



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 08:49 AM UTC

PDB ID : 9KHS / pdb_00009khs
EMDB ID : EMD-62353
Title : Cryo-EM structure of Ufd2/Ubc4-Ub in complex with K29-linked diUb
(monomeric conformation)
Authors : Ai, H.S.; Tong, Z.B.; Liu, L.
Deposited on : 2024-11-11
Resolution : 4.31 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:

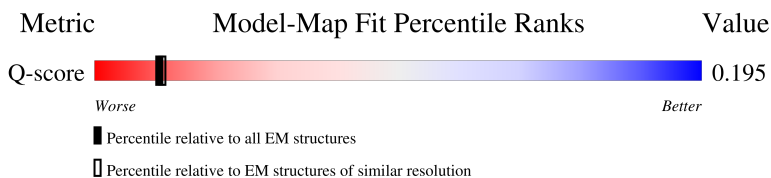
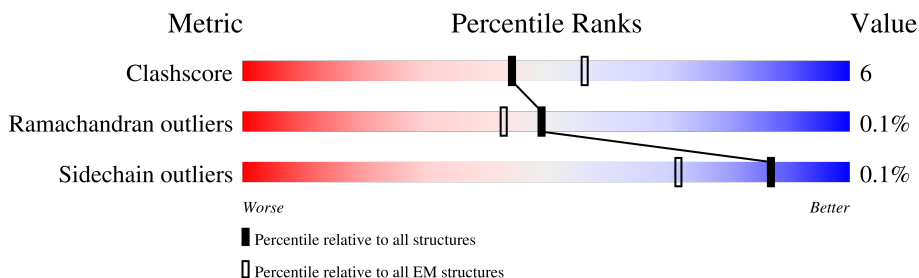
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.31 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.



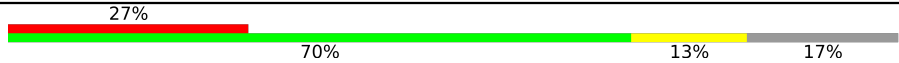
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3904 (3.81 - 4.80)

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	B	148	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>32%</p> </div> <div style="text-align: center;"> <p>84%</p> </div> <div style="text-align: center;"> <p>16%</p> </div> </div>
2	D	77	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>12%</p> </div> <div style="text-align: center;"> <p>86%</p> </div> <div style="text-align: center;"> <p>14%</p> </div> </div>
3	E	76	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>33%</p> </div> <div style="text-align: center;"> <p>78%</p> </div> <div style="text-align: center;"> <p>22%</p> </div> </div>
4	C	76	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>86%</p> </div> <div style="text-align: center;"> <p>76%</p> </div> <div style="text-align: center;"> <p>24%</p> </div> </div>

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Mol	Chain	Length	Quality of chain
5	A	961	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a red segment (27%), a green segment (70%), a yellow segment (13%), and a grey segment (17%). The percentages are labeled above or below the segments.</p>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9327 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 Ubiquitin-conjugating enzyme E2 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	148	1161	747	189	222	3	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	22	SER	CYS	engineered mutation	UNP P15731
B	108	SER	CYS	engineered mutation	UNP P15731

- Molecule 2 is a protein called Polyubiquitin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	77	606	379	105	120	2	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	48	CYS	LYS	engineered mutation	UNP P0CG48
D	77	ASP	-	expression tag	UNP P0CG48

- Molecule 3 is a protein called Polyubiquitin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	E	76	591	372	101	117	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	29	ARG	LYS	engineered mutation	UNP P0CG48

- Molecule 4 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	C	76	538	332	98	108	0	0

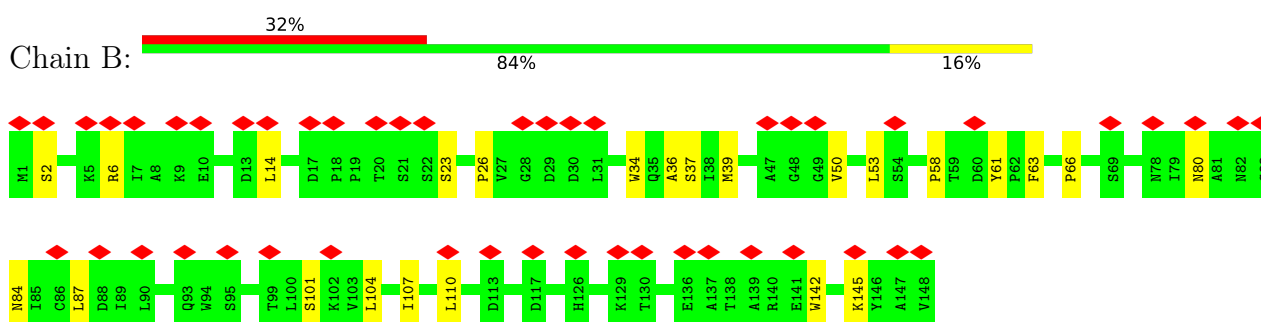
- Molecule 5 is a protein called E4 ubiquitin-protein ligase UFD2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	802	6431	4155	1054	1200	22	7	0

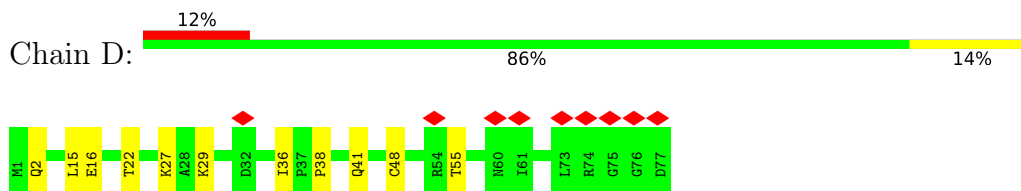
3 Residue-property plots [i](#)

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.

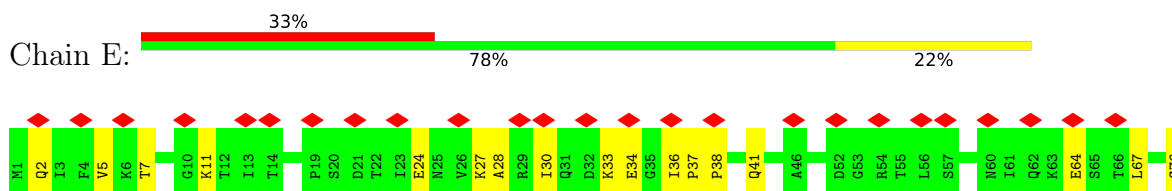
- Molecule 1: Ubiquitin-conjugating enzyme E2 4



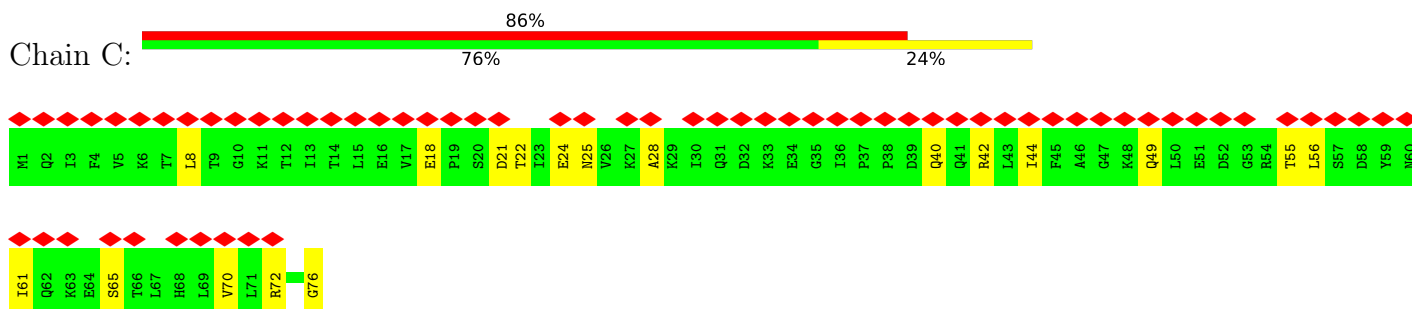
- Molecule 2: Polyubiquitin-C



- Molecule 3: Polyubiquitin-C



- Molecule 4: Ubiquitin



• Molecule 5: E4 ubiquitin-protein ligase UFD2



MET	THR	ALA	ILE	GLU	ASP	ILE	LEU	GLN	GLN	THR	THR	ASP	PRO	SER	THR	ARG	ASP	ARG	GLY	TYR	TYR	SER	LEU	LEU	LEU	LYS	SER	GLU	GLU	VAL	PRO	PRO	GLN	GLY	GLY	ASP	PHE	ILE	ASP	VAL	ASP	THR	THR	LEU	LEU	LEU	LEU	TYR	GLN	LEU	LEU	GLU	ASN	GLY	ALA	LEU	ASP	ILE	ASP	LYS	PRO	PRO	PHE	GLU	TYR	LEU						
ASN	ASP	CYS	PHE	ARG	ARG	ASN	GLN	GLN	GLN	THR	THR	ASP	THR	LYS	LYS	LYS	PRO	PRO	ARG	GLY	ALA	ALA	SER	SER	LEU	LEU	HIS	SER	THR	THR	PHE	GLN	GLN	ILE	ILE	ASP	ASP	ARG	ARG	THR	LEU	LEU	VAL	ILE	GLY	VAL	ASP	TYR	GLY	VAL	VAL	VAL	ALA	LEU	LEU	GLN	ILE	GLN	GLU	ASN	GLY	ALA	PHE	ILE	ASP	ASN	TYR	TYR	ASN	GLU	TYR	LEU
V121	S122	N123	V124	N125	S126	Y127	K188	T128	D129	F130	L131	S132	Q133	I134	I135	Q136	R137	A138	I139	L140	E141	G142	T143	A144	P208	L145	D146	L147	L148	N149	A150	V151	F152	P153	T154	L155	L156	E157	Y158	C159	N160	K161	H162	V163	S164	H165	F166	D167	L168	N169	E170	S171	V172	I173	Y174	N175	N176	V177	L178	T179	I180											
F181	E182	L183	F184	V185	T186	F187	K188	P189	I190	A191	E192	I193	F194	I197	D198	G199	F200	F201	A202	D203	C206	K207	P208	Q209	E212	R297	A298	D299	P302	E305	N309	G310	S313	N314	V320	A231	R321	F322	S323	Q324	L327	S330	I334	K336	F342	N343	N344	Q254																								
A255	E256	H257	I261	D262	F266	I267	V268	D269	K270	L271	V272	R273	L276	N277	S278	R279	T280	D281	M282	I289	A290	N291	K292	R297	A298	D299	P302	E305	N309	G310	S313	N314	V320	A231	R321	F322	S323	Q324	L327	S330	I334	K336	F342	N343	N344																											
R356	L357	N358	S359	D360	R372	LYS	THR	ALA	ASP	S377	K378	P379	I382	Y395	E404	E405	K406	M407	G408	S409	E410	I411	K412	I418	E419	K420	I421	K422	K423	I424	A425	A426	N427	H428	D429	V430	F431	A432	R433	F434	I435	T436	A437	Q438	L439	E443	K444	K447	T448	T449	E450																					
S451	Q457	Q458	F459	F460	A461	H462	Q466	D471	C474	T478	F479	R482	F490	P491	F492	K493	Q494	I495	K496	L497	PRO	LEU	I1E	PRO	ASP	GLN	ILE	GLY	VAL	GLU	ASN	VAL	ASP	ASN	ALA	ASP	F514	L515	R516	F431	A432	R433	F434	I435	T436	A437	Q438	L439	E443	K444	K447	T448	T449	E450																		
Y637	Y640	Q645	P648	I649	F650	L555	G556	C568	P569	E570	T593	M600	M601	F604	E605	H606	D607	L615	V623	K627	THR	GLY	SER	SER	GLY	VAL	GLU	ASN	VAL	ASP	ASN	ALA	ASP	F514	L515	R516	F431	A432	R433	F434	I435	T436	A437	Q438	L439	E443	K444	K447	T448	T449	E450																					
L692	S693	N694	L695	A696	E697	V698	H699	N700	E704	N707	ARG	ALA	ARG	GLY	ALA	PRO	PRO	THR	ARG	GLU	GLU	D720	K721	E722	L723	Q724	T725	R726	A730	S737	S744	S752	K753	D754	P762	E763	I764	R767	M771	L772	N773	Y774	N775	S778	K783	C784	G785																									
E786	L787	K788	V789	K790	D791	P792	Q793	S794	Y795	S796	F797	N798	P799	L806	L813	S814	S817	E818	S821	A822	K825	R828	S829	F830	H831	R832	R837	A838	V839	D840	I841	L842	G843	R844	K845	T846	G847	L848	A849	E852	F853	L854	L857	F860	A861	N862	K863	A864	E865																							
K869	A870	D871	E872	D875	G878	G879	D880	V881	P882	D883	E884	F885	L886	D887	P888	L889	M890	I893	H894	K895	D896	P897	V898	L899	L900	P901	A902	S903	K904	N905	N906	I907	D908	R909	A914	S918	D919	S920	T921	D922	N925	R926	N927	P928	L929	L931	E932	D933	I934	T935	P936																					
N937	E938	E939	L940	R941	Q942	K943	I944	L945	C946	F947	K948	K949	Q950	K951	K952	E953	E954	A955	LYS	HIS	LYS	ALA	SER	GLU																																																

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	191564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.182	Depositor
Minimum map value	-0.161	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0165	Depositor
Map size (\AA)	219.58, 219.58, 219.58	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0979, 1.0979, 1.0979	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	B	0.25	0/1197	0.57	0/1634
2	D	0.28	0/612	0.63	0/824
3	E	0.25	0/597	0.56	0/805
4	C	0.26	0/543	0.58	0/735
5	A	0.24	0/6596	0.57	1/8920 (0.0%)
All	All	0.25	0/9545	0.57	1/12918 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	531	VAL	N-CA-C	-5.24	107.72	112.12

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1161	0	1145	16	0
2	D	606	0	625	12	0
3	E	591	0	607	12	0
4	C	538	0	496	13	0
5	A	6431	0	6365	73	0
All	All	9327	0	9238	118	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 6.

The worst 5 of 118 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:D:29:LYS:NZ	3:E:76:GLY:HA2	1.95	0.80
5:A:482:ARG:HH12	5:A:492:PHE:HE1	1.31	0.76
5:A:297:ARG:HD3	5:A:395:TYR:HA	1.76	0.66
2:D:29:LYS:HZ1	3:E:76:GLY:HA2	1.63	0.62
1:B:14:LEU:HD11	1:B:101:SER:HB3	1.83	0.61

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	B	146/148 (99%)	141 (97%)	5 (3%)	0	100	100
2	D	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
3	E	74/76 (97%)	74 (100%)	0	0	100	100
4	C	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
5	A	799/961 (83%)	768 (96%)	30 (4%)	1 (0%)	48	83
All	All	1168/1338 (87%)	1124 (96%)	43 (4%)	1 (0%)	49	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	491	PRO

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	B	130/130 (100%)	130 (100%)	0	100	100
2	D	69/69 (100%)	69 (100%)	0	100	100
3	E	66/68 (97%)	66 (100%)	0	100	100
4	C	50/68 (74%)	50 (100%)	0	100	100
5	A	708/867 (82%)	707 (100%)	1 (0%)	88	88
All	All	1023/1202 (85%)	1022 (100%)	1 (0%)	87	88

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	881	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
5	A	254	GLN
5	A	343	ASN
5	A	702	GLN
5	A	291	ASN
5	A	344	ASN

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](#)

There are no ligands in this entry.

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.

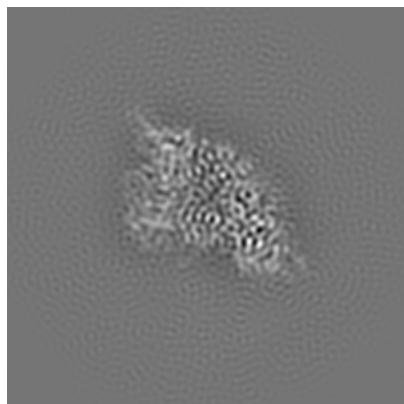
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62353. These allow visual inspection of the internal detail of the map and identification of artifacts.

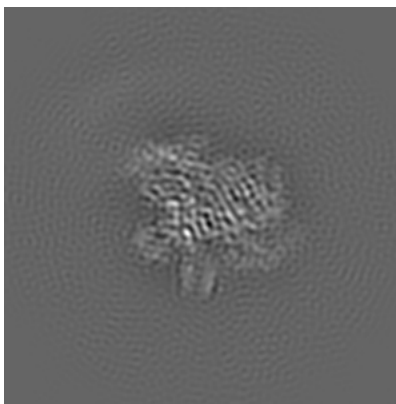
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

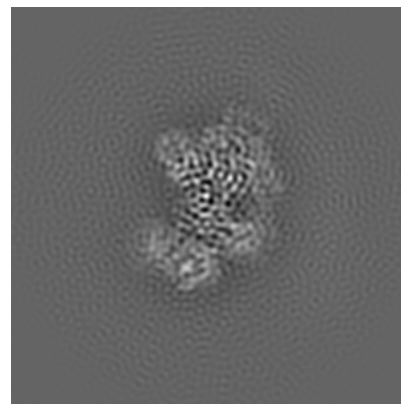
6.1.1 Primary map



X

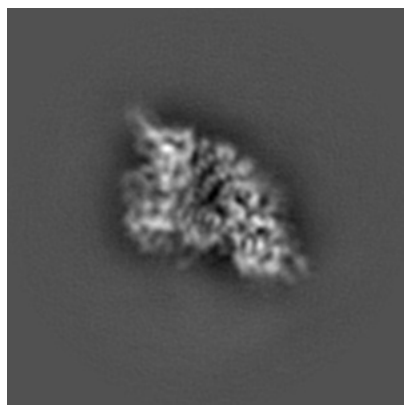


Y

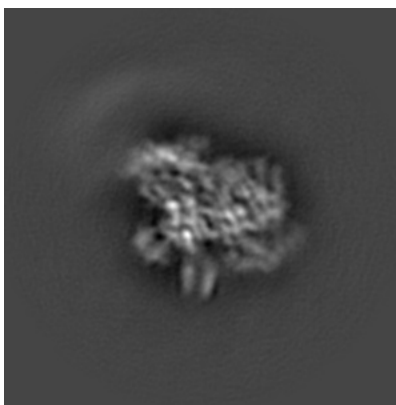


Z

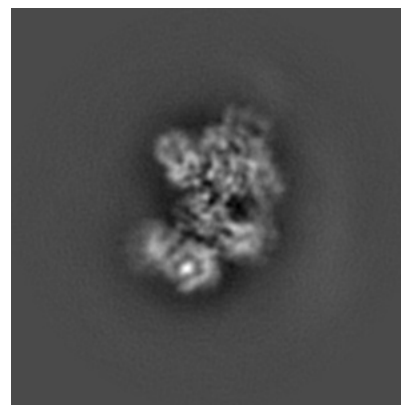
6.1.2 Raw map



X



Y

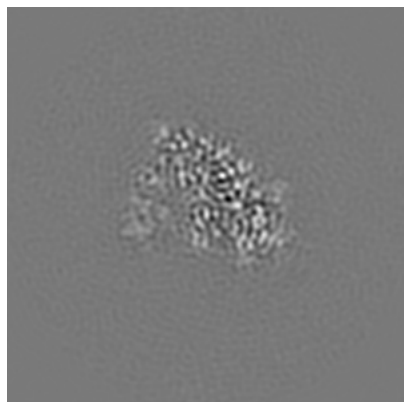


Z

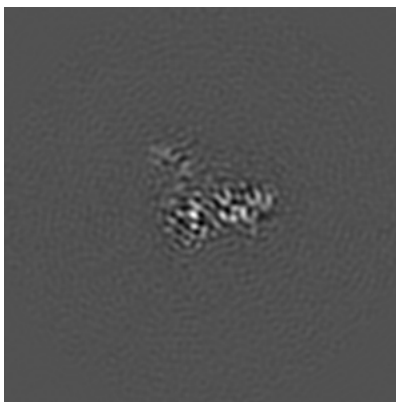
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

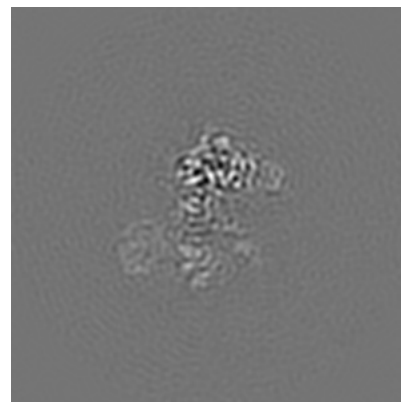
6.2.1 Primary map



X Index: 100

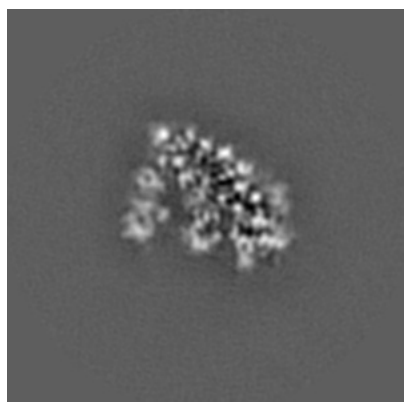


Y Index: 100

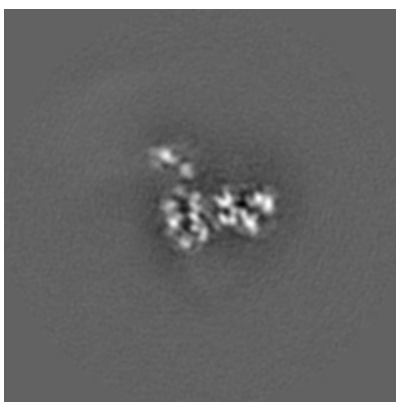


Z Index: 100

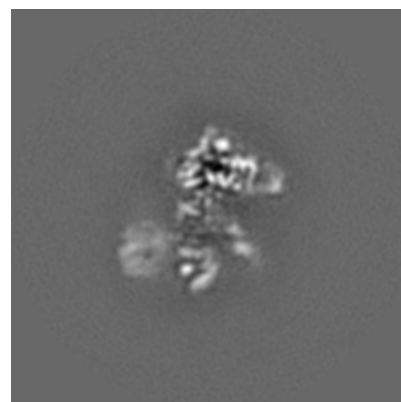
6.2.2 Raw map



X Index: 100



Y Index: 100

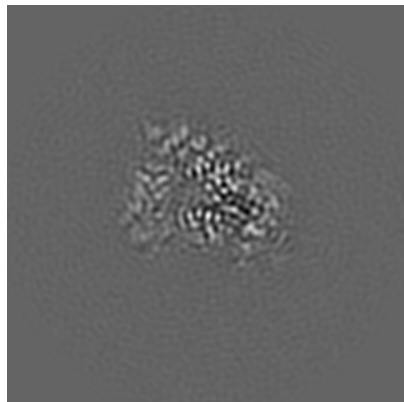


Z Index: 100

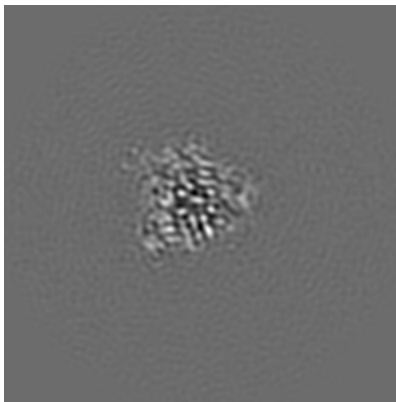
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

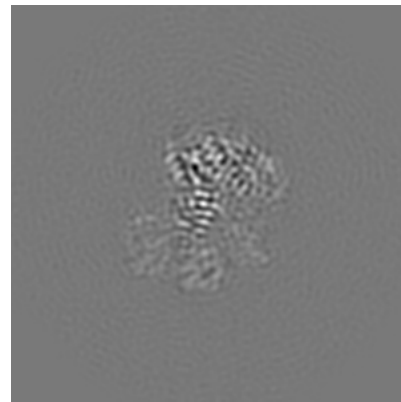
6.3.1 Primary map



X Index: 96

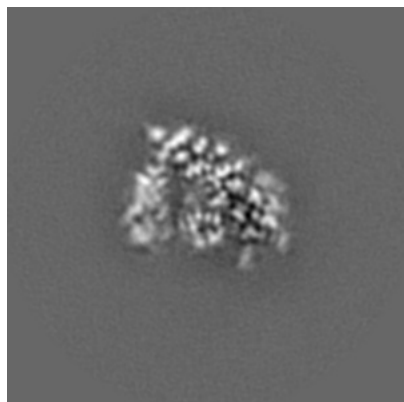


Y Index: 121

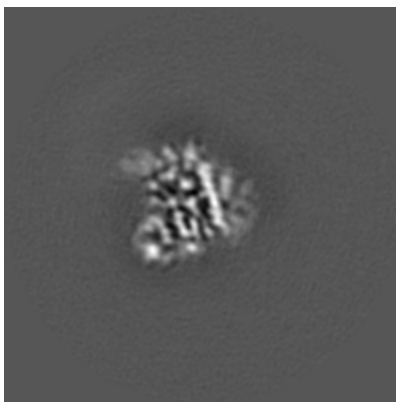


Z Index: 94

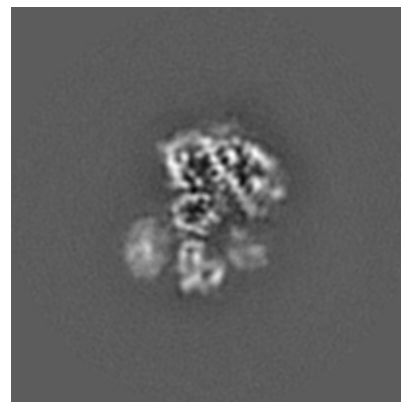
6.3.2 Raw map



X Index: 97



Y Index: 123

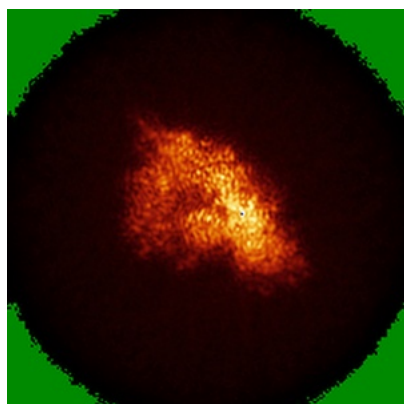


Z Index: 92

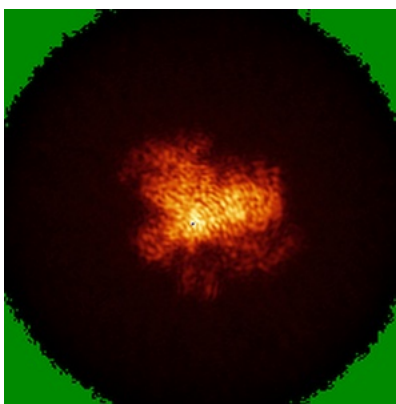
The images above show the largest variance slices of the map in three orthogonal directions.

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

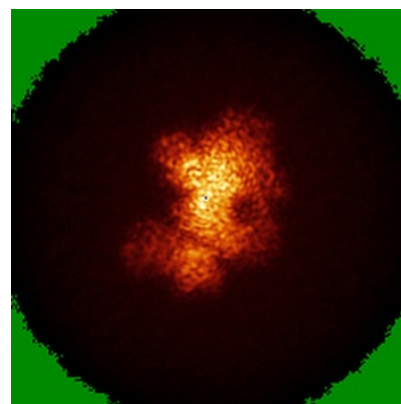
6.4.1 Primary map



X

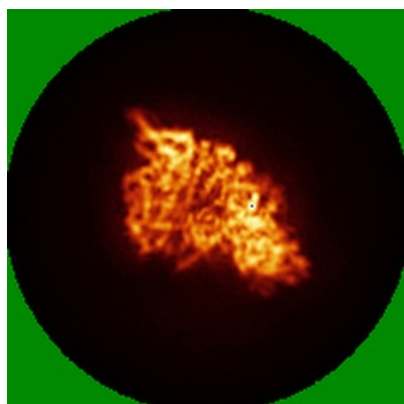


Y

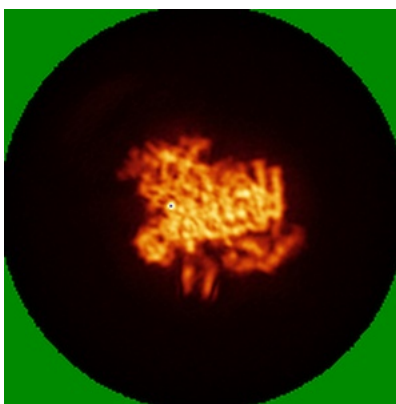


Z

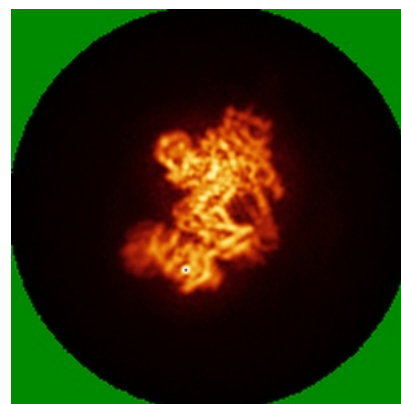
6.4.2 Raw map



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.

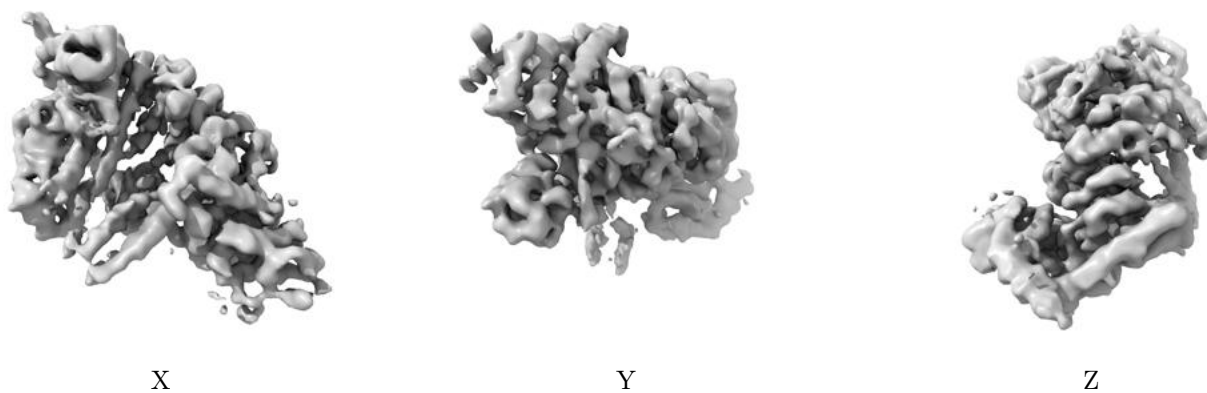
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0165. 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.

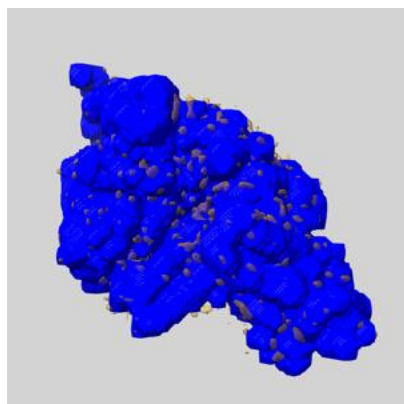
6.6 Mask visualisation [i](#)

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

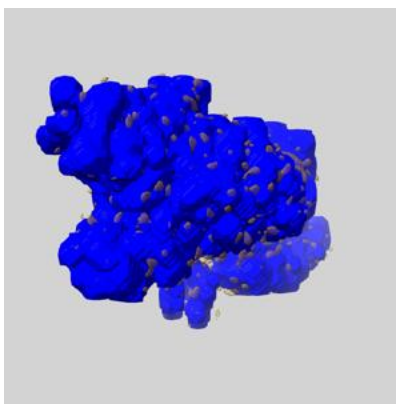
A mask typically either:

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

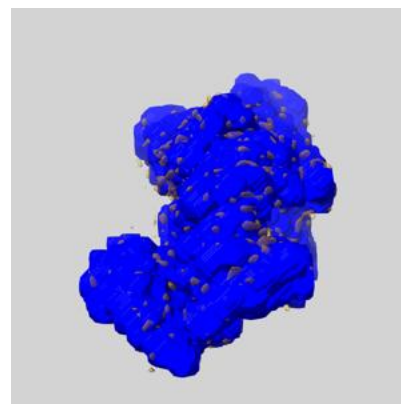
6.6.1 emd_62353_msk_1.map [i](#)



X



Y

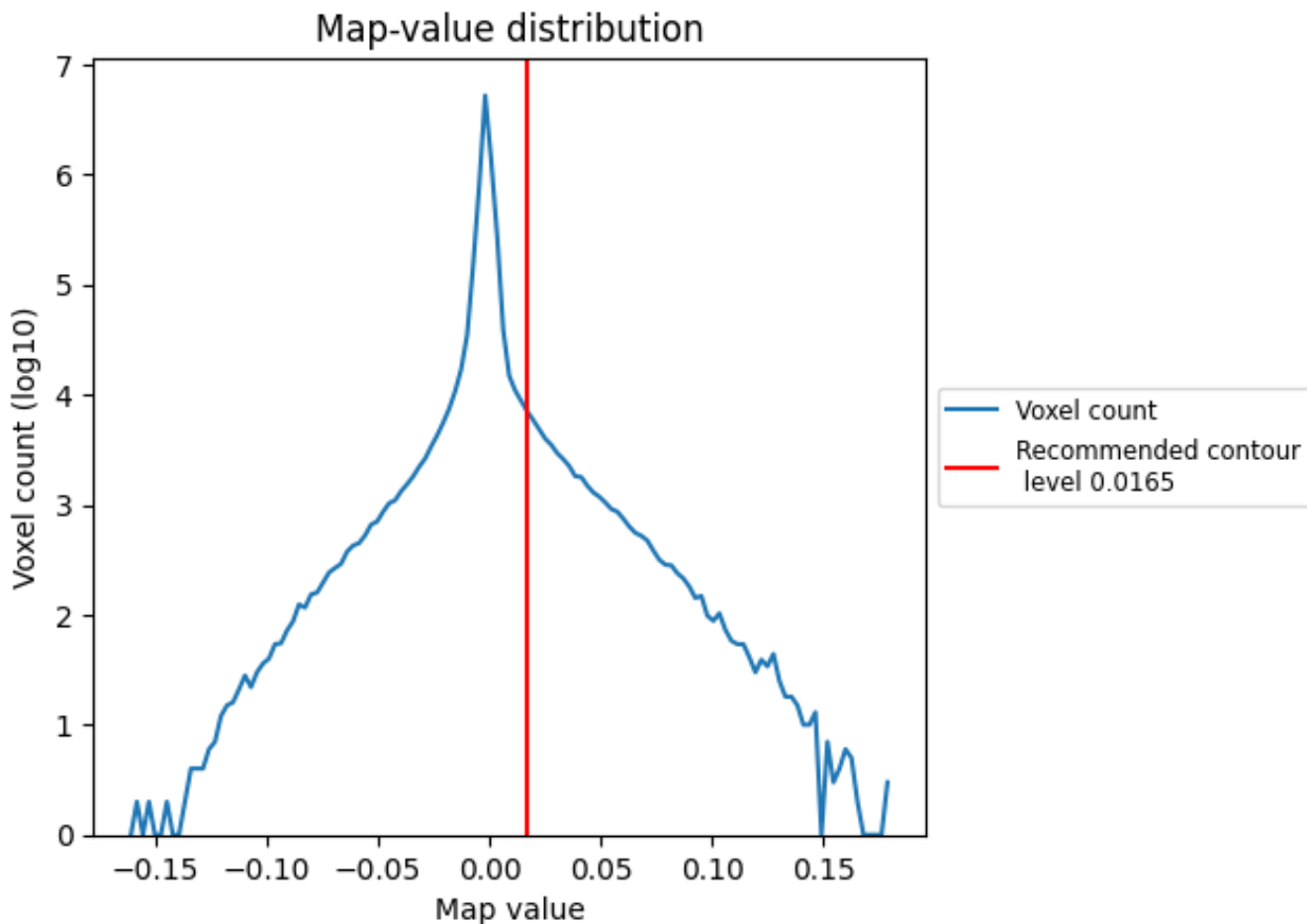


Z

7 Map analysis [i](#)

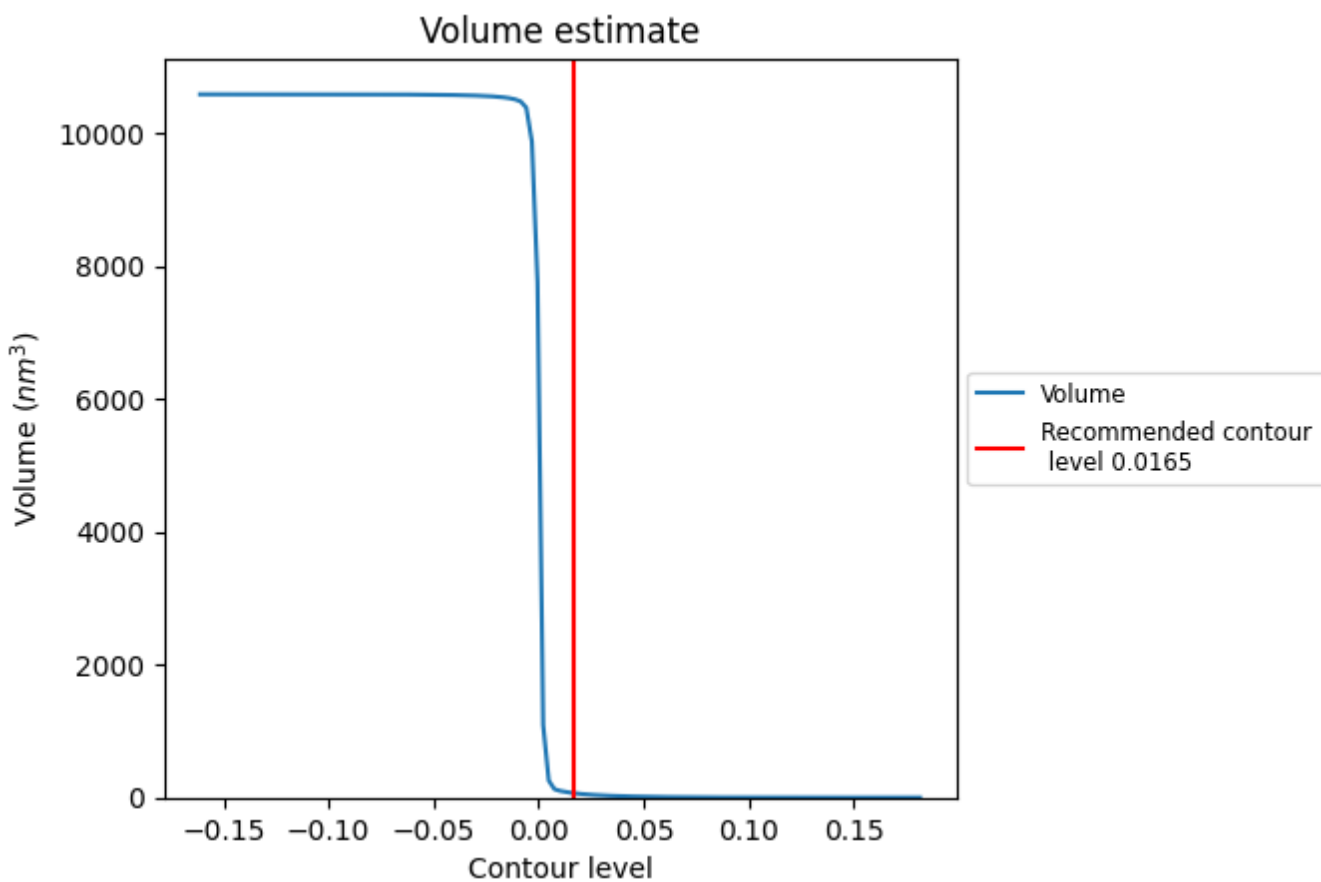
This section contains the results of statistical analysis of the map.

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.

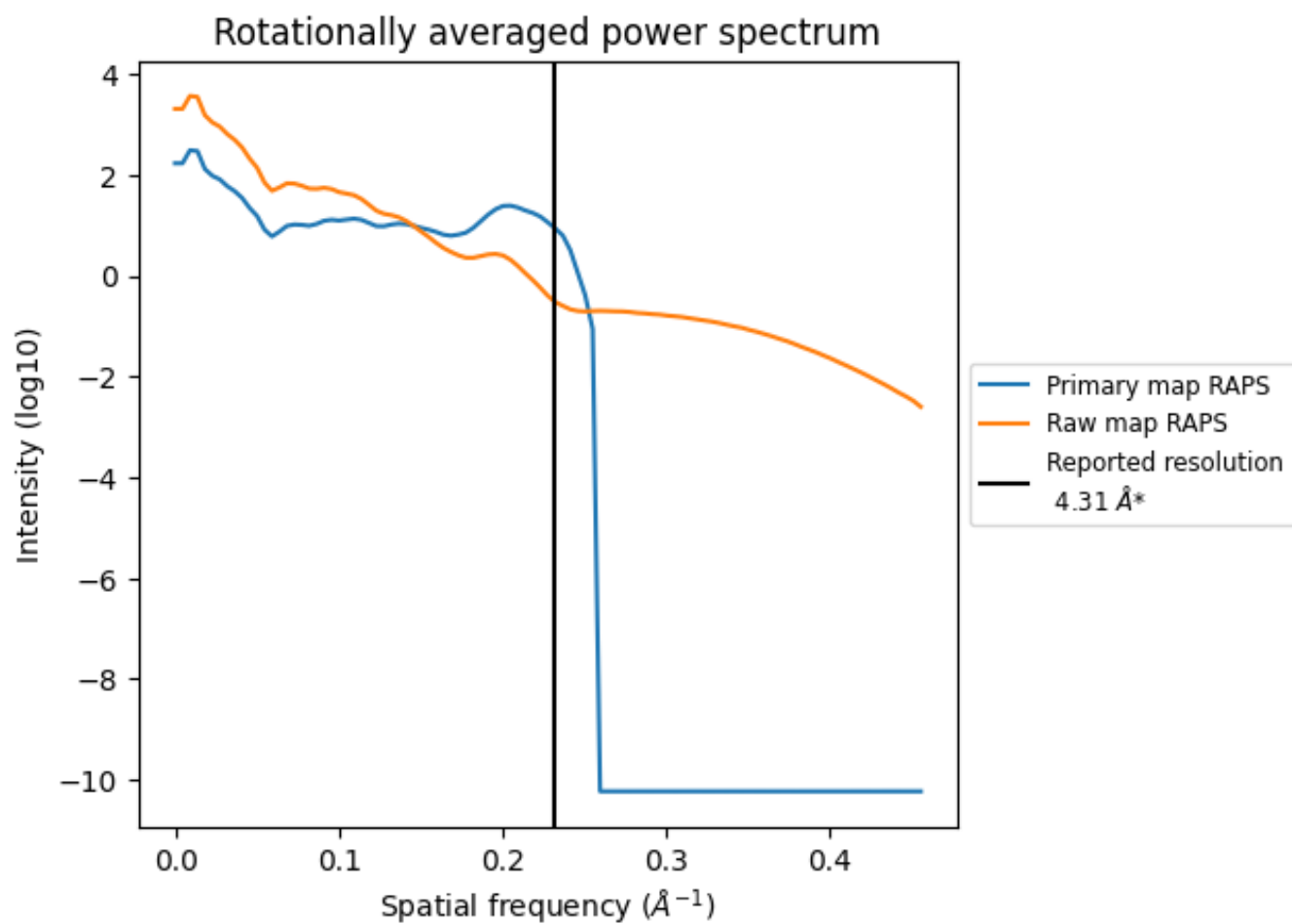
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 67 nm³; this corresponds to an approximate mass of 61 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 [i](#)

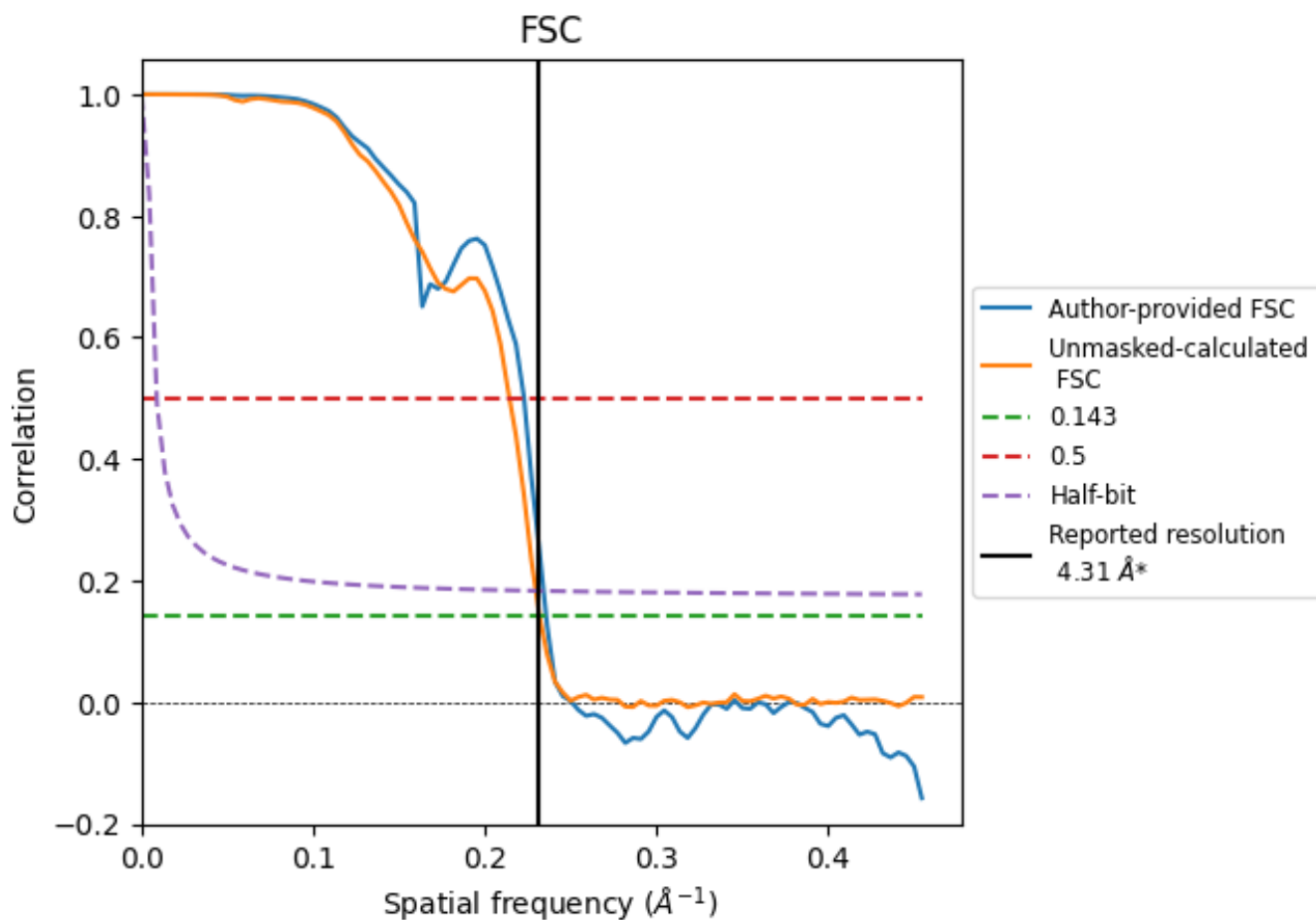


*Reported resolution corresponds to spatial frequency of 0.232 Å⁻¹

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 0.232 Å⁻¹

8.2 Resolution estimates [i](#)

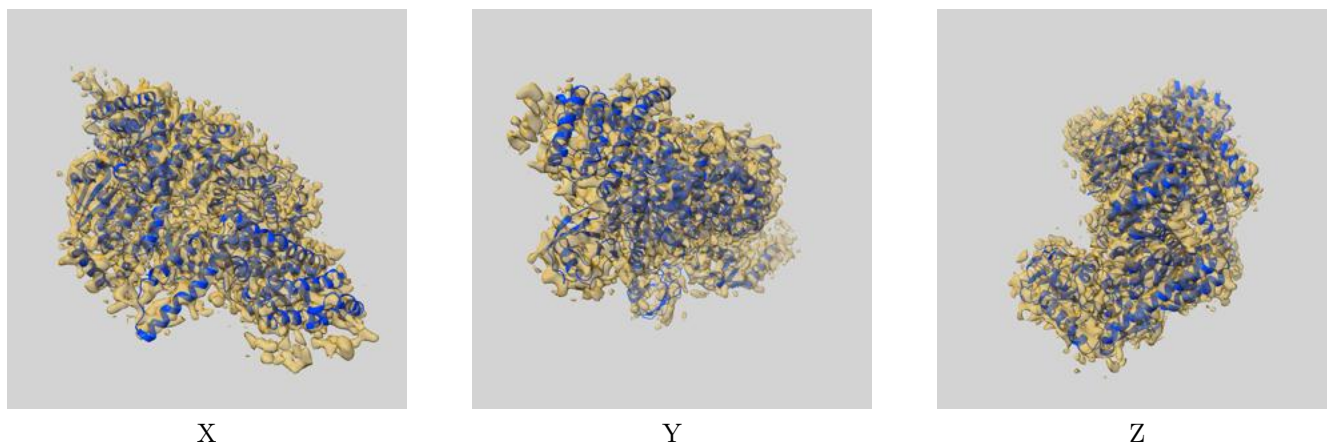
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.31	-	-
Author-provided FSC curve	4.23	4.48	4.26
Unmasked-calculated*	4.31	4.66	4.34

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

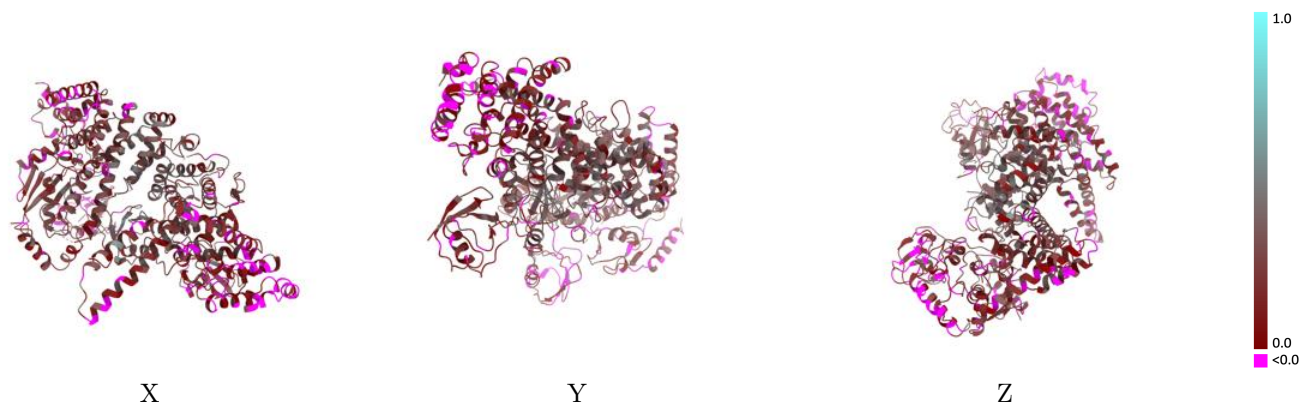
This section contains information regarding the fit between EMDB map EMD-62353 and PDB model 9KHS. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



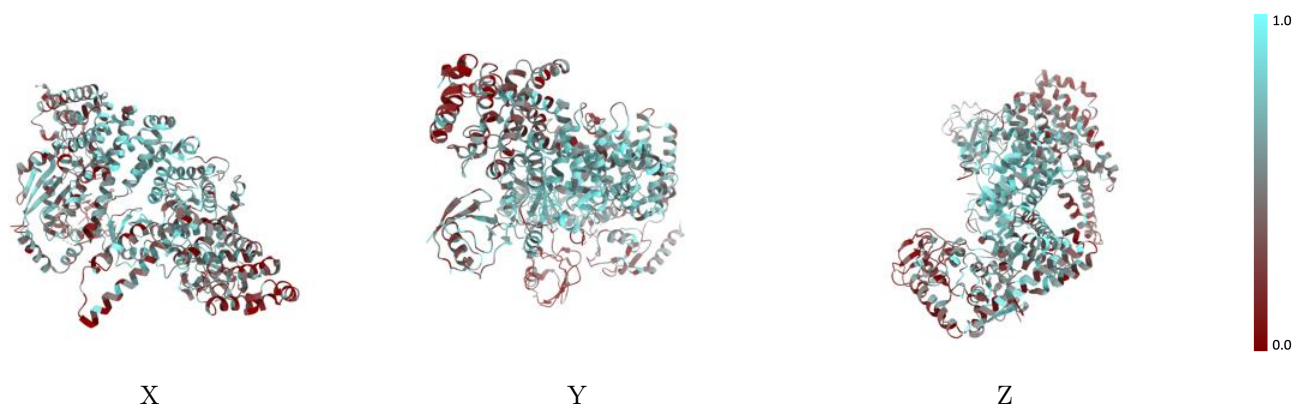
The images above show the 3D surface view of the map at the recommended contour level 0.0165 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



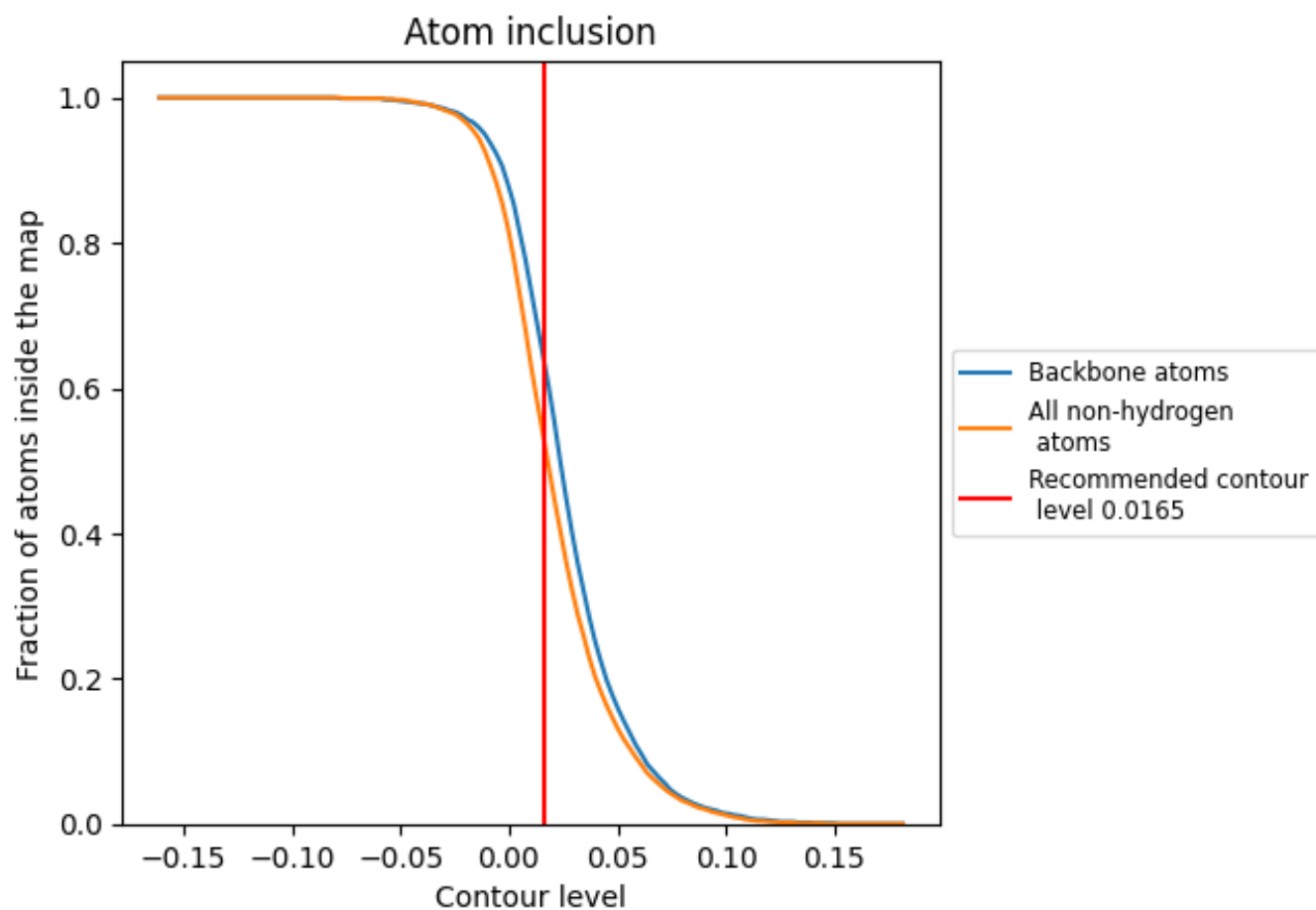
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0165).

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 52% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.0165) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5230	0.1950
A	0.5350	0.1960
B	0.5380	0.1960
C	0.1840	0.0630
D	0.6570	0.3080
E	0.5310	0.1840

