



wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 07:01 PM UTC

PDB ID : 7M2W / pdb_00007m2w
EMDB ID : EMD-23635
Title : Engineered disulfide cross-linked closed conformation of the Yeast gamma-TuRC(SS)
Authors : Brilot, A.F.; Lyon, A.S.; Zelter, A.; Viswanath, S.; Maxwell, A.; MacCoss, M.J.; Muller, E.G.; Sali, A.; Davis, T.N.; Agard, D.A.
Deposited on : 2021-03-17
Resolution : 3.00 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:

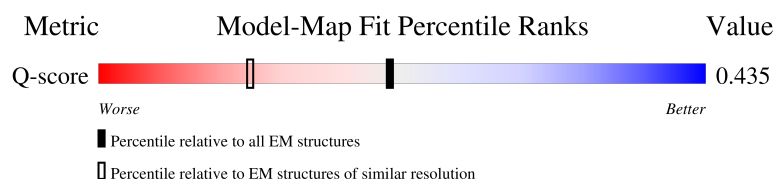
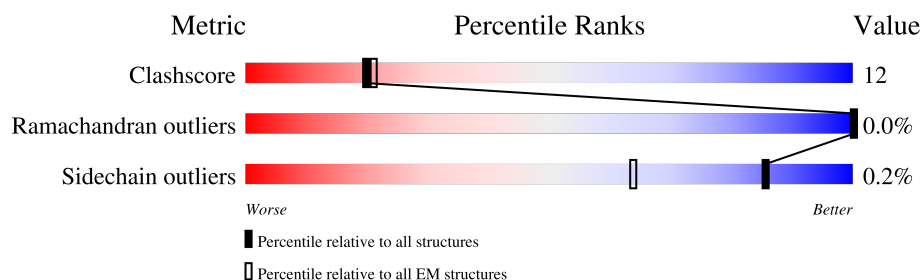
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



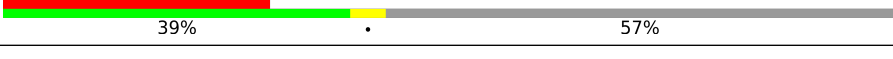
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	14% 65% 31% .
1	B	473	13% 63% 30% 7%
1	C	473	10% 67% 27% 6%
1	D	473	19% 62% 32% 5%

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Mol	Chain	Length	Quality of chain
2	E	823	
2	G	823	
3	F	846	
3	H	846	
4	K	220	
4	U	220	
4	X	220	
4	Y	220	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 39366 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
1	B	441	Total	C	N	O	S	0	0
			3450	2159	585	688	18		
1	A	453	Total	C	N	O	S	0	0
			3547	2218	599	711	19		
1	C	445	Total	C	N	O	S	0	0
			3481	2176	589	698	18		
1	D	447	Total	C	N	O	S	0	0
			3500	2189	591	701	19		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	58	CYS	SER	engineered mutation	UNP P53378
B	288	CYS	GLY	engineered mutation	UNP P53378
A	58	CYS	SER	engineered mutation	UNP P53378
A	288	CYS	GLY	engineered mutation	UNP P53378
C	58	CYS	SER	engineered mutation	UNP P53378
C	288	CYS	GLY	engineered mutation	UNP P53378
D	58	CYS	SER	engineered mutation	UNP P53378
D	288	CYS	GLY	engineered mutation	UNP P53378

- Molecule 2 is a protein called Spindle pole body component SPC97.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	707	Total	C	N	O	S	0	0
			5899	3796	991	1083	29		
2	G	712	Total	C	N	O	S	0	0
			5935	3819	997	1090	29		

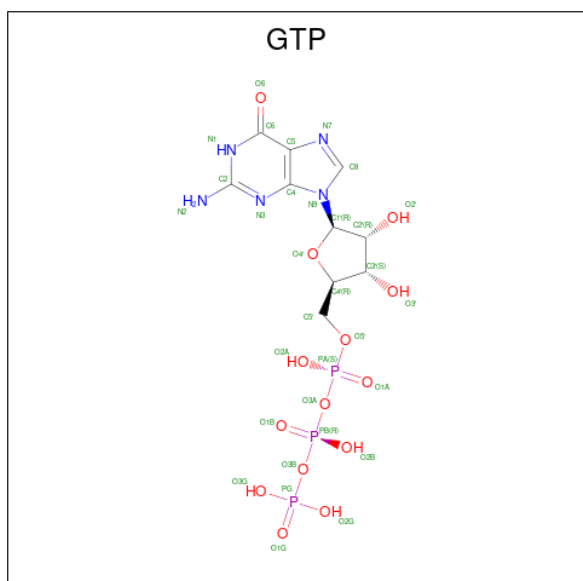
- Molecule 3 is a protein called Spindle pole body component SPC98.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	674	Total	C	N	O	S	0	0
			5569	3601	920	1032	16		
3	H	674	Total	C	N	O	S	0	0
			5569	3601	920	1032	16		

- Molecule 4 is a protein called Spindle pole body component 110.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	42	Total	C	N	O		0	0
			352	215	61	76			
4	K	95	Total	C	N	O	S	0	0
			792	488	142	160	2		
4	X	42	Total	C	N	O		0	0
			352	215	61	76			
4	Y	95	Total	C	N	O	S	0	0
			792	488	142	160	2		

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

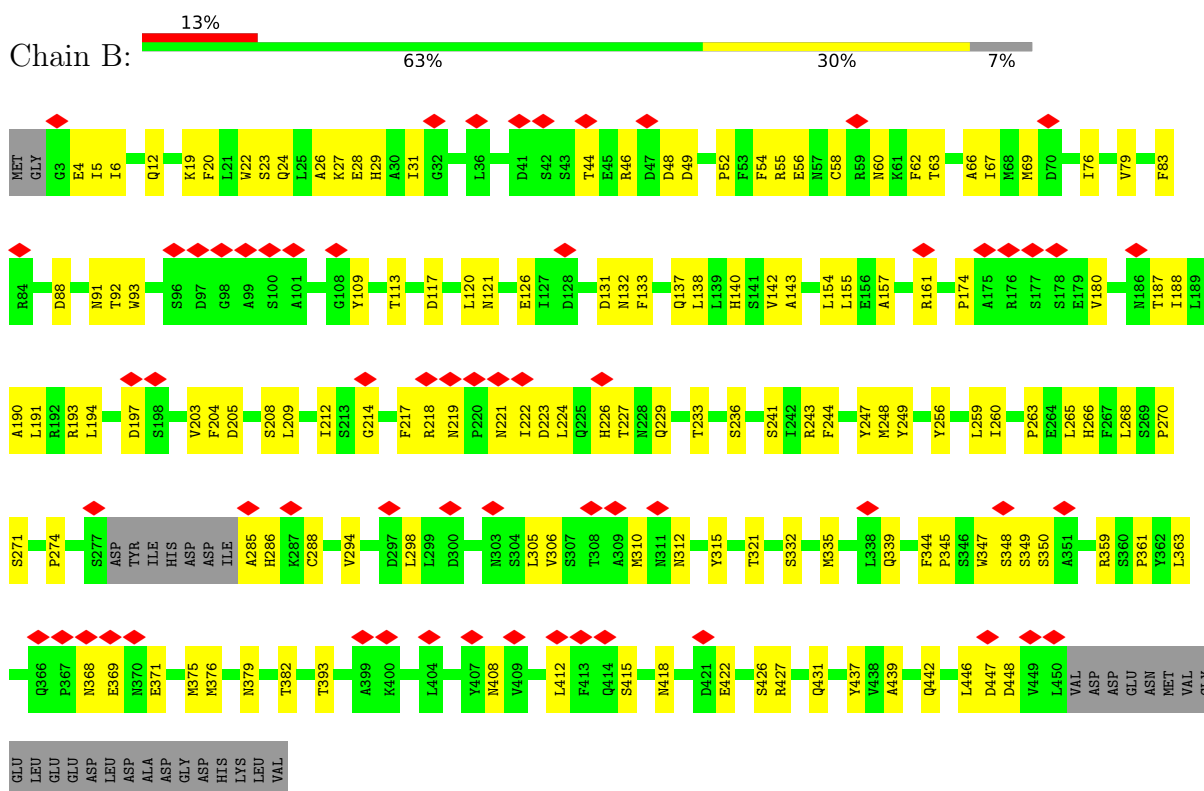


Mol	Chain	Residues	Atoms					AltConf
5	B	1	Total	C	N	O	P	0
			32	10	5	14	3	
5	A	1	Total	C	N	O	P	0
			32	10	5	14	3	
5	C	1	Total	C	N	O	P	0
			32	10	5	14	3	
5	D	1	Total	C	N	O	P	0
			32	10	5	14	3	

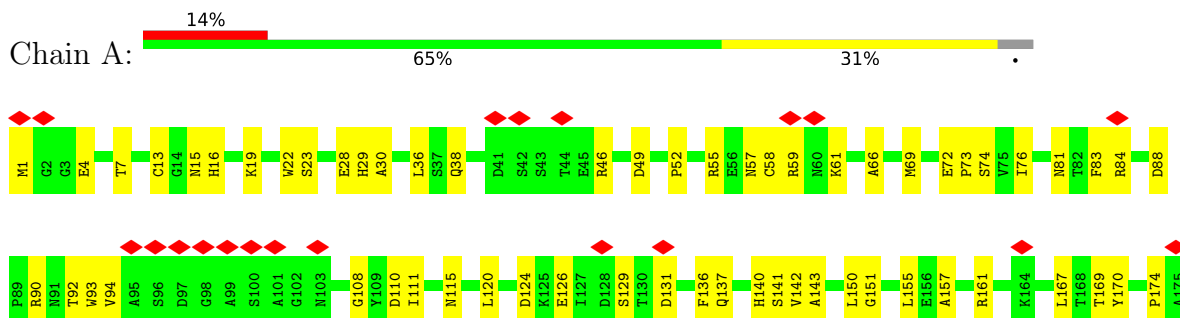
3 Residue-property plots

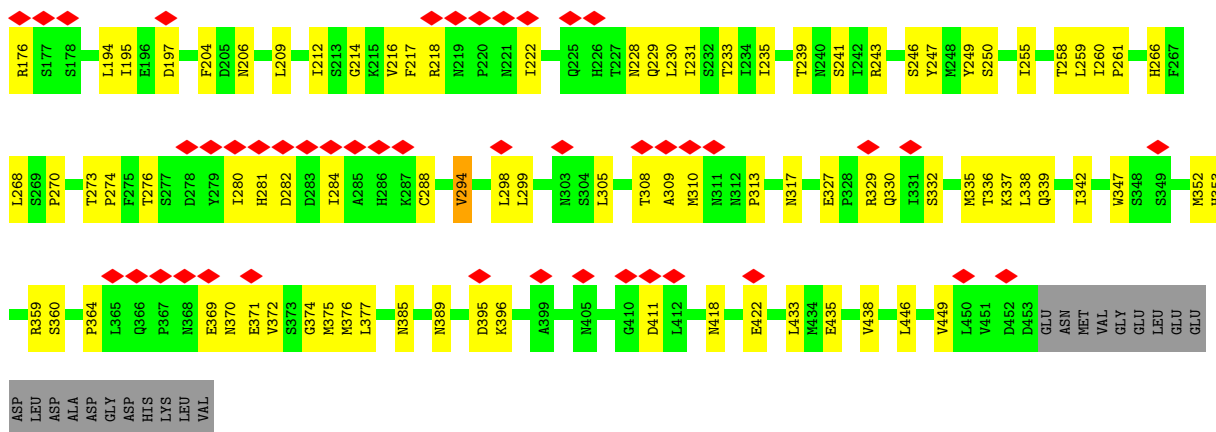
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

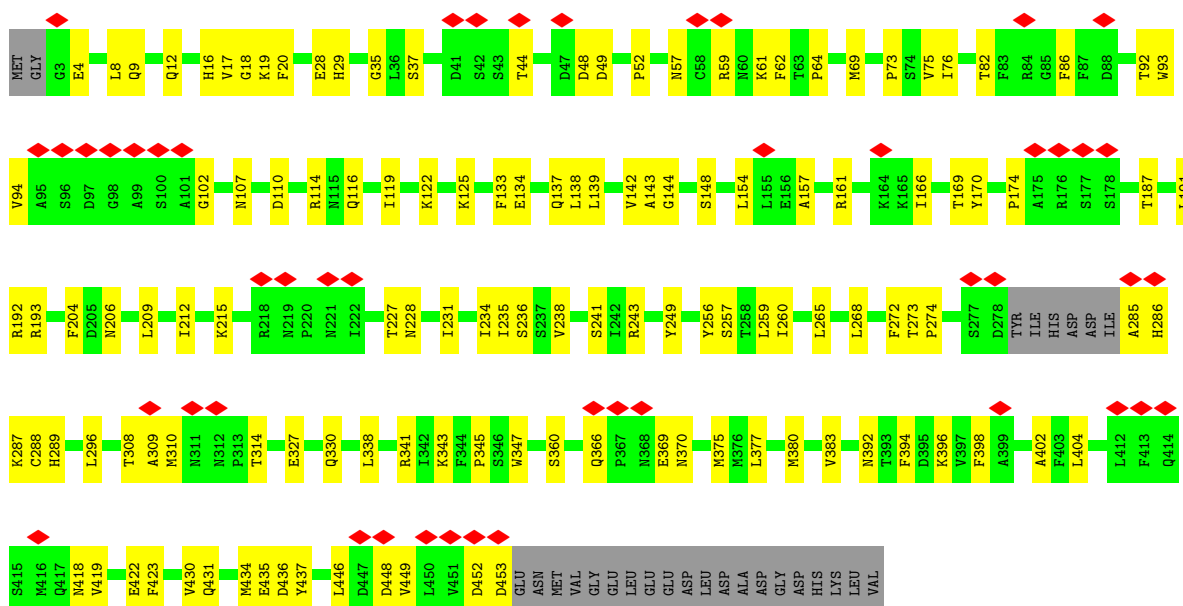


• Molecule 1: Tubulin gamma chain

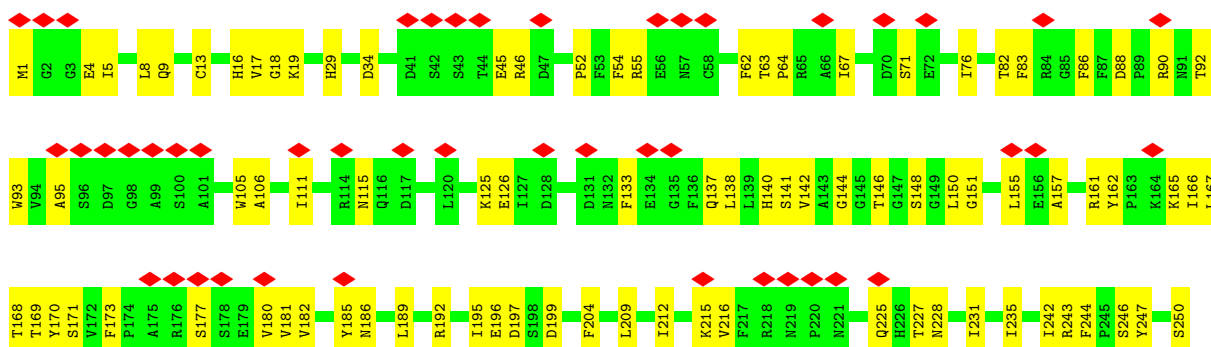


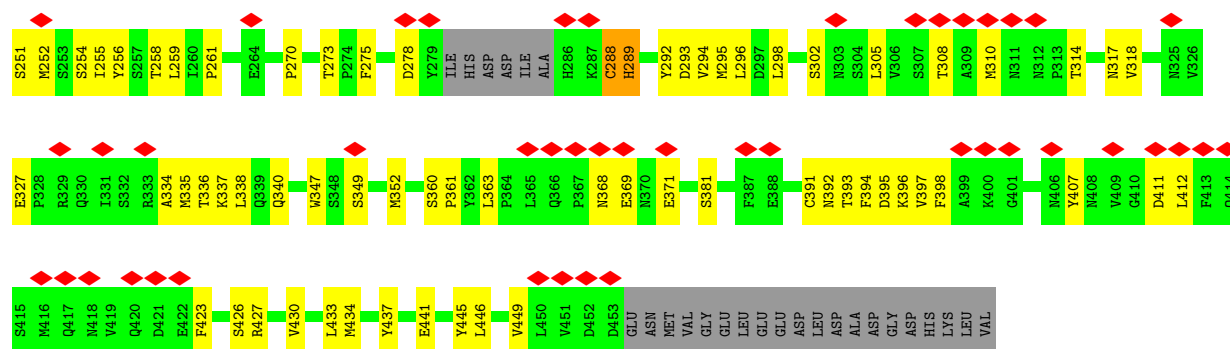


● Molecule 1: Tubulin gamma chain

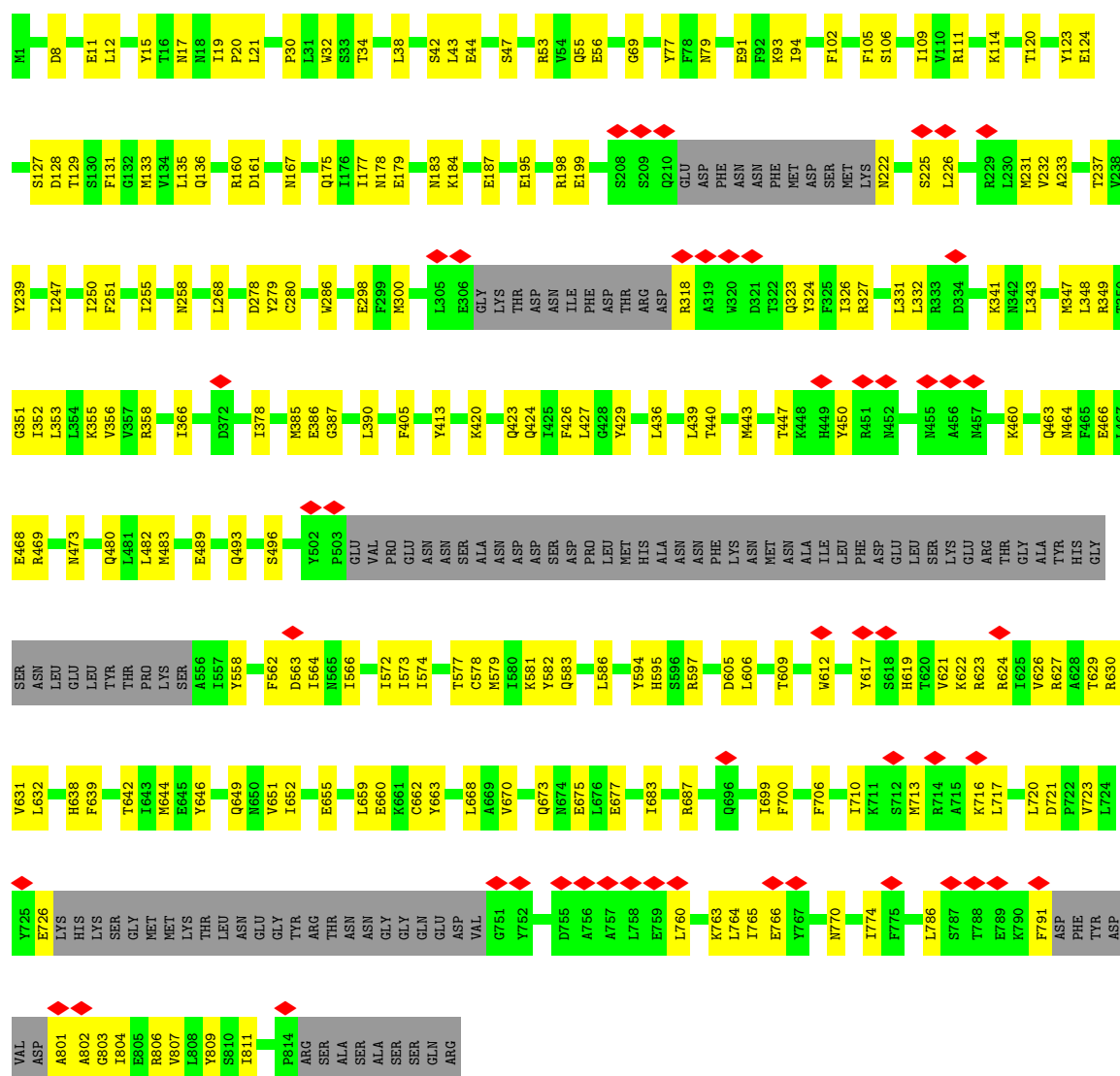


● Molecule 1: Tubulin gamma chain





• Molecule 2: Spindle pole body component SPC97



• Molecule 2: Spindle pole body component SPC97



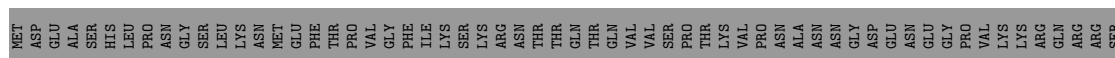


P508	R328	P210	HIS	GLU	MET
R509	L341	T213	LEU	THR	GLU
Y510	L341	T213	LEU	THR	GLU
V520	W349	N215	PRO	MET	GLU
H527	L350	S218	VAL	TRP	THR
L528	Y359	H222	ARG	HIS	LEU
V537	D363	F225	ALA	LEU	PHE
I538	D363	F225	PRO	GLY	ILE
L541	D374	E226	TYR	LYS	ILE
R544	D375	A227	THR	PHE	GLU
H550	D376	G228	GLU	LEU	GLU
W555	F377	L229	ALA	ASP	ALA
D561	I378	F241	SER	LEU	ALA
Y562	Y379	I246	PHE	PHE	GLN
P566	H380	I246	GLU	GLY	LEU
L570	I381	S247	ASN	ILE	LEU
Y574	P382	K251	MET	GLN	SER
R575	I383	I257	ASP	THR	GLN
R576	I402	N259	ARG	ASP	SER
E582	F403	V272	PHE	ASP	HIS
Y583	G406	L280	GLU	LEU	LEU
F589	F411	R286	ARG	MET	GLN
L590	F425	E286	ARG	LYS	THR
W591	Y429	I287	MET	LEU	VAL
Y598	T443	Y288	VAL	SER	ASP
F599	E447	I291	SER	VAL	VAL
Y600	Q452	R295	PRO	GLN	ASN
E603	M461	R299	SER	SER	LEU
S607	L477	F300	THR	TYR	LEU
I610	I480	T301	TYR	ALA	ALA
T611	L481	L304	S163	LYS	THR
R612	L482	E305	D183	ILE	GLN
S613	M483	E306	I184	VAL	GLY
F614	S486	D310	Y187	LYS	PRO
R615	D487	T311	V188	SER	LEU
R618	F488	F312	S189	SER	ILE
G619	M489	E315	T196	GLY	PHE
Y620	D490	L316	F202	ASN	TYR
N621	I493	R317	D203	GLU	LYS
	I499	I318	H204	ASN	LEU
	N497	F319	F205	ALA	LEU
	D498	K320	Q206	ASN	ASP
	I499	T207	I207	HIS	SER

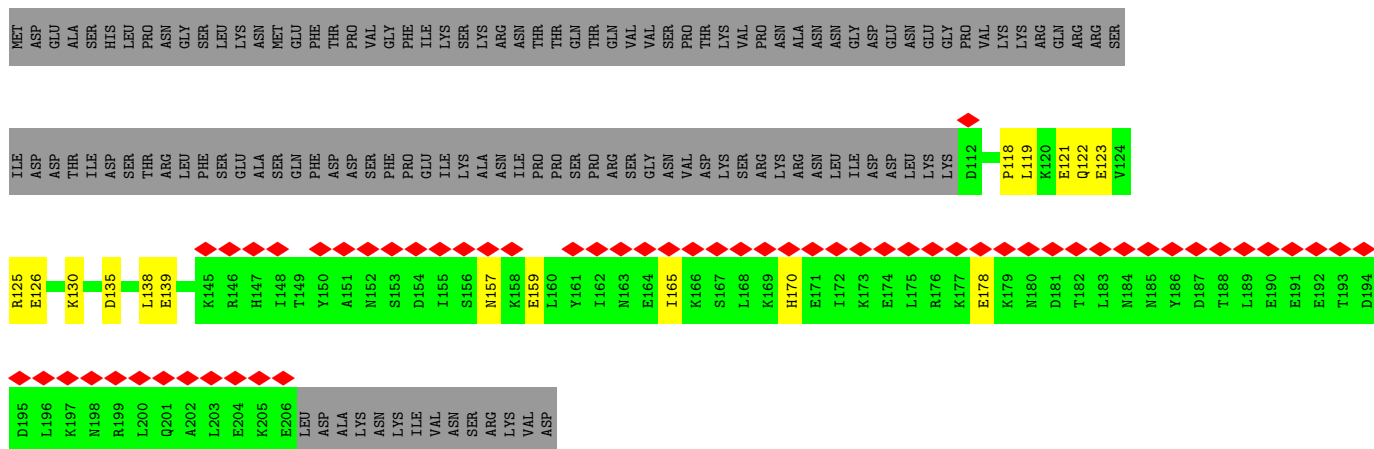
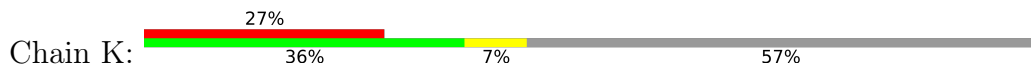
- Molecule 3: Spindle pole body component SPC98



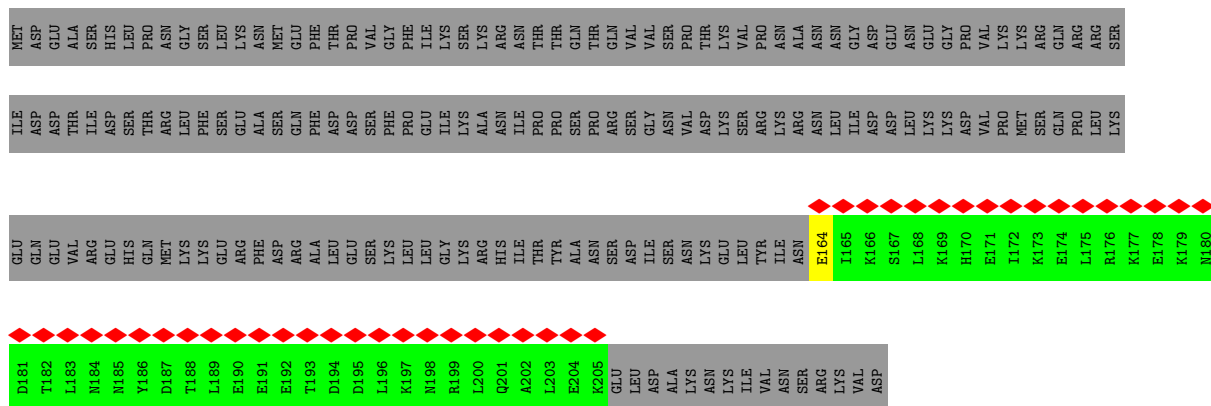
- Molecule 4: Spindle pole body component 110



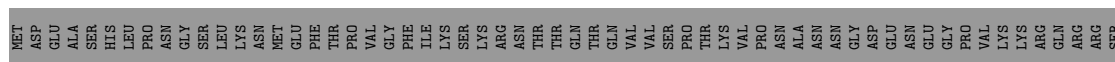
- Molecule 4: Spindle pole body component 110



- Molecule 4: Spindle pole body component 110



- Molecule 4: Spindle pole body component 110



LEU	ASP	ALA	LYS	ASN	LYS	ILE	VAL	ASN	SER	ARG	LYS	VAL	ASP																											ASP																			
H147	I148	T149	Y150	A151	N152	S153	D154	I155	S156	N157	K158	E159	L160	Y161	I162	N163	E164	I165	K166	S167	L168	K169	H170	E171	I172	K173	E174	L175	R176	K177	E178	K179	N180	D181	T182	L183	N184	N185	Y186	D187	T188	L189	E190	E191	E192	T193	D194	D195	L196	K197	N198	R199	L200	Q201	A202	L203	E204	K205	E206
ILE	ASP	THR	ILE	ASP	SER	THR	ARG	LEU	PHE	SER	GLU	ALA	SER	GLN	PHE	ASP	PHE	PRO	GLU	ILE	LYS	ALA	ASN	PRO	PRO	SER	PRO	ARG	SER	GLY	ASN	VAL	ASP	LYS	SER	ARG	LYS	ARG	ASN	LEU	ILE	ASP	ASP	LEU	LYS	LYS	D112	E121	L142	L143	G144	K145	R146						

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=0°, rise=0.1 Å, axial sym=C1	Depositor
Number of segments used	148911	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Final reconstruction in cis-TEM	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	72	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	47214	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	32.981	Depositor
Minimum map value	-18.020	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.632	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	635.4, 635.4, 635.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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

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	0.17	0/3622	0.41	0/4920
1	B	0.17	0/3522	0.43	1/4782 (0.0%)
1	C	0.17	0/3553	0.40	0/4825
1	D	0.22	0/3573	0.46	0/4851
2	E	0.19	0/6015	0.39	0/8119
2	G	0.19	0/6052	0.39	0/8170
3	F	0.19	0/5688	0.39	0/7688
3	H	0.18	0/5688	0.40	0/7688
4	K	0.71	0/800	0.95	0/1069
4	U	0.81	0/353	0.93	0/471
4	X	0.74	0/353	1.22	0/471
4	Y	0.82	0/800	1.32	0/1069
All	All	0.26	0/40019	0.48	1/54123 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	58	CYS	N-CA-C	5.78	118.32	111.33

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3547	0	3398	112	0
1	B	3450	0	3315	110	0
1	C	3481	0	3336	91	0
1	D	3500	0	3354	132	0
2	E	5899	0	5954	185	0
2	G	5935	0	5996	141	0
3	F	5569	0	5588	129	0
3	H	5569	0	5588	140	0
4	K	792	0	788	17	0
4	U	352	0	347	4	0
4	X	352	0	347	0	0
4	Y	792	0	788	41	0
5	A	32	0	11	4	0
5	B	32	0	12	2	0
5	C	32	0	12	1	0
5	D	32	0	11	5	0
All	All	39366	0	38845	973	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 12.

The worst 5 of 973 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:G:34:THR:HG21	4:K:178:GLU:OE2	1.12	1.30
2:E:226:LEU:HD11	4:Y:146:ARG:CZ	1.62	1.28
2:G:34:THR:CG2	4:K:178:GLU:OE2	2.03	1.06
2:E:226:LEU:CD1	4:Y:146:ARG:NH1	2.20	1.05
2:E:226:LEU:HG	4:Y:146:ARG:HG3	1.38	1.05

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	451/473 (95%)	429 (95%)	22 (5%)	0	100	100
1	B	437/473 (92%)	416 (95%)	21 (5%)	0	100	100
1	C	441/473 (93%)	414 (94%)	27 (6%)	0	100	100
1	D	443/473 (94%)	418 (94%)	24 (5%)	1 (0%)	43	76
2	E	695/823 (84%)	666 (96%)	29 (4%)	0	100	100
2	G	700/823 (85%)	675 (96%)	25 (4%)	0	100	100
3	F	670/846 (79%)	638 (95%)	32 (5%)	0	100	100
3	H	670/846 (79%)	642 (96%)	28 (4%)	0	100	100
4	K	93/220 (42%)	91 (98%)	2 (2%)	0	100	100
4	U	40/220 (18%)	40 (100%)	0	0	100	100
4	X	40/220 (18%)	40 (100%)	0	0	100	100
4	Y	93/220 (42%)	88 (95%)	5 (5%)	0	100	100
All	All	4773/6110 (78%)	4557 (96%)	215 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	288	CYS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	404/421 (96%)	403 (100%)	1 (0%)	87	92
1	B	393/421 (93%)	392 (100%)	1 (0%)	86	91
1	C	397/421 (94%)	397 (100%)	0	100	100
1	D	399/421 (95%)	397 (100%)	2 (0%)	81	89
2	E	663/766 (87%)	663 (100%)	0	100	100
2	G	668/766 (87%)	668 (100%)	0	100	100
3	F	628/787 (80%)	627 (100%)	1 (0%)	87	92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	H	628/787 (80%)	628 (100%)	0	100	100
4	K	89/206 (43%)	88 (99%)	1 (1%)	65	83
4	U	40/206 (19%)	39 (98%)	1 (2%)	42	72
4	X	40/206 (19%)	39 (98%)	1 (2%)	42	72
4	Y	89/206 (43%)	87 (98%)	2 (2%)	45	74
All	All	4438/5614 (79%)	4428 (100%)	10 (0%)	85	92

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	X	164	GLU
4	Y	145	LYS
4	Y	165	ILE
1	D	289	HIS
3	F	614	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	539	ASN
4	X	184	ASN
3	F	660	ASN
2	G	649	GLN
1	A	420	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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
5	GTP	C	501	-	33,34,34	0.97	1 (3%)	50,54,54	1.57	9 (18%)
5	GTP	B	501	-	33,34,34	0.94	1 (3%)	50,54,54	1.60	8 (16%)
5	GTP	D	501	-	33,34,34	1.00	2 (6%)	50,54,54	1.57	9 (18%)
5	GTP	A	501	-	33,34,34	0.98	1 (3%)	50,54,54	1.54	9 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GTP	C	501	-	-	6/22/38/38	0/3/3/3
5	GTP	B	501	-	-	6/22/38/38	0/3/3/3
5	GTP	D	501	-	-	3/22/38/38	0/3/3/3
5	GTP	A	501	-	-	6/22/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	501	GTP	C2-N3	2.31	1.38	1.33
5	C	501	GTP	C2-N3	2.21	1.38	1.33
5	A	501	GTP	C2-N3	2.19	1.38	1.33
5	B	501	GTP	C2-N3	2.13	1.38	1.33
5	D	501	GTP	PA-O3A	2.05	1.61	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	501	GTP	C5-C4-N3	-5.12	120.25	128.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	501	GTP	C5-C4-N3	-5.10	120.28	128.39
5	C	501	GTP	C5-C4-N3	-5.03	120.38	128.39
5	A	501	GTP	C5-C4-N3	-4.91	120.58	128.39
5	B	501	GTP	C2-N3-C4	4.68	120.35	112.30

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

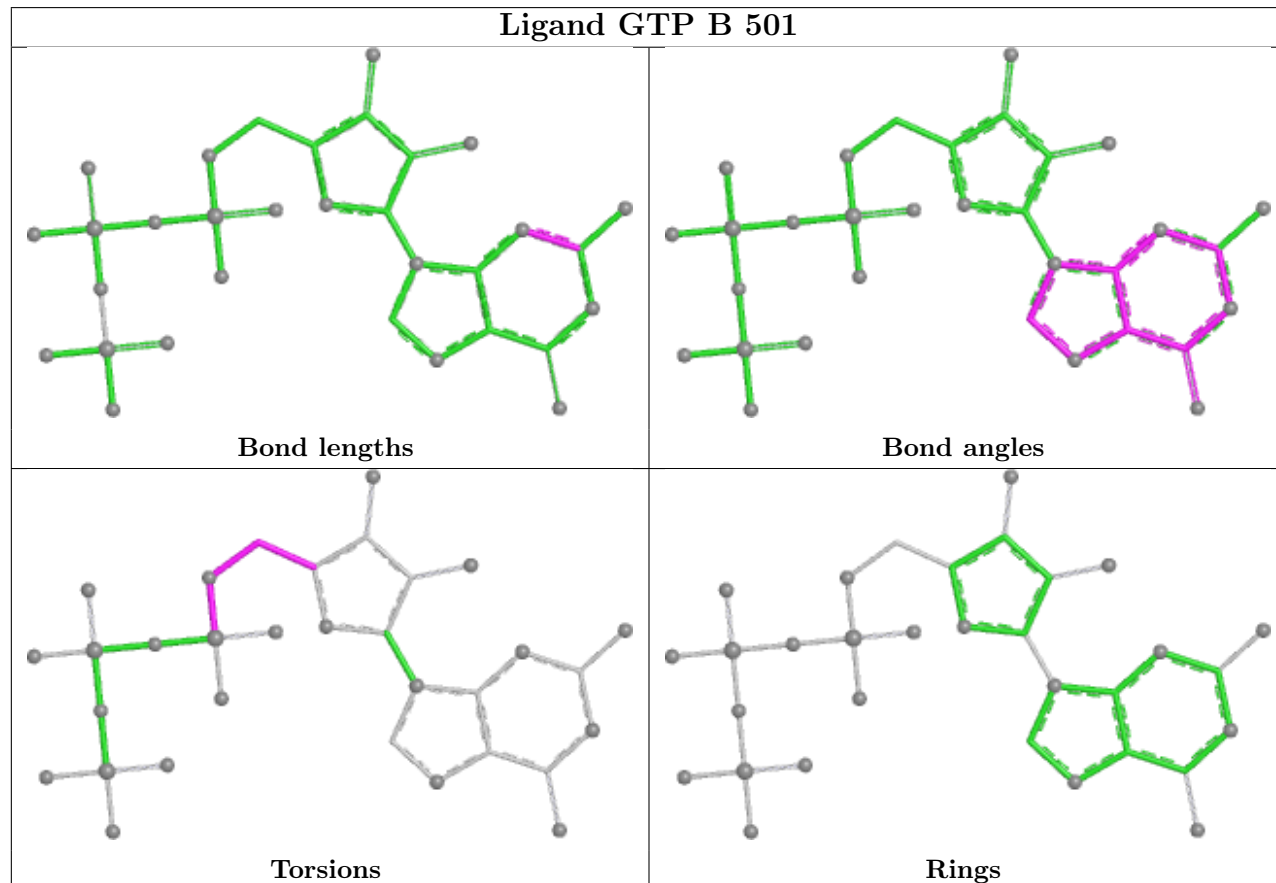
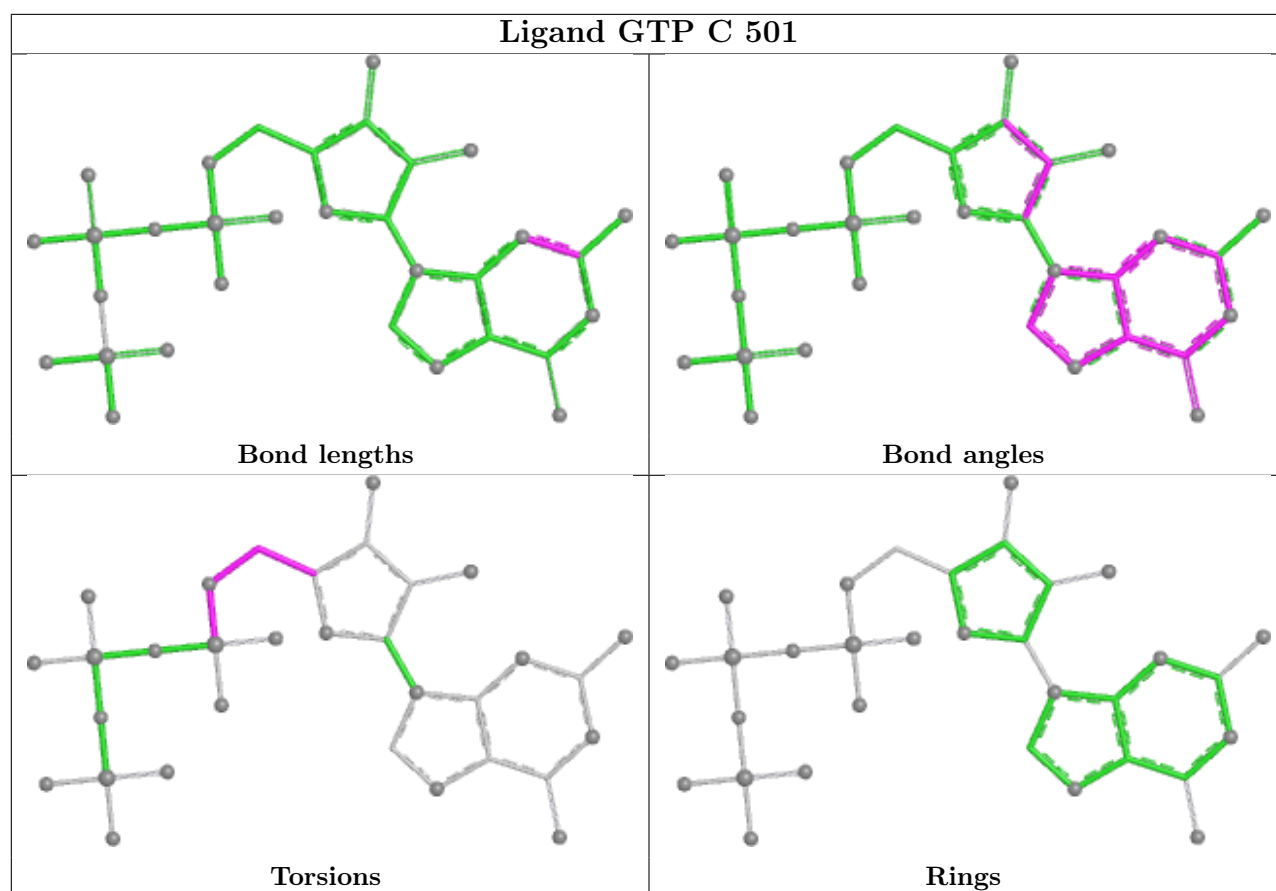
Mol	Chain	Res	Type	Atoms
5	B	501	GTP	C5'-O5'-PA-O3A
5	B	501	GTP	C5'-O5'-PA-O2A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	C5'-O5'-PA-O3A
5	C	501	GTP	C5'-O5'-PA-O1A

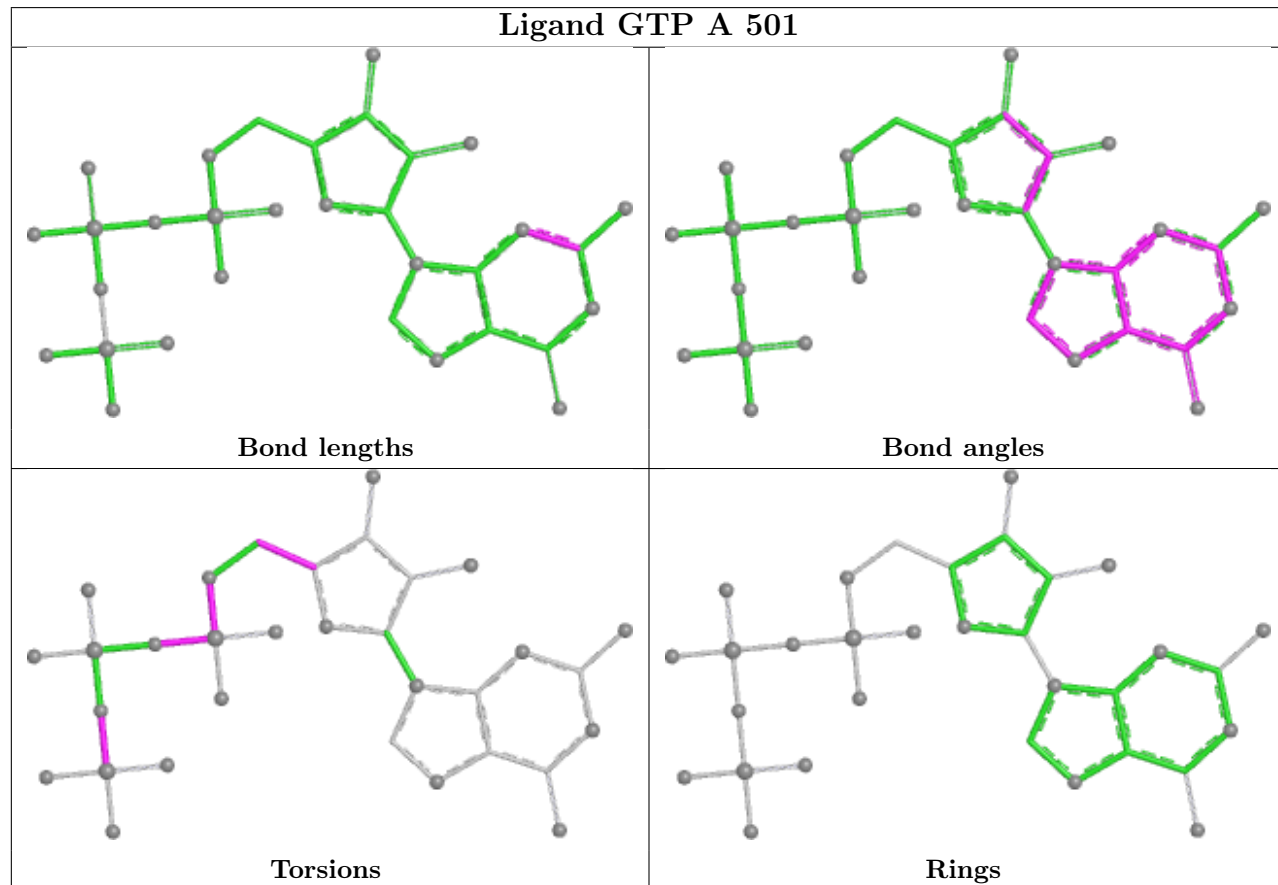
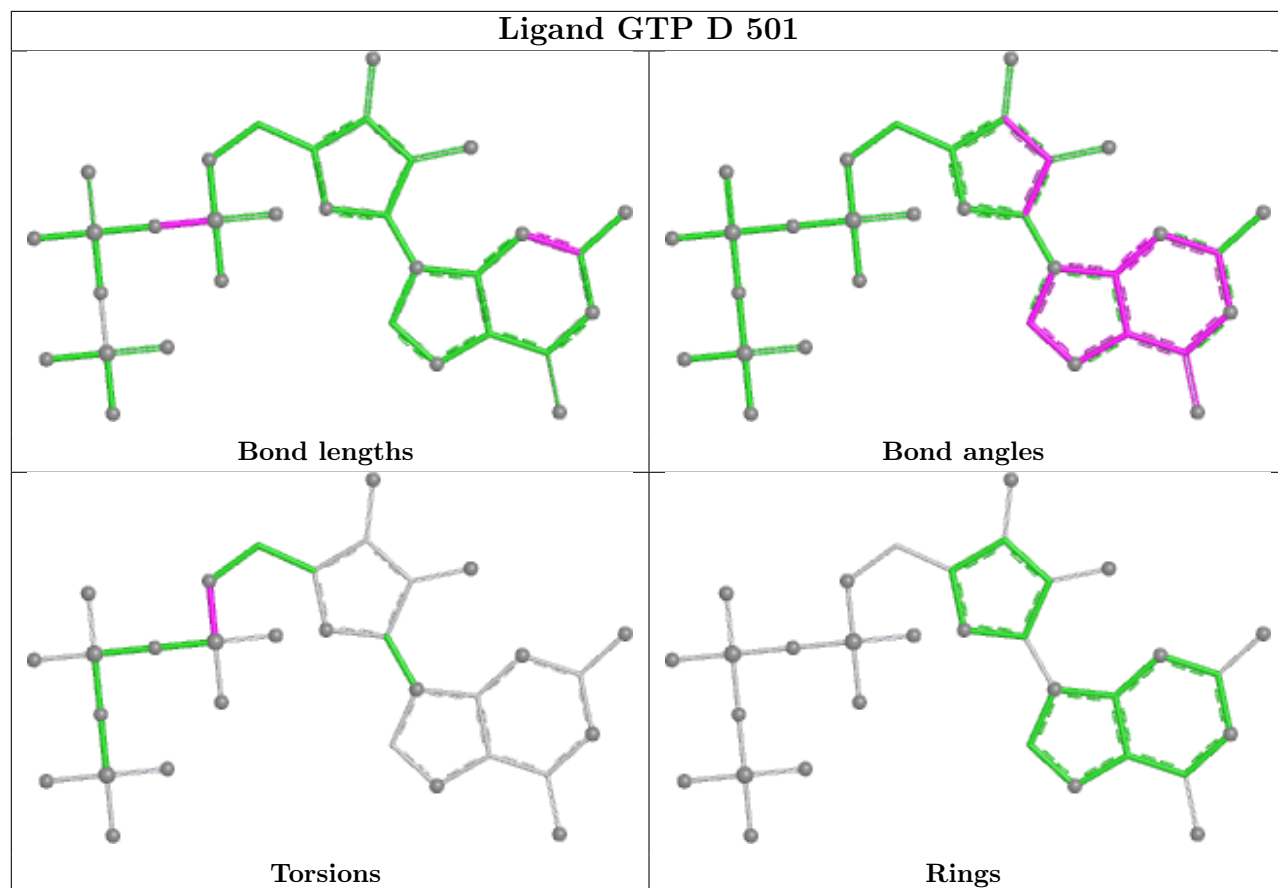
There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	501	GTP	1	0
5	B	501	GTP	2	0
5	D	501	GTP	5	0
5	A	501	GTP	4	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.

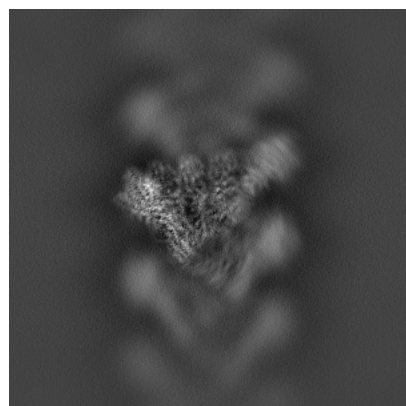
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23635. These allow visual inspection of the internal detail of the map and identification of artifacts.

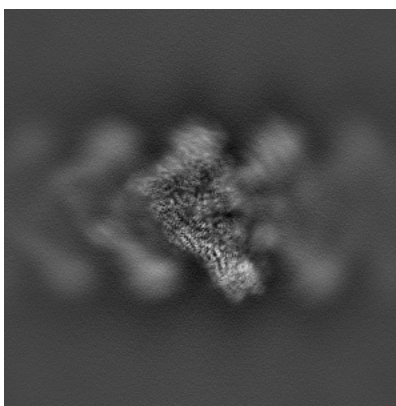
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

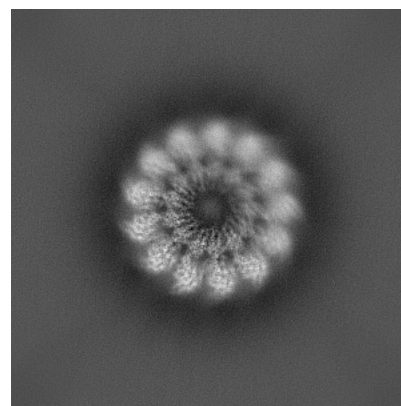
6.1.1 Primary map



X

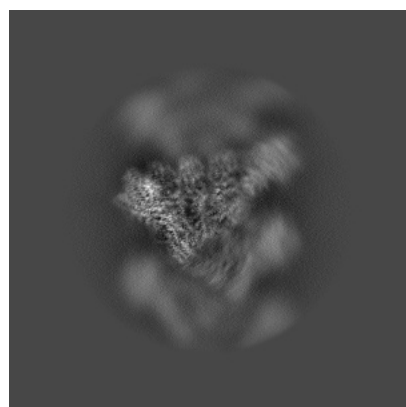


Y

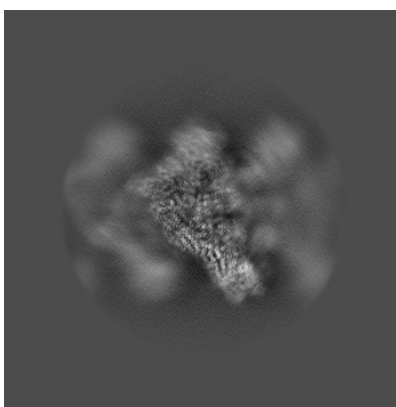


Z

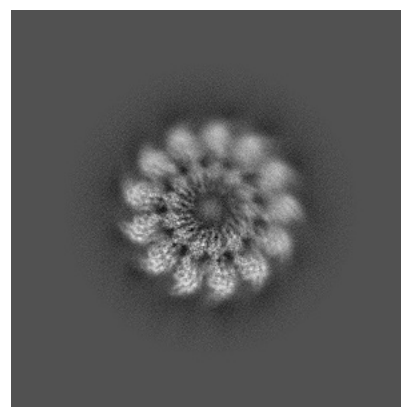
6.1.2 Raw map



X



Y

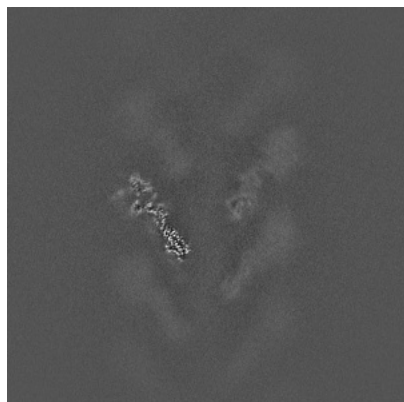


Z

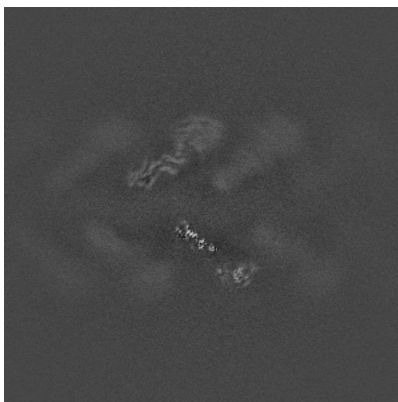
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

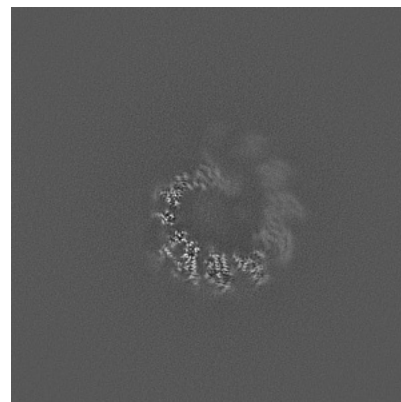
6.2.1 Primary map



X Index: 300

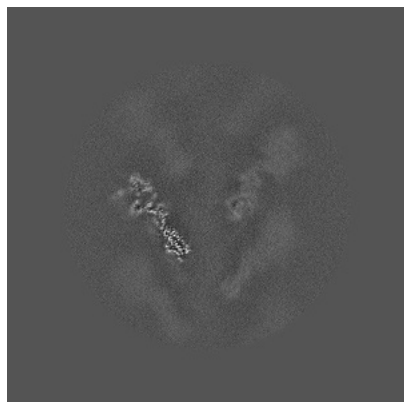


Y Index: 300

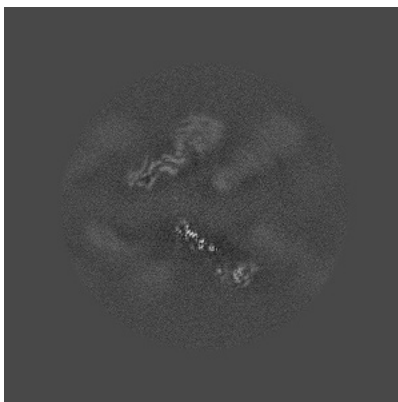


Z Index: 300

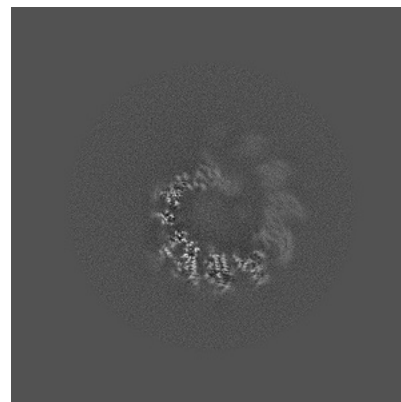
6.2.2 Raw map



X Index: 300



Y Index: 300



Z Index: 300

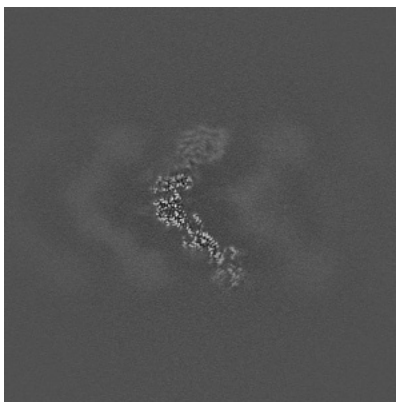
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

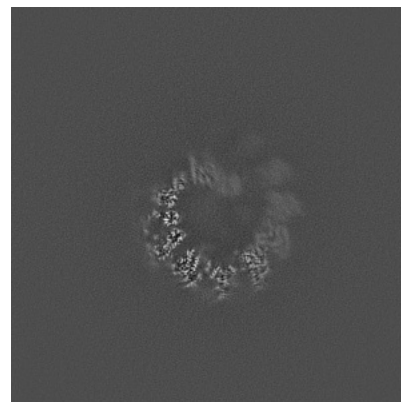
6.3.1 Primary map



X Index: 260

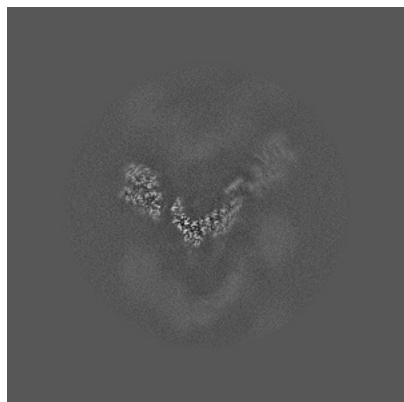


Y Index: 251

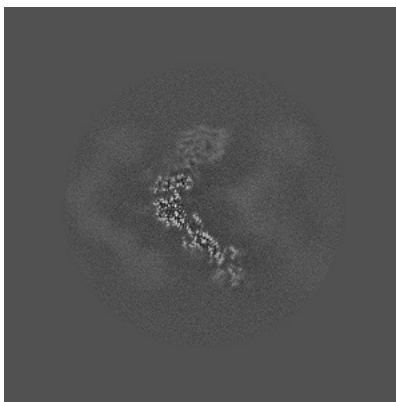


Z Index: 308

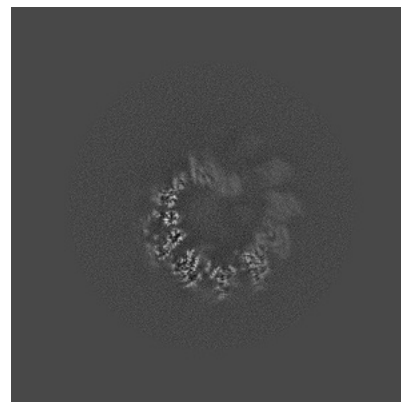
6.3.2 Raw map



X Index: 260



Y Index: 251

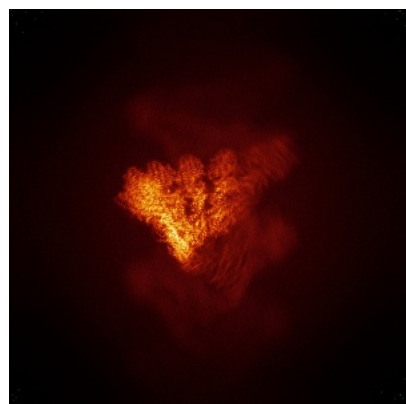


Z Index: 308

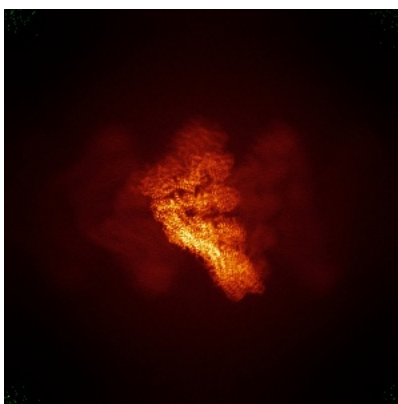
The images above show the largest variance slices of the map in three orthogonal directions.

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

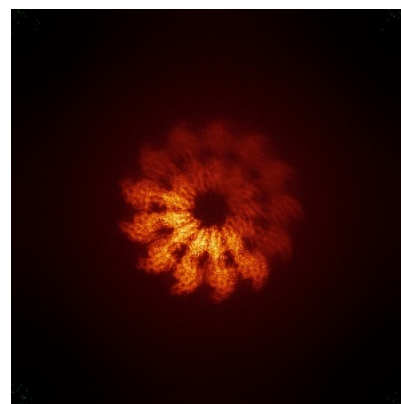
6.4.1 Primary map



X

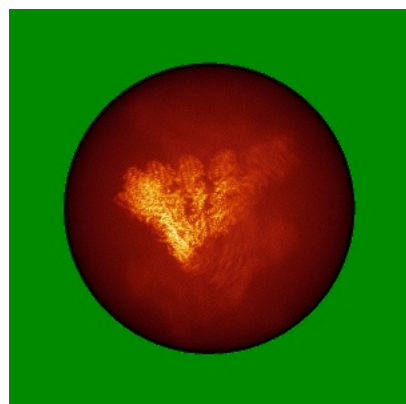


Y

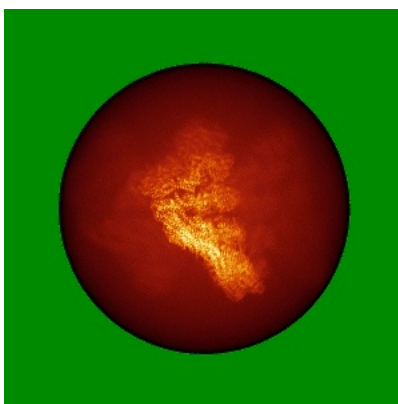


Z

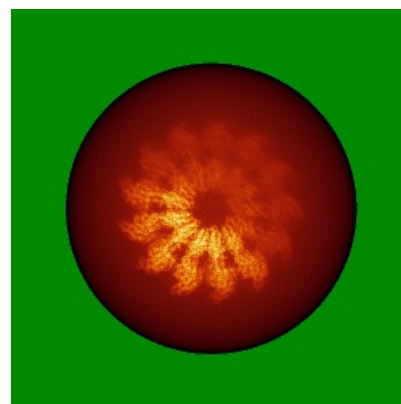
6.4.2 Raw map



X



Y

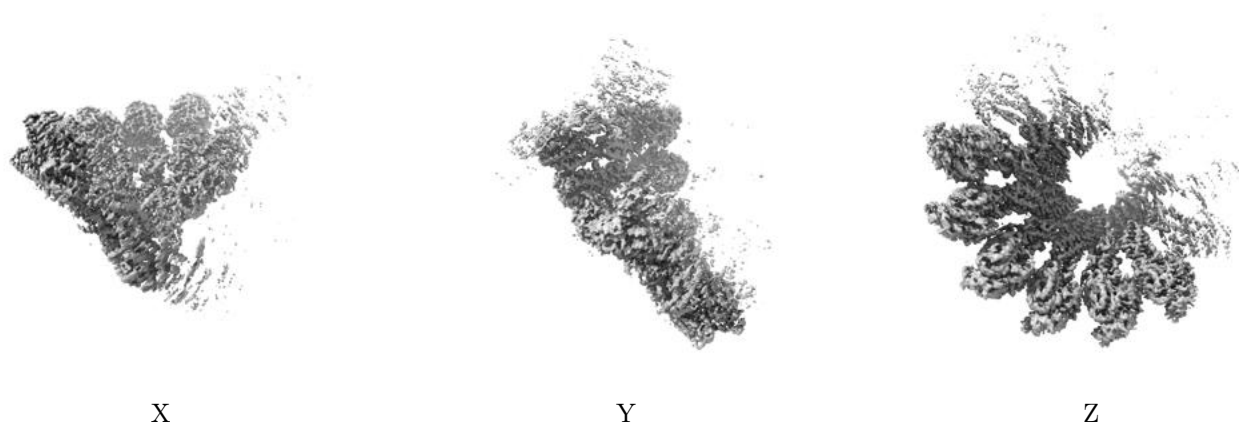


Z

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.

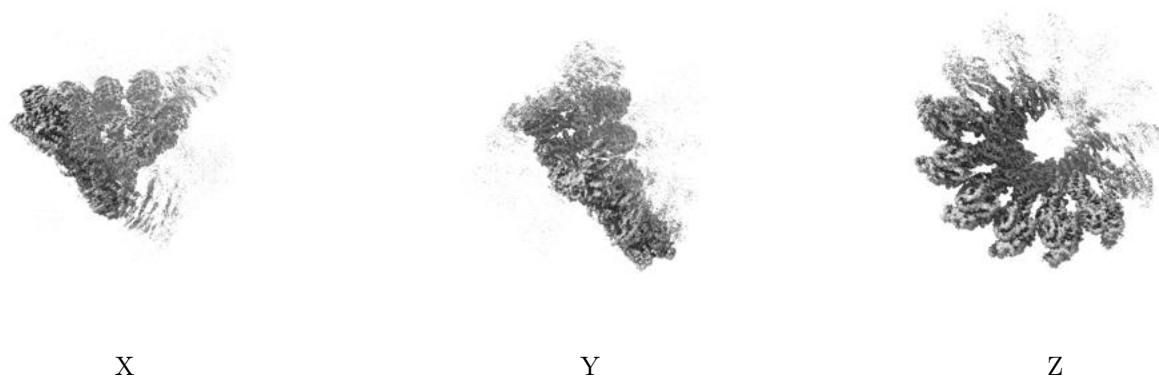
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.5. 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.

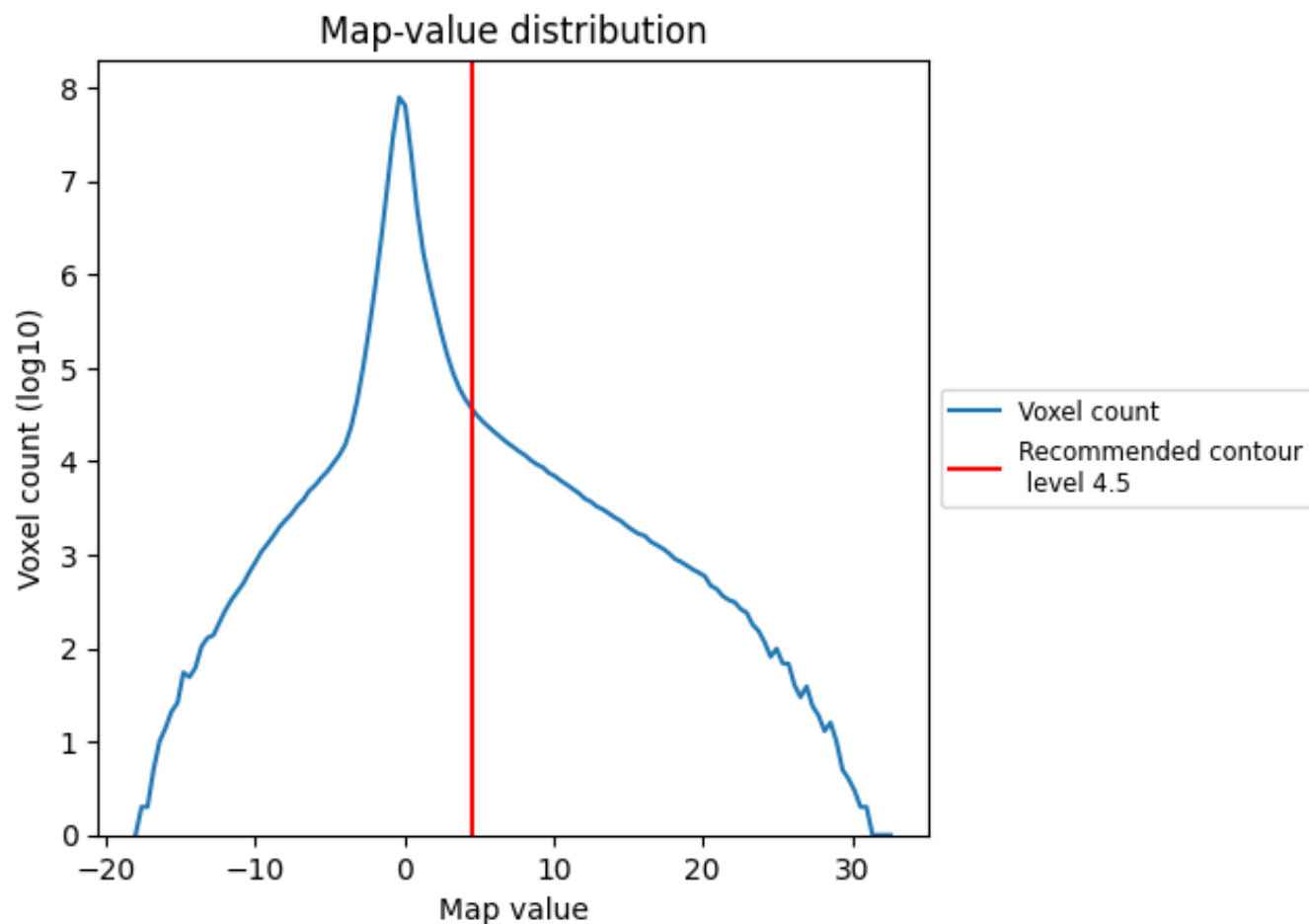
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

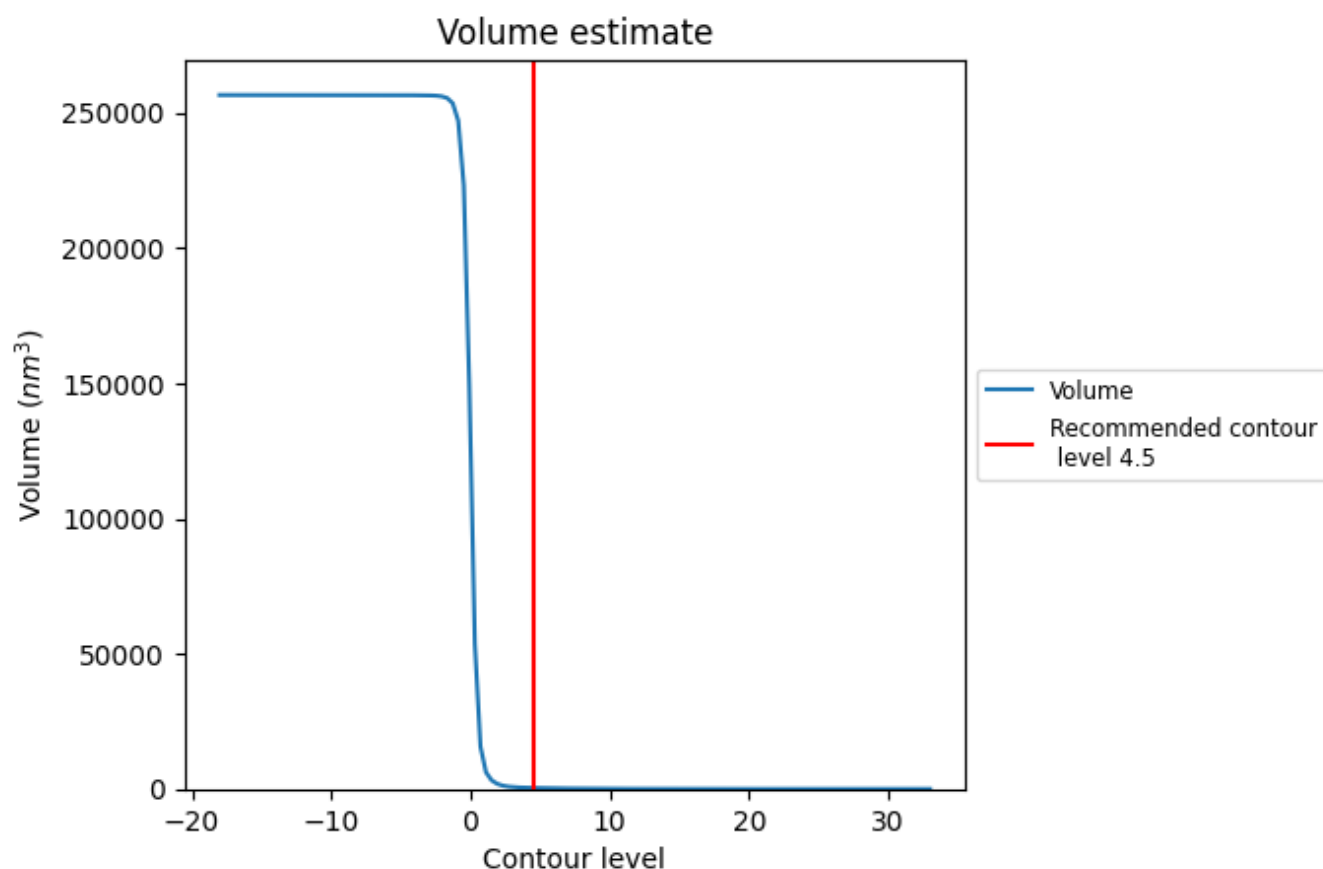
This section contains the results of statistical analysis of the map.

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.

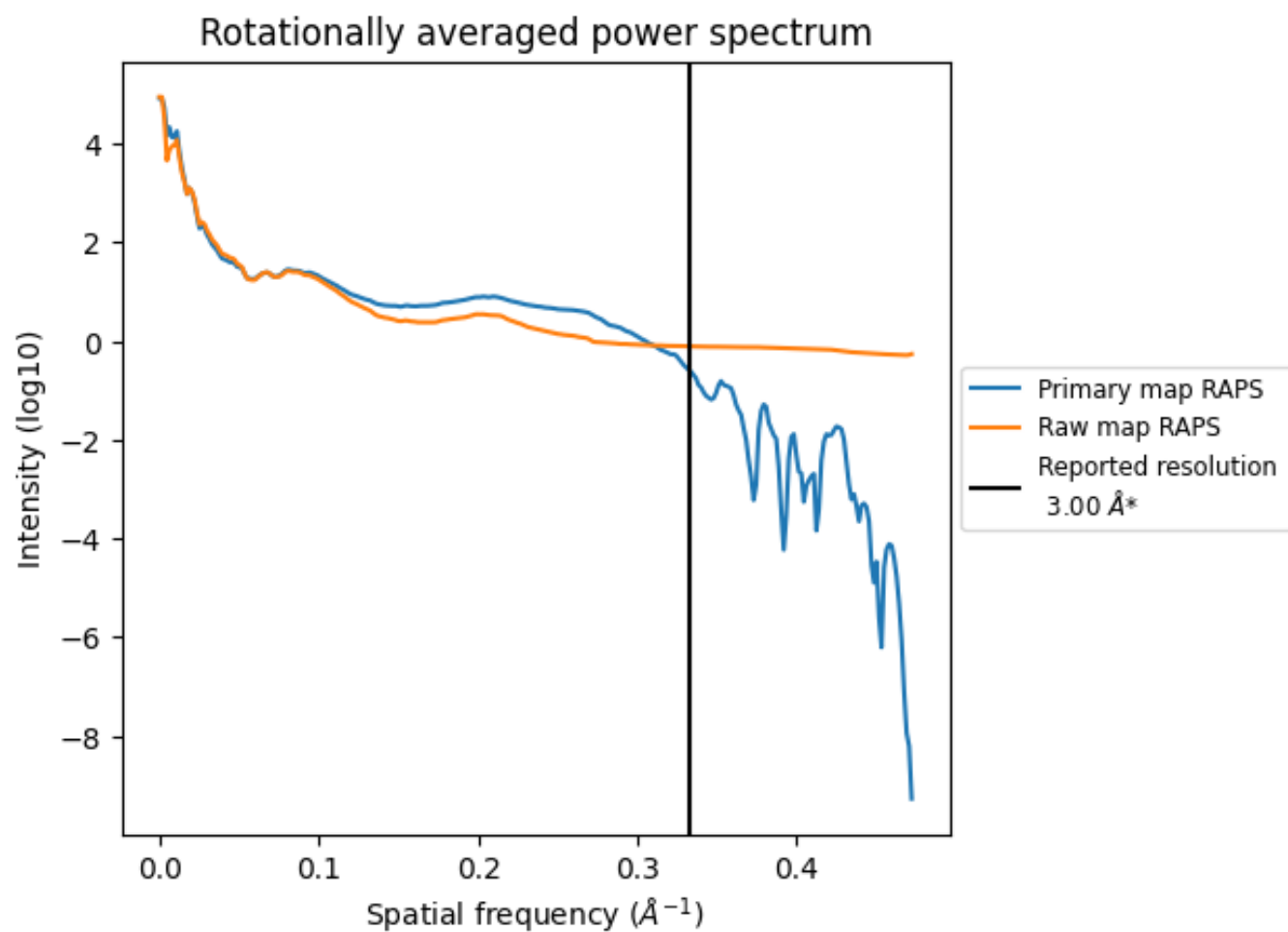
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 374 nm^3 ; this corresponds to an approximate mass of 338 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 ⓘ

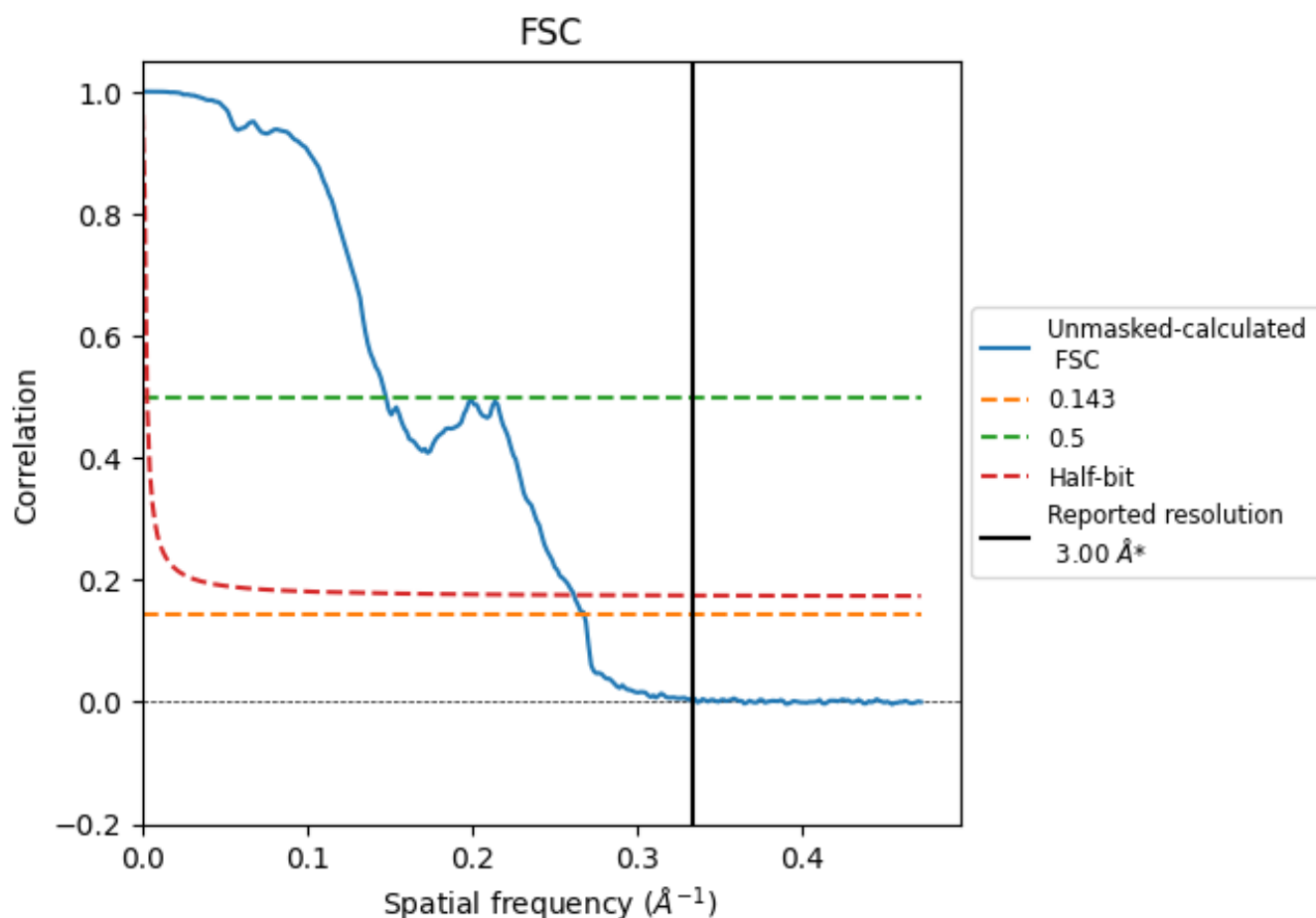


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

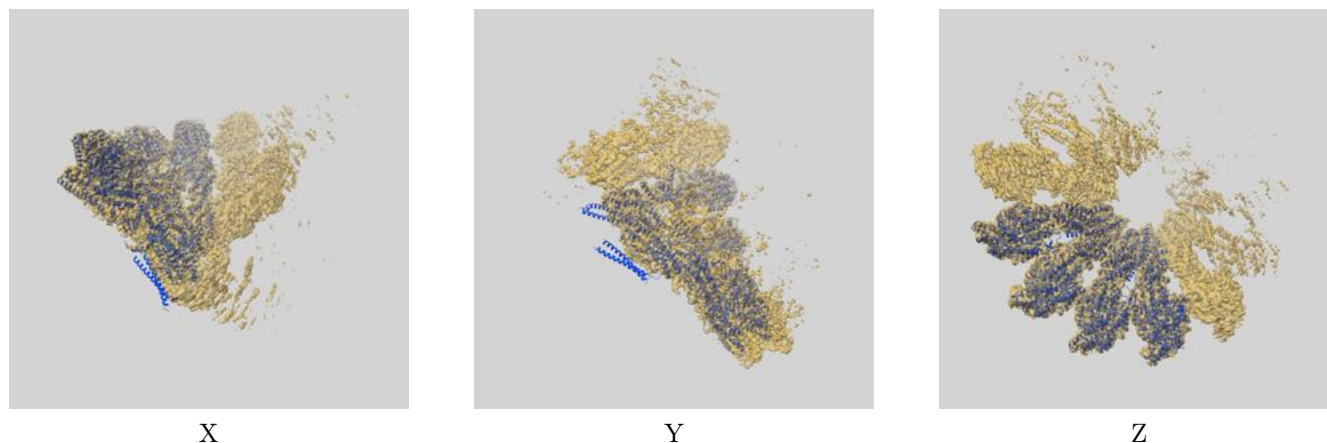
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.73	6.77	3.82

*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 3.73 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

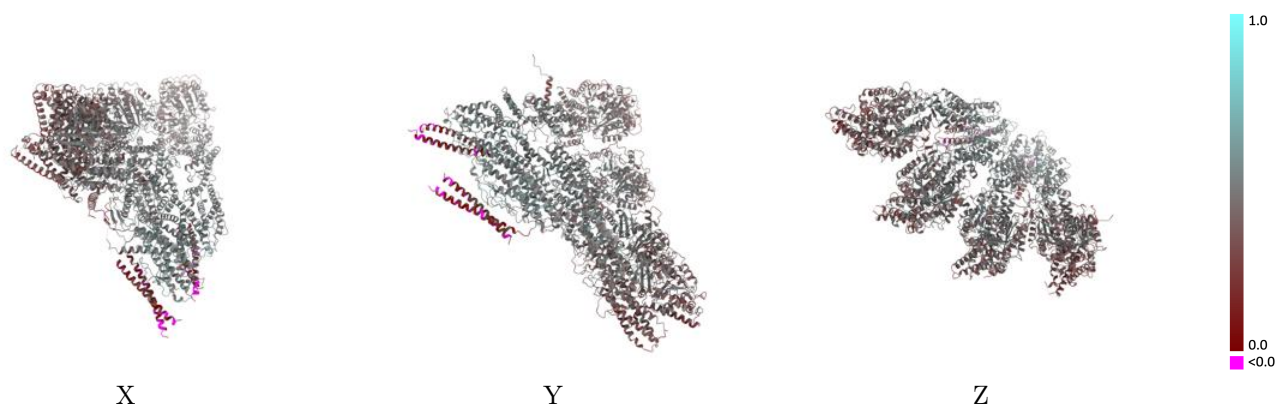
This section contains information regarding the fit between EMDB map EMD-23635 and PDB model 7M2W. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



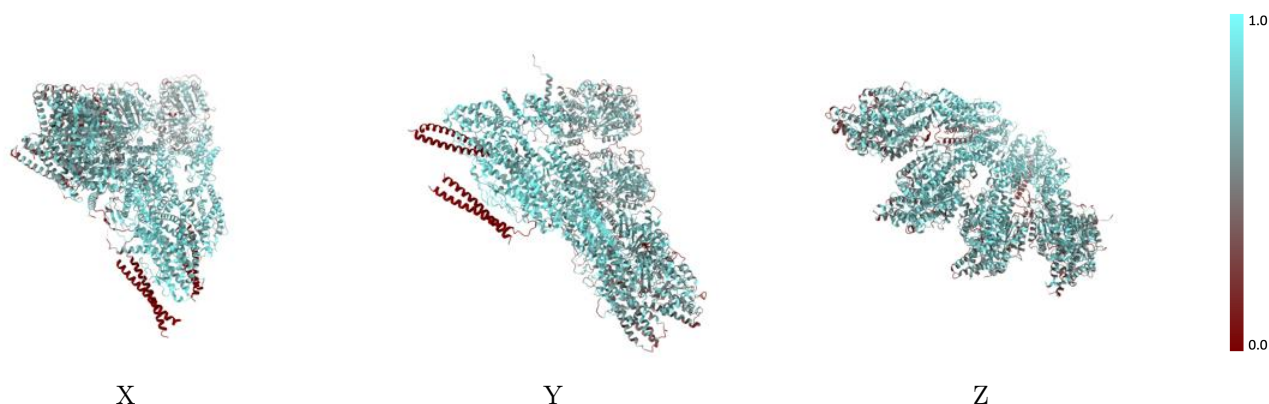
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



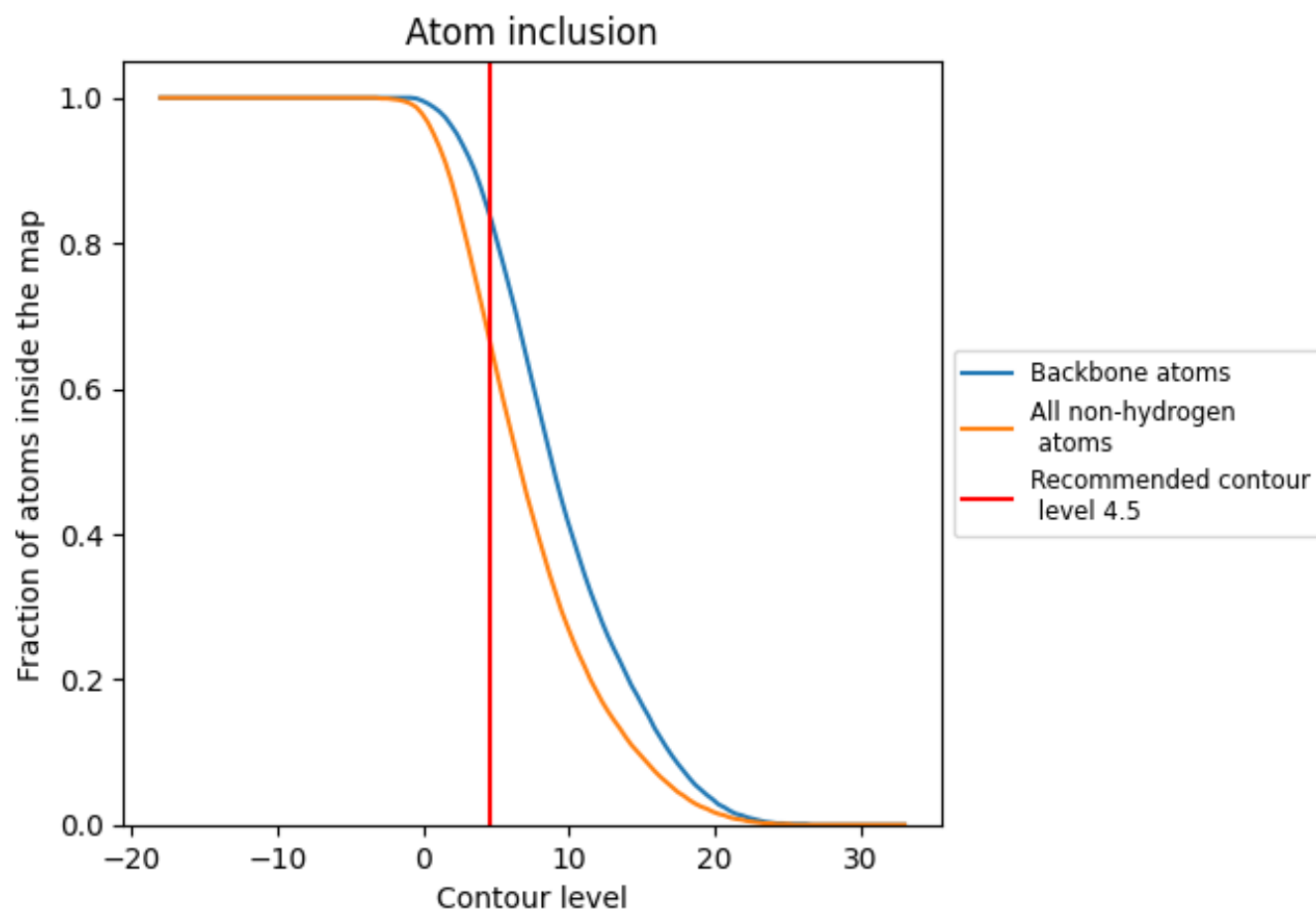
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 67% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6700	 0.4350
A	 0.6500	 0.4400
B	 0.6250	 0.4000
C	 0.6910	 0.4420
D	 0.6000	 0.3980
E	 0.7240	 0.4580
F	 0.7520	 0.4800
G	 0.7500	 0.4730
H	 0.7230	 0.4490
K	 0.2810	 0.2800
U	 0.0030	 0.1610
X	 0.0000	 0.1730
Y	 0.2320	 0.2170

