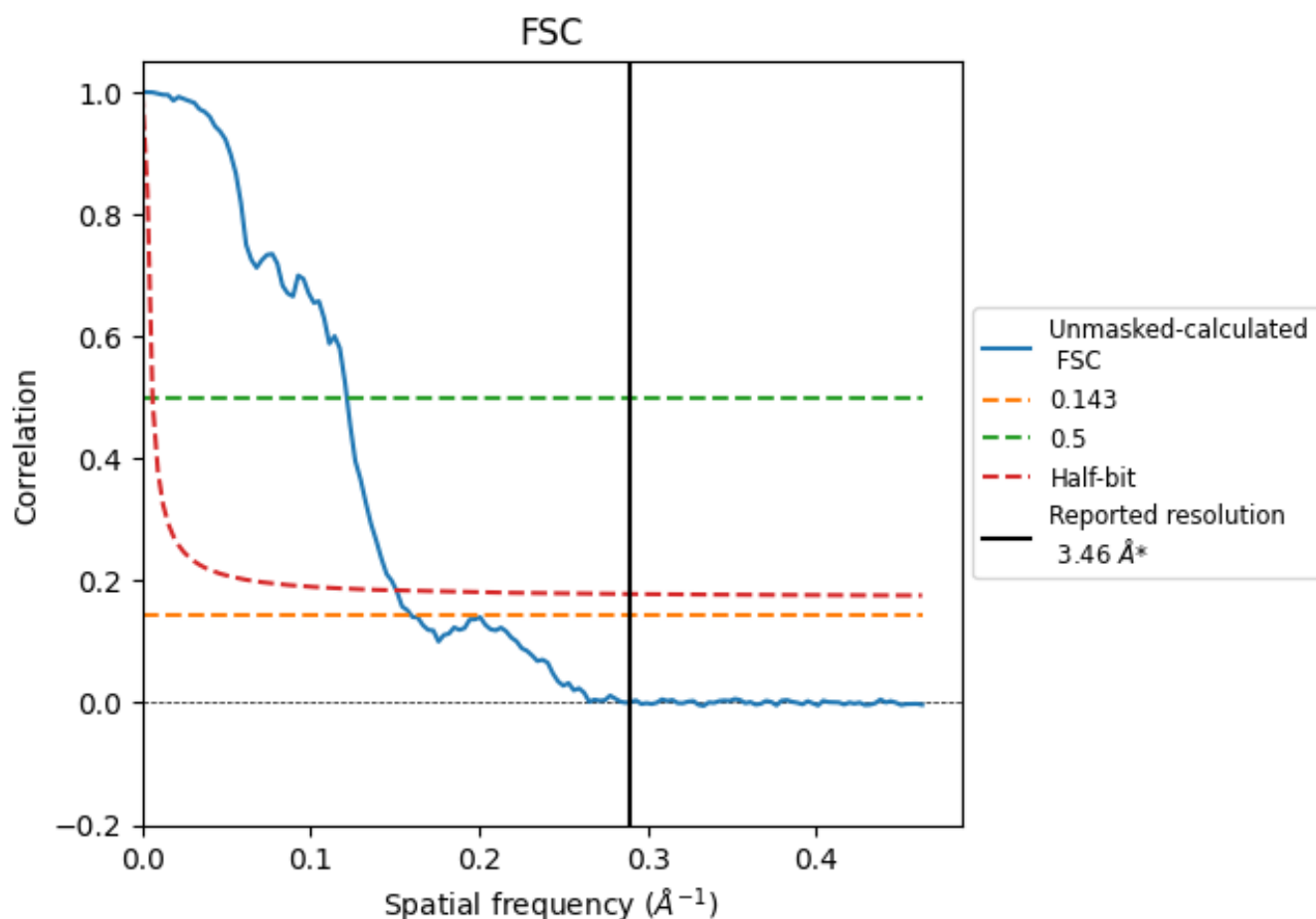


8 Fourier-Shell correlation [i](#)

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 $0.289 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

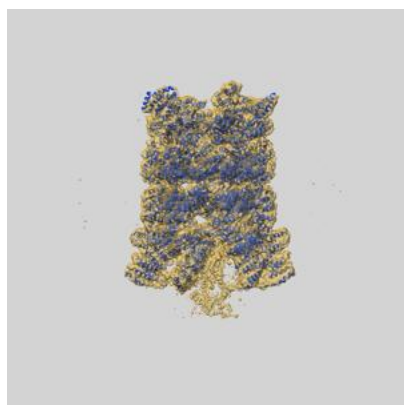
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.46	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.26	8.24	6.63

*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 6.26 differs from the reported value 3.46 by more than 10 %

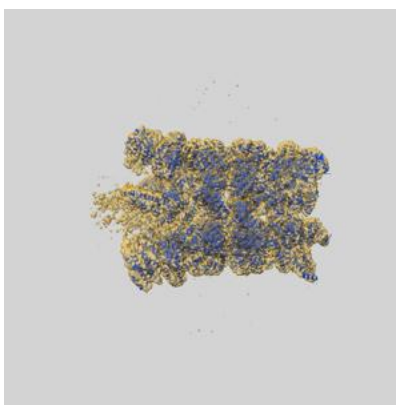
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-65990 and PDB model 9WID. Per-residue inclusion information can be found in section [3](#) on page [8](#).

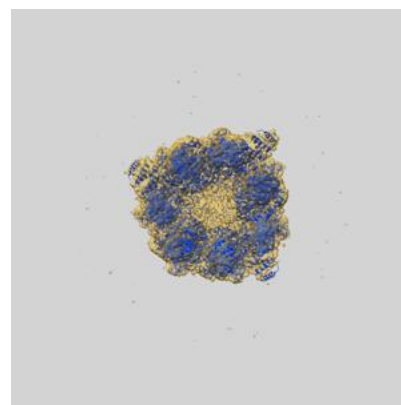
9.1 Map-model overlay [i](#)



X



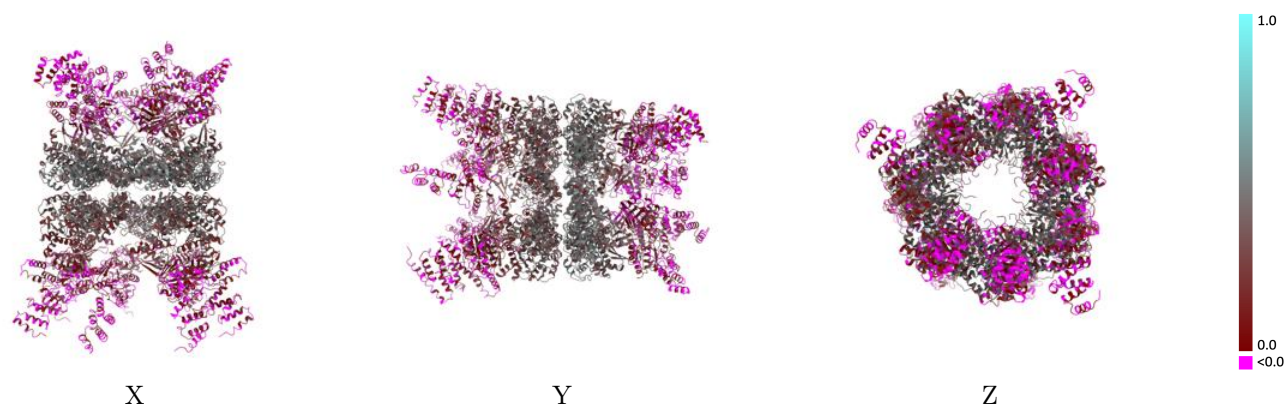
Y



Z

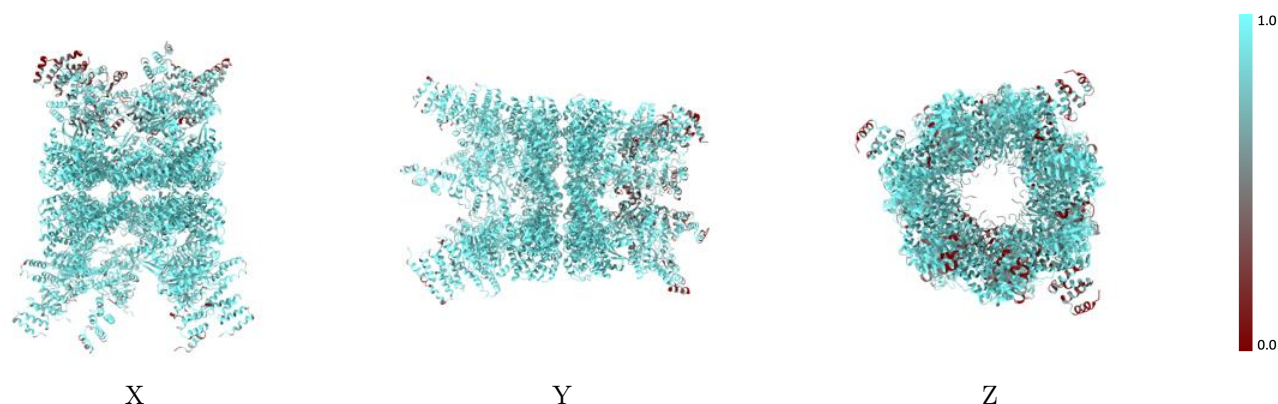
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



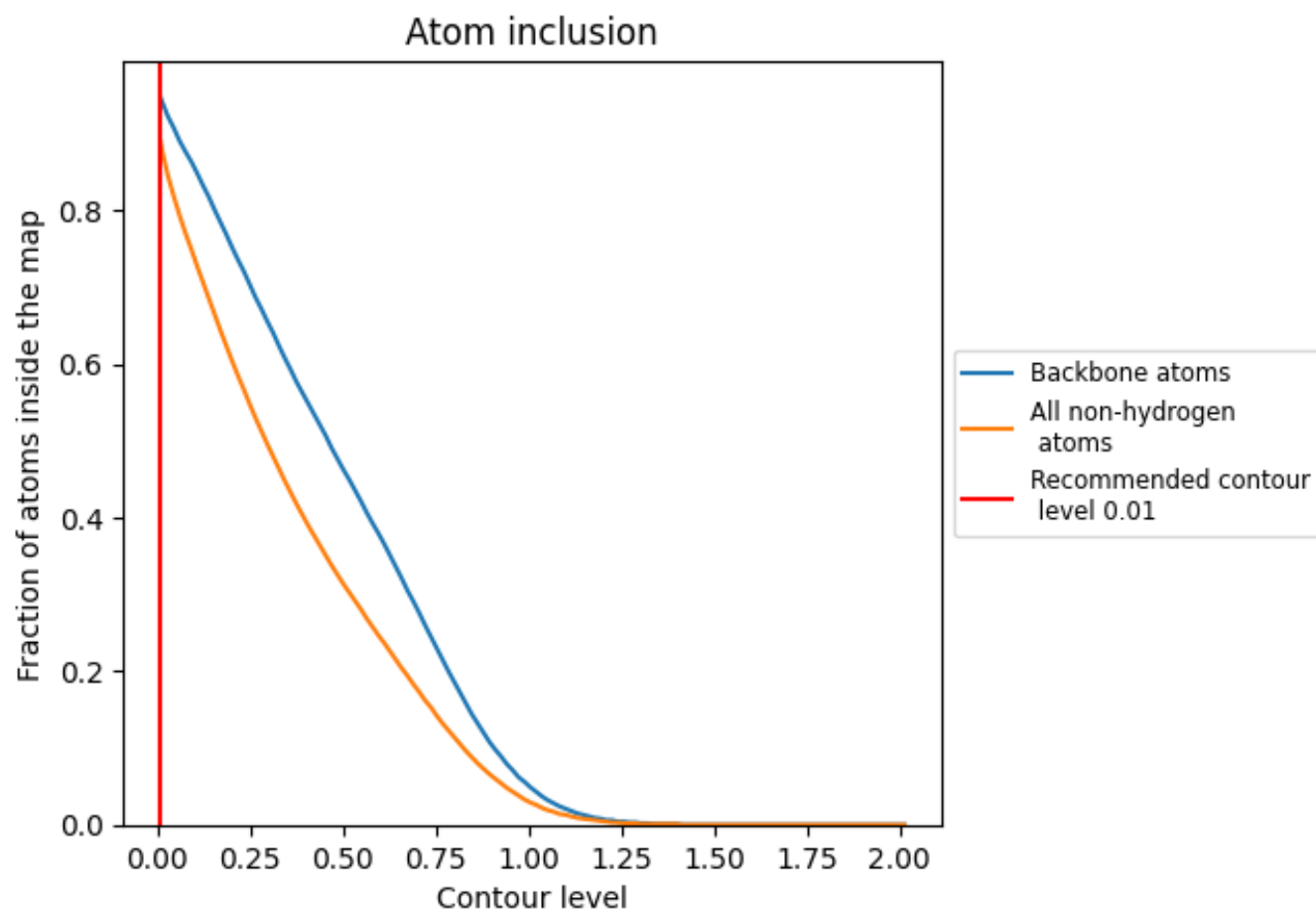
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 89% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8900	 0.2320
0	 0.9350	 0.2440
1	 0.8300	 0.0190
2	 0.8200	 0.0260
3	 0.7740	 0.0170
4	 0.9460	 0.2610
5	 0.9310	 0.2350
6	 0.9280	 0.2400
7	 0.9250	 0.2410
8	 0.9310	 0.2470
9	 0.9350	 0.2500
B	 0.6330	 0.0160
F	 0.7100	 0.0350
G	 0.9250	 0.3320
H	 0.8880	 0.2570
I	 0.8110	 0.0380
J	 0.9220	 0.3000
K	 0.8280	 0.0160
M	 0.4880	 -0.0250
N	 0.8800	 0.2860
O	 0.9170	 0.3180
P	 0.7710	 0.0820
T	 0.5830	 -0.0110
U	 0.8870	 0.2800
V	 0.8800	 0.2790
W	 0.5650	 -0.0460
x	 0.8580	 0.0550
y	 0.8060	 0.0360
z	 0.8270	 0.0230

