



wwPDB EM Validation Summary Report ⓘ

Mar 1, 2026 – 07:08 AM UTC

PDB ID : 7NTX / pdb_00007ntx
EMDB ID : EMD-10889
Title : Vip3Bc1 tetramer in processed, activated state
Authors : Thompson, R.F.; Byrne, M.J.; Iadanza, M.I.
Deposited on : 2021-03-11
Resolution : 4.75 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:

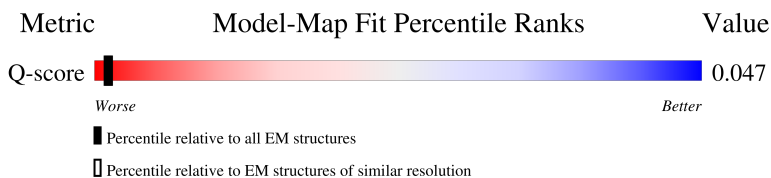
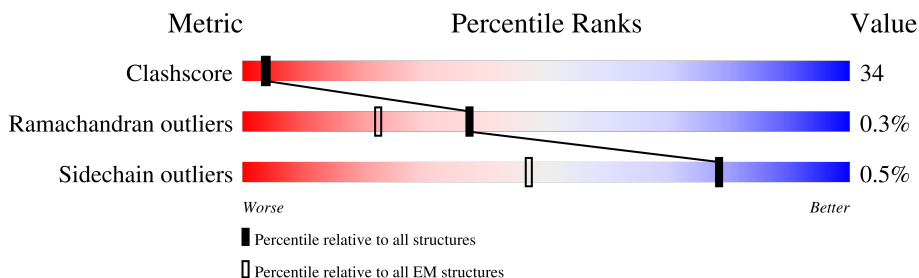
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.75 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	1575 (4.30 - 5.30)

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	803	<p>25% (Poor fit), 40% (0 outliers), 40% (1 outlier), 19% (Not modelled)</p>
1	B	803	<p>26% (Poor fit), 39% (0 outliers), 41% (1 outlier), 19% (Not modelled)</p>
1	C	803	<p>25% (Poor fit), 39% (0 outliers), 41% (1 outlier), 19% (Not modelled)</p>
1	D	803	<p>26% (Poor fit), 38% (0 outliers), 42% (1 outlier), 19% (Not modelled)</p>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 20848 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 Vegetative insecticidal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	648	Total 5212	C 3328	N 843	O 1029	S 12	0	0
1	B	648	Total 5212	C 3328	N 843	O 1029	S 12	0	0
1	C	648	Total 5212	C 3328	N 843	O 1029	S 12	0	0
1	D	648	Total 5212	C 3328	N 843	O 1029	S 12	0	0



MET	VAL	LEU	GLN	LYS	ASN	TRP	MET	GLN	ARG	MET	ILE	ILE	VAL	ASP	ASN	ASN	LEU	LEU	VAL	ASN	VAL	ARG	ALA	PRO	LEU	PRO	SER	SER	PHE	PHE	GLY	GLY	ILE	ILE	THR	THR	LYS	ASP	ASP	ILE	ILE	GLY	MET	GLY	MET	ILE	PHE	PHE	LYS	THR	ASP	THR	THR	THR	GLY	VAL	SER	ASN	ALA	ALA	LEU	THR	LEU	ALA	ASP	GLU	ILE	ILE	LEU	LYS	ASN	GLN	ASN	ASN	GLY	ASP	GLY	ASN	VAL	VAL	LYS	Q141	H143	L168	T177	E178	I179	A182	I186	V189	N190	F193	L196	T197	S198	THR	VAL	GLU	LYS	LYS	ASN	ASN	PRO	LYS	SER	TYR	TYR	ASN	ASP	ASN	THR	THR	VAL	THR	LYS	E214	L219	L222	T223	E224	L225	T230	K231	N232	D233	M234	D235	L241	Q242	N252	L265	K268	E269	N270	V271	T272	T273	R274	E277	I278	V281	Y282	M283	F284	L285	T289	A295	T300	R303	T309	D310	S311	I311	D312	Q315	I316	H319	G323	K324	R326	E327	I330	N331	I332	L333	F334	T335	L336	S337	N338	N339	F340	S341	N342	P343	S344	Y345	S346	K347	N348	R349	G350	S351	D352	I353	S354	D355	P356	K357	V358	V359	L360	E361	A362	A363	P364	G365	Y366	A367	L368	I369	G370	F371	E372	D376	P377	L378	P379	I380	L381	K382	G383	Y384	Q385	A386	R387	L388	K389	P390	M391	Y392	Q393	R396	E397	S398	M399	S400	E401	T402	I403	Y404	D406	I407	H408	K409	L410	F411	K414	Q418	K419	Y420	Y421	I422	K423	D424	I425	E426	F427	P428	E429	G430	Y431	T434	K435	I436	V437	F438	E439	K440	R441	L442	N443	Q444	L445	G446	Y447	E448	V449	F453	Y454	D455	P456	S457	T458	I461	D462	M464	K465	V466	K467	V468	E469	S470	W471	K472	E473	K474	S475	C476	E477	E478	D479	S480	C481	E482	D483	Y485	S486	I487	I488	G494	I495	Y496	M497	P498	L499	G500	V501	V502	S503	E504	T505	F506	L507	D508	H509	I510	Y511	G512	F513	G514	L515	R516	W517	D518	N519	E519	Q522	A523	F524	T525	G526	K527	S528	E529	S530	Y531	R532	L533	E534	S535	L536	L537	E538	T539	D540	L541	L542	N543	N544	E545	T546	Y547	L548	S551	P552	D553	G554	Y555	I556	S558	I559	V560	E561	N562	W563	N564	L565	T566	S567	D568	H569	G571	T572	S573	R574	A575	N576	N577	N578	N579	A580	F581	V582	D583	K584	A585	D586	I587	E588	K589	S589	S590	G591	L594	Y595	T596	H597	K598	D599	G600	E601	F602	S603	Q604	F605	I606	G607	N608	K609	L610	K611	K612	K613	T614	N615	V616	V617	I618	Q619	Y620	V621	I622	K623	G624	R625	P626	A627	I628	Y629	L630	K631	N632	N633	K634	D635	T636	L637	F638	E639	D640	T641	K642	N643	M644	F645	S646	D647	Q649	T650	V651	T652	K653	K654	F655	M656	S657	G658	V659	N660	P661	E663	I664	Y665	F666	L667	F668	K669	N670	Q671	Y674	A675	A676	W677	G678	N679	N680	F681	I682	L683	L684	E685	I686	K687	S688	L689	E690	F691	L692	P693	Q694	M695	L696	K697	P698	E699	D700	W701	I702	P703	S704	G705	N706	V707	Q708	M709	K710	D711	G712	G713	R714	L715	E716	I717	L718	G719	Y722	F723	K724	Q725	F726	I727	K728	L729	E730	N731	D732	S733	T734	Y735	H736	L737	R738	L739	S740	V741	K742	G743	T744	G745	R746	V747	S748	I749	I750	D751	E752	S753	K754	Y755	L756	L757	F758	V759	N760	V761	K762	D763	E764	D765	L766	T767	R768	V769	I770	K771	N772	S774	S775	K776	G777	C779	F780	I781	A782	L783	E784	G785	T786	E789	N790	S791	T792	T793	I794	F795	S796	N797	V798	S799	I800	V801	K802	E803
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	158763	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 ($e^-/\text{\AA}^2$)	70.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.779	Depositor
Minimum map value	-0.787	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.100	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	319.50003, 319.50003, 319.50003	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	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	A	0.53	4/5311 (0.1%)	0.96	10/7183 (0.1%)
1	B	0.53	3/5311 (0.1%)	0.97	13/7183 (0.2%)
1	C	0.53	4/5311 (0.1%)	0.96	12/7183 (0.2%)
1	D	0.52	3/5311 (0.1%)	0.97	13/7183 (0.2%)
All	All	0.53	14/21244 (0.1%)	0.97	48/28732 (0.2%)

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	2
1	B	0	3
1	C	0	2
1	D	0	3
All	All	0	10

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	336	LEU	N-CA	8.70	1.57	1.46
1	C	336	LEU	N-CA	8.61	1.57	1.46
1	B	336	LEU	C-N	7.69	1.43	1.33
1	D	336	LEU	C-N	7.58	1.42	1.33
1	C	335	THR	N-CA	7.26	1.54	1.45

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	334	PRO	O-C-N	-12.61	105.61	122.64
1	C	334	PRO	O-C-N	-12.51	105.75	122.64
1	B	335	THR	CB-CA-C	12.27	134.84	110.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	335	THR	CB-CA-C	11.65	133.61	110.42
1	A	335	THR	CA-C-O	-10.40	109.36	121.11

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	303	ARG	Sidechain
1	A	334	PRO	Mainchain
1	B	303	ARG	Sidechain
1	B	334	PRO	Mainchain
1	B	335	THR	Peptide

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	A	5212	0	5169	327	0
1	B	5212	0	5169	362	0
1	C	5212	0	5169	343	0
1	D	5212	0	5168	362	0
All	All	20848	0	20675	1394	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 34.

The worst 5 of 1394 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:275:GLY:HA2	1:A:505:THR:CG2	1.16	1.64
1:A:278:ILE:HG13	1:A:336:LEU:CD1	1.27	1.60
1:A:278:ILE:CG1	1:A:336:LEU:HD13	1.32	1.58
1:C:275:GLY:CA	1:C:505:THR:CG2	1.84	1.53
1:C:275:GLY:HA2	1:C:505:THR:CG2	1.17	1.53

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	644/803 (80%)	576 (89%)	66 (10%)	2 (0%)	36	71
1	B	644/803 (80%)	580 (90%)	62 (10%)	2 (0%)	36	71
1	C	644/803 (80%)	578 (90%)	64 (10%)	2 (0%)	36	71
1	D	644/803 (80%)	579 (90%)	63 (10%)	2 (0%)	36	71
All	All	2576/3212 (80%)	2313 (90%)	255 (10%)	8 (0%)	37	71

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	336	LEU
1	B	335	THR
1	C	336	LEU
1	D	335	THR
1	A	334	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	A	592/730 (81%)	588 (99%)	4 (1%)	76	79
1	B	592/730 (81%)	590 (100%)	2 (0%)	86	84
1	C	592/730 (81%)	589 (100%)	3 (0%)	81	82
1	D	592/730 (81%)	589 (100%)	3 (0%)	81	82
All	All	2368/2920 (81%)	2356 (100%)	12 (0%)	78	82

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	336	LEU
1	C	565	ILE
1	D	741	VAL
1	D	225	LEU
1	A	565	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	148	GLN
1	C	708	GLN
1	D	576	ASN
1	C	155	GLN
1	C	348	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

There are no chain breaks in this entry.

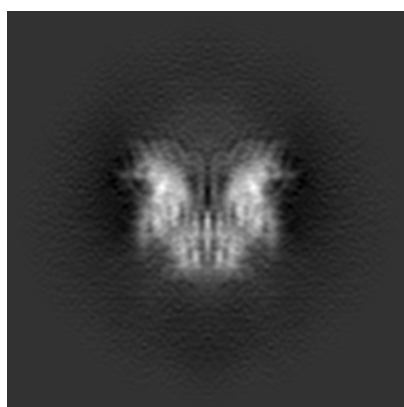
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10889. These allow visual inspection of the internal detail of the map and identification of artifacts.

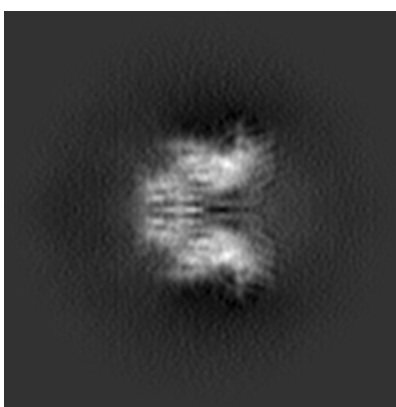
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

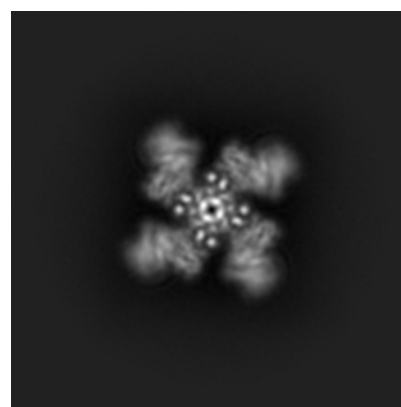
6.1.1 Primary map



X



Y

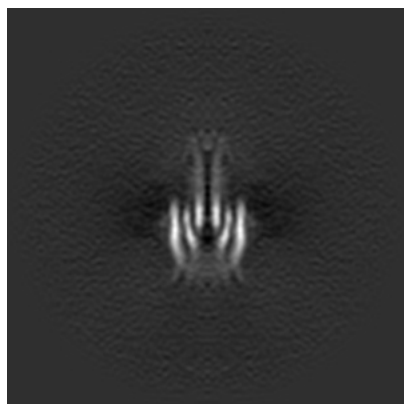


Z

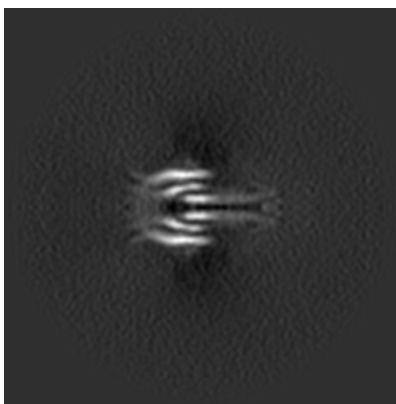
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

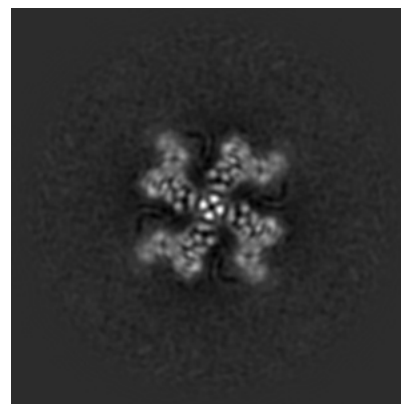
6.2.1 Primary map



X Index: 150



Y Index: 150

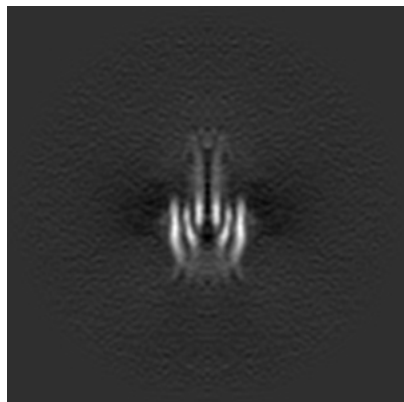


Z Index: 150

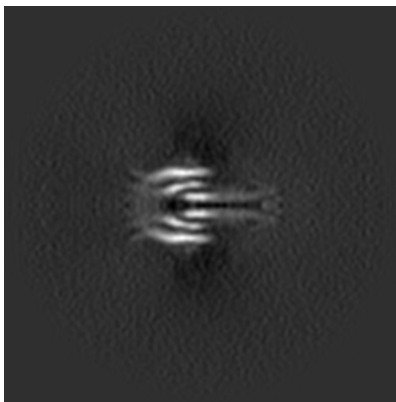
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

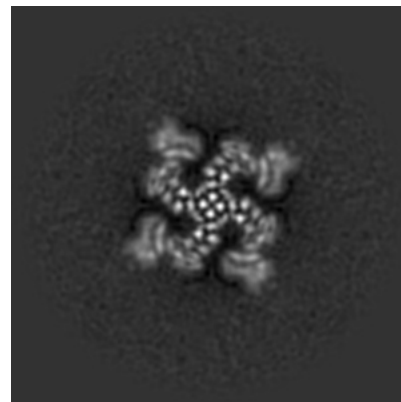
6.3.1 Primary map



X Index: 150



Y Index: 150

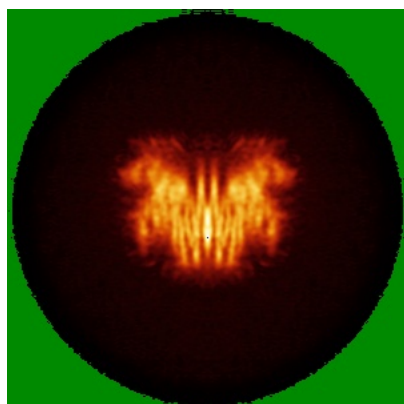


Z Index: 143

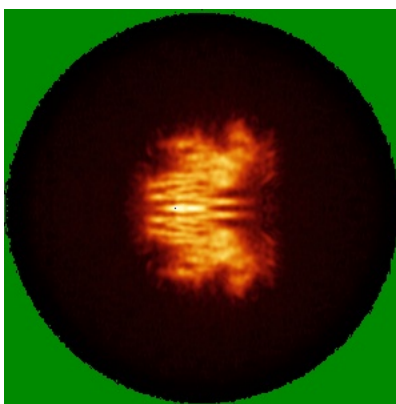
The images above show the largest variance slices of the map in three orthogonal directions.

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

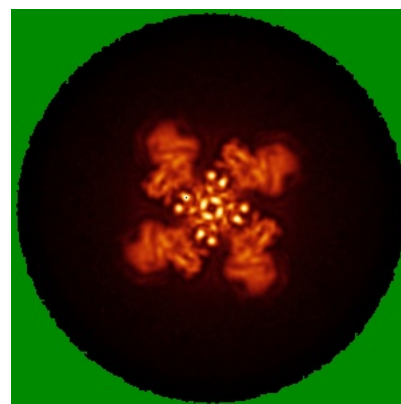
6.4.1 Primary map



X



Y



Z

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 0.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

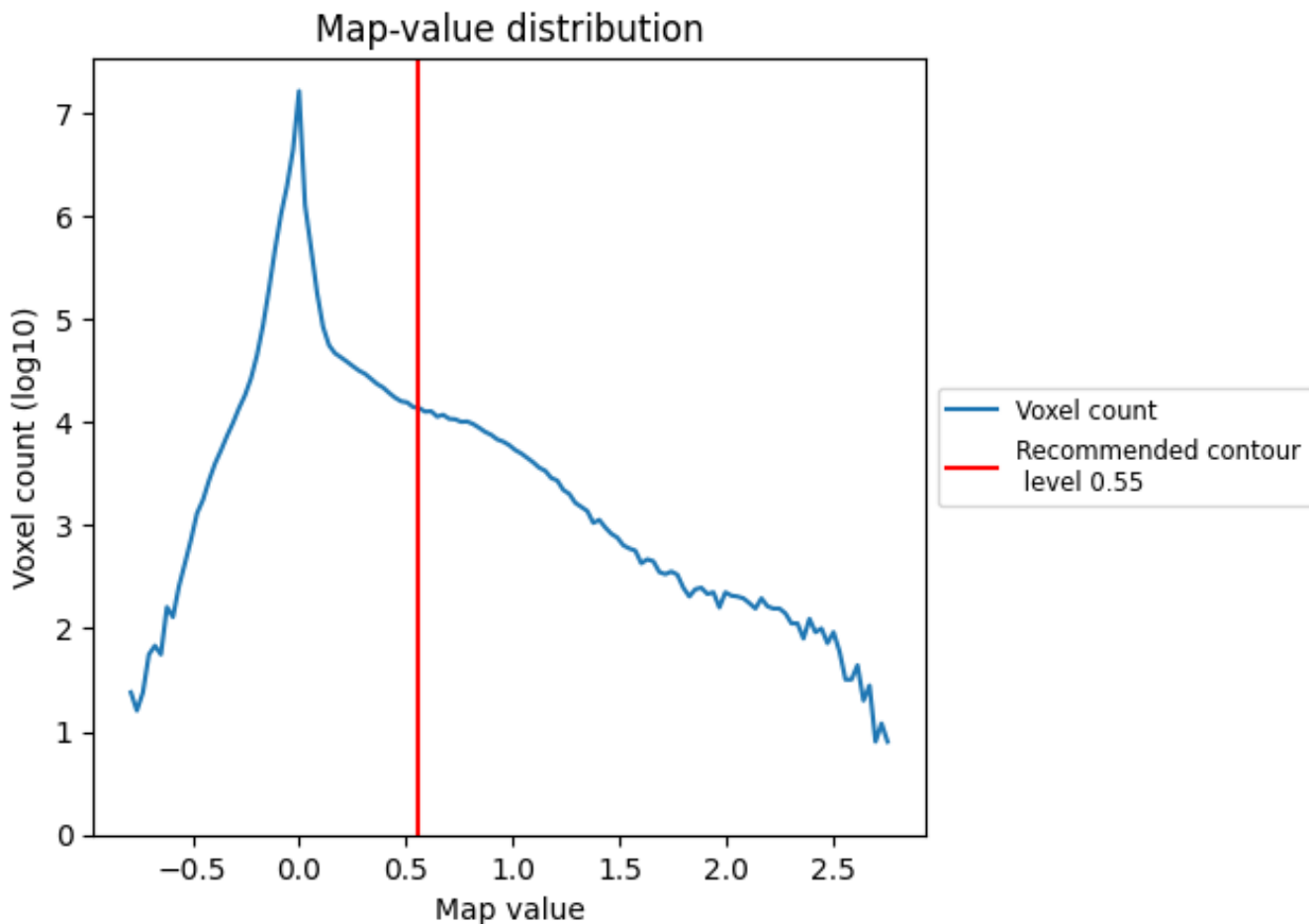
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

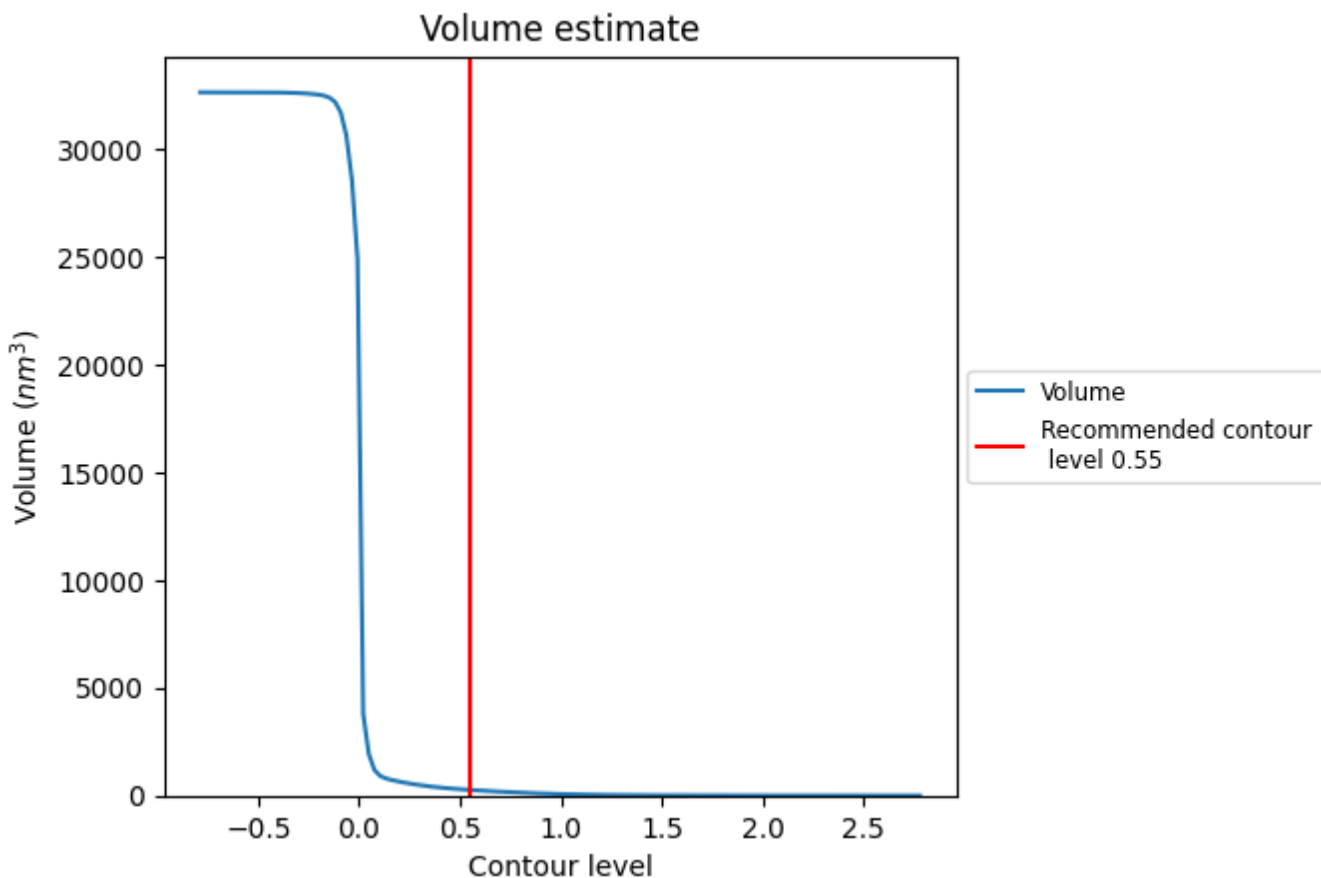
This section contains the results of statistical analysis of the map.

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.

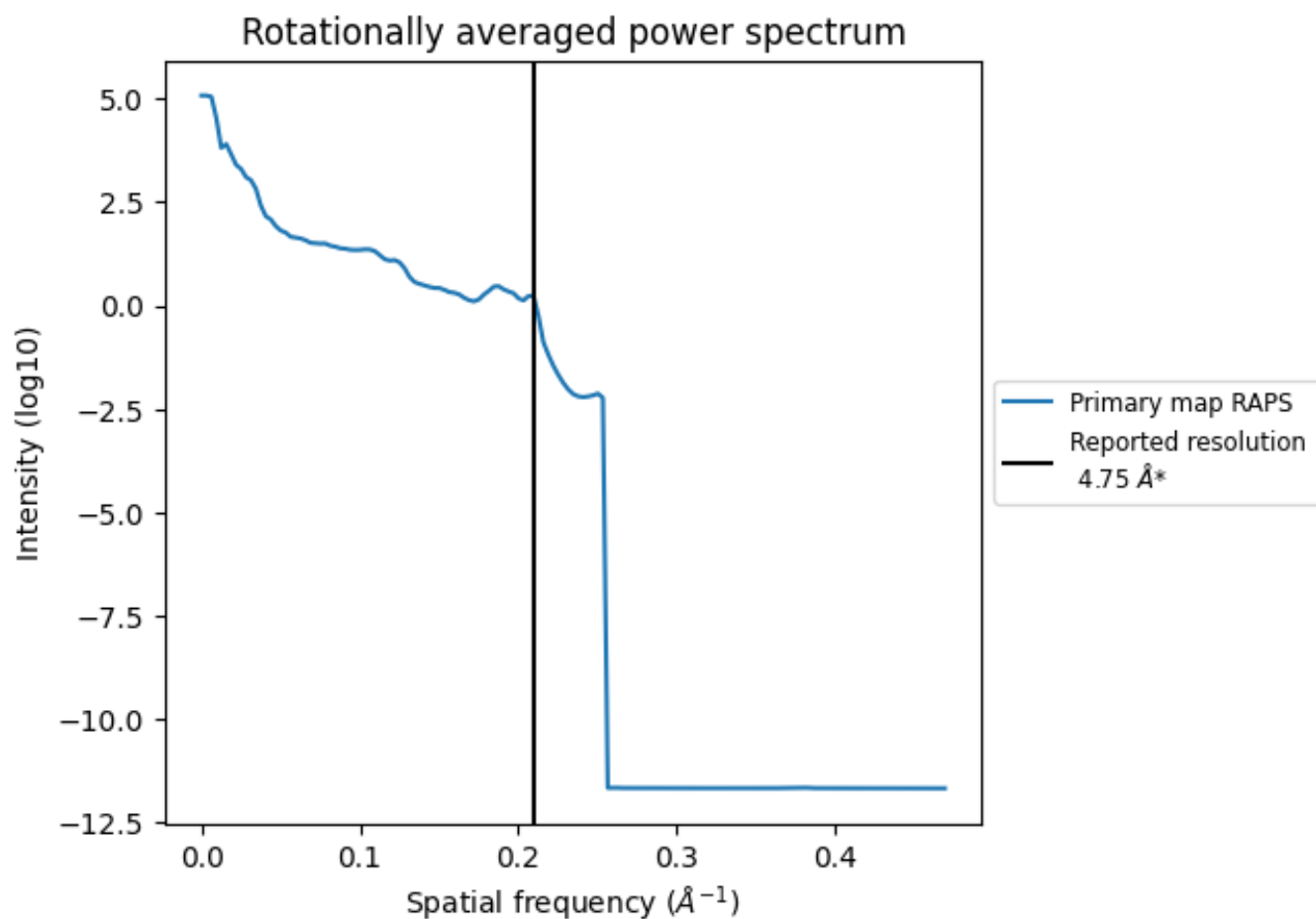
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 261 nm^3 ; this corresponds to an approximate mass of 236 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](#)

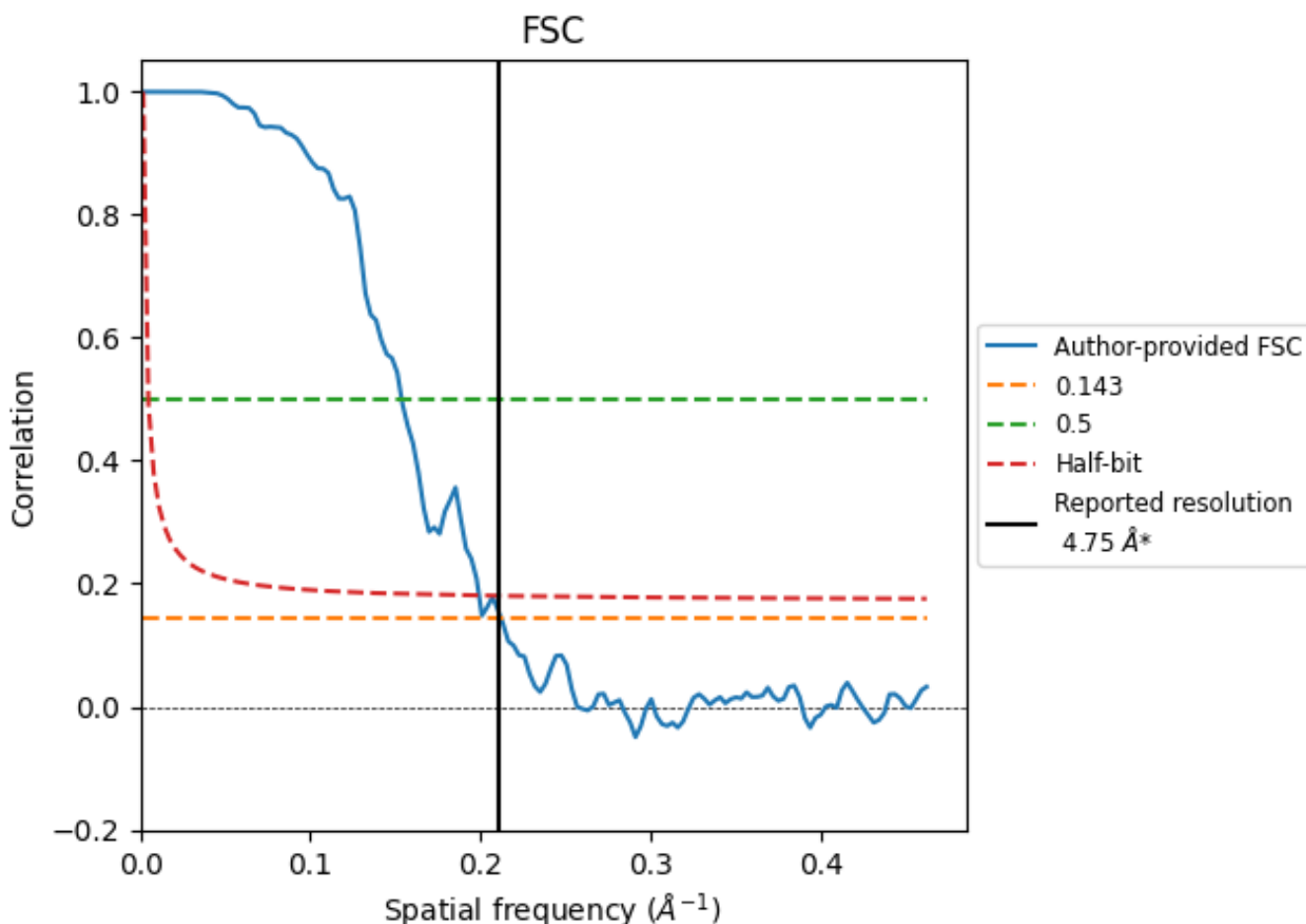


*Reported resolution corresponds to spatial frequency of 0.211 Å⁻¹

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 0.211 Å⁻¹

8.2 Resolution estimates [i](#)

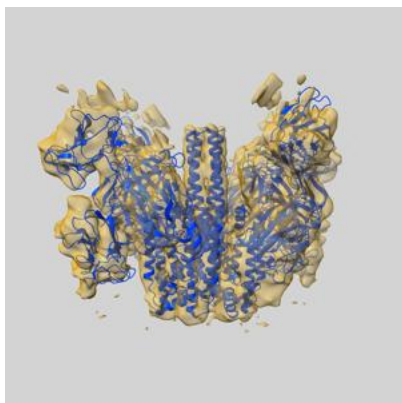
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.75	-	-
Author-provided FSC curve	4.71	6.51	5.02
Unmasked-calculated*	-	-	-

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

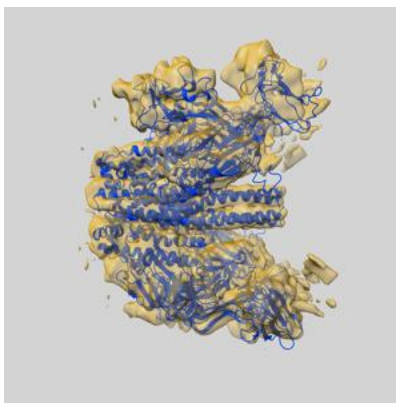
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10889 and PDB model 7NTX. Per-residue inclusion information can be found in section 3 on page 4.

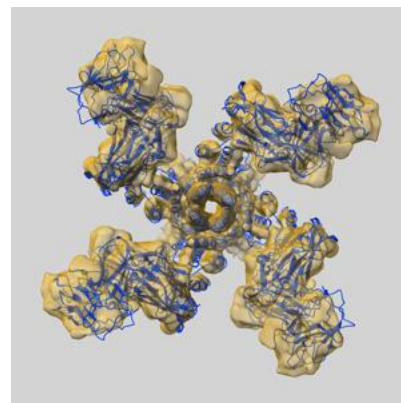
9.1 Map-model overlay [i](#)



X



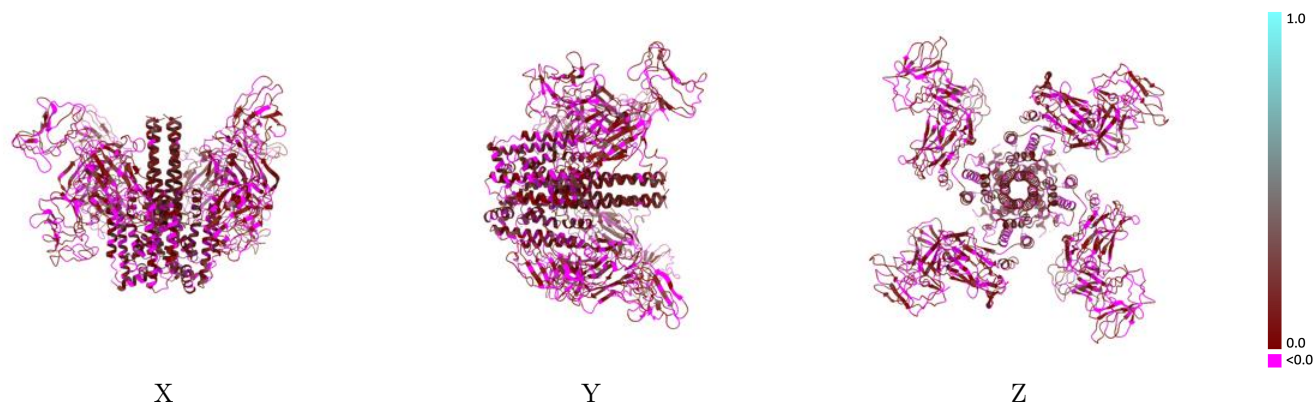
Y



Z

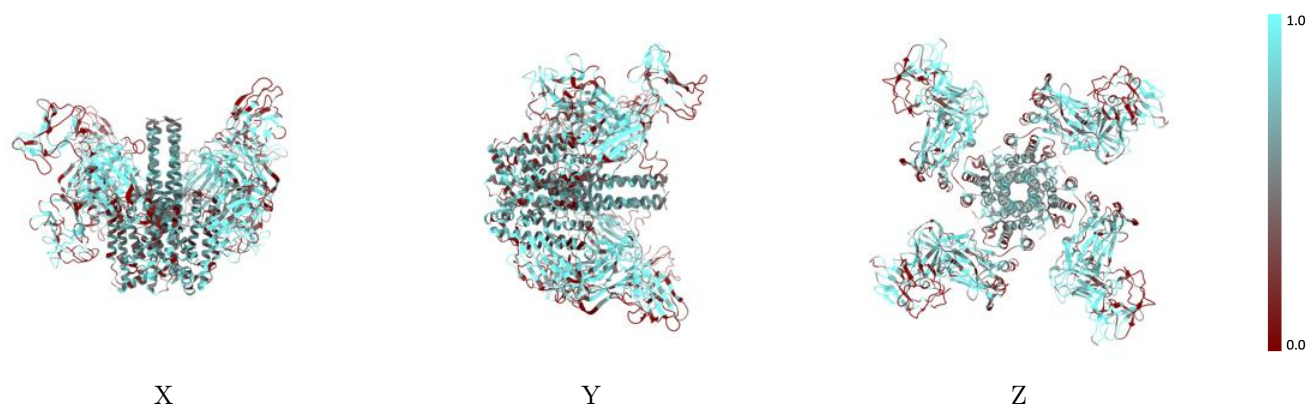
The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



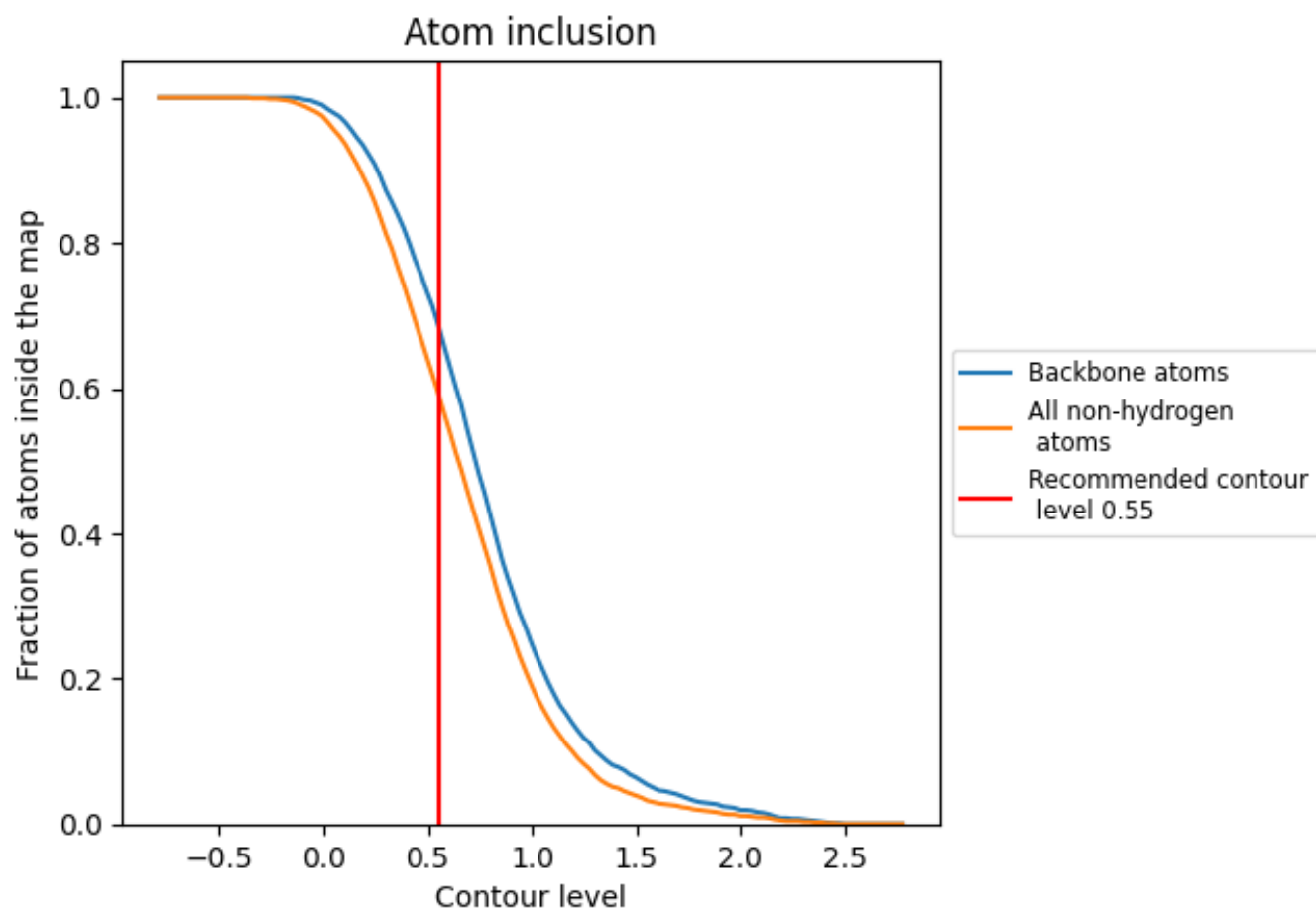
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.55).











9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 59% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5930	 0.0470
A	 0.5930	 0.0510
B	 0.5920	 0.0460
C	 0.5940	 0.0500
D	 0.5920	 0.0410

