



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 08:54 PM UTC

PDB ID : 8RG7 / pdb_00008rg7
EMDB ID : EMD-19130
Title : BmrA E504-R6G-25uMATP-Mg
Authors : Gobet, A.; Zarkadas, E.; Schoehn, G.; Falson, P.; Chaptal, V.
Deposited on : 2023-12-13
Resolution : 3.90 Å(reported)
Based on initial model : 6r81

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

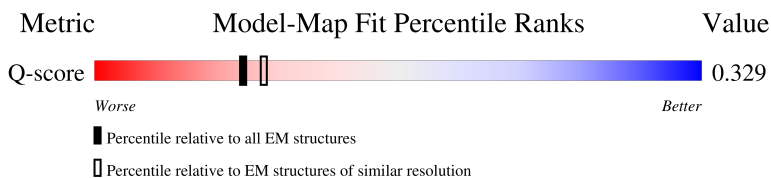
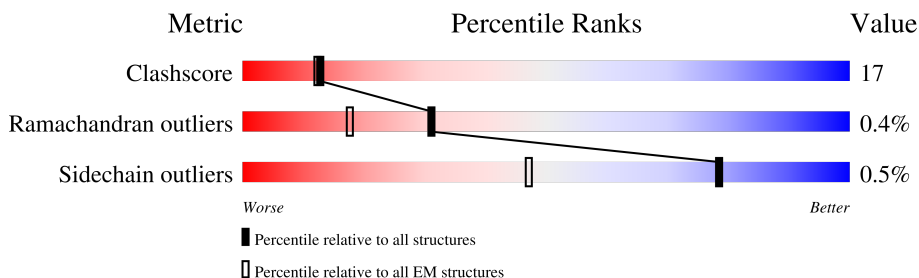
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	8855 (3.40 - 4.40)

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	599	
1	B	599	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8868 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.

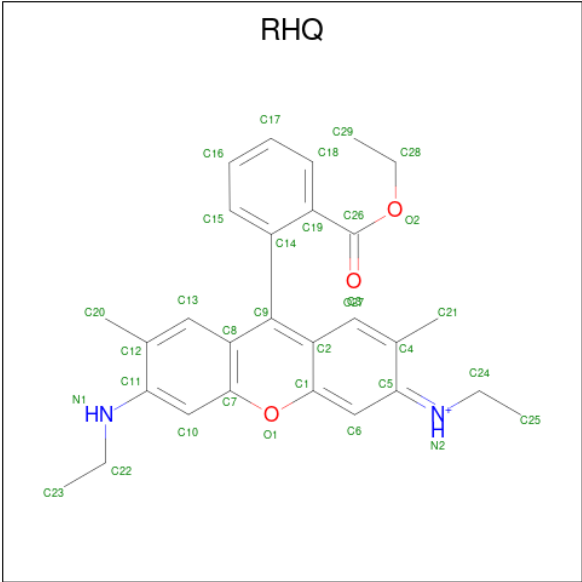
- Molecule 1 is a protein called Multidrug resistance ABC transporter ATP-binding/permease protein BmrA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	572	Total	C	N	O	S	0	0
			4401	2825	734	824	18		
1	B	572	Total	C	N	O	S	0	0
			4401	2825	734	824	18		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	initiating methionine	UNP O06967
A	-8	SER	-	expression tag	UNP O06967
A	-7	SER	-	expression tag	UNP O06967
A	-6	SER	-	expression tag	UNP O06967
A	-5	HIS	-	expression tag	UNP O06967
A	-4	HIS	-	expression tag	UNP O06967
A	-3	HIS	-	expression tag	UNP O06967
A	-2	HIS	-	expression tag	UNP O06967
A	-1	HIS	-	expression tag	UNP O06967
A	0	HIS	-	expression tag	UNP O06967
A	504	ALA	GLU	engineered mutation	UNP O06967
B	-9	MET	-	initiating methionine	UNP O06967
B	-8	SER	-	expression tag	UNP O06967
B	-7	SER	-	expression tag	UNP O06967
B	-6	SER	-	expression tag	UNP O06967
B	-5	HIS	-	expression tag	UNP O06967
B	-4	HIS	-	expression tag	UNP O06967
B	-3	HIS	-	expression tag	UNP O06967
B	-2	HIS	-	expression tag	UNP O06967
B	-1	HIS	-	expression tag	UNP O06967
B	0	HIS	-	expression tag	UNP O06967
B	504	ALA	GLU	engineered mutation	UNP O06967

- Molecule 2 is RHODAMINE 6G (CCD ID: RHQ) (formula: C₂₈H₃₁N₂O₃).

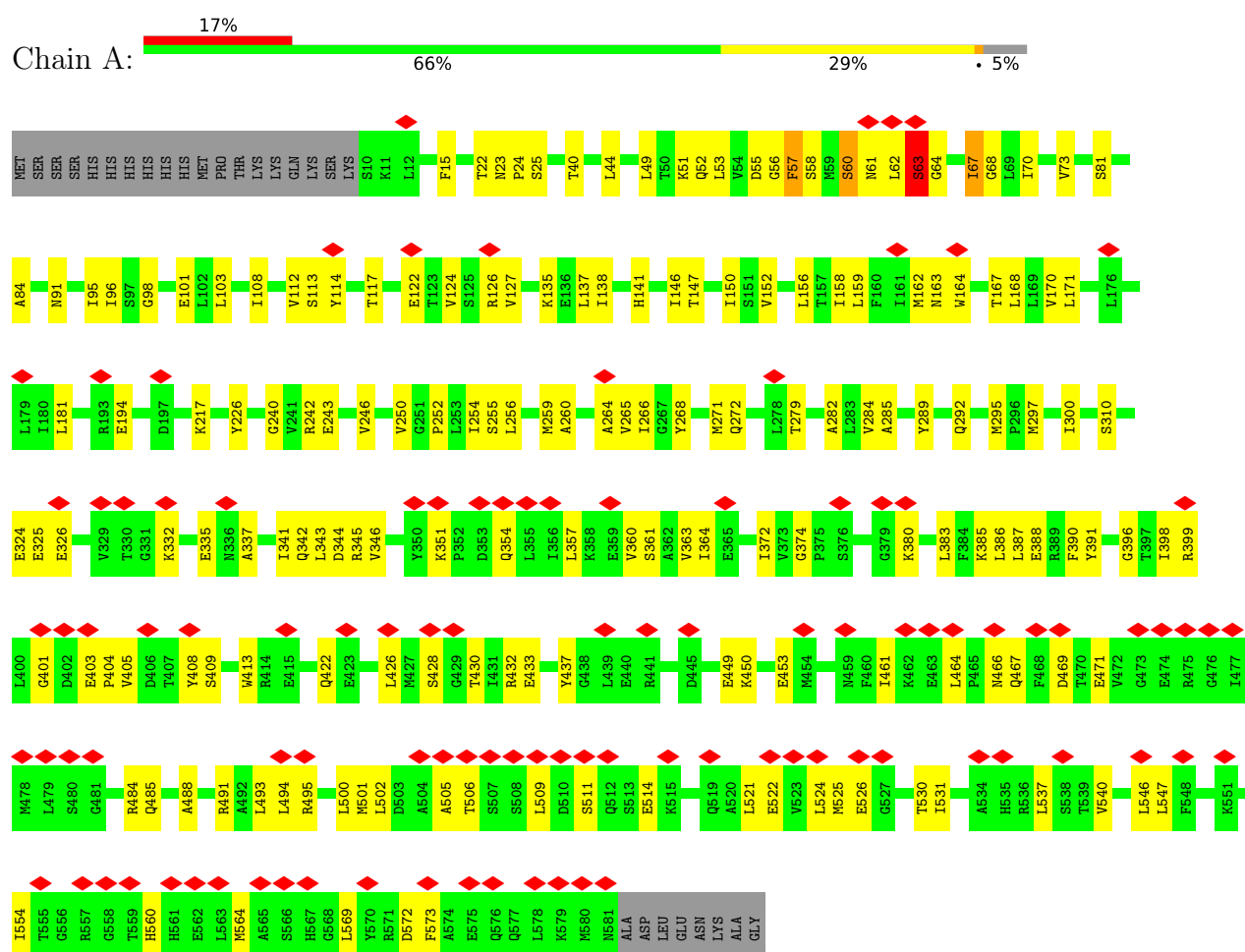


Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			33	28	2	3	
2	B	1	Total	C	N	O	0
			33	28	2	3	

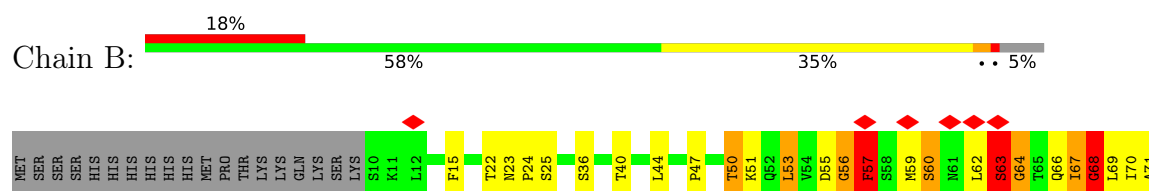
3 Residue-property plots

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: Multidrug resistance ABC transporter ATP-binding/permease protein BmrA



- Molecule 1: Multidrug resistance ABC transporter ATP-binding/permease protein BmrA



G568	L569	Y570	R571	D572	F573	A574	E575	Q576	Q577	L578	X579	M580	N581	ALA	ASP	LEU	GLU	ASN	LYS	ALA	GLY																																		
A504	A505	T506	S507	S508	L509	D510	S511	Q512	S513	E514	K515	S516	Q519	A520	L521	E522	V523	L524	N525	E526	G527	R528	T529	T530	L531	V532	L533	A534	H535	R536	L537	S538	T539	V540	V541	D542	A543	D544	L547	F548	V549	E550	K551	Q552	E553	I554	R557	G558	T559	H560	H561	E562	A565	S566	H567
C436	Y437	G438	L439	E440	R441	D442	V443	T444	D445	A446	E447	E453	M454	A457	L458	N459	F460	I461	K462	E463	L464	Q467	F468	D469	T470	E471	V472	G473	E474	R475	G476	I477	M478	L479	S480	R484	Q485	R486	I487	A488	L489	A490	R491	A492	L493	L494	R495	N496	P497	S498	L499	L500	M501	L502	D503
V369	T370	A371	I372	V373	G378	G379	K380	T381	T382	L383	F384	K385	L386	R389	F390	Y391	A395	I398	R399	L400	G401	D402	E403	P404	V405	D406	T407	Y408	S409	L410	E411	S412	W413	R414	E415	H416	I417	G418	Y419	Q422	E423	S424	P425	L426	M427	S428	G429	T430	I431	R432	E433	M434	L435		
A282	L283	V284	A285	F286	I287	L288	Y289	L290	L293	T294	M295	P296	M297	I300	Q308	K309	S310	I311	E315	R316	M317	E325	E326	D327	T328	Q333	I334	E335	N336	A337	Q342	L343	D344	R345	V346	S347	F348	G349	Y350	K351	P352	D353	Q354	L355	I356	L357	K358	E359	V360	E365	A366				
I180	L181	M188	R193	E194	D197	N207	Q208	R214	L215	V216	K217	Y226	T233	S234	G240	V241	R242	E243	A244	K245	V246	Q247	S248	P252	L253	I254	S255	L256	V257	L258	M259	A260	A261	A264	V265	I266	G267	Y268	M271	Q272	V273	S274	S275	G276	E277	L278	T279								
L72	V73	T85	N89	Y90	N91	I95	G98	E101	L102	L103	W104	K105	S113	Y114	T117	N118	A119	E122	T123	V124	S125	R126	V127	D130	T131	E136	L137	I138	H141	T147	G148	V152	L156	T157	I158	L159	F160	I161	M162	L168	L176	L179													

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	150715	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38.79	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.972	Depositor
Minimum map value	-0.620	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.026	Depositor
Recommended contour level	0.195	Depositor
Map size (Å)	269.312, 269.312, 269.312	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.052, 1.052, 1.052	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: RHQ

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	0.33	6/4468 (0.1%)	0.53	9/6047 (0.1%)
1	B	0.38	3/4468 (0.1%)	0.67	15/6047 (0.2%)
All	All	0.36	9/8936 (0.1%)	0.61	24/12094 (0.2%)

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	B	0	3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	51	LYS	C-O	10.31	1.36	1.24
1	B	64	GLY	C-O	8.50	1.34	1.23
1	B	56	GLY	C-O	-7.63	1.14	1.23
1	A	52	GLN	C-O	7.48	1.33	1.24
1	A	64	GLY	C-O	6.14	1.31	1.23

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	404	PRO	CA-N-CD	-17.09	88.07	112.00
1	B	402	ASP	N-CA-C	-9.28	98.29	111.56
1	B	401	GLY	N-CA-C	-9.12	101.82	115.32
1	B	67	ILE	N-CA-C	-8.25	101.22	110.62
1	B	400	LEU	N-CA-C	-7.68	94.44	110.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	402	ASP	Mainchain
1	B	50	THR	Mainchain
1	B	57	PHE	Mainchain

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	4401	0	4573	137	0
1	B	4401	0	4573	179	0
2	A	33	0	29	5	0
2	B	33	0	28	4	0
All	All	8868	0	9203	299	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 17.

The worst 5 of 299 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:A:449:GLU:OE2	1:A:450:LYS:HG3	1.56	1.04
1:A:181:LEU:HD11	1:A:254:ILE:HG13	1.57	0.87
1:A:342:GLN:HB3	1:A:399:ARG:HB3	1.54	0.86
1:B:502:LEU:HD22	1:B:532:VAL:HG13	1.63	0.80
1:A:271:MET:HG2	1:B:57:PHE:HB3	1.61	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	570/599 (95%)	527 (92%)	42 (7%)	1 (0%)	43	74
1	B	570/599 (95%)	510 (90%)	56 (10%)	4 (1%)	18	53
All	All	1140/1198 (95%)	1037 (91%)	98 (9%)	5 (0%)	31	64

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	SER
1	B	60	SER
1	B	404	PRO
1	B	69	LEU
1	B	68	GLY

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	482/506 (95%)	480 (100%)	2 (0%)	84	83
1	B	482/506 (95%)	479 (99%)	3 (1%)	78	80
All	All	964/1012 (95%)	959 (100%)	5 (0%)	78	82

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ASP

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Mol	Chain	Res	Type
1	A	63	SER
1	B	53	LEU
1	B	63	SER
1	B	404	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	299	GLN
1	B	292	GLN
1	B	434	ASN
1	B	560	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	RHQ	B	601	-	35,36,36	3.96	15 (42%)	49,51,51	5.38	12 (24%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	RHQ	A	601	-	35,36,36	3.93	16 (45%)	49,51,51	5.10	13 (26%)

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	RHQ	B	601	-	-	6/15/21/21	0/4/4/4
2	RHQ	A	601	-	-	6/15/21/21	0/4/4/4

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	RHQ	C2-C1	-11.70	1.19	1.43
2	A	601	RHQ	C2-C1	-11.69	1.19	1.43
2	B	601	RHQ	C6-C5	9.62	1.62	1.42
2	B	601	RHQ	C3-C2	-9.33	1.15	1.41
2	A	601	RHQ	C3-C2	-9.17	1.16	1.41

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	RHQ	C4-C5-N2	25.49	153.62	117.22
2	A	601	RHQ	C4-C5-N2	22.65	149.56	117.22
2	A	601	RHQ	C6-C5-C4	-15.79	92.33	119.14
2	B	601	RHQ	C6-C5-C4	-15.67	92.52	119.14
2	B	601	RHQ	C18-C19-C26	-13.75	90.84	118.66

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

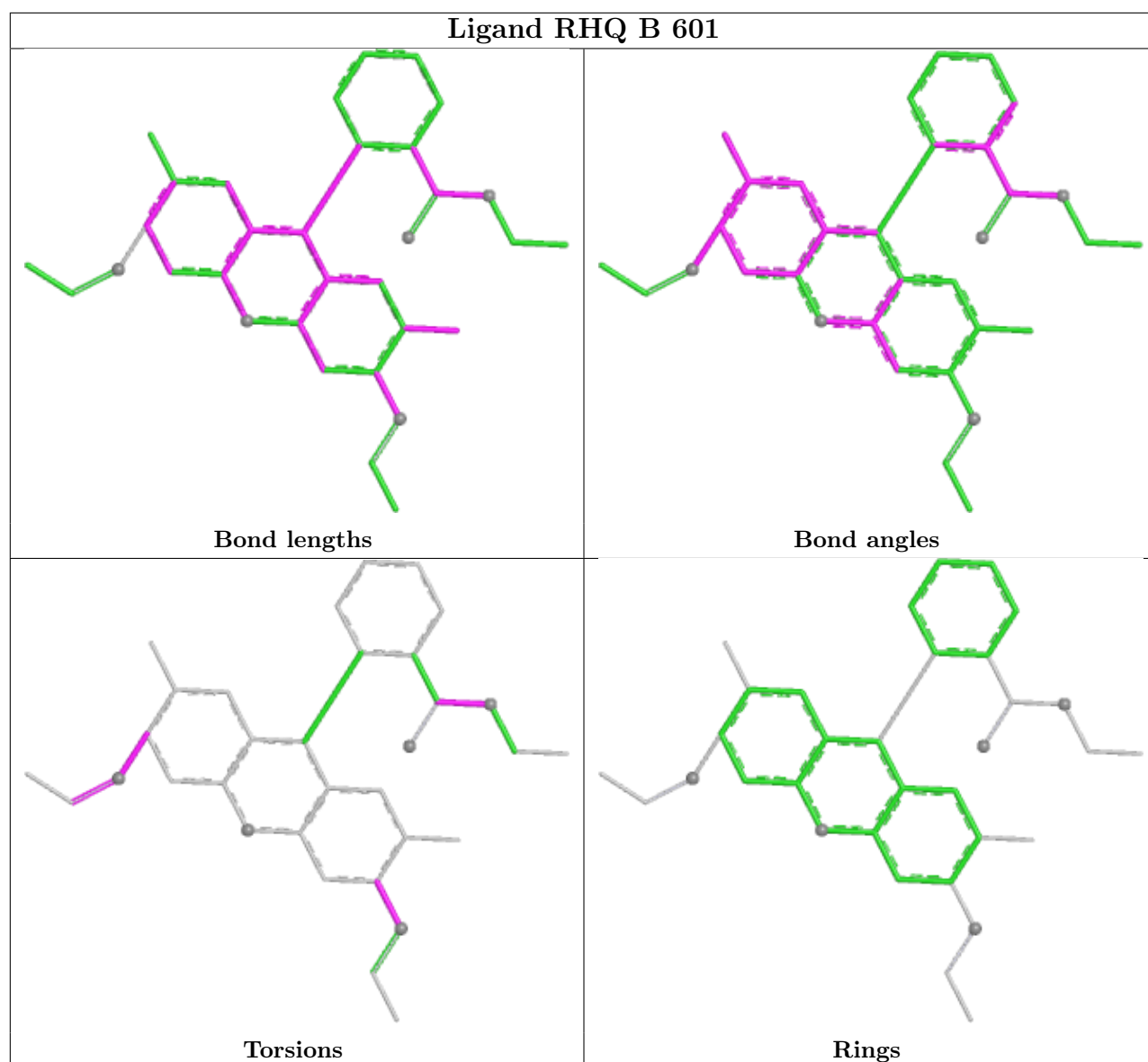
Mol	Chain	Res	Type	Atoms
2	A	601	RHQ	C6-C5-N2-C24
2	A	601	RHQ	O27-C26-O2-C28
2	B	601	RHQ	C6-C5-N2-C24
2	B	601	RHQ	C25-C24-N2-C5
2	B	601	RHQ	O27-C26-O2-C28

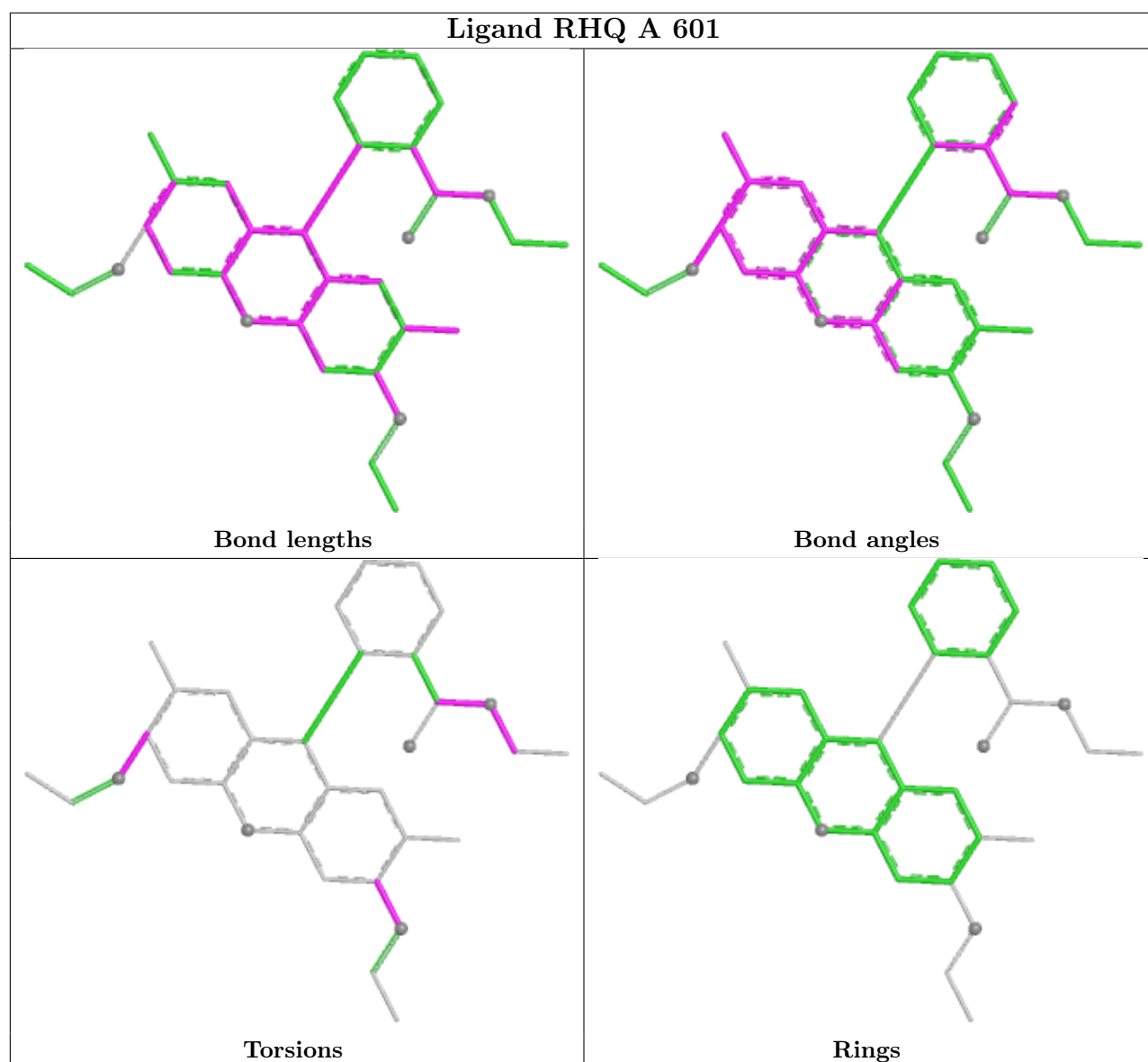
There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	RHQ	4	0
2	A	601	RHQ	5	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.

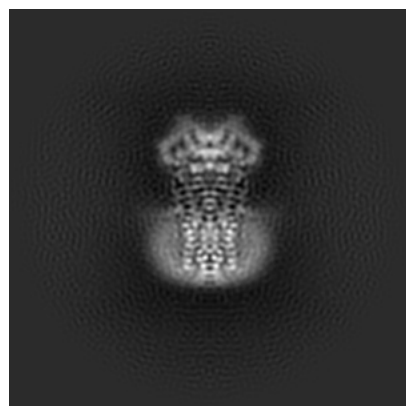
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19130. These allow visual inspection of the internal detail of the map and identification of artifacts.

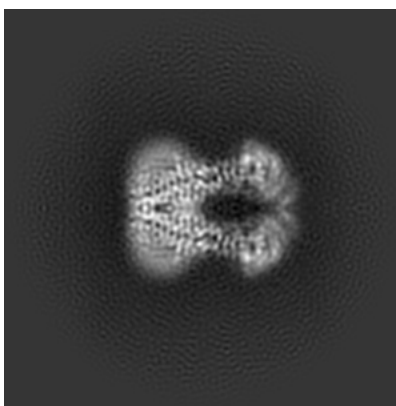
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

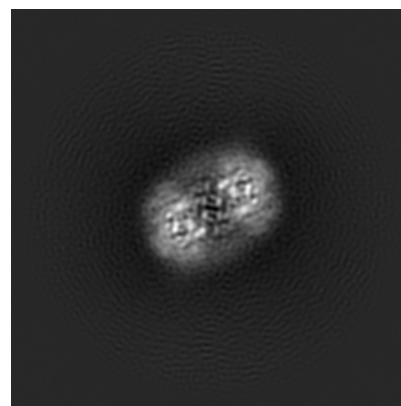
6.1.1 Primary map



X

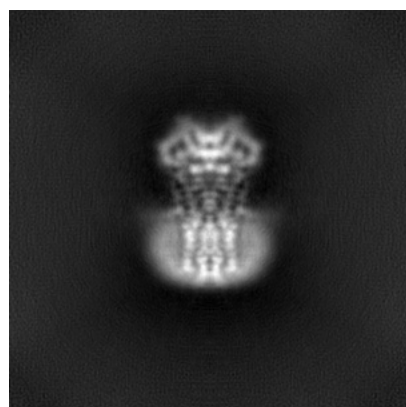


Y

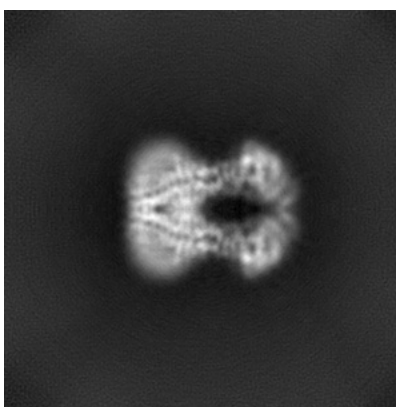


Z

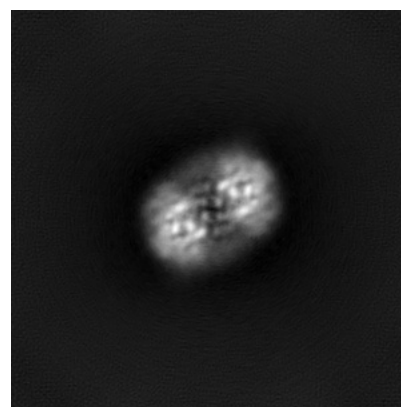
6.1.2 Raw map



X



Y

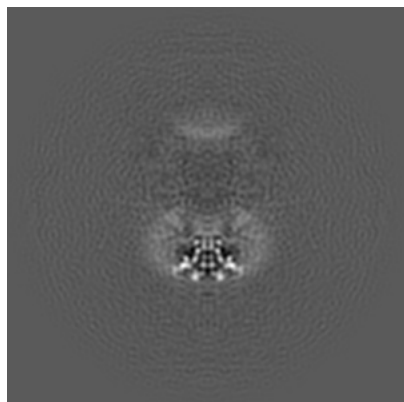


Z

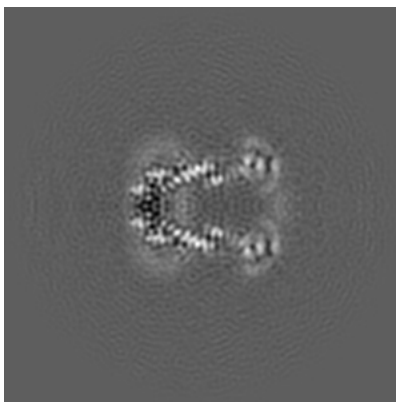
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

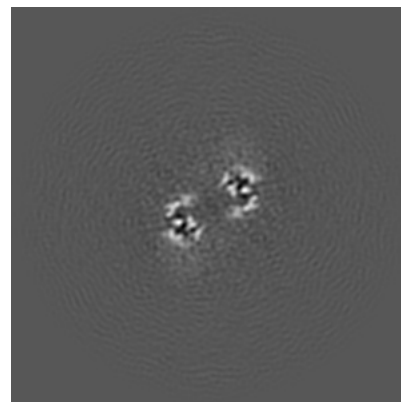
6.2.1 Primary map



X Index: 128

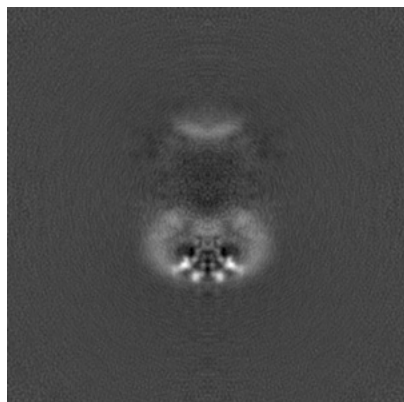


Y Index: 128

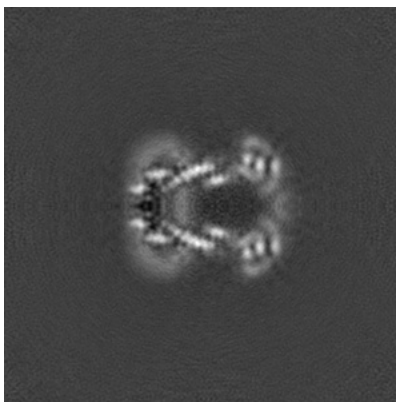


Z Index: 128

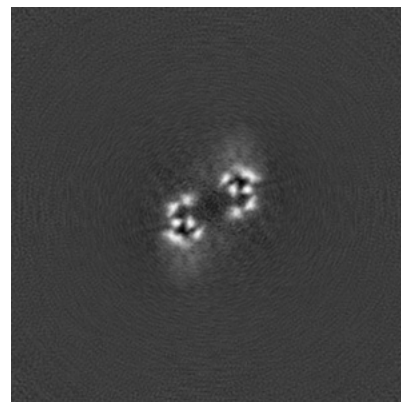
6.2.2 Raw map



X Index: 128



Y Index: 128

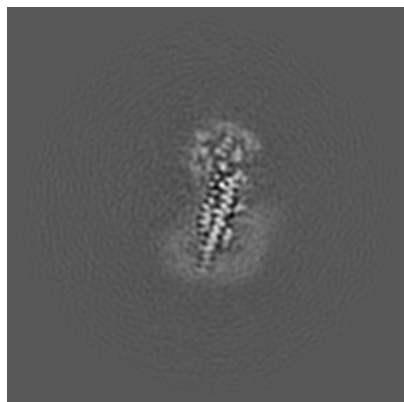


Z Index: 128

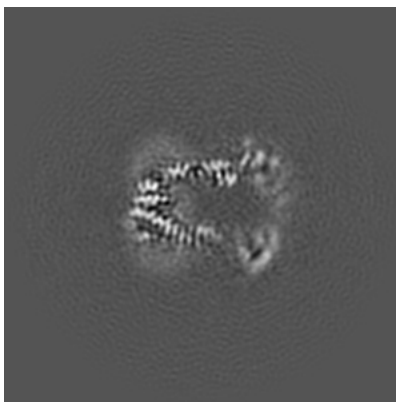
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

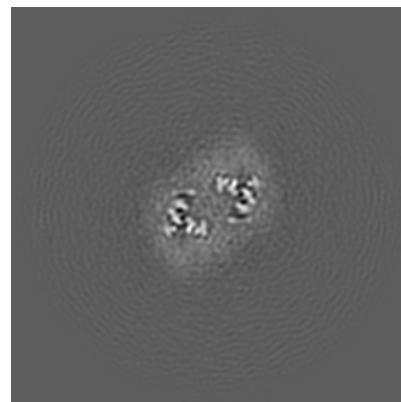
6.3.1 Primary map



X Index: 150

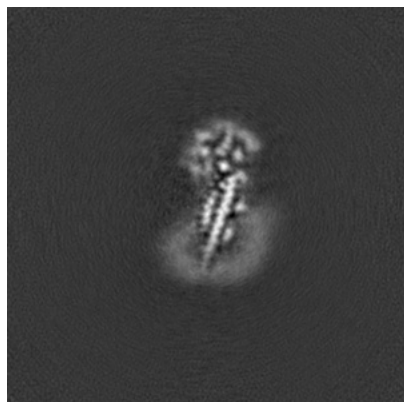


Y Index: 132

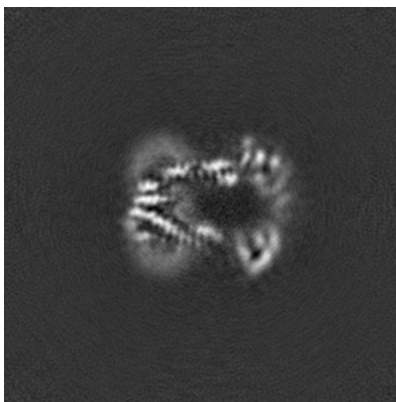


Z Index: 117

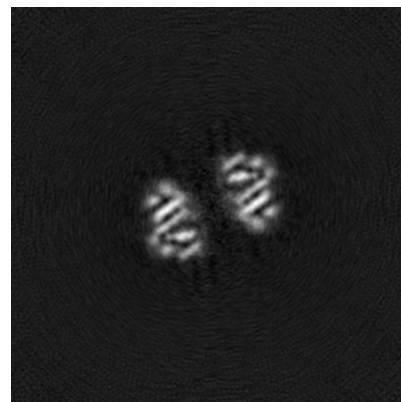
6.3.2 Raw map



X Index: 151



Y Index: 132

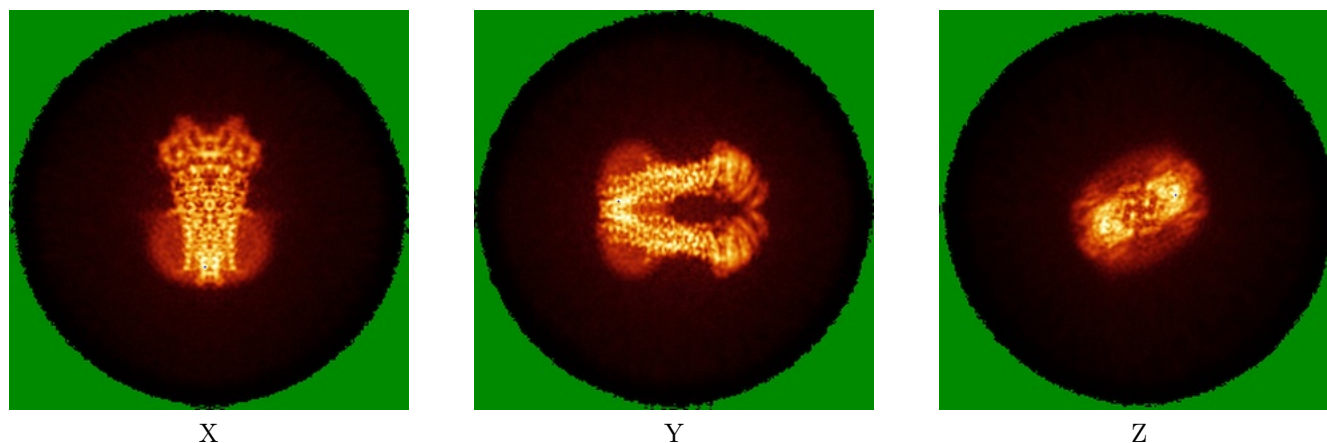


Z Index: 163

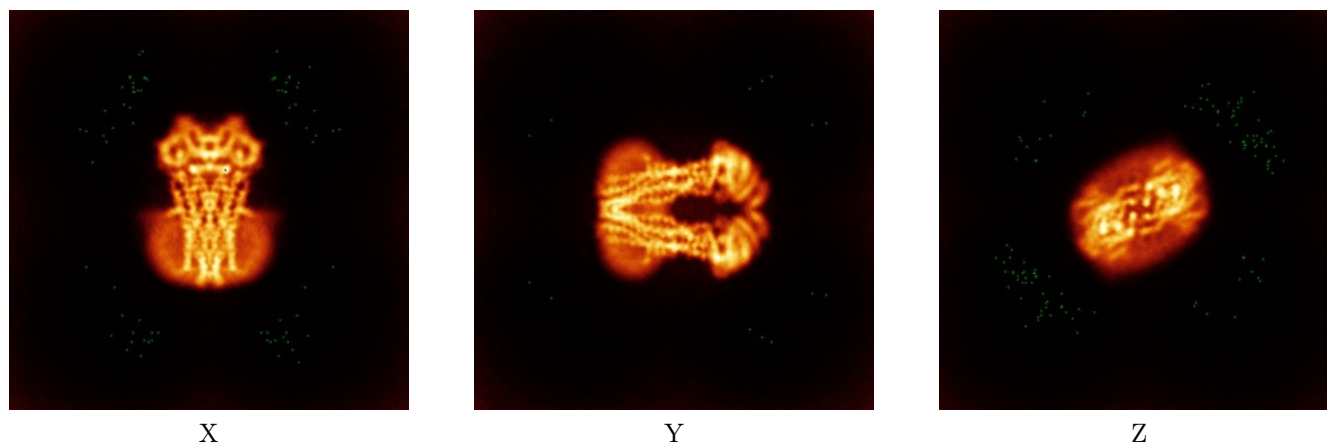
The images above show the largest variance slices of the map in three orthogonal directions.

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.

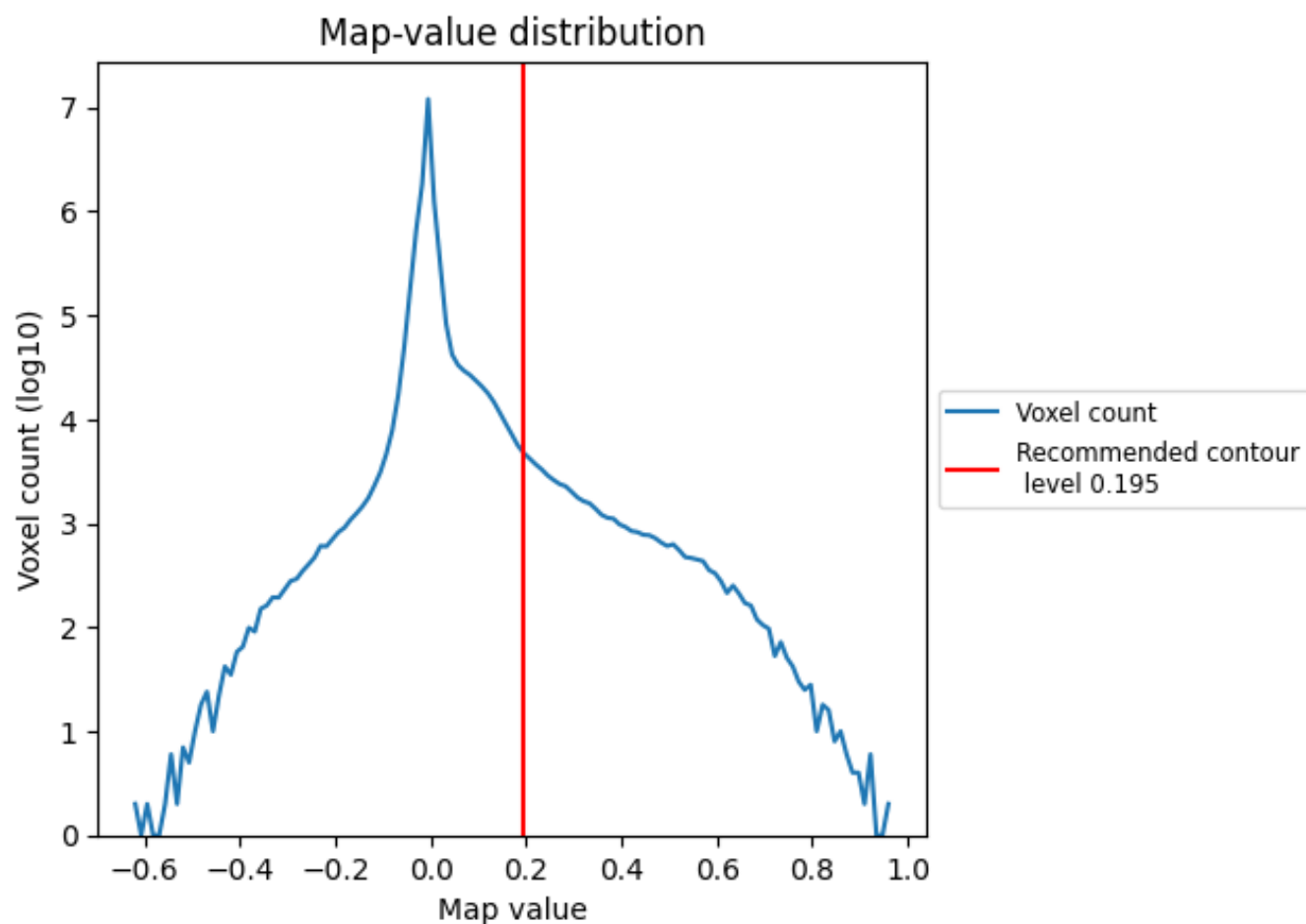
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

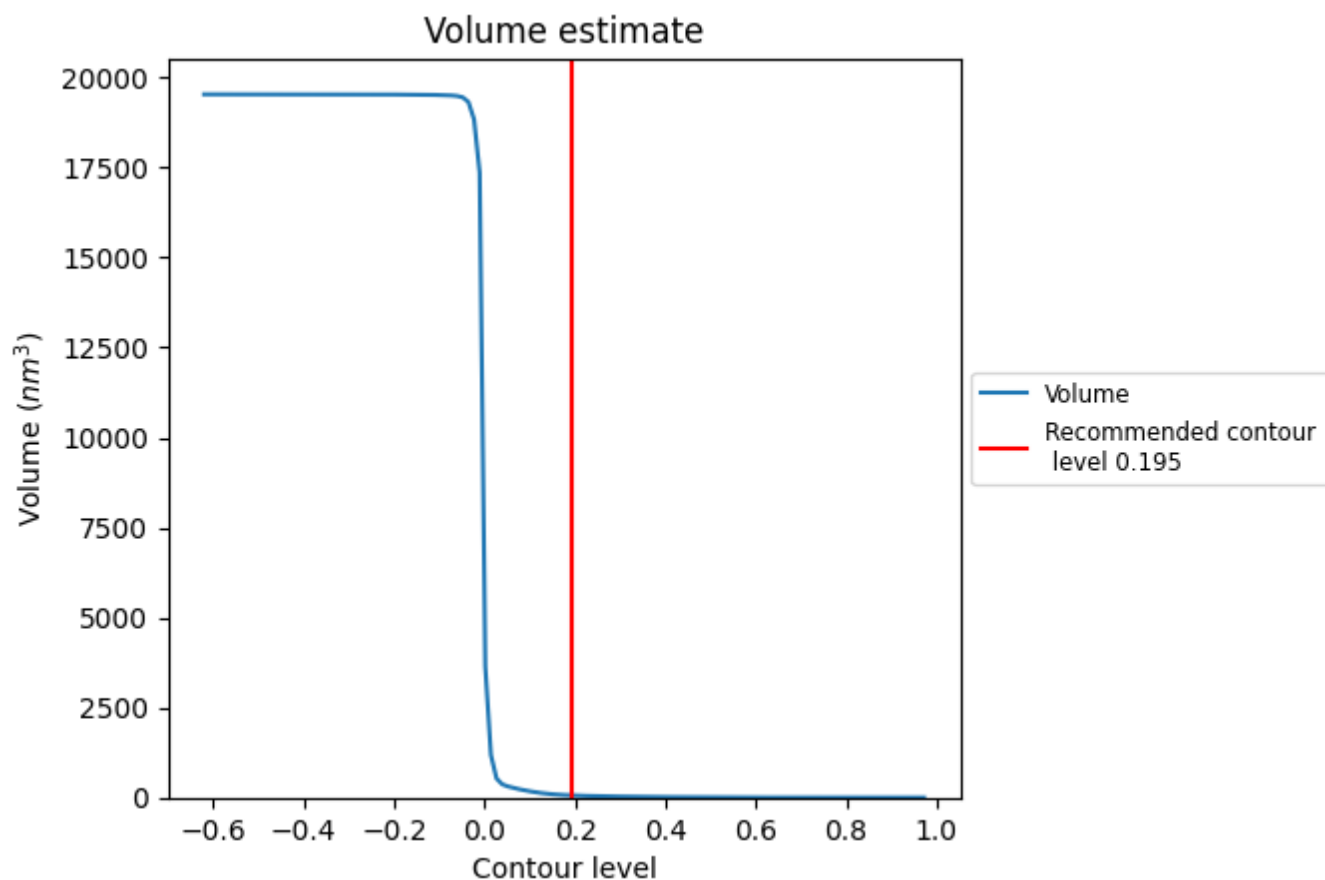
This section contains the results of statistical analysis of the map.

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.

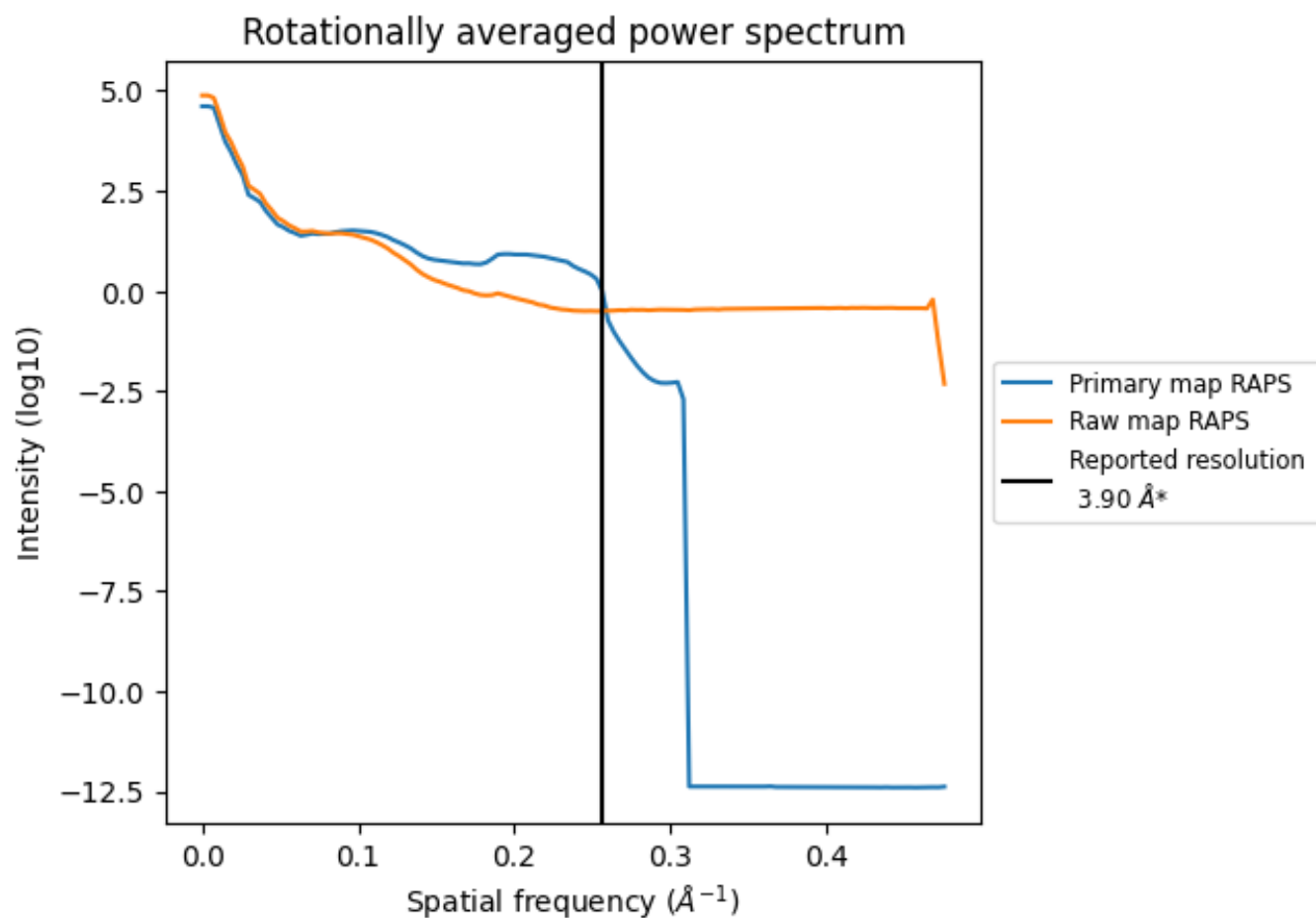
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 59 nm³; this corresponds to an approximate mass of 53 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 ⓘ

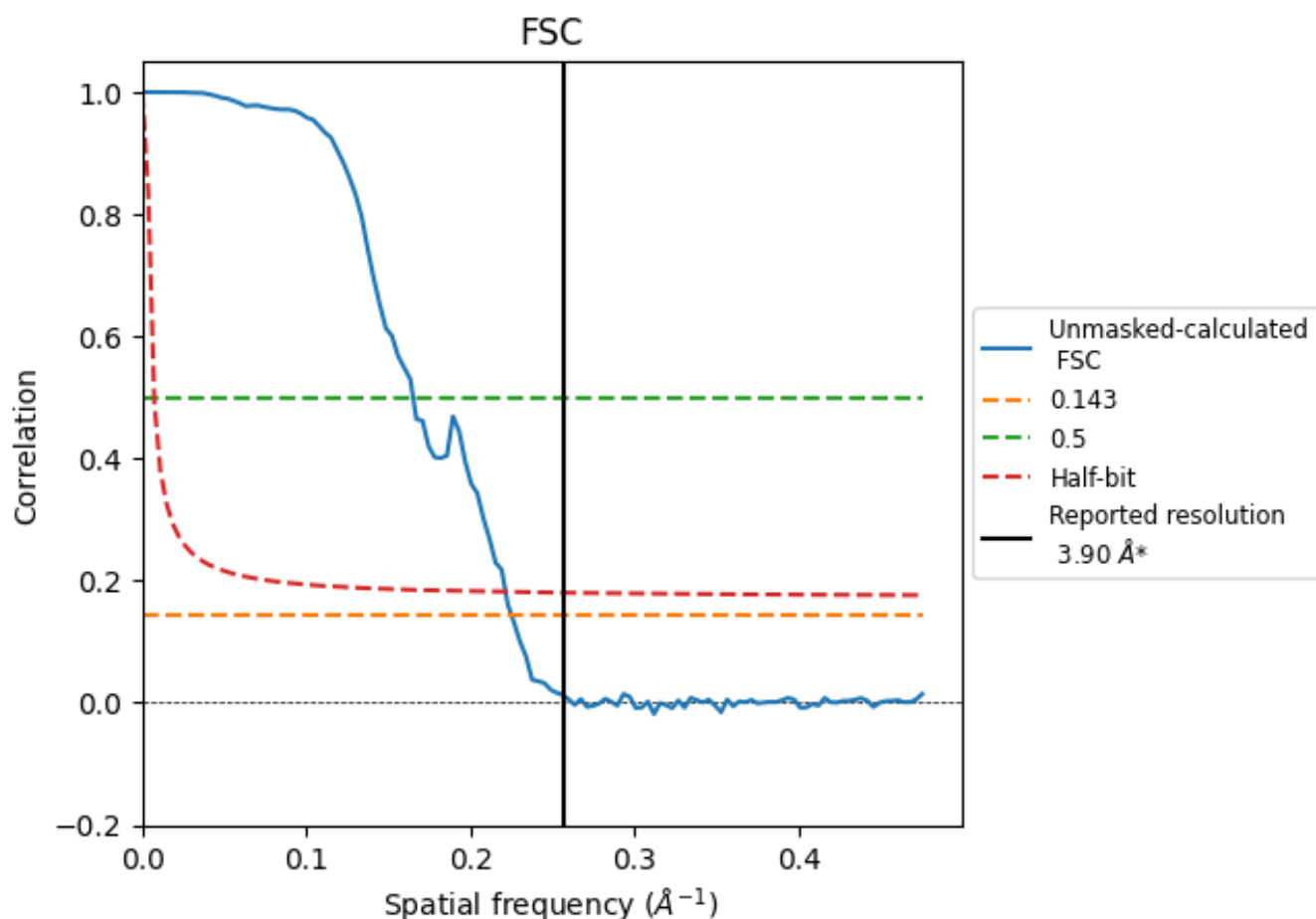


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.44	6.06	4.51

*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 4.44 differs from the reported value 3.9 by more than 10 %

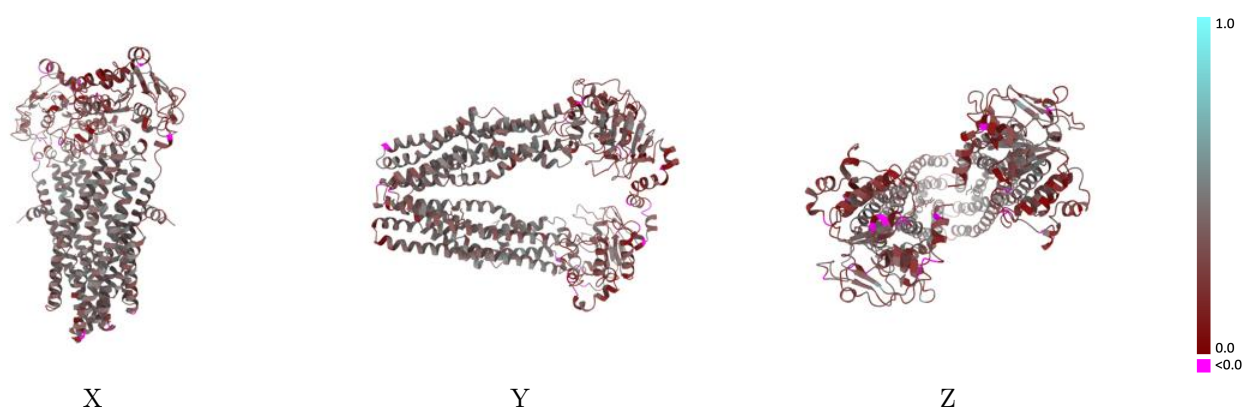
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19130 and PDB model 8RG7. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)

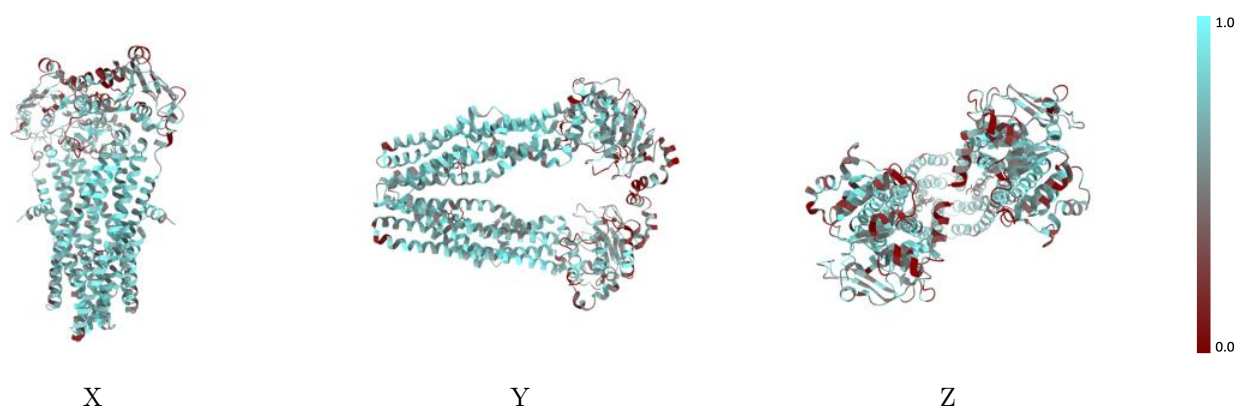
This section was not generated.

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



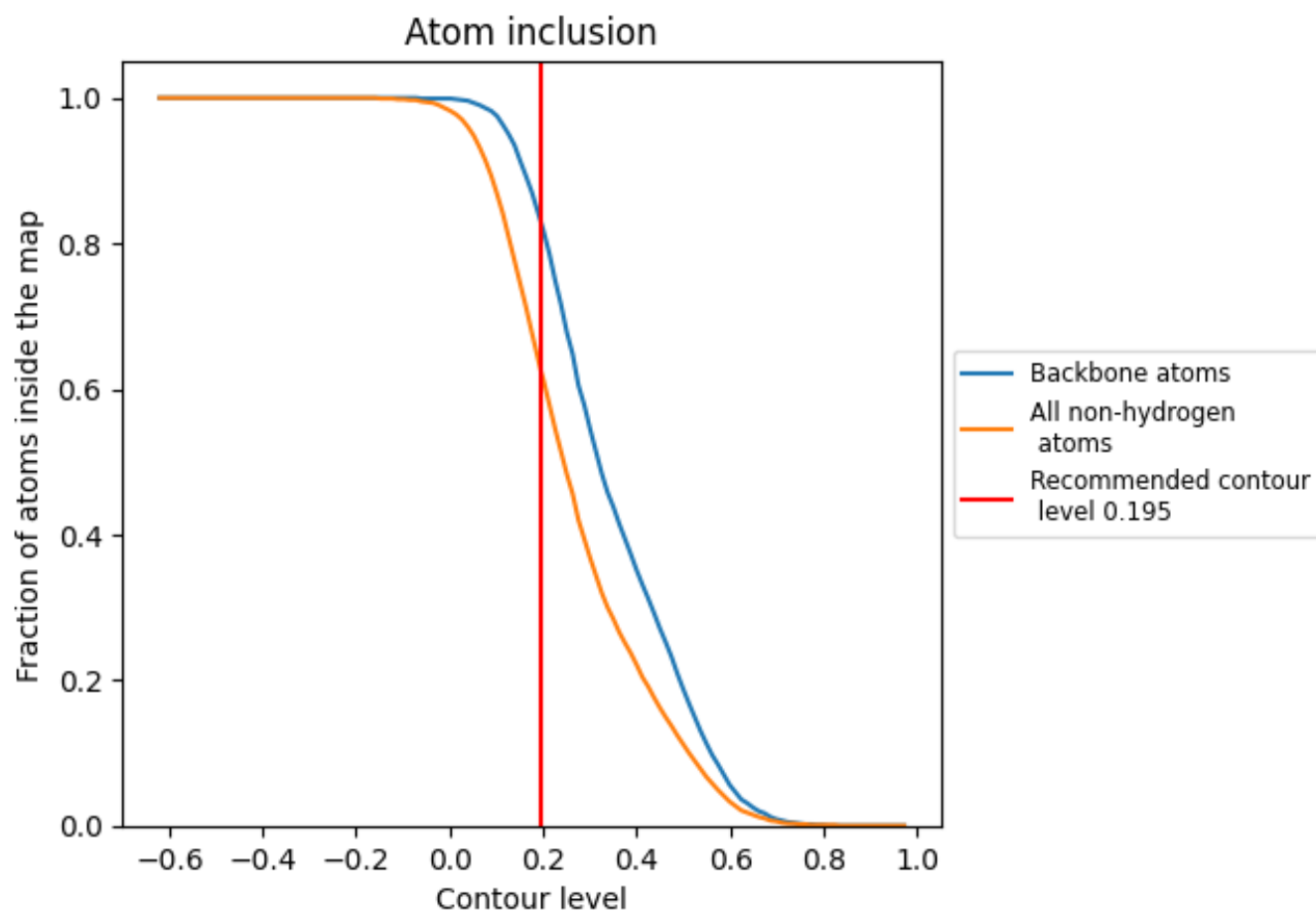
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.195).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 62% 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 (0.195) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6250	0.3290
A	0.6290	0.3330
B	0.6220	0.3250

