



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 10:14 PM UTC

PDB ID : 8HAS / pdb_00008has
EMDB ID : EMD-34607
Title : NARROW LEAF 1-close from Japonica
Authors : Zhang, S.J.; He, Y.J.; Wang, N.; Zhang, W.J.; Liu, C.M.
Deposited on : 2022-10-26
Resolution : 2.89 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

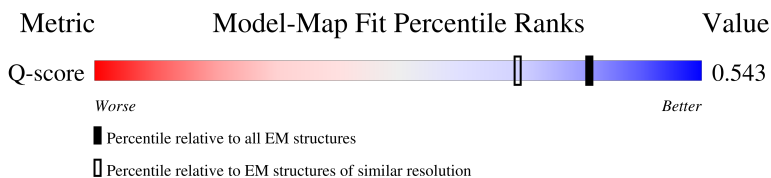
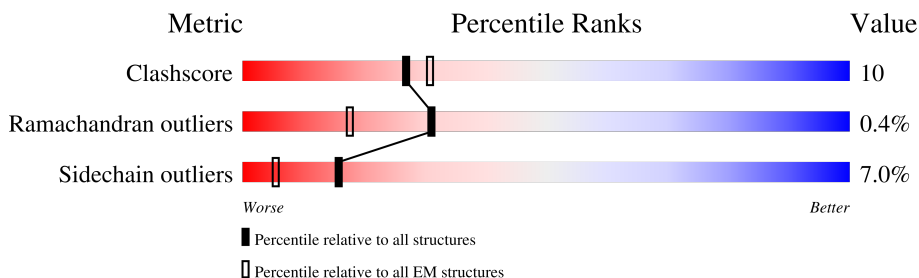
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 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	12148 (2.39 - 3.39)

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	582	
1	B	582	
1	C	582	
1	D	582	

Continued on next page...

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Mol	Chain	Length	Quality of chain
1	E	582	44%13%39%
1	F	582	47%12%39%

2 Entry composition [i](#)

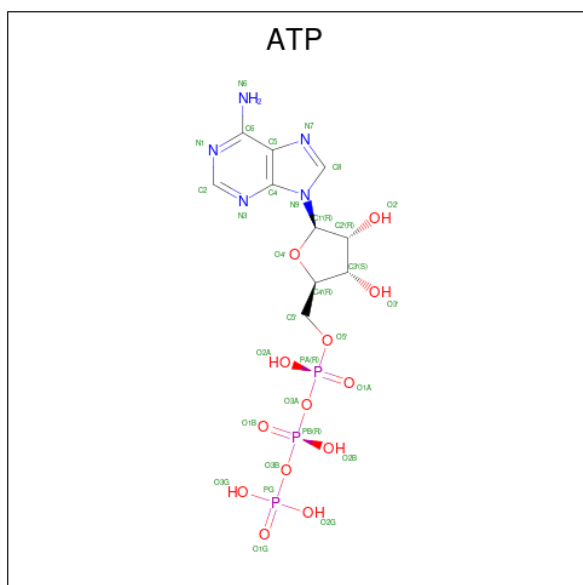
There are 2 unique types of molecules in this entry. The entry contains 16712 atoms, of which 72 are hydrogens and 0 are deuteriums.

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 Protein NARROW LEAF 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	360	Total	C	N	O	S	0	0
			2766	1751	479	525	11		
1	B	357	Total	C	N	O	S	0	0
			2745	1738	475	521	11		
1	C	359	Total	C	N	O	S	0	0
			2757	1745	478	523	11		
1	D	358	Total	C	N	O	S	0	0
			2753	1744	475	523	11		
1	E	353	Total	C	N	O	S	0	0
			2714	1720	469	514	11		
1	F	354	Total	C	N	O	S	0	0
			2719	1723	471	514	11		

- Molecule 2 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
2	A	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
2	B	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
2	C	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
2	D	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
2	E	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
2	F	1	Total 43	C 10	H 12	N 5	O 13	P 3	0

PRO	ARG	SER	ILE	THR	ASN	LEU	ASN	ASN	PRO	PRO	SER	GLU	GLU	GLU	LEU	LEU	MET	SER	LEU	HIS	LEU	GLY	ASP	ARG	GLU	PRO	LYS	THR	ARG	LEU	GLY	GLU	GLU	ALA	ASP	ASP	ALA	ASN	THR	VAL	GLN	GLN	ASN	GLU	GLU	GLU	HIS	LEU	VAL	ALA	THR	SER	ASN	PHE	VAL	GLY	MET	SER	PRO	VAL	ARG	ASP	ASP	GLN	VAL	ALA	ILE	PRO	GLU
T409	A410	M411	L415	T418	M425	W426	T427	D431	L432	G433	R434	D437	R438	L439	E440	L441	D442	I443	M447	E448	S449	L450	Q451	ASP	ALA	VAL	GLN	GLN	GLN	ASN	THR	VAL	GLN	GLN	ARG	PHE	ALA	LEU	VAL	ALA	ALA	VAL	ALA	ASN	THR	SER	ALA	VAL	GLY	MET	SER	PRO	VAL	ARG	ASP	ASP	GLN	VAL	ALA	ILE	PRO	GLU							
E285	V288	R289	A290	D291	I295	D300	F301	D302	V306	D318	V319	K320	L324	L328	V336	R341	T347	L355	D359	E360	I363	T367	V372	D380	L388	L391	T392	S393	Q394	D395	G396	E397	R400	G403	I404	G407	G408																																
W162	V165	D166	V167	F170	S171	Y172	TYR	GLY	ALA	PRO	ALA	GLN	THR	PRO	LYS	GLU	Q183	G194	S195	I199	Q204	E209	I217	R220	K225	L230	T231	N232	H233	H234	V235	A236	V237	D238	L239	D240	Y241	P242	N243	M246	P249	L254	E264	T282																									

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	670053	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF amplitude correction was performed following 3D reconstruction	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.641	Depositor
Minimum map value	-2.266	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.107	Depositor
Recommended contour level	0.32	Depositor
Map size ($\text{\AA}$)	214.76, 214.76, 214.76	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0738, 1.0738, 1.0738	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

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	0.29	1/2821 (0.0%)	0.57	2/3827 (0.1%)
1	B	0.28	1/2800 (0.0%)	0.58	3/3798 (0.1%)
1	C	0.30	1/2812 (0.0%)	0.62	7/3816 (0.2%)
1	D	0.22	0/2809	0.48	1/3812 (0.0%)
1	E	0.42	4/2769 (0.1%)	0.64	7/3758 (0.2%)
1	F	0.24	1/2774 (0.0%)	0.49	0/3764
All	All	0.30	8/16785 (0.0%)	0.57	20/22775 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2
1	F	0	1
All	All	0	3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	142	LYS	CA-C	-8.49	1.44	1.53
1	E	122	ARG	C-O	-8.02	1.15	1.24
1	C	233	HIS	C-O	-6.13	1.16	1.24
1	F	233	HIS	C-O	-5.83	1.16	1.24
1	B	233	HIS	C-O	-5.75	1.16	1.24

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	TYR	N-CA-C	-13.01	93.48	110.39
1	E	241	TYR	CA-C-N	11.08	133.69	119.84
1	E	241	TYR	C-N-CA	11.08	133.69	119.84
1	C	241	TYR	CA-C-N	10.19	132.58	119.84
1	C	241	TYR	C-N-CA	10.19	132.58	119.84

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	288	VAL	Peptide
1	C	439	LEU	Peptide
1	F	439	LEU	Peptide

5.2 Too-close contacts ⓘ

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	2766	0	2741	54	0
1	B	2745	0	2719	54	0
1	C	2757	0	2730	62	0
1	D	2753	0	2720	53	0
1	E	2714	0	2689	67	0
1	F	2719	0	2696	46	0
2	A	31	12	12	0	0
2	B	31	12	12	3	0
2	C	31	12	12	2	0
2	D	31	12	12	2	0
2	E	31	12	12	1	0
2	F	31	12	12	2	0
All	All	16640	72	16367	327	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 10.

The worst 5 of 327 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)
1:E:238:ASP:HB2	1:E:244:GLN:NE2	1.80	0.96
1:C:234:HIS:CE1	1:C:291:ASP:OD2	2.25	0.88
1:C:414:ARG:H	1:C:425:ASN:HA	1.49	0.77
1:D:224:ASN:OD1	1:D:224:ASN:N	2.19	0.76
1:C:234:HIS:ND1	1:C:291:ASP:OD2	2.19	0.74

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	356/582 (61%)	342 (96%)	14 (4%)	0	100	100
1	B	353/582 (61%)	343 (97%)	10 (3%)	0	100	100
1	C	355/582 (61%)	335 (94%)	16 (4%)	4 (1%)	11	36
1	D	354/582 (61%)	339 (96%)	15 (4%)	0	100	100
1	E	349/582 (60%)	330 (95%)	14 (4%)	5 (1%)	9	30
1	F	350/582 (60%)	336 (96%)	14 (4%)	0	100	100
All	All	2117/3492 (61%)	2025 (96%)	83 (4%)	9 (0%)	31	59

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	303	ILE
1	E	241	TYR
1	E	303	ILE
1	E	239	LEU
1	E	412	ARG

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	301/488 (62%)	287 (95%)	14 (5%)	23	56
1	B	299/488 (61%)	279 (93%)	20 (7%)	15	43
1	C	300/488 (62%)	281 (94%)	19 (6%)	16	45
1	D	299/488 (61%)	271 (91%)	28 (9%)	8	26
1	E	296/488 (61%)	271 (92%)	25 (8%)	10	31
1	F	296/488 (61%)	277 (94%)	19 (6%)	16	44
All	All	1791/2928 (61%)	1666 (93%)	125 (7%)	16	40

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	173	TYR
1	F	235	VAL
1	D	347	THR
1	F	230	LEU
1	F	328	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	283	ASN
1	D	329	ASN
1	F	411	ASN
1	E	224	ASN
1	F	375	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](#)

6 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$
2	ATP	B	601	-	32,33,33	2.81	21 (65%)	48,52,52	2.85	18 (37%)
2	ATP	A	601	-	32,33,33	2.79	20 (62%)	48,52,52	2.86	22 (45%)
2	ATP	D	601	-	32,33,33	2.62	19 (59%)	48,52,52	2.91	19 (39%)
2	ATP	E	601	-	32,33,33	2.79	20 (62%)	48,52,52	2.79	22 (45%)
2	ATP	C	601	-	32,33,33	2.62	19 (59%)	48,52,52	2.91	19 (39%)
2	ATP	F	601	-	32,33,33	2.72	19 (59%)	48,52,52	2.87	21 (43%)

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
2	ATP	B	601	-	-	9/22/38/38	0/3/3/3
2	ATP	A	601	-	-	6/22/38/38	0/3/3/3
2	ATP	D	601	-	-	9/22/38/38	0/3/3/3
2	ATP	E	601	-	-	7/22/38/38	0/3/3/3
2	ATP	C	601	-	-	9/22/38/38	0/3/3/3
2	ATP	F	601	-	-	7/22/38/38	0/3/3/3

The worst 5 of 118 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	ATP	C5-N7	-7.01	1.26	1.39
2	D	601	ATP	C5-N7	-6.31	1.27	1.39
2	C	601	ATP	C5-N7	-6.27	1.27	1.39
2	F	601	ATP	C5-N7	-6.01	1.28	1.39
2	E	601	ATP	C5-N7	-5.40	1.29	1.39

The worst 5 of 121 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	ATP	C5-C4-N3	-9.15	114.11	126.72
2	D	601	ATP	C5-C4-N3	-9.14	114.14	126.72
2	F	601	ATP	C5-C4-N3	-8.78	114.63	126.72
2	E	601	ATP	C5-C4-N3	-8.73	114.70	126.72
2	A	601	ATP	C5-C4-N3	-8.71	114.72	126.72

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	ATP	PB-O3B-PG-O2G
2	B	601	ATP	C5'-O5'-PA-O1A
2	C	601	ATP	C5'-O5'-PA-O3A
2	D	601	ATP	C5'-O5'-PA-O3A
2	E	601	ATP	PB-O3B-PG-O3G

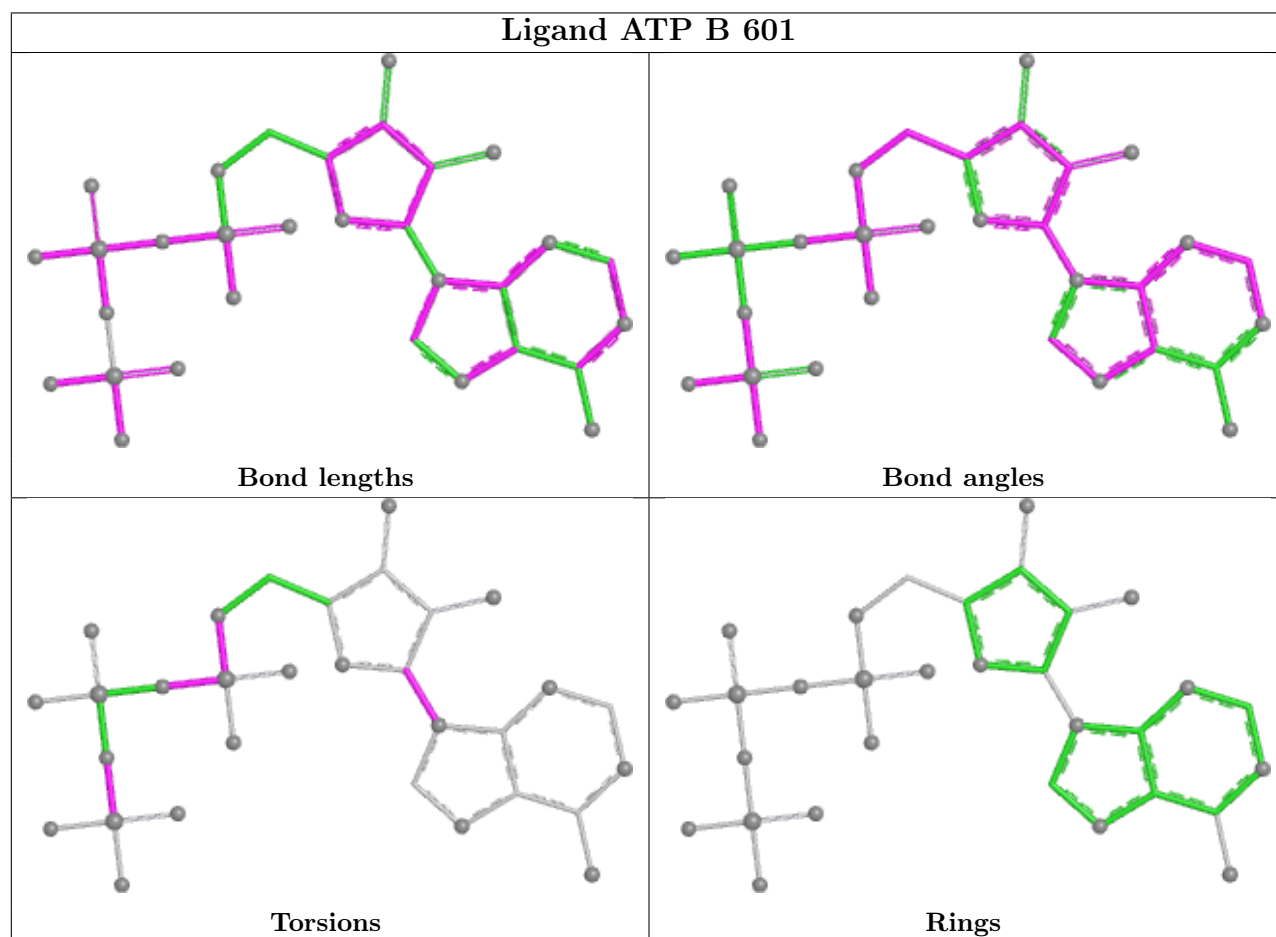
There are no ring outliers.

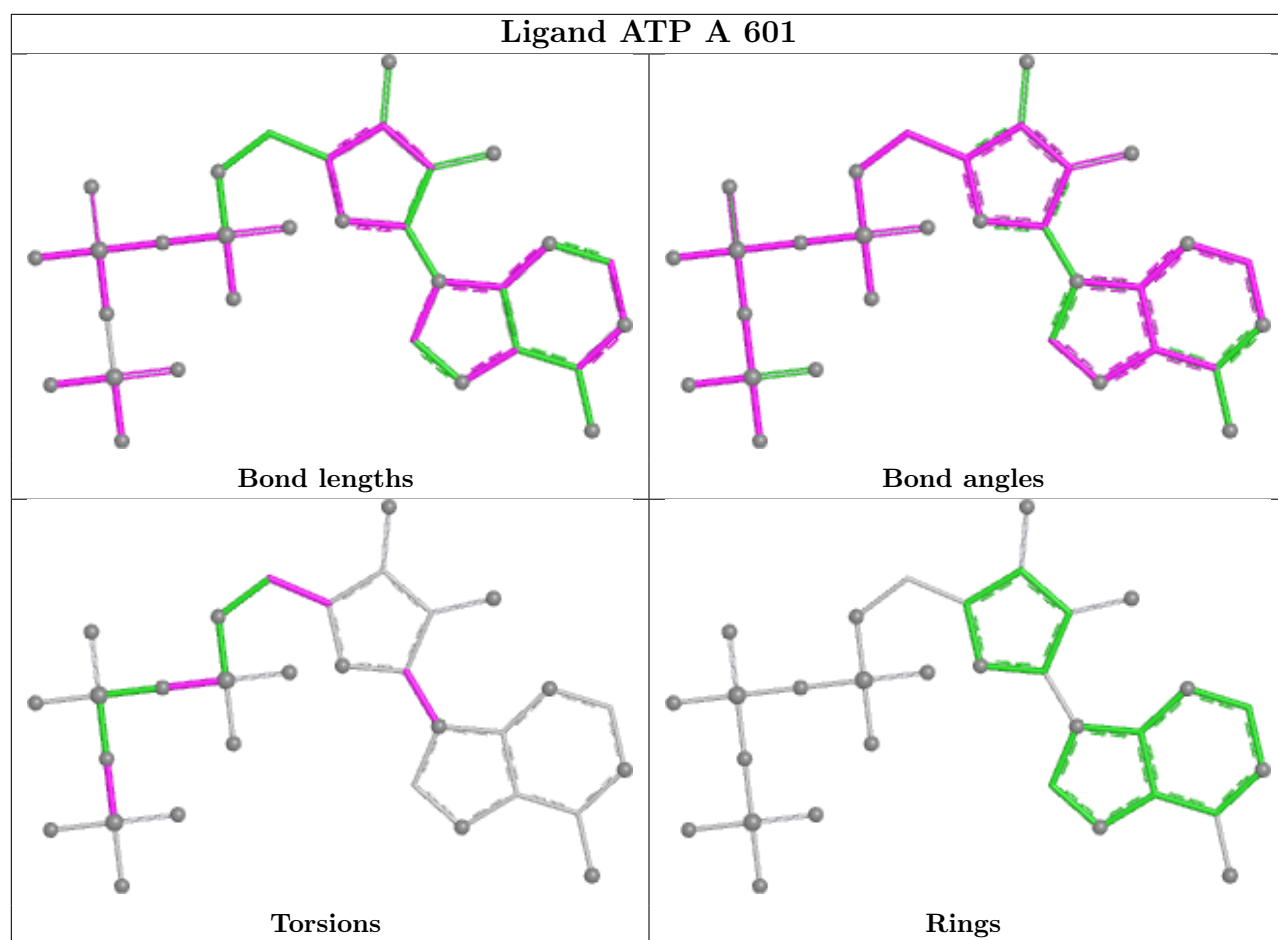
5 monomers are involved in 10 short contacts:

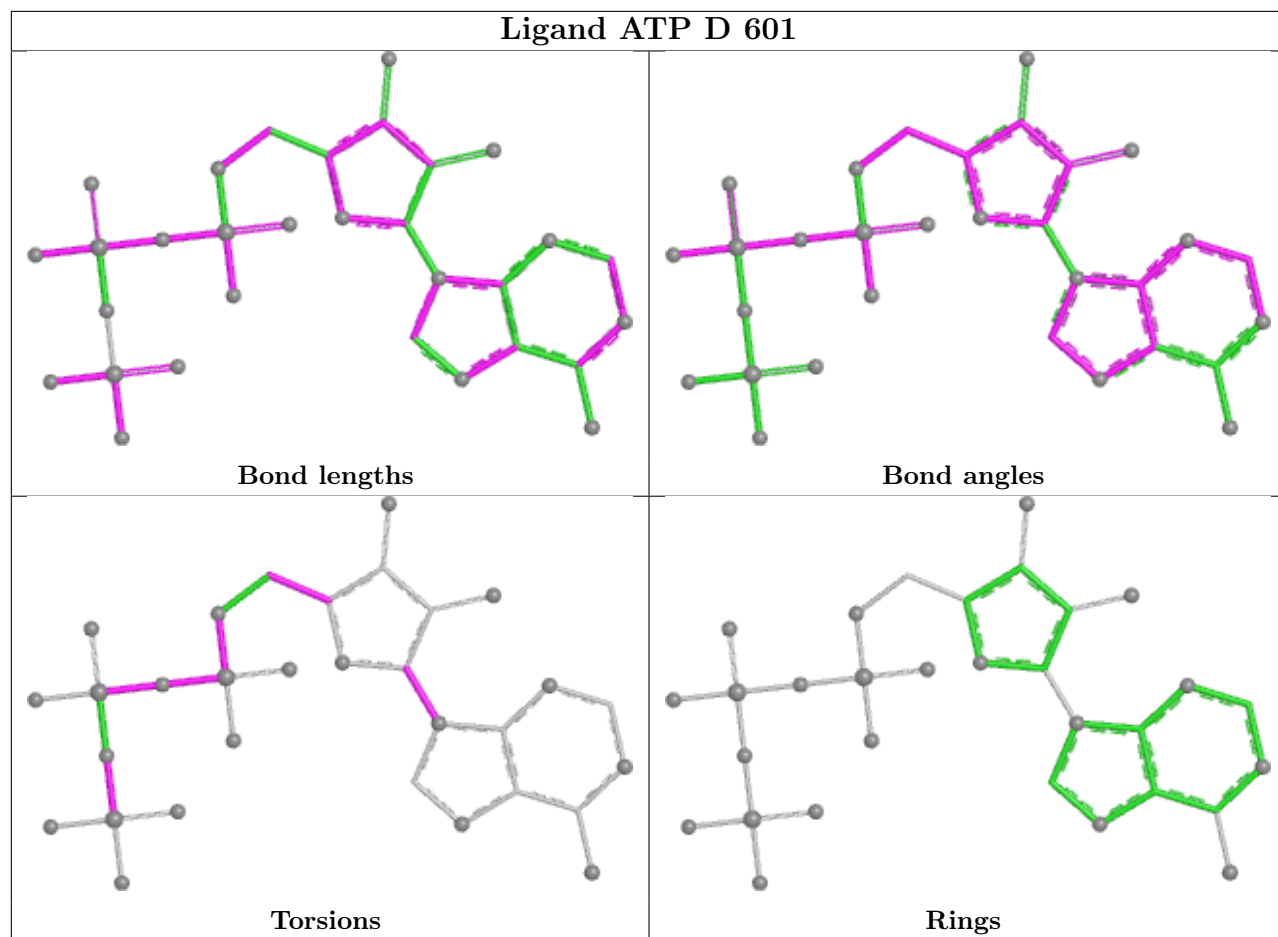
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	ATP	3	0
2	D	601	ATP	2	0
2	E	601	ATP	1	0
2	C	601	ATP	2	0
2	F	601	ATP	2	0

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

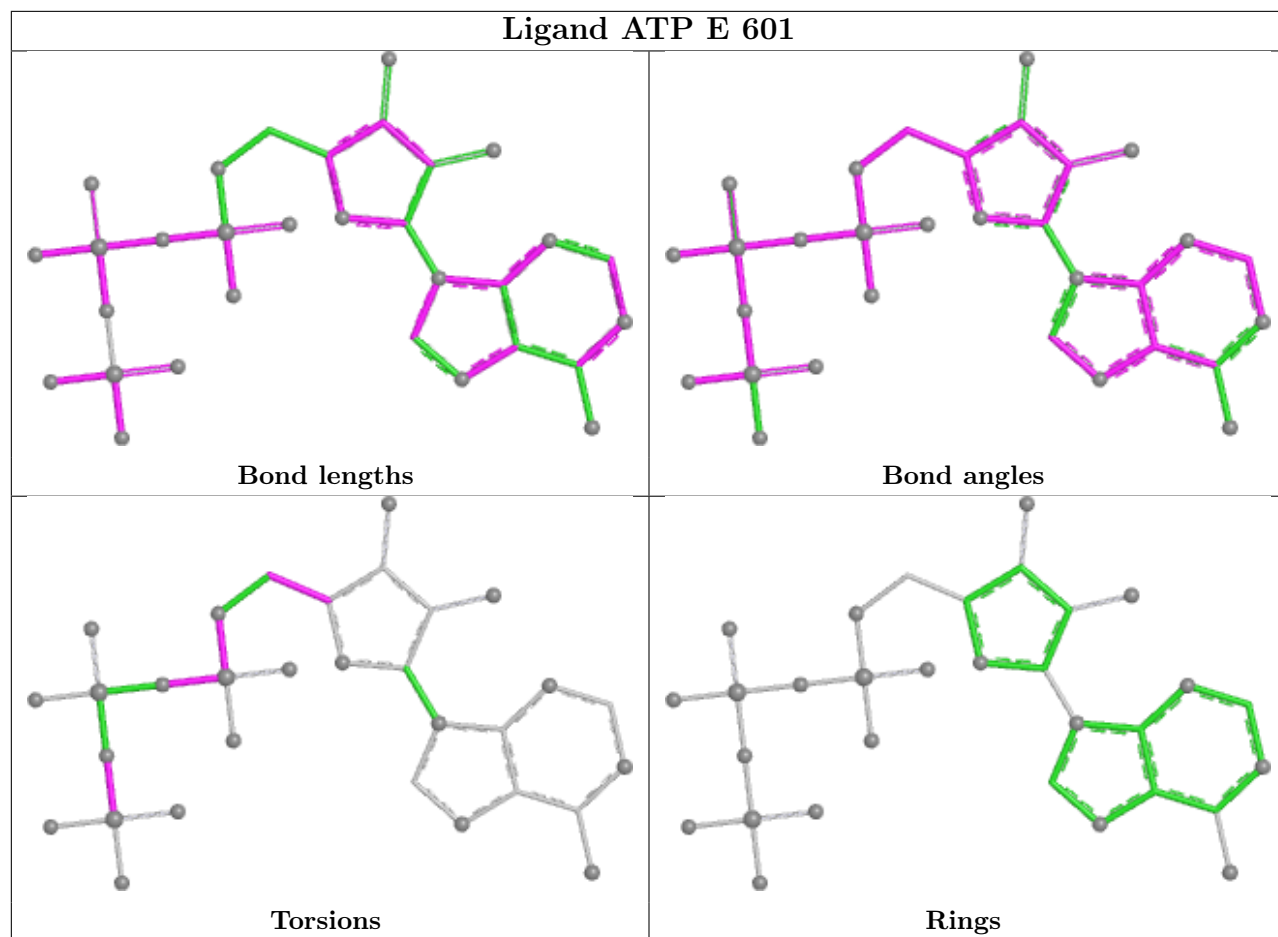
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

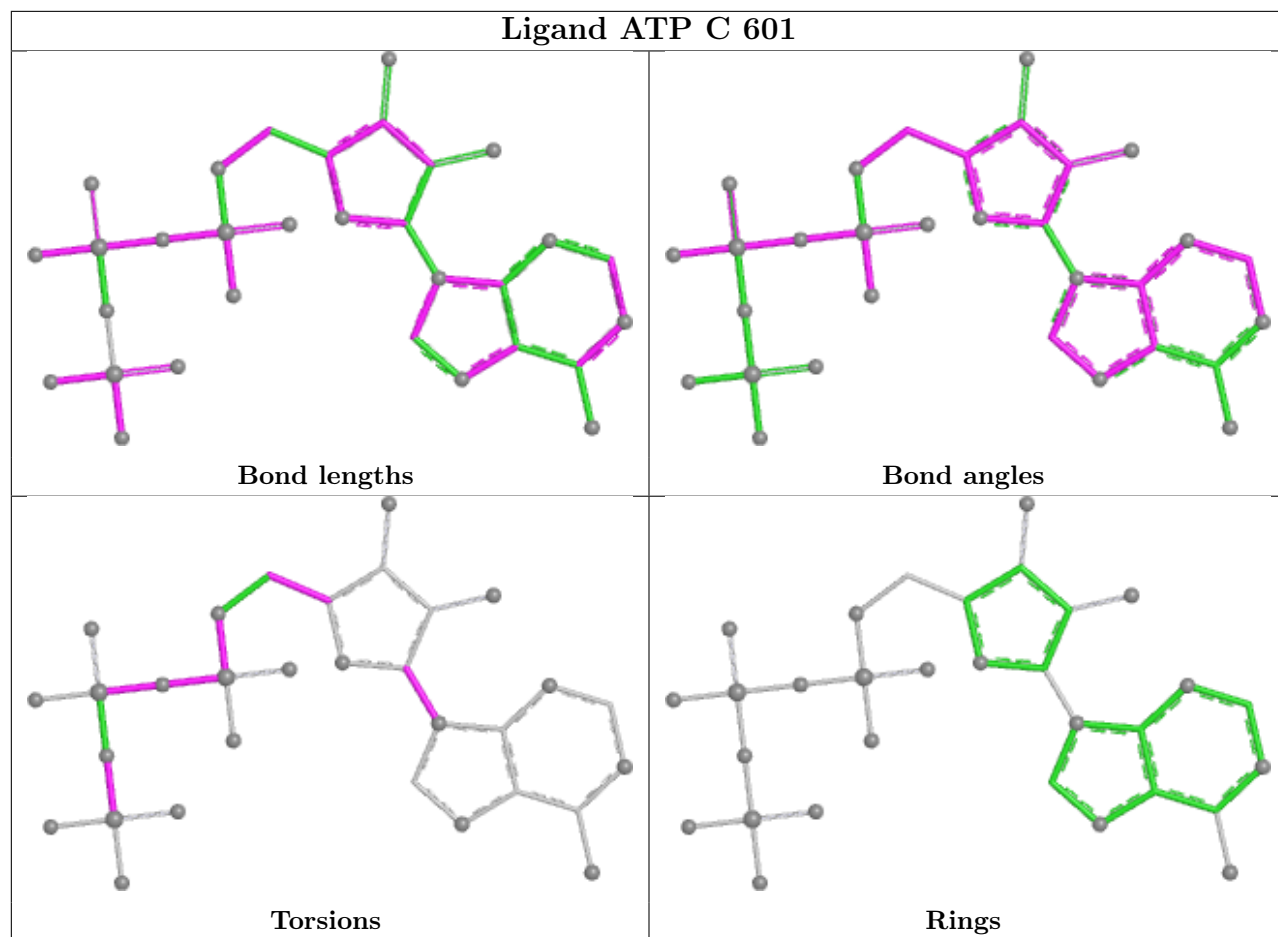


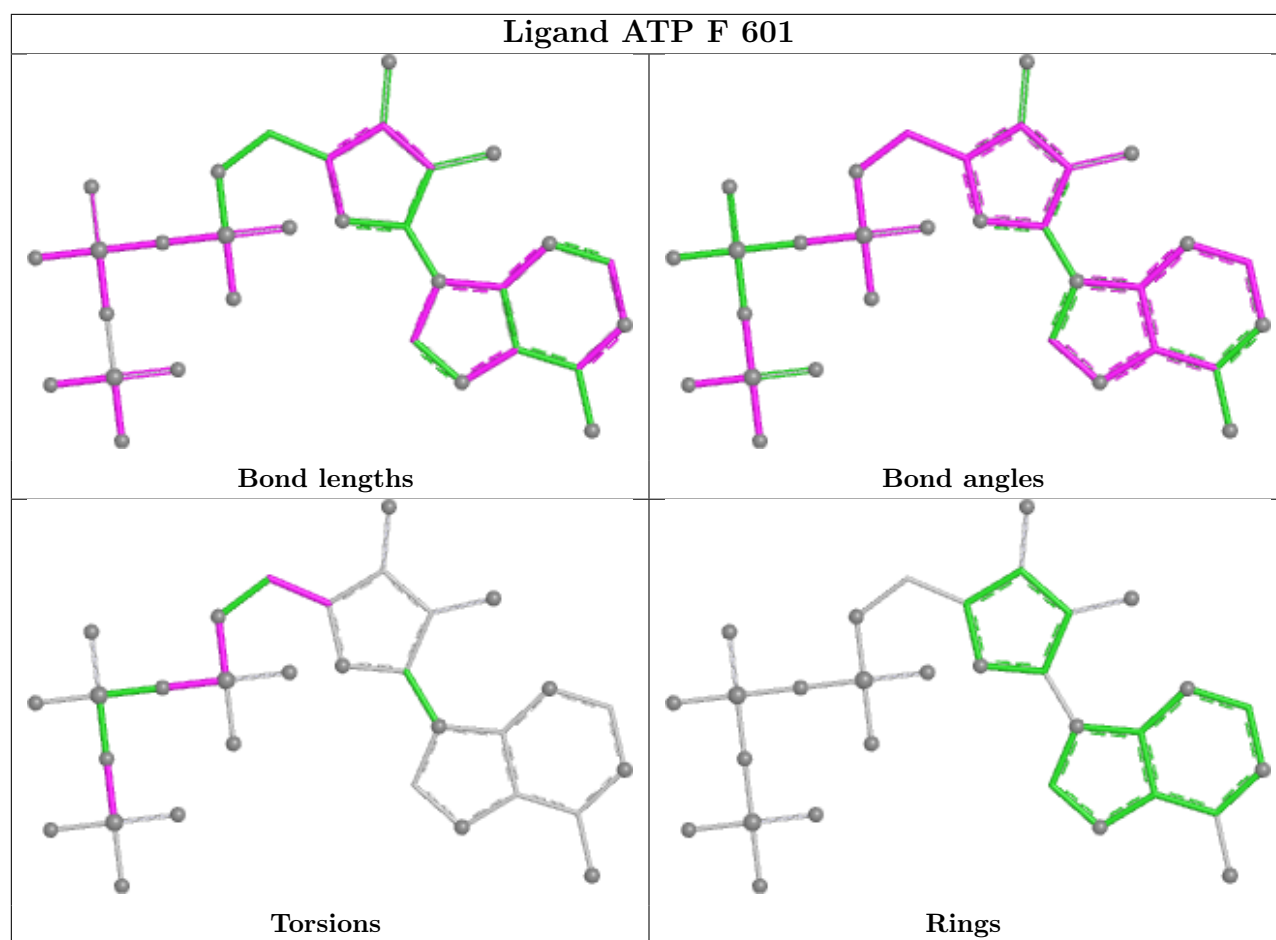




Ligand ATP E 601







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.

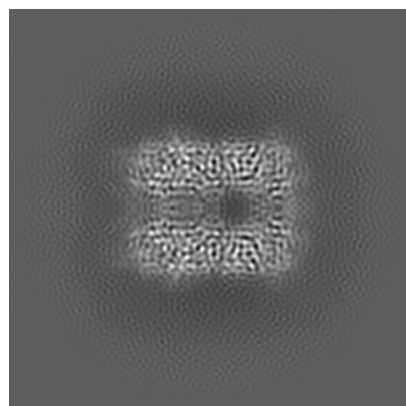
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34607. These allow visual inspection of the internal detail of the map and identification of artifacts.

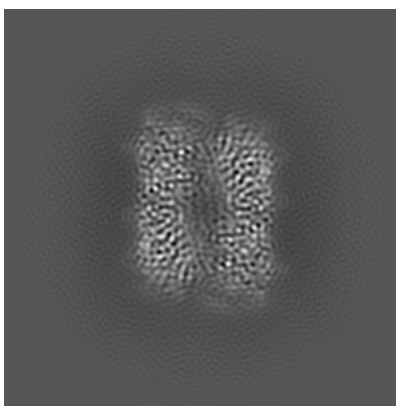
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

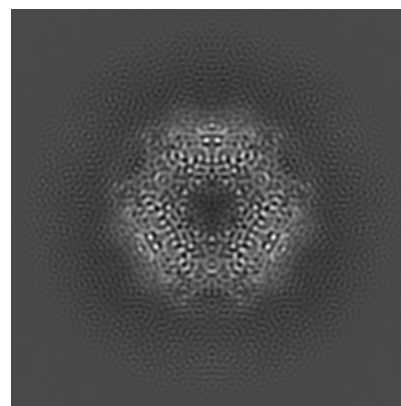
6.1.1 Primary map



X

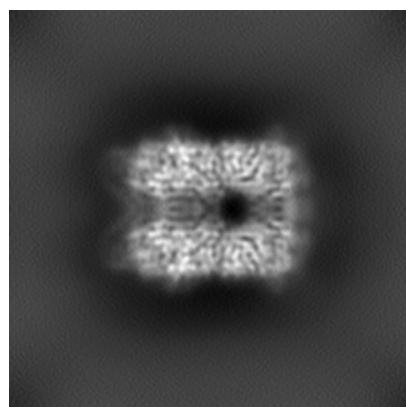


Y

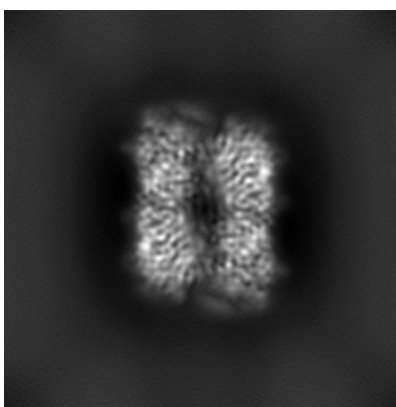


Z

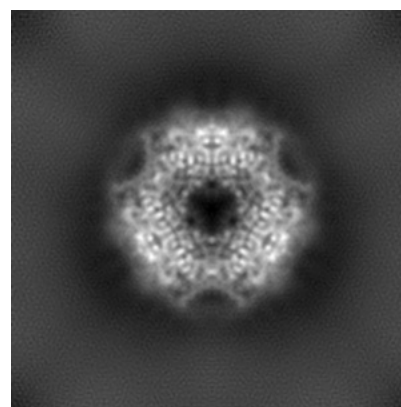
6.1.2 Raw map



X



Y

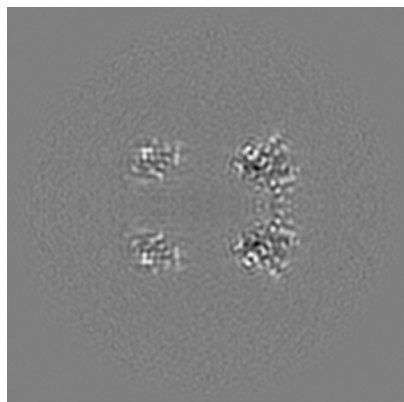


Z

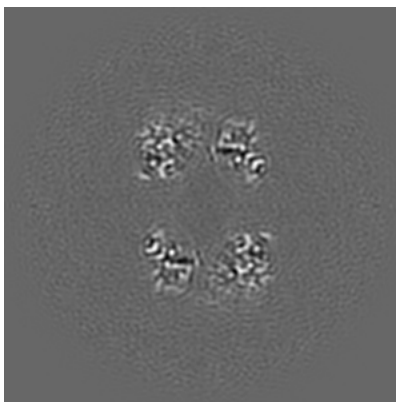
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

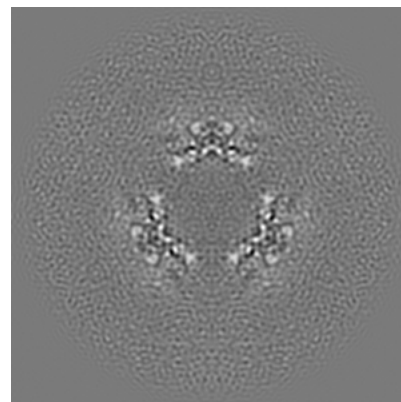
6.2.1 Primary map



X Index: 100

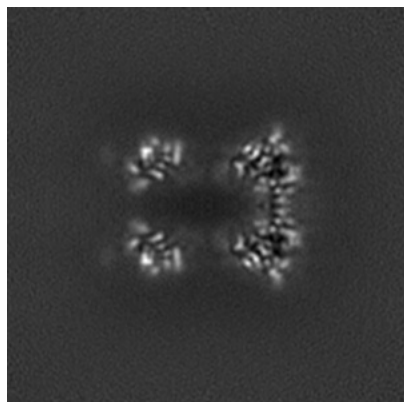


Y Index: 100

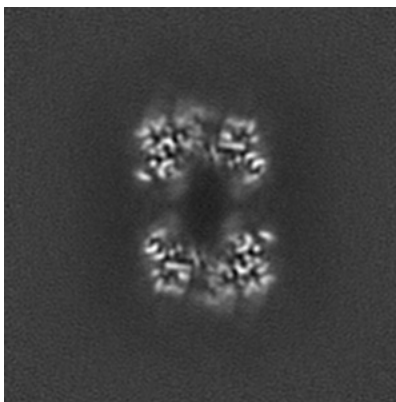


Z Index: 100

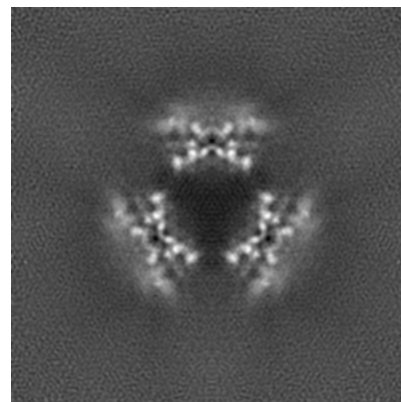
6.2.2 Raw map



X Index: 100



Y Index: 100

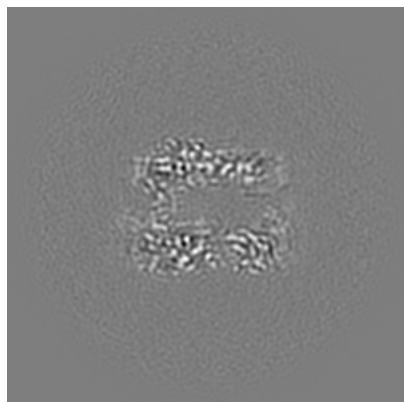


Z Index: 100

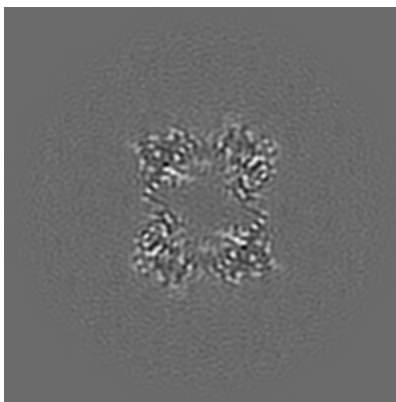
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

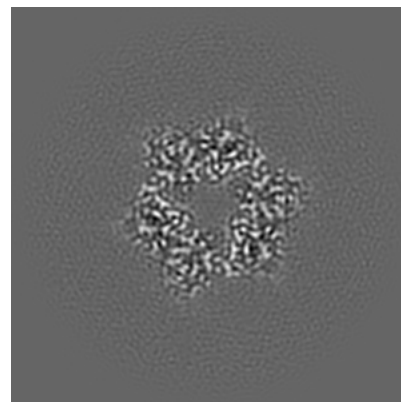
6.3.1 Primary map



X Index: 79

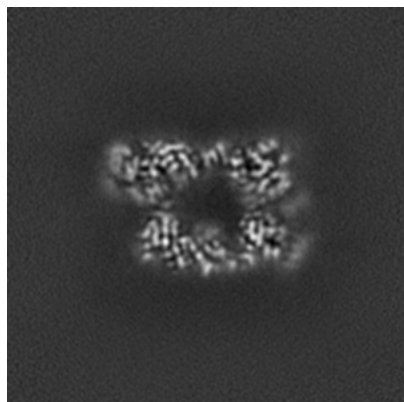


Y Index: 83

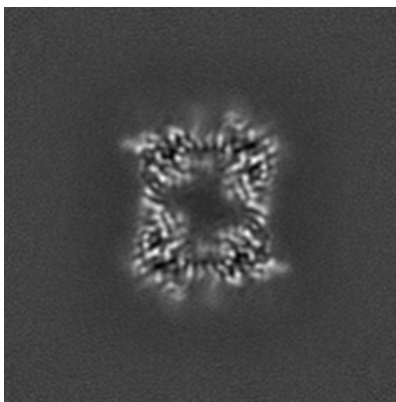


Z Index: 79

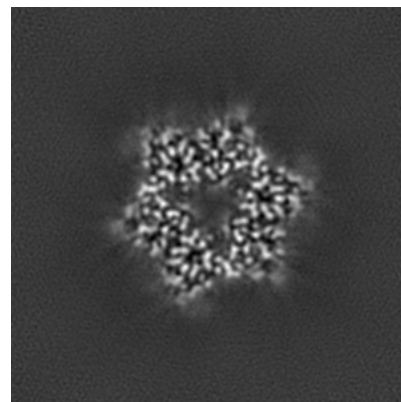
6.3.2 Raw map



X Index: 115



Y Index: 84

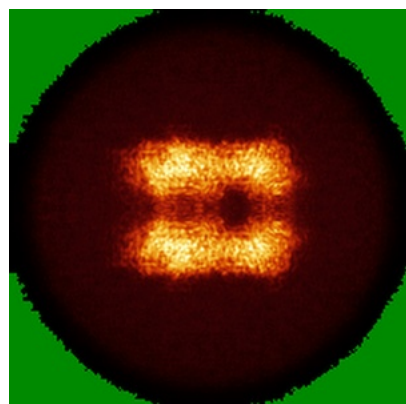


Z Index: 79

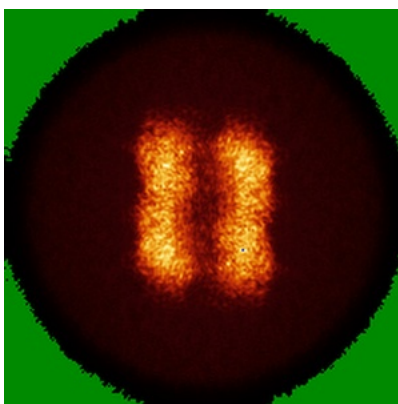
The images above show the largest variance slices of the map in three orthogonal directions.

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

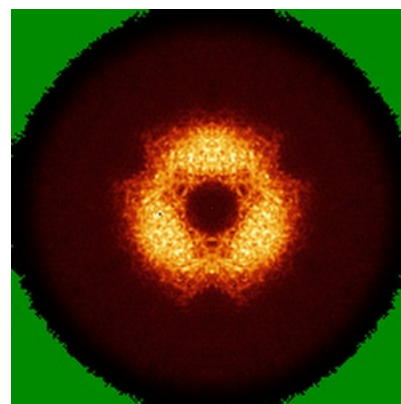
6.4.1 Primary map



X

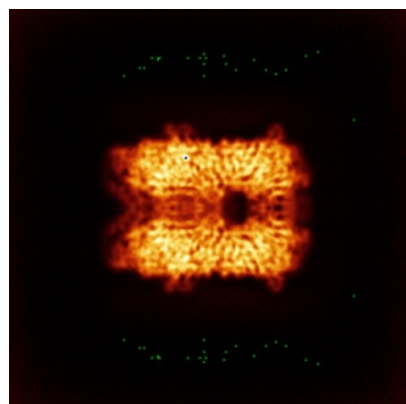


Y

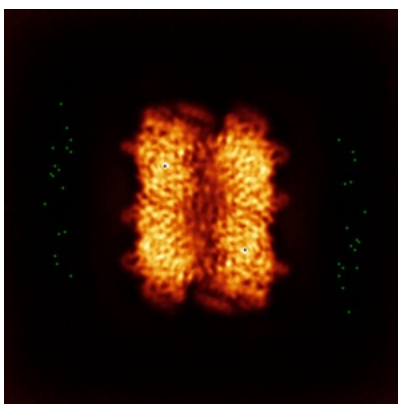


Z

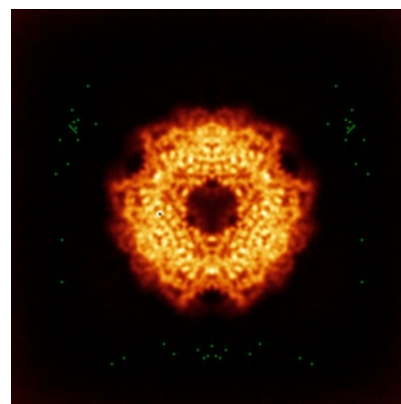
6.4.2 Raw map



X



Y

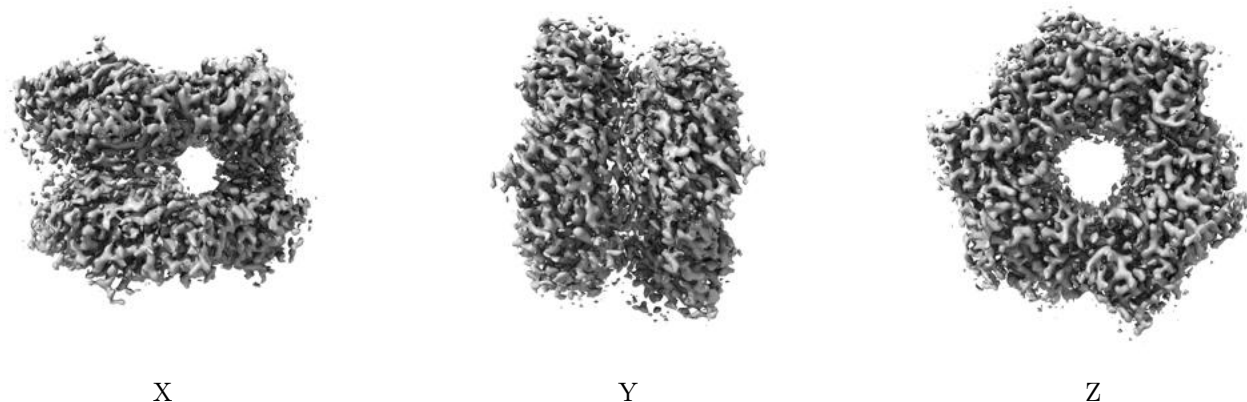


Z

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 0.32. 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.

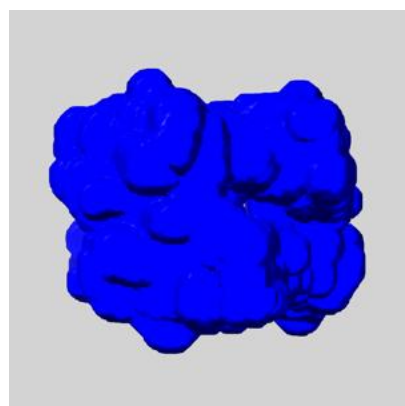
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

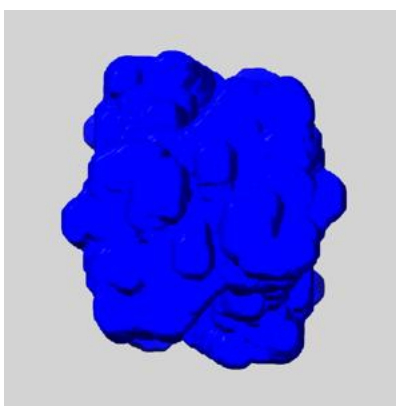
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

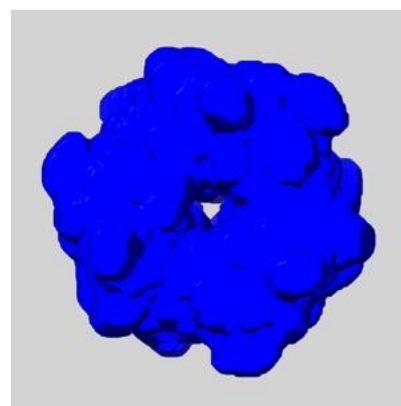
6.6.1 emd_34607_msk_1.map [i](#)



X



Y

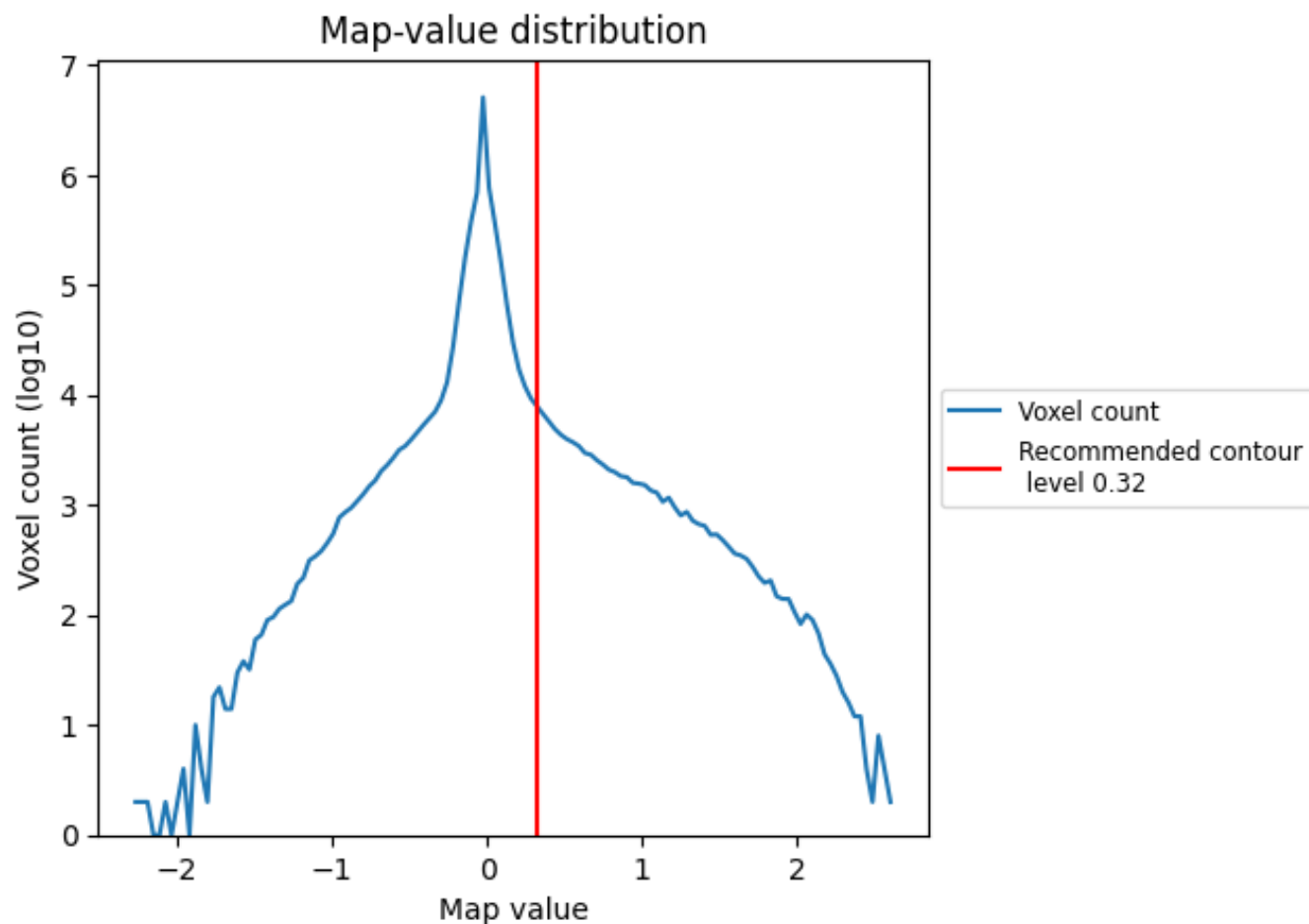


Z

7 Map analysis [i](#)

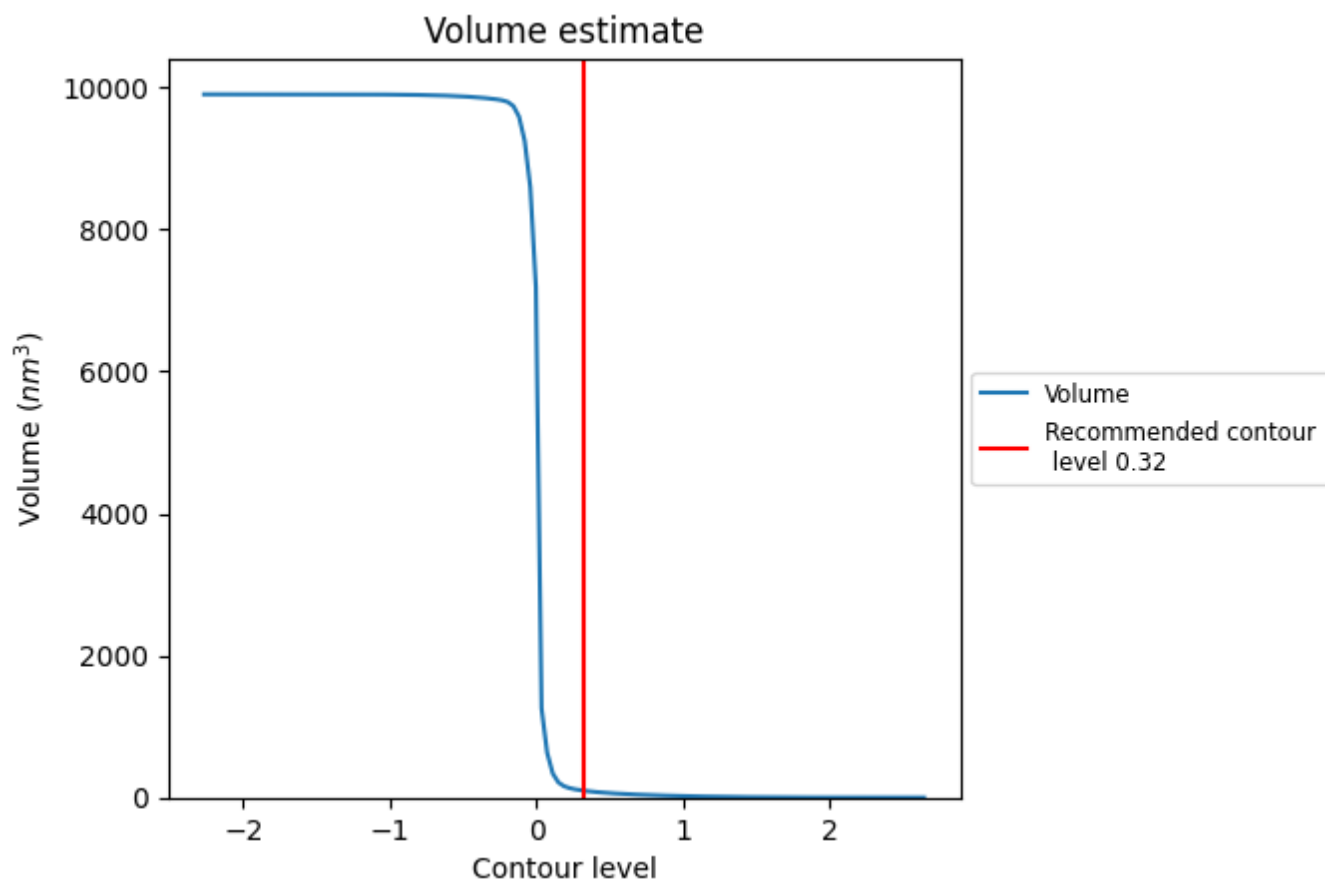
This section contains the results of statistical analysis of the map.

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.

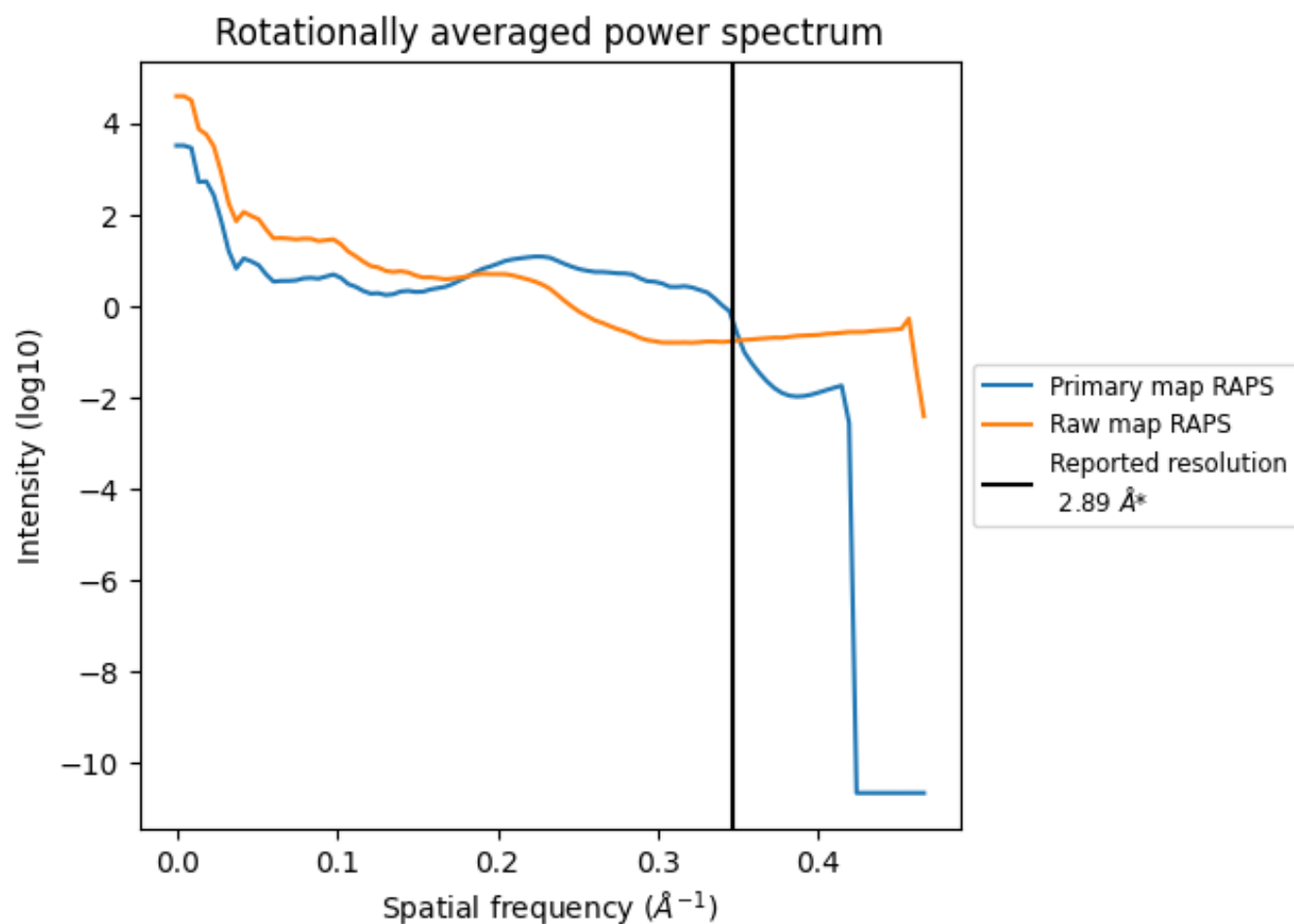
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 98 nm³; this corresponds to an approximate mass of 89 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 ⓘ

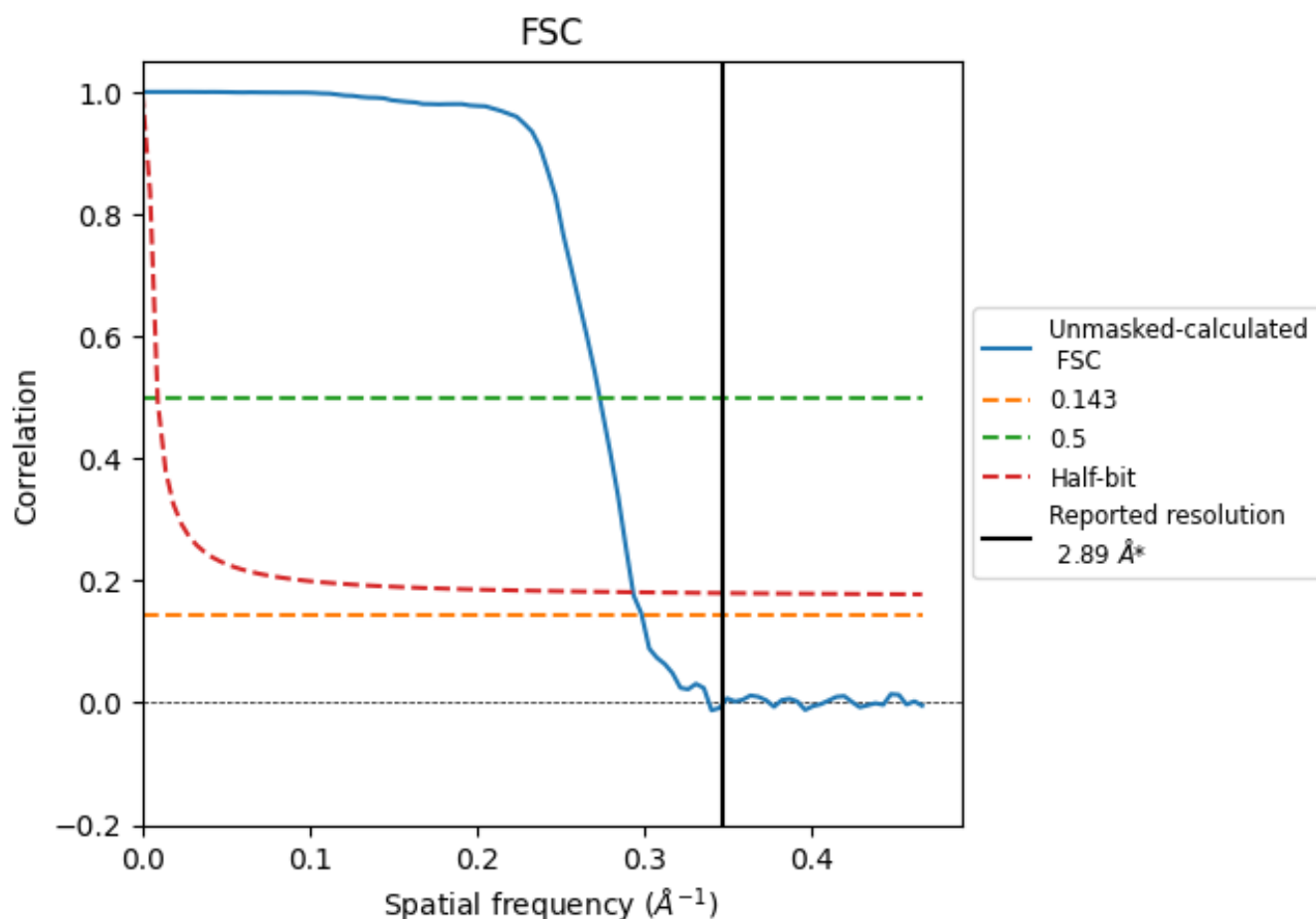


*Reported resolution corresponds to spatial frequency of 0.346 Å⁻¹

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 0.346 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.89	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.35	3.66	3.41

*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 3.35 differs from the reported value 2.89 by more than 10 %

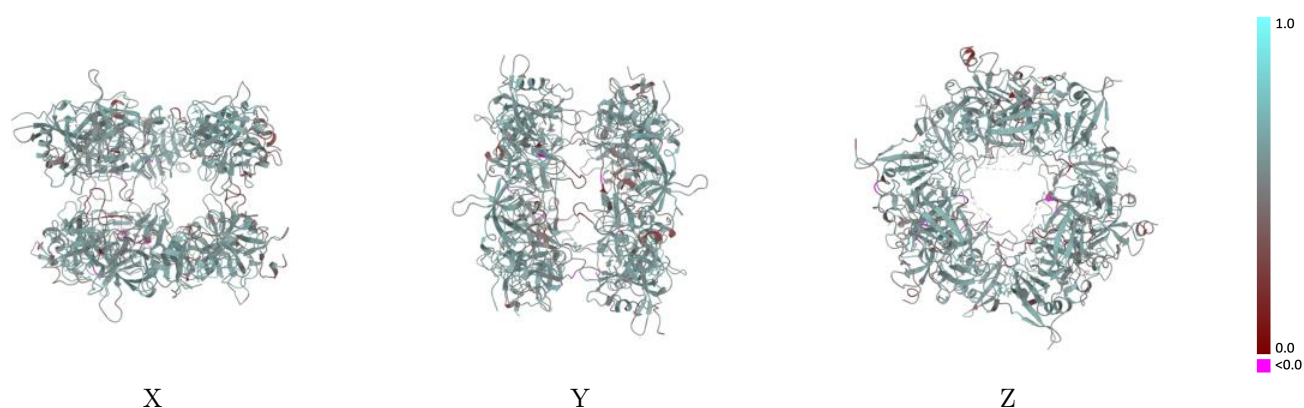
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34607 and PDB model 8HAS. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

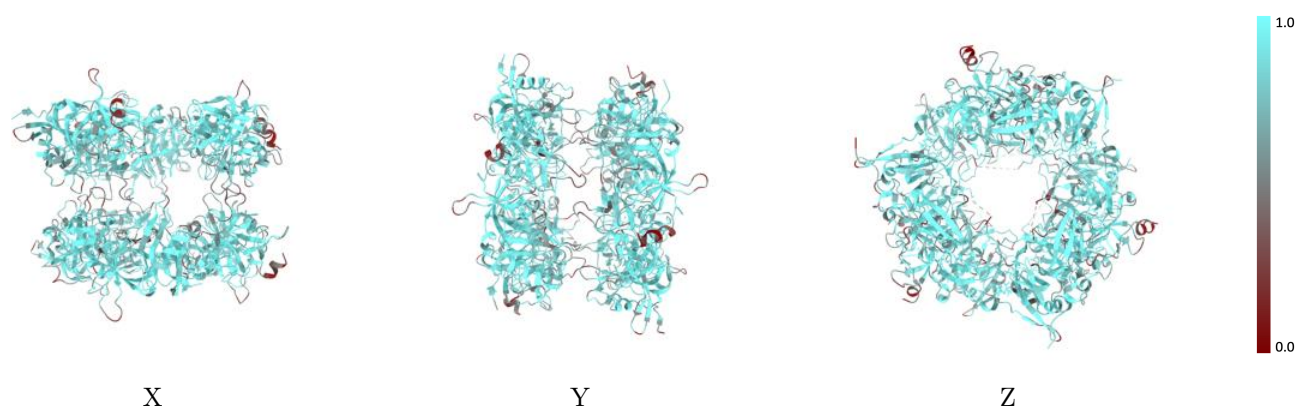
This section was not generated.

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



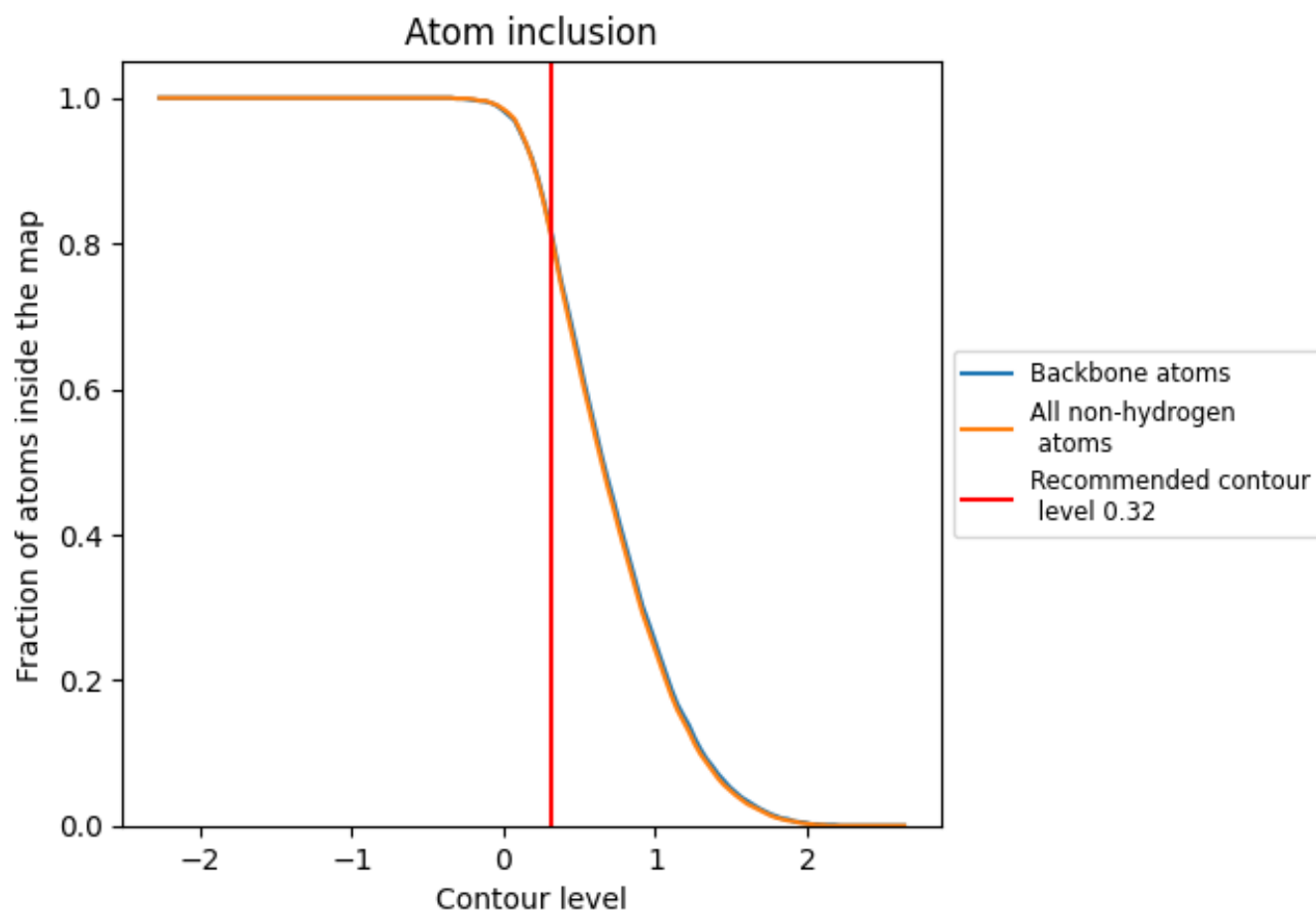
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.32).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 80% 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 (0.32) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8050	0.5430
A	0.8030	0.5430
B	0.8060	0.5440
C	0.7980	0.5420
D	0.8060	0.5450
E	0.8040	0.5390
F	0.8180	0.5430

1.0

0.0

<0.0