



# wwPDB EM Validation Summary Report ⓘ

Jan 15, 2025 – 08:34 PM JST

PDB ID : 8YIX  
EMDB ID : EMD-39332  
Title : Cryo-EM structure of human proteasome assembly intermediate half-proteasome  
Authors : Han, Y.; Han, Q.; Tang, Q.; Zhang, Y.; Liu, K.  
Deposited on : 2024-02-29  
Resolution : 2.91 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

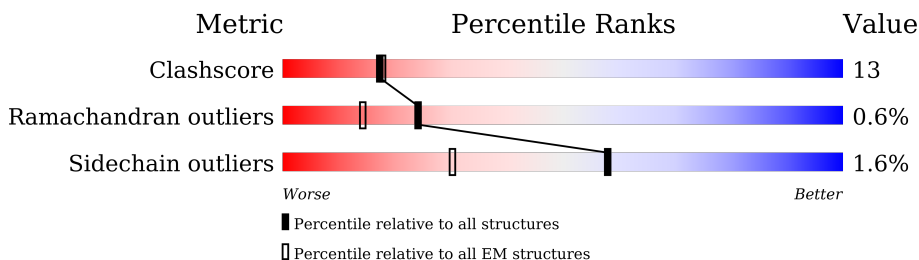
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.91 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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  $\geq 3$ , 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	234	 76% 21% 5%
2	B	261	 72% 23% 5%
3	C	248	 75% 20% 5%
4	D	241	 77% 23%
5	E	263	 73% 17% 9%
6	F	255	 77% 17% 5%
7	G	246	 76% 23%
8	H	277	 64% 21% 14%

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Mol	Chain	Length	Quality of chain
9	I	205	
10	J	201	
11	K	263	
12	L	241	
13	M	253	
14	N	239	
15	f	288	
16	g	264	
17	h	141	

## 2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 29572 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 Proteasome subunit alpha type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	232	Total	C	N	O	S	0	0
			1797	1146	304	340	7		

- Molecule 2 is a protein called Proteasome subunit alpha type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	246	Total	C	N	O	S	0	0
			1903	1202	323	368	10		

- Molecule 3 is a protein called Proteasome subunit alpha type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	236	Total	C	N	O	S	0	0
			1827	1148	322	352	5		

- Molecule 4 is a protein called Proteasome subunit alpha type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	241	Total	C	N	O	S	0	0
			1844	1161	305	366	12		

- Molecule 5 is a protein called Proteasome subunit alpha type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	239	Total	C	N	O	S	1	0
			1879	1179	339	349	12		

- Molecule 6 is a protein called Proteasome subunit alpha type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	241	Total	C	N	O	S	1	0
			1873	1189	321	351	12		

- Molecule 7 is a protein called Proteasome subunit alpha type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	245	Total	C	N	O	S	0	0
			1899	1204	320	361	14		

- Molecule 8 is a protein called Proteasome subunit beta type-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	238	Total	C	N	O	S	1	0
			1807	1147	307	341	12		

- Molecule 9 is a protein called Proteasome subunit beta type-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	200	Total	C	N	O	S	1	0
			1568	999	262	289	18		

- Molecule 10 is a protein called Proteasome subunit beta type-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	196	Total	C	N	O	S	2	0
			1581	1013	269	289	10		

- Molecule 11 is a protein called Proteasome subunit beta type-5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	228	Total	C	N	O	S	2	0
			1764	1117	312	323	12		

- Molecule 12 is a protein called Proteasome subunit beta type-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	197	Total	C	N	O	S	1	0
			1514	960	260	283	11		

- Molecule 13 is a protein called Proteasome subunit beta type-4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	205	Total	C	N	O	S	1	0
			1597	1008	275	303	11		

- Molecule 14 is a protein called Proteasome subunit beta type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	188	Total	C	N	O	S	1	0
			1434	904	239	278	13		

- Molecule 15 is a protein called Proteasome assembly chaperone 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	f	277	Total	C	N	O	S	0	0
			2217	1412	372	414	19		

- Molecule 16 is a protein called Proteasome assembly chaperone 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	g	264	Total	C	N	O	S	0	0
			2062	1323	336	388	15		

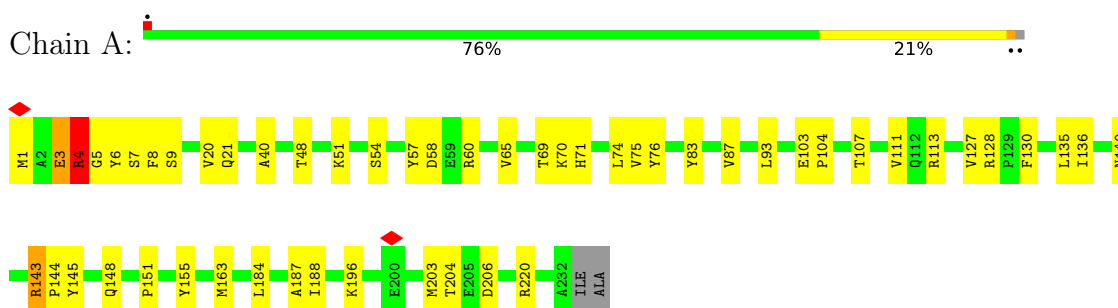
- Molecule 17 is a protein called Proteasome maturation protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	h	127	Total	C	N	O	S	0	0
			1006	638	168	195	5		

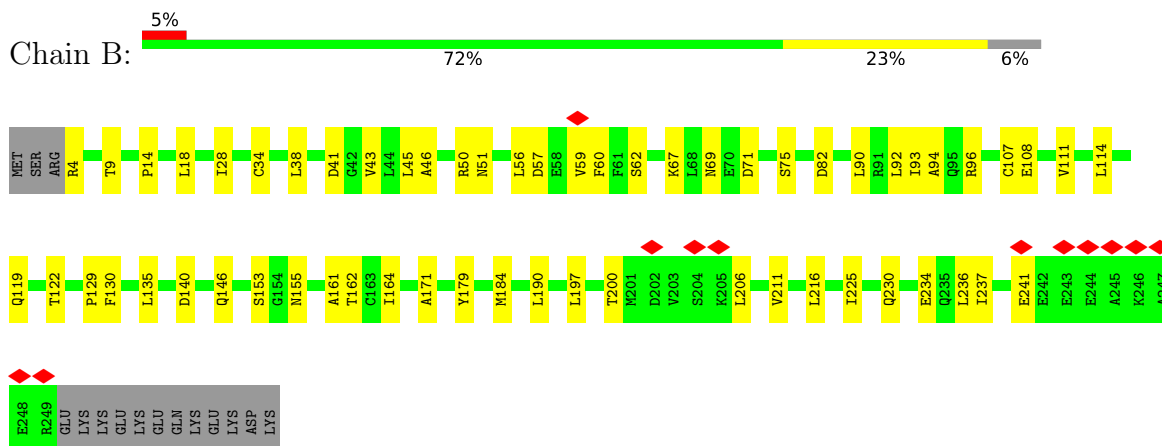
### 3 Residue-property plots [i](#)

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.

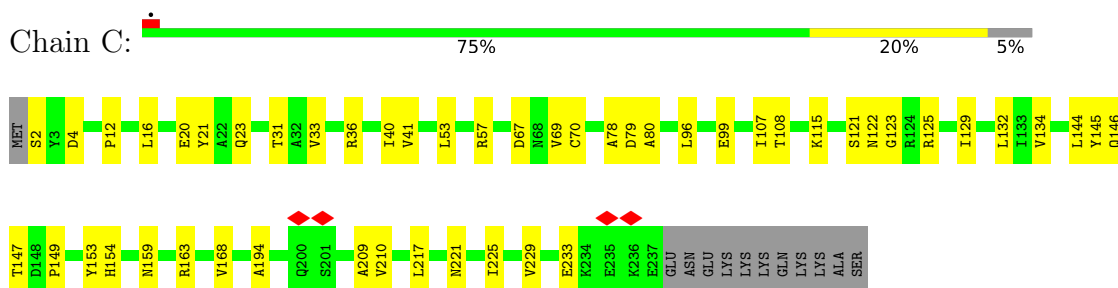
- Molecule 1: Proteasome subunit alpha type-2




- Molecule 2: Proteasome subunit alpha type-4

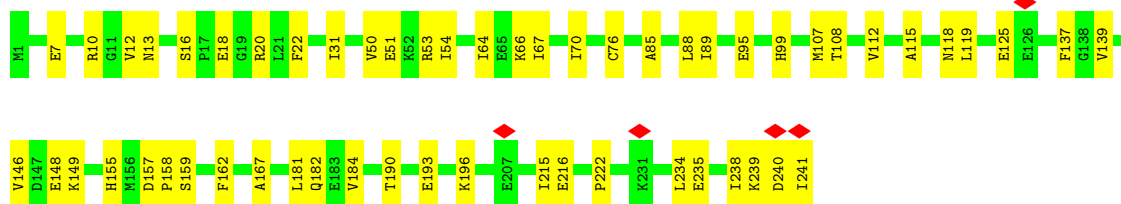


- Molecule 3: Proteasome subunit alpha type-7



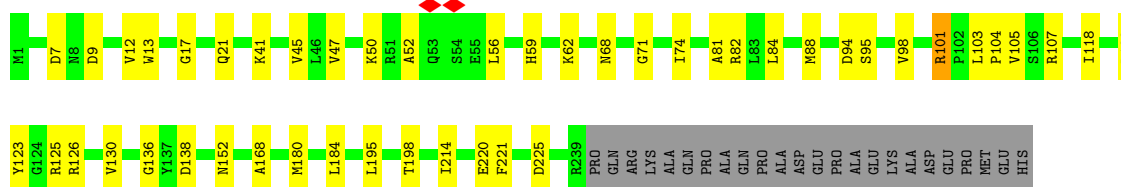
- Molecule 4: Proteasome subunit alpha type-5

Chain D:  77% 23%




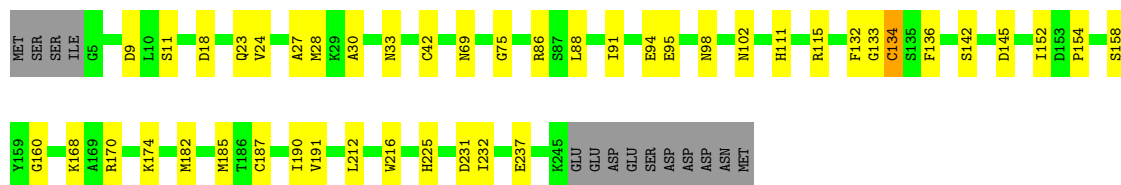
• Molecule 5: Proteasome subunit alpha type-1

Chain E:  73% 17% 9%




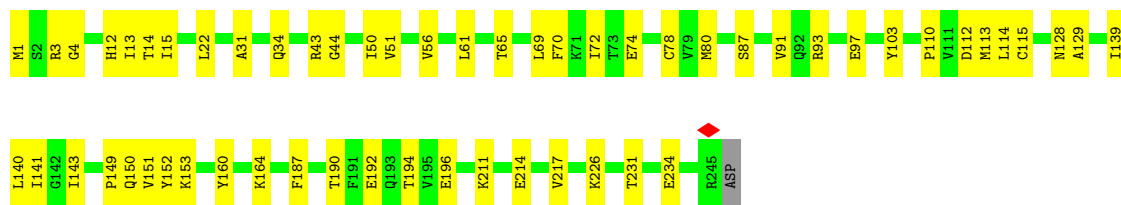
• Molecule 6: Proteasome subunit alpha type-3

Chain F:  77% 17% 5%



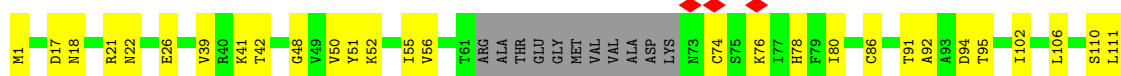
• Molecule 7: Proteasome subunit alpha type-6

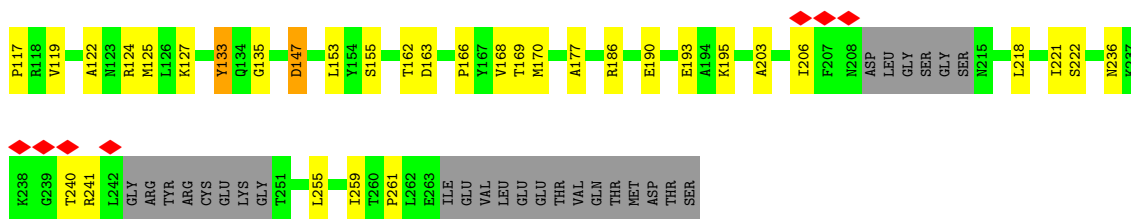
Chain G:  76% 23%



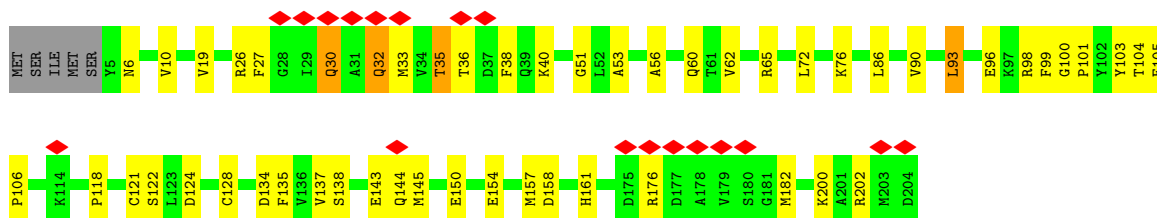
• Molecule 8: Proteasome subunit beta type-7

Chain H:  64% 21% 14%

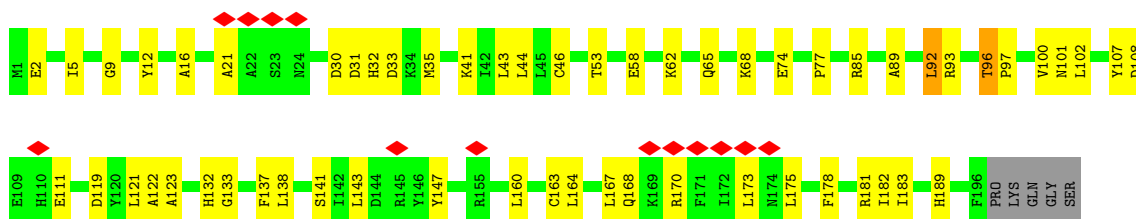




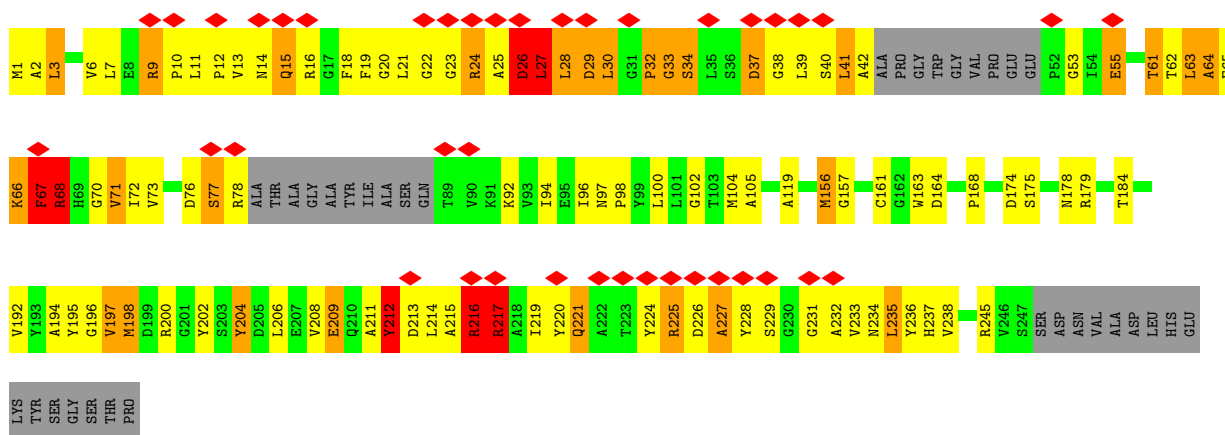
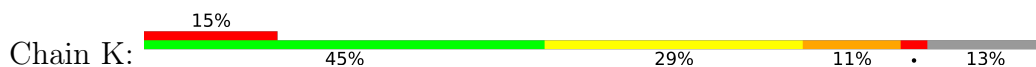
• Molecule 9: Proteasome subunit beta type-3

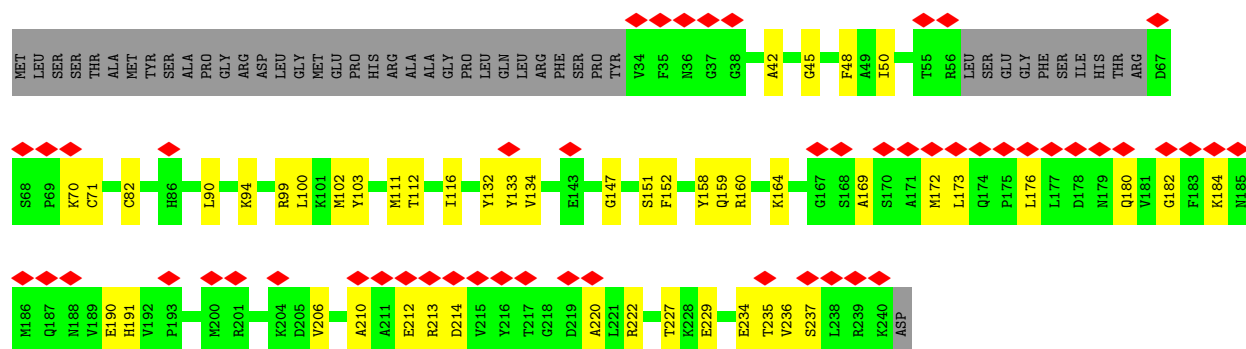


• Molecule 10: Proteasome subunit beta type-2

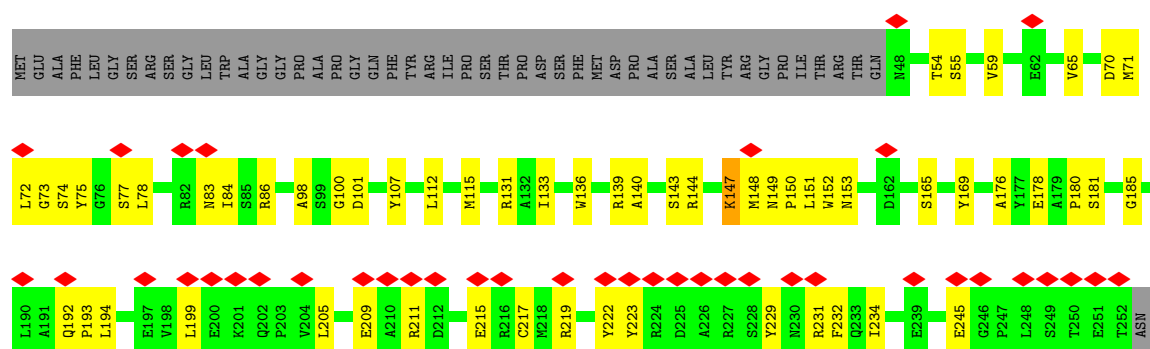


• Molecule 11: Proteasome subunit beta type-5

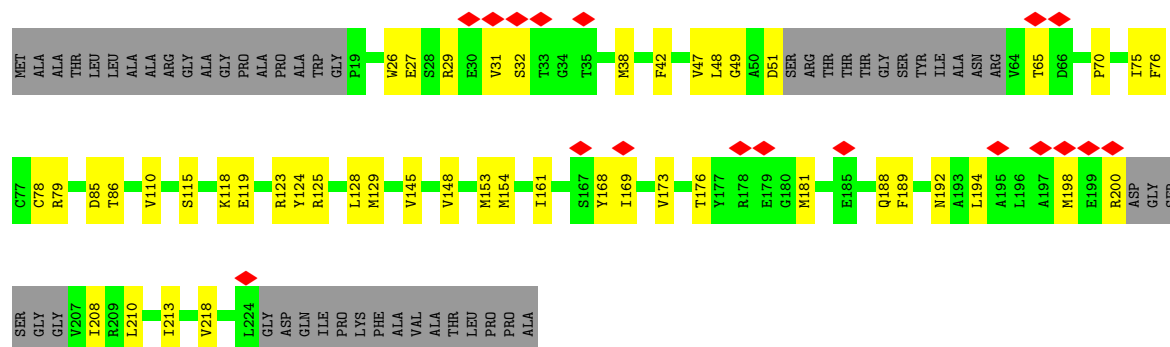




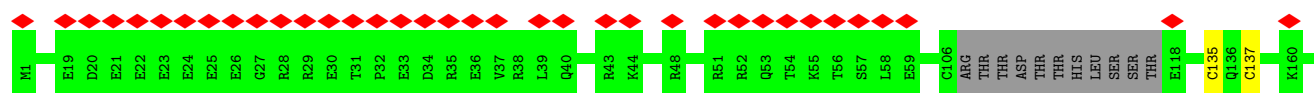
• Molecule 13: Proteasome subunit beta type-4



• Molecule 14: Proteasome subunit beta type-6

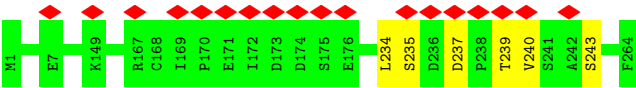


• Molecule 15: Proteasome assembly chaperone 1

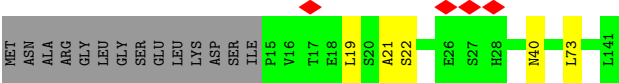
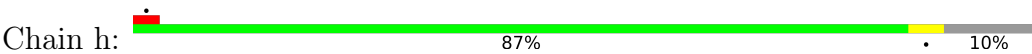




• Molecule 16: Proteasome assembly chaperone 2



• Molecule 17: Proteasome maturation protein



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	310562	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI 12	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	49.41	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	5.128	Depositor
Minimum map value	-3.506	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.161	Depositor
Recommended contour level	0.592	Depositor
Map size (Å)	316.49997, 316.49997, 316.49997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	0.70	0/1836	0.60	0/2489
2	B	0.65	0/1933	0.58	0/2613
3	C	0.62	0/1853	0.55	0/2509
4	D	0.57	0/1873	0.59	0/2528
5	E	0.62	0/1917	0.59	0/2589
6	F	0.63	0/1911	0.54	0/2575
7	G	0.65	0/1933	0.55	0/2613
8	H	0.56	0/1841	0.60	1/2492 (0.0%)
9	I	0.56	0/1597	0.59	1/2154 (0.0%)
10	J	0.53	0/1620	0.54	1/2191 (0.0%)
11	K	0.68	0/1803	1.05	8/2428 (0.3%)
12	L	0.43	0/1541	0.53	0/2075
13	M	0.42	0/1630	0.53	0/2205
14	N	0.46	0/1463	0.55	0/1979
15	f	0.54	1/2262 (0.0%)	0.62	1/3061 (0.0%)
16	g	0.58	0/2108	0.59	0/2858
17	h	0.61	0/1025	0.73	2/1381 (0.1%)
All	All	0.59	1/30146 (0.0%)	0.62	14/40740 (0.0%)

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	1
8	H	0	1
9	I	0	1
10	J	0	1
11	K	0	5
13	M	0	1
15	f	0	1
17	h	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	f	135	CYS	CB-SG	5.18	1.91	1.82

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	67	PHE	CB-CA-C	-19.09	72.21	110.40
11	K	212	TYR	CB-CG-CD2	-14.32	112.41	121.00
11	K	212	TYR	CB-CG-CD1	12.74	128.65	121.00
15	f	135	CYS	CA-CB-SG	7.77	127.98	114.00
11	K	67	PHE	N-CA-CB	-7.53	97.05	110.60

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	4	ARG	Sidechain
8	H	133	TYR	Peptide
9	I	99	PHE	Peptide
10	J	96	THR	Peptide
11	K	9	ARG	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1797	0	1770	35	0
2	B	1903	0	1876	39	0
3	C	1827	0	1812	34	0
4	D	1844	0	1832	53	0
5	E	1879	0	1872	33	0
6	F	1873	0	1855	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1899	0	1902	33	0
8	H	1807	0	1828	40	0
9	I	1568	0	1580	39	0
10	J	1581	0	1585	41	0
11	K	1764	0	1758	223	0
12	L	1514	0	1527	38	0
13	M	1597	0	1580	66	0
14	N	1434	0	1395	32	0
15	f	2217	0	2227	0	0
16	g	2062	0	2092	0	0
17	h	1006	0	1003	0	0
All	All	29572	0	29494	641	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 13.

The worst 5 of 641 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)
4:D:107:MET:CE	11:K:39:LEU:HD21	1.21	1.63
6:F:132:PHE:CZ	11:K:1:MET:CE	2.12	1.33
4:D:107:MET:HE3	11:K:39:LEU:CD2	1.59	1.32
4:D:107:MET:CE	11:K:39:LEU:CD2	2.10	1.30
6:F:132:PHE:CZ	11:K:1:MET:HE1	1.71	1.25

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	230/234 (98%)	218 (95%)	11 (5%)	1 (0%)	30 59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	244/261 (94%)	233 (96%)	11 (4%)	0	100	100
3	C	234/248 (94%)	223 (95%)	10 (4%)	1 (0%)	30	59
4	D	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
5	E	238/263 (90%)	228 (96%)	10 (4%)	0	100	100
6	F	240/255 (94%)	235 (98%)	5 (2%)	0	100	100
7	G	243/246 (99%)	231 (95%)	11 (4%)	1 (0%)	30	59
8	H	231/277 (83%)	209 (90%)	22 (10%)	0	100	100
9	I	199/205 (97%)	182 (92%)	17 (8%)	0	100	100
10	J	196/201 (98%)	178 (91%)	17 (9%)	1 (0%)	25	55
11	K	224/263 (85%)	181 (81%)	28 (12%)	15 (7%)	1	2
12	L	194/241 (80%)	173 (89%)	21 (11%)	0	100	100
13	M	204/253 (81%)	193 (95%)	11 (5%)	0	100	100
14	N	183/239 (77%)	162 (88%)	21 (12%)	0	100	100
15	f	273/288 (95%)	242 (89%)	31 (11%)	0	100	100
16	g	262/264 (99%)	235 (90%)	24 (9%)	3 (1%)	12	36
17	h	125/141 (89%)	110 (88%)	14 (11%)	1 (1%)	16	44
All	All	3759/4120 (91%)	3457 (92%)	279 (7%)	23 (1%)	24	51

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
11	K	61	THR
11	K	64	ALA
11	K	67	PHE
11	K	197	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	186/191 (97%)	181 (97%)	5 (3%)	40	72
2	B	198/221 (90%)	197 (100%)	1 (0%)	86	95
3	C	191/211 (90%)	191 (100%)	0	100	100
4	D	201/203 (99%)	201 (100%)	0	100	100
5	E	203/224 (91%)	202 (100%)	1 (0%)	86	95
6	F	195/212 (92%)	192 (98%)	3 (2%)	60	84
7	G	206/210 (98%)	206 (100%)	0	100	100
8	H	196/228 (86%)	194 (99%)	2 (1%)	73	90
9	I	169/174 (97%)	164 (97%)	5 (3%)	36	69
10	J	169/171 (99%)	169 (100%)	0	100	100
11	K	179/202 (89%)	148 (83%)	31 (17%)	1	4
12	L	162/199 (81%)	161 (99%)	1 (1%)	84	94
13	M	169/206 (82%)	169 (100%)	0	100	100
14	N	150/181 (83%)	148 (99%)	2 (1%)	65	86
15	f	251/262 (96%)	249 (99%)	2 (1%)	79	92
16	g	237/237 (100%)	234 (99%)	3 (1%)	65	86
17	h	117/128 (91%)	116 (99%)	1 (1%)	75	91
All	All	3179/3460 (92%)	3122 (98%)	57 (2%)	58	81

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	K	68	ARG
16	g	243	SER
11	K	192	VAL
16	g	239	THR
14	N	181[A]	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
11	K	237	HIS
13	M	153	ASN
17	h	80	GLN
15	f	280	ASN
9	I	30	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](#)

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.

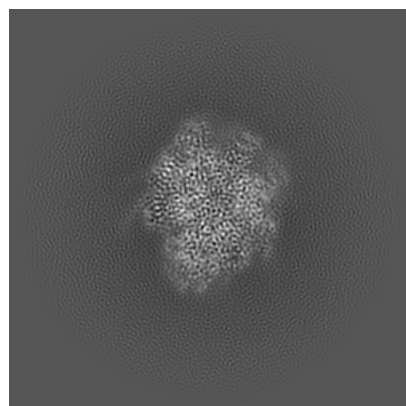
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39332. These allow visual inspection of the internal detail of the map and identification of artifacts.

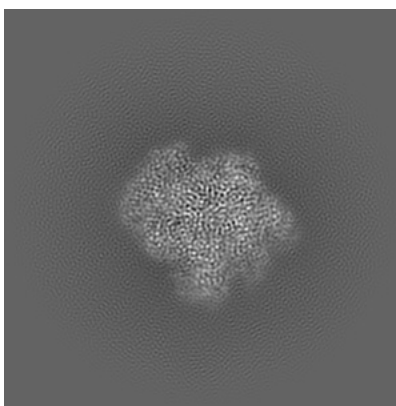
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

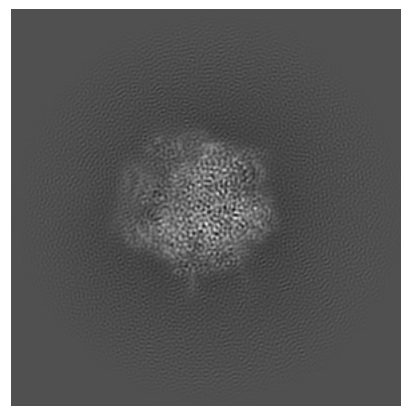
#### 6.1.1 Primary map



X

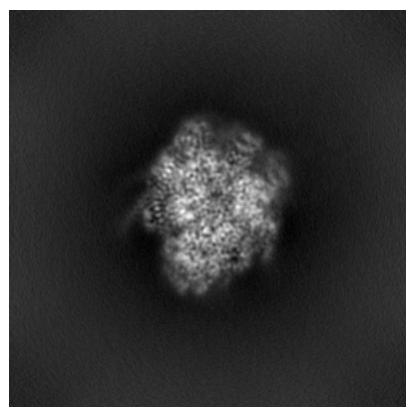


Y

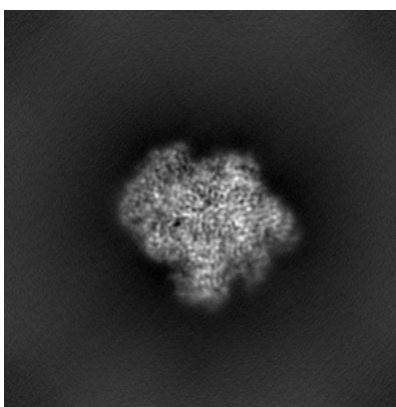


Z

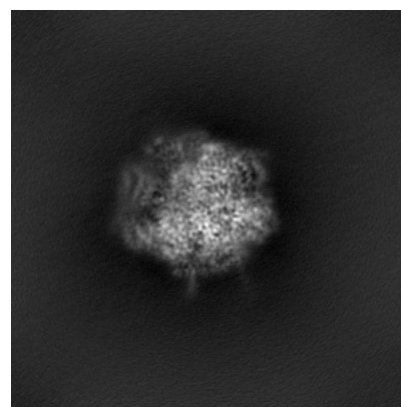
#### 6.1.2 Raw map



X



Y

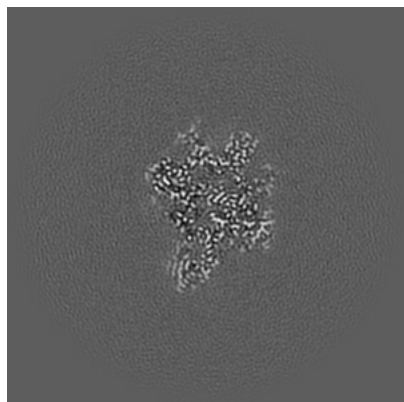


Z

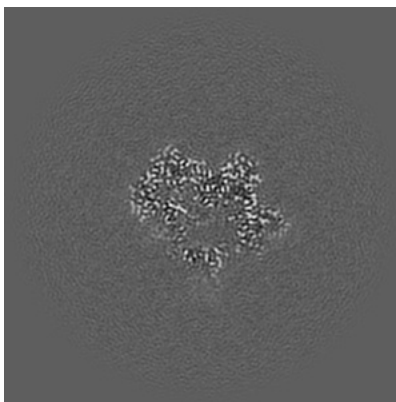
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

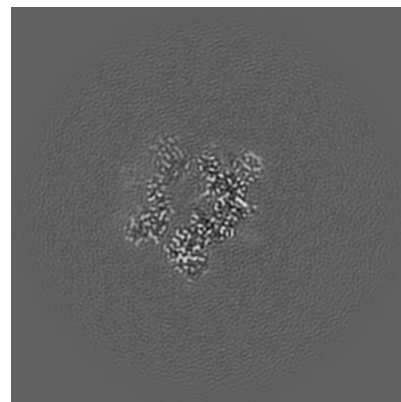
### 6.2.1 Primary map



X Index: 150

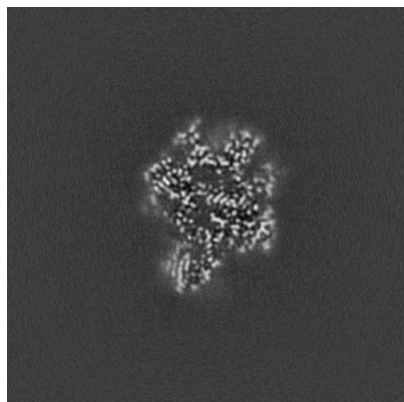


Y Index: 150

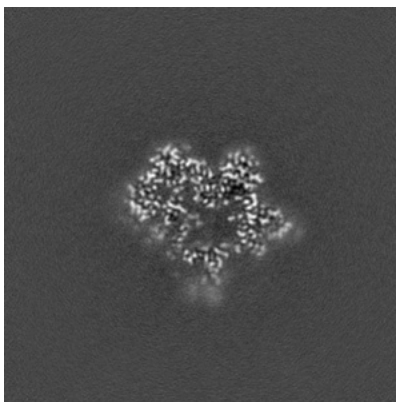


Z Index: 150

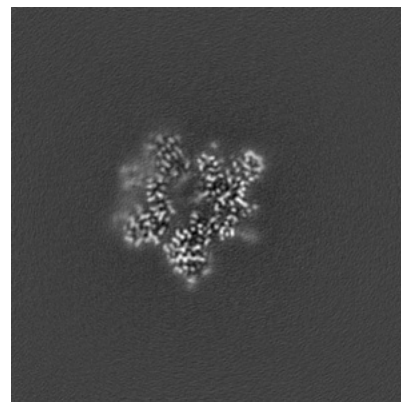
### 6.2.2 Raw map



X Index: 150



Y Index: 150

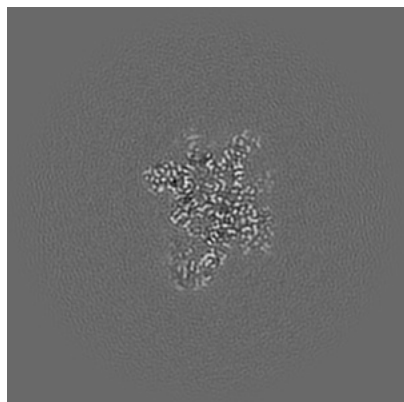


Z Index: 150

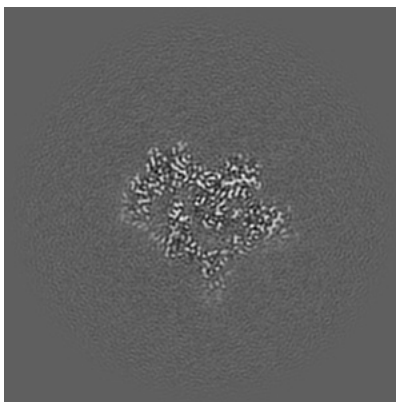
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

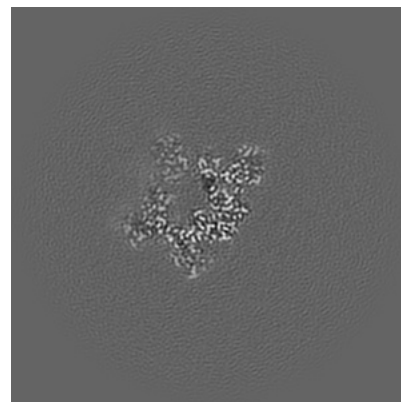
### 6.3.1 Primary map



X Index: 153

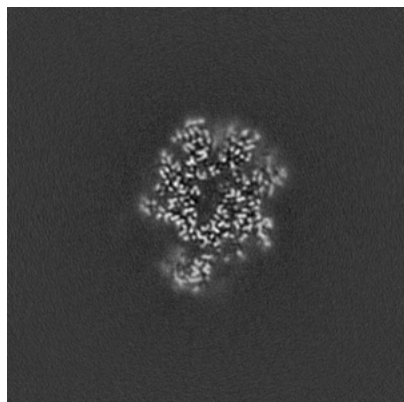


Y Index: 143

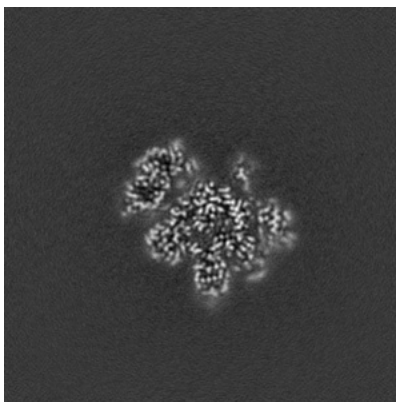


Z Index: 156

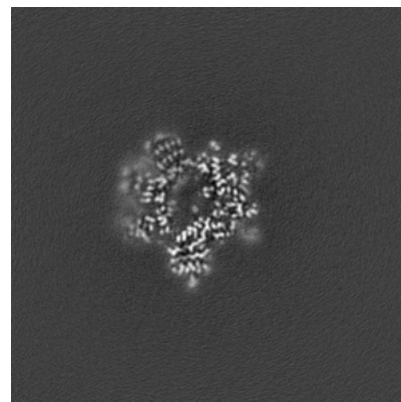
### 6.3.2 Raw map



X Index: 146



Y Index: 134

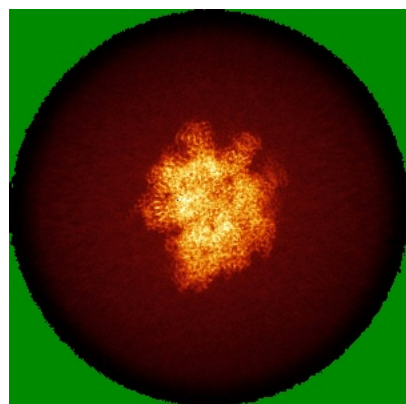


Z Index: 147

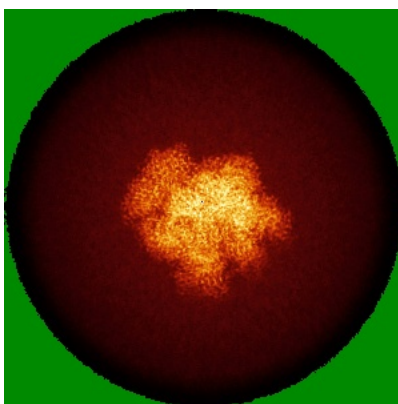
The images above show the largest variance slices of the map in three orthogonal directions.

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

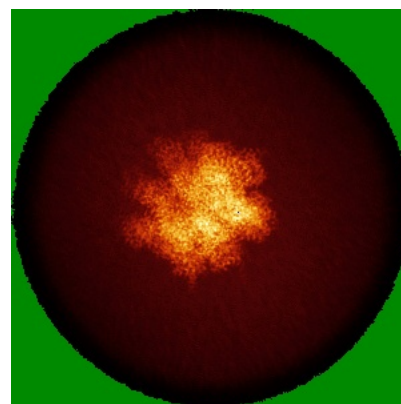
### 6.4.1 Primary map



X

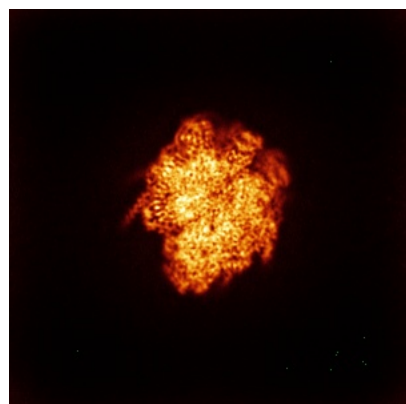


Y

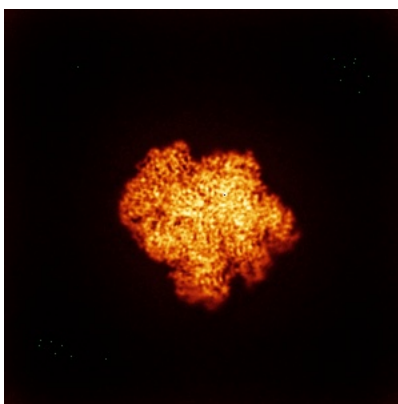


Z

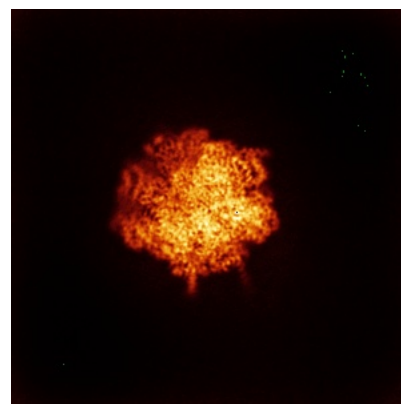
### 6.4.2 Raw map



X



Y

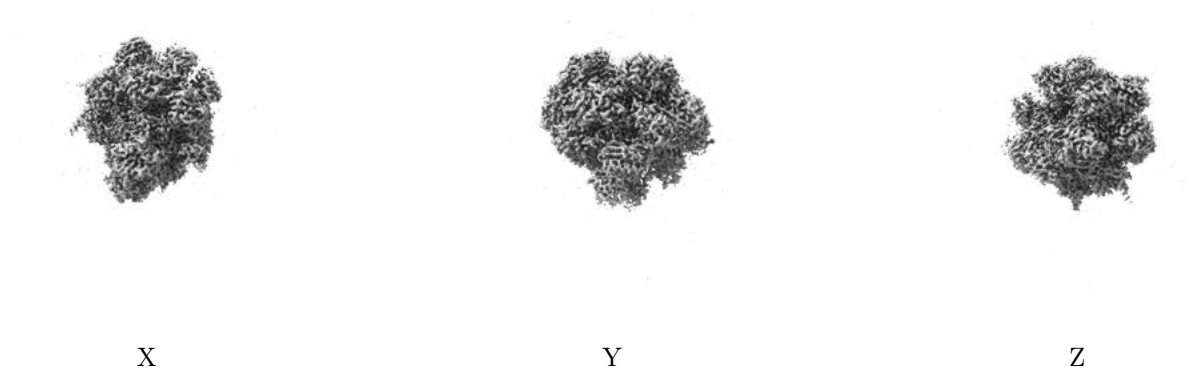


Z

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.

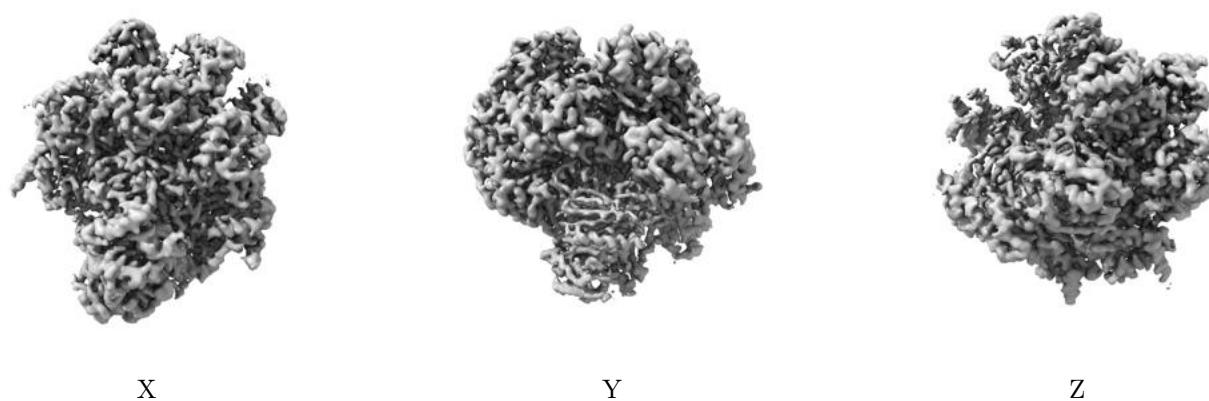
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.592. 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.

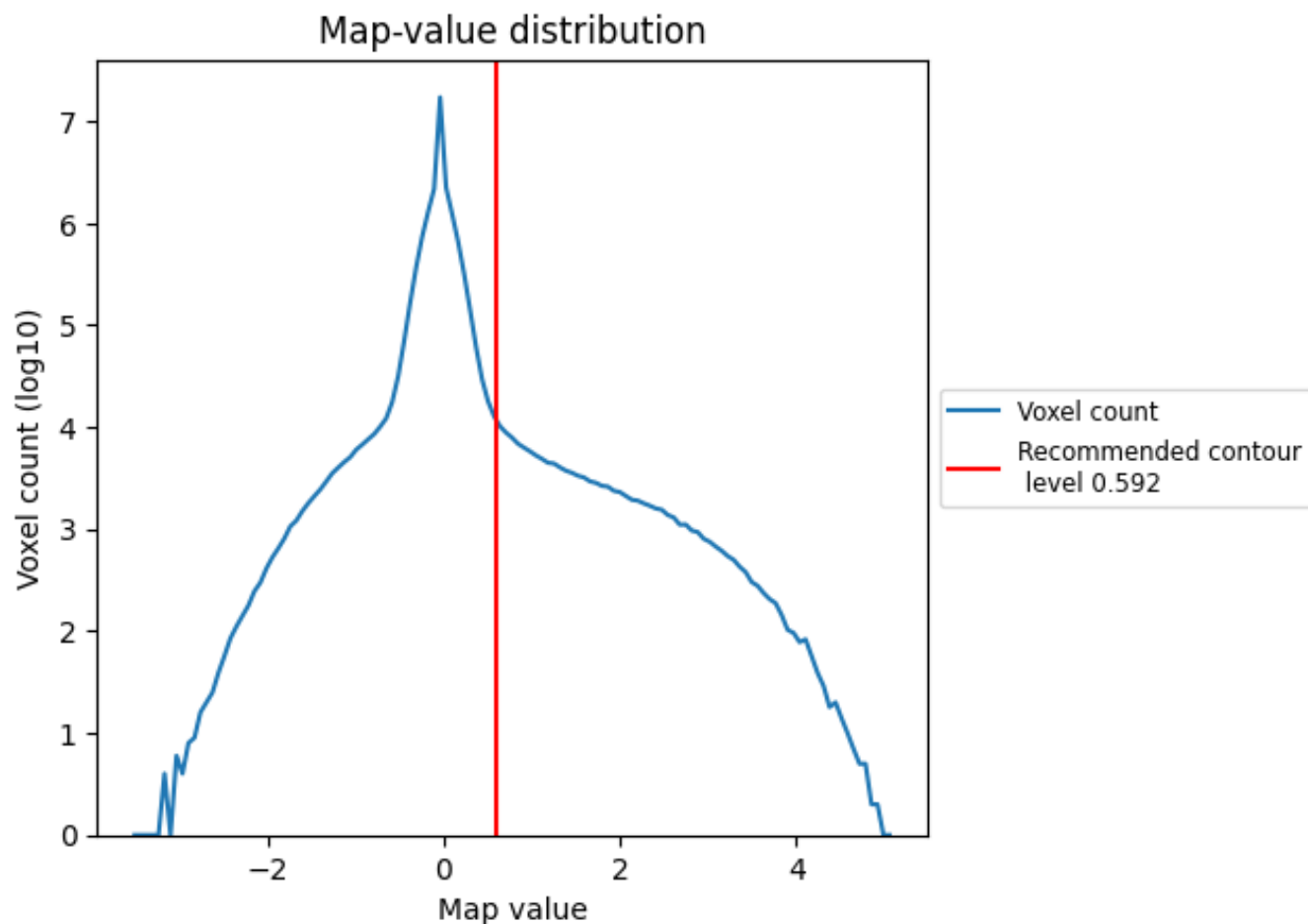
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

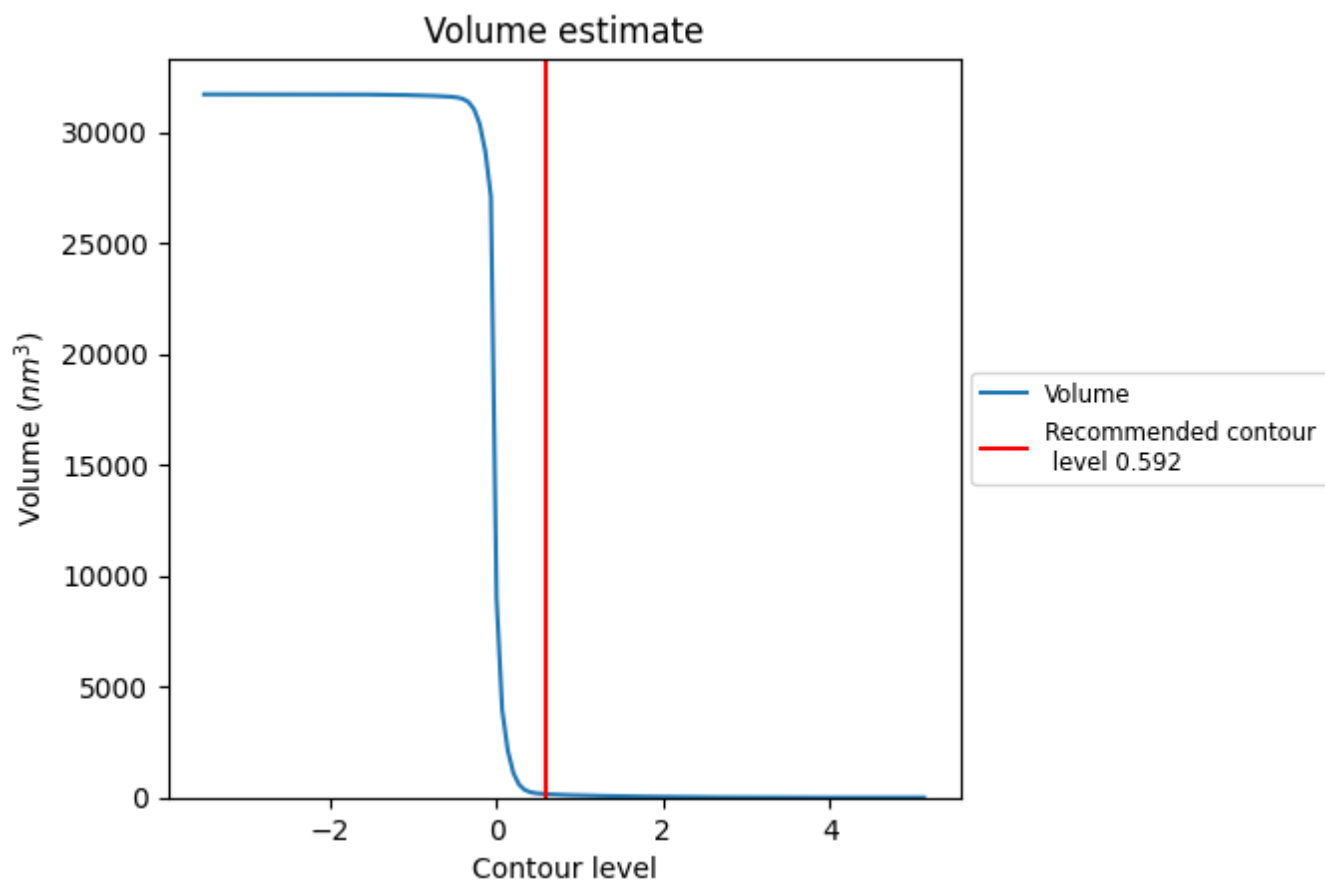
This section contains the results of statistical analysis of the map.

### 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.

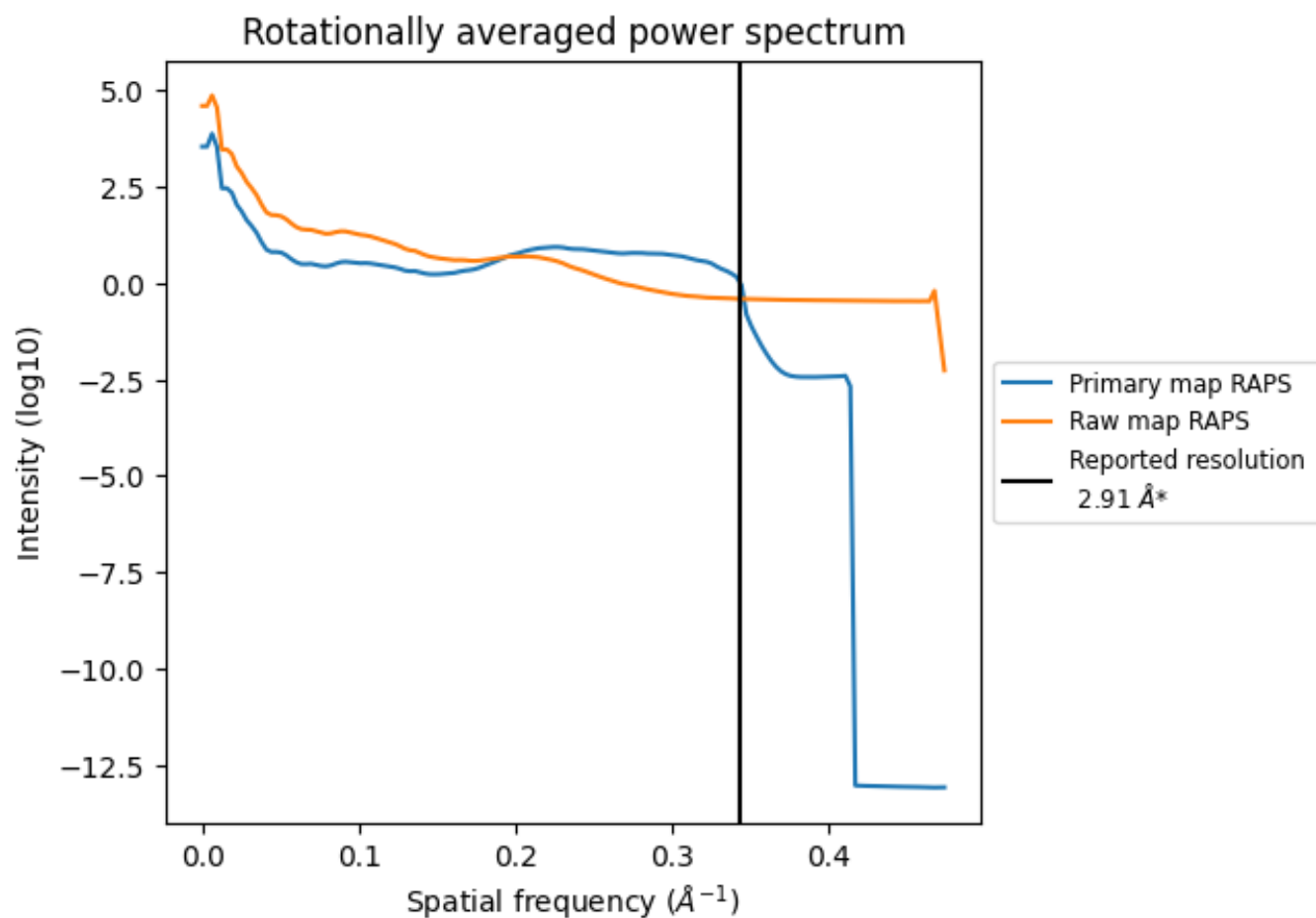
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 157 nm<sup>3</sup>; this corresponds to an approximate mass of 142 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 ⓘ

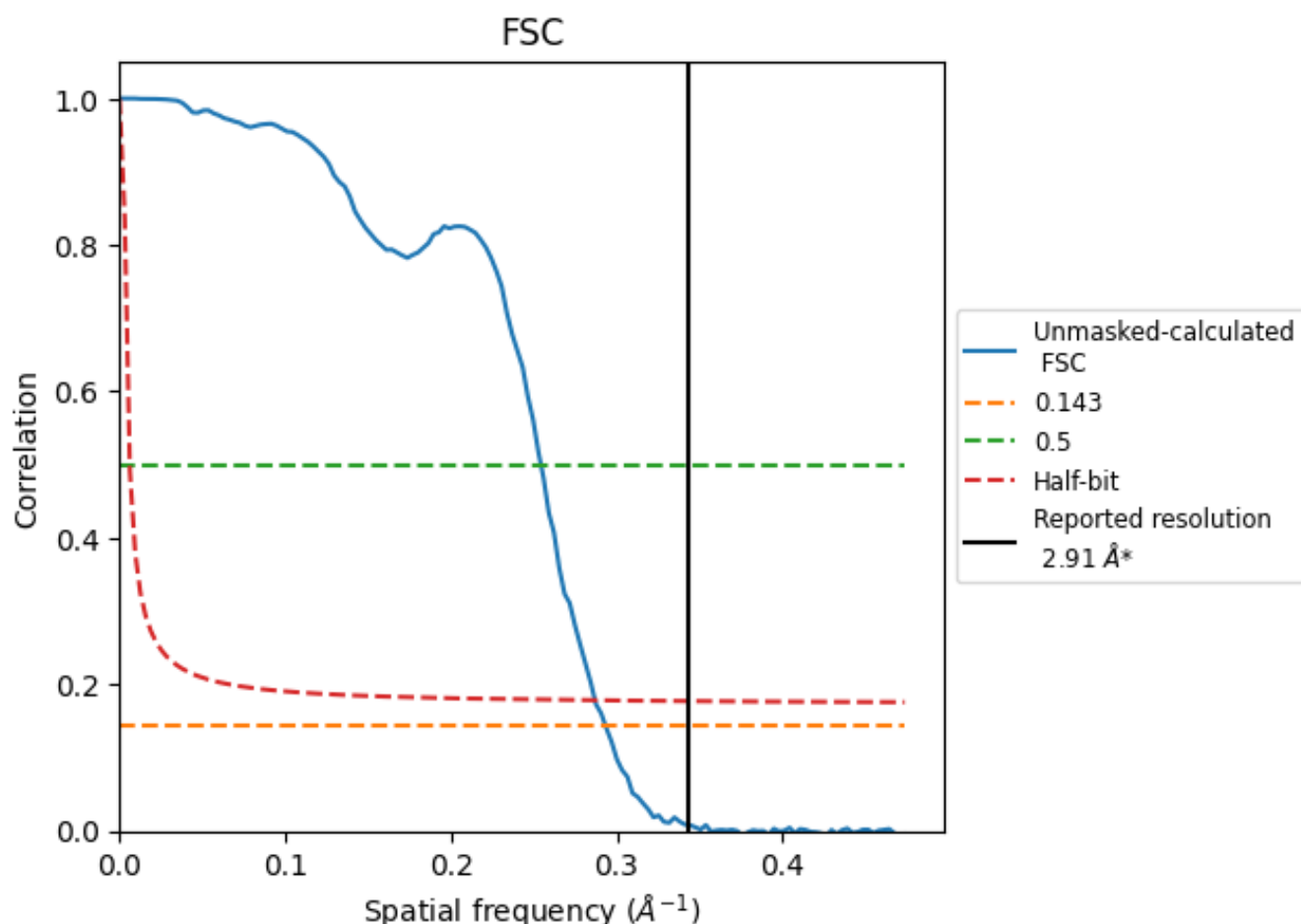


\*Reported resolution corresponds to spatial frequency of 0.344  $\text{\AA}^{-1}$

## 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 0.344  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

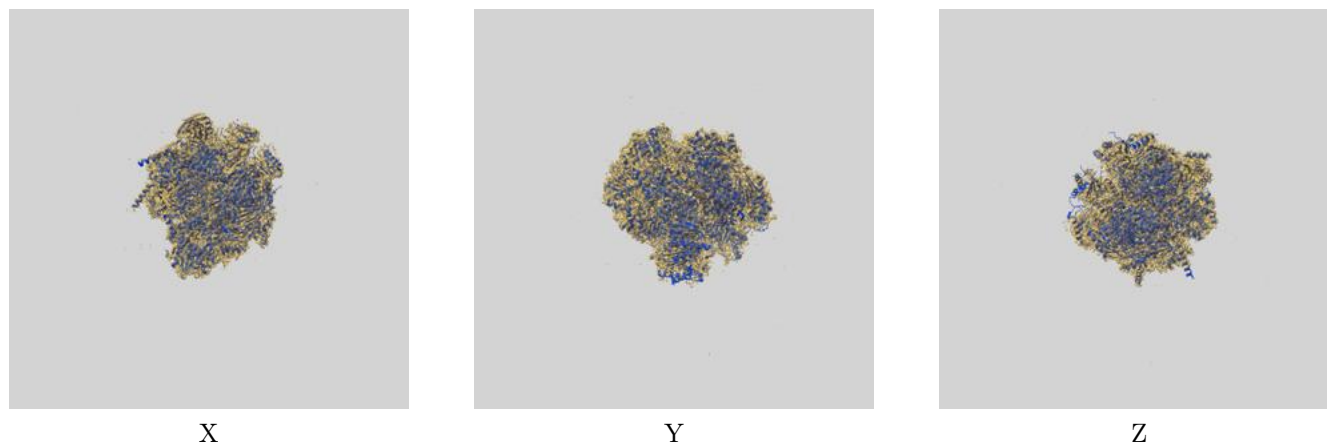
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.91	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.41	3.93	3.49

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.41 differs from the reported value 2.91 by more than 10 %

## 9 Map-model fit [i](#)

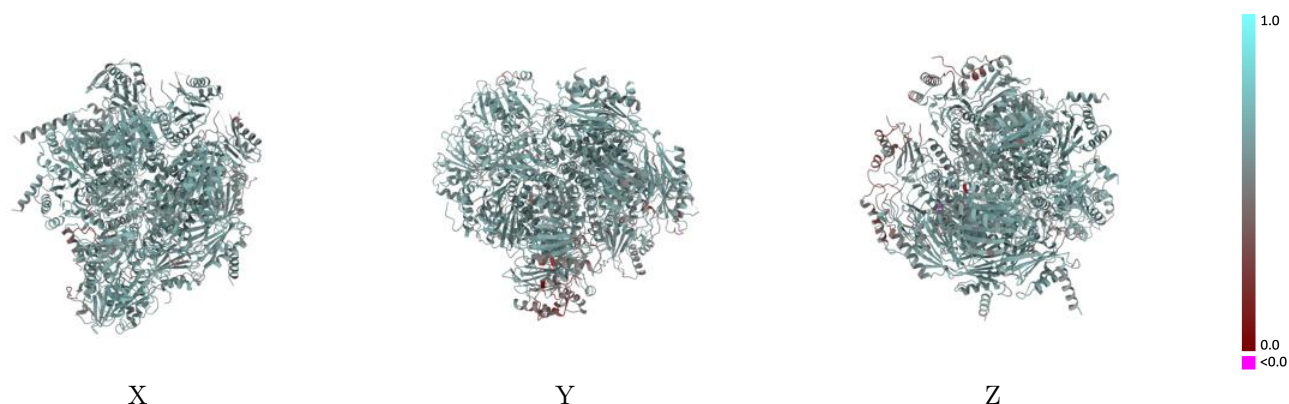
This section contains information regarding the fit between EMDB map EMD-39332 and PDB model 8YIX. Per-residue inclusion information can be found in section [3](#) on page [7](#).

### 9.1 Map-model overlay [i](#)



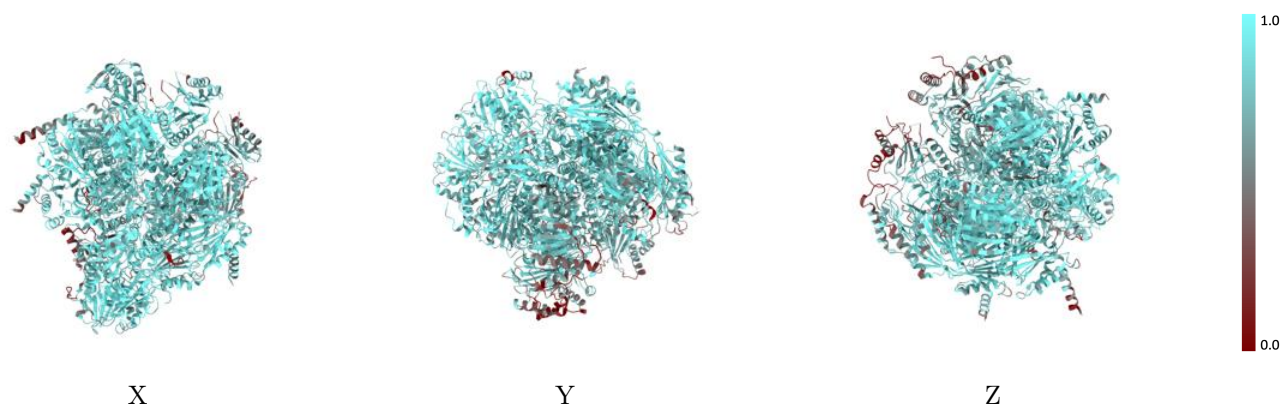
The images above show the 3D surface view of the map at the recommended contour level 0.592 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



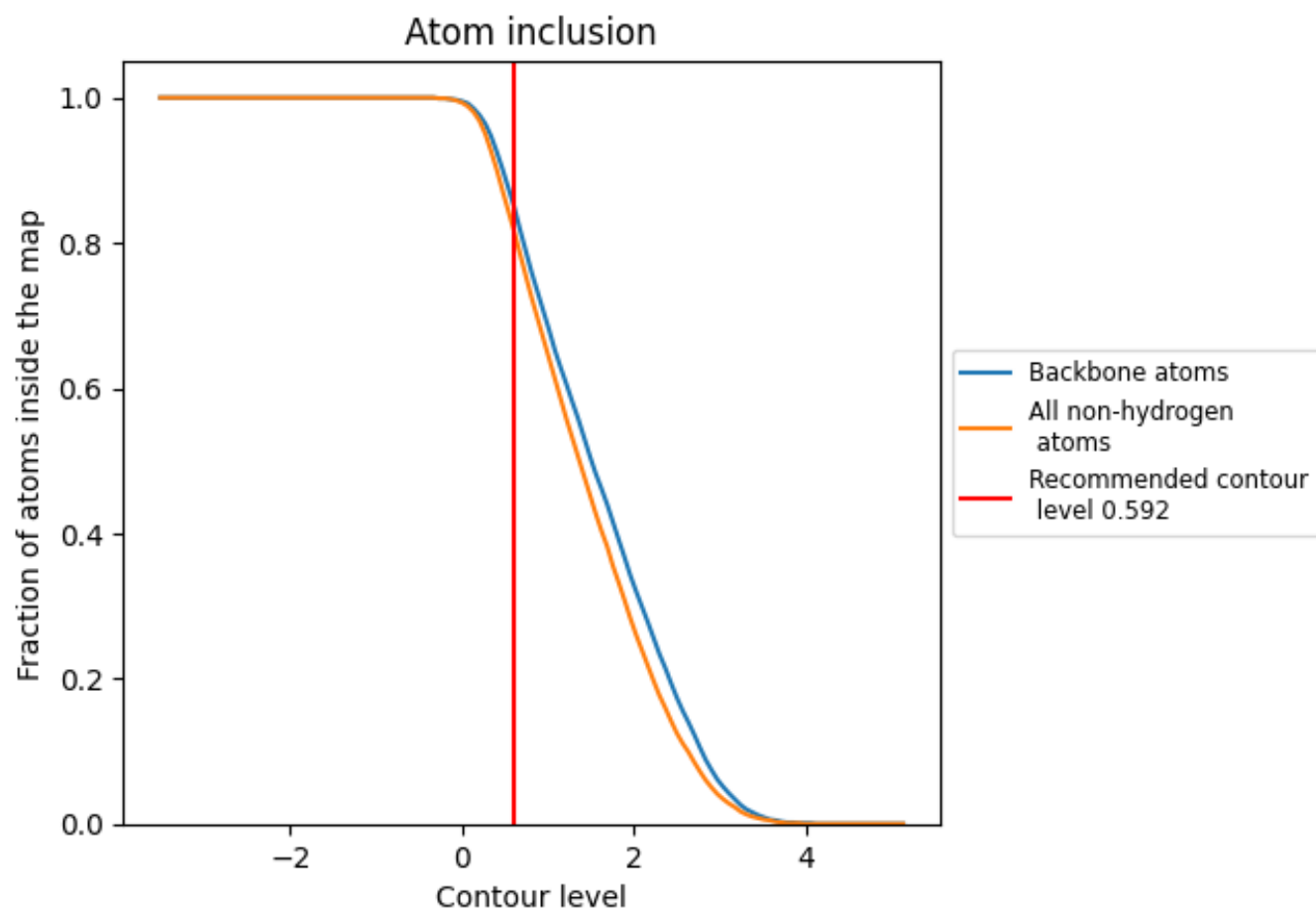
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.592).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% 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 (0.592) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8220</div>	<div><div></div>0.5890</div>
A	<div><div></div>0.9190</div>	<div><div></div>0.6170</div>
B	<div><div></div>0.8690</div>	<div><div></div>0.6090</div>
C	<div><div></div>0.9000</div>	<div><div></div>0.6210</div>
D	<div><div></div>0.8570</div>	<div><div></div>0.5980</div>
E	<div><div></div>0.9090</div>	<div><div></div>0.6190</div>
F	<div><div></div>0.8990</div>	<div><div></div>0.6140</div>
G	<div><div></div>0.9090</div>	<div><div></div>0.6170</div>
H	<div><div></div>0.8470</div>	<div><div></div>0.5970</div>
I	<div><div></div>0.8200</div>	<div><div></div>0.5840</div>
J	<div><div></div>0.8040</div>	<div><div></div>0.5820</div>
K	<div><div></div>0.7200</div>	<div><div></div>0.5520</div>
L	<div><div></div>0.6010</div>	<div><div></div>0.5050</div>
M	<div><div></div>0.6420</div>	<div><div></div>0.5430</div>
N	<div><div></div>0.7310</div>	<div><div></div>0.5630</div>
f	<div><div></div>0.7540</div>	<div><div></div>0.5610</div>
g	<div><div></div>0.8550</div>	<div><div></div>0.6000</div>
h	<div><div></div>0.8710</div>	<div><div></div>0.6030</div>

1.0

0.0

<0.0