



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 01:31 AM UTC

PDB ID : 9NLW / pdb_00009nlw
EMDB ID : EMD-49524
Title : Y20S (Sec18-Sec17-Sec9-Sso1-Snc1) EDTA - Class 6
Authors : Khan, Y.A.; Brunger, A.T.
Deposited on : 2025-03-03
Resolution : 3.73 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

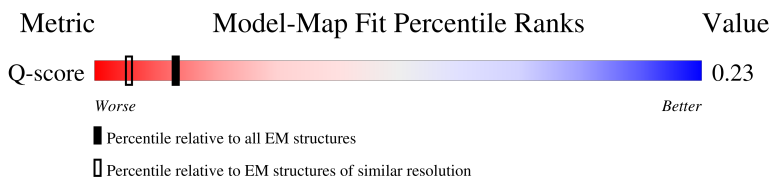
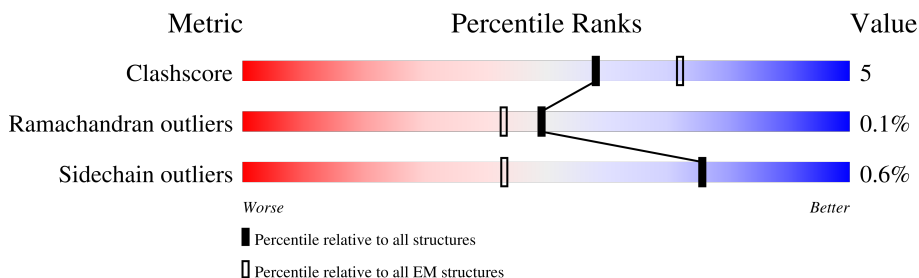
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.73 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	10415 (3.23 - 4.23)

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	761	
1	B	761	
1	C	761	
1	D	761	

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Mol	Chain	Length	Quality of chain
1	E	761	10% 85% 8% 7%
1	F	761	• 60% • 36%
2	G	293	9% 71% 17% 11%
2	H	293	5% 79% 18% •
2	I	293	10% 78% 14% 8%
3	J	97	• 53% 9% 38%
4	K	269	• 25% 6% • 67%
5	L	222	• 46% 12% 42%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 78921 atoms, of which 39482 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 Vesicular-fusion protein SEC18.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	506	Total	C	H	N	O	S	0	0
			7969	2484	4032	680	755	18		
1	B	726	Total	C	H	N	O	S	0	0
			11393	3577	5722	983	1088	23		
1	C	741	Total	C	H	N	O	S	0	0
			11638	3647	5853	1008	1107	23		
1	D	741	Total	C	H	N	O	S	0	0
			11638	3647	5853	1008	1107	23		
1	E	709	Total	C	H	N	O	S	0	0
			11140	3502	5601	958	1058	21		
1	F	490	Total	C	H	N	O	S	0	0
			7719	2402	3905	659	735	18		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P18759
A	-1	ALA	-	expression tag	UNP P18759
A	0	HIS	-	expression tag	UNP P18759
B	-2	GLY	-	expression tag	UNP P18759
B	-1	ALA	-	expression tag	UNP P18759
B	0	HIS	-	expression tag	UNP P18759
C	-2	GLY	-	expression tag	UNP P18759
C	-1	ALA	-	expression tag	UNP P18759
C	0	HIS	-	expression tag	UNP P18759
D	-2	GLY	-	expression tag	UNP P18759
D	-1	ALA	-	expression tag	UNP P18759
D	0	HIS	-	expression tag	UNP P18759
E	-2	GLY	-	expression tag	UNP P18759
E	-1	ALA	-	expression tag	UNP P18759
E	0	HIS	-	expression tag	UNP P18759
F	-2	GLY	-	expression tag	UNP P18759
F	-1	ALA	-	expression tag	UNP P18759
F	0	HIS	-	expression tag	UNP P18759

- Molecule 2 is a protein called Alpha-soluble NSF attachment protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	G	260	Total	C	H	N	O	S	0	0
			3994	1277	1961	331	414	11		
2	H	284	Total	C	H	N	O	S	0	0
			4388	1398	2157	373	449	11		
2	I	271	Total	C	H	N	O	S	0	0
			4200	1339	2070	350	431	10		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	0	GLY	-	expression tag	UNP P32602
H	0	GLY	-	expression tag	UNP P32602
I	0	GLY	-	expression tag	UNP P32602

- Molecule 3 is a protein called Synaptobrevin homolog 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	J	60	Total	C	H	N	O	S	0	0
			938	282	470	92	92	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	GLY	-	expression tag	UNP P31109
J	-2	ALA	-	expression tag	UNP P31109
J	-1	SER	-	expression tag	UNP P31109
J	0	HIS	-	expression tag	UNP P31109

- Molecule 4 is a protein called Protein SSO1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	K	89	Total	C	H	N	O	S	0	0
			1390	426	692	126	144	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-3	GLY	-	expression tag	UNP P32867
K	-2	ALA	-	expression tag	UNP P32867
K	-1	SER	-	expression tag	UNP P32867
K	0	HIS	-	expression tag	UNP P32867

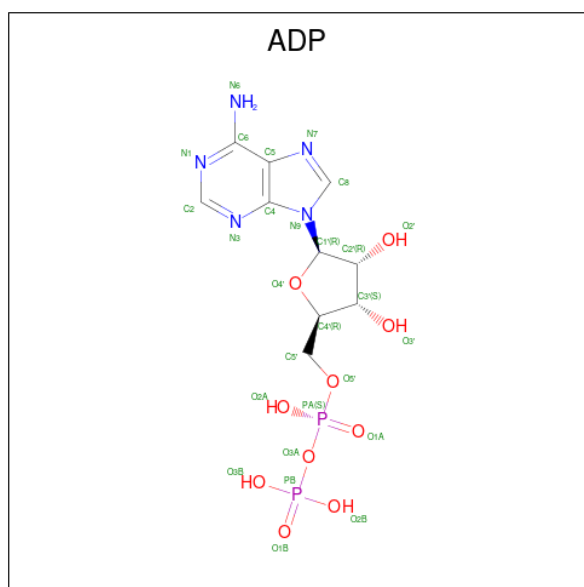
- Molecule 5 is a protein called Protein transport protein SEC9.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	L	129	Total	C	H	N	O	S	0	0
			2049	614	1034	186	208	7		

There are 4 discrepancies between the modelled and reference sequences:

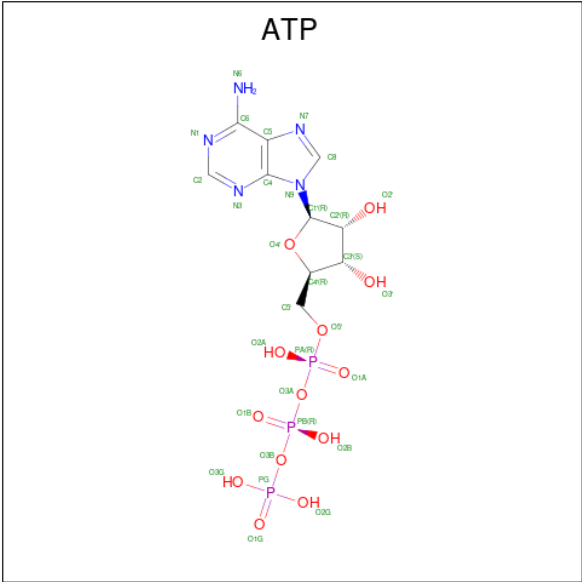
Chain	Residue	Modelled	Actual	Comment	Reference
L	429	GLY	-	expression tag	UNP P40357
L	430	ALA	-	expression tag	UNP P40357
L	431	SER	-	expression tag	UNP P40357
L	432	HIS	-	expression tag	UNP P40357

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

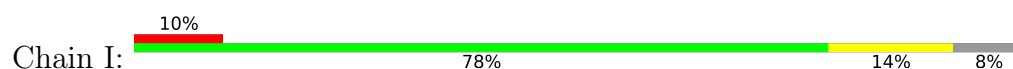


Mol	Chain	Residues	Atoms						AltConf
6	A	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	
6	E	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	

- Molecule 7 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
7	A	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	B	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	B	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	C	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	C	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	D	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	D	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	E	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
7	F	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64857	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.023	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00245	Depositor
Map size ($\text{\AA}$)	322.224, 322.224, 322.224	wwPDB
Map dimensions	294, 294, 294	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.096, 1.096, 1.096	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: ATP, ADP

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	0.19	0/3990	0.32	0/5378
1	B	0.18	0/5761	0.31	0/7776
1	C	0.19	0/5878	0.31	0/7936
1	D	0.18	0/5878	0.33	0/7936
1	E	0.17	0/5628	0.31	0/7597
1	F	0.17	0/3861	0.29	0/5201
2	G	0.18	0/2060	0.35	0/2755
2	H	0.23	0/2266	0.41	0/3040
2	I	0.17	0/2160	0.31	0/2894
3	J	0.31	0/470	0.60	0/628
4	K	0.23	0/701	0.45	0/941
5	L	0.42	0/1016	0.74	0/1355
All	All	0.19	0/39669	0.35	0/53437

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3937	4032	4032	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5671	5722	5722	34	0
1	C	5785	5853	5853	28	0
1	D	5785	5853	5853	38	0
1	E	5539	5601	5601	50	0
1	F	3814	3905	3905	23	0
2	G	2033	1961	1963	54	0
2	H	2231	2157	2159	80	0
2	I	2130	2070	2072	44	0
3	J	468	470	470	9	0
4	K	698	692	692	23	0
5	L	1015	1034	1034	39	0
6	A	27	12	12	0	0
6	E	27	12	12	0	0
7	A	31	12	12	0	0
7	B	62	24	24	0	0
7	C	62	24	24	1	0
7	D	62	24	24	3	0
7	E	31	12	12	0	0
7	F	31	12	12	0	0
All	All	39439	39482	39488	373	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 5.

The worst 5 of 373 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:H:196:TRP:CZ2	5:L:453:ASP:HA	1.82	1.15
2:G:150:GLN:HG2	2:H:89:SER:HB3	1.36	1.03
3:J:56:ARG:HG3	5:L:623:GLN:OE1	1.62	0.98
2:H:196:TRP:CH2	5:L:453:ASP:HA	2.00	0.97
1:F:461:GLU:O	1:F:465:LEU:HD12	1.72	0.89

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	500/761 (66%)	475 (95%)	24 (5%)	1 (0%)	43	71
1	B	720/761 (95%)	694 (96%)	25 (4%)	1 (0%)	48	78
1	C	739/761 (97%)	700 (95%)	37 (5%)	2 (0%)	36	65
1	D	739/761 (97%)	708 (96%)	29 (4%)	2 (0%)	36	65
1	E	703/761 (92%)	666 (95%)	36 (5%)	1 (0%)	48	78
1	F	480/761 (63%)	465 (97%)	15 (3%)	0	100	100
2	G	248/293 (85%)	248 (100%)	0	0	100	100
2	H	280/293 (96%)	279 (100%)	1 (0%)	0	100	100
2	I	263/293 (90%)	263 (100%)	0	0	100	100
3	J	58/97 (60%)	58 (100%)	0	0	100	100
4	K	87/269 (32%)	85 (98%)	2 (2%)	0	100	100
5	L	125/222 (56%)	124 (99%)	1 (1%)	0	100	100
All	All	4942/6033 (82%)	4765 (96%)	170 (3%)	7 (0%)	49	78

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	515	ILE
1	B	625	SER
1	C	220	ASN
1	C	223	ARG
1	D	233	ASP

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	440/656 (67%)	439 (100%)	1 (0%)	87	86
1	B	631/656 (96%)	629 (100%)	2 (0%)	86	83
1	C	643/656 (98%)	639 (99%)	4 (1%)	78	79
1	D	643/656 (98%)	639 (99%)	4 (1%)	78	79
1	E	614/656 (94%)	613 (100%)	1 (0%)	87	86
1	F	428/656 (65%)	428 (100%)	0	100	100
2	G	216/245 (88%)	216 (100%)	0	100	100
2	H	237/245 (97%)	237 (100%)	0	100	100
2	I	227/245 (93%)	227 (100%)	0	100	100
3	J	48/82 (58%)	48 (100%)	0	100	100
4	K	75/234 (32%)	65 (87%)	10 (13%)	4	20
5	L	115/201 (57%)	111 (96%)	4 (4%)	32	54
All	All	4317/5188 (83%)	4291 (99%)	26 (1%)	76	79

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	K	174	SER
4	K	182	ARG
5	L	634	ASP
4	K	178	LEU
4	K	183	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	373	ASN
5	L	473	ASN
1	F	325	ASN
2	I	255	GLN
1	E	504	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 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$
7	ATP	C	801	-	32,33,33	0.76	2 (6%)	48,52,52	0.51	0
7	ATP	C	802	-	32,33,33	0.60	1 (3%)	48,52,52	0.52	0
7	ATP	A	802	-	32,33,33	0.51	0	48,52,52	0.56	0
7	ATP	D	801	-	32,33,33	0.69	2 (6%)	48,52,52	0.58	0
7	ATP	D	802	-	32,33,33	0.44	0	48,52,52	0.48	0
7	ATP	B	802	-	32,33,33	0.84	2 (6%)	48,52,52	0.54	0
7	ATP	B	801	-	32,33,33	0.85	2 (6%)	48,52,52	0.55	0
7	ATP	E	802	-	32,33,33	0.57	1 (3%)	48,52,52	0.48	0
6	ADP	A	801	-	28,29,29	1.36	5 (17%)	43,45,45	1.84	8 (18%)
7	ATP	F	801	-	32,33,33	0.63	2 (6%)	48,52,52	0.60	0
6	ADP	E	801	-	28,29,29	1.37	5 (17%)	43,45,45	1.78	10 (23%)

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
7	ATP	C	801	-	-	3/22/38/38	0/3/3/3
7	ATP	C	802	-	-	1/22/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	ATP	A	802	-	-	5/22/38/38	0/3/3/3
7	ATP	D	801	-	-	7/22/38/38	0/3/3/3
7	ATP	D	802	-	-	9/22/38/38	0/3/3/3
7	ATP	B	802	-	-	4/22/38/38	0/3/3/3
7	ATP	B	801	-	-	3/22/38/38	0/3/3/3
7	ATP	E	802	-	-	2/22/38/38	0/3/3/3
6	ADP	A	801	-	-	5/16/32/32	0/3/3/3
7	ATP	F	801	-	-	7/22/38/38	0/3/3/3
6	ADP	E	801	-	-	4/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	801	ADP	C5-C4	4.36	1.46	1.39
6	A	801	ADP	C5-C4	4.34	1.46	1.39
7	B	801	ATP	PB-O3B	-3.50	1.55	1.59
7	B	802	ATP	PA-O3A	-3.45	1.55	1.59
7	C	801	ATP	PB-O3B	-2.96	1.56	1.59

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	801	ADP	C5-C4-N3	-5.75	118.80	126.72
6	E	801	ADP	C5-C4-N3	-5.42	119.25	126.72
6	A	801	ADP	N3-C4-N9	4.80	135.34	127.17
6	E	801	ADP	N3-C4-N9	4.27	134.43	127.17
6	A	801	ADP	C2-N3-C4	3.70	120.86	111.83

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

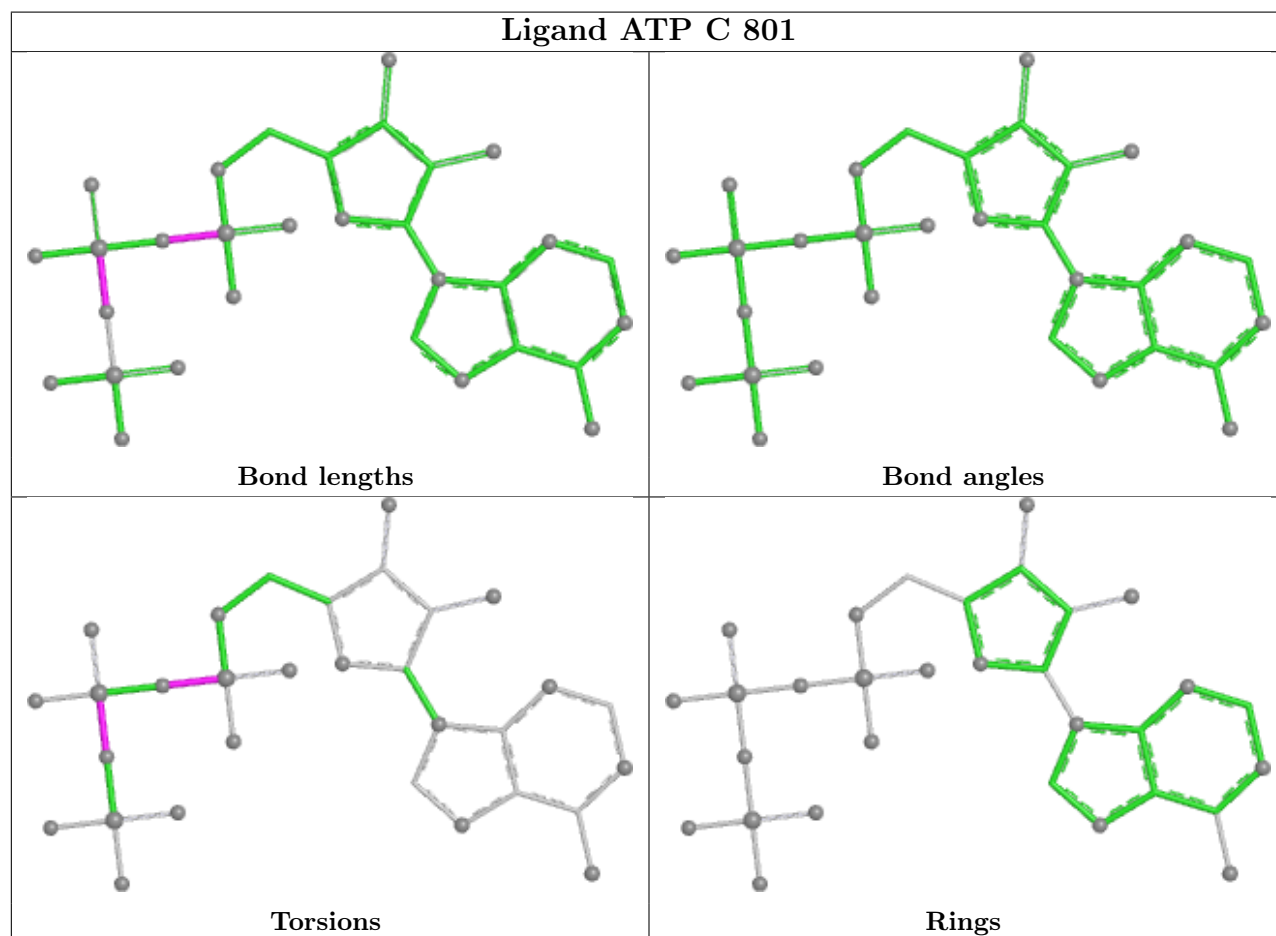
Mol	Chain	Res	Type	Atoms
6	E	801	ADP	O4'-C4'-C5'-O5'
6	E	801	ADP	C3'-C4'-C5'-O5'
6	E	801	ADP	O4'-C1'-N9-C8
6	E	801	ADP	O4'-C1'-N9-C4
7	A	802	ATP	C5'-O5'-PA-O2A

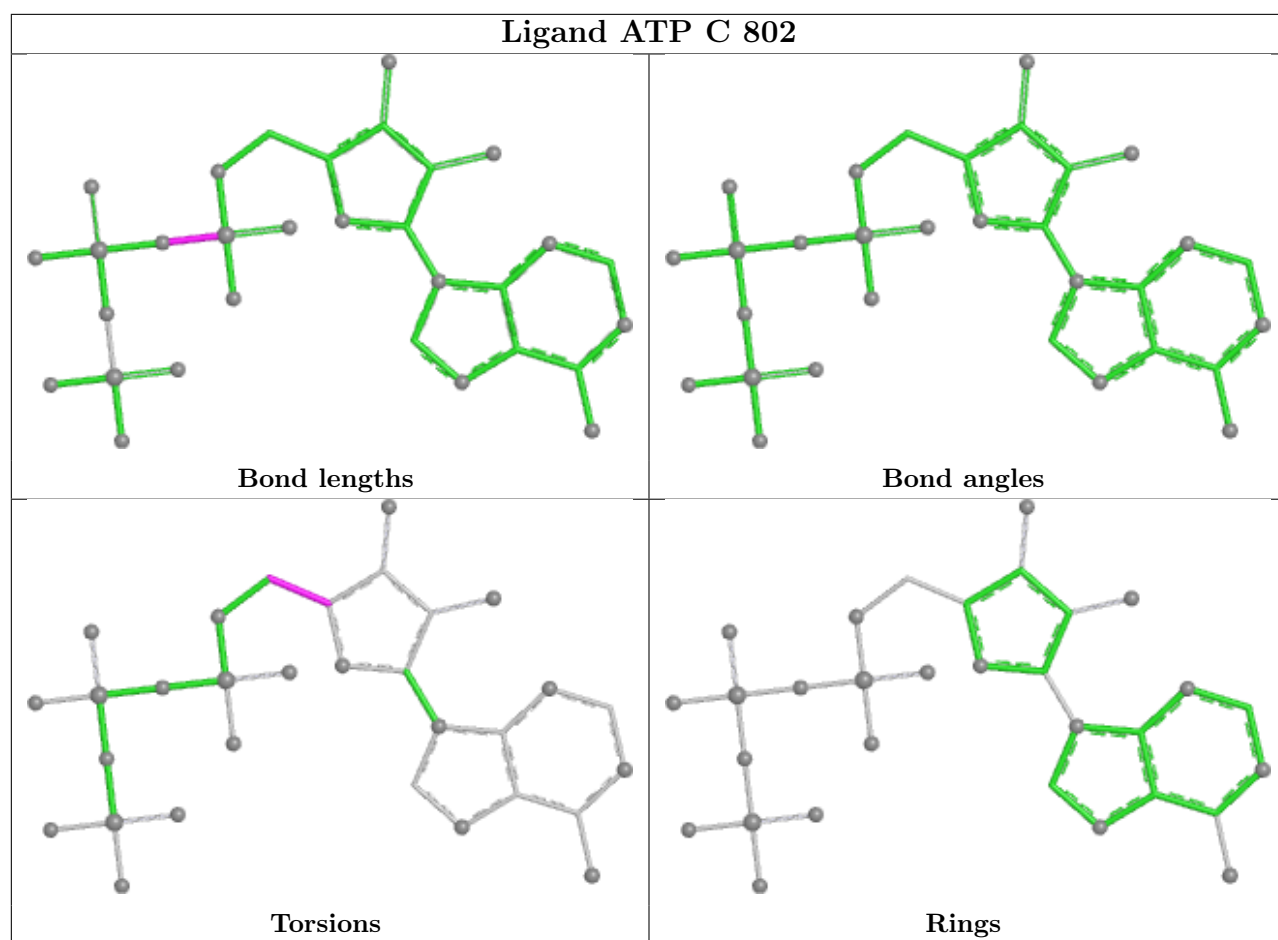
There are no ring outliers.

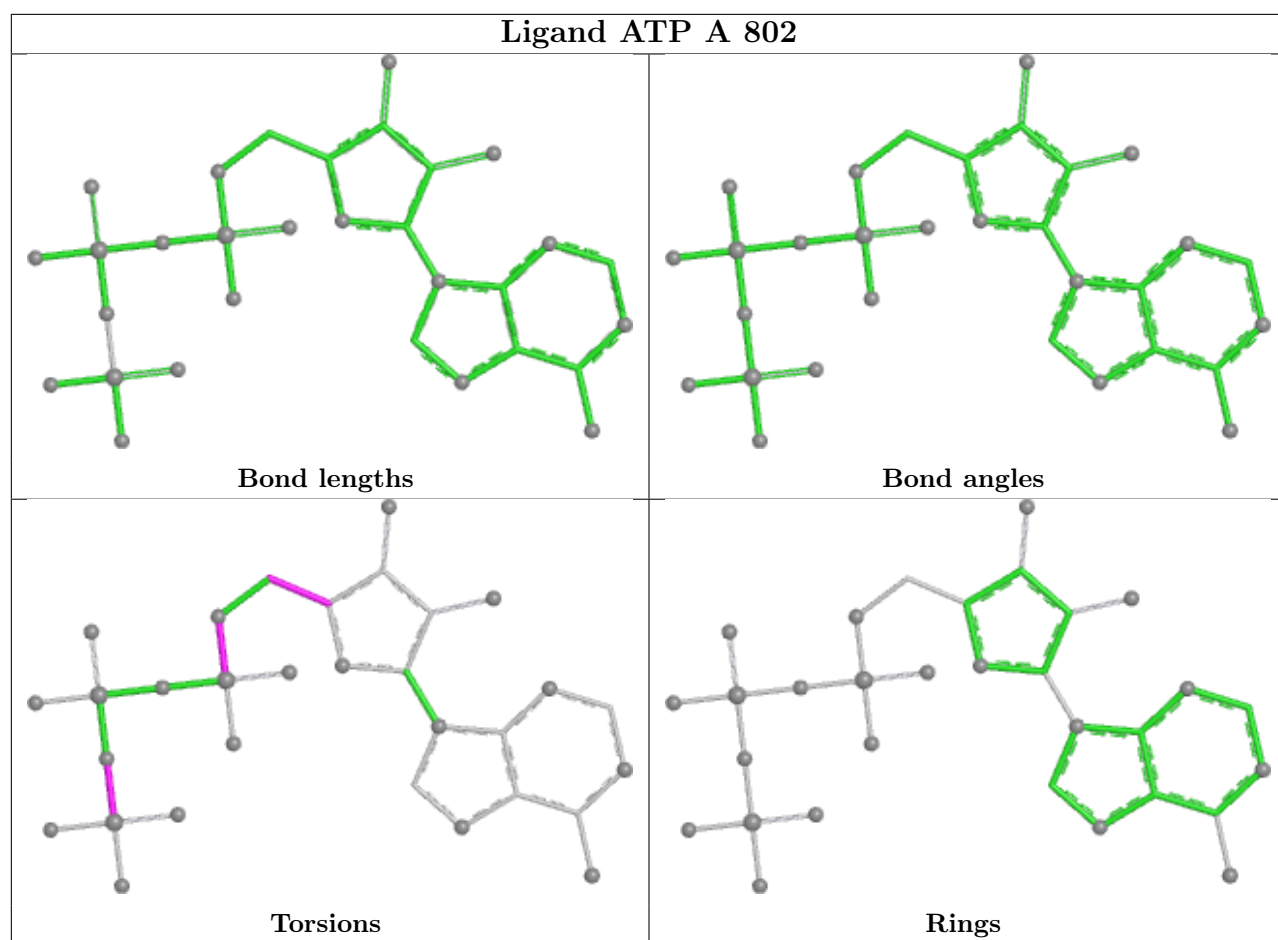
3 monomers are involved in 4 short contacts:

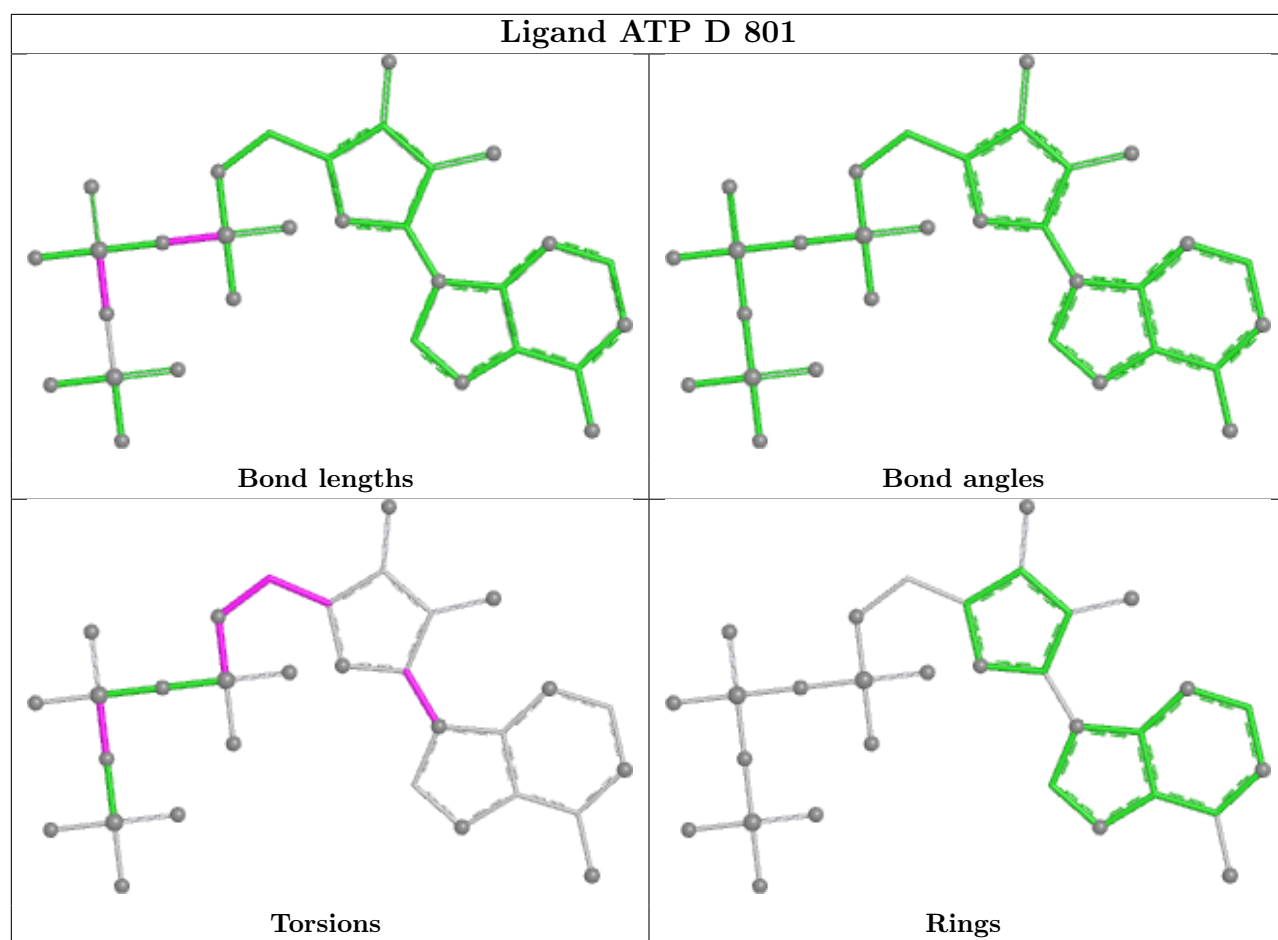
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	801	ATP	1	0
7	D	801	ATP	2	0
7	D	802	ATP	1	0

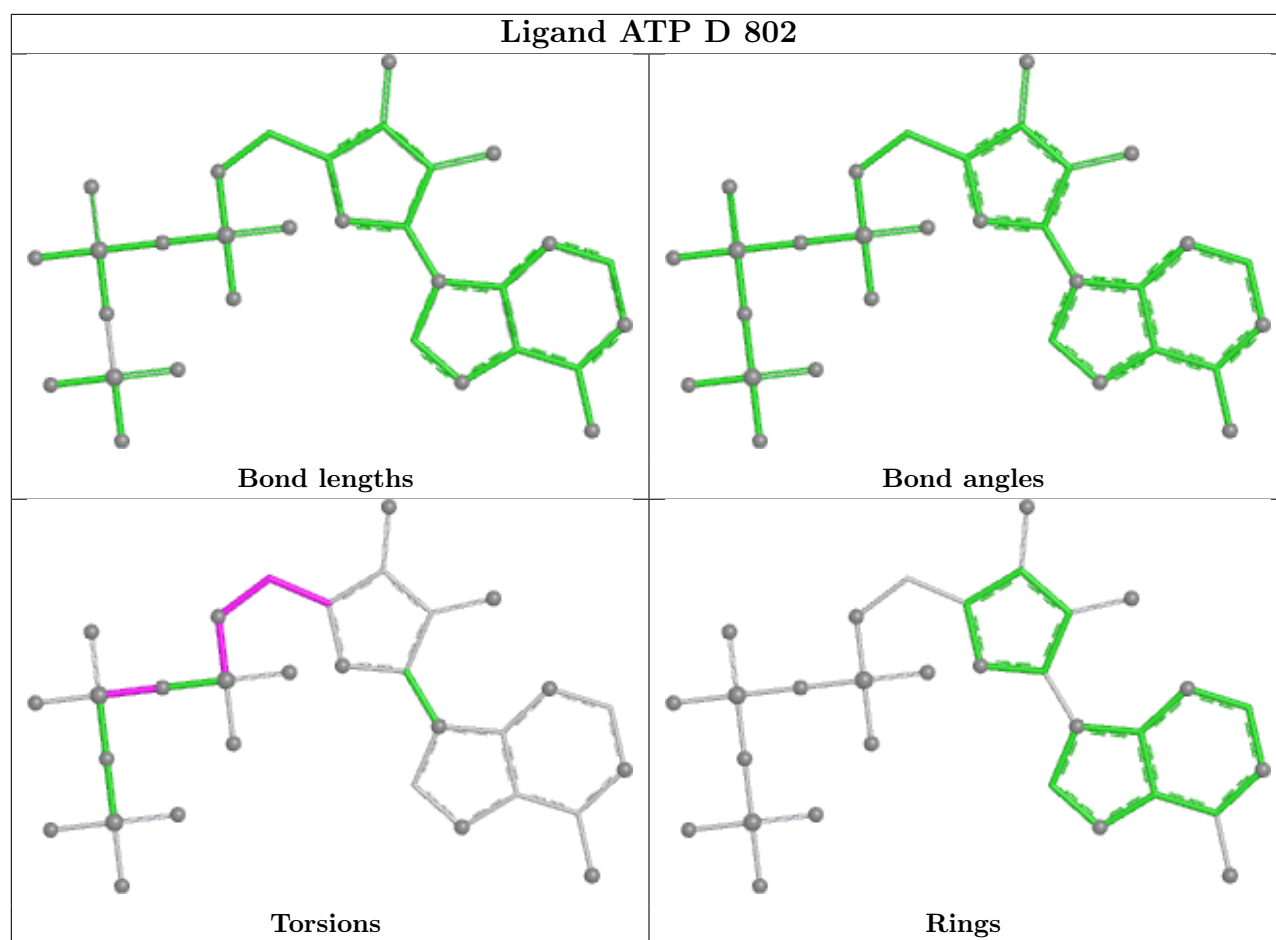
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

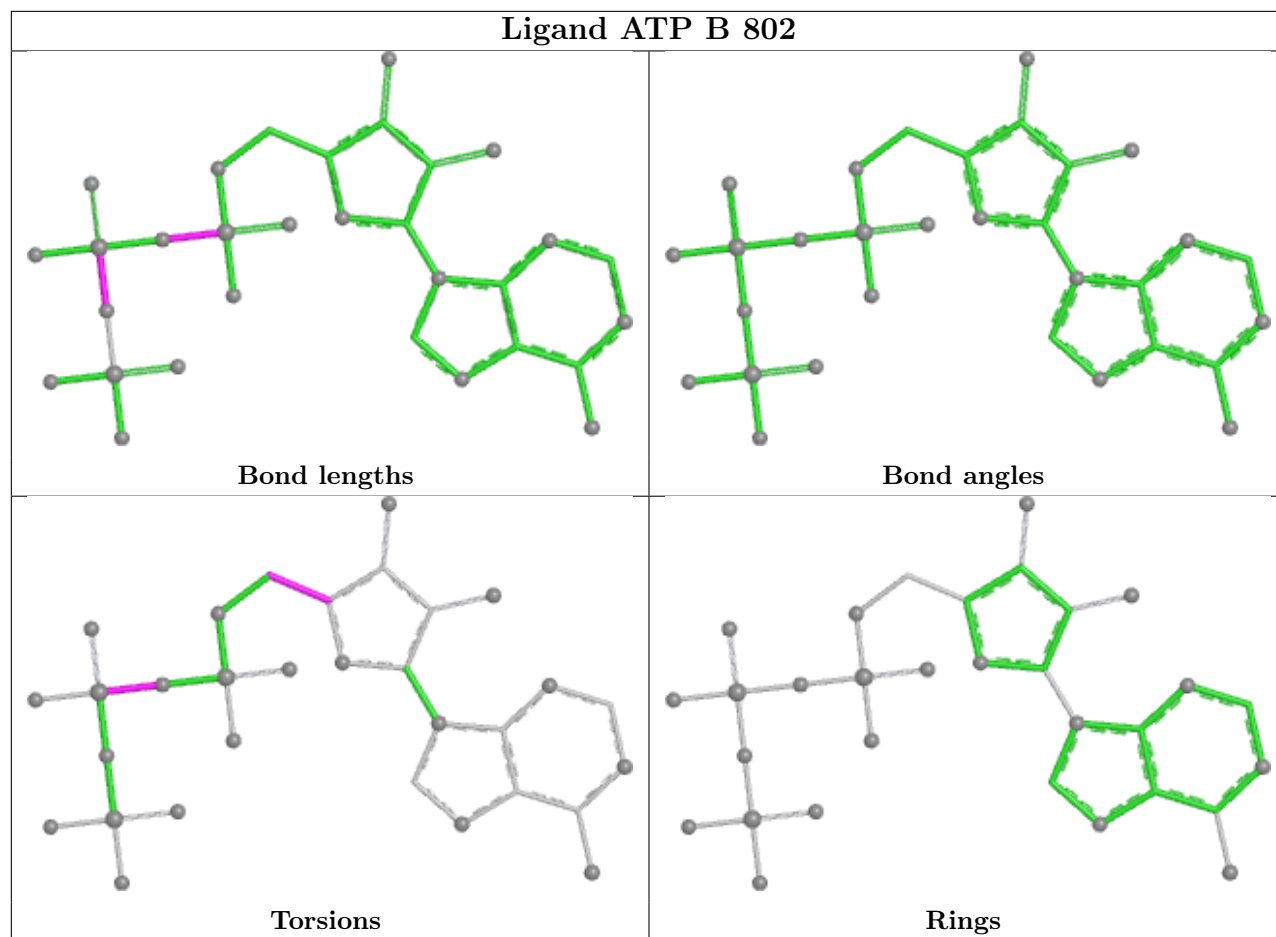


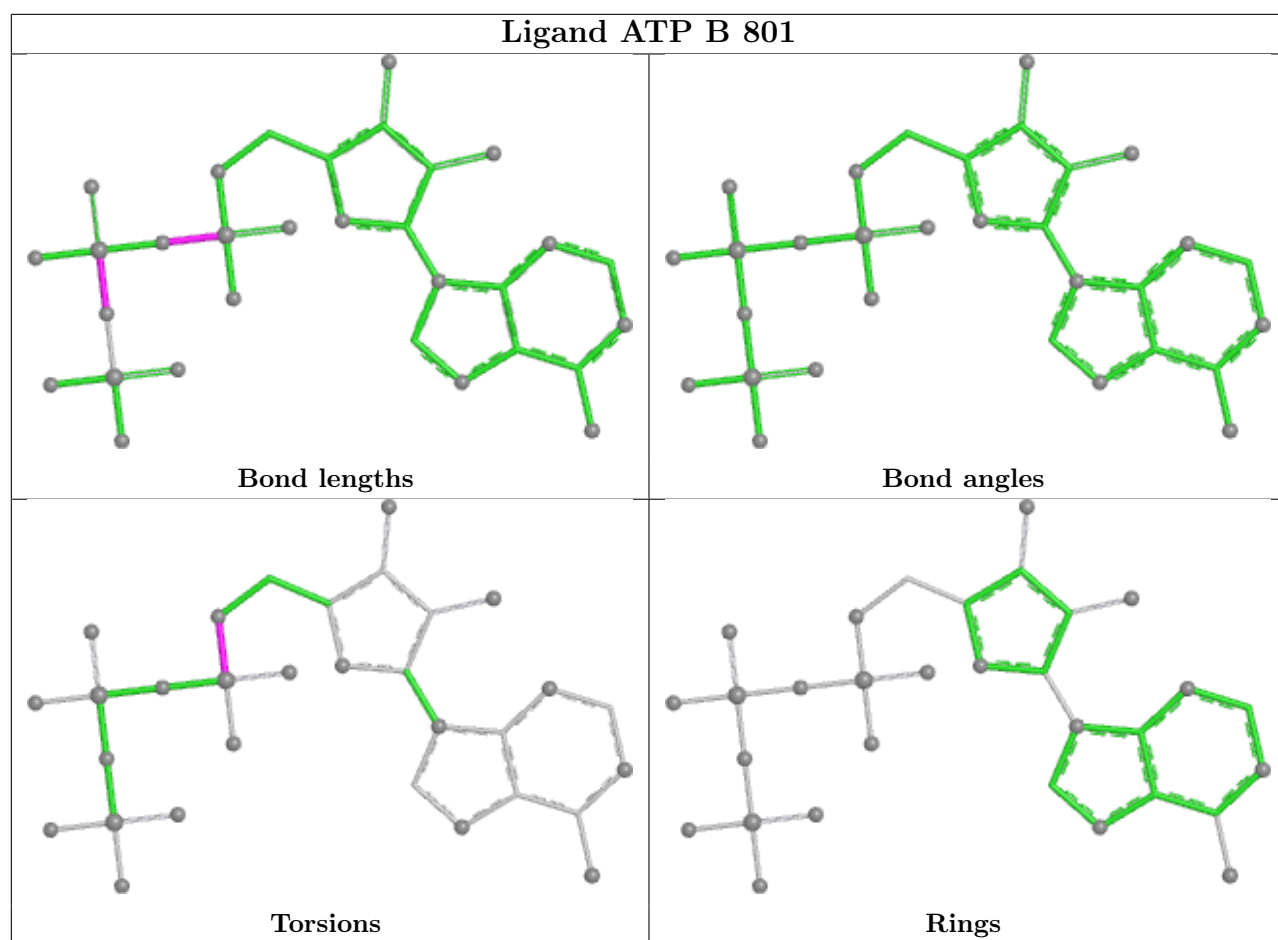




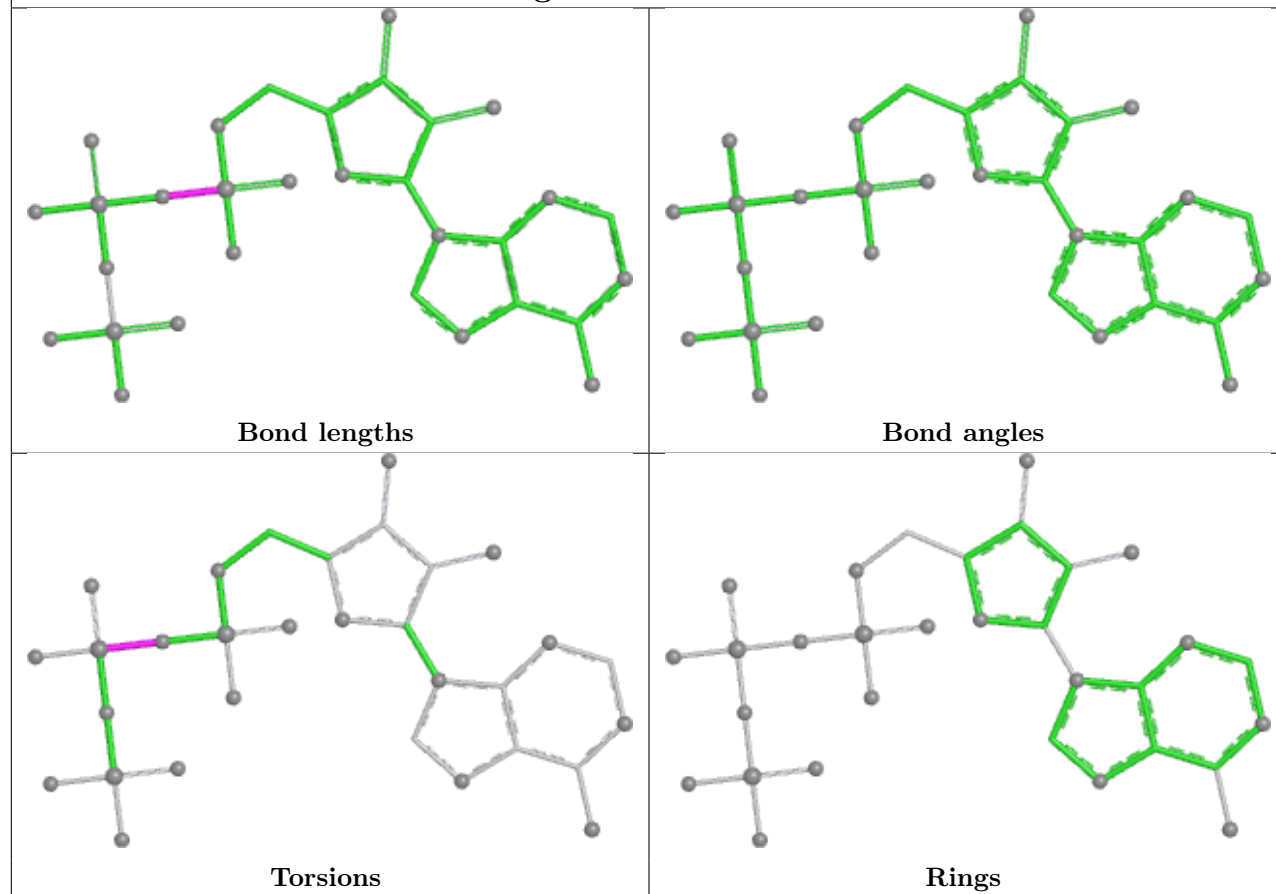




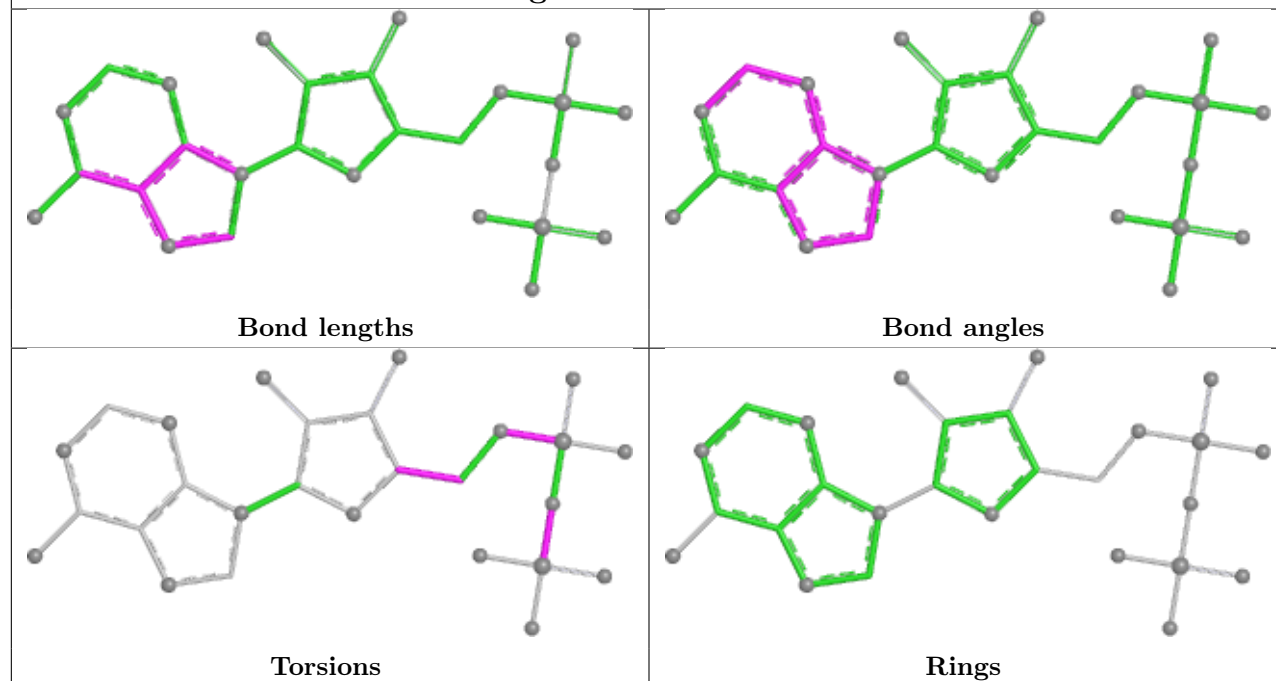




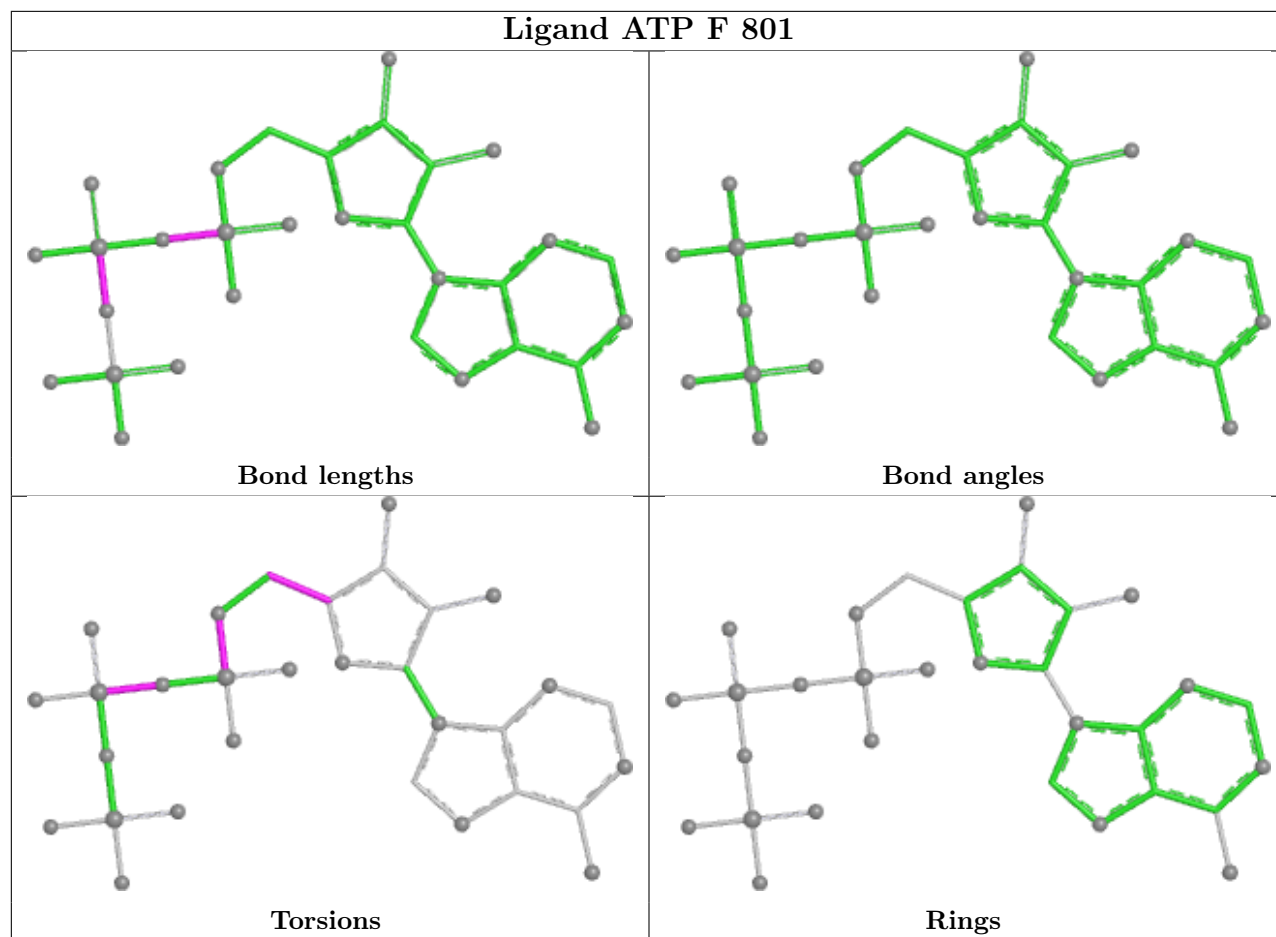
Ligand ATP E 802



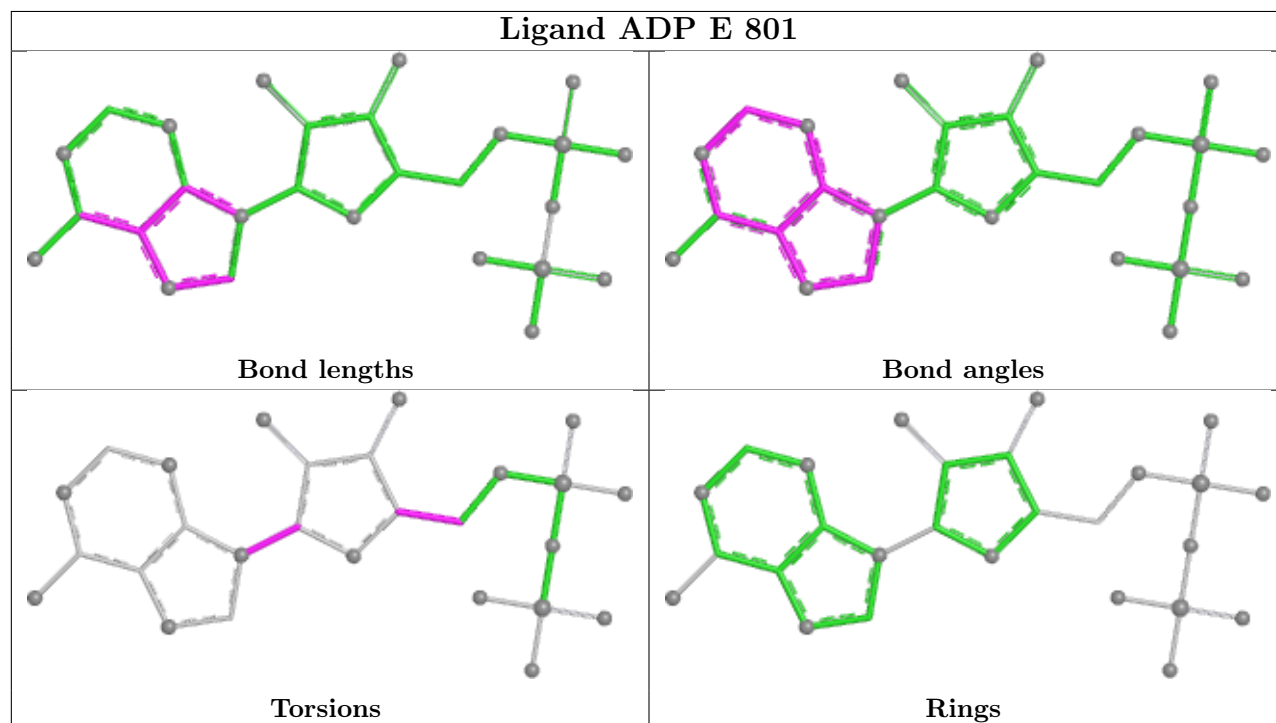
Ligand ADP A 801



Ligand ATP F 801



Ligand ADP E 801



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.

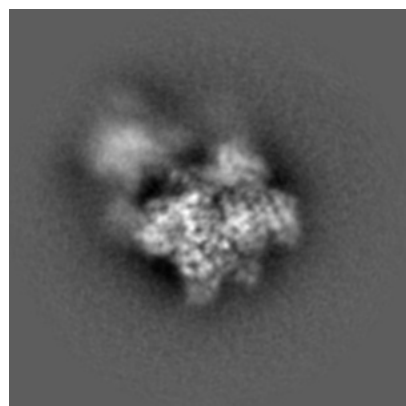
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49524. These allow visual inspection of the internal detail of the map and identification of artifacts.

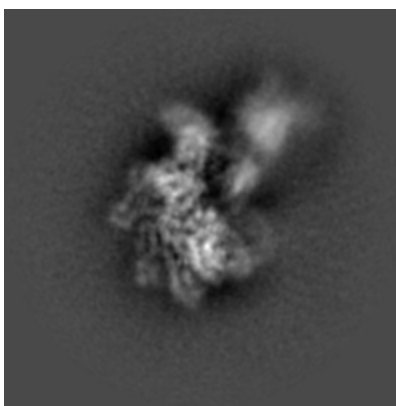
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

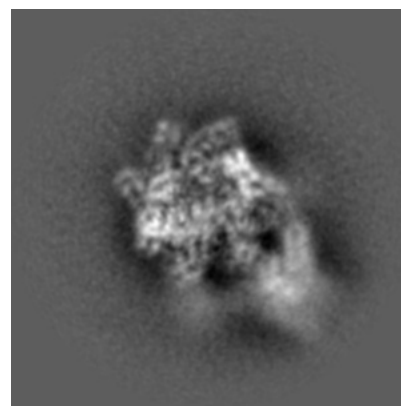
6.1.1 Primary map



X

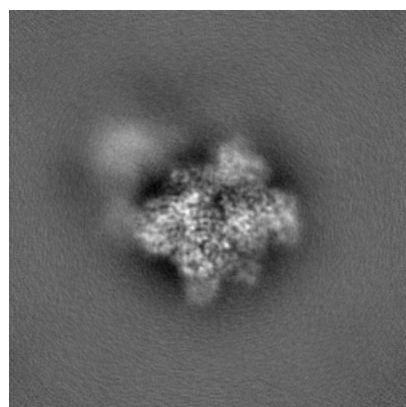


Y

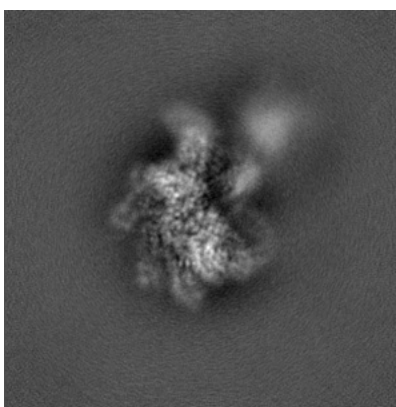


Z

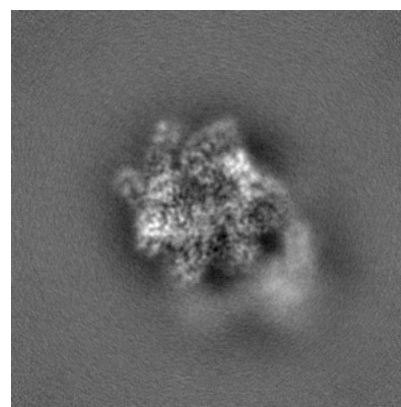
6.1.2 Raw map



X



Y

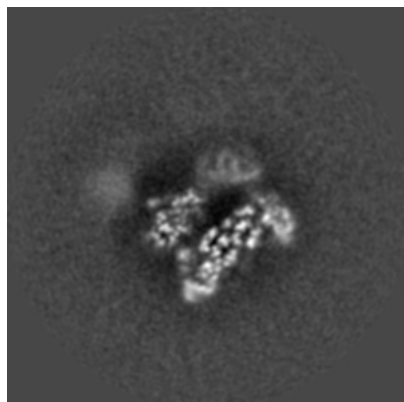


Z

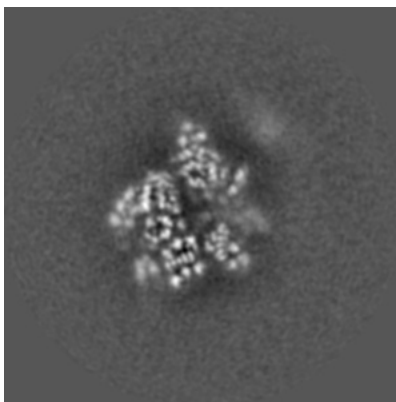
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

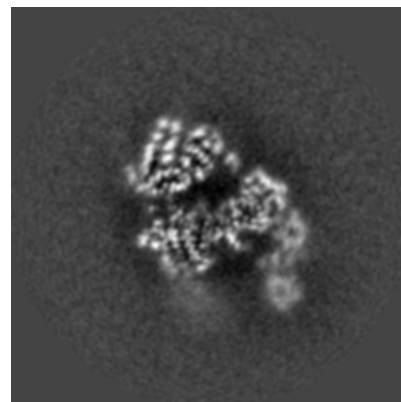
6.2.1 Primary map



X Index: 147

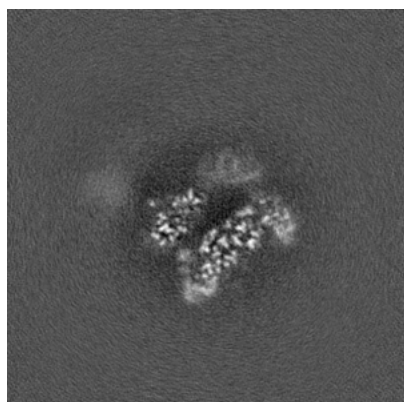


Y Index: 147

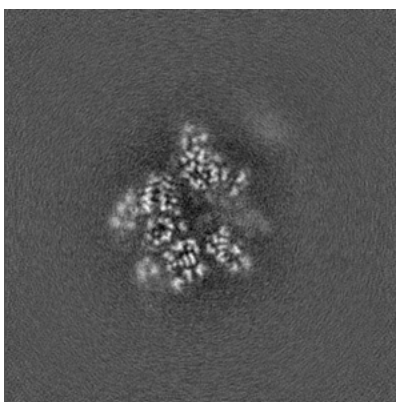


Z Index: 147

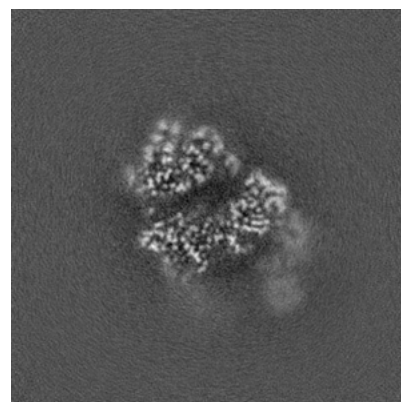
6.2.2 Raw map



X Index: 147



Y Index: 147

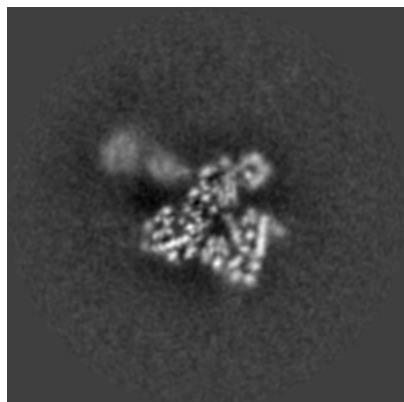


Z Index: 147

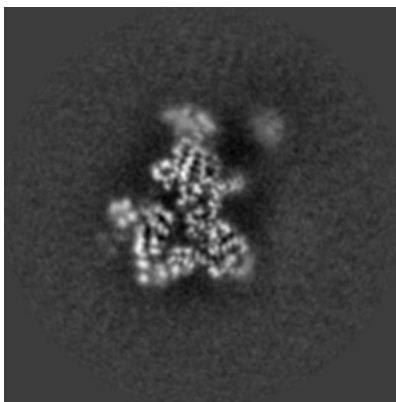
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

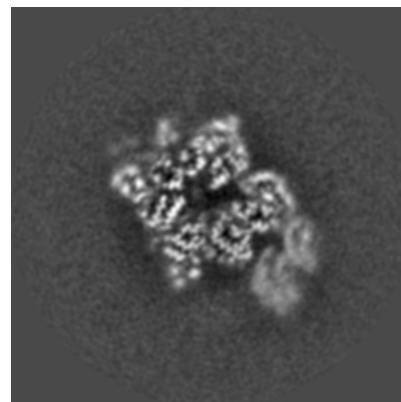
6.3.1 Primary map



X Index: 169

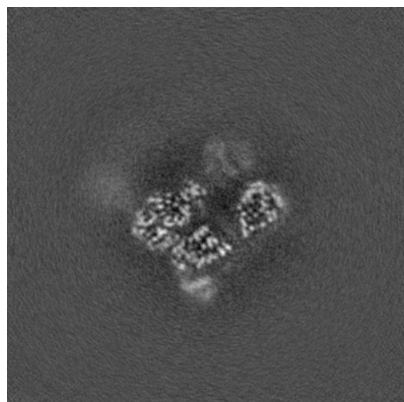


Y Index: 133

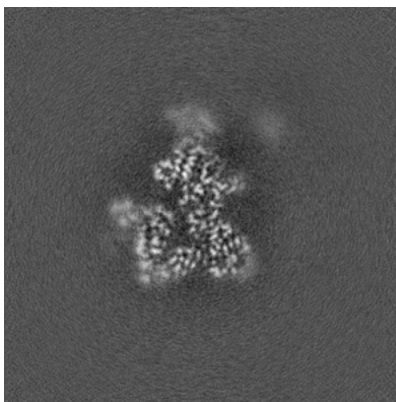


Z Index: 137

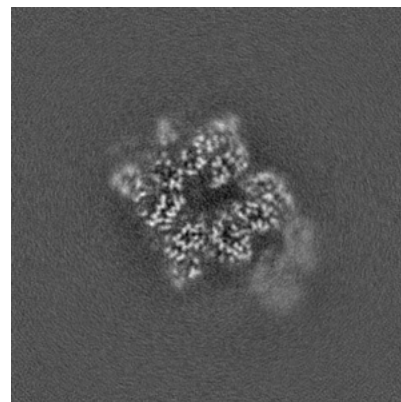
6.3.2 Raw map



X Index: 135



Y Index: 133

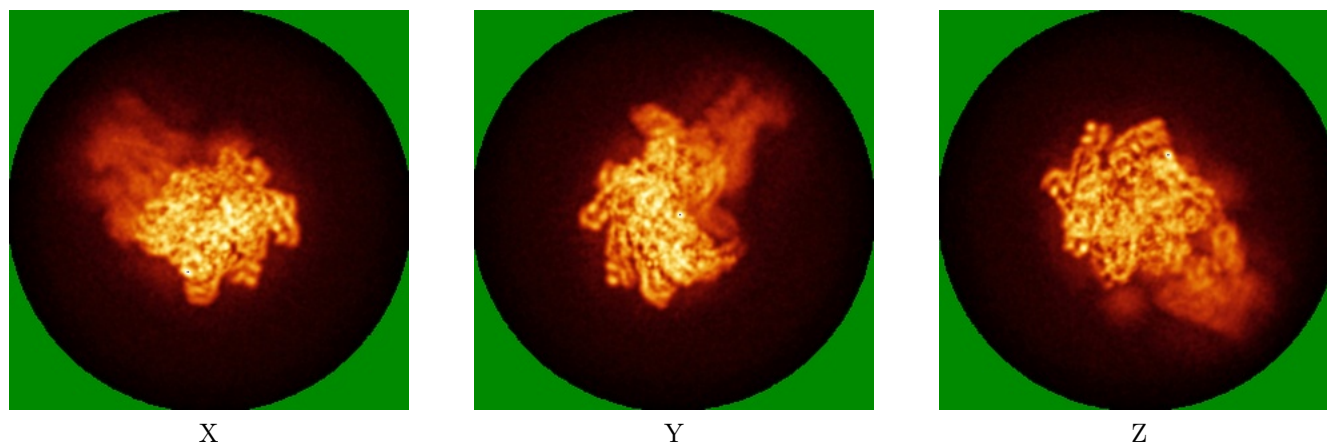


Z Index: 138

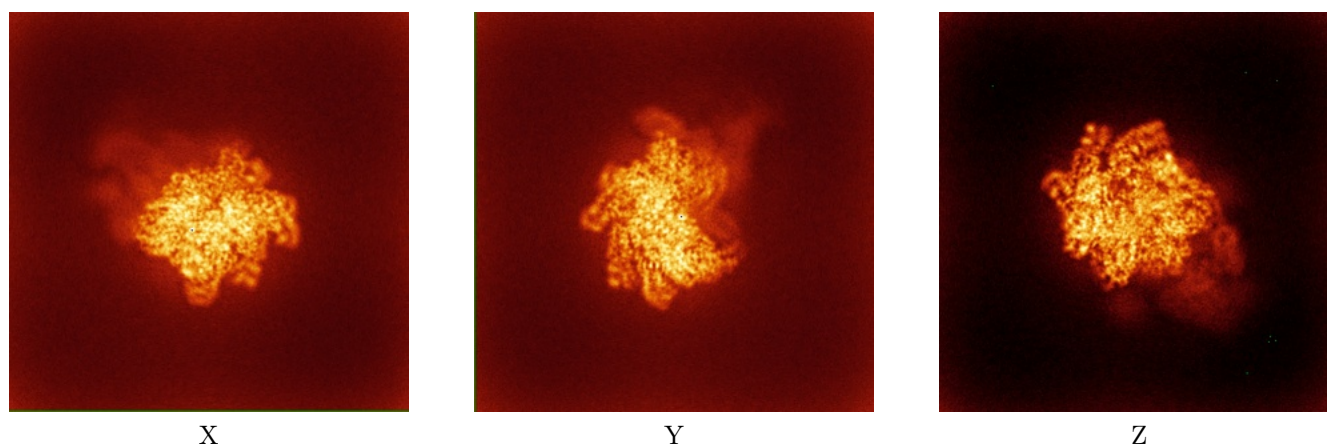
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

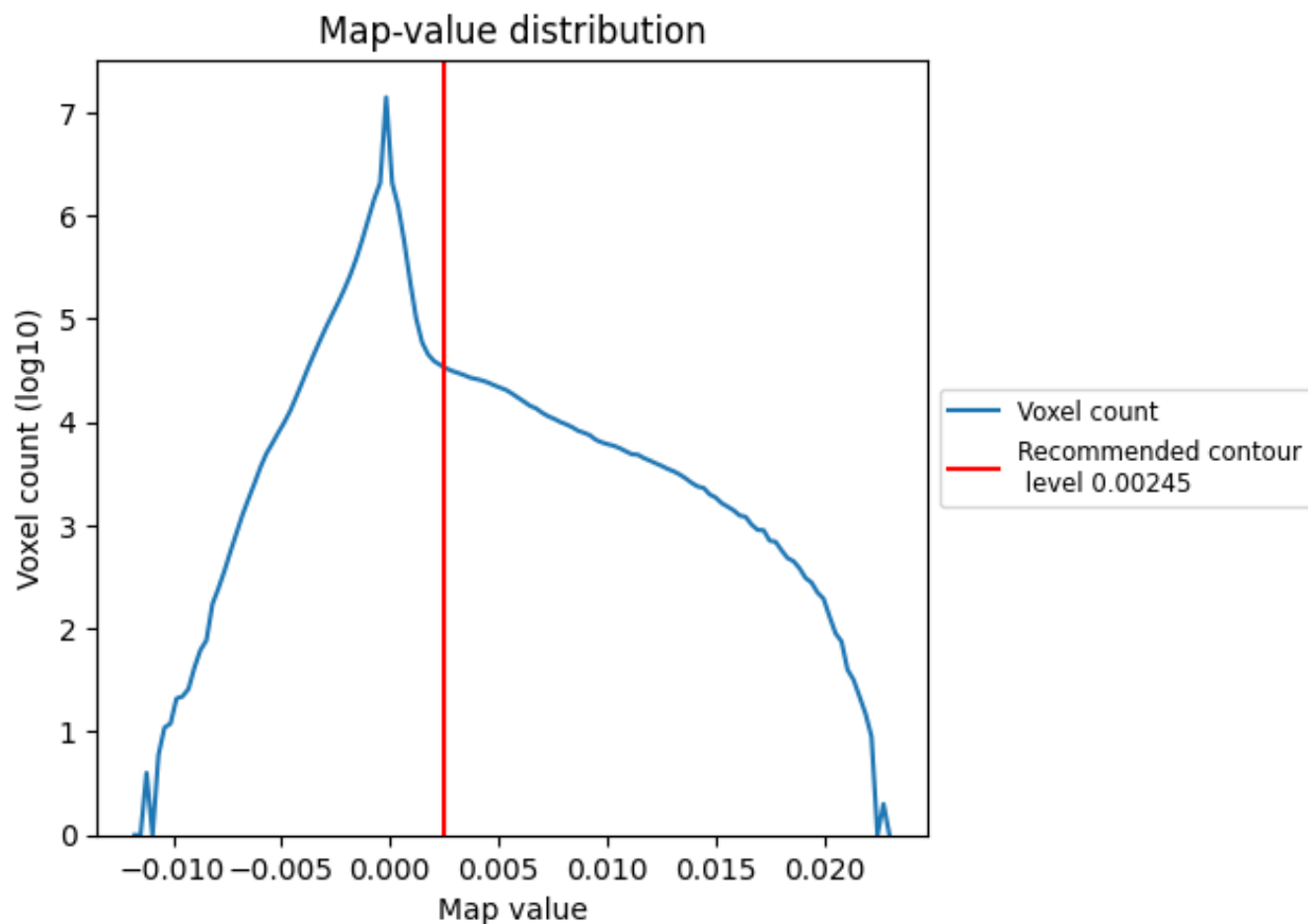
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

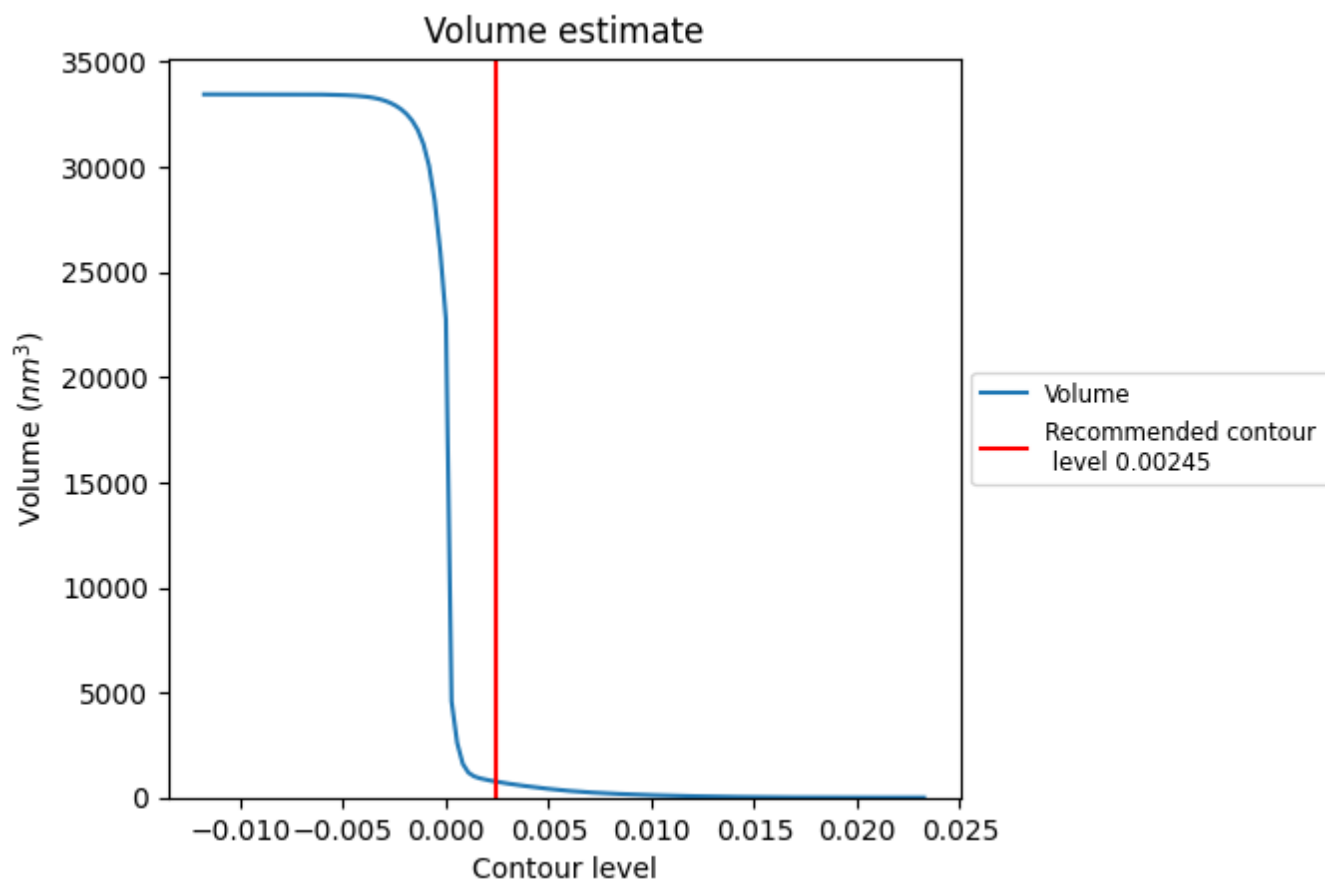
This section contains the results of statistical analysis of the map.

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.

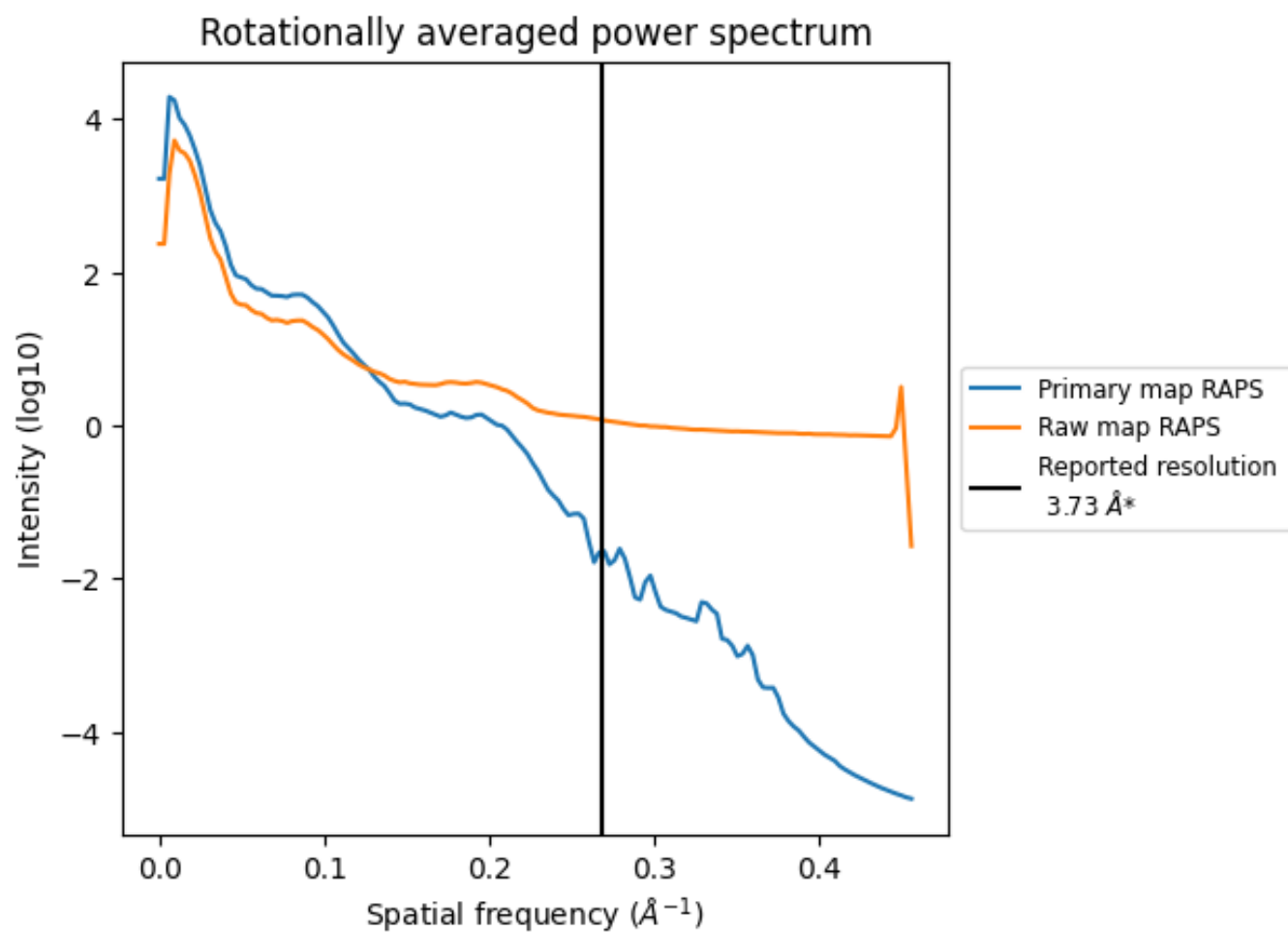
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 756 nm³; this corresponds to an approximate mass of 683 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 ⓘ

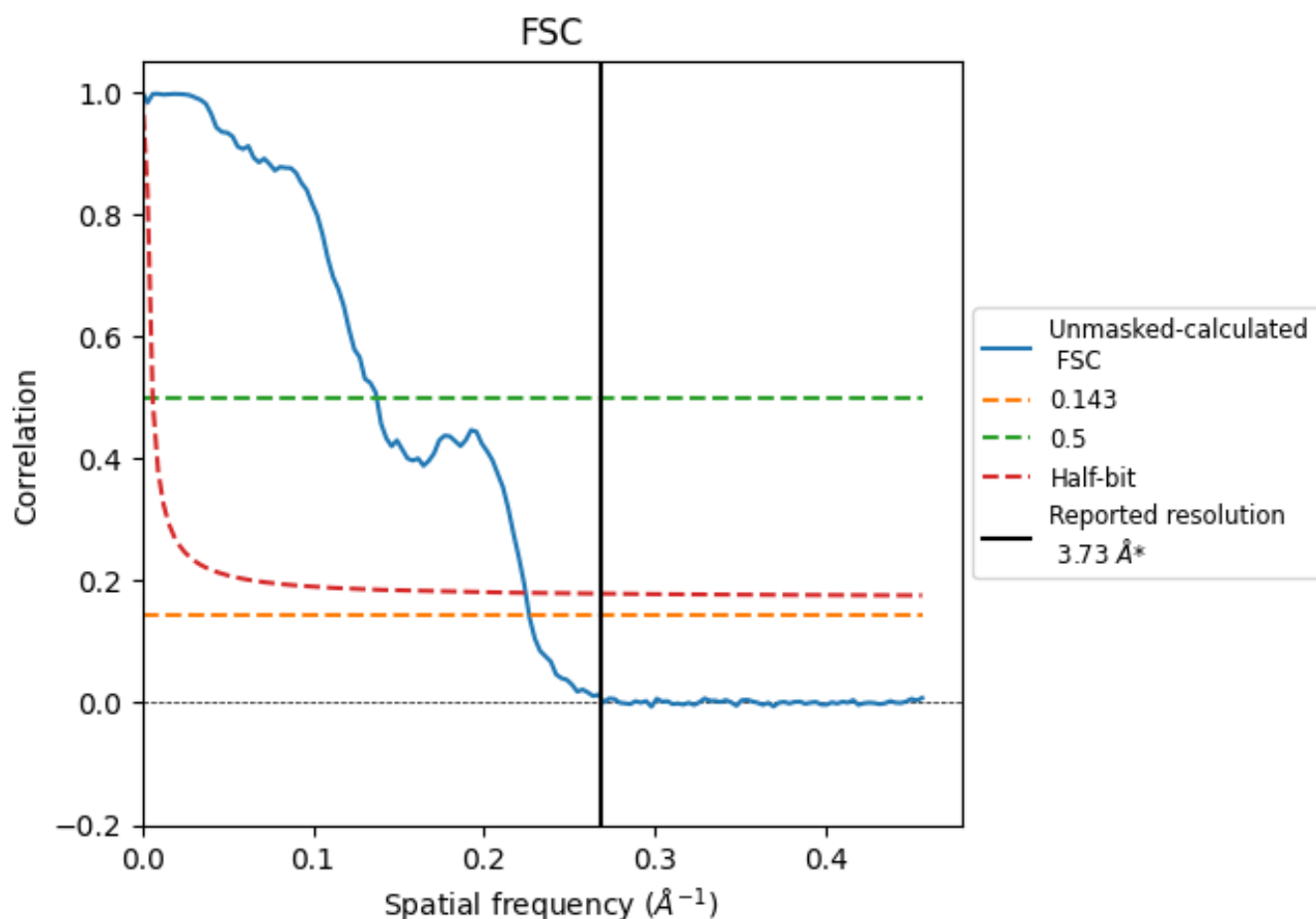


*Reported resolution corresponds to spatial frequency of 0.268 Å⁻¹

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 0.268 Å⁻¹

8.2 Resolution estimates [i](#)

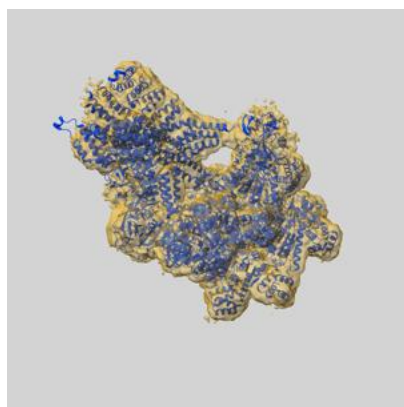
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.73	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.42	7.30	4.46

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

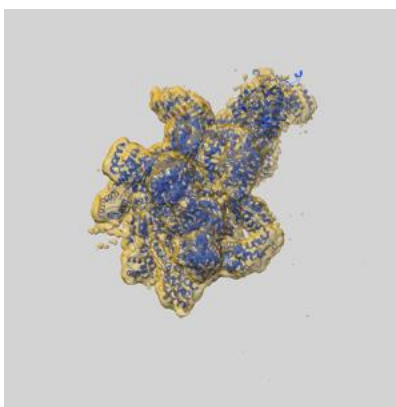
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49524 and PDB model 9NLW. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

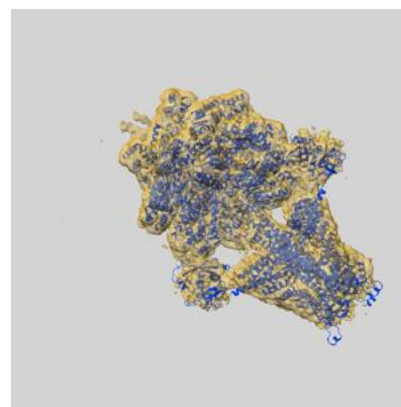
9.1 Map-model overlay [i](#)



X



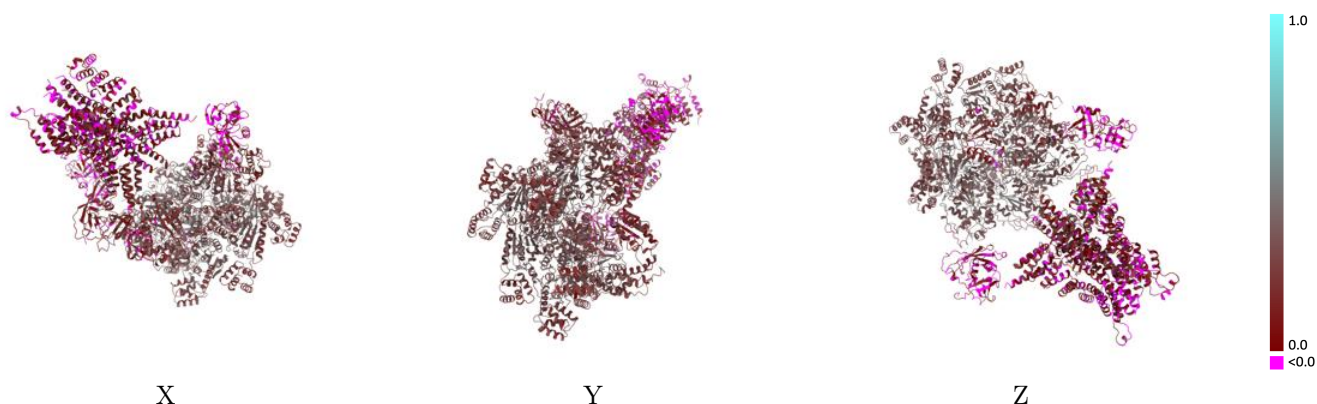
Y



Z

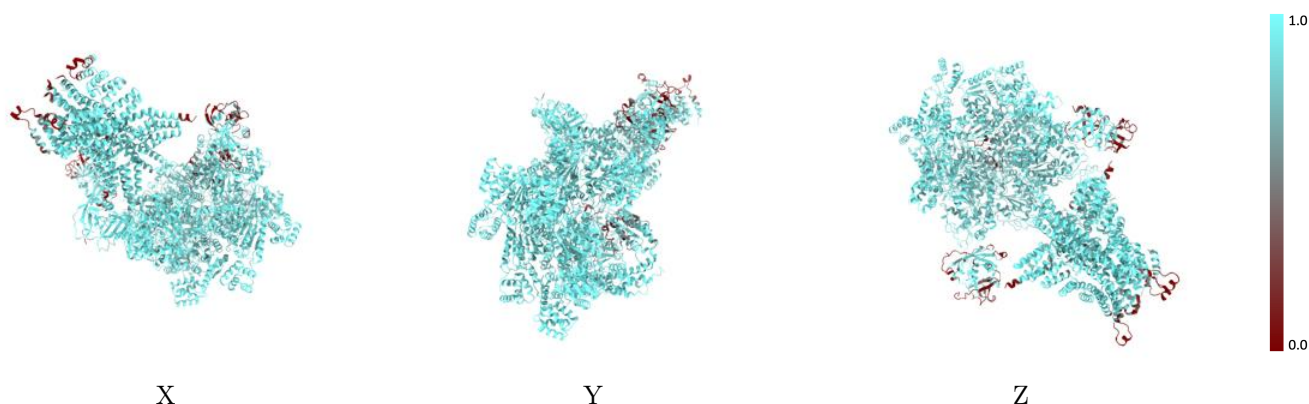
The images above show the 3D surface view of the map at the recommended contour level 0.00245 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



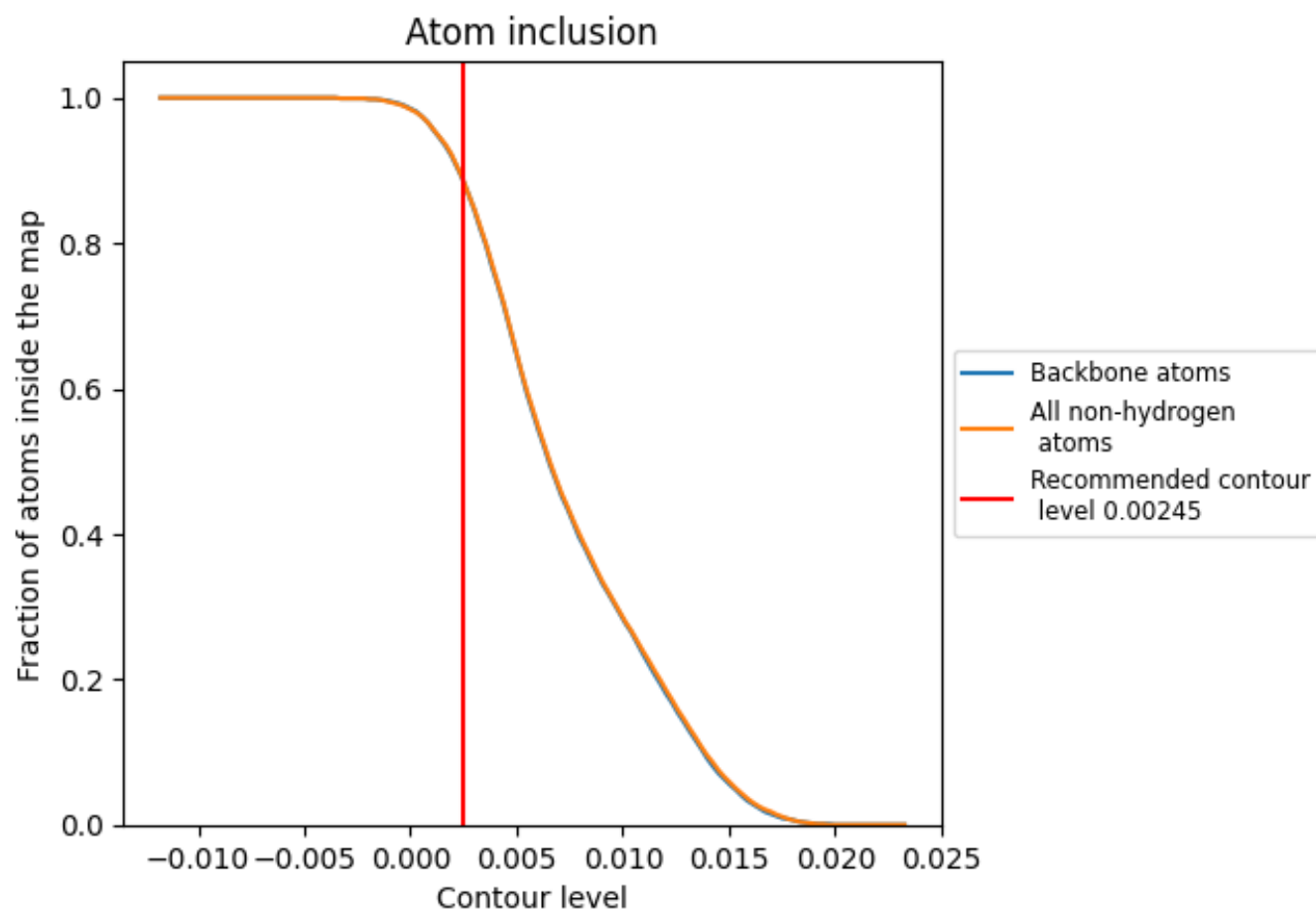
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00245).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 89% 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 (0.00245) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8900	0.2300
A	0.9380	0.3210
B	0.8410	0.2530
C	0.9330	0.2820
D	0.9380	0.2890
E	0.8420	0.2230
F	0.8700	0.2480
G	0.8510	0.0730
H	0.8960	0.1150
I	0.8590	0.0750
J	0.9200	0.1060
K	0.9000	0.1400
L	0.9550	0.0980

1.0

0.0

<0.0