



Full wwPDB EM Validation Report ⓘ

Mar 26, 2026 – 06:29 PM UTC

PDB ID : 8OW0 / pdb_00008ow0
EMDB ID : EMD-17226
Title : Cryo-EM structure of CBF1-CCAN bound topologically to a centromeric CENP-A nucleosome
Authors : Dendooven, T.D.; Zhang, Z.; Yang, J.; McLaughlin, S.; Schwabb, J.; Scheres, S.; Yatskevich, S.; Barford, D.
Deposited on : 2023-04-26
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM Validation 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 : **FAILED**
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

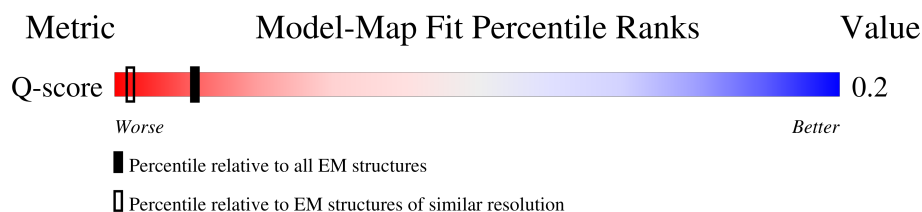
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	14717 (2.90 - 3.90)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 74349 atoms, of which 36378 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 DNA chain called C0N3 DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	D	121	Total	C	H	N	O	P	0	0
			3839	1180	1364	446	728	121		

- Molecule 2 is a DNA chain called C0N3 DNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	E	120	Total	C	H	N	O	P	0	0
			3818	1173	1352	456	717	120		

- Molecule 3 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	79	Total	C	H	N	O	0	0
			1283	393	658	120	112		
3	f	79	Total	C	H	N	O	0	0
			1292	395	665	120	112		

- Molecule 4 is a protein called Histone H2B.1.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	d	95	Total	C	H	N	O	S	0	0
			1489	461	754	129	144	1		
4	h	94	Total	C	H	N	O	S	0	0
			1478	458	749	128	142	1		

- Molecule 5 is a protein called Histone H3-like centromeric protein CSE4.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	e	97	Total	C	H	N	O	S	0	0
			1585	498	804	139	140	4		
5	a	97	Total	C	H	N	O	S	0	0
			1585	498	804	139	140	4		

- Molecule 6 is a protein called Histone H2A.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	97	Total	C	H	N	O	0	0
			1530	467	785	146	132		
6	c	97	Total	C	H	N	O	0	0
			1518	464	776	146	132		

- Molecule 7 is a protein called Centromere-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	101	Total	C	H	N	O	0	0
			1668	507	846	152	161		
7	B	107	Total	C	H	N	O	0	0
			1773	542	897	161	171		

- Molecule 8 is a protein called Inner kinetochore subunit MCM16.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	171	Total	C	H	N	O	0	0
			2865	890	1453	247	273		

- Molecule 9 is a protein called Inner kinetochore subunit CTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	667	Total	C	H	N	O	0	0
			10917	3499	5512	905	971		

- Molecule 10 is a protein called Inner kinetochore subunit MCM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	219	Total	C	H	N	O	0	0
			3566	1113	1804	304	340		

- Molecule 11 is a protein called Inner kinetochore subunit IML3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	241	Total	C	H	N	O	0	0
			3887	1244	1946	320	366		

- Molecule 12 is a protein called Inner kinetochore subunit CHL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	N	391	Total	C	H	N	O	S	0	0
			6373	2053	3207	537	563	13		

- Molecule 13 is a protein called Inner kinetochore subunit MCM21.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	O	241	Total	C	H	N	O	S	0	0
			3976	1277	1997	328	369	5		

- Molecule 14 is a protein called Inner kinetochore subunit CTF19.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	P	257	Total	C	H	N	O	S	0	0
			4308	1358	2192	366	378	14		

- Molecule 15 is a protein called Inner kinetochore subunit OKP1.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	Q	258	Total	C	H	N	O	S	0	0
			4347	1357	2201	375	405	9		

- Molecule 16 is a protein called Inner kinetochore subunit CNN1.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	T	92	Total	C	H	N	O	S	0	0
			1543	488	782	125	144	4		

- Molecule 17 is a protein called Inner kinetochore subunit AME1.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	U	184	Total	C	H	N	O	S	0	0
			2965	928	1480	255	299	3		

- Molecule 18 is a protein called Inner kinetochore subunit WIP1.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	W	69	Total	C	H	N	O	S	0	0
			1111	348	560	96	105	2		

- Molecule 19 is a protein called Inner kinetochore subunit NKP1.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	Y	223	Total	C	H	N	O	S	0	0
			3308	1027	1645	281	349	6		

- Molecule 20 is a protein called Inner kinetochore subunit NKP2.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	Z	151	Total	C	H	N	O	S	0	0
			2325	740	1145	204	235	1		

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100311	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.975	Depositor
Minimum map value	-0.638	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.149	Depositor
Map size (Å)	307.08, 307.08, 307.08	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.853, 0.853, 0.853	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

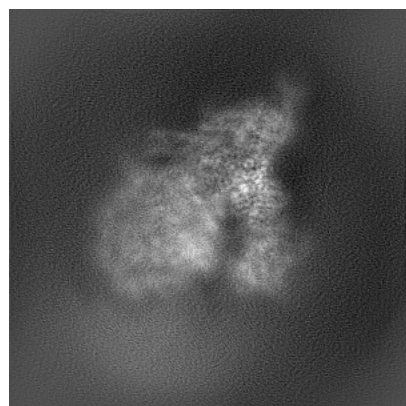
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17226. These allow visual inspection of the internal detail of the map and identification of artifacts.

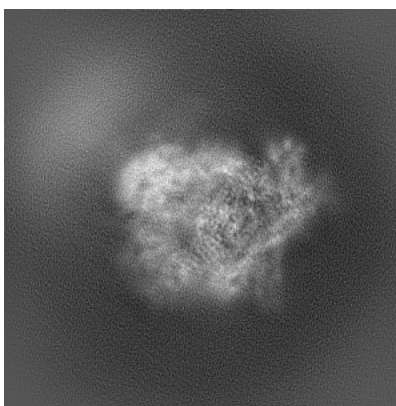
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

5.1 Orthogonal projections [i](#)

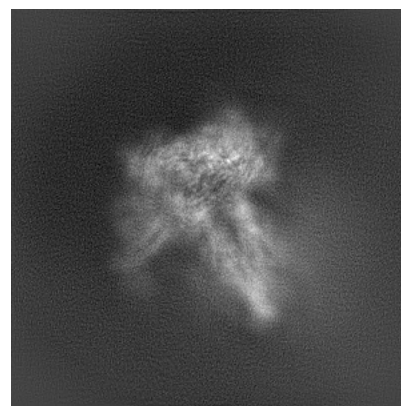
5.1.1 Primary map



X

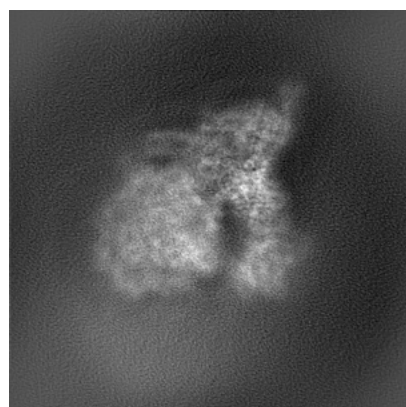


Y

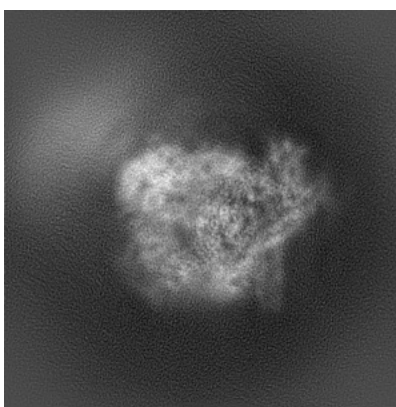


Z

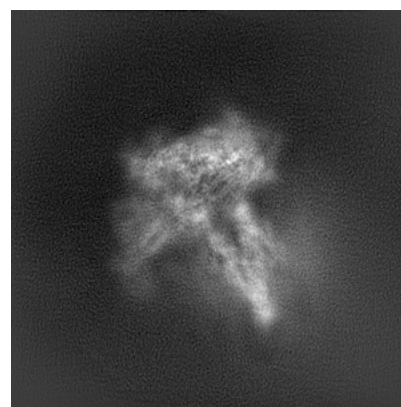
5.1.2 Raw map



X



Y

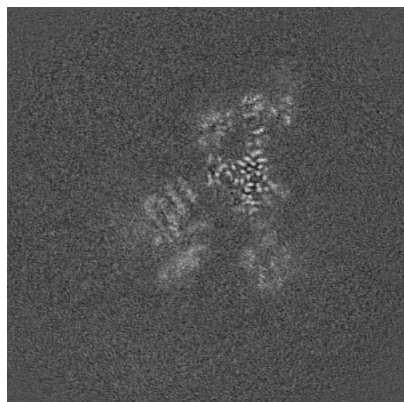


Z

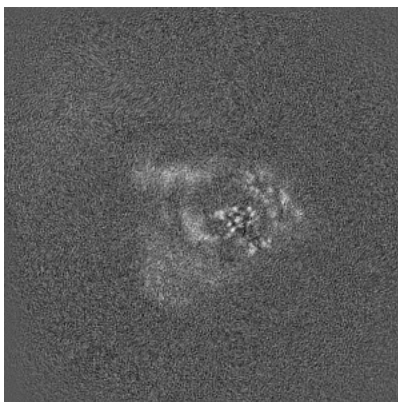
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

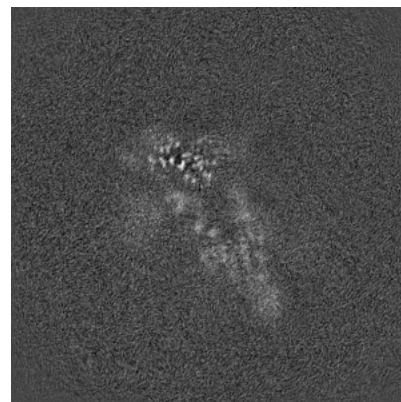
5.2.1 Primary map



X Index: 180

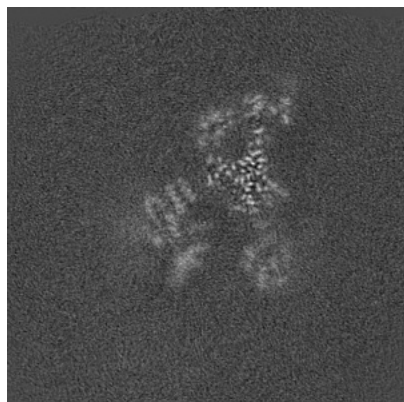


Y Index: 180



Z Index: 180

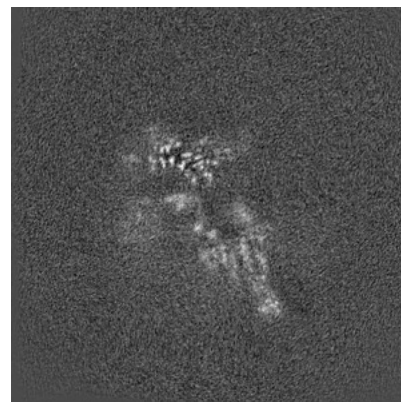
5.2.2 Raw map



X Index: 180



Y Index: 180

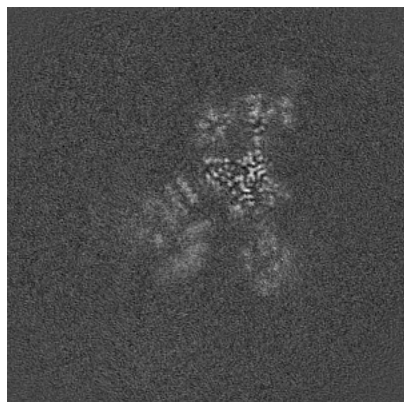


Z Index: 180

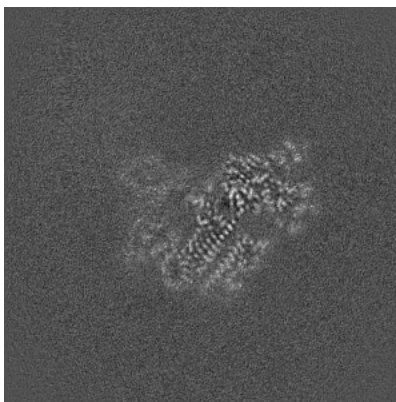
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

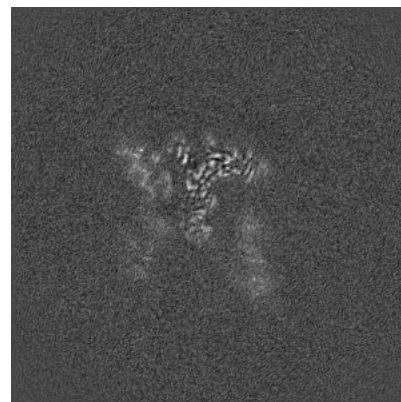
5.3.1 Primary map



X Index: 178

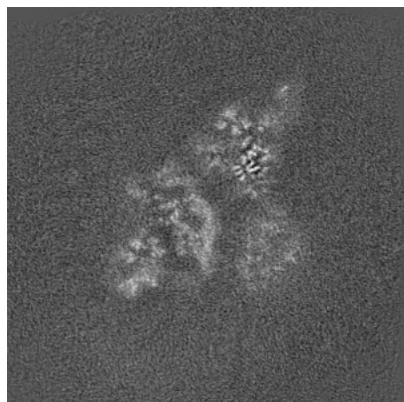


Y Index: 223

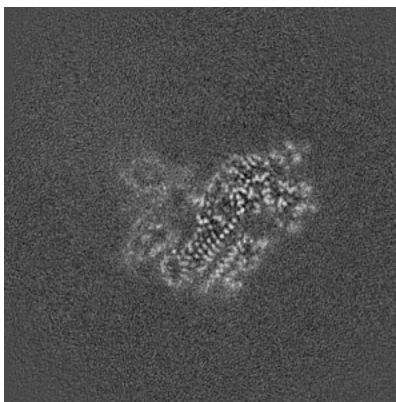


Z Index: 200

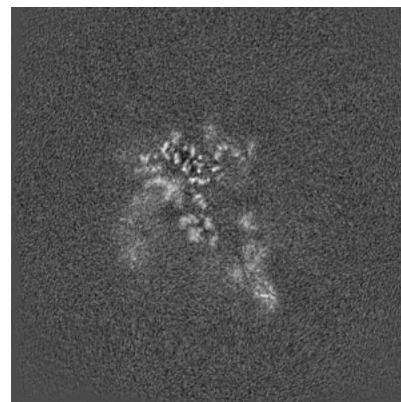
5.3.2 Raw map



X Index: 207



Y Index: 223

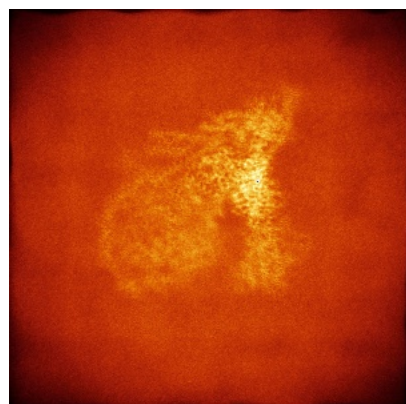


Z Index: 191

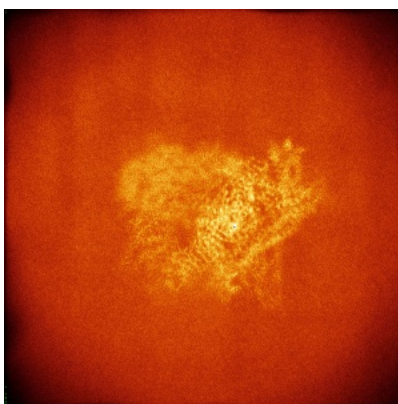
The images above show the largest variance slices of the map in three orthogonal directions.

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

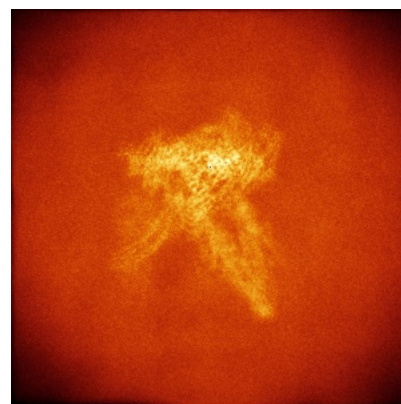
5.4.1 Primary map



X

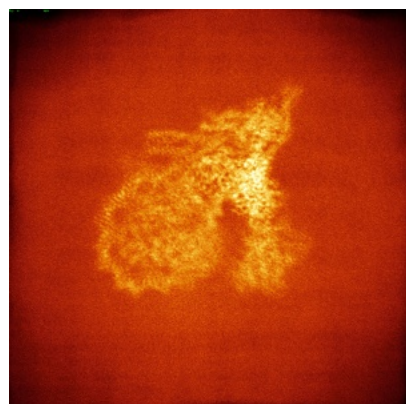


Y

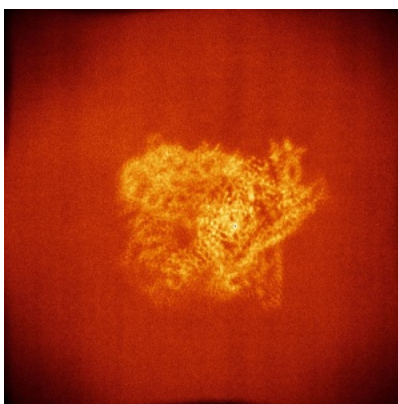


Z

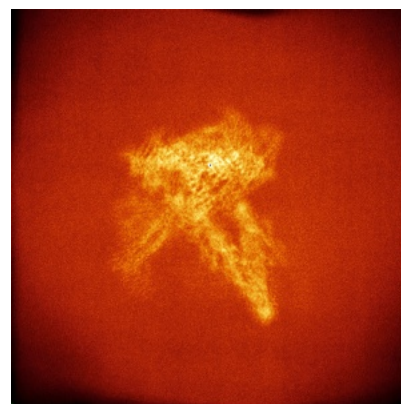
5.4.2 Raw map



X



Y

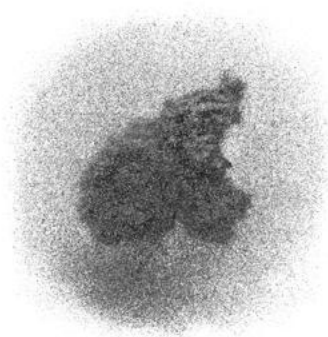


Z

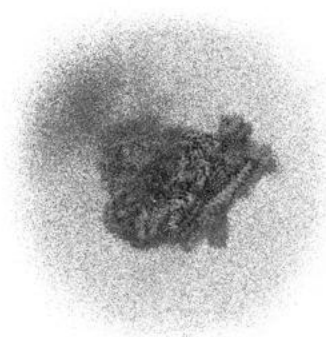
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



X



Y



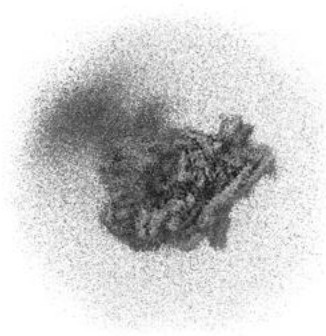
Z

The images above show the 3D surface view of the map at the recommended contour level 0.149. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

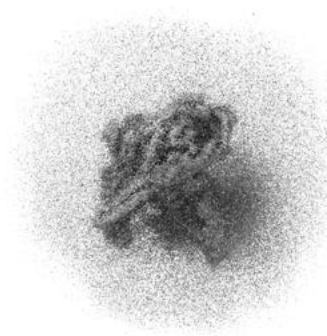
5.5.2 Raw map



X



Y



Z

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

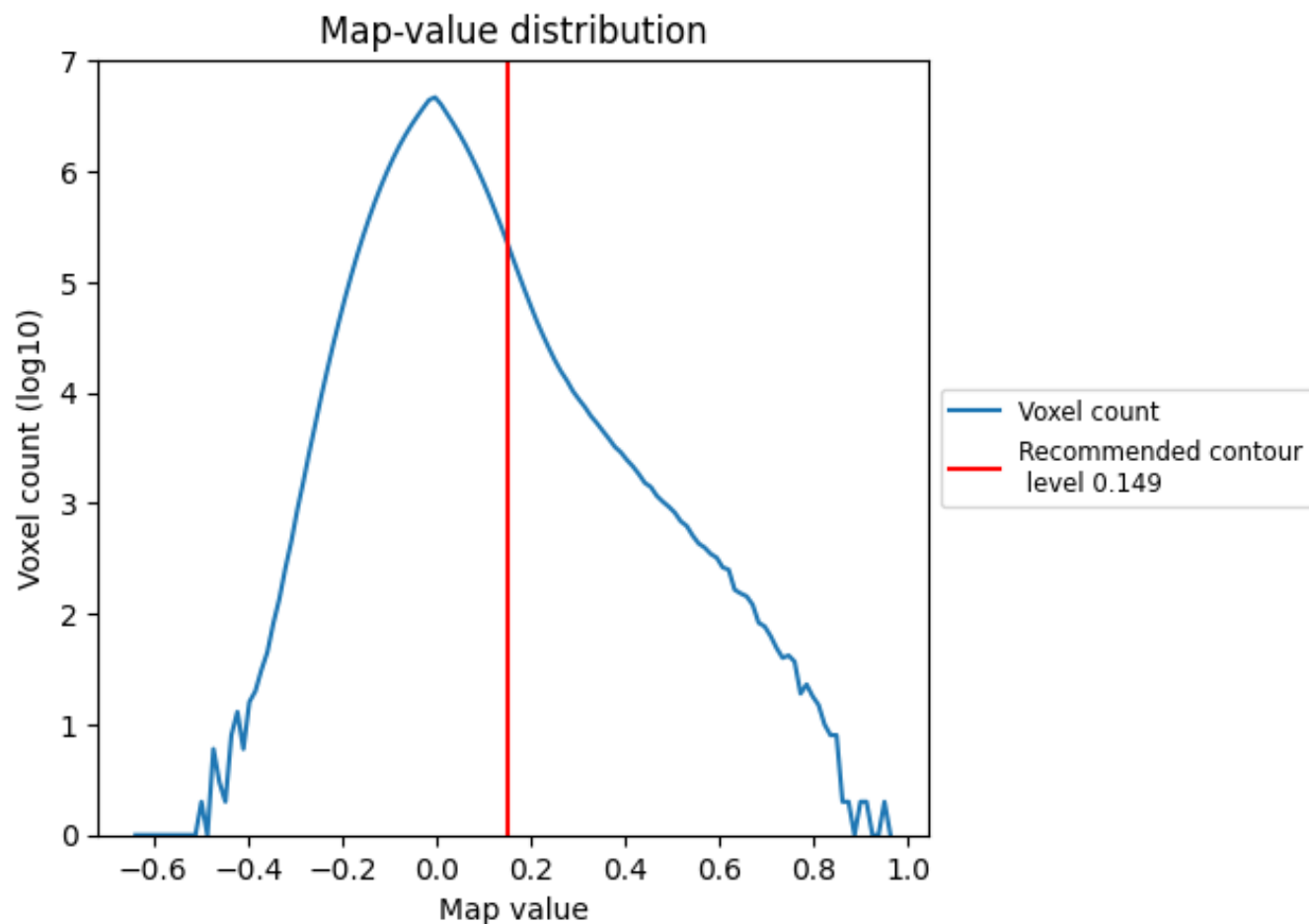
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

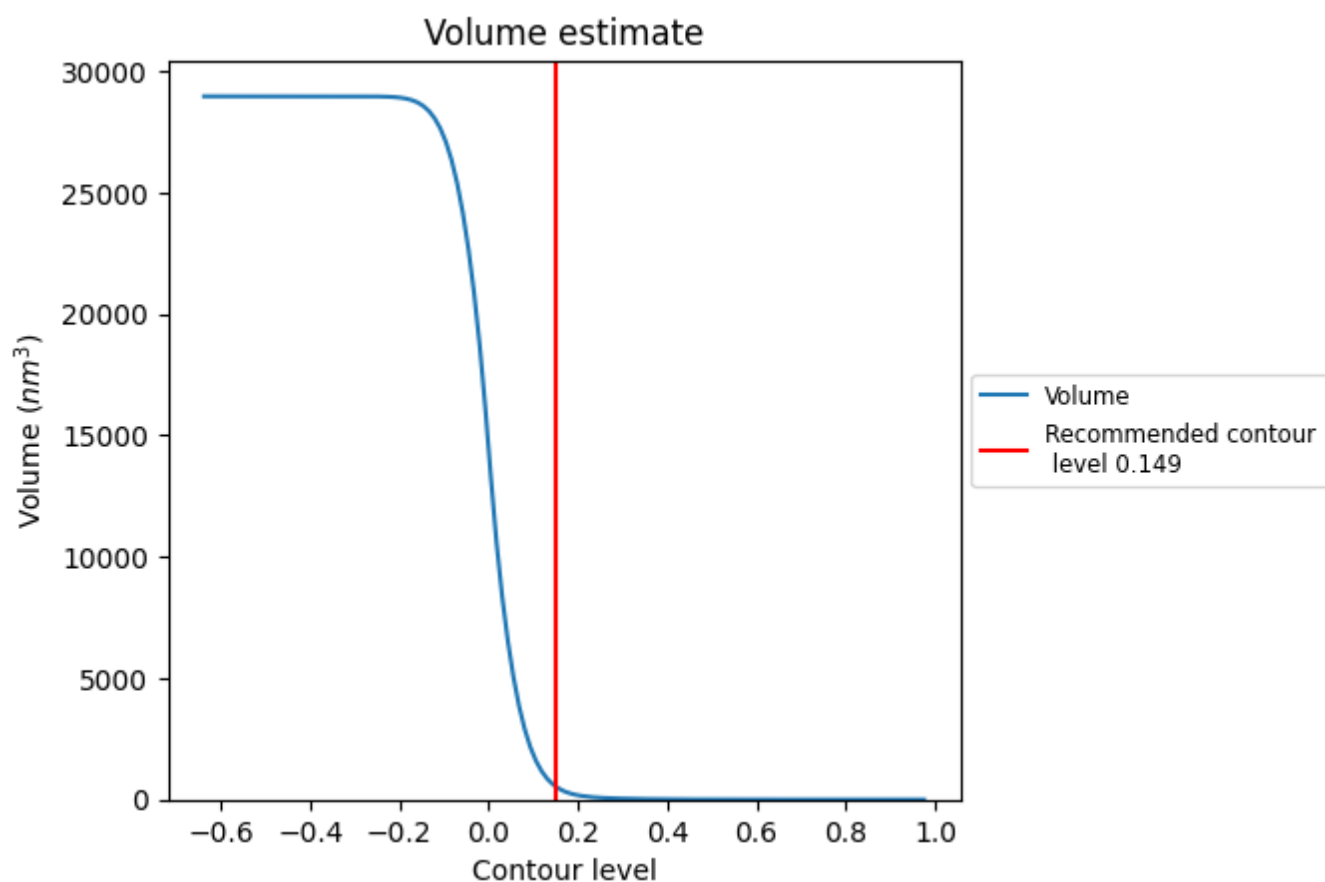
This section contains the results of statistical analysis of the map.

6.1 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.

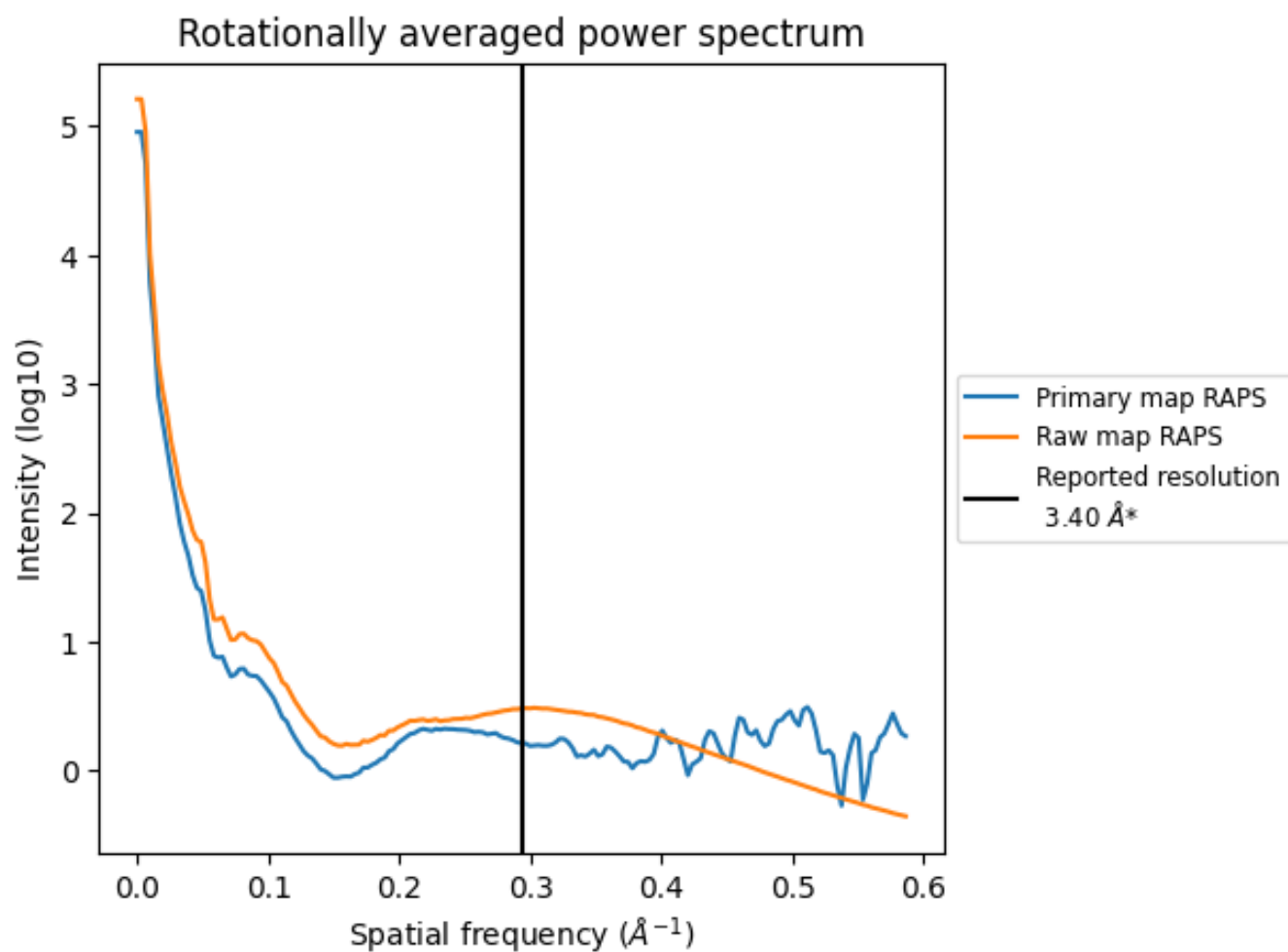
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 558 nm³; this corresponds to an approximate mass of 504 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

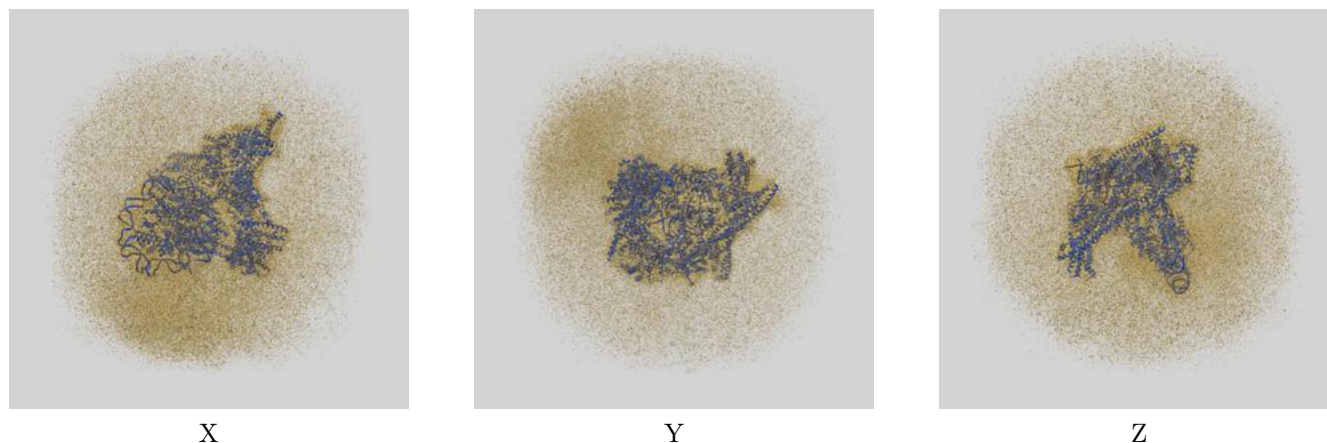
7 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

8 Map-model fit [i](#)

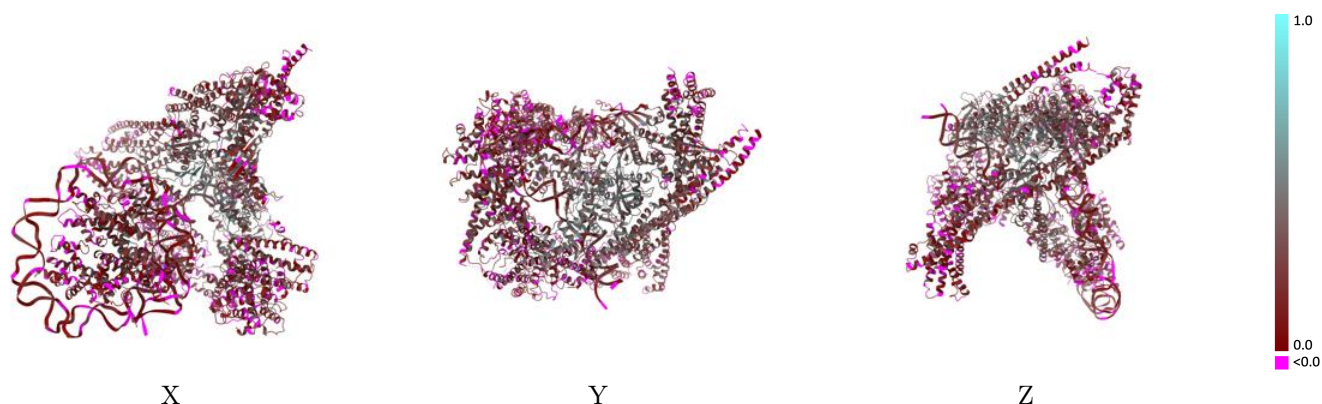
This section contains information regarding the fit between EMDB map EMD-17226 and PDB model 8OW0. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



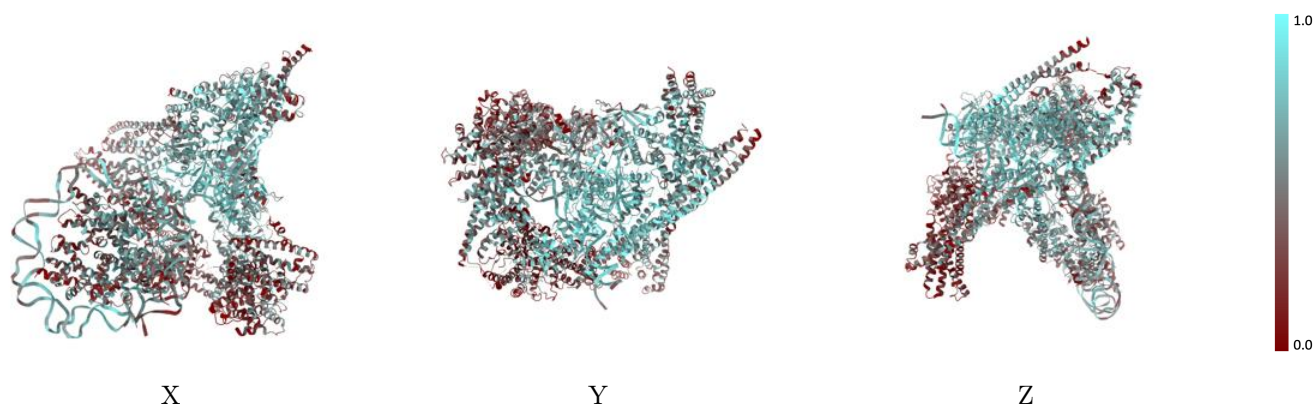
The images above show the 3D surface view of the map at the recommended contour level 0.149 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



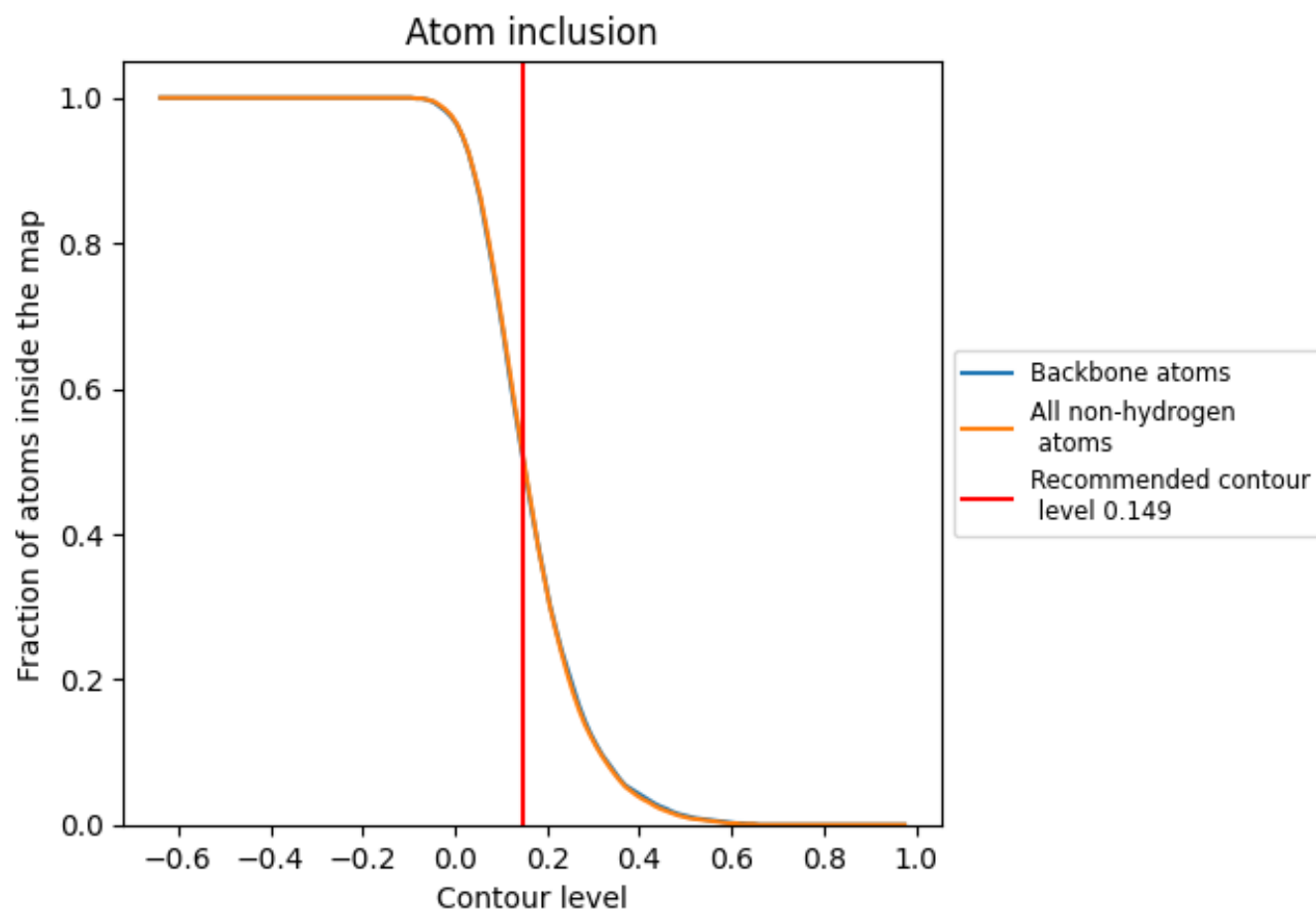
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 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 (0.149).

8.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.149) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5040	 0.2000
A	 0.6230	 0.2460
B	 0.6160	 0.2560
D	 0.6500	 0.1180
E	 0.6310	 0.1180
H	 0.3430	 0.1690
I	 0.3090	 0.1390
K	 0.2700	 0.1110
L	 0.7110	 0.3680
N	 0.7610	 0.3930
O	 0.5950	 0.2980
P	 0.6370	 0.2680
Q	 0.4470	 0.1870
T	 0.1620	 0.0820
U	 0.4960	 0.2180
W	 0.1680	 0.0750
Y	 0.5140	 0.2100
Z	 0.4550	 0.1870
a	 0.3850	 0.0900
b	 0.5060	 0.1370
c	 0.5620	 0.2270
d	 0.5720	 0.2160
e	 0.3810	 0.1090
f	 0.5220	 0.1800
g	 0.3920	 0.1290
h	 0.4620	 0.1600

