0/3620	0.39	0/4917
1	k	0.24	0/3520	0.40	0/4779
1	l	0.24	0/3620	0.39	0/4917
1	m	0.24	0/3504	0.40	0/4757
1	n	0.24	0/3620	0.40	0/4917
2	C	0.95	6/5890 (0.1%)	0.42	1/7949 (0.0%)
2	E	0.24	0/5961	0.38	0/8045
2	G	0.23	0/5961	0.38	0/8045
2	I	0.23	0/5961	0.38	0/8045
2	K	0.23	0/5961	0.38	0/8045
2	M	0.23	0/5961	0.38	0/8045
2	O	0.23	0/5961	0.38	0/8045
3	D	0.25	0/5507	0.36	0/7443
3	F	0.24	0/5676	0.37	0/7672
3	H	0.24	0/5676	0.36	0/7672
3	J	0.24	0/5676	0.36	0/7672
3	L	0.24	0/5676	0.36	0/7672
3	N	0.24	0/5676	0.36	0/7672
3	P	0.24	0/5676	0.37	0/7672
4	Ab	0.24	0/3384	0.40	0/4589
4	Ac	0.25	0/3514	0.41	0/4766
4	Ad	0.25	0/3514	0.41	0/4766
4	Ae	0.25	0/3514	0.41	0/4766

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	Af	0.24	0/3514	0.41	0/4766
4	Ag	0.25	0/3514	0.41	0/4766
4	Ah	0.24	0/3514	0.41	0/4766
4	Ai	0.24	0/3514	0.39	0/4766
4	Aj	0.24	0/3514	0.39	0/4766
4	Ak	0.24	0/3514	0.40	0/4766
4	Al	0.24	0/3514	0.40	0/4766
4	Am	0.24	0/3514	0.40	0/4766
4	An	0.24	0/3514	0.40	0/4766
4	Ao	0.24	0/3514	0.41	0/4766
4	Ap	0.87	6/3514 (0.2%)	0.41	0/4766
4	Aq	0.24	0/3514	0.41	0/4766
4	Ar	0.24	0/3514	0.39	0/4766
5	Bb	0.25	0/3318	0.42	0/4493
5	Bc	1.23	1/3416 (0.0%)	0.45	2/4627 (0.0%)
5	Bd	0.25	0/3416	0.42	0/4627
5	Be	0.24	0/3416	0.41	0/4627
5	Bf	0.24	0/3416	0.41	0/4627
5	Bg	0.24	0/3416	0.41	0/4627
5	Bh	0.24	0/3416	0.41	0/4627
5	Bi	0.24	0/3416	0.40	0/4627
5	Bj	0.24	0/3416	0.41	0/4627
5	Bk	0.24	0/3416	0.40	0/4627
5	Bl	0.24	0/3416	0.41	0/4627
5	Bm	0.24	0/3416	0.40	0/4627
5	Bn	0.24	0/3416	0.42	0/4627
5	Bo	0.24	0/3416	0.40	0/4627
5	Bp	0.24	0/3416	0.41	0/4627
5	Bq	0.24	0/3416	0.40	0/4627
5	Br	0.24	0/3416	0.41	0/4627
6	Sa	0.23	0/353	0.39	0/471
6	Sb	0.22	0/521	0.39	0/698
6	Sc	0.22	0/353	0.35	0/471
6	Sd	0.22	0/720	0.36	0/960
6	Se	0.22	0/353	0.36	0/471
6	Sf	0.22	0/729	0.35	0/972
6	Sg	0.22	0/353	0.36	0/471
6	Sh	0.22	0/720	0.35	0/960
6	Si	0.21	0/353	0.34	0/471
6	Sj	0.22	0/729	0.36	0/972
6	Sk	0.22	0/353	0.38	0/471
6	Sl	0.22	0/720	0.36	0/960
6	Sm	0.23	0/171	0.35	0/224

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
6	Sn	0.22	0/550	0.39	0/729
All	All	0.33	13/255704 (0.0%)	0.39	3/346161 (0.0%)

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
4	Ab	0	2
4	Ac	0	2
4	Ad	0	2
4	Ae	0	2
4	Af	0	2
4	Ag	0	2
4	Ah	0	2
4	Ai	0	2
4	Aj	0	2
4	Ak	0	2
4	Al	0	2
4	Am	0	2
4	An	0	2
4	Ao	0	2
4	Ap	0	1
4	Aq	0	3
4	Ar	0	1
5	Bb	0	1
5	Bd	0	1
5	Bf	0	1
5	Bh	0	1
5	Bj	0	1
5	Bl	0	1
5	Bn	0	1
All	All	0	40

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	Bc	391	ARG	CB-CG	70.11	3.41	1.52
2	C	320	TRP	CE3-CZ3	51.60	2.26	1.38
4	Ap	347	TRP	CE3-CZ3	33.02	1.94	1.38
2	C	320	TRP	CZ3-CH2	28.17	1.85	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	320	TRP	CE2-CZ2	26.02	1.83	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Bc	391	ARG	CA-CB-CG	8.95	133.09	113.40
2	C	320	TRP	CE3-CZ3-CH2	-7.12	113.37	121.20
5	Bc	391	ARG	CB-CG-CD	7.04	129.91	111.60

There are no chirality outliers.

5 of 40 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	Ac	35	HIS	Peptide
4	Ac	36	LEU	Peptide
4	Ad	35	HIS	Peptide
4	Ad	36	LEU	Peptide
5	Bd	424	GLN	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	436/473 (92%)	419 (96%)	17 (4%)	0	100	100
1	b	451/473 (95%)	444 (98%)	7 (2%)	0	100	100
1	c	437/473 (92%)	431 (99%)	6 (1%)	0	100	100
1	d	451/473 (95%)	444 (98%)	7 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	e	435/473 (92%)	428 (98%)	7 (2%)	0	100	100
1	f	451/473 (95%)	441 (98%)	10 (2%)	0	100	100
1	g	437/473 (92%)	428 (98%)	9 (2%)	0	100	100
1	h	451/473 (95%)	443 (98%)	8 (2%)	0	100	100
1	i	435/473 (92%)	428 (98%)	7 (2%)	0	100	100
1	j	451/473 (95%)	443 (98%)	8 (2%)	0	100	100
1	k	437/473 (92%)	428 (98%)	9 (2%)	0	100	100
1	l	451/473 (95%)	444 (98%)	7 (2%)	0	100	100
1	m	435/473 (92%)	428 (98%)	7 (2%)	0	100	100
1	n	451/473 (95%)	445 (99%)	6 (1%)	0	100	100
2	C	681/823 (83%)	648 (95%)	33 (5%)	0	100	100
2	E	689/823 (84%)	675 (98%)	14 (2%)	0	100	100
2	G	689/823 (84%)	674 (98%)	15 (2%)	0	100	100
2	I	689/823 (84%)	674 (98%)	15 (2%)	0	100	100
2	K	689/823 (84%)	676 (98%)	13 (2%)	0	100	100
2	M	689/823 (84%)	672 (98%)	17 (2%)	0	100	100
2	O	689/823 (84%)	678 (98%)	11 (2%)	0	100	100
3	D	645/846 (76%)	623 (97%)	22 (3%)	0	100	100
3	F	668/846 (79%)	651 (98%)	17 (2%)	0	100	100
3	H	668/846 (79%)	646 (97%)	22 (3%)	0	100	100
3	J	668/846 (79%)	649 (97%)	19 (3%)	0	100	100
3	L	668/846 (79%)	646 (97%)	22 (3%)	0	100	100
3	N	668/846 (79%)	646 (97%)	22 (3%)	0	100	100
3	P	668/846 (79%)	650 (97%)	18 (3%)	0	100	100
4	Ab	419/447 (94%)	396 (94%)	22 (5%)	1 (0%)	47	81
4	Ac	438/447 (98%)	408 (93%)	28 (6%)	2 (0%)	29	69
4	Ad	438/447 (98%)	408 (93%)	28 (6%)	2 (0%)	29	69
4	Ae	438/447 (98%)	410 (94%)	26 (6%)	2 (0%)	29	69
4	Af	438/447 (98%)	410 (94%)	26 (6%)	2 (0%)	29	69
4	Ag	438/447 (98%)	410 (94%)	27 (6%)	1 (0%)	47	81
4	Ah	438/447 (98%)	412 (94%)	24 (6%)	2 (0%)	29	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Ai	438/447 (98%)	410 (94%)	28 (6%)	0	100	100
4	Aj	438/447 (98%)	413 (94%)	25 (6%)	0	100	100
4	Ak	438/447 (98%)	411 (94%)	25 (6%)	2 (0%)	29	69
4	Al	438/447 (98%)	414 (94%)	24 (6%)	0	100	100
4	Am	438/447 (98%)	412 (94%)	26 (6%)	0	100	100
4	An	438/447 (98%)	415 (95%)	23 (5%)	0	100	100
4	Ao	438/447 (98%)	413 (94%)	25 (6%)	0	100	100
4	Ap	438/447 (98%)	421 (96%)	17 (4%)	0	100	100
4	Aq	438/447 (98%)	414 (94%)	22 (5%)	2 (0%)	29	69
4	Ar	438/447 (98%)	423 (97%)	15 (3%)	0	100	100
5	Bb	410/457 (90%)	398 (97%)	12 (3%)	0	100	100
5	Bc	425/457 (93%)	415 (98%)	10 (2%)	0	100	100
5	Bd	425/457 (93%)	410 (96%)	15 (4%)	0	100	100
5	Be	425/457 (93%)	411 (97%)	14 (3%)	0	100	100
5	Bf	425/457 (93%)	414 (97%)	11 (3%)	0	100	100
5	Bg	425/457 (93%)	416 (98%)	9 (2%)	0	100	100
5	Bh	425/457 (93%)	413 (97%)	12 (3%)	0	100	100
5	Bi	425/457 (93%)	416 (98%)	9 (2%)	0	100	100
5	Bj	425/457 (93%)	411 (97%)	14 (3%)	0	100	100
5	Bk	425/457 (93%)	417 (98%)	8 (2%)	0	100	100
5	Bl	425/457 (93%)	412 (97%)	13 (3%)	0	100	100
5	Bm	425/457 (93%)	416 (98%)	9 (2%)	0	100	100
5	Bn	425/457 (93%)	412 (97%)	13 (3%)	0	100	100
5	Bo	425/457 (93%)	419 (99%)	6 (1%)	0	100	100
5	Bp	425/457 (93%)	418 (98%)	7 (2%)	0	100	100
5	Bq	425/457 (93%)	420 (99%)	5 (1%)	0	100	100
5	Br	425/457 (93%)	418 (98%)	7 (2%)	0	100	100
6	Sa	40/944 (4%)	40 (100%)	0	0	100	100
6	Sb	60/944 (6%)	60 (100%)	0	0	100	100
6	Sc	40/944 (4%)	40 (100%)	0	0	100	100
6	Sd	83/944 (9%)	81 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	Se	40/944 (4%)	40 (100%)	0	0	100	100
6	Sf	84/944 (9%)	82 (98%)	2 (2%)	0	100	100
6	Sg	40/944 (4%)	40 (100%)	0	0	100	100
6	Sh	83/944 (9%)	81 (98%)	2 (2%)	0	100	100
6	Si	40/944 (4%)	40 (100%)	0	0	100	100
6	Sj	84/944 (9%)	82 (98%)	2 (2%)	0	100	100
6	Sk	40/944 (4%)	40 (100%)	0	0	100	100
6	Sl	83/944 (9%)	81 (98%)	2 (2%)	0	100	100
6	Sm	18/944 (2%)	18 (100%)	0	0	100	100
6	Sn	62/944 (7%)	60 (97%)	2 (3%)	0	100	100
All	All	31111/46889 (66%)	30123 (97%)	972 (3%)	16 (0%)	54	86

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	Af	404	ALA
4	Ae	404	ALA
4	Ad	404	ALA
4	Ac	404	ALA
4	Ah	404	ALA

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	a	391/420 (93%)	389 (100%)	2 (0%)	88	93
1	b	403/420 (96%)	403 (100%)	0	100	100
1	c	392/420 (93%)	392 (100%)	0	100	100
1	d	403/420 (96%)	403 (100%)	0	100	100
1	e	391/420 (93%)	391 (100%)	0	100	100
1	f	403/420 (96%)	403 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	g	392/420 (93%)	392 (100%)	0	100	100
1	h	403/420 (96%)	403 (100%)	0	100	100
1	i	391/420 (93%)	391 (100%)	0	100	100
1	j	403/420 (96%)	403 (100%)	0	100	100
1	k	392/420 (93%)	392 (100%)	0	100	100
1	l	403/420 (96%)	403 (100%)	0	100	100
1	m	391/420 (93%)	391 (100%)	0	100	100
1	n	403/420 (96%)	403 (100%)	0	100	100
2	C	649/766 (85%)	647 (100%)	2 (0%)	92	95
2	E	658/766 (86%)	656 (100%)	2 (0%)	92	95
2	G	658/766 (86%)	656 (100%)	2 (0%)	92	95
2	I	658/766 (86%)	656 (100%)	2 (0%)	92	95
2	K	658/766 (86%)	656 (100%)	2 (0%)	92	95
2	M	658/766 (86%)	657 (100%)	1 (0%)	93	96
2	O	658/766 (86%)	657 (100%)	1 (0%)	93	96
3	D	607/787 (77%)	603 (99%)	4 (1%)	84	90
3	F	626/787 (80%)	626 (100%)	0	100	100
3	H	626/787 (80%)	626 (100%)	0	100	100
3	J	626/787 (80%)	626 (100%)	0	100	100
3	L	626/787 (80%)	626 (100%)	0	100	100
3	N	626/787 (80%)	626 (100%)	0	100	100
3	P	626/787 (80%)	626 (100%)	0	100	100
4	Ab	359/381 (94%)	357 (99%)	2 (1%)	86	92
4	Ac	375/381 (98%)	373 (100%)	2 (0%)	88	93
4	Ad	375/381 (98%)	373 (100%)	2 (0%)	88	93
4	Ae	375/381 (98%)	374 (100%)	1 (0%)	92	95
4	Af	375/381 (98%)	374 (100%)	1 (0%)	92	95
4	Ag	375/381 (98%)	374 (100%)	1 (0%)	92	95
4	Ah	375/381 (98%)	374 (100%)	1 (0%)	92	95
4	Ai	375/381 (98%)	373 (100%)	2 (0%)	88	93
4	Aj	375/381 (98%)	374 (100%)	1 (0%)	92	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Ak	375/381 (98%)	373 (100%)	2 (0%)	88	93
4	Al	375/381 (98%)	374 (100%)	1 (0%)	92	95
4	Am	375/381 (98%)	373 (100%)	2 (0%)	88	93
4	An	375/381 (98%)	374 (100%)	1 (0%)	92	95
4	Ao	375/381 (98%)	375 (100%)	0	100	100
4	Ap	375/381 (98%)	375 (100%)	0	100	100
4	Aq	375/381 (98%)	374 (100%)	1 (0%)	92	95
4	Ar	375/381 (98%)	375 (100%)	0	100	100
5	Bb	355/392 (91%)	355 (100%)	0	100	100
5	Bc	366/392 (93%)	366 (100%)	0	100	100
5	Bd	366/392 (93%)	366 (100%)	0	100	100
5	Be	366/392 (93%)	366 (100%)	0	100	100
5	Bf	366/392 (93%)	366 (100%)	0	100	100
5	Bg	366/392 (93%)	366 (100%)	0	100	100
5	Bh	366/392 (93%)	366 (100%)	0	100	100
5	Bi	366/392 (93%)	366 (100%)	0	100	100
5	Bj	366/392 (93%)	366 (100%)	0	100	100
5	Bk	366/392 (93%)	366 (100%)	0	100	100
5	Bl	366/392 (93%)	366 (100%)	0	100	100
5	Bm	366/392 (93%)	366 (100%)	0	100	100
5	Bn	366/392 (93%)	366 (100%)	0	100	100
5	Bo	366/392 (93%)	366 (100%)	0	100	100
5	Bp	366/392 (93%)	366 (100%)	0	100	100
5	Bq	366/392 (93%)	366 (100%)	0	100	100
5	Br	366/392 (93%)	366 (100%)	0	100	100
6	Sa	40/901 (4%)	40 (100%)	0	100	100
6	Sb	58/901 (6%)	57 (98%)	1 (2%)	60	78
6	Sc	40/901 (4%)	40 (100%)	0	100	100
6	Sd	79/901 (9%)	78 (99%)	1 (1%)	69	81
6	Se	40/901 (4%)	40 (100%)	0	100	100
6	Sf	80/901 (9%)	79 (99%)	1 (1%)	69	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	Sg	40/901 (4%)	40 (100%)	0	100	100
6	Sh	79/901 (9%)	78 (99%)	1 (1%)	69	81
6	Si	40/901 (4%)	40 (100%)	0	100	100
6	Sj	80/901 (9%)	79 (99%)	1 (1%)	69	81
6	Sk	40/901 (4%)	40 (100%)	0	100	100
6	Sl	79/901 (9%)	78 (99%)	1 (1%)	69	81
6	Sm	20/901 (2%)	20 (100%)	0	100	100
6	Sn	61/901 (7%)	60 (98%)	1 (2%)	62	79
All	All	27867/42506 (66%)	27822 (100%)	45 (0%)	93	96

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	Ai	403	ARG
4	Ab	113	ARG
4	Al	113	ARG
4	An	113	ARG
6	Sd	146	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 426 such sidechains are listed below:

Mol	Chain	Res	Type
4	Ah	230	ASN
4	Al	18	ASN
5	Bo	291	GLN
4	Ag	207	ASN
4	Aj	102	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 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
8	GTP	h	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.67	7 (21%)
8	GTP	f	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.65	7 (21%)
8	GTP	d	501	-	26,34,34	1.13	2 (7%)	32,54,54	1.66	7 (21%)
8	GTP	j	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.66	7 (21%)
8	GTP	e	501	-	26,34,34	1.10	2 (7%)	32,54,54	1.61	7 (21%)
8	GTP	b	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.66	7 (21%)
8	GTP	g	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.61	7 (21%)
8	GTP	l	501	-	26,34,34	1.11	2 (7%)	32,54,54	1.62	7 (21%)
8	GTP	k	501	-	26,34,34	1.10	2 (7%)	32,54,54	1.62	7 (21%)
8	GTP	c	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.61	7 (21%)
8	GTP	m	501	-	26,34,34	1.10	2 (7%)	32,54,54	1.63	7 (21%)
8	GTP	i	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.62	7 (21%)
8	GTP	n	501	-	26,34,34	1.12	2 (7%)	32,54,54	1.66	7 (21%)
9	GDP	a	501	-	24,30,30	0.96	1 (4%)	30,47,47	1.32	4 (13%)

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
8	GTP	h	501	-	-	5/18/38/38	0/3/3/3
8	GTP	f	501	-	-	4/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GTP	d	501	-	-	4/18/38/38	0/3/3/3
8	GTP	j	501	-	-	4/18/38/38	0/3/3/3
8	GTP	e	501	-	-	5/18/38/38	0/3/3/3
8	GTP	b	501	-	-	4/18/38/38	0/3/3/3
8	GTP	g	501	-	-	5/18/38/38	0/3/3/3
8	GTP	l	501	-	-	4/18/38/38	0/3/3/3
8	GTP	k	501	-	-	5/18/38/38	0/3/3/3
8	GTP	c	501	-	-	4/18/38/38	0/3/3/3
8	GTP	m	501	-	-	4/18/38/38	0/3/3/3
8	GTP	i	501	-	-	4/18/38/38	0/3/3/3
8	GTP	n	501	-	-	5/18/38/38	0/3/3/3
9	GDP	a	501	-	-	3/12/32/32	0/3/3/3

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	d	501	GTP	C5-C6	-4.06	1.39	1.47
8	j	501	GTP	C5-C6	-4.02	1.39	1.47
8	f	501	GTP	C5-C6	-4.01	1.39	1.47
8	n	501	GTP	C5-C6	-4.00	1.39	1.47
8	b	501	GTP	C5-C6	-4.00	1.39	1.47

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	n	501	GTP	PA-O3A-PB	-3.91	119.40	132.83
8	b	501	GTP	PA-O3A-PB	-3.91	119.42	132.83
8	d	501	GTP	PA-O3A-PB	-3.90	119.44	132.83
8	h	501	GTP	PA-O3A-PB	-3.90	119.45	132.83
8	j	501	GTP	PA-O3A-PB	-3.89	119.47	132.83

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	b	501	GTP	C5'-O5'-PA-O3A
8	b	501	GTP	C5'-O5'-PA-O2A
8	c	501	GTP	C5'-O5'-PA-O1A
8	c	501	GTP	C5'-O5'-PA-O2A

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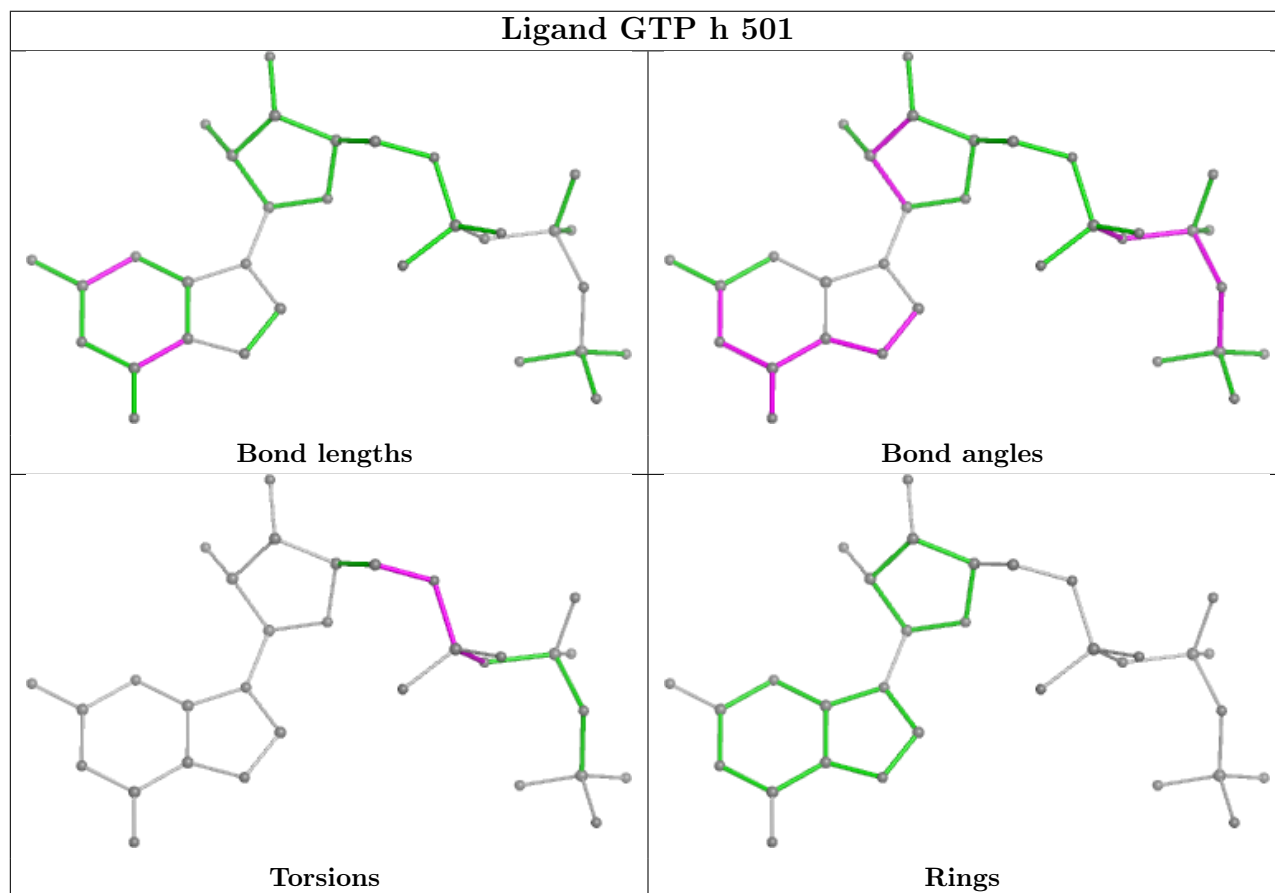
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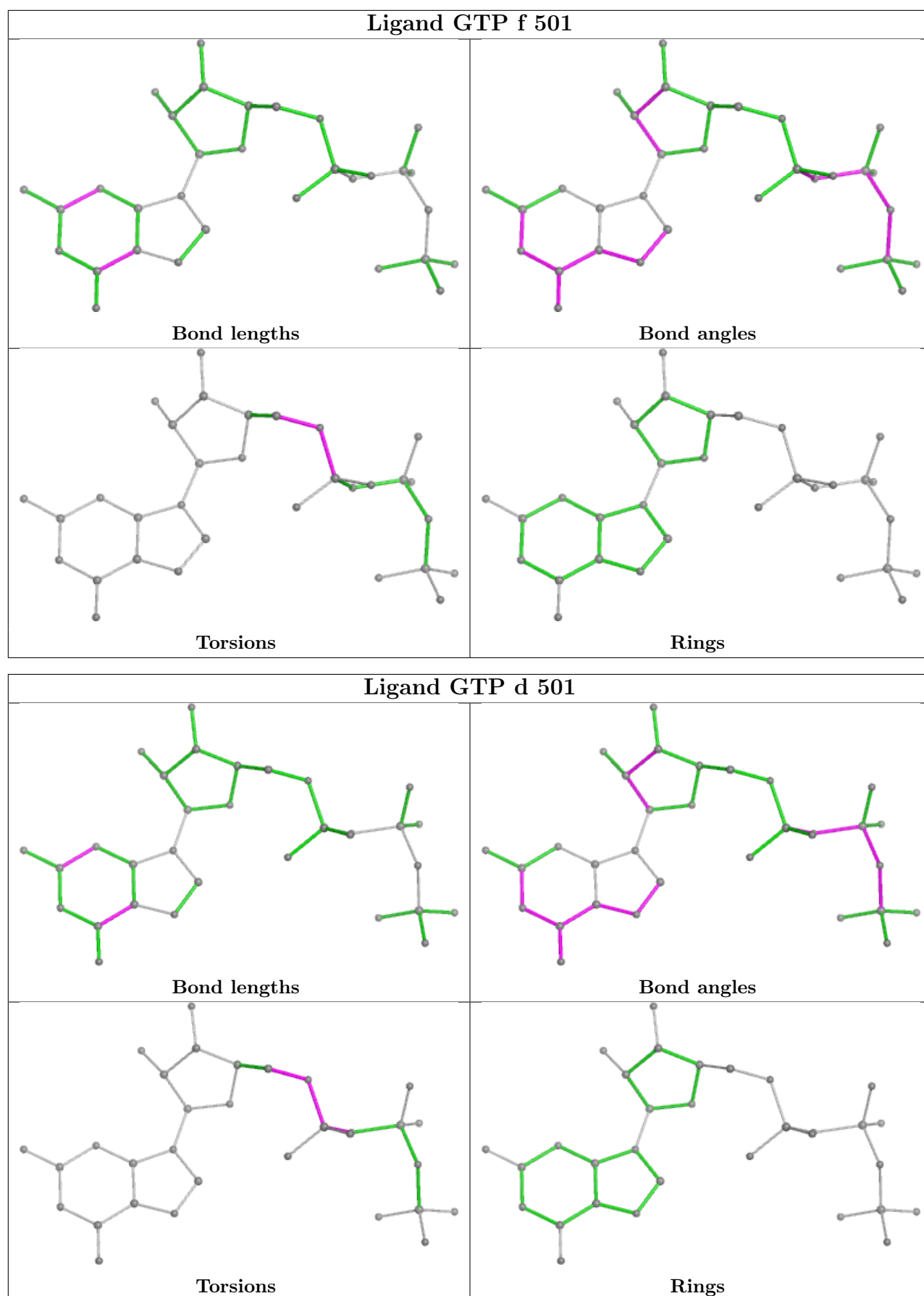
Mol	Chain	Res	Type	Atoms
8	d	501	GTP	C5'-O5'-PA-O3A

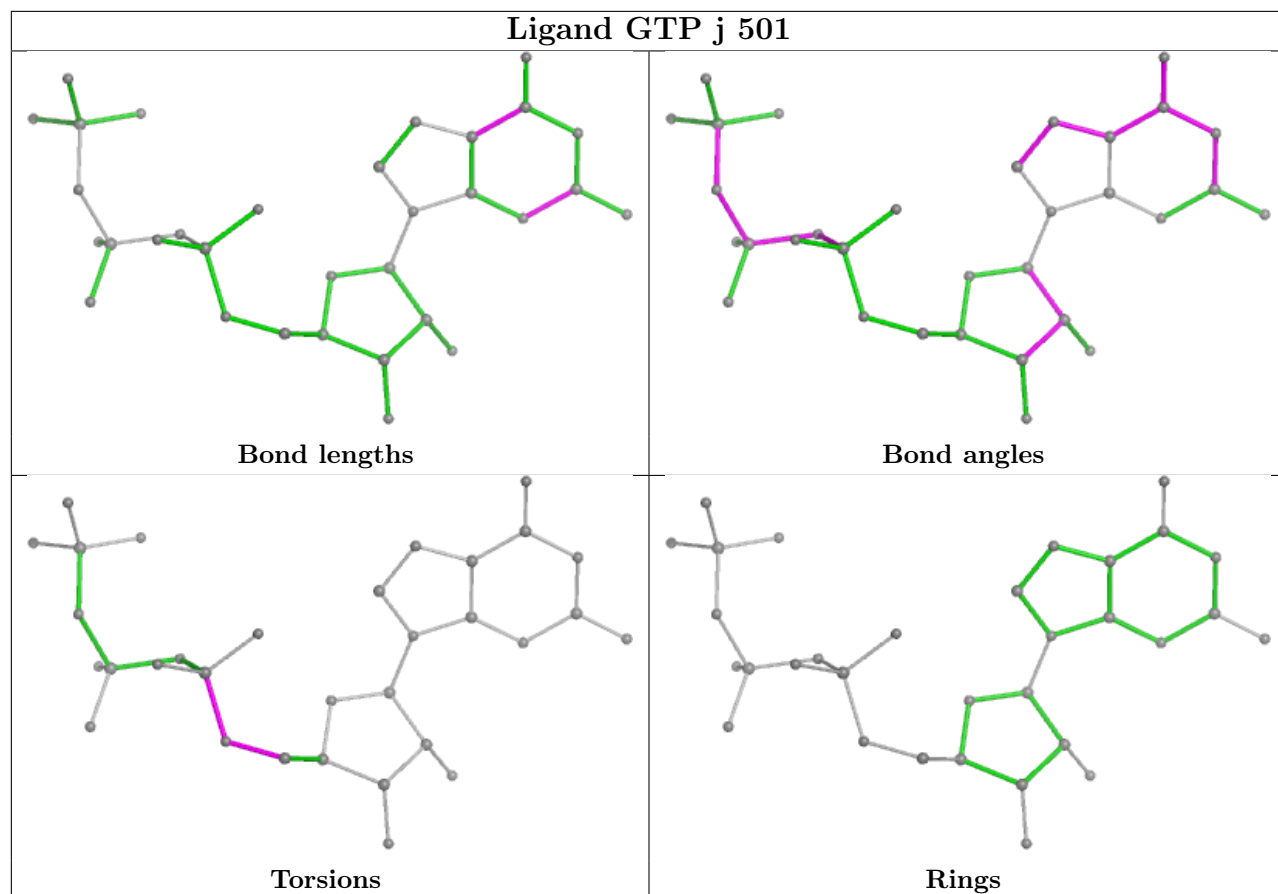
There are no ring outliers.

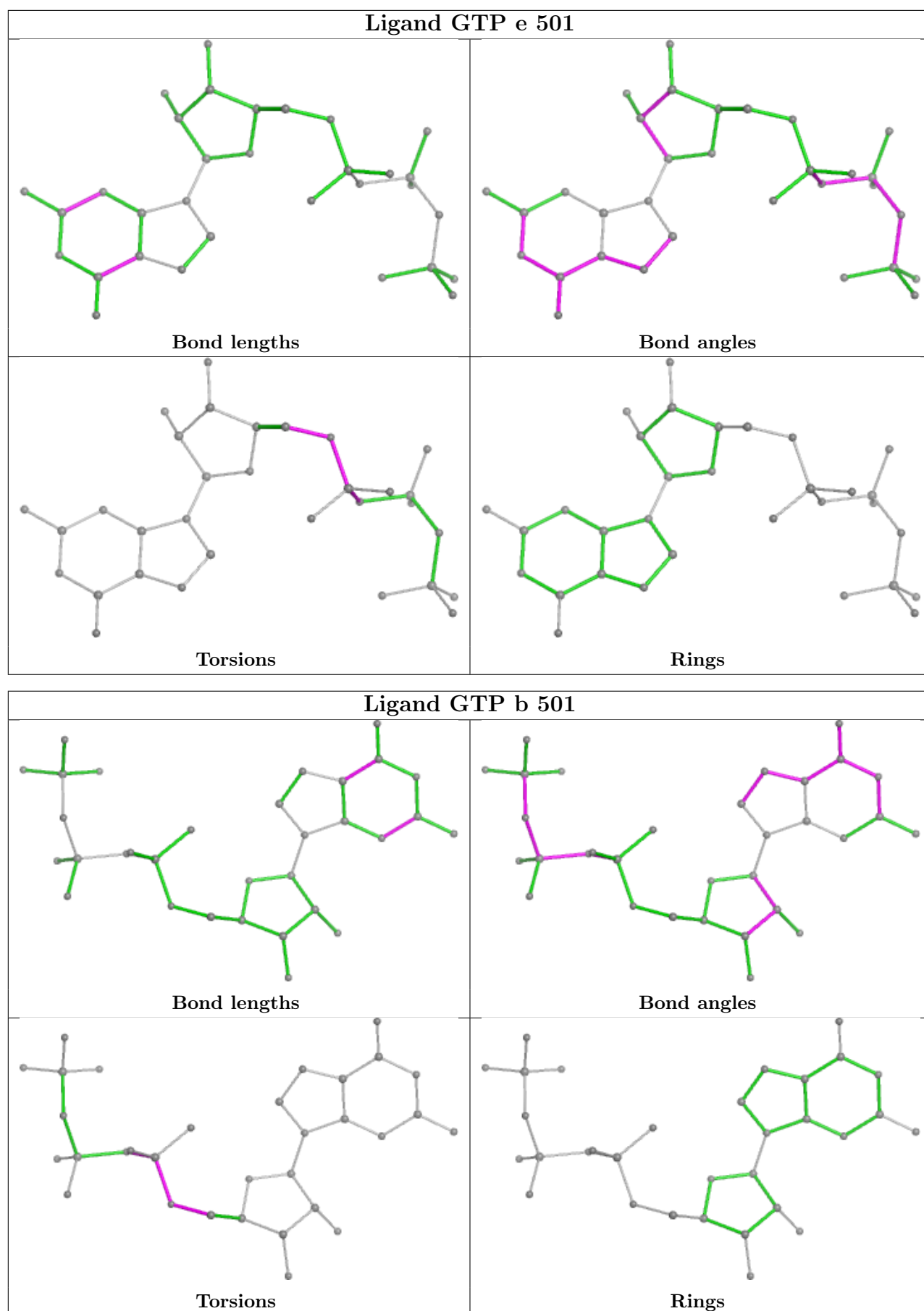
No monomer is involved in short contacts.

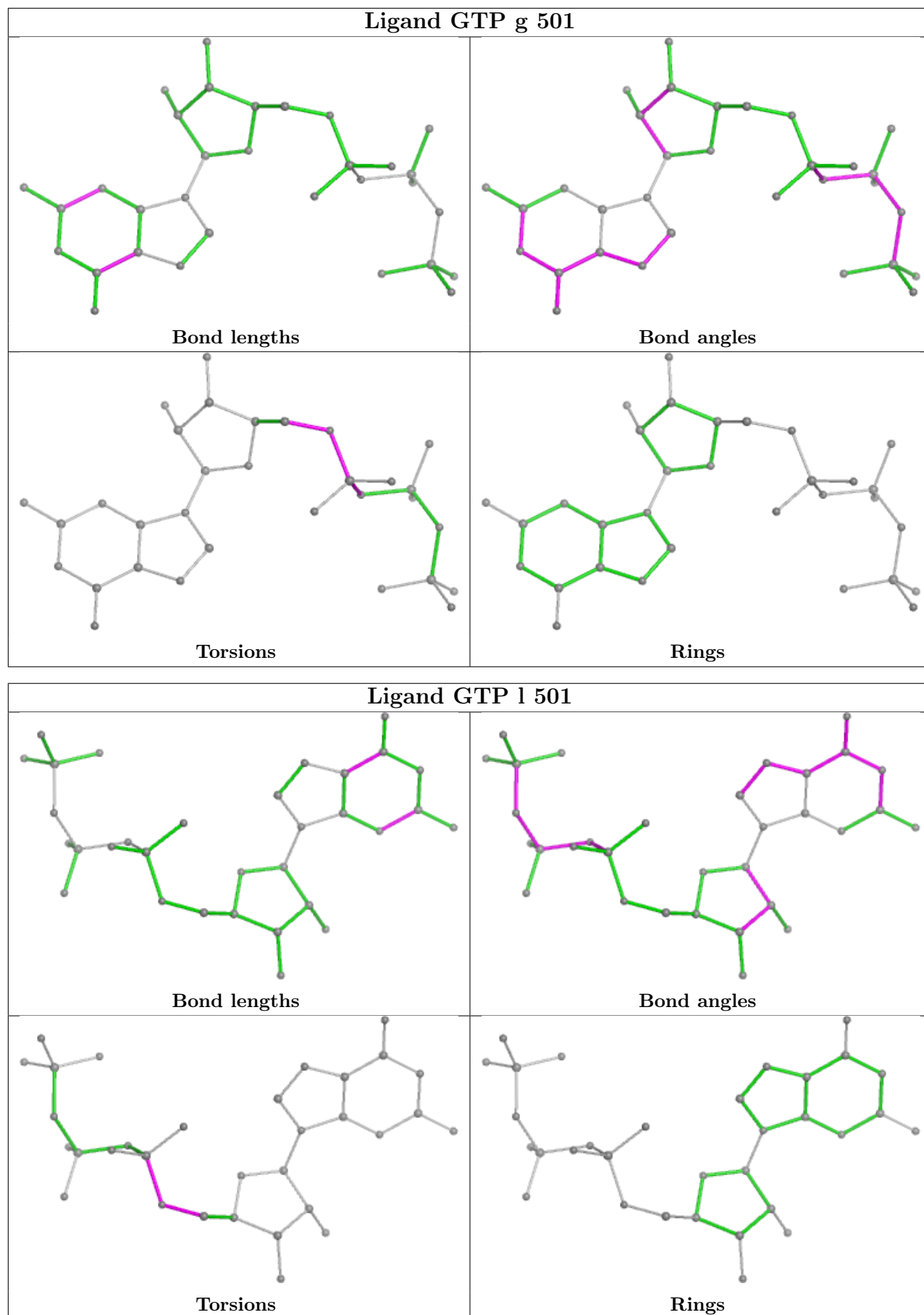
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

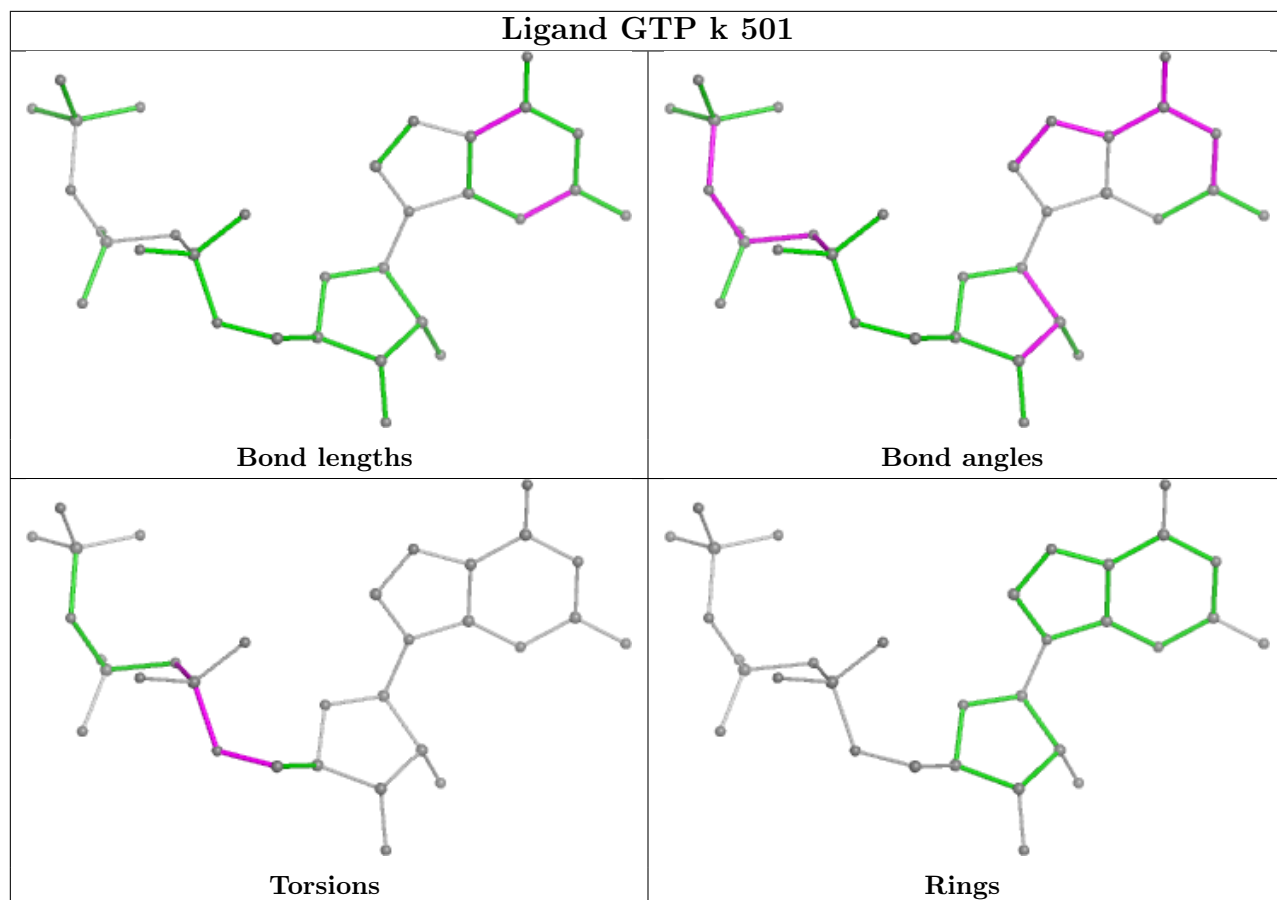


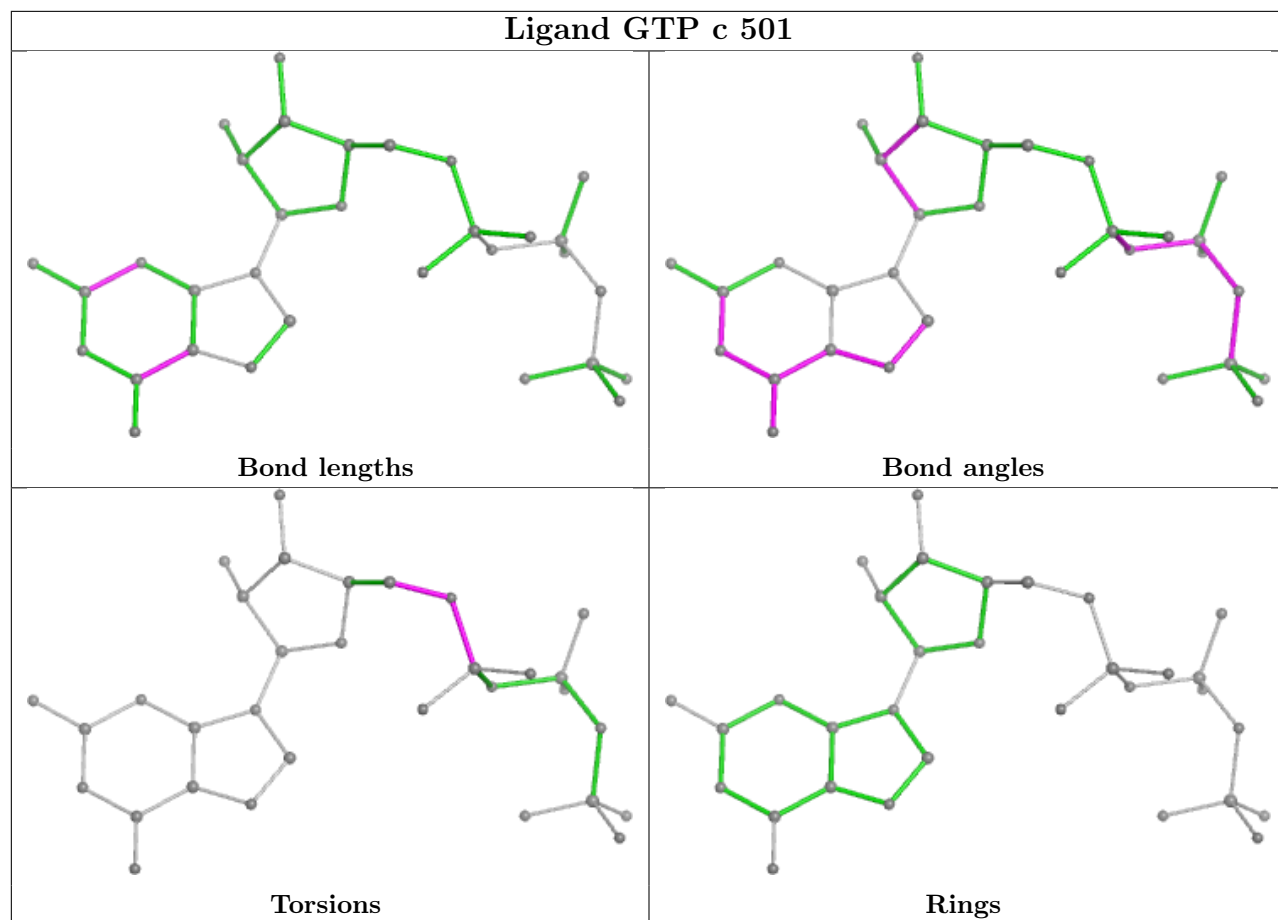


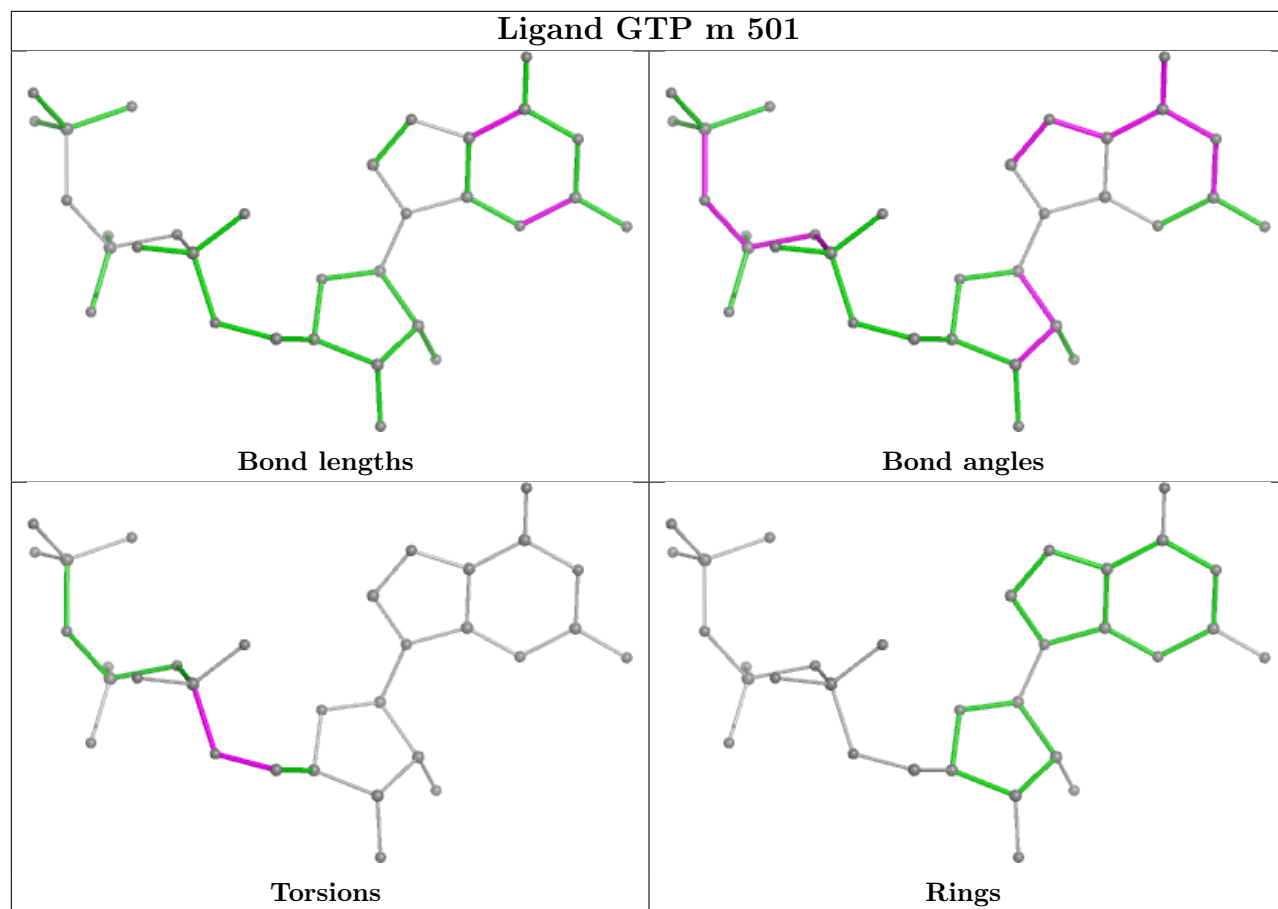


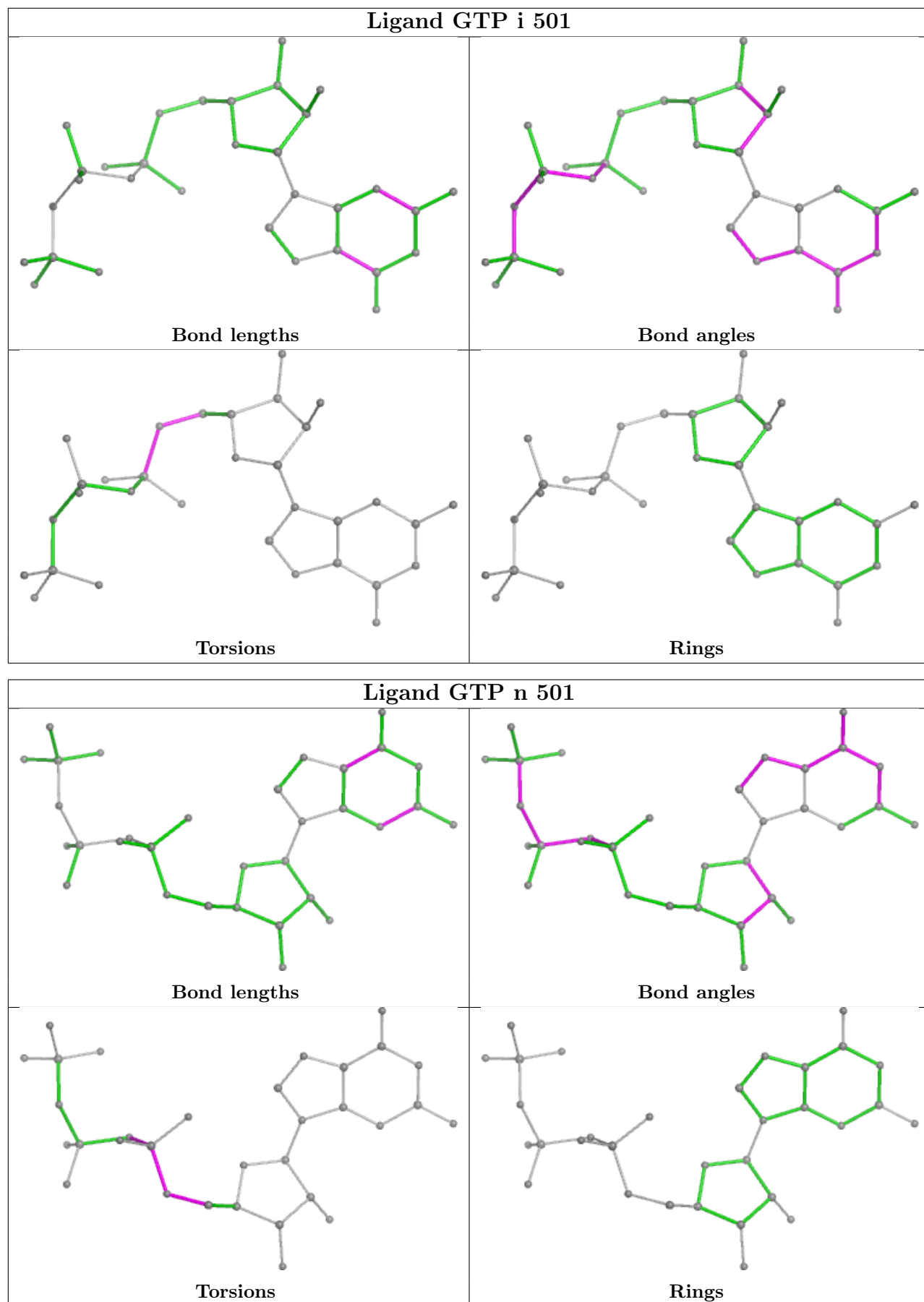


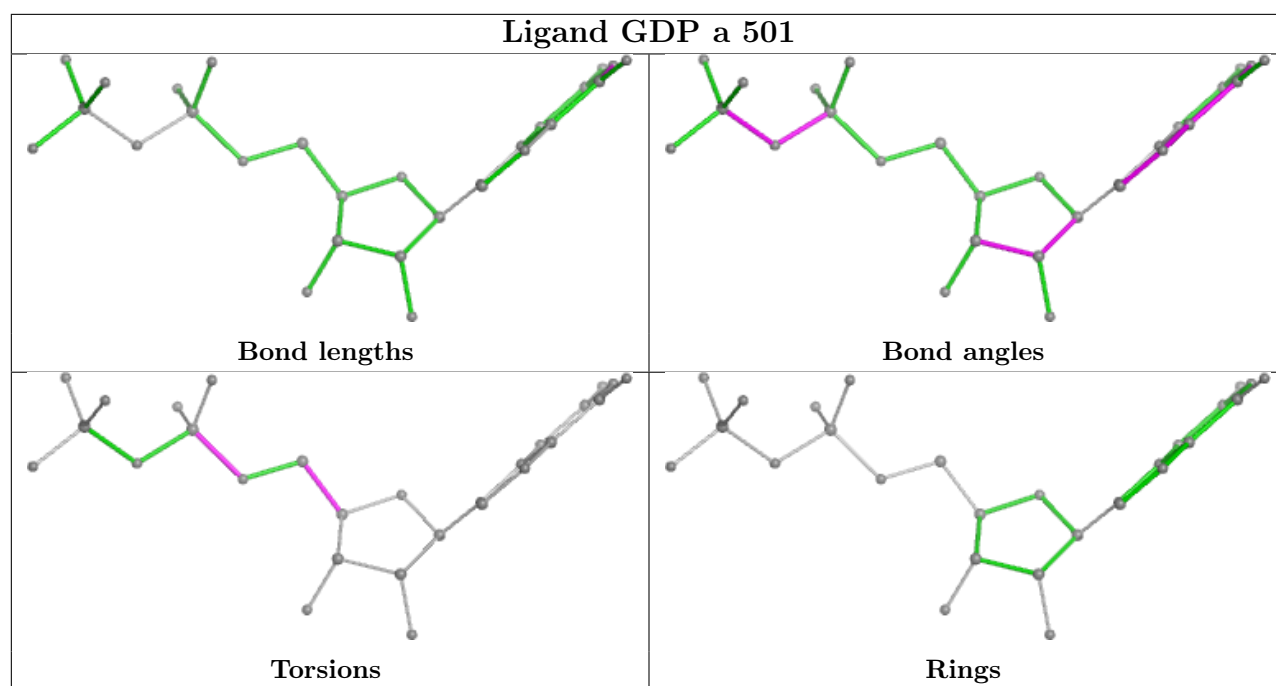












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

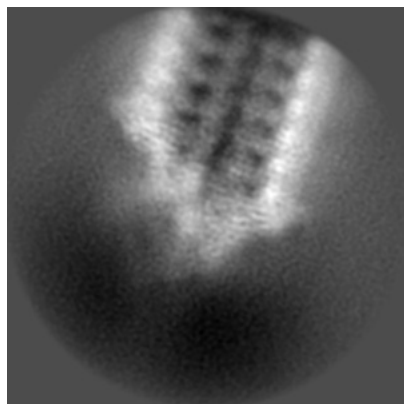
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-18665. These allow visual inspection of the internal detail of the map and identification of artifacts.

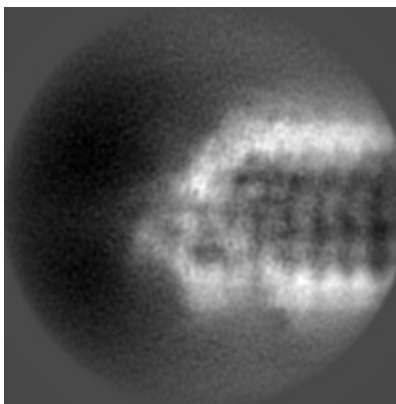
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

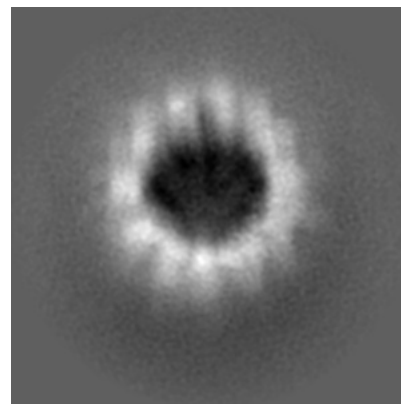
6.1.1 Primary map



X

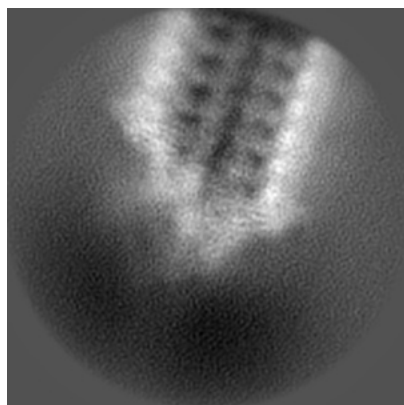


Y

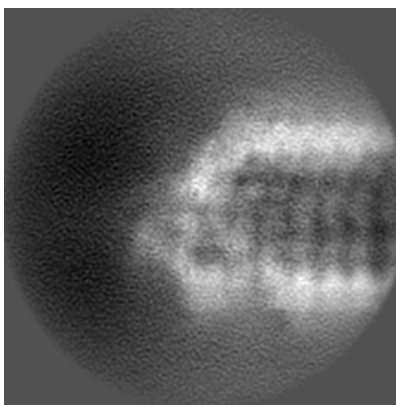


Z

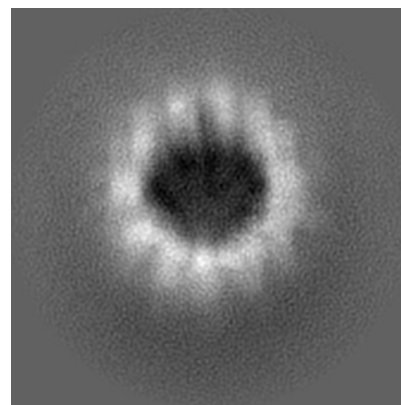
6.1.2 Raw map



X



Y

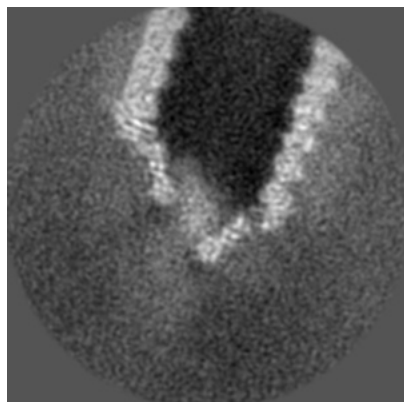


Z

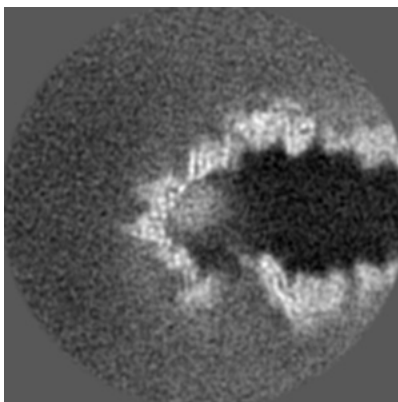
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

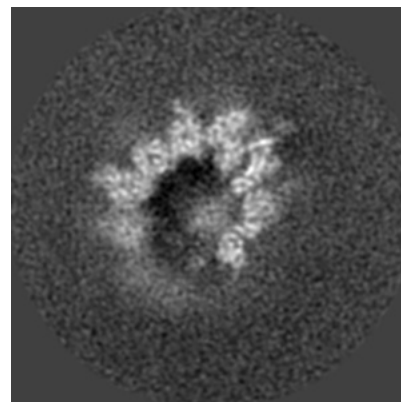
6.2.1 Primary map



X Index: 84

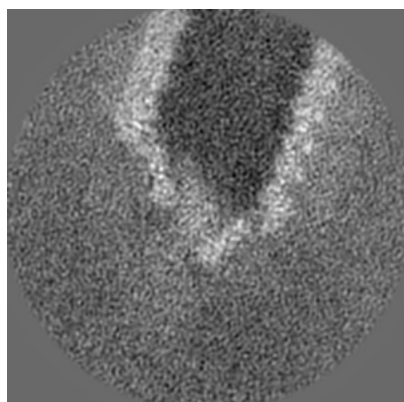


Y Index: 84

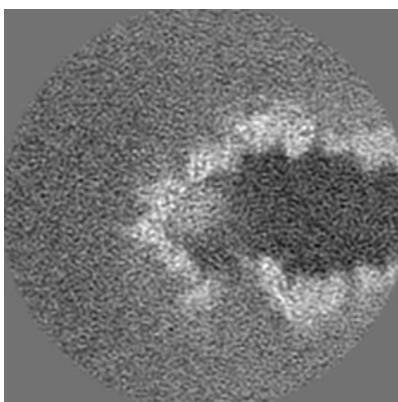


Z Index: 84

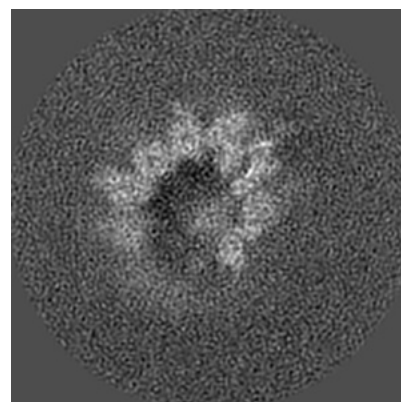
6.2.2 Raw map



X Index: 84



Y Index: 84

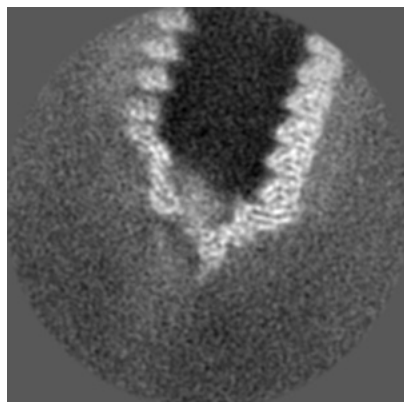


Z Index: 84

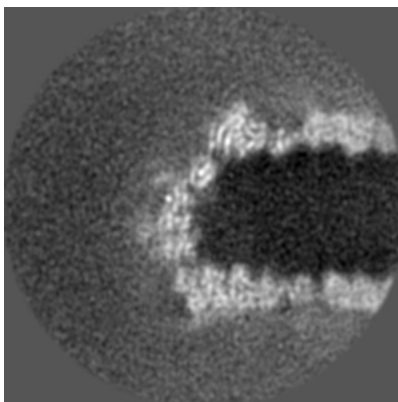
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

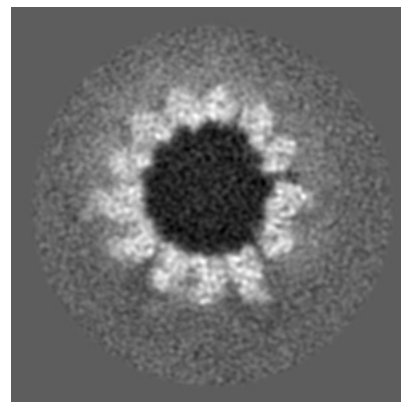
6.3.1 Primary map



X Index: 89

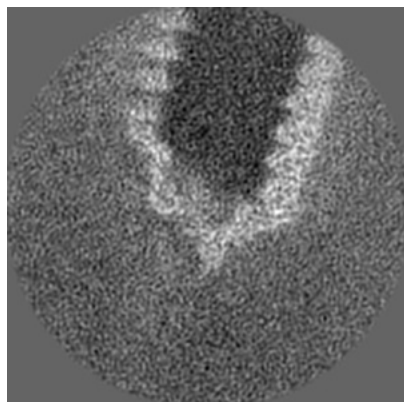


Y Index: 94

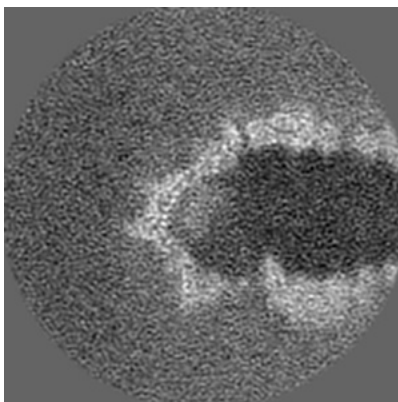


Z Index: 124

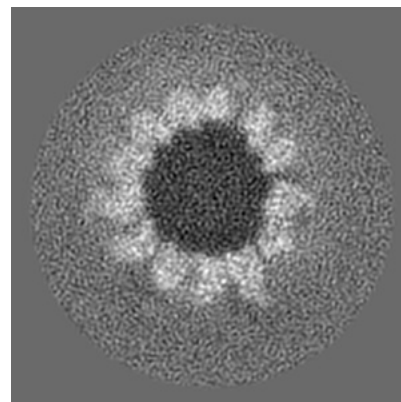
6.3.2 Raw map



X Index: 89



Y Index: 86

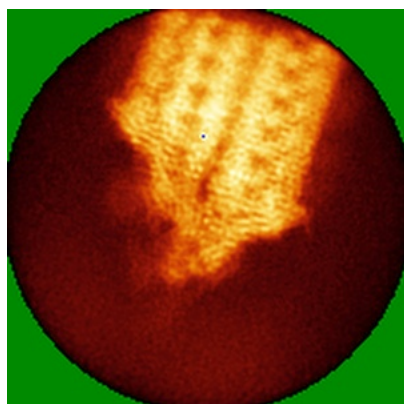


Z Index: 123

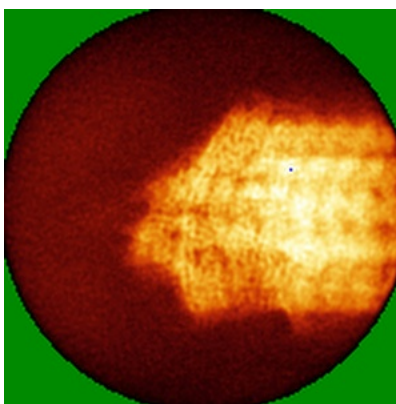
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

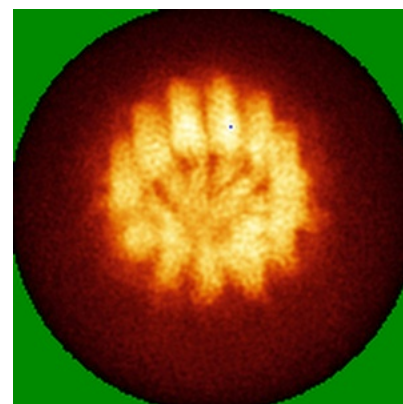
6.4.1 Primary map



X

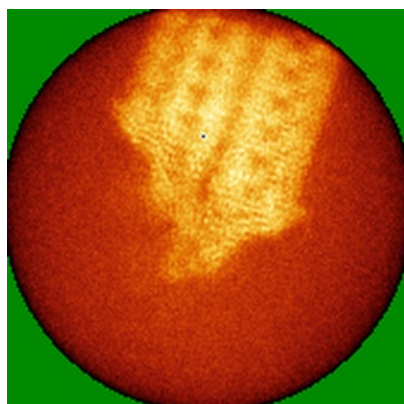


Y

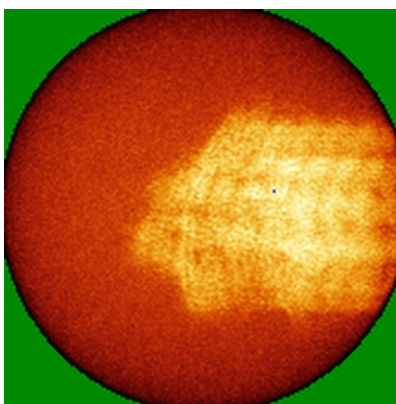


Z

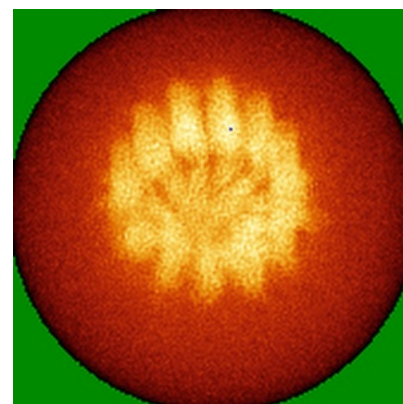
6.4.2 Raw map



X



Y

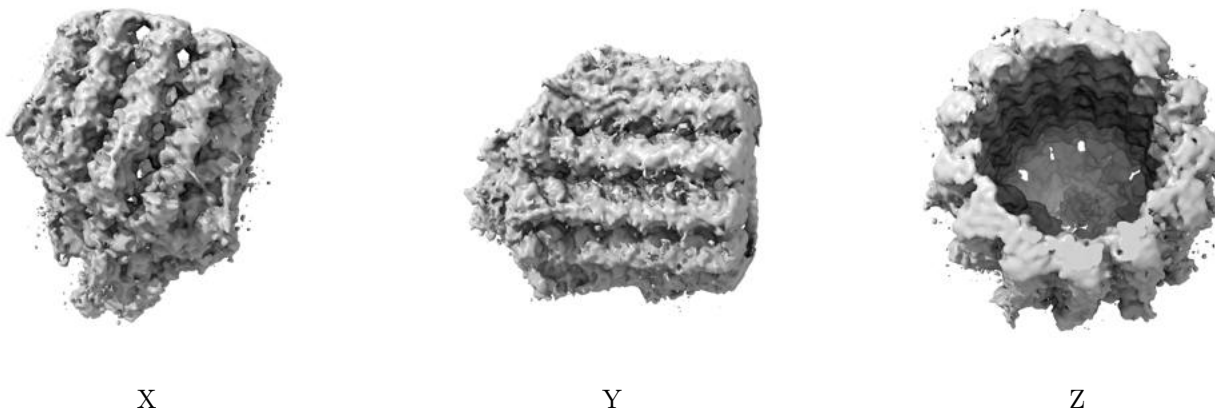


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

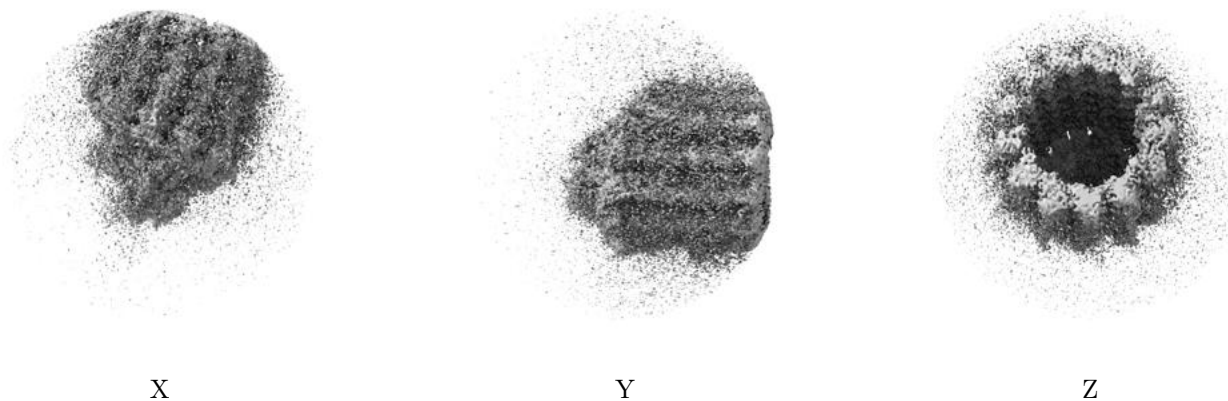
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.243. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

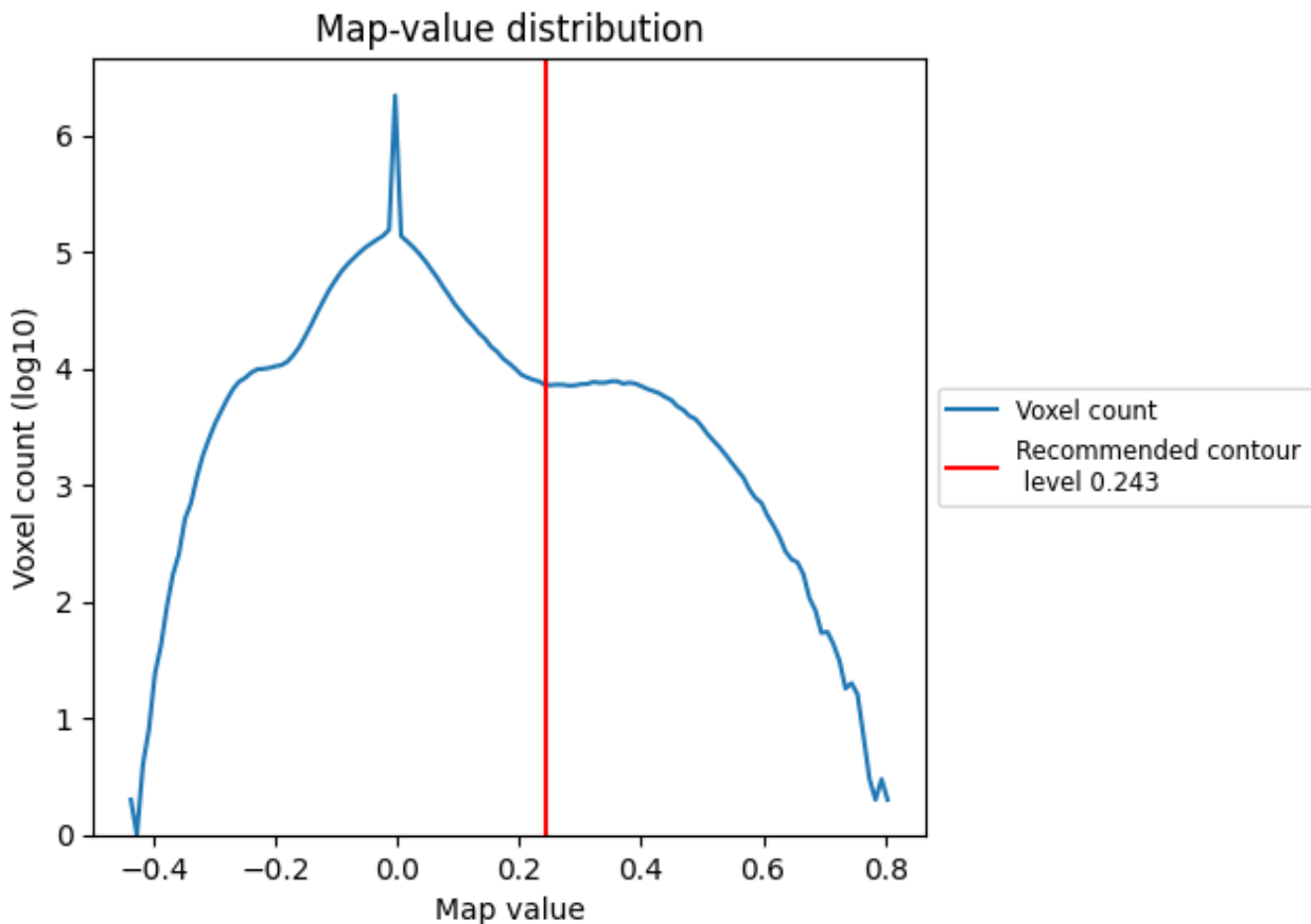
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

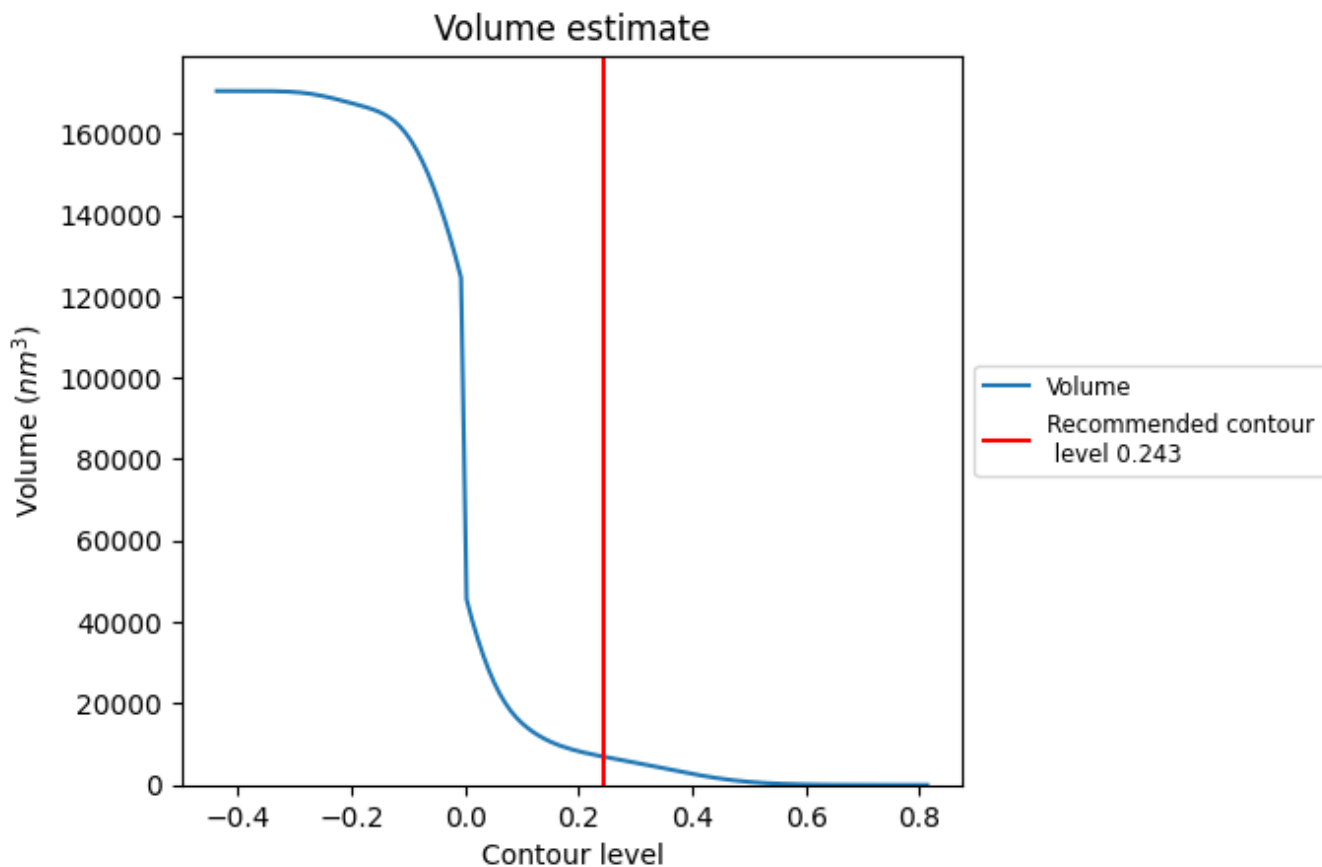
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

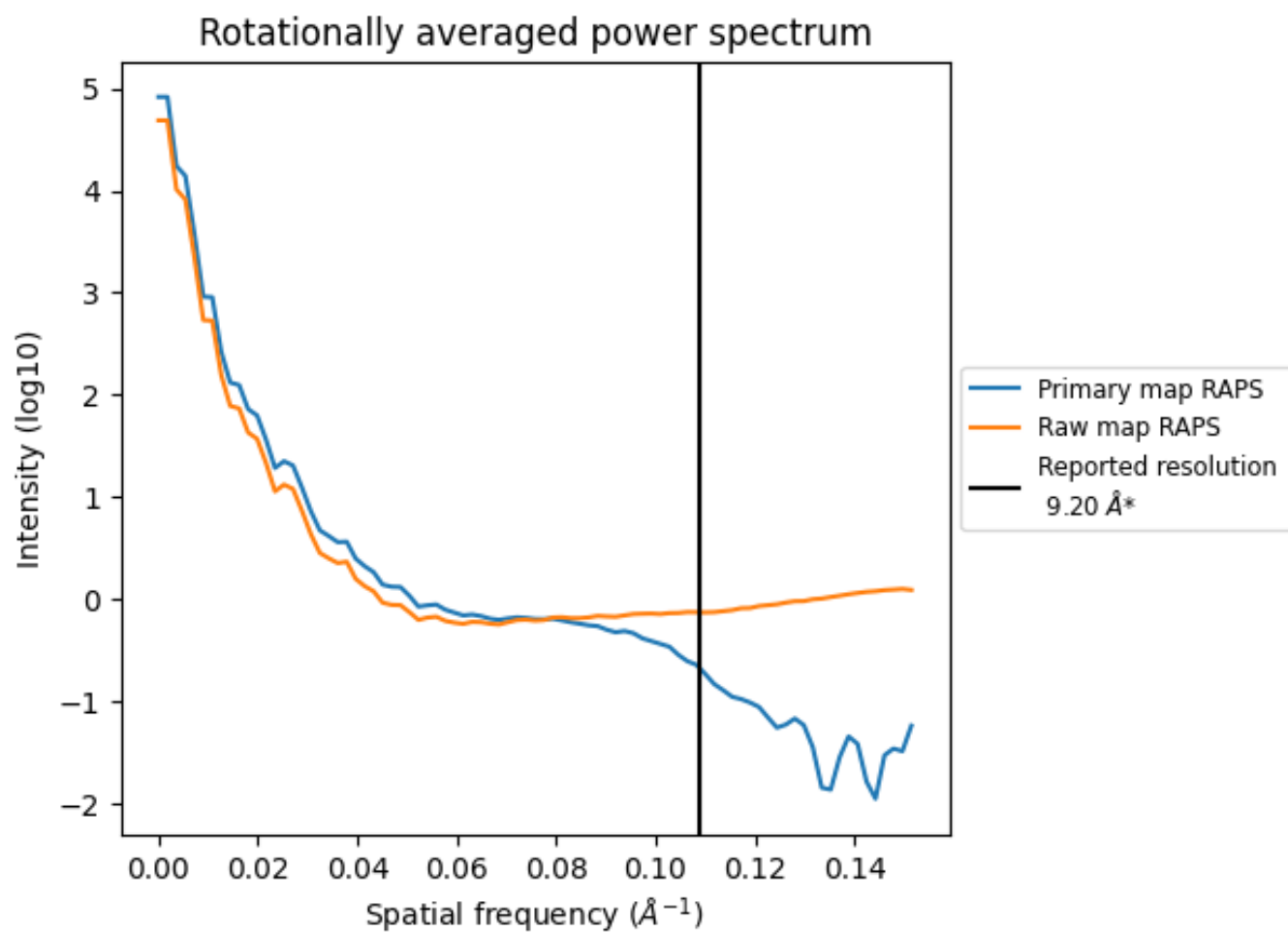
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 69720 nm³; this corresponds to an approximate mass of 6298 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i

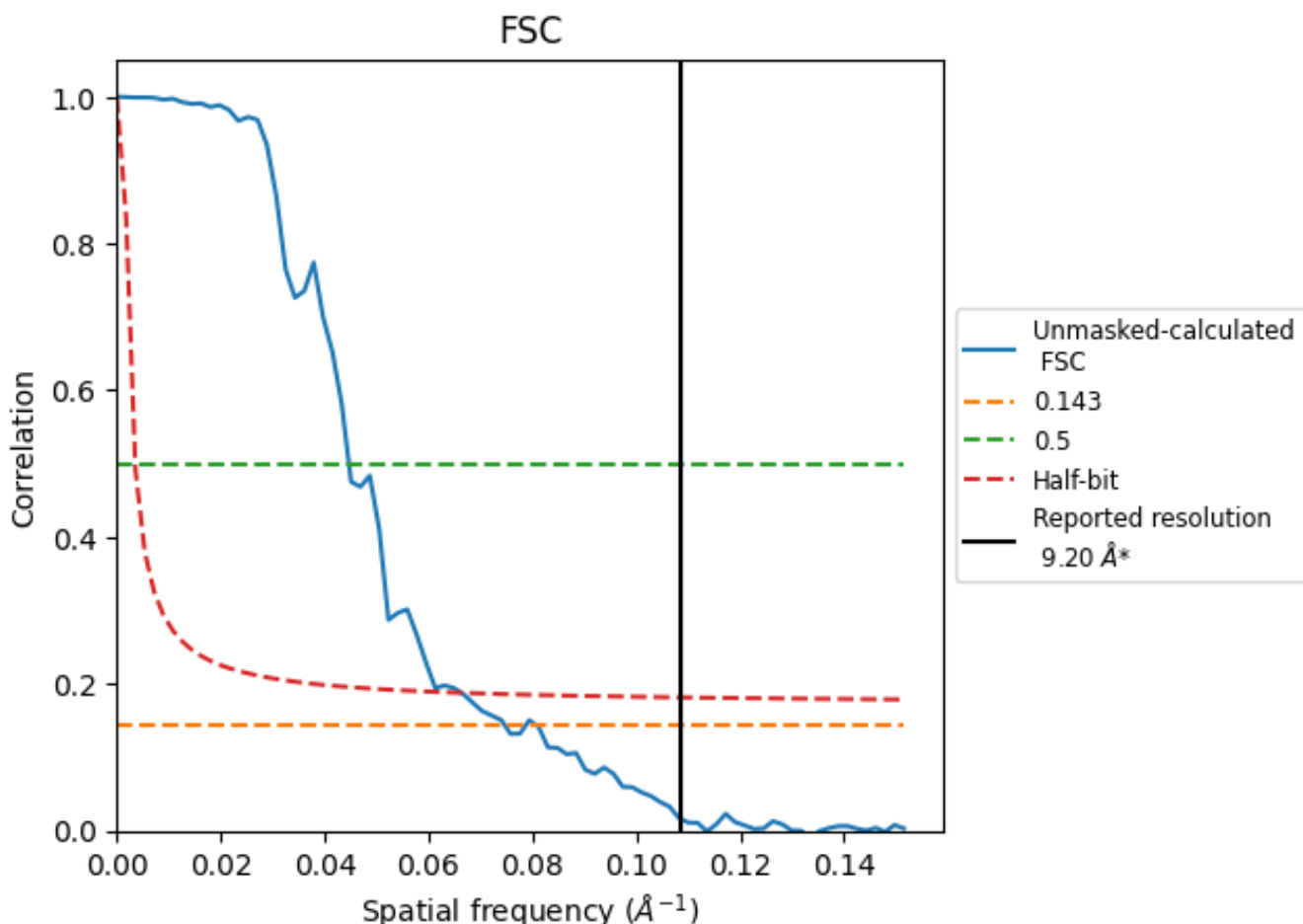


*Reported resolution corresponds to spatial frequency of 0.109 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.109 Å⁻¹

8.2 Resolution estimates [i](#)

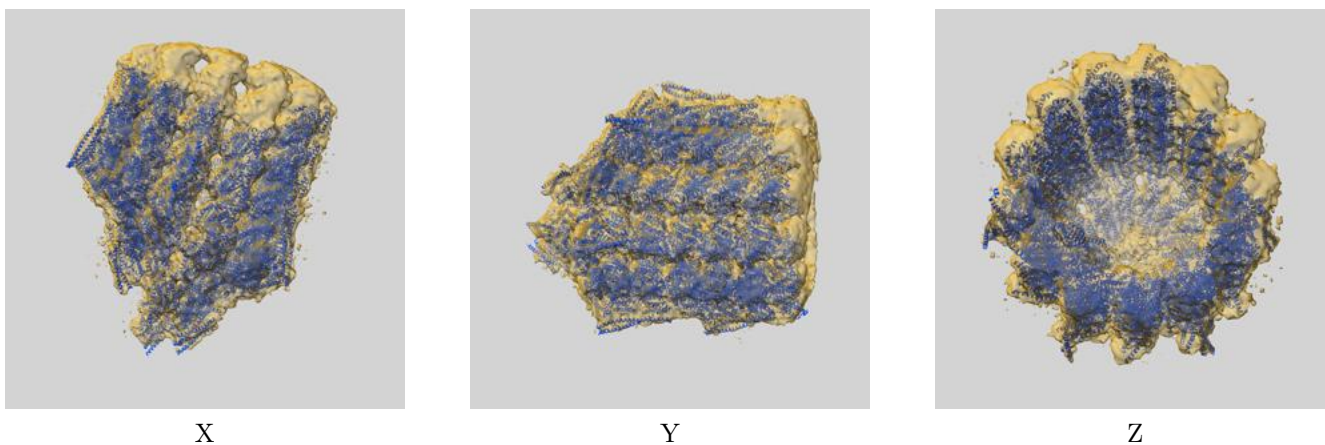
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	13.39	22.37	15.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 13.39 differs from the reported value 9.2 by more than 10 %

9 Map-model fit [i](#)

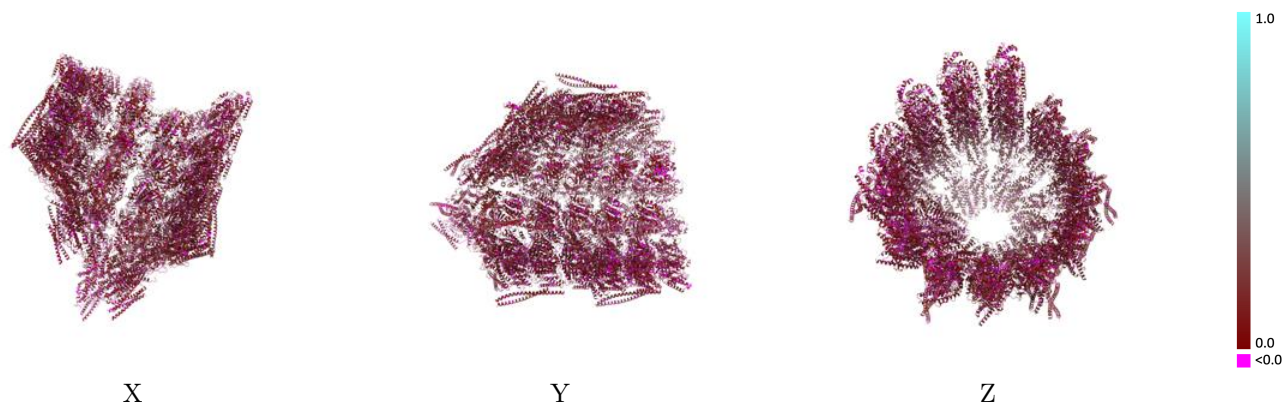
This section contains information regarding the fit between EMDB map EMD-18665 and PDB model 8QV2. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



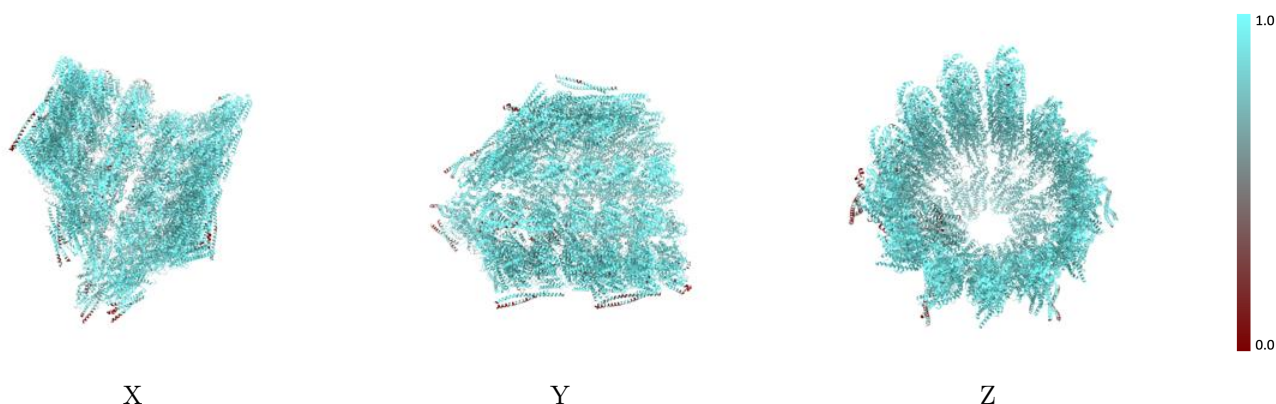
The images above show the 3D surface view of the map at the recommended contour level 0.243 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



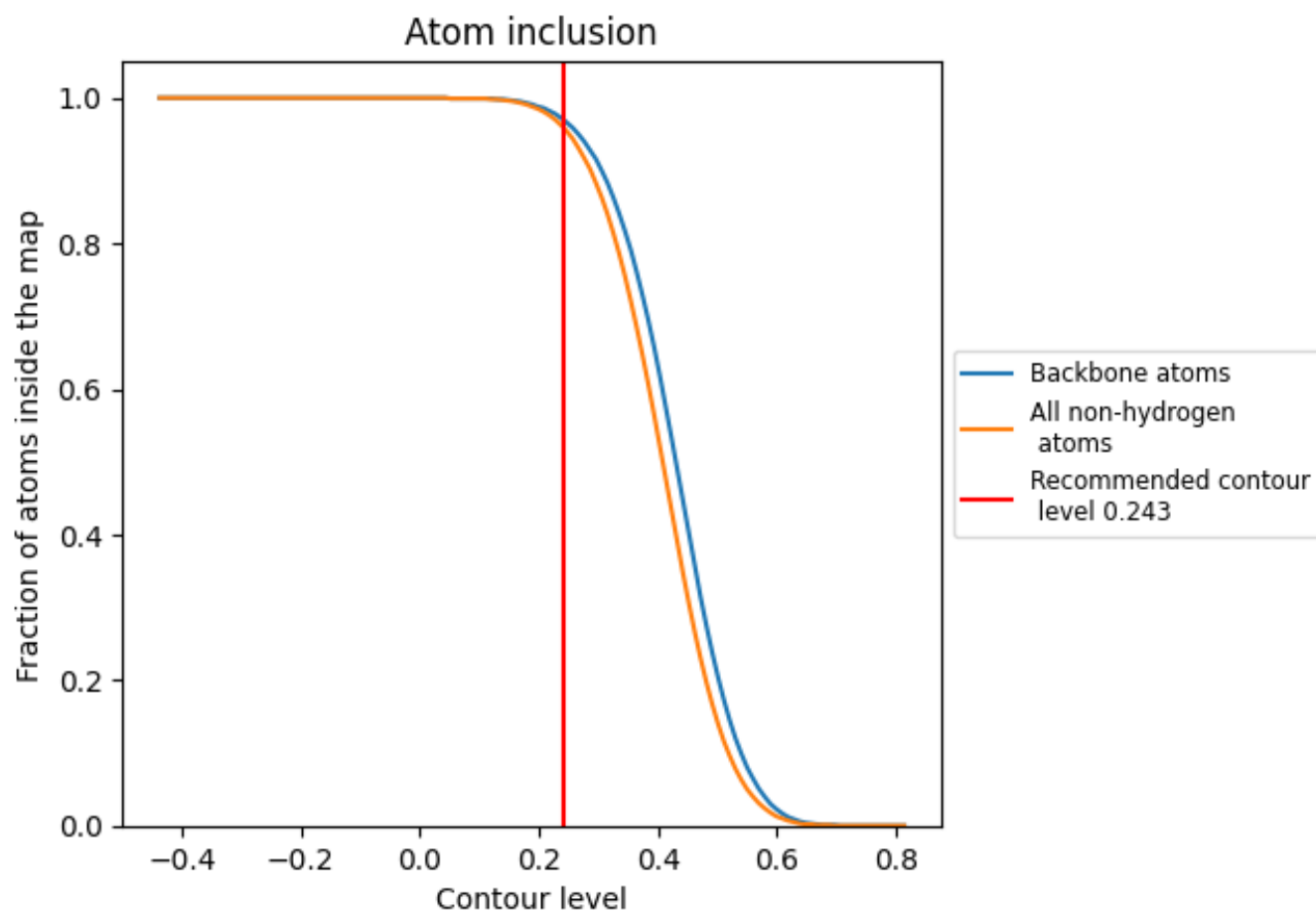
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.243).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.243) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9580	 0.1120
Ab	 0.9440	 0.1110
Ac	 0.9720	 0.1250
Ad	 0.9880	 0.1140
Ae	 0.9940	 0.1170
Af	 0.9880	 0.1180
Ag	 0.9860	 0.1160
Ah	 0.9790	 0.1150
Ai	 0.9870	 0.1150
Aj	 0.9910	 0.1020
Ak	 0.9880	 0.1080
Al	 0.9900	 0.0960
Am	 0.9730	 0.0950
An	 0.9640	 0.0940
Ao	 0.9520	 0.0980
Ap	 0.9870	 0.1090
Aq	 0.9920	 0.0910
Ar	 0.9890	 0.1050
Bb	 0.9670	 0.1060
Bc	 0.9830	 0.1210
Bd	 0.9910	 0.1180
Be	 0.9910	 0.1130
Bf	 0.9940	 0.1190
Bg	 0.9900	 0.1190
Bh	 0.9800	 0.1190
Bi	 0.9850	 0.1030
Bj	 0.9860	 0.1090
Bk	 0.9840	 0.1030
Bl	 0.9850	 0.0960
Bm	 0.9530	 0.0870
Bn	 0.8850	 0.0870
Bo	 0.9550	 0.0980
Bp	 0.9610	 0.0930
Bq	 0.9810	 0.1080
Br	 0.9800	 0.0970































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Chain	Atom inclusion	Q-score
C	 0.8970	 0.0510
D	 0.9500	 0.1130
E	 0.9780	 0.1230
F	 0.9750	 0.1350
G	 0.9860	 0.1310
H	 0.9740	 0.1320
I	 0.9820	 0.1320
J	 0.9640	 0.1390
K	 0.9770	 0.1360
L	 0.9680	 0.1340
M	 0.9820	 0.1290
N	 0.9630	 0.1240
O	 0.9490	 0.1110
P	 0.8820	 0.1170
Sa	 0.5480	 0.0830
Sb	 0.5750	 0.0560
Sc	 0.7580	 0.0840
Sd	 0.8080	 0.0790
Se	 0.8440	 0.1210
Sf	 0.8570	 0.1040
Sg	 0.8820	 0.1220
Sh	 0.8240	 0.1100
Si	 0.8100	 0.0930
Sj	 0.8550	 0.0980
Sk	 0.7870	 0.1070
Sl	 0.7450	 0.0870
Sm	 0.7280	 0.1040
Sn	 0.8090	 0.0680
Ua	 0.8810	 0.1450
Ub	 0.4550	 0.1070
Uc	 0.9370	 0.1680
Ud	 0.7850	 0.1590
Ue	 0.8840	 0.1860
Uf	 0.7420	 0.1810
Ug	 0.9070	 0.1510
Uh	 0.8440	 0.1800
Ui	 0.8240	 0.1680
Uj	 0.6150	 0.1720
Uk	 0.8660	 0.1610
Ul	 0.5340	 0.1570
Um	 0.5490	 0.1280
Un	 0.3450	 0.0990

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Chain	Atom inclusion	Q-score
a	 0.7820	 0.0430
b	 0.9450	 0.1000
c	 0.9670	 0.1090
d	 0.9830	 0.1120
e	 0.9850	 0.1230
f	 0.9810	 0.1180
g	 0.9620	 0.1230
h	 0.9670	 0.1140
i	 0.9750	 0.1140
j	 0.9820	 0.1150
k	 0.9800	 0.1030
l	 0.9750	 0.1010
m	 0.9700	 0.1050
n	 0.9450	 0.0920