



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 01:34 PM UTC

PDB ID : 8RGN / pdb_00008rgn
EMDB ID : EMD-19135
Title : BmrA E504-R6G-70uMATPMg
Authors : Gobet, A.; Zarkadas, E.; Schoehn, G.; Falson, P.; Chaptal, V.
Deposited on : 2023-12-14
Resolution : 3.70 Å(reported)
Based on initial model : 6r72

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

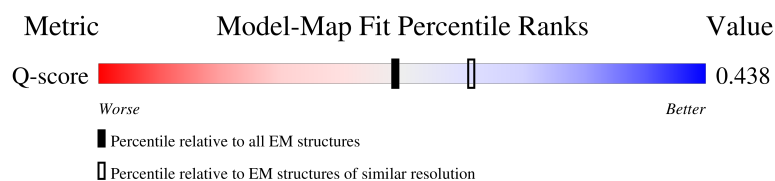
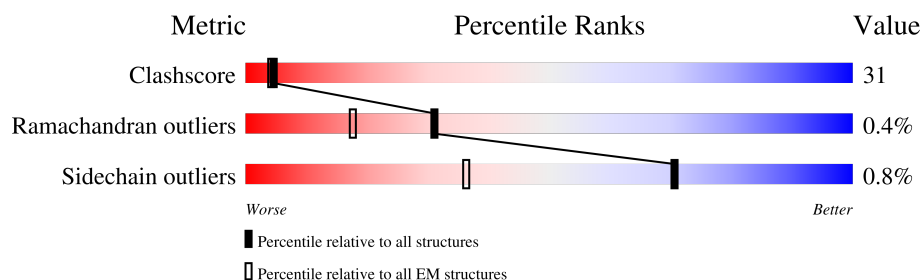
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	9% 47% 47% ...
1	B	599	9% 47% 48% ...

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9031 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	578	Total	C	N	O	S	0	0
			4448	2853	742	835	18		
1	B	578	Total	C	N	O	S	0	0
			4448	2853	742	835	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 33	C 28	N 2	O 3	0
2	B	1	Total 33	C 28	N 2	O 3	0

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{13}\text{P}_3$).



Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total 31	C 10	N 5	O 13	P 3	0
3	B	1	Total 31	C 10	N 5	O 13	P 3	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Mg 1	0
4	B	1	Total 1	Mg 1	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		AltConf
5	A	3	Total 3	O 3	0
5	B	2	Total 2	O 2	0

T530	A452	S376	F291	I209	L137	M59	MET
T533	A457	K380	Q292	L210	I138	S60	SER
A534			I293	P211	T139	S61	SER
H535	F460	K385	M295	I213	L214	L62	HIS
L537	I461	L387	P296	L215	S143	S63	HIS
S538	L464	E388	Q299		G144	G64	HIS
T539	P465	R389	I300	A218	F145	T85	HIS
V540	M466	F390	T301	S219	I146	Q66	HIS
V541	Q467	Y391	T302		T147	G148	HIS
D542	F468	S392	F303	Y226	I149	I67	MET
	D469	P393	F504	G227	I150	G68	PRO
Q645	T470	T394	T305	R228	L150	L69	THR
L546	E471	A395	Q306	G229	V152	V73	LYS
L547	V472		L307	K230	I153	F74	GLN
	G473	R398	Q308	M231	G154	F75	LYS
I554	E474	R399	K309	L236	S155		LYS
		L400	S310		L156	V76	SER
R557	M478	G401	I311	L239	T157	Q77	K9
	L479	D402	M317	G240	I158	A78	S10
L563	Q483	E403	I318	V241	F160	S81	K11
M564		V405	E319	R242	I161	A87	L12
	I489	D406	L320	E243	M162	L88	K13
H567	A490	T407	L321	V250	N163	N89	P14
G568	A491	Y408			W164		L18
L569	A492	S409	E326	V257	K165		V19
V570	A493		D327	L258	L166	Q93	R20
R571	L494	W413	T328		T167	G92	R21
	R495	I417	V329	A261	L168	G88	T22
E575			T330	L262	L169	L99	M23
Q576	T499	Q422	G331	L263	V170		P24
Q577	M501	E423	L343	V263	L171	L103	K28
L578	L502	S424	D344	A264	V172	W104	L33
K579	D503		R345	V265	V173	K105	L34
M580	A504	M427	V346	I266		K106	A34
N581	A505	S428	S347	G267	L176	L107	V37
A582	T506	G429	Y350	Y268	A177	I108	V38
D583	S507	T430		G269	A178	K109	T39
L584	S508	I431	D353	G270	L179	P111	T40
	L509	R432	I356	M271	L180	V112	L41
E585	D510	E433	L357	Q272	L181	S113	W42
N586	S511	N434	K358	V273	V182	Y114	S43
LYS	Q512	C435	E359	S274	M188	F115	L44
ALA	S513	Y437	V360	S275	I191	D116	L45
GLY	E514		S361	G276	T195	T117	I46
	V517	E440	A366	E277		N118	P47
	Q518	R441		L278	T195	A119	L48
	Q519	D442	A366	T279	E198	S120	L49
	A520	V443	A366	A280	T199	G121	L49
	L521	T444	V369	G281	S124		T50
	L524	D445	T370	A282	S125		K51
	M525	A446	A371	L283	A200		Q52
		E447	I372		R201		V27
	R528	I448	V373	T203	F202		T128
			G374	N207	T203		L53
			P375	L287	N129		V54
				L288	D130		D55
				L290	E136		G56
							F57
							S58

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	123402	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 ($e^-/\text{\AA}^2$)	37.95	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.798	Depositor
Minimum map value	-2.743	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.381	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: RHQ, MG, 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	0.36	0/4515	0.88	29/6110 (0.5%)
1	B	0.39	0/4515	1.00	25/6110 (0.4%)
All	All	0.38	0/9030	0.94	54/12220 (0.4%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	470	THR	N-CA-C	-27.37	62.82	108.26
1	B	467	GLN	N-CA-C	-20.11	88.64	113.38
1	B	118	ASN	N-CA-C	-19.08	78.29	109.40
1	A	443	VAL	N-CA-C	-18.34	81.71	108.12
1	B	446	ALA	N-CA-C	-17.67	92.15	113.88

There are no chirality outliers.

There are no planarity outliers.

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	4448	0	4618	308	0
1	B	4448	0	4618	301	0
2	A	33	0	31	0	0
2	B	33	0	31	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	31	0	12	2	0
3	B	31	0	12	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0
All	All	9031	0	9322	564	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 31.

The worst 5 of 564 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:466:ASN:HB3	1:A:468:PHE:CE2	1.55	1.40
1:A:466:ASN:CB	1:A:468:PHE:CE2	2.16	1.28
1:A:466:ASN:HB3	1:A:468:PHE:CD2	1.75	1.22
1:B:121:GLY:O	1:B:124:VAL:HG22	1.51	1.11
1:A:466:ASN:CB	1:A:468:PHE:CD2	2.41	0.99

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	576/599 (96%)	549 (95%)	25 (4%)	2 (0%)	36 65
1	B	576/599 (96%)	549 (95%)	24 (4%)	3 (0%)	24 56
All	All	1152/1198 (96%)	1098 (95%)	49 (4%)	5 (0%)	31 60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	466	ASN
1	B	466	ASN
1	A	469	ASP
1	B	469	ASP
1	B	444	THR

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	487/506 (96%)	483 (99%)	4 (1%)	73	76
1	B	487/506 (96%)	483 (99%)	4 (1%)	73	76
All	All	974/1012 (96%)	966 (99%)	8 (1%)	70	76

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	542	ASP
1	B	467	GLN
1	B	344	ASP
1	A	542	ASP
1	B	448	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	581	ASN
1	B	434	ASN
1	B	581	ASN
1	B	545	GLN
1	A	545	GLN

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](#)

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	ATP	B	602	4	32,33,33	1.30	5 (15%)	48,52,52	1.78	8 (16%)
2	RHQ	B	601	-	35,36,36	1.73	8 (22%)	49,51,51	1.20	5 (10%)
2	RHQ	A	601	-	35,36,36	1.73	8 (22%)	49,51,51	1.20	5 (10%)
3	ATP	A	602	4	32,33,33	1.29	4 (12%)	48,52,52	1.78	8 (16%)

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	ATP	B	602	4	-	4/22/38/38	0/3/3/3
2	RHQ	B	601	-	-	8/15/21/21	0/4/4/4
2	RHQ	A	601	-	-	8/15/21/21	0/4/4/4
3	ATP	A	602	4	-	4/22/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	RHQ	C11-N1	4.93	1.50	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	RHQ	C11-N1	4.93	1.50	1.37
3	B	602	ATP	C5-C4	4.39	1.46	1.39
3	A	602	ATP	C5-C4	4.32	1.46	1.39
2	B	601	RHQ	O2-C26	4.02	1.43	1.33

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	ATP	C5-C4-N3	-6.02	118.42	126.72
3	A	602	ATP	C5-C4-N3	-6.00	118.46	126.72
3	B	602	ATP	N3-C4-N9	4.90	135.50	127.17
3	A	602	ATP	N3-C4-N9	4.87	135.45	127.17
3	A	602	ATP	C2-N3-C4	3.77	121.04	111.83

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	RHQ	C4-C5-N2-C24
2	A	601	RHQ	C6-C5-N2-C24
2	A	601	RHQ	C19-C26-O2-C28
2	B	601	RHQ	C4-C5-N2-C24
2	B	601	RHQ	C6-C5-N2-C24

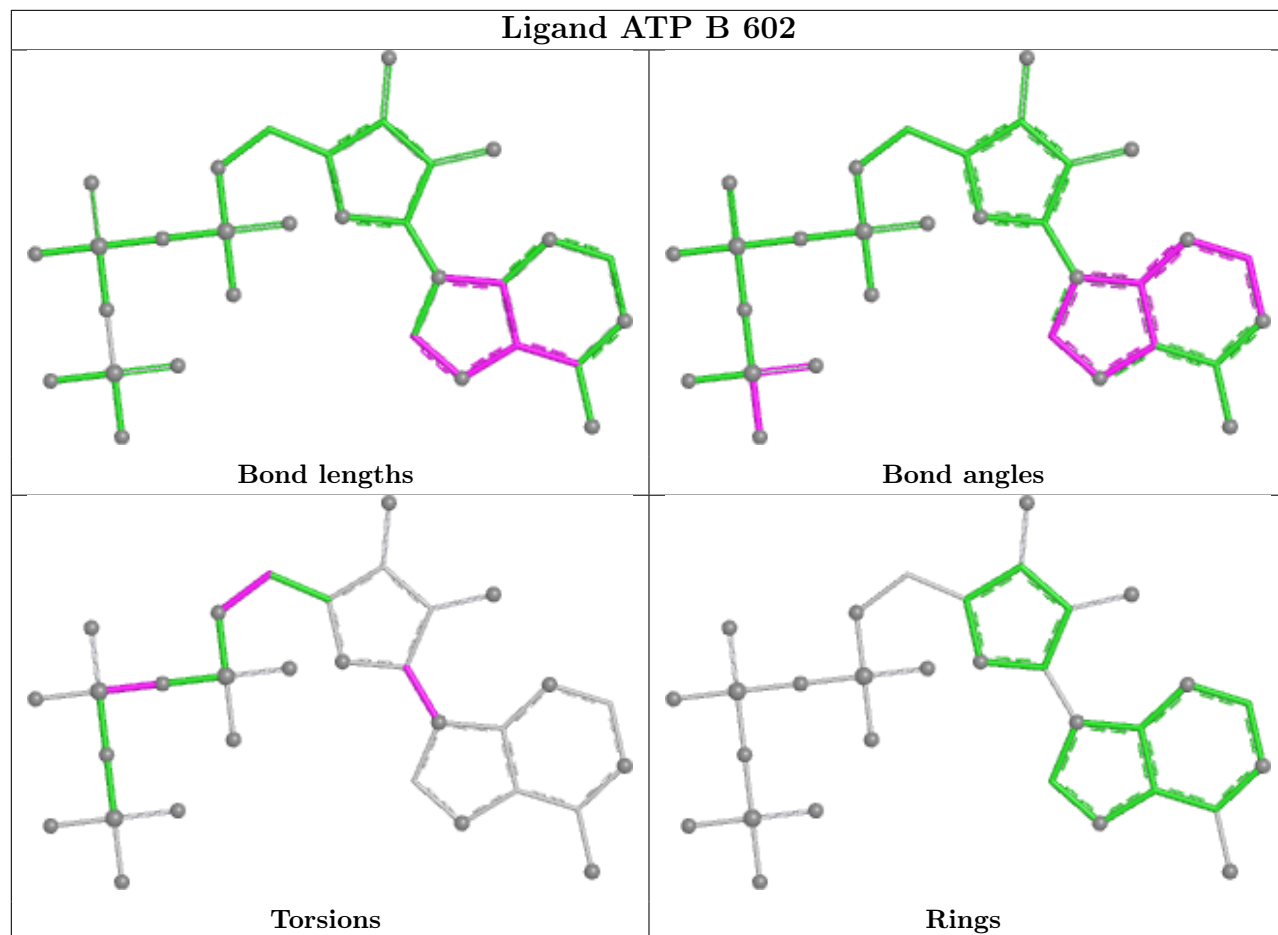
There are no ring outliers.

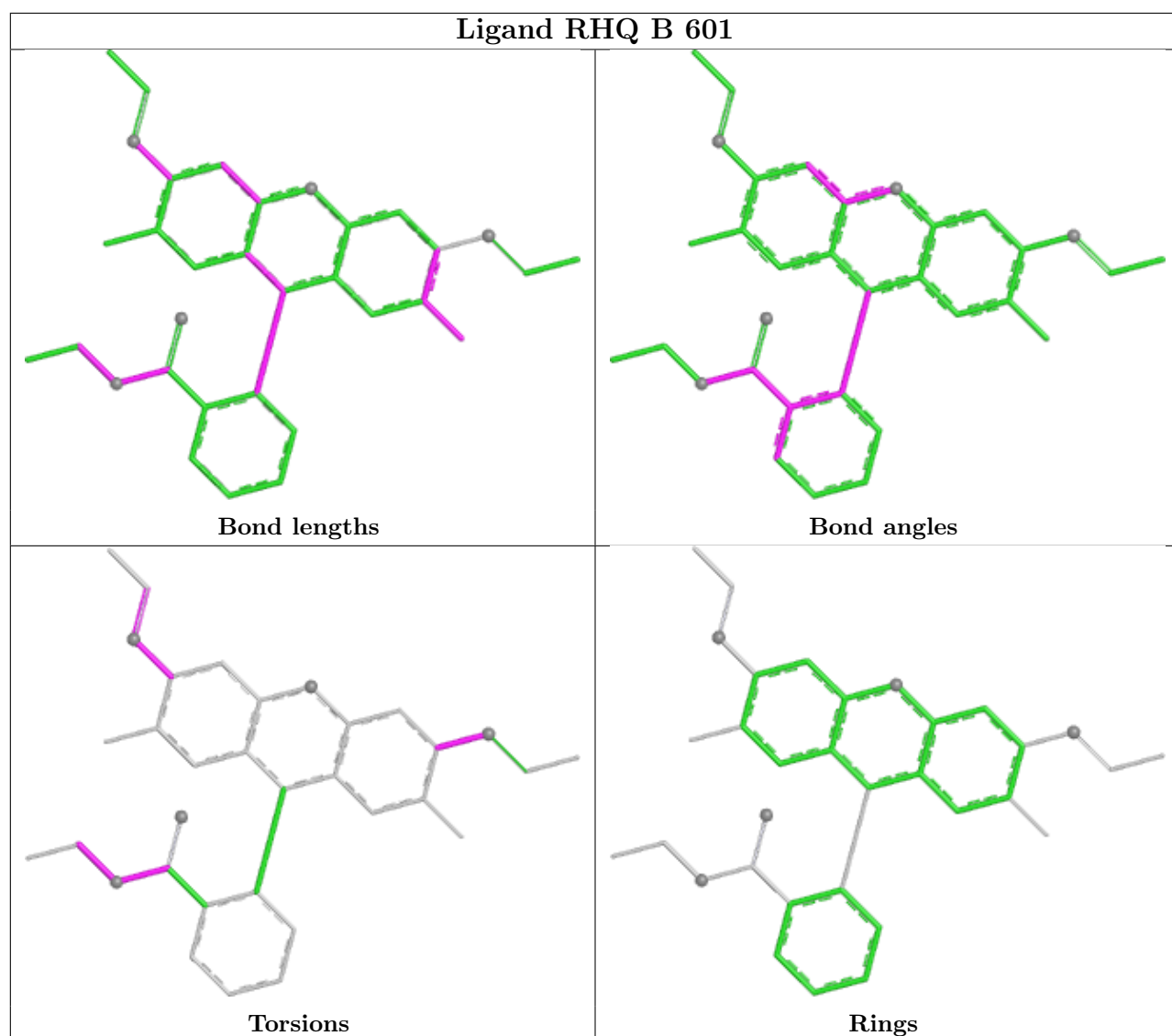
2 monomers are involved in 4 short contacts:

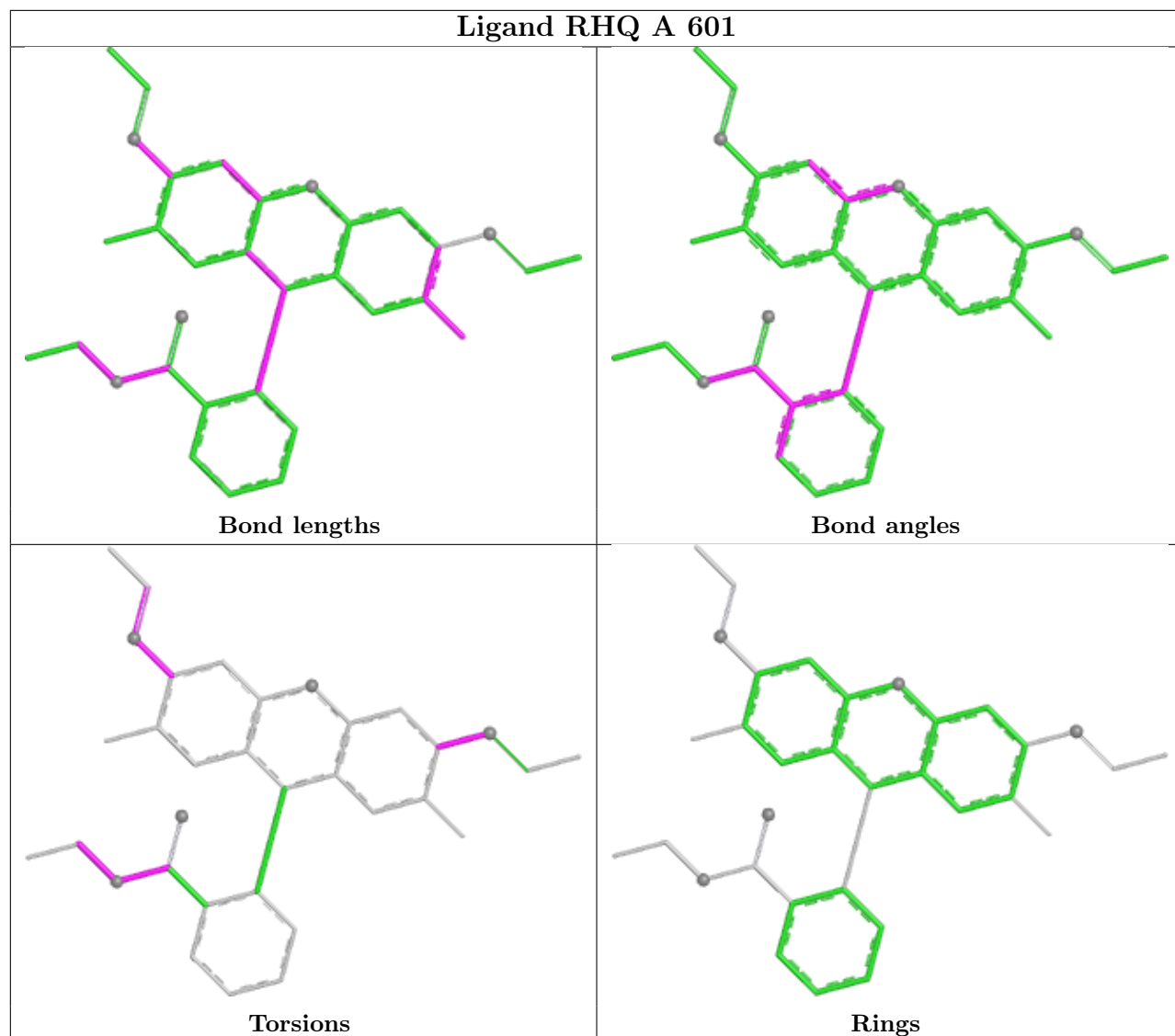
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	ATP	2	0
3	A	602	ATP	2	0

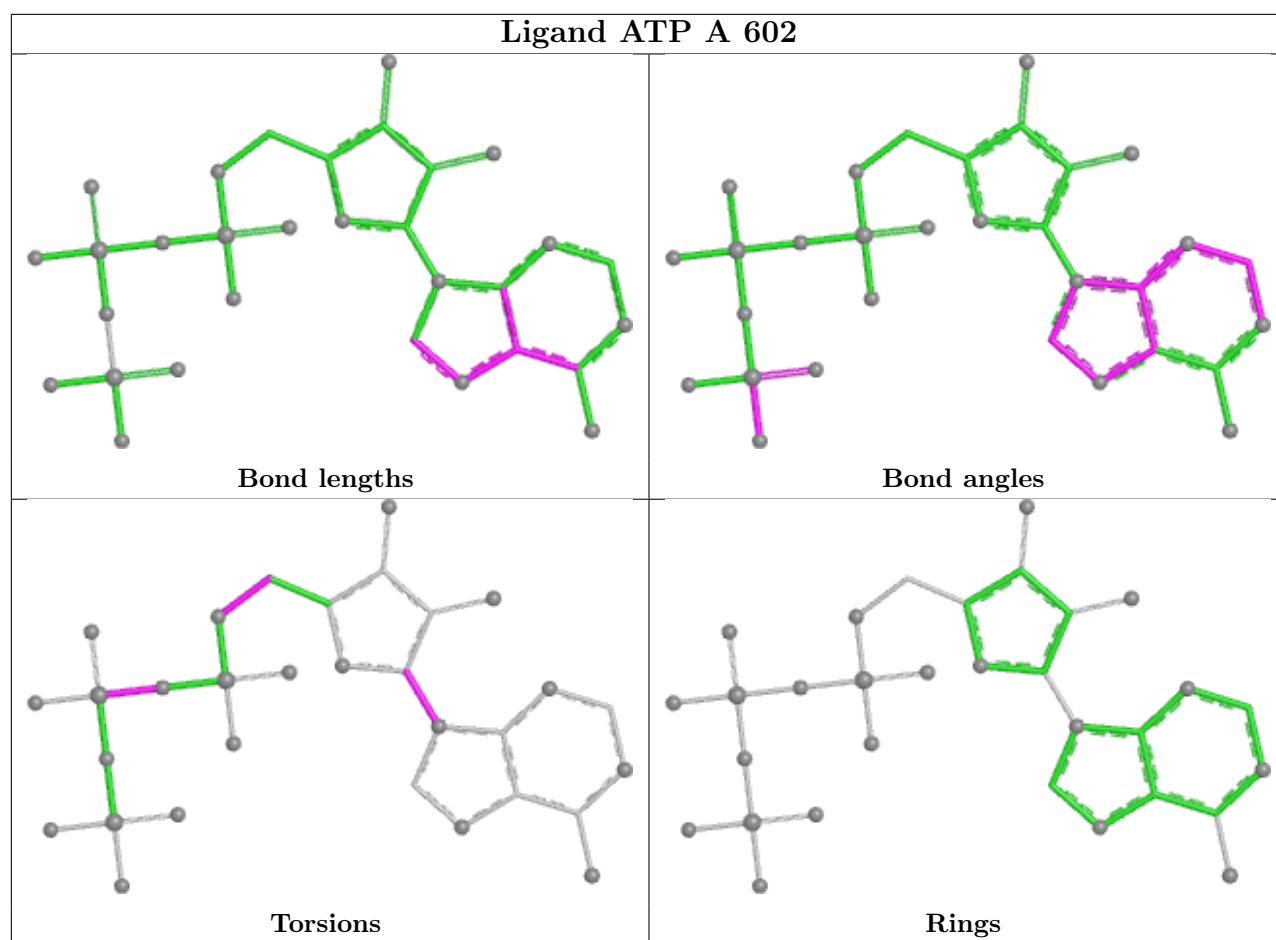
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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









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.

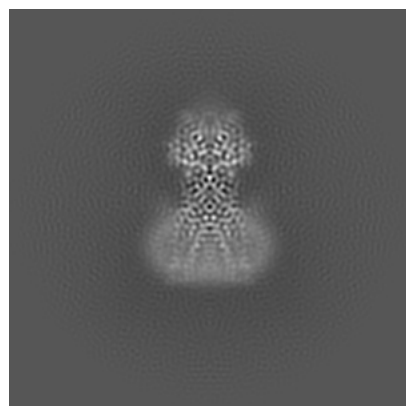
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19135. These allow visual inspection of the internal detail of the map and identification of artifacts.

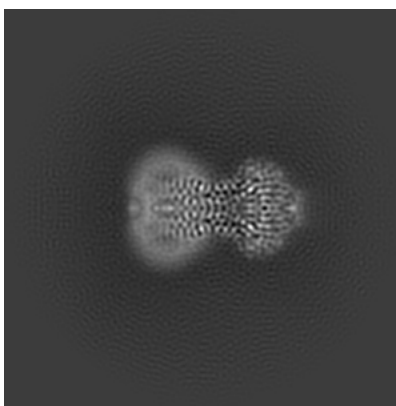
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

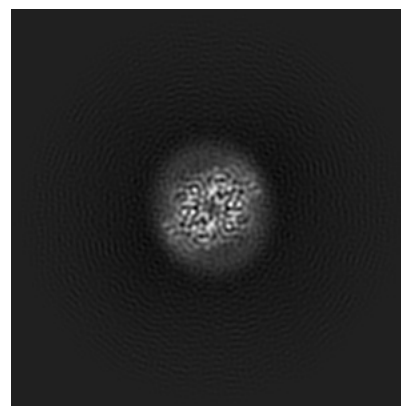
6.1.1 Primary map



X

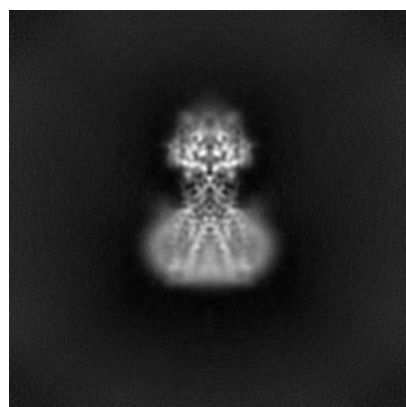


Y

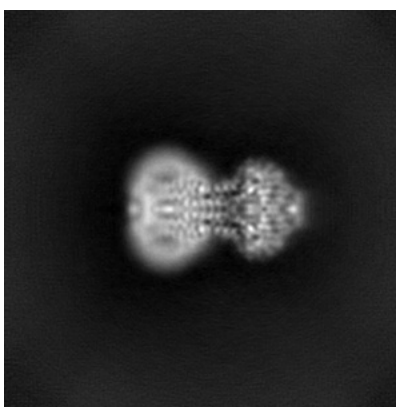


Z

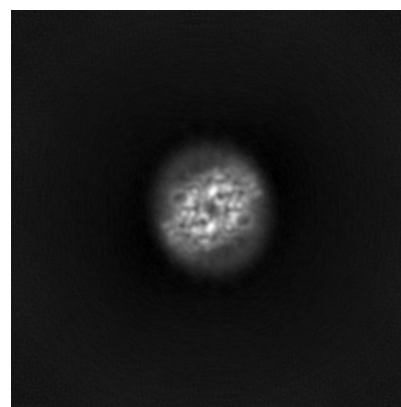
6.1.2 Raw map



X



Y

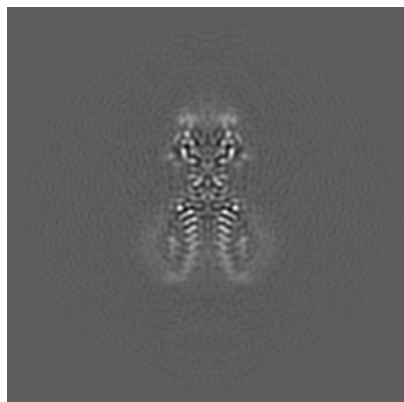


Z

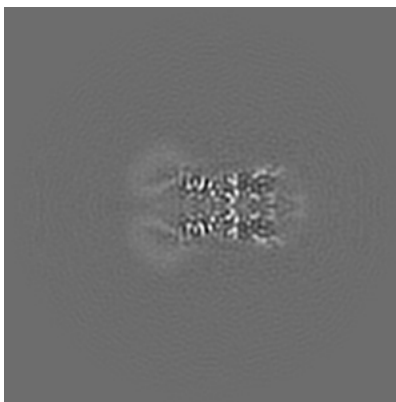
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

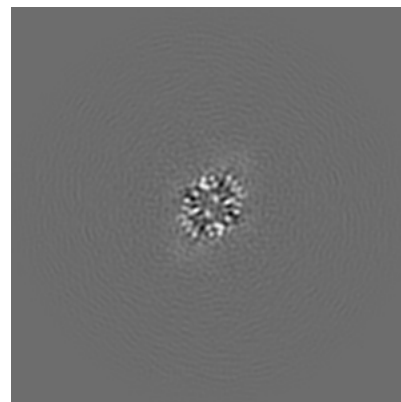
6.2.1 Primary map



X Index: 128

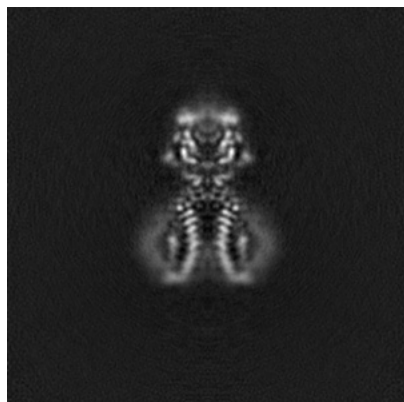


Y Index: 128

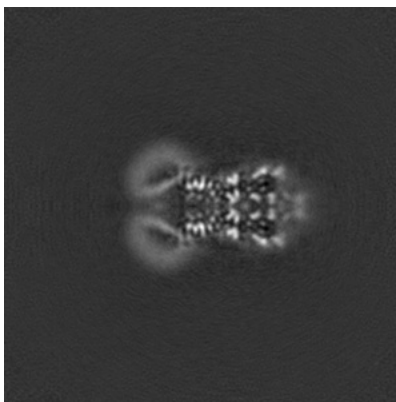


Z Index: 128

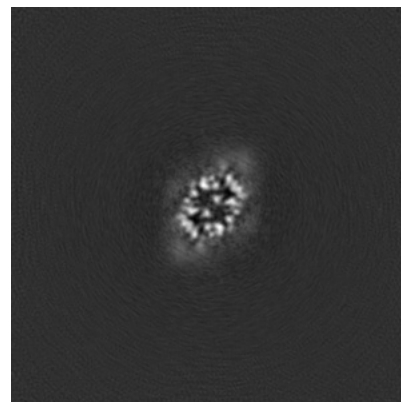
6.2.2 Raw map



X Index: 128



Y Index: 128

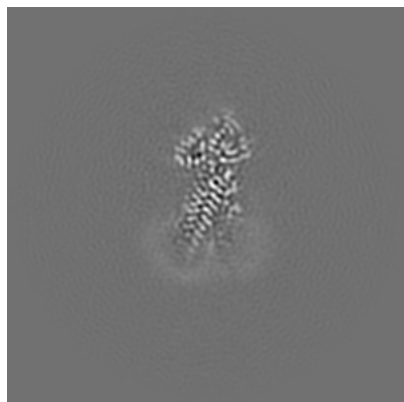


Z Index: 128

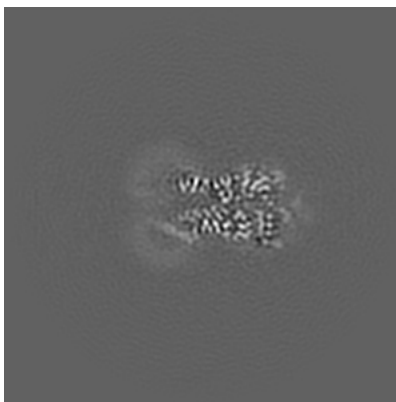
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

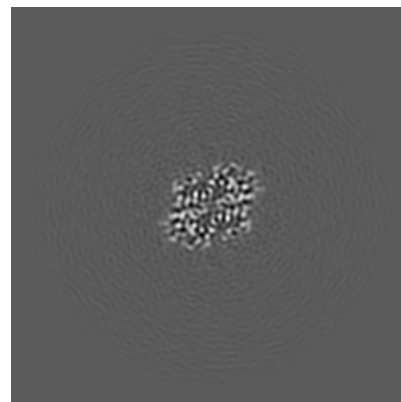
6.3.1 Primary map



X Index: 140

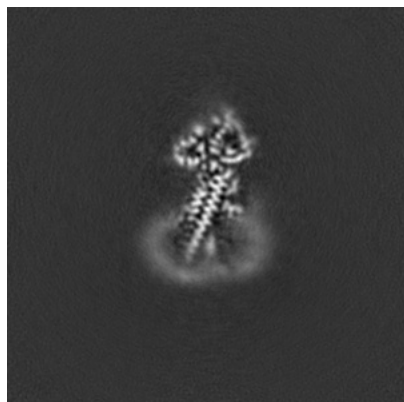


Y Index: 125

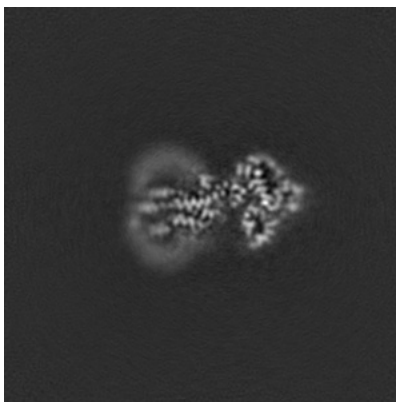


Z Index: 163

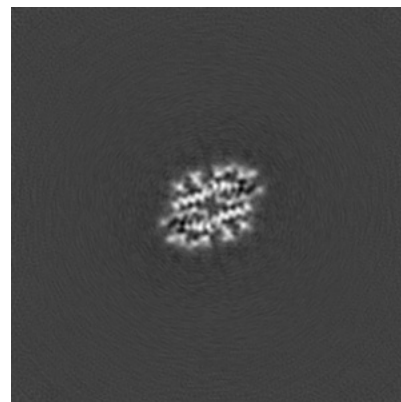
6.3.2 Raw map



X Index: 141



Y Index: 140

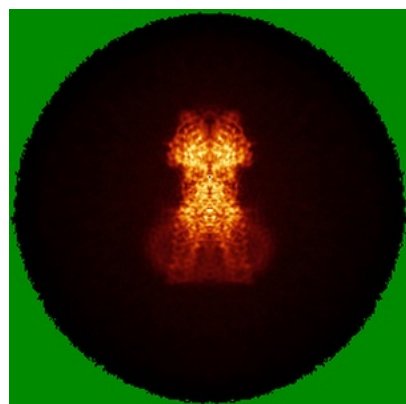


Z Index: 165

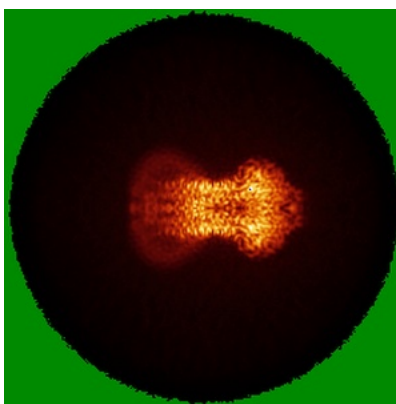
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

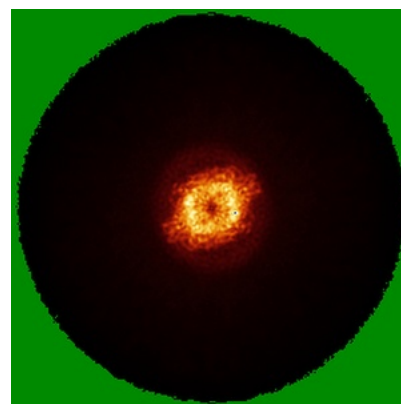
6.4.1 Primary map



X

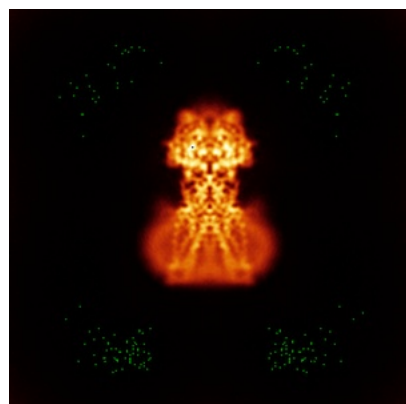


Y

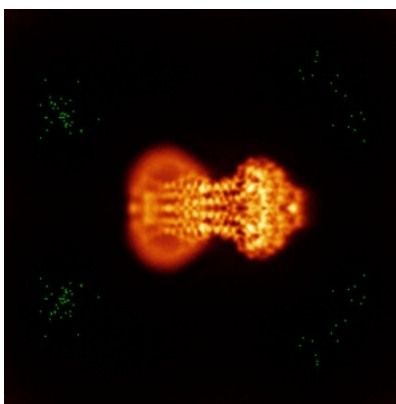


Z

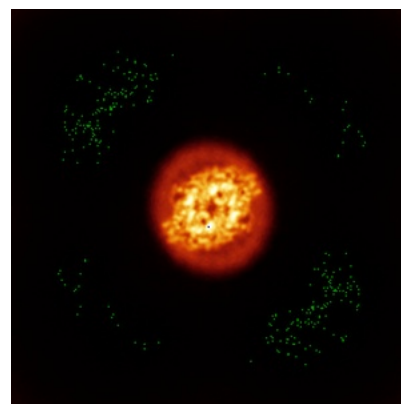
6.4.2 Raw map



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.

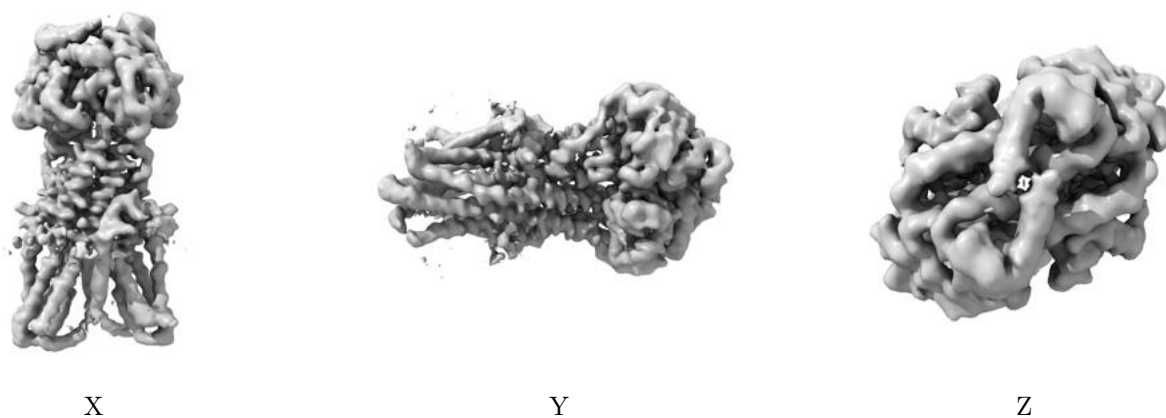
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.381. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

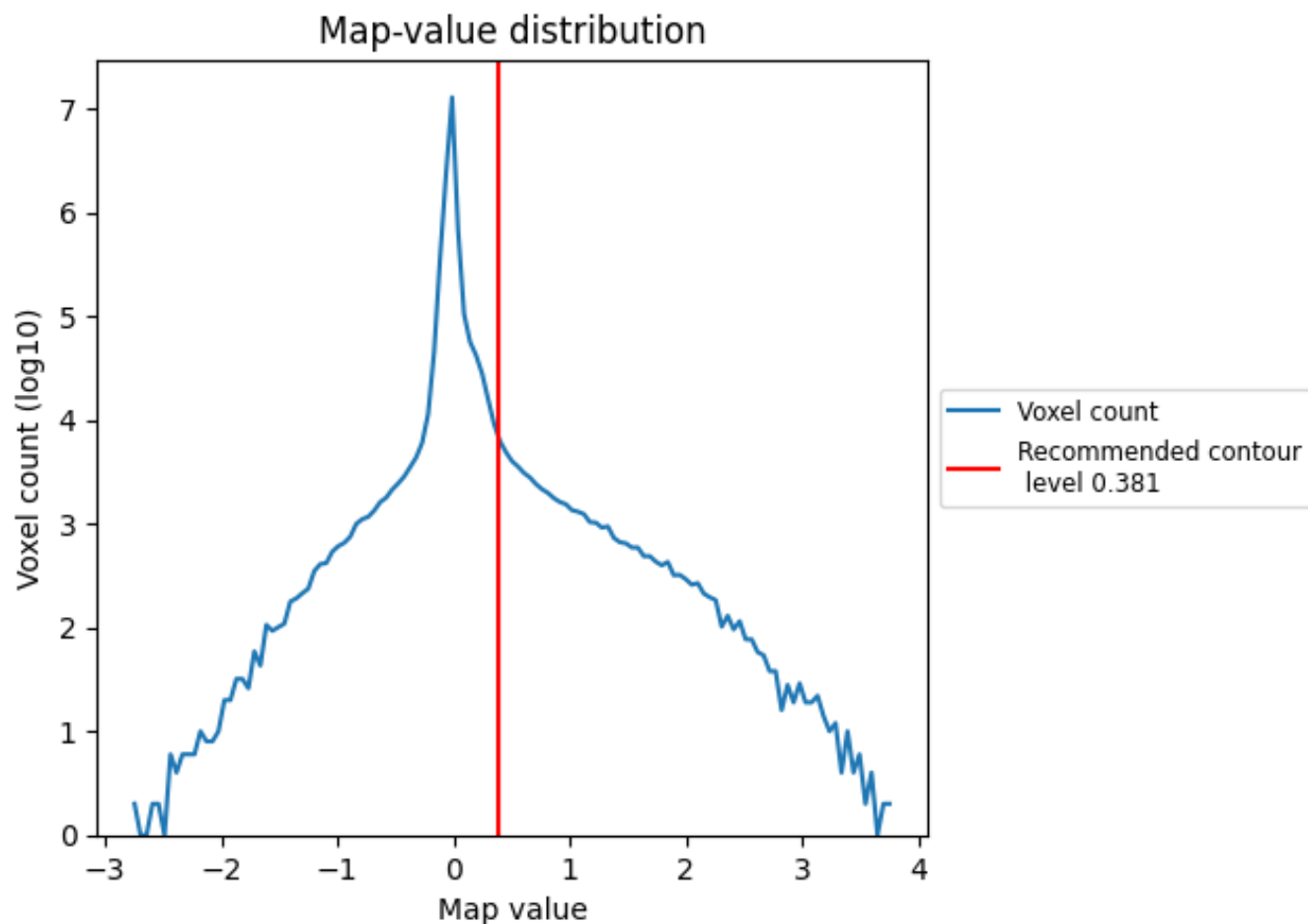
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

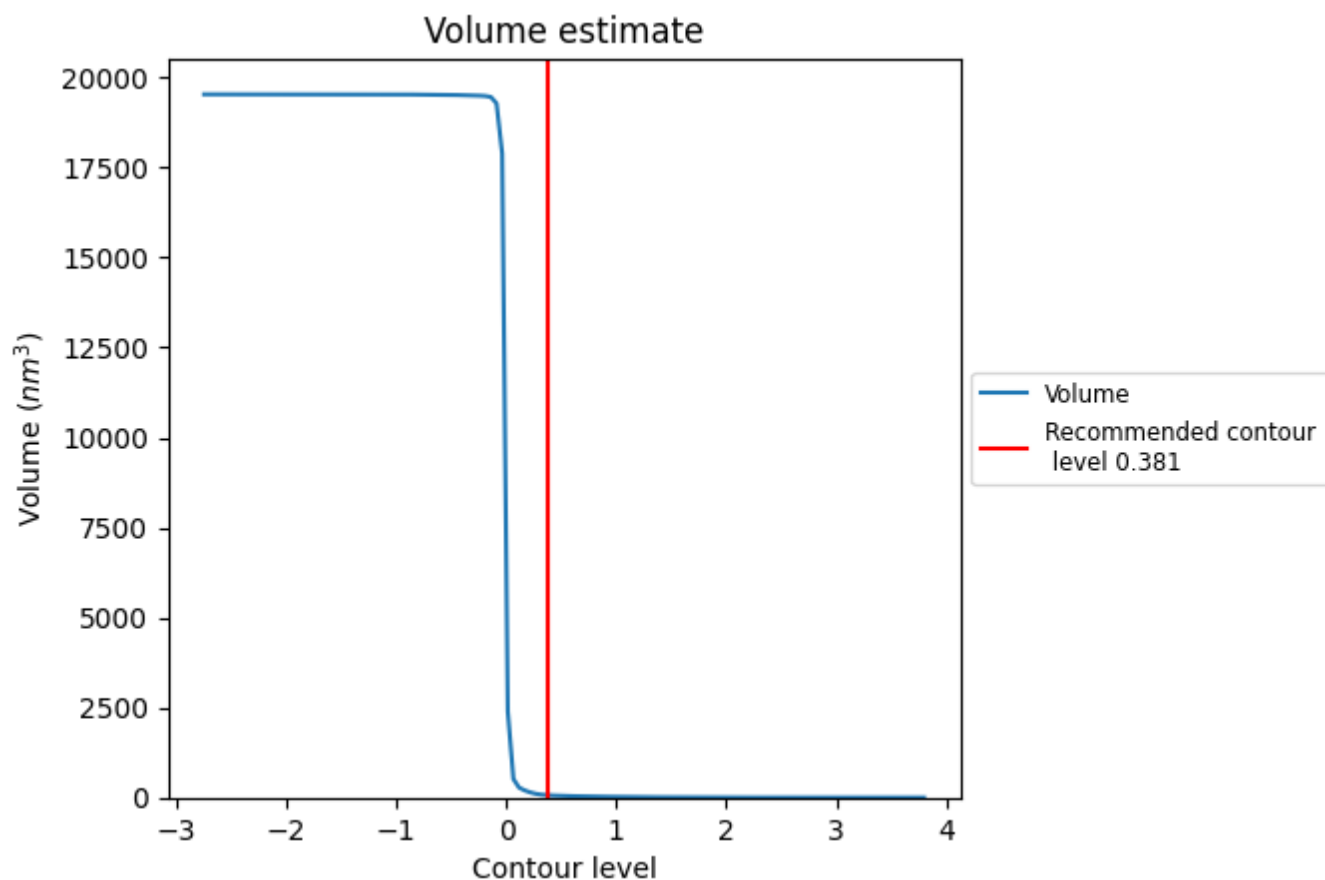
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

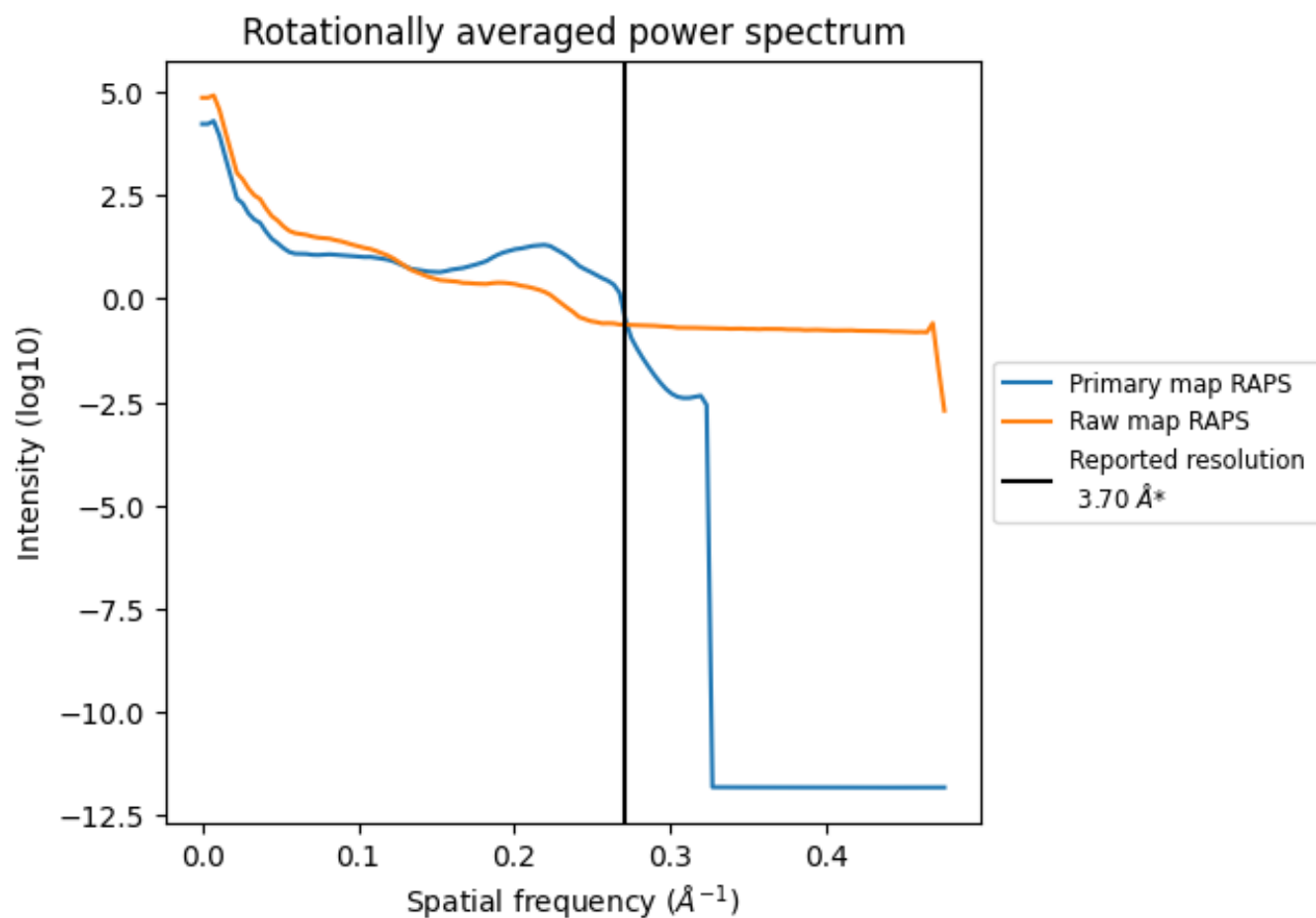
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 64 nm³; this corresponds to an approximate mass of 58 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 ⓘ

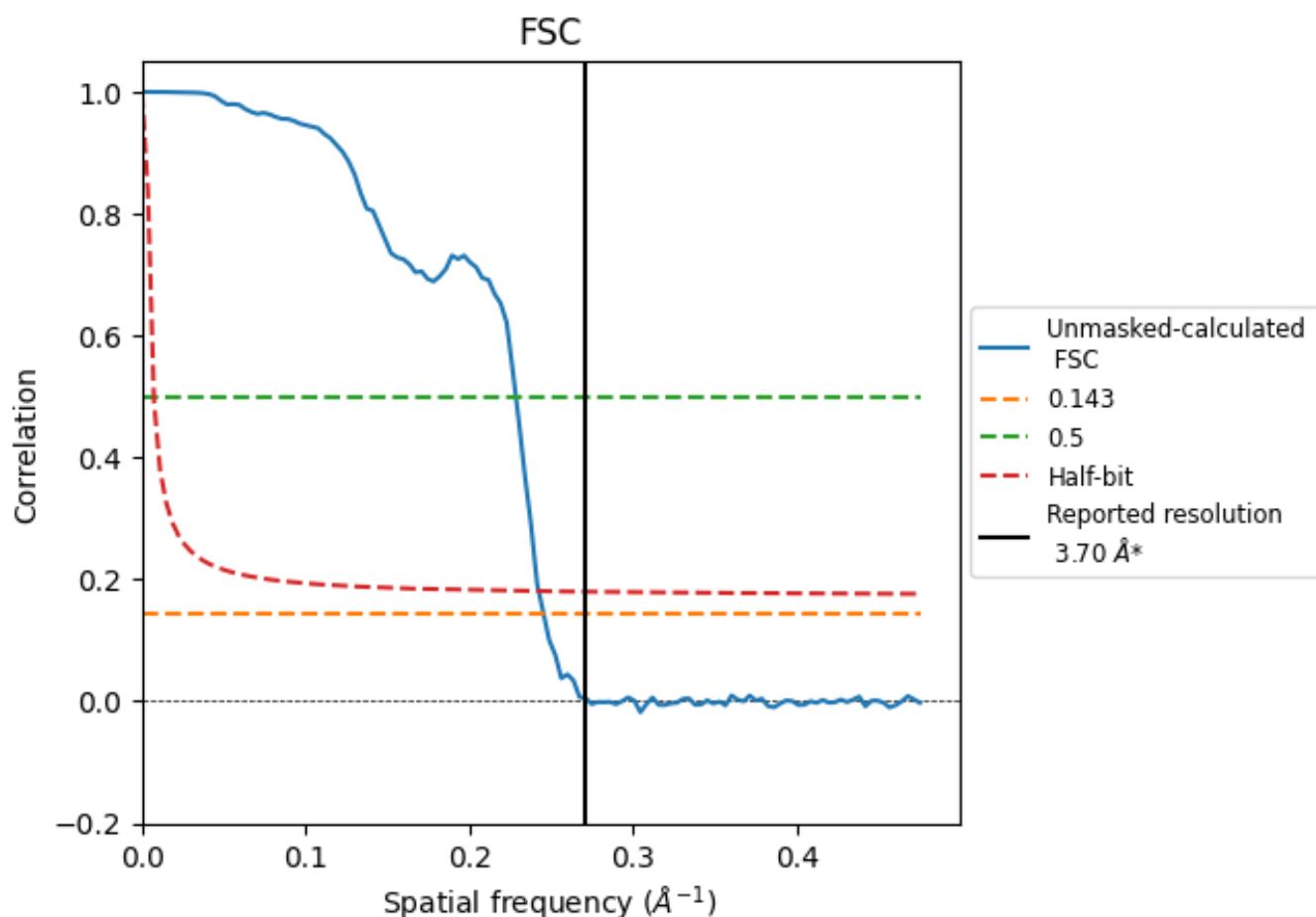


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

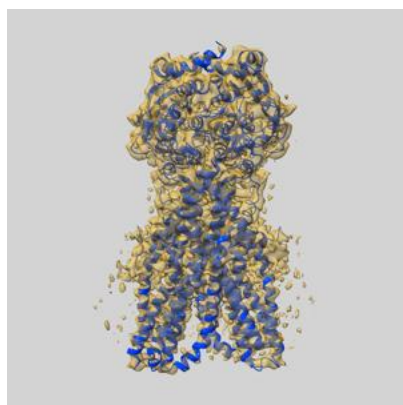
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.08	4.38	4.13

*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 4.08 differs from the reported value 3.7 by more than 10 %

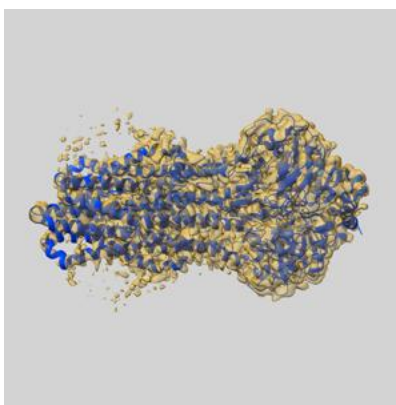
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19135 and PDB model 8RGN. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

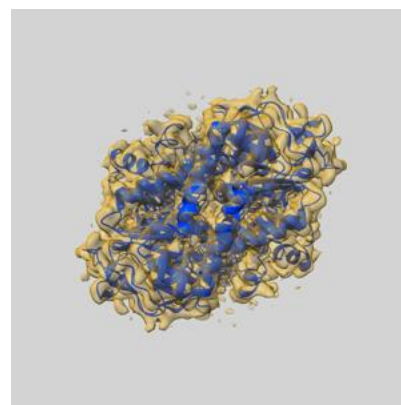
9.1 Map-model overlay [i](#)



X



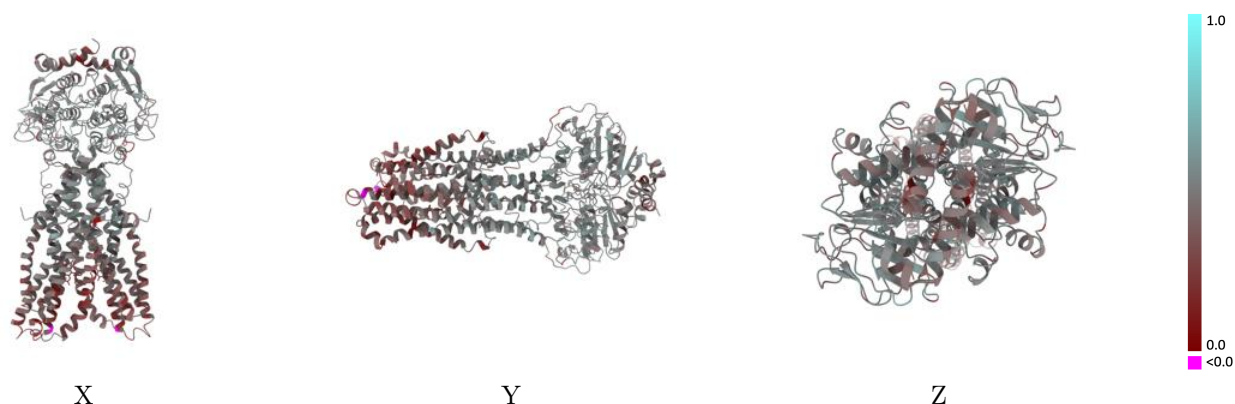
Y



Z

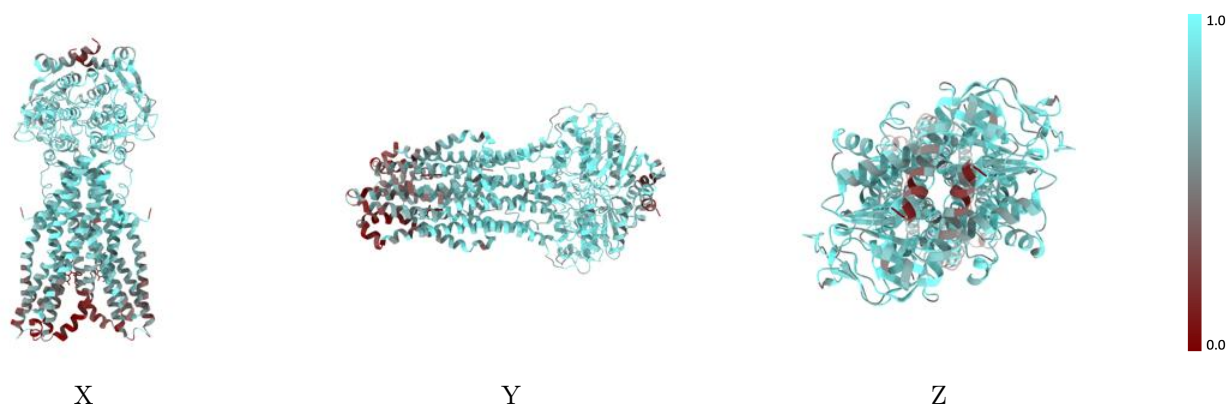
The images above show the 3D surface view of the map at the recommended contour level 0.381 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



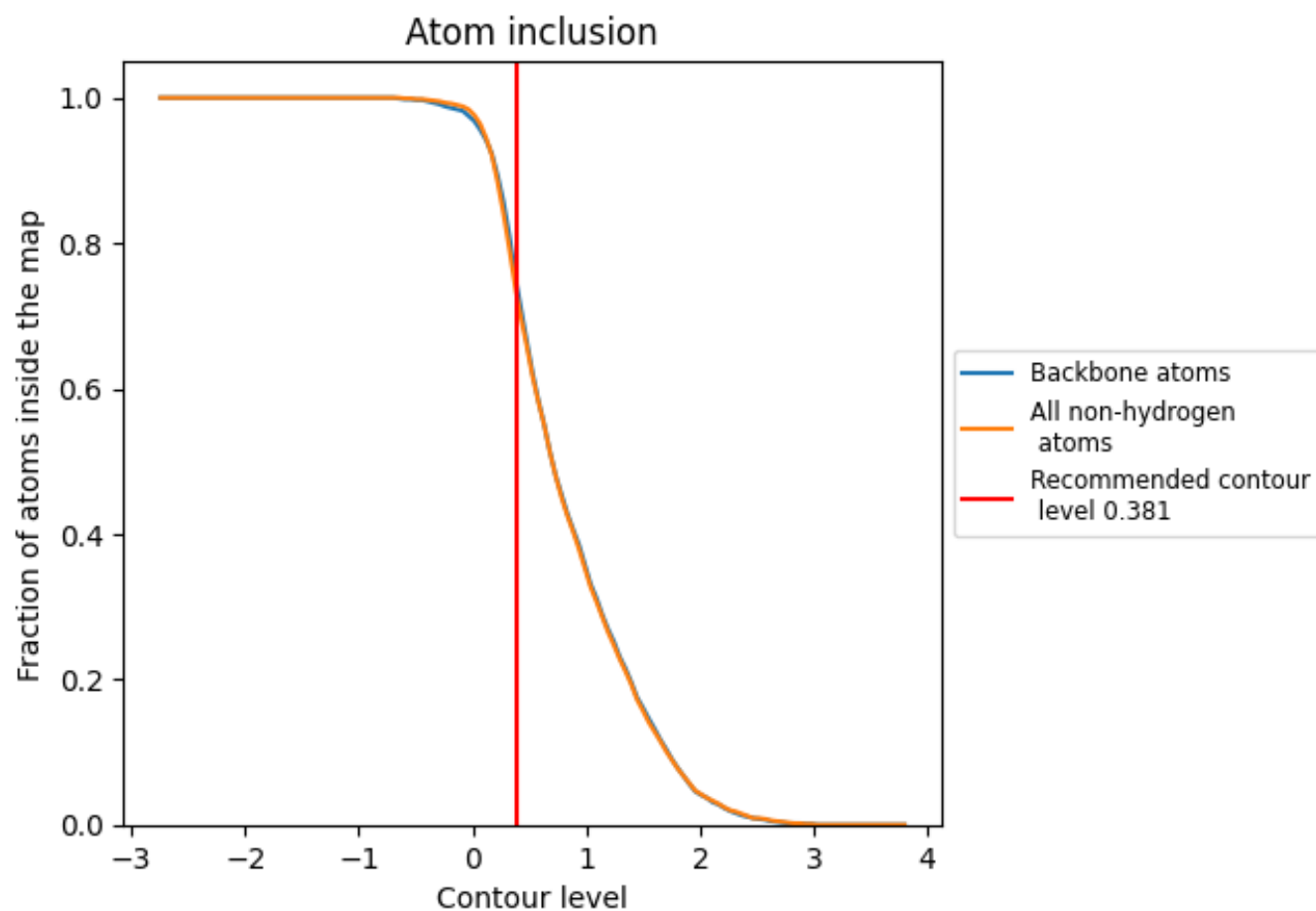
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.381).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 73% 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 (0.381) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7340	0.4380
A	0.7350	0.4380
B	0.7380	0.4380

