



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:27 AM UTC

PDB ID : 9L45 / pdb_00009l45
EMDB ID : EMD-62806
Title : ATR-ATRIP bound with VE-822
Authors : Wang, G.
Deposited on : 2024-12-19
Resolution : 3.95 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:

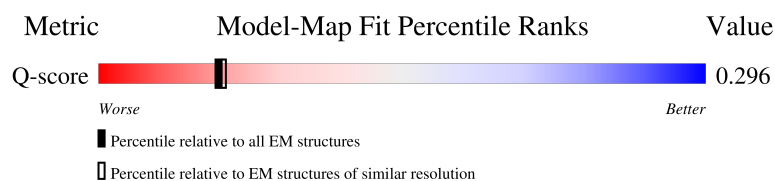
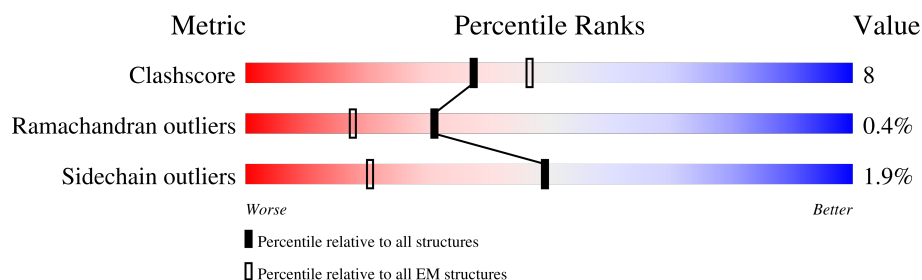
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.95 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	7707 (3.45 - 4.45)

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	2644	
1	B	2644	
2	C	791	
2	D	791	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 54714 atoms, of which 21335 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.

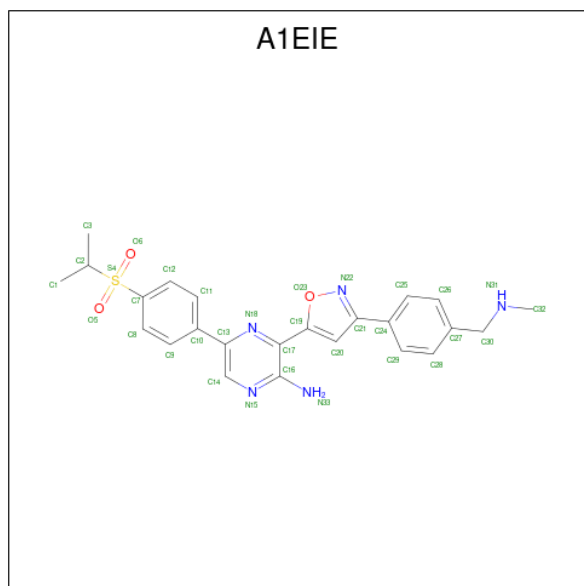
- Molecule 1 is a protein called Serine/threonine-protein kinase ATR.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	2459	Total	C	H	N	O	S	0	0
			24402	8972	9737	2768	2875	50		
1	B	2489	Total	C	H	N	O	S	0	0
			23559	8802	9100	2729	2890	38		

- Molecule 2 is a protein called ATR-interacting protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	D	366	Total	C	H	N	O	S	0	0
			3198	1203	1195	388	399	13		
2	C	380	Total	C	H	N	O	S	0	0
			3409	1258	1291	407	441	12		

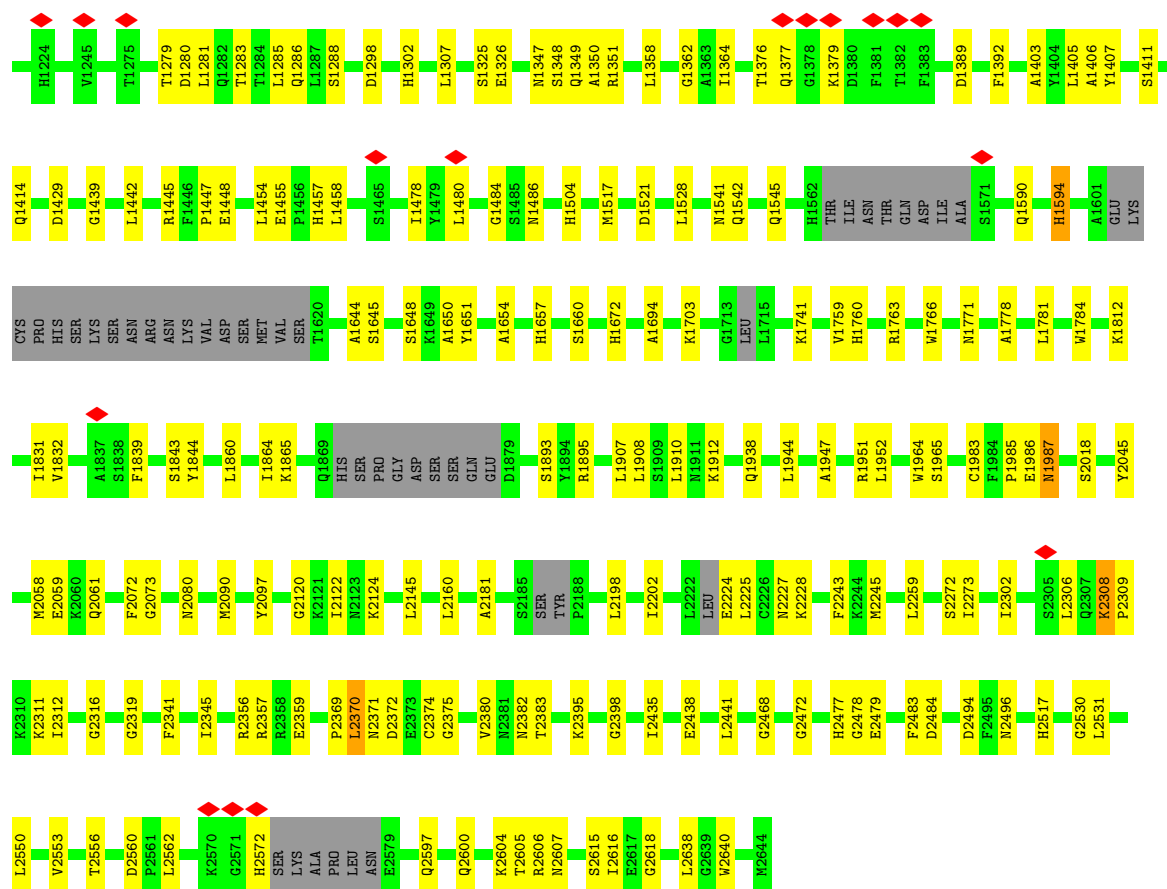
- Molecule 3 is VE-822 (CCD ID: A1EIE) (formula: $C_{24}H_{25}N_5O_3S$) (labeled as "Ligand of Interest" by depositor).



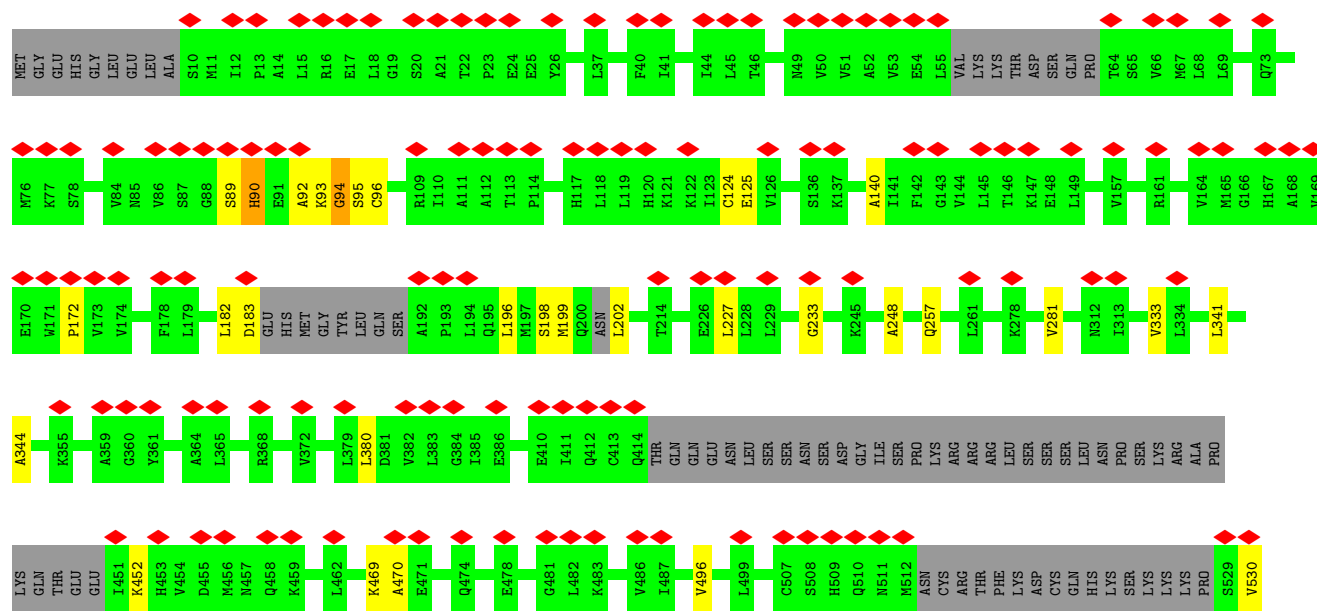
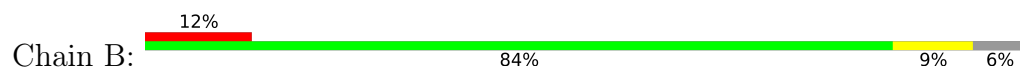
Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	
3	B	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	
3	B	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	
3	B	1	Total	C	H	N	O	S	0
			36	24	3	5	3	1	

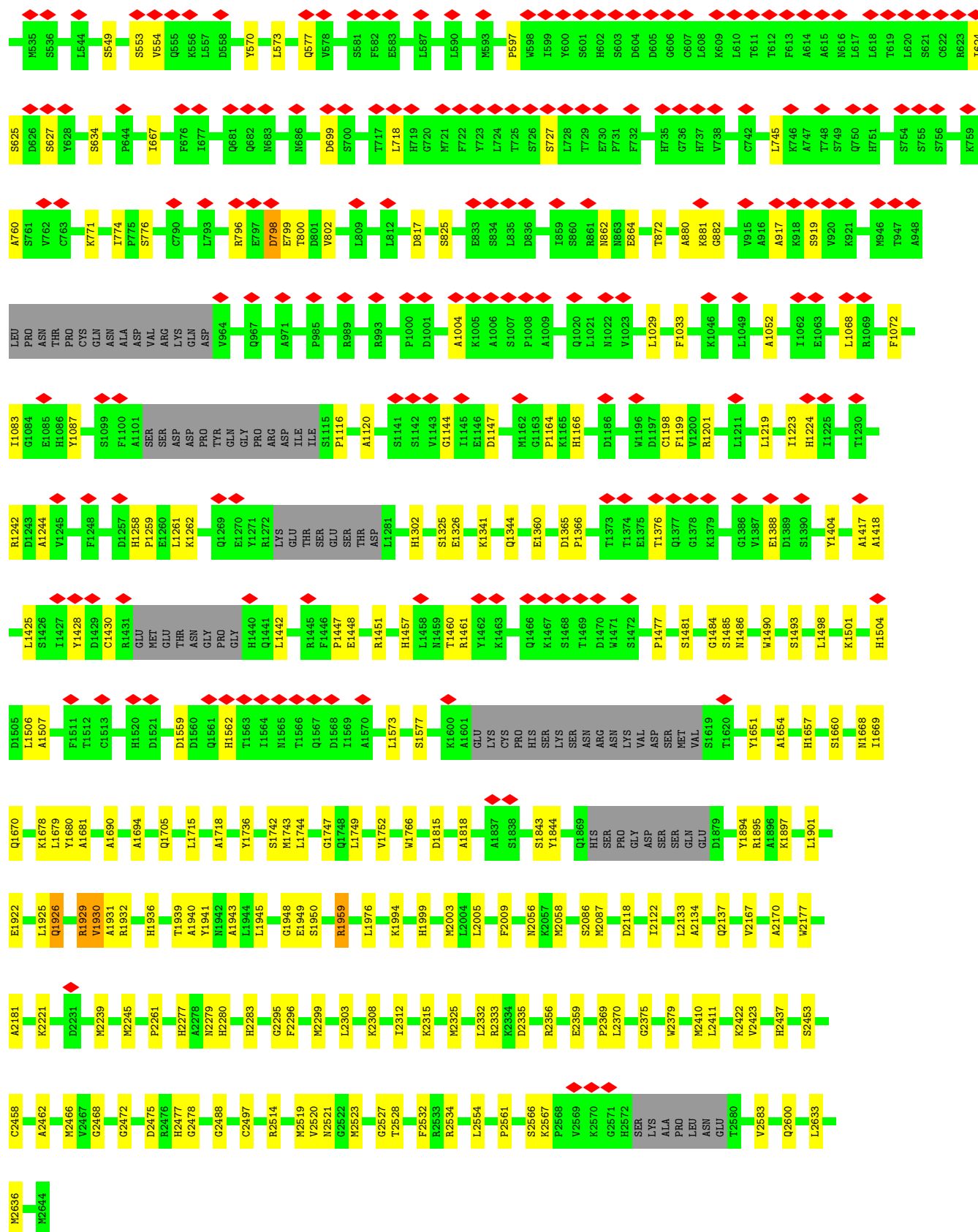
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	D	1	Total	Zn	0
			1	1	
4	C	1	Total	Zn	0
			1	1	

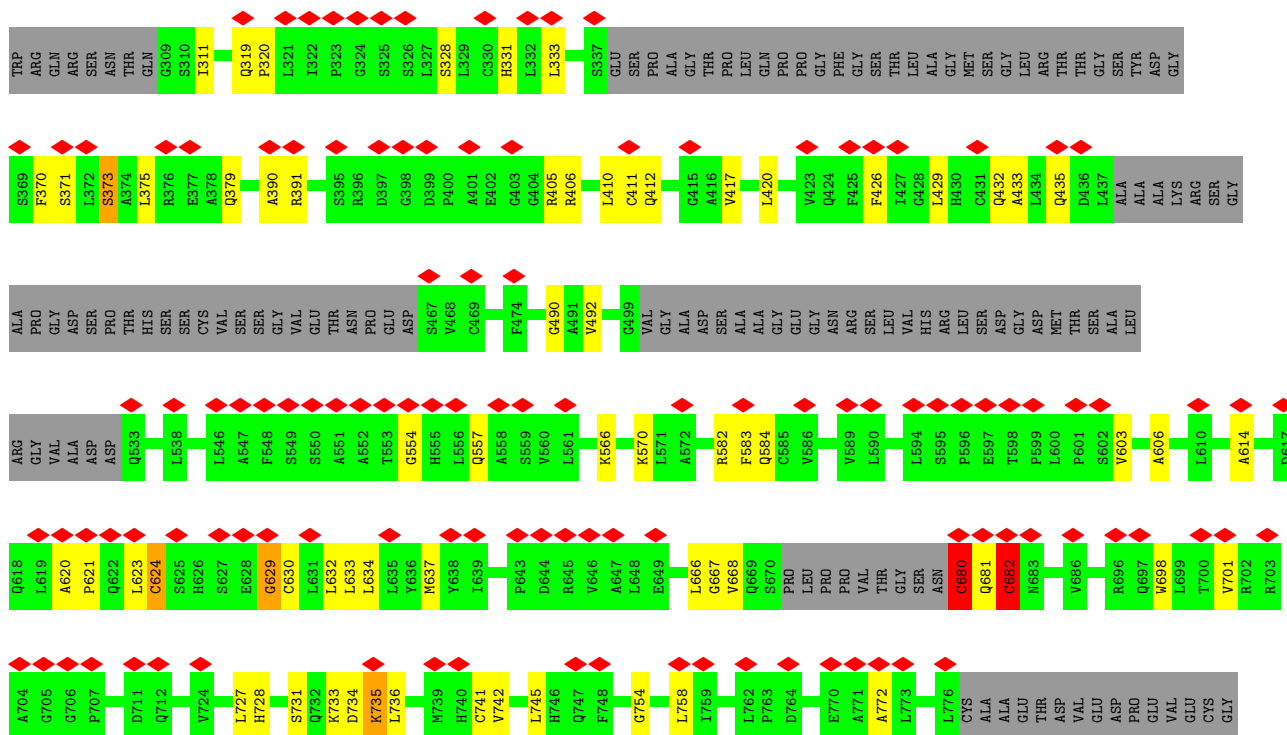
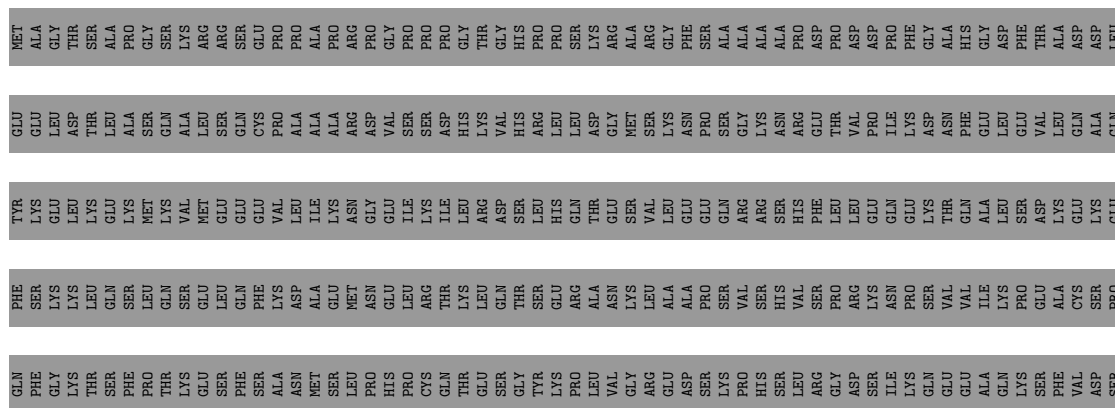


• Molecule 1: Serine/threonine-protein kinase ATR

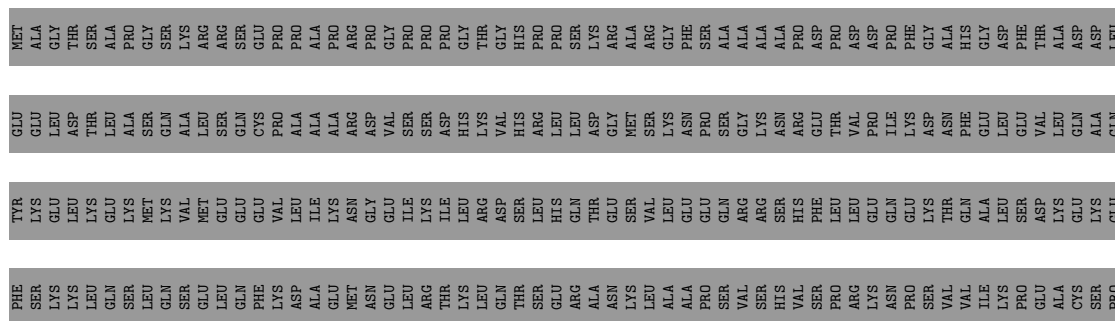




• Molecule 2: ATR-interacting protein



Chain C:



GLN	PHE	GLY	LYS	THR	SER	PHE	PRO	THR	LYS	GLU	SER	PHE	SER	ALA	MET	SER	LEU	PRO	HIS	PRO	CYS	GLN	THR	GLU	SER	GLY	LYS	PRO	LEU	VAL	GLY	ARG	GLY	ASP	SER	ILE	LYS	GLN	GLU	GLU	ALA	GLN	LYS	SER	PHE	VAL	ASP	SER								
TRP	ARG	GLN	ARG	SER	ASN	THR	Q308	P320	L321	I322	P323	G324	S325	S326	L327	S328	L329	C330	H331	L332	L333	S334	S335	S336	S337	E338	S339	PRO	ALA	GLY	THR	PRO	LEU	GLN	PRO	PRO	GLY	PHE	SER	THR	LEU	ALA	GLY	MET	SER	GLY	LEU	ARG	THR	GLY	VAL	THR	SER	ASP	G368	S369
A378	Q379	A382	C385	V389	A390	R391	N392	E393	D397	G398	D399	R405	R406	A407	G415	F419	L422	A433	L437	A438	A439	A440	R441	ARG	SER	GLY	ALA	PRO	GLY	PRO	GLY	ASP	SER	THR	PRO	HIS	SER	SER	CYS	VAL	SER	SER	GLY	VAL	THR	GLU	THR	ASN	P464	S467						
E472	H484	L485	H488	C499	V500	G501	ALA	ASP	SER	ALA	ALA	GLY	GLU	GLY	ASN	ARG	SER	LEU	VAL	ARG	LEU	SER	ASP	GLY	ASP	THR	SER	ALA	LEU	ARG	GLY	VAL	ALA	ASP	GLN	G534	A547	F548	S549	S550	A551	A552	T553	G554	H555	A558	S559	T562	Q563	C564						
L565	K566	K570	V586	S595	P596	E597	T598	A620	P621	Q622	L623	C624	S627	E628	G629	C630	L631	L632	M637	P643	D644	R645	Q651	L666	G667	V668	Q669	PRO	PRO	PRO	VAL	THR	GLY	SER	N679	C680	G681	C682	V687	Q697	R703	A704	G705	G706	P707											
P708	R709	T710	D711	R714	R715	T716	V717	R718	L725	G729	L730	S731	H740	C741	V744	Q747	P763	D764	E769	E770	A771	A772	L773	L776	C777	A778	ALA	GLU	THR	ASP	VAL	GLU	ASP	PRO	GLU	VAL	GLU	CYS	GLY																	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66141	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.595	Depositor
Minimum map value	-0.747	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.067	Depositor
Recommended contour level	0.255	Depositor
Map size (Å)	308.16, 308.16, 308.16	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: A1EIE, ZN

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	0.46	21/14824 (0.1%)	0.55	22/20386 (0.1%)
1	B	0.40	10/14600 (0.1%)	0.52	13/20134 (0.1%)
2	C	0.56	3/2126 (0.1%)	0.87	12/2926 (0.4%)
2	D	0.52	0/2011	0.97	7/2774 (0.3%)
All	All	0.45	34/33561 (0.1%)	0.60	54/46220 (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	A	0	2
1	B	0	3
2	C	0	2
2	D	0	1
All	All	0	8

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1594	HIS	ND1-CE1	5.40	1.38	1.32
1	B	1224	HIS	ND1-CE1	5.39	1.38	1.32
1	B	2437	HIS	ND1-CE1	5.38	1.38	1.32
1	A	2572	HIS	ND1-CE1	5.33	1.37	1.32
1	A	160	HIS	ND1-CE1	5.33	1.37	1.32

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	708	PRO	N-CA-CB	-17.19	85.20	103.25
2	D	680	CYS	CB-CA-C	-17.01	77.78	110.10
1	B	1930	VAL	N-CA-C	-10.98	102.77	113.53
2	C	628	GLU	N-CA-C	-10.59	96.55	110.53
2	D	682	CYS	CB-CA-C	-10.27	93.74	110.79

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2496	ASN	Mainchain
1	A	797	GLU	Peptide
1	B	1929	ARG	Sidechain
1	B	1959	ARG	Sidechain
1	B	796	ARG	Sidechain

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	14665	9737	9833	195	0
1	B	14459	9100	9181	152	0
2	C	2118	1291	1311	38	0
2	D	2003	1195	1203	36	0
3	A	33	3	0	0	0
3	B	99	9	0	5	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	33379	21335	21528	414	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 8.

The worst 5 of 414 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:C:378:ALA:HB1	2:C:422:LEU:HA	1.36	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:896:LEU:HA	1:A:904:SER:HA	1.57	0.85
1:B:1430:CYS:HA	1:B:1442:LEU:CB	2.10	0.82
1:B:281:VAL:HA	1:B:333:VAL:CB	2.10	0.80
2:C:630:CYS:CB	2:C:682:CYS:HB3	2.11	0.80

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	2429/2644 (92%)	2300 (95%)	126 (5%)	3 (0%)	48	81
1	B	2463/2644 (93%)	2345 (95%)	109 (4%)	9 (0%)	30	65
2	C	370/791 (47%)	346 (94%)	19 (5%)	5 (1%)	9	39
2	D	356/791 (45%)	327 (92%)	25 (7%)	4 (1%)	11	44
All	All	5618/6870 (82%)	5318 (95%)	279 (5%)	21 (0%)	31	65

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	603	SER
1	A	1986	GLU
1	B	90	HIS
1	B	1668	ASN
2	D	371	SER

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	717/2363 (30%)	708 (99%)	9 (1%)	61	72
1	B	621/2363 (26%)	613 (99%)	8 (1%)	61	72
2	C	91/678 (13%)	88 (97%)	3 (3%)	33	56
2	D	74/678 (11%)	65 (88%)	9 (12%)	5	21
All	All	1503/6082 (25%)	1474 (98%)	29 (2%)	49	67

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1929	ARG
2	C	570	LYS
2	D	311	ILE
2	D	680	CYS
1	B	1959	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2559	HIS
2	C	563	GLN
1	B	788	HIS
1	B	1349	GLN
1	B	1672	HIS

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

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	A1EIE	B	2701	-	36,36,36	0.41	1 (2%)	45,52,52	0.44	1 (2%)
3	A1EIE	B	2703	-	36,36,36	0.37	0	45,52,52	0.40	0
3	A1EIE	A	2701	-	36,36,36	0.40	0	45,52,52	0.52	1 (2%)
3	A1EIE	B	2702	-	36,36,36	0.38	0	45,52,52	0.52	1 (2%)

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
3	A1EIE	B	2701	-	-	14/27/27/27	0/4/4/4
3	A1EIE	B	2703	-	-	15/27/27/27	0/4/4/4
3	A1EIE	A	2701	-	-	8/27/27/27	0/4/4/4
3	A1EIE	B	2702	-	-	7/27/27/27	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2701	A1EIE	C30-N31	2.03	1.49	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2701	A1EIE	C19-C17-N18	-2.54	110.10	115.55
3	B	2702	A1EIE	C19-C17-N18	-2.40	110.41	115.55
3	B	2701	A1EIE	C19-C17-N18	-2.15	110.95	115.55

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

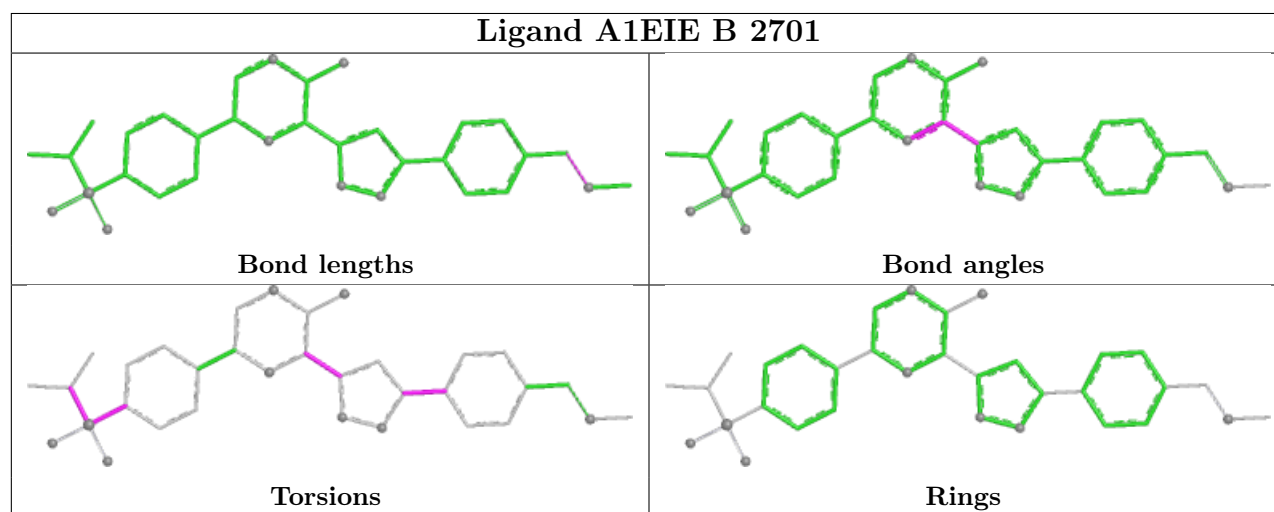
Mol	Chain	Res	Type	Atoms
3	A	2701	A1EIE	N18-C17-C19-O23
3	A	2701	A1EIE	C1-C2-S4-C7
3	A	2701	A1EIE	C1-C2-S4-O5
3	A	2701	A1EIE	C1-C2-S4-O6
3	A	2701	A1EIE	C3-C2-S4-C7

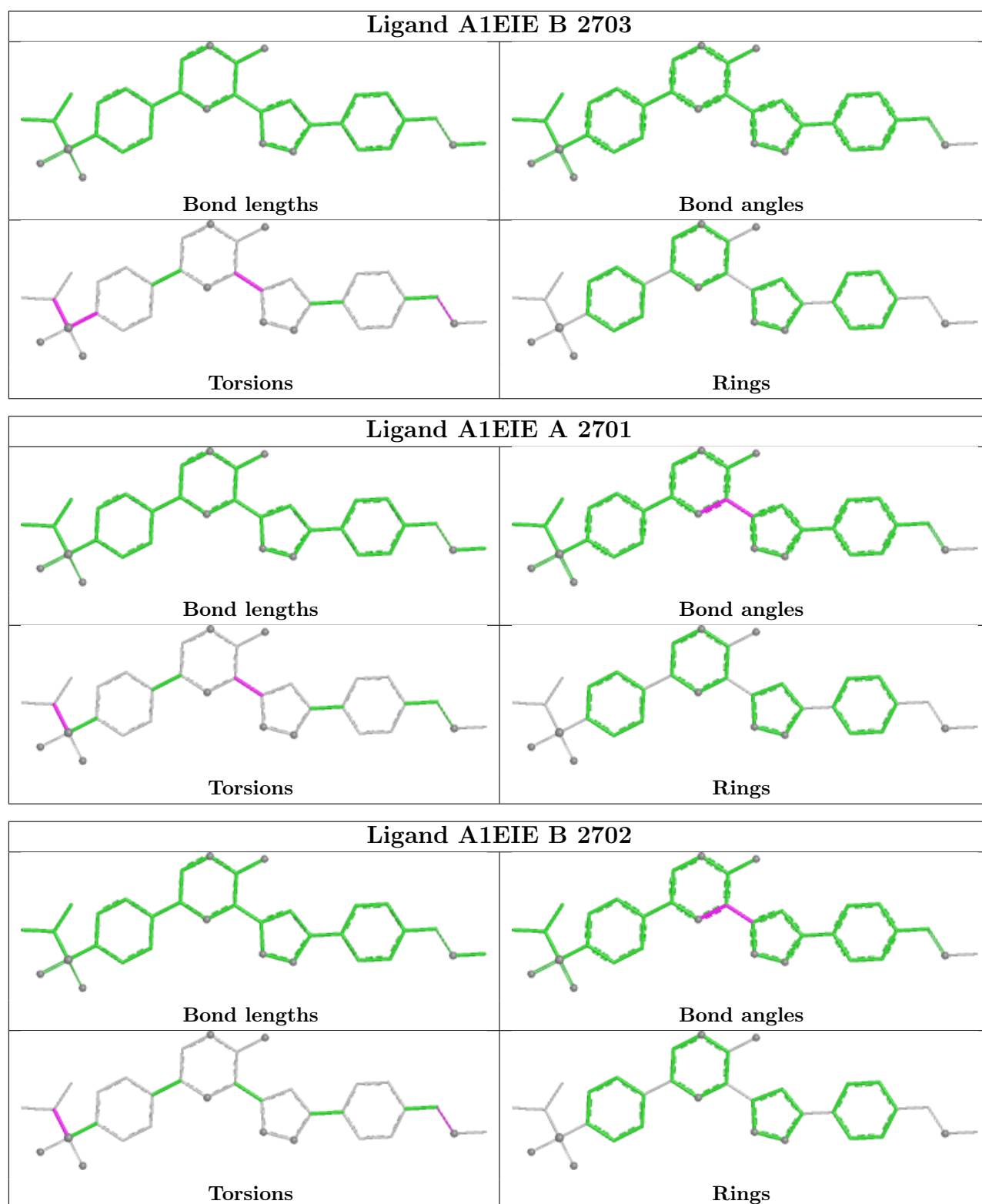
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2701	A1EIE	2	0
3	B	2703	A1EIE	3	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

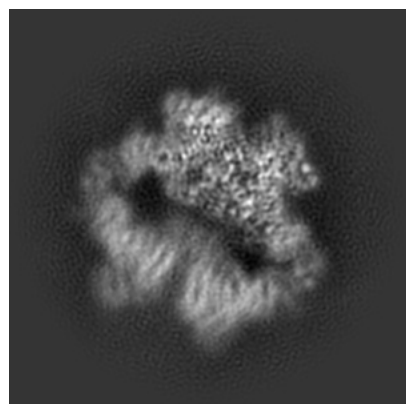
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62806. These allow visual inspection of the internal detail of the map and identification of artifacts.

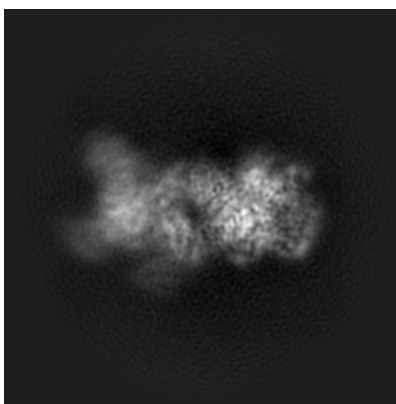
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

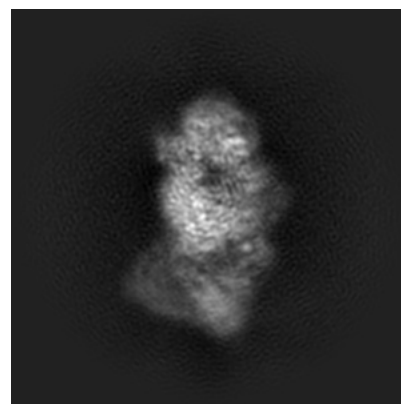
6.1.1 Primary map



X

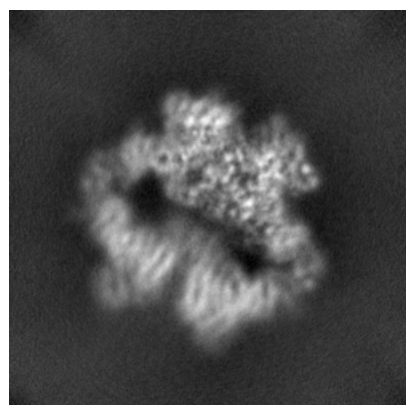


Y

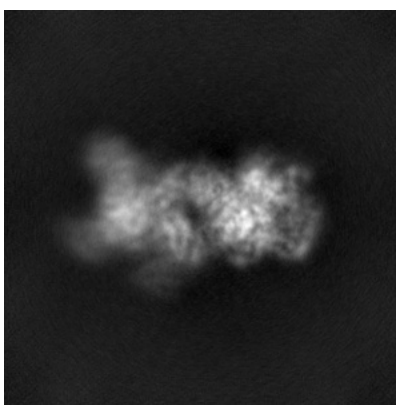


Z

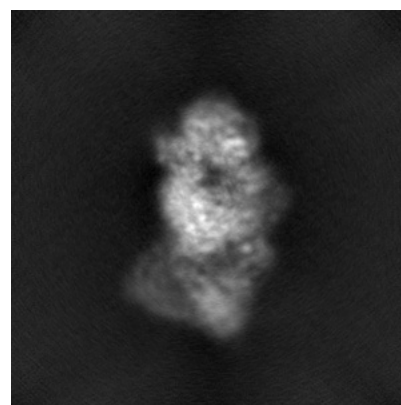
6.1.2 Raw map



X



Y

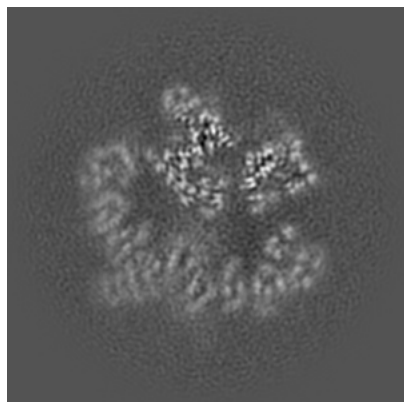


Z

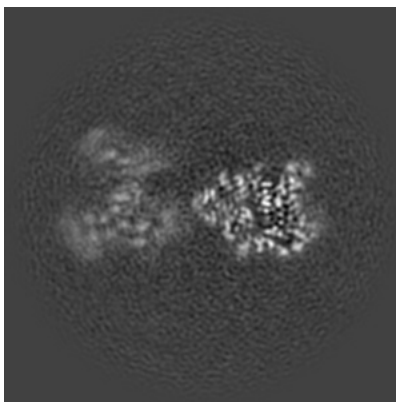
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

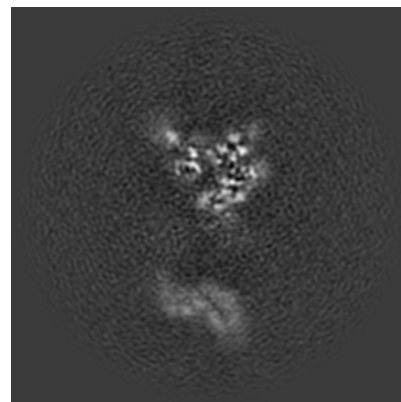
6.2.1 Primary map



X Index: 144

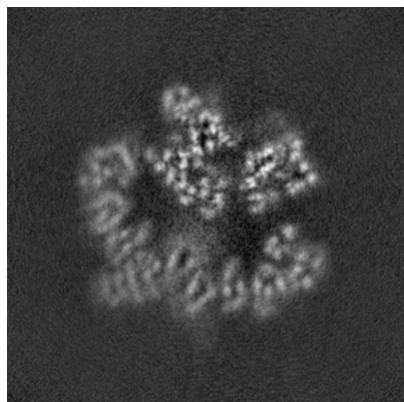


Y Index: 144

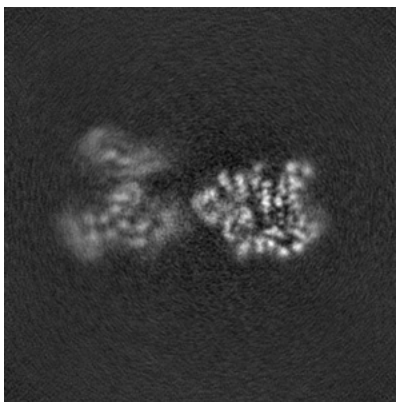


Z Index: 144

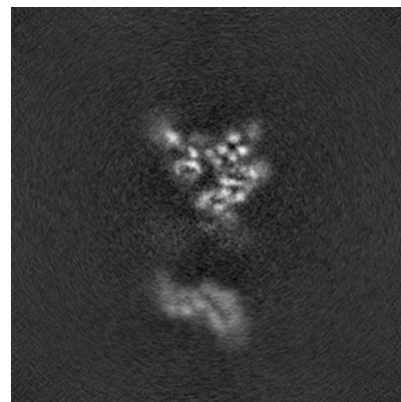
6.2.2 Raw map



X Index: 144



Y Index: 144

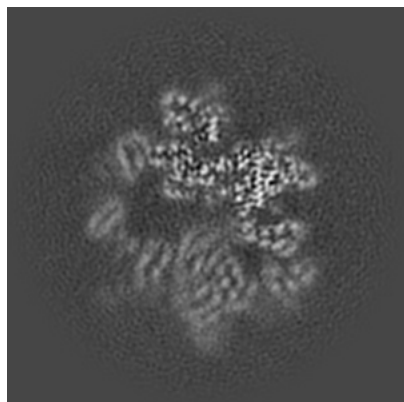


Z Index: 144

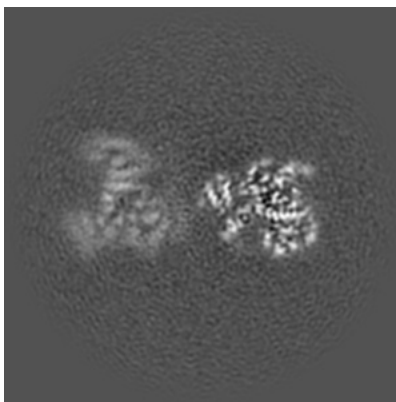
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

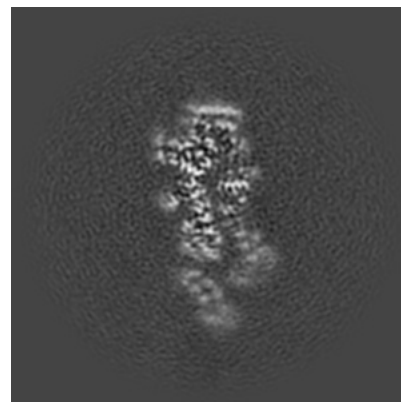
6.3.1 Primary map



X Index: 133

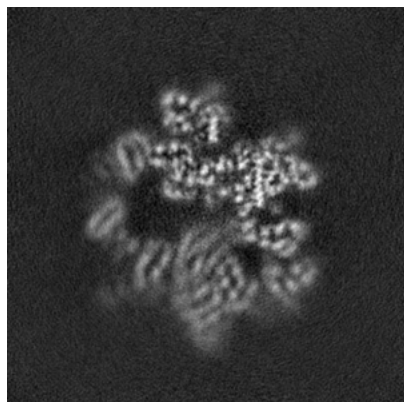


Y Index: 139

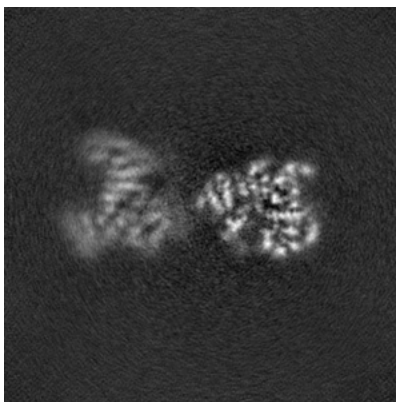


Z Index: 173

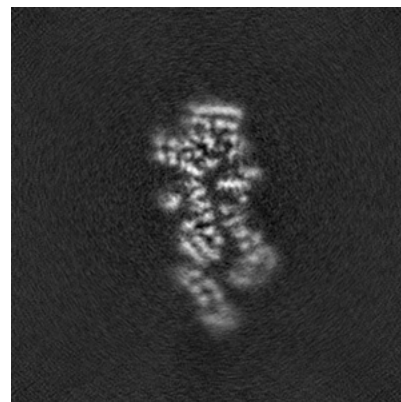
6.3.2 Raw map



X Index: 133



Y Index: 140

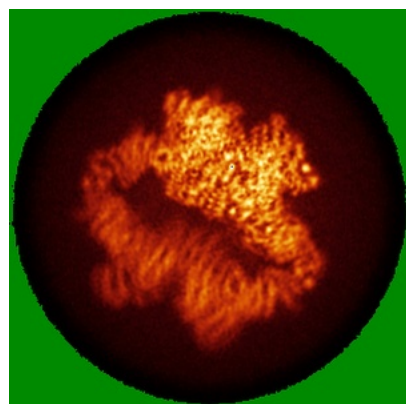


Z Index: 174

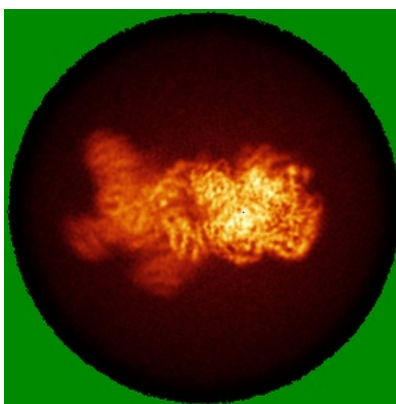
The images above show the largest variance slices of the map in three orthogonal directions.

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

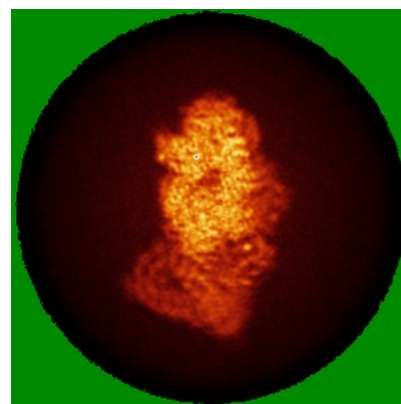
6.4.1 Primary map



X

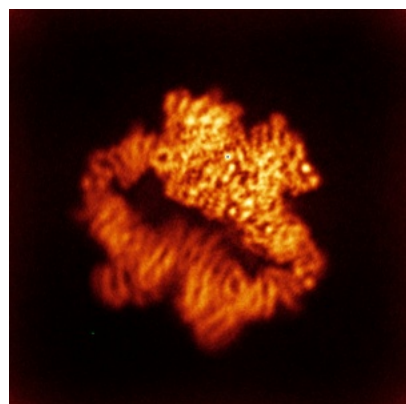


Y

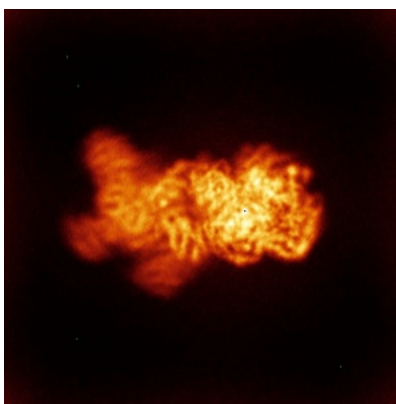


Z

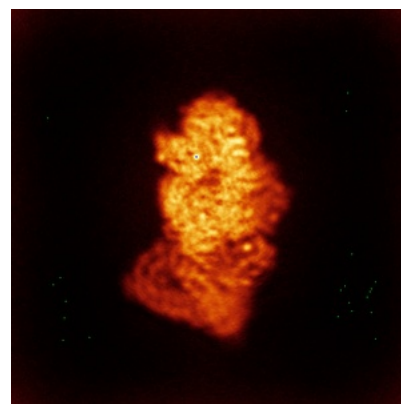
6.4.2 Raw map



X



Y

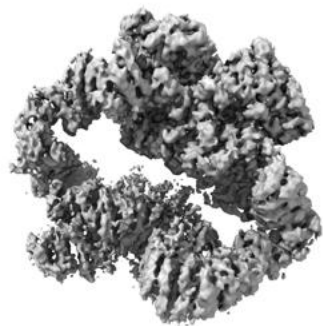


Z

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



X



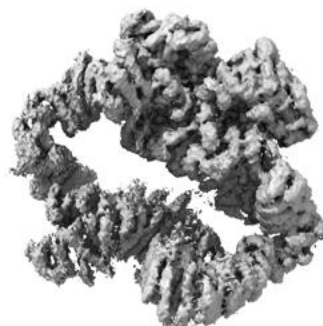
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.255. 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



X



Y



Z

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.

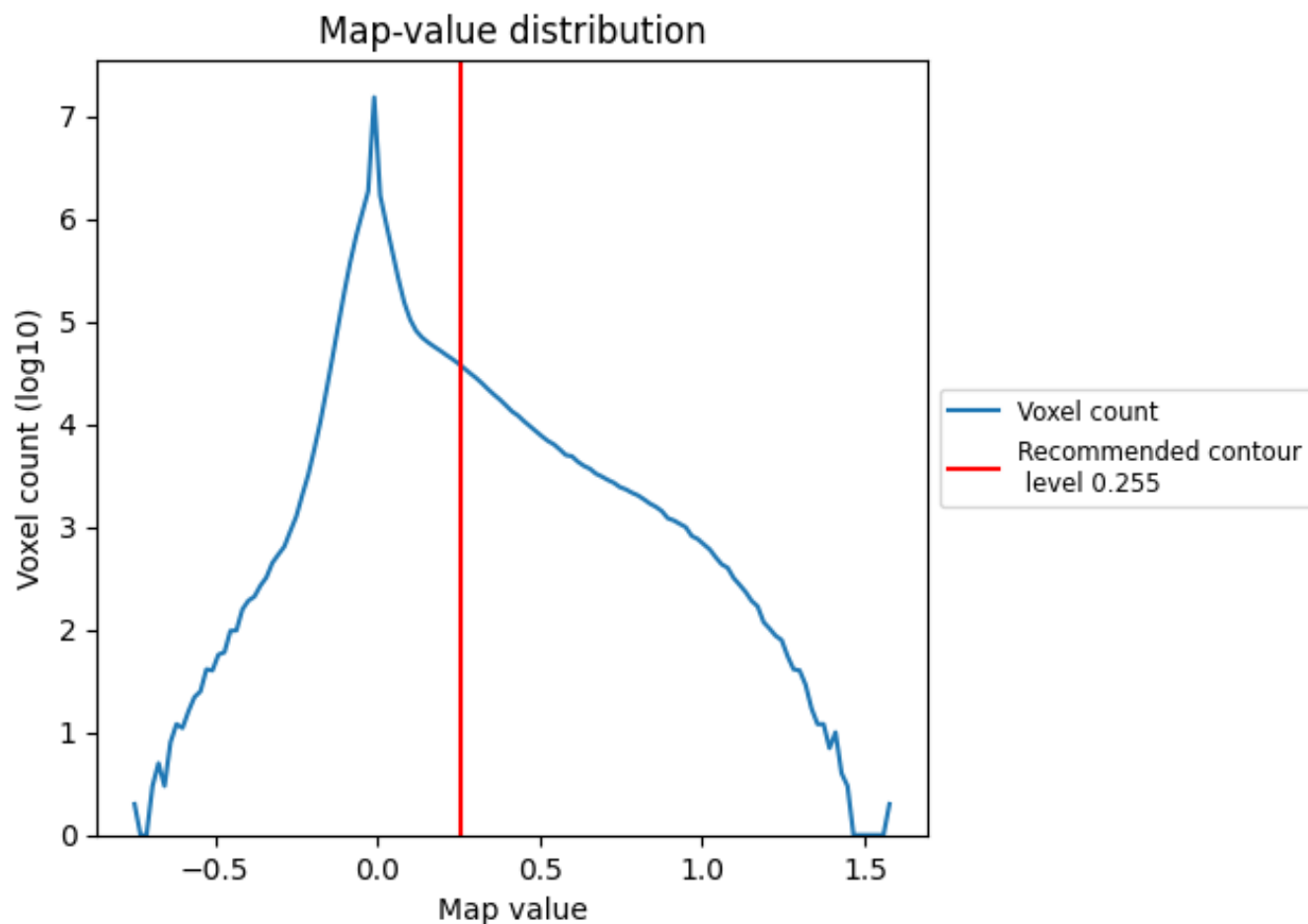
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

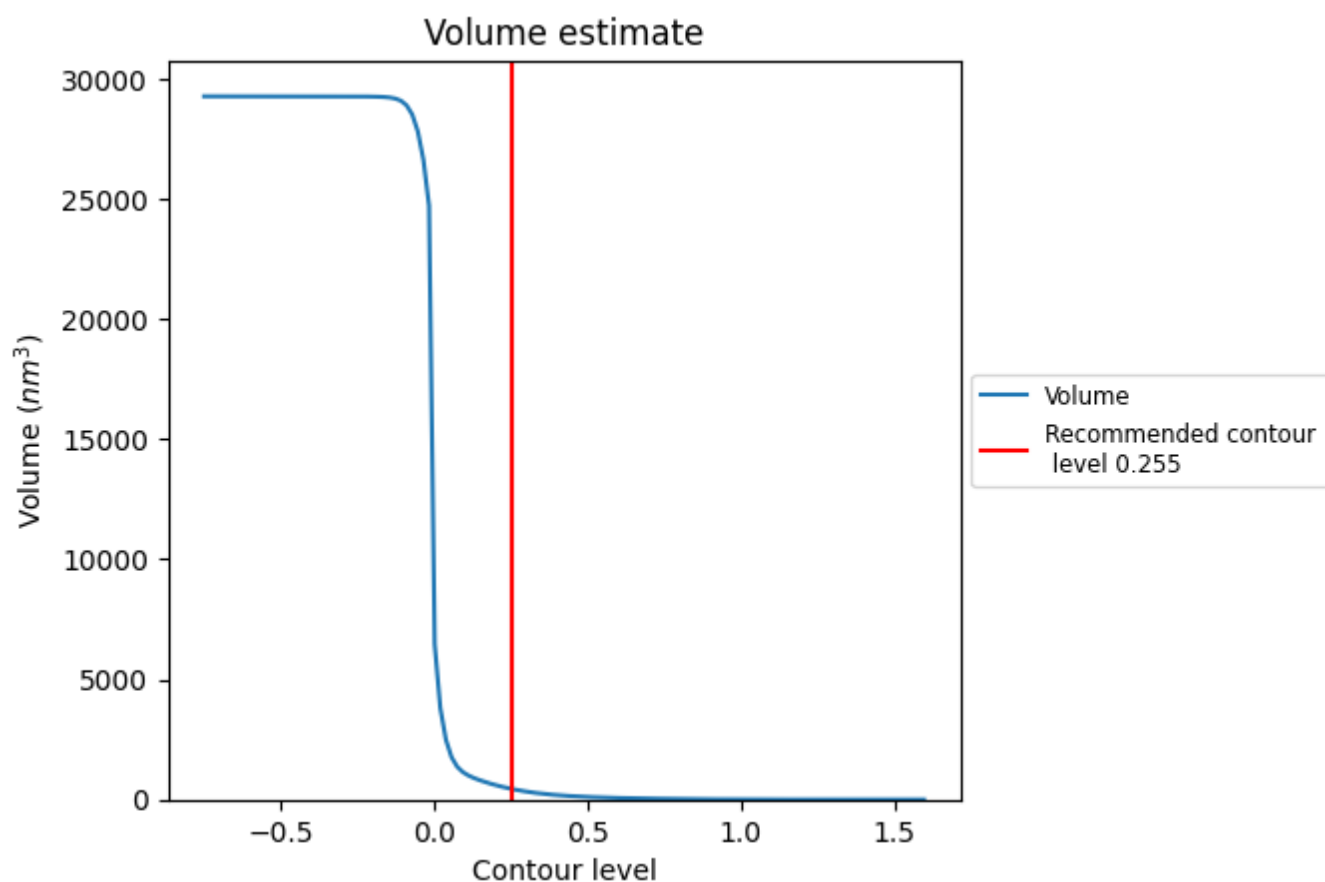
This section contains the results of statistical analysis of the map.

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.

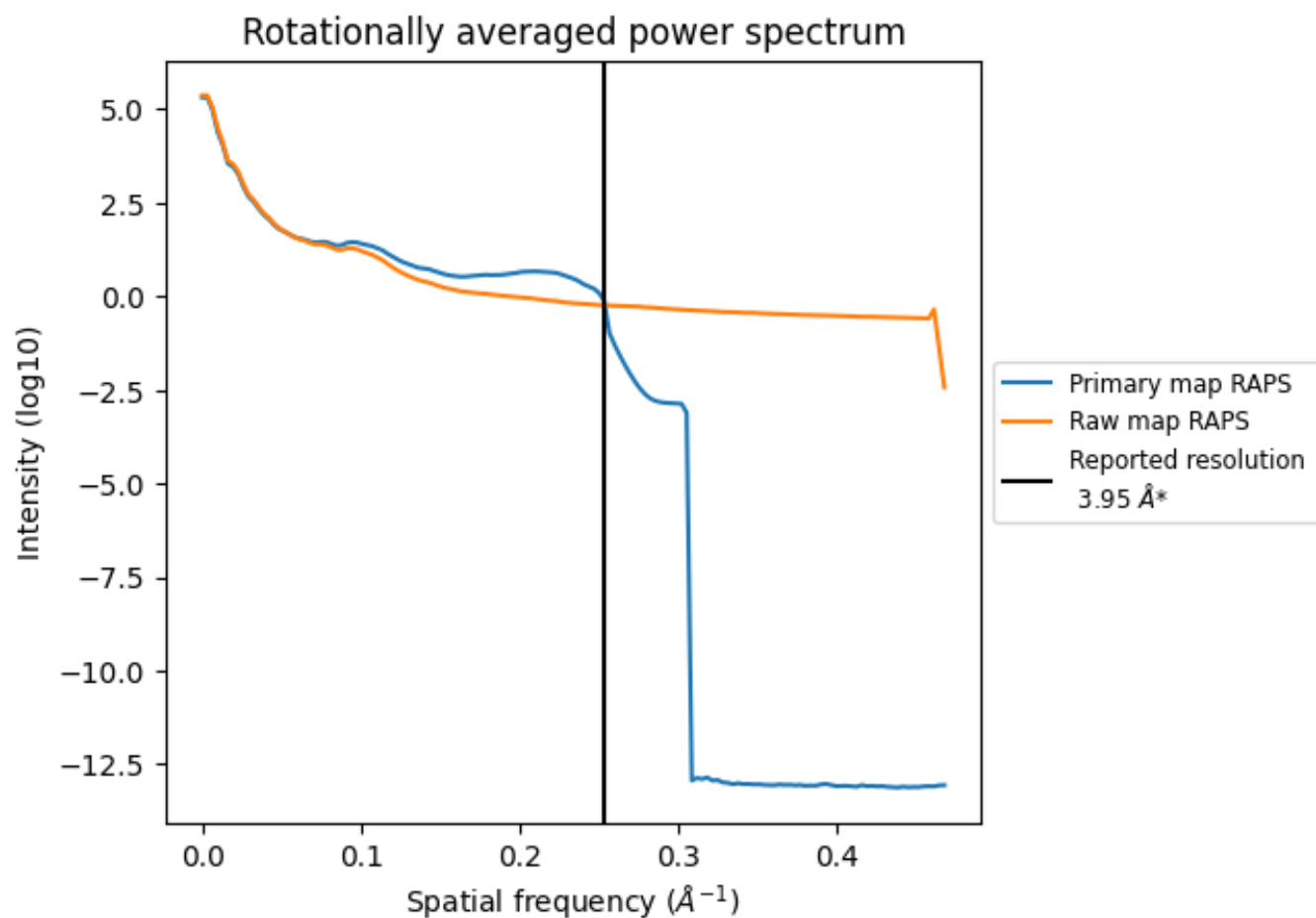
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 438 nm³; this corresponds to an approximate mass of 396 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 ⓘ

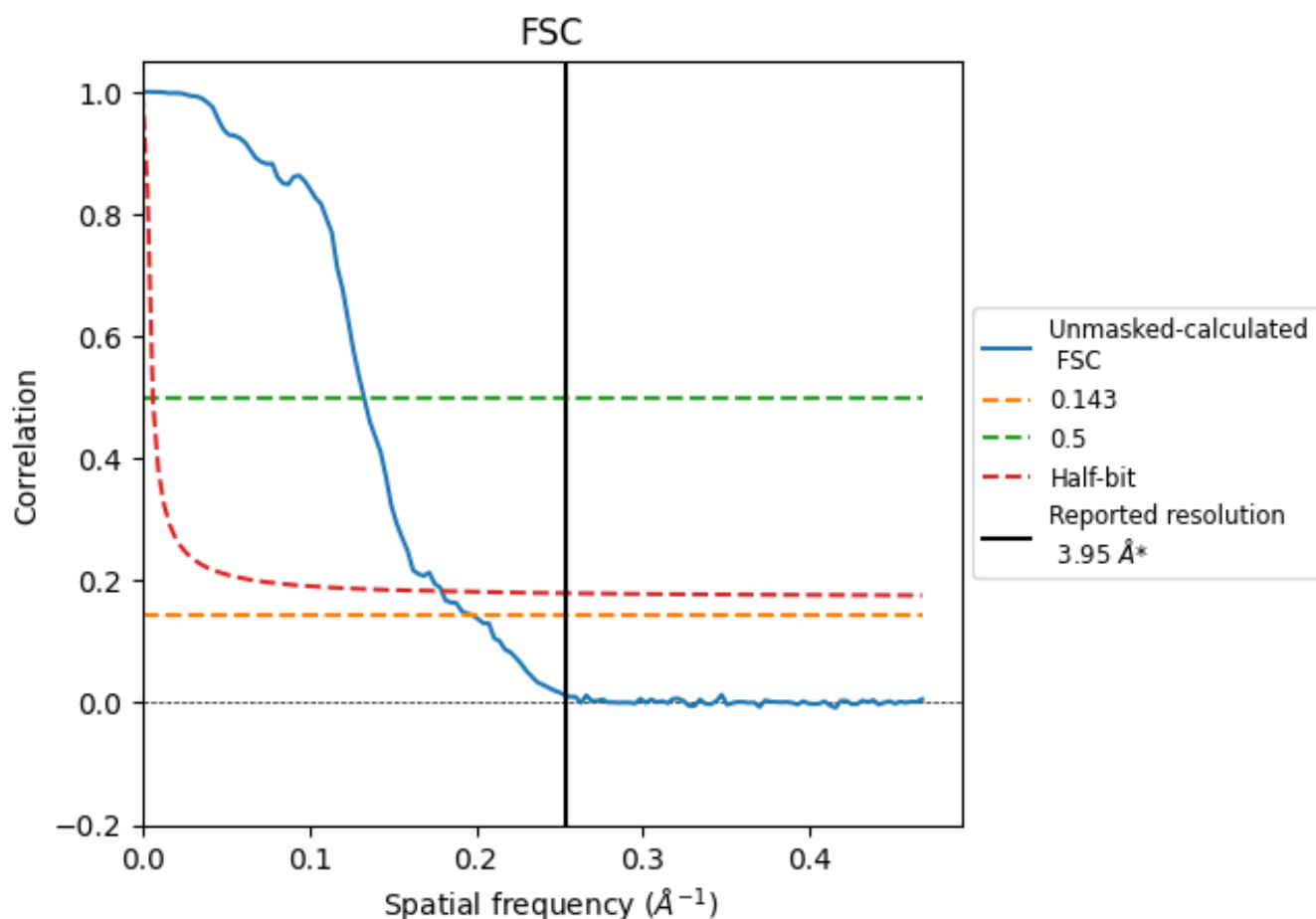


*Reported resolution corresponds to spatial frequency of 0.253 Å⁻¹

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 0.253 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

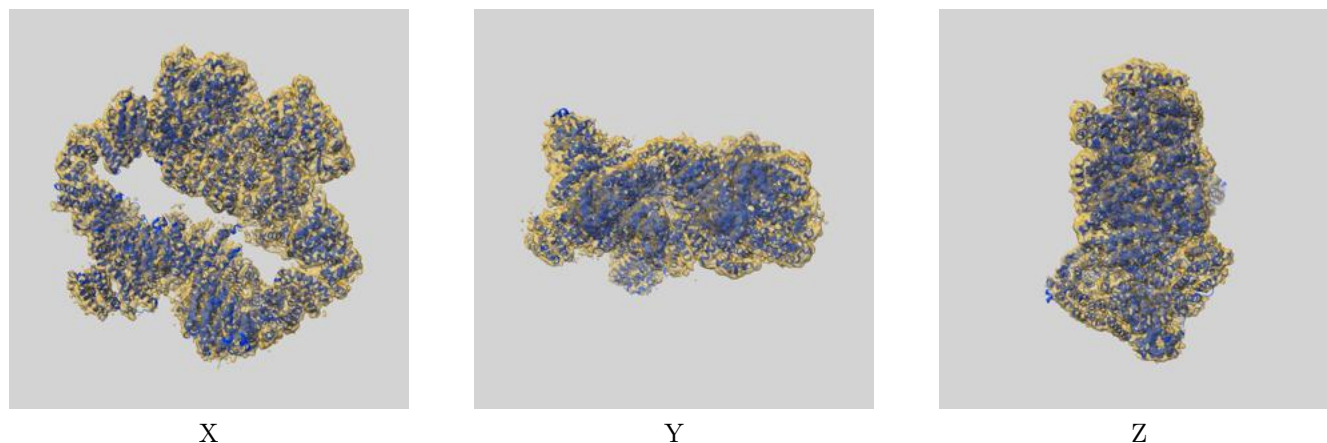
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.95	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.05	7.52	5.57

*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 5.05 differs from the reported value 3.95 by more than 10 %

9 Map-model fit [i](#)

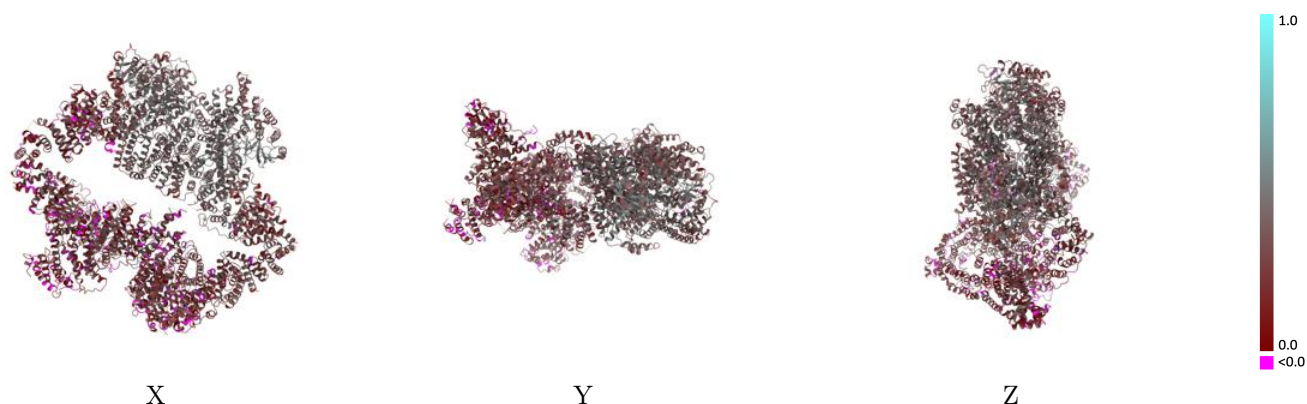
This section contains information regarding the fit between EMDB map EMD-62806 and PDB model 9L45. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.255 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](#)

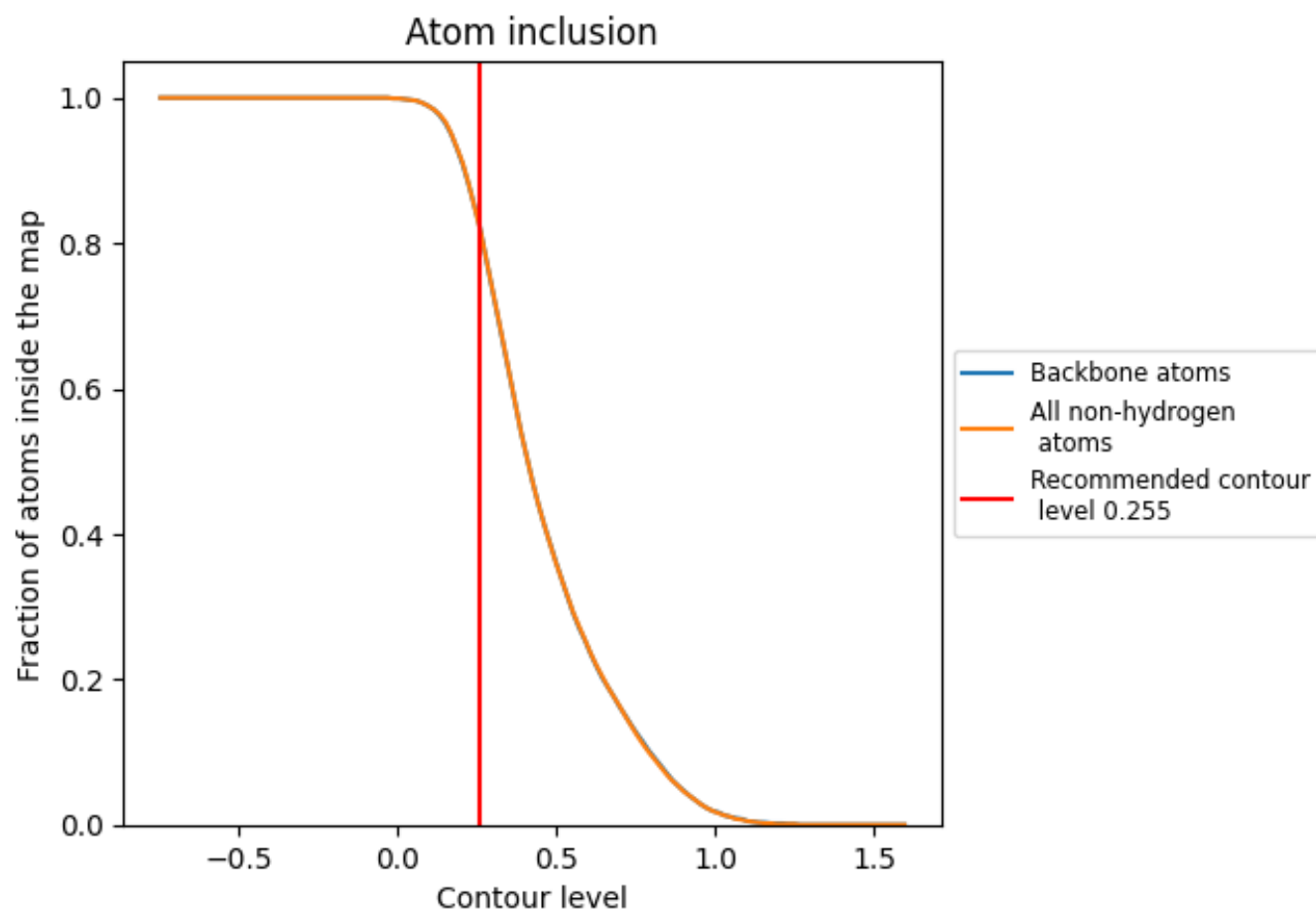


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 83% 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 (0.255) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8270	0.2960
A	0.8820	0.3240
B	0.8150	0.2950
C	0.7110	0.2070
D	0.6090	0.1930

