



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:22 PM UTC

PDB ID : 7BWA / pdb_00007bwa
EMDB ID : EMD-30231
Title : Cryo-EM Structure for the Ectodomain of the Full-length Human Insulin Receptor in Complex with 2 Insulin
Authors : Yu, D.; Zhang, X.; Sun, J.; Li, X.; Wu, Z.; Han, X.; Fan, C.; Ma, Y.; Ouyang, Q.; Wang, T.
Deposited on : 2020-04-14
Resolution : 4.90 Å (reported)
Based on initial model : 6PXV

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

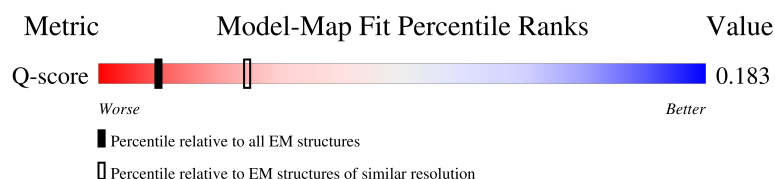
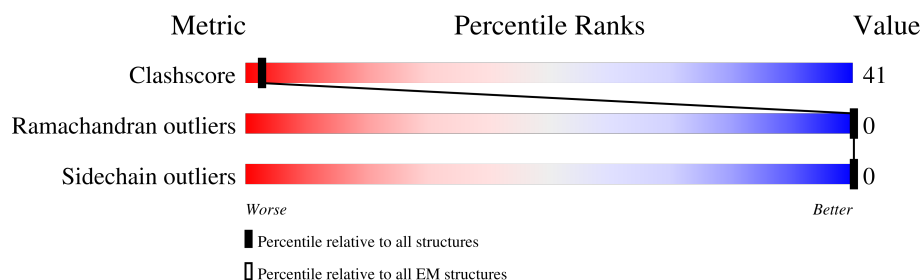
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 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	1274 (4.40 - 5.40)

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	1355	12% 18% 32% 50%
1	C	1355	14% 18% 32% 50%
2	D	74	22% 35% 30% 35%
2	E	74	20% 35% 30% 35%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11670 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 Insulin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	674	Total	C	N	O	S	0	0
			5459	3472	938	1008	41		
1	C	674	Total	C	N	O	S	0	0
			5459	3472	938	1008	41		

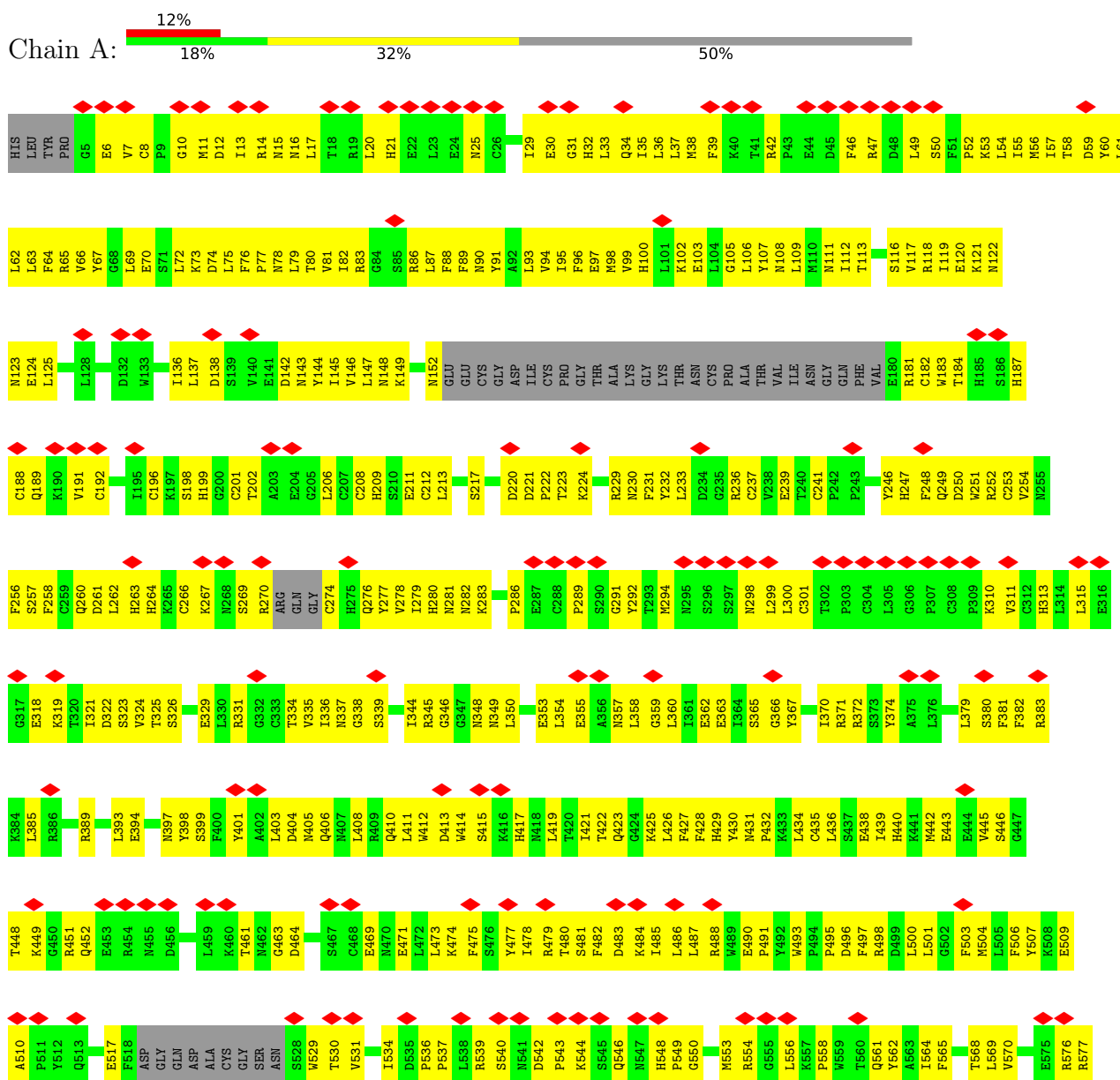
- Molecule 2 is a protein called Insulin fusion.

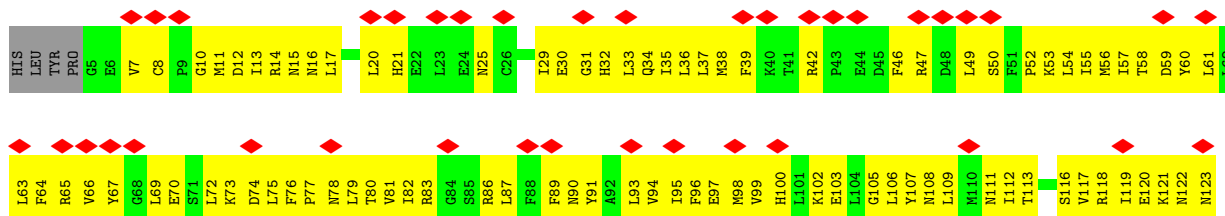
Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	48	Total	C	N	O	S	0	0
			376	238	61	71	6		
2	E	48	Total	C	N	O	S	0	0
			376	238	61	71	6		

3 Residue-property plots

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: Insulin receptor





GLY	SER	ILE	ARG	ILE	D813	SER	T704	LEU	G580	A510	E444	R383	L315	V254	S186	E124
PRO	GLU	TYR	GLU	VAL	A581	PRO	F705	ASP	A581	GLY	V445	K384	E316	M255	H187	L125
GLU	GLY	CYS	LEU	GLY	K582	GLU	E706	TYR	K582	GLY	S446	L385	G317	F256	C188	L128
HIS	LEU	LEU	LEU	PRO	S583	HIS	D707	LEU	S583	ASP	G447	R386	E318	S257	Q189	A129
ARG	PRO	GLY	GLY	VAL	D584	ARG	L709	LEU	D584	ASP	T448	L387	K319	F258	K190	T130
P758	THR	THR	THR	THR	I585	P758	H710	LEU	I585	ASP	K449	I388	T321	Q259	V191	T130
F759	THR	THR	THR	THR	I586	F759	N711	LEU	I586	ASP	G450	R389	T320	C259	C192	D132
E760	THR	THR	THR	THR	V587	E760	N712	LEU	V587	GLY	R451	R390	D322	P193	P193	I131
K761	THR	THR	THR	THR	V588	K761	V713	LEU	V588	GLN	Q452	G390	S323	T194	T194	T130
V762	THR	THR	THR	THR	Q589	V762	V714	LEU	Q589	ASP	R453	T392	S325	H263	H263	D132
V763	THR	THR	THR	THR	T590	V763	V715	LEU	T590	CYS	R454	L393	T326	H264	H264	I135
N764	THR	THR	THR	THR	D591	N764	V716	LEU	D591	GLY	N455	E394	S326	K265	K136	I135
K765	THR	THR	THR	THR	N594	K765	L717	LEU	N594	SER	M456	R397	E329	K197	L137	L137
E766	THR	THR	THR	THR	P595	E766	R718	LEU	P595	ASN	L459	N397	L330	K267	L138	D138
S767	THR	THR	THR	THR	S596	S767	L719	LEU	S596	ASN	K460	Y398	R331	M268	S139	S139
L768	THR	THR	THR	THR	L599	L768	THR	LEU	L599	GLY	T461	Y399	R332	G200	V140	V140
V769	THR	THR	THR	THR	P601	V769	THR	LEU	P601	GLY	M462	S399	T334	S269	E141	E141
T770	THR	THR	THR	THR	D602	T770	THR	LEU	D602	GLY	D464	F400	T335	T202	T202	D142
S771	THR	THR	THR	THR	I603	S771	THR	LEU	I603	GLY	G463	Y401	N336	A203	A203	N143
G772	THR	THR	THR	THR	V604	G772	THR	LEU	V604	GLY	D464	L403	N337	E204	E204	Y144
L773	THR	THR	THR	THR	S605	L773	THR	LEU	S605	GLY	C468	D404	G338	G205	G205	I145
H774	THR	THR	THR	THR	N606	H774	THR	LEU	N606	GLY	E469	N405	S339	L206	L206	V146
R775	THR	THR	THR	THR	S607	R775	THR	LEU	S607	GLY	N470	M407	L340	C207	C207	L147
F776	THR	THR	THR	THR	Q610	F776	THR	LEU	Q610	GLY	E471	L408	I341	Q276	Q276	L147
T777	THR	THR	THR	THR	I611	T777	THR	LEU	I611	GLY	L472	R409	T344	Y277	Y277	K149
G778	THR	THR	THR	THR	L612	G778	THR	LEU	L612	GLY	L473	Q410	R345	V278	V278	D150
R780	THR	THR	THR	THR	L613	R780	THR	LEU	L613	GLY	K474	L411	G346	I279	I279	E211
E781	THR	THR	THR	THR	L614	E781	THR	LEU	L614	GLY	F475	L412	G347	H280	H280	C212
L783	THR	THR	THR	THR	M615	L783	THR	LEU	M615	GLY	F475	D413	N348	N281	N281	D151
Q784	THR	THR	THR	THR	K616	Q784	THR	LEU	K616	GLY	L478	N414	N349	N282	N282	L213
A785	THR	THR	THR	THR	P617	A785	THR	LEU	P617	GLY	L479	N415	L350	C284	C284	M152
C786	THR	THR	THR	THR	Q618	C786	THR	LEU	Q618	GLY	T480	S416	E353	I285	I285	GLU
ASN	THR	THR	THR	THR	M619	ASN	THR	LEU	M619	GLY	T481	H417	E354	P286	P286	GLU
GLN	THR	THR	THR	THR	S619	GLN	THR	LEU	S619	GLY	F482	N418	E355	E287	E287	CYS
ASP	THR	THR	THR	THR	D620	ASP	THR	LEU	D620	GLY	K483	L419	A356	C788	C788	ASP
PRO	THR	THR	THR	THR	P621	PRO	THR	LEU	P621	GLY	L485	T420	N357	D221	D221	ILE
GLU	THR	THR	THR	THR	M622	GLU	THR	LEU	M622	GLY	L486	I421	L358	P222	P222	CYS
ALA	THR	THR	THR	THR	G623	ALA	THR	LEU	G623	GLY	L487	T422	G359	G291	G291	THR
VAL	THR	THR	THR	THR	L556	VAL	THR	LEU	L556	GLY	R488	Q423	L360	Y292	Y292	LYS
LEU	THR	THR	THR	THR	K557	LEU	THR	LEU	K557	GLY	M489	G424	I361	T293	T293	GLY
THR	THR	THR	THR	THR	P558	THR	THR	LEU	P558	GLY	E490	K425	E362	M294	M294	LYS
ASP	THR	THR	THR	THR	Q561	ASP	THR	LEU	Q561	GLY	F491	L426	E363	N295	N295	THR
LEU	THR	THR	THR	THR	Y562	LEU	THR	LEU	Y562	GLY	M492	F427	I364	S296	S296	ASN
HIS	THR	THR	THR	THR	A563	HIS	THR	LEU	A563	GLY	D493	F428	S365	S297	S297	CYS
CYS	THR	THR	THR	THR	I564	CYS	THR	LEU	I564	GLY	R498	H429	G366	C237	C237	PRO
VAL	THR	THR	THR	THR	F565	VAL	THR	LEU	F565	GLY	L500	N431	Y367	N298	N298	ALA
ARG	THR	THR	THR	THR	T568	ARG	THR	LEU	T568	GLY	L499	P432	I370	L299	L299	THR
LEU	THR	THR	THR	THR	K632	LEU	THR	LEU	K632	GLY	D499	L434	R371	L300	L300	VAL
ALA	THR	THR	THR	THR	S633	ALA	THR	LEU	S633	GLY	L501	P432	R372	E239	E239	ILE
THR	THR	THR	THR	THR	B634	THR	THR	LEU	B634	GLY	G502	L436	Y374	C241	C241	ASN
SER	THR	THR	THR	THR	E574	SER	THR	LEU	E574	GLY	F503	S437	E374	Y246	Y246	GLN
LEU	THR	THR	THR	THR	D575	LEU	THR	LEU	D575	GLY	E438	E437	L379	H247	H247	PHE
GLU	THR	THR	THR	THR	A576	GLU	THR	LEU	A576	GLY	I439	I439	L305	R248	R248	VAL
VAL	THR	THR	THR	THR	R576	VAL	THR	LEU	R576	GLY	H440	H440	G306	F248	F248	THR
PRO	THR	THR	THR	THR	R577	PRO	THR	LEU	R577	GLY	K441	K441	F307	Q249	Q249	THR
THR	THR	THR	THR	THR	Y578	THR	THR	LEU	Y578	GLY	M442	M442	F381	D250	D250	THR
D812	THR	THR	THR	THR	Y579	D812	THR	LEU	Y579	GLY	E509	E509	F382	W251	W251	C182
														R252	R252	W183
														C253	C253	T184
																H185

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	368511	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 ($e^-/\text{\AA}^2$)	50.0	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	43796	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.098	Depositor
Minimum map value	-0.070	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.023	Depositor
Map size (Å)	219.2, 219.2, 219.2	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	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	0.22	0/5589	0.46	0/7569
1	C	0.22	0/5589	0.46	0/7569
2	D	0.22	0/383	0.41	0/518
2	E	0.22	0/383	0.41	0/518
All	All	0.22	0/11944	0.46	0/16174

There are no bond length outliers.

There are no bond angle outliers.

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	A	5459	0	5329	462	0
1	C	5459	0	5329	466	0
2	D	376	0	346	26	0
2	E	376	0	346	25	0
All	All	11670	0	11350	946	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 41.

The worst 5 of 946 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:C:436:LEU:HD21	1:C:577:ARG:CD	1.74	1.16
1:A:576:ARG:HD3	1:A:579:TYR:CE1	1.89	1.08
1:A:484:LYS:HA	1:A:553:MET:O	1.57	1.02
1:C:484:LYS:HA	1:C:553:MET:O	1.57	1.01
1:C:469:GLU:HA	1:C:577:ARG:HH12	1.21	0.99

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	660/1355 (49%)	571 (86%)	89 (14%)	0	100	100
1	C	660/1355 (49%)	571 (86%)	89 (14%)	0	100	100
2	D	44/74 (60%)	39 (89%)	5 (11%)	0	100	100
2	E	44/74 (60%)	39 (89%)	5 (11%)	0	100	100
All	All	1408/2858 (49%)	1220 (87%)	188 (13%)	0	100	100

There are no Ramachandran outliers to report.

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	618/1212 (51%)	618 (100%)	0	100	100
1	C	618/1212 (51%)	618 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	43/65 (66%)	43 (100%)	0	100	100
2	E	43/65 (66%)	43 (100%)	0	100	100
All	All	1322/2554 (52%)	1322 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	25	ASN
1	C	627	HIS
1	C	263	HIS
1	C	470	ASN
1	C	199	HIS

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.

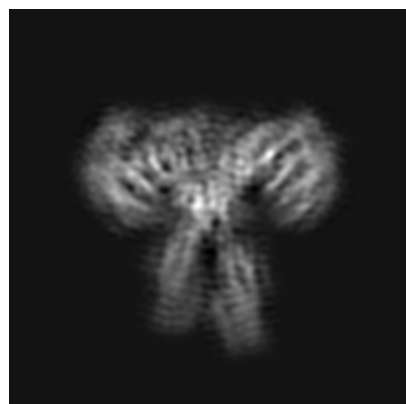
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30231. These allow visual inspection of the internal detail of the map and identification of artifacts.

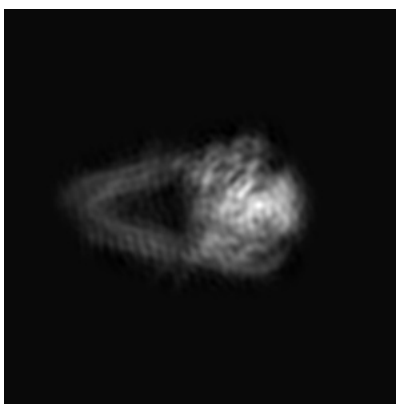
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

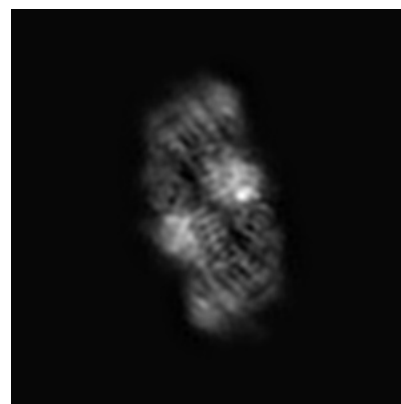
6.1.1 Primary map



X

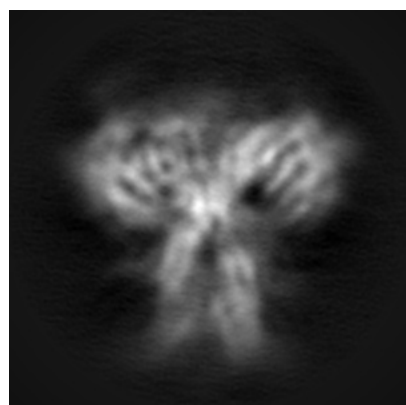


Y

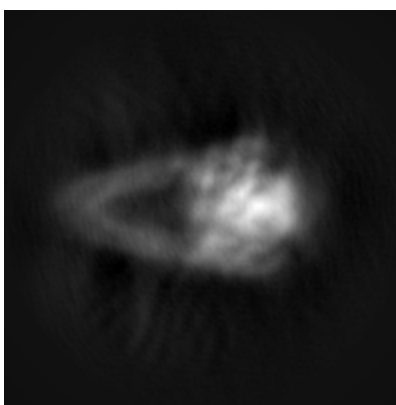


Z

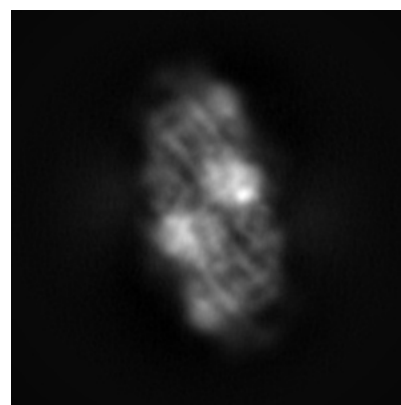
6.1.2 Raw map



X



Y

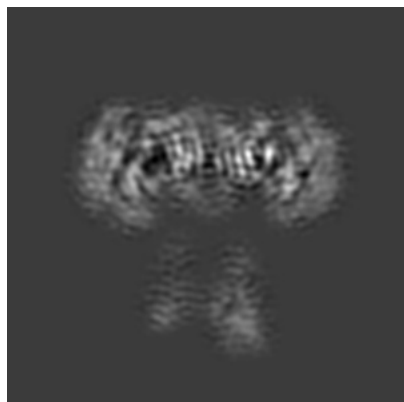


Z

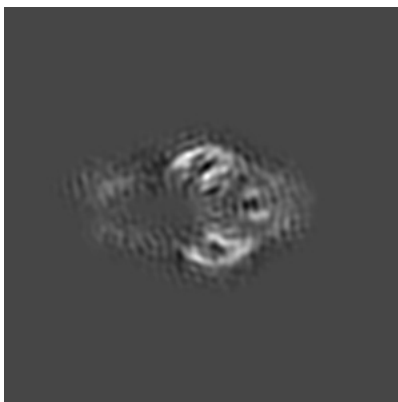
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

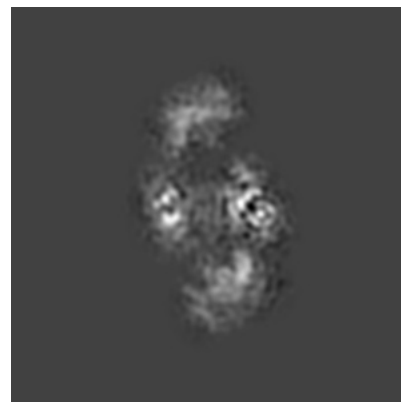
6.2.1 Primary map



X Index: 80

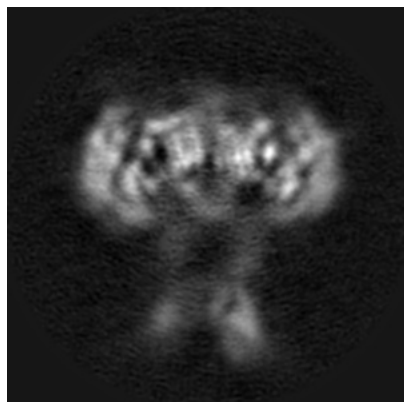


Y Index: 80

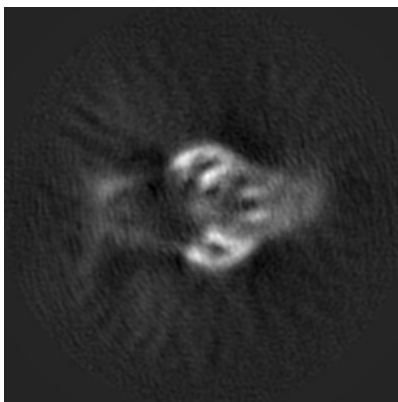


Z Index: 80

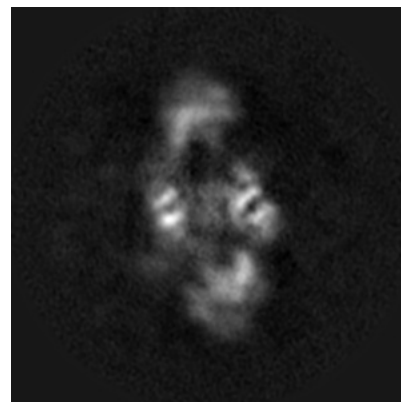
6.2.2 Raw map



X Index: 80



Y Index: 80

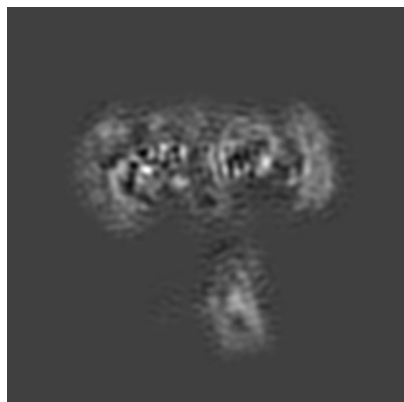


Z Index: 80

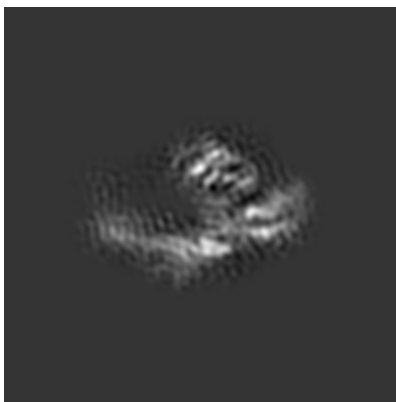
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 85

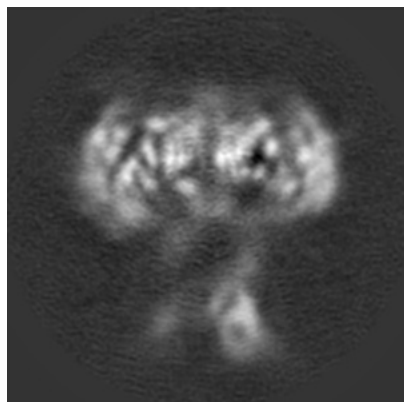


Y Index: 75

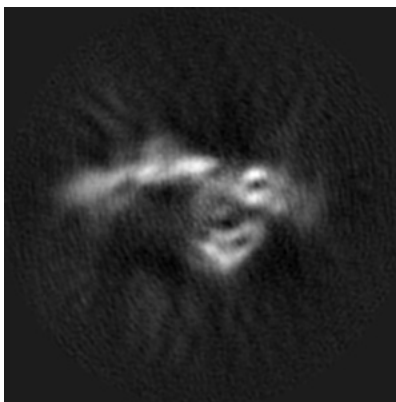


Z Index: 98

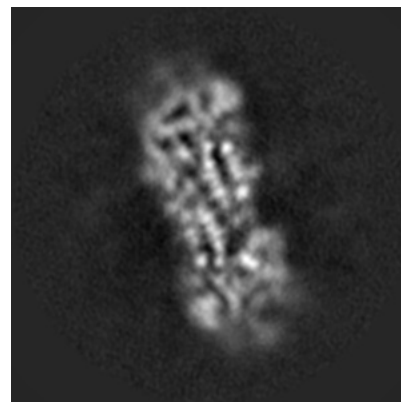
6.3.2 Raw map



X Index: 82



Y Index: 86



Z Index: 98

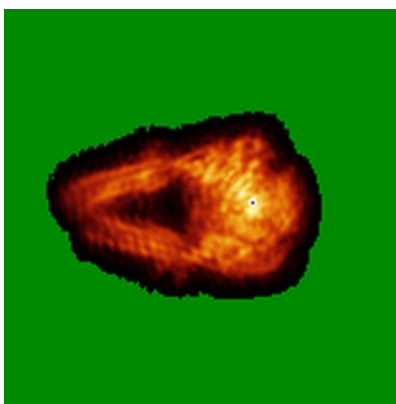
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

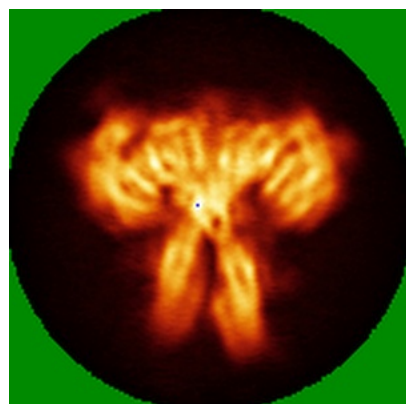


Y

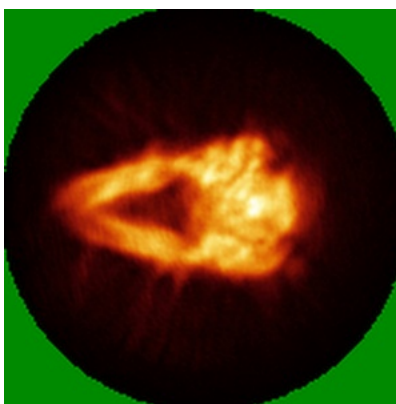


Z

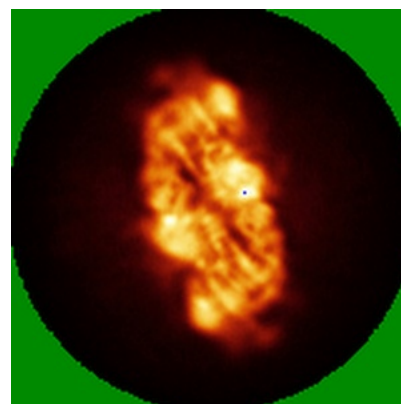
6.4.2 Raw map



X



Y

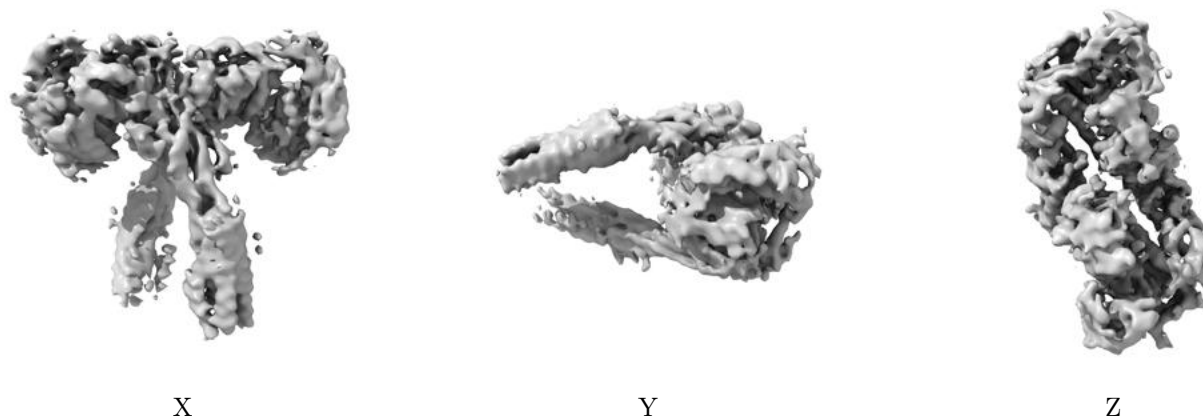


Z

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 0.023. 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.

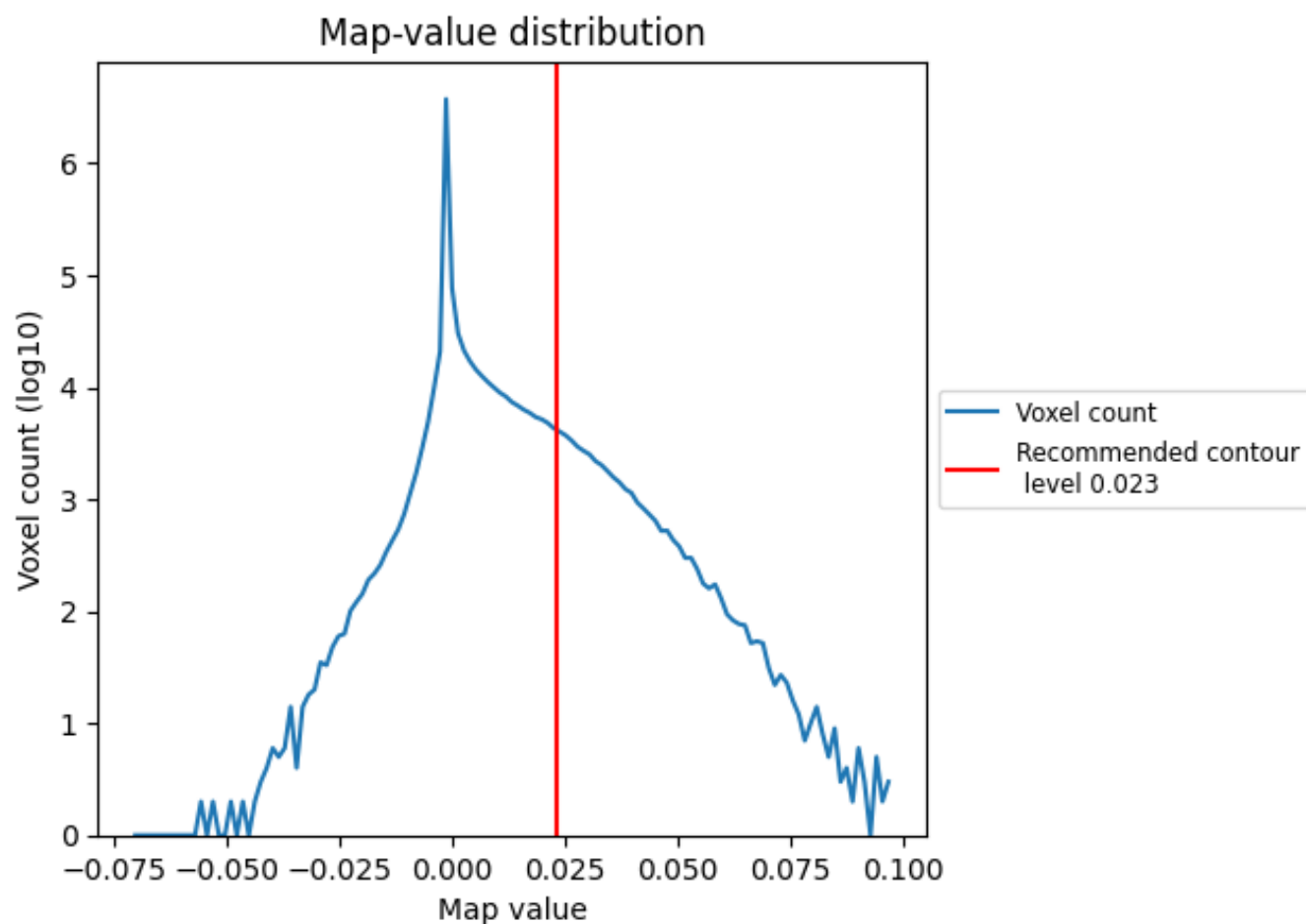
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

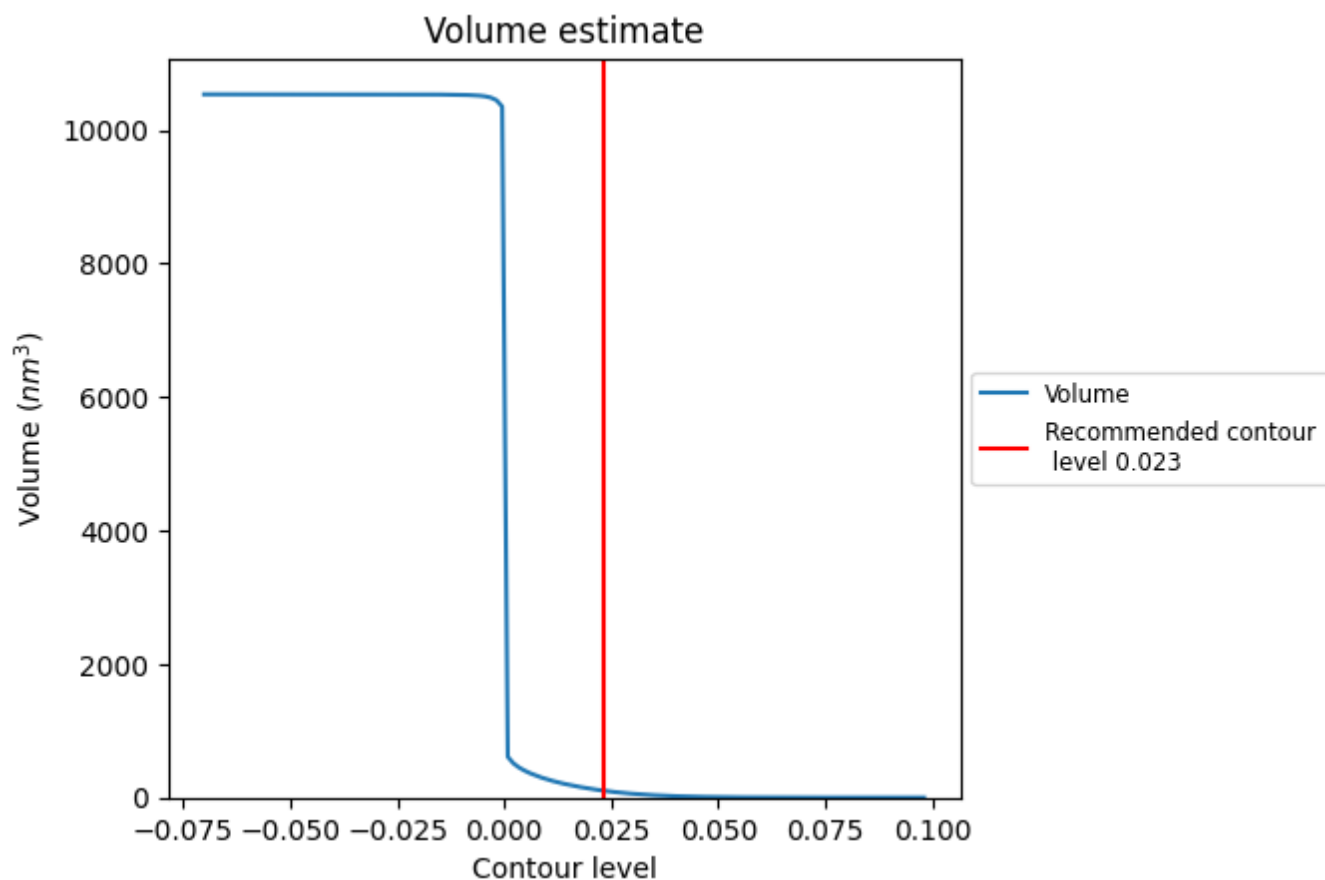
This section contains the results of statistical analysis of the map.

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.

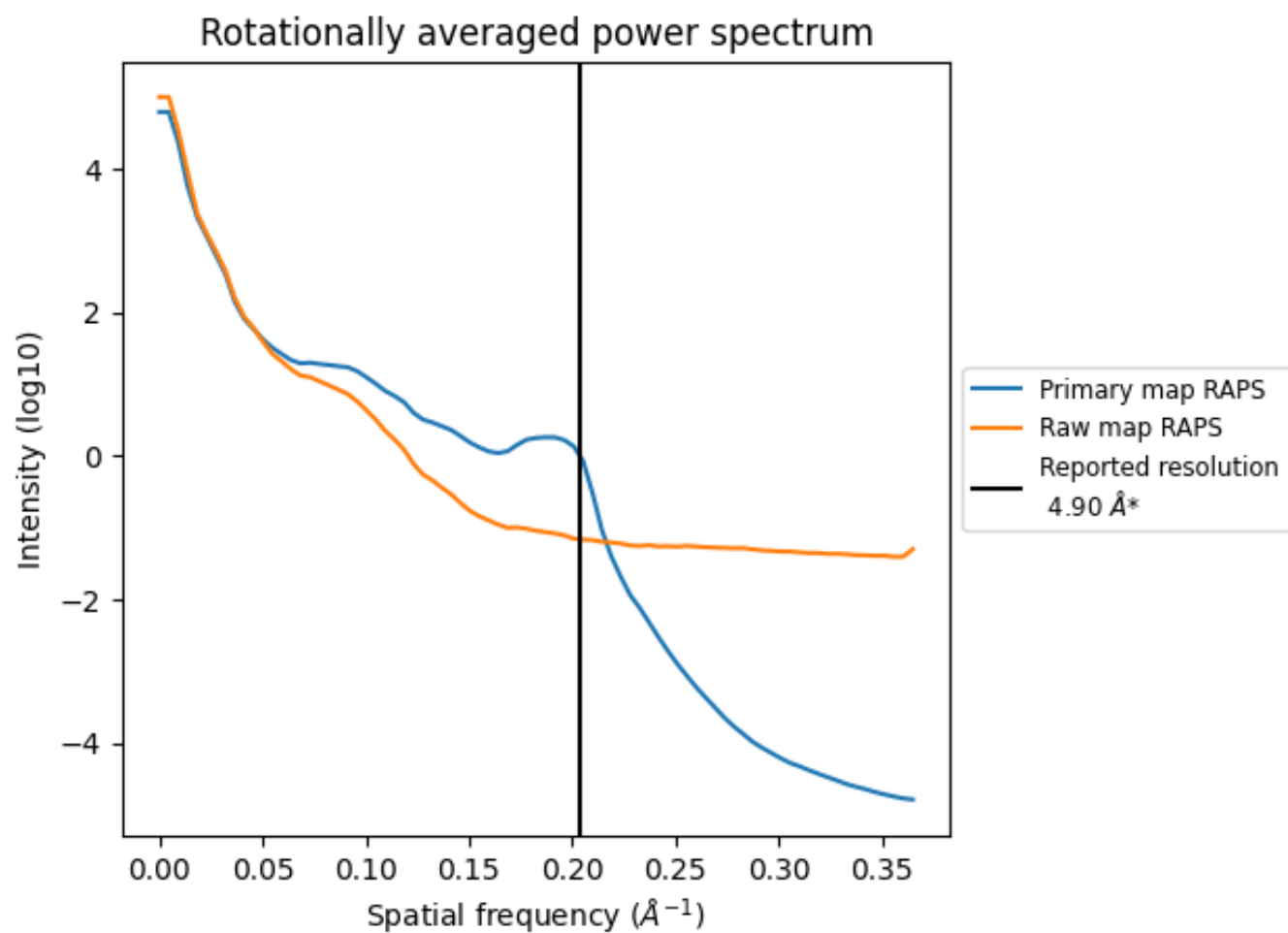
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 105 nm³; this corresponds to an approximate mass of 95 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 ⓘ

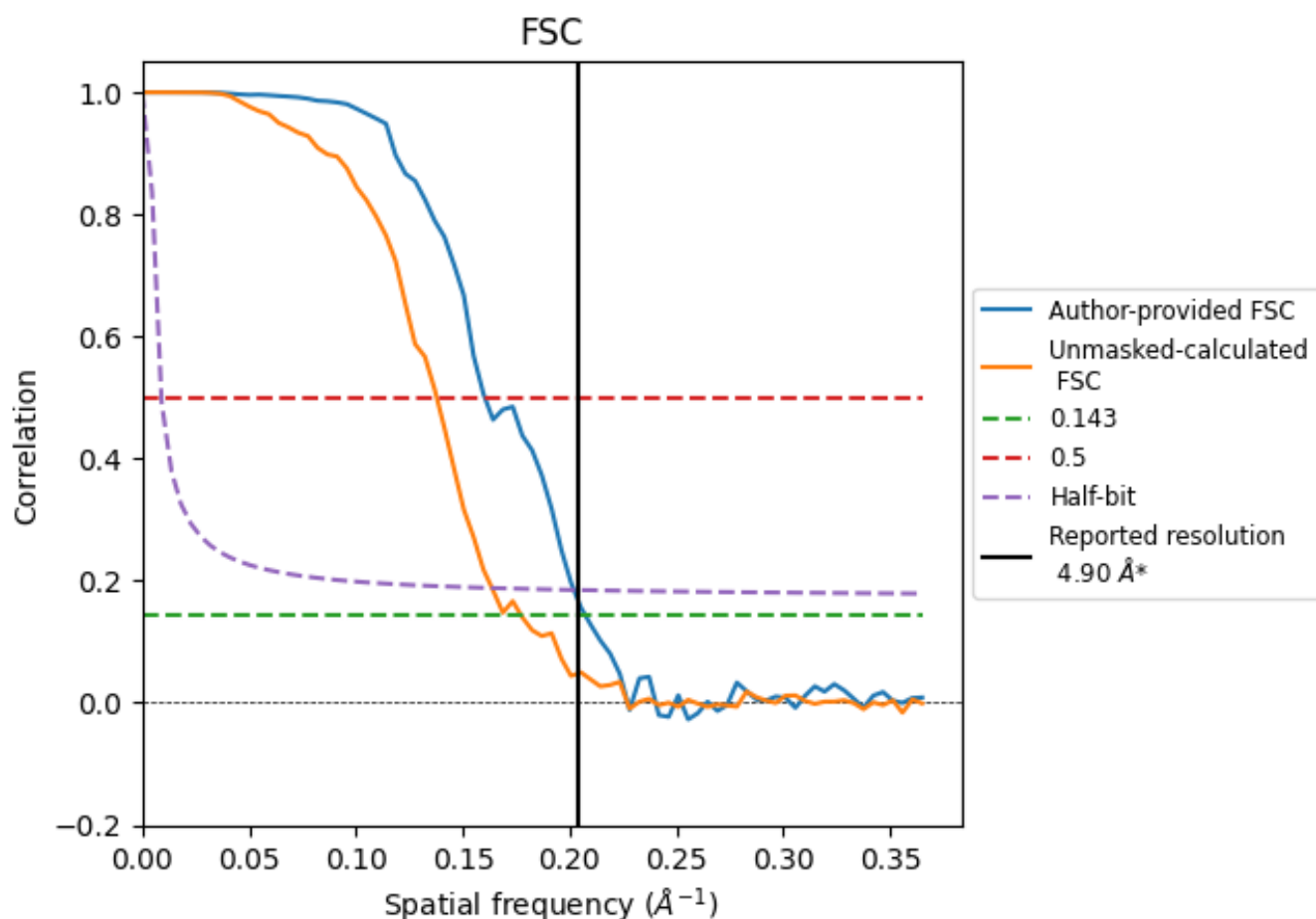


*Reported resolution corresponds to spatial frequency of 0.204 $\text{\AA}^{-1}$

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 $0.204 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

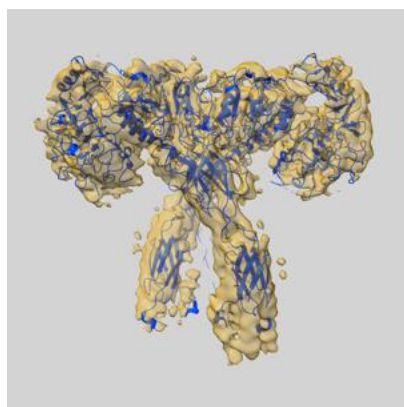
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.82	6.24	4.95
Unmasked-calculated*	5.64	7.26	6.11

*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 5.64 differs from the reported value 4.9 by more than 10 %

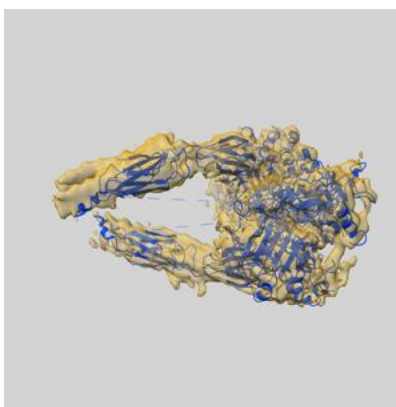
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30231 and PDB model 7BWA. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

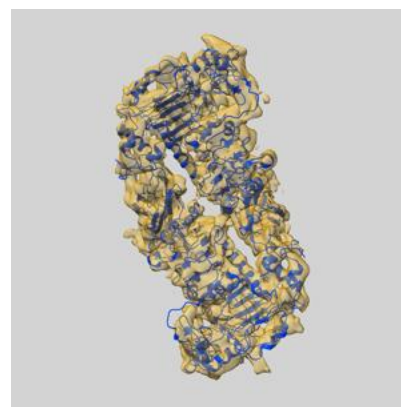
9.1 Map-model overlay [i](#)



X



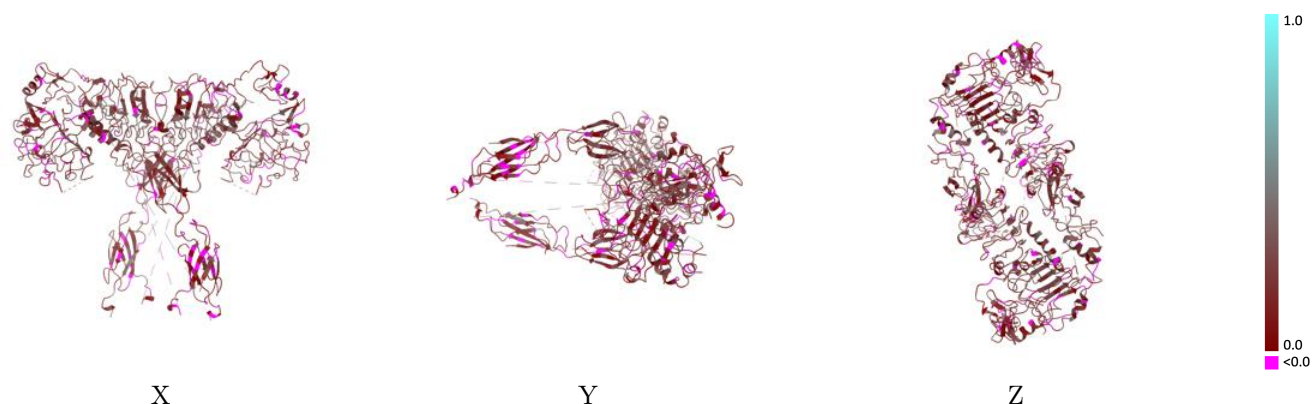
Y



Z

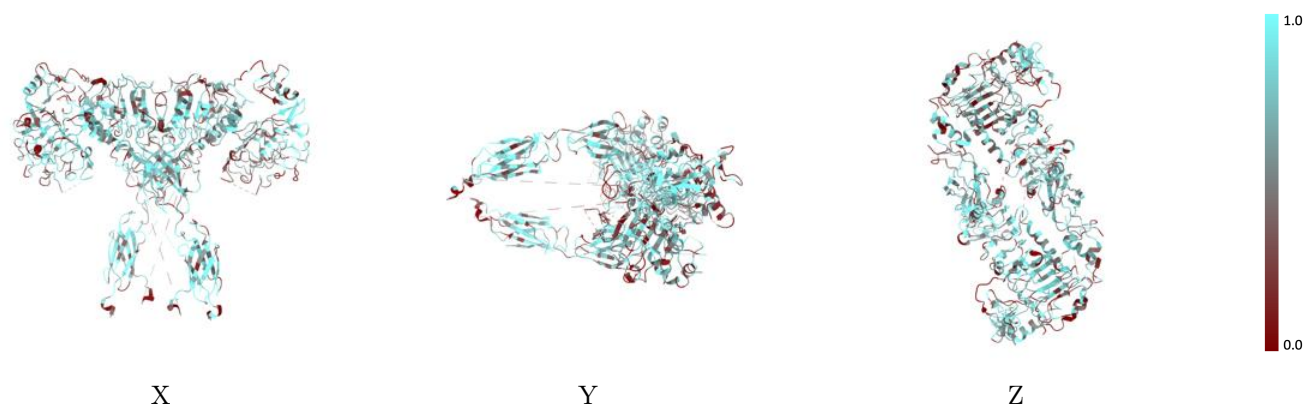
The images above show the 3D surface view of the map at the recommended contour level 0.023 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



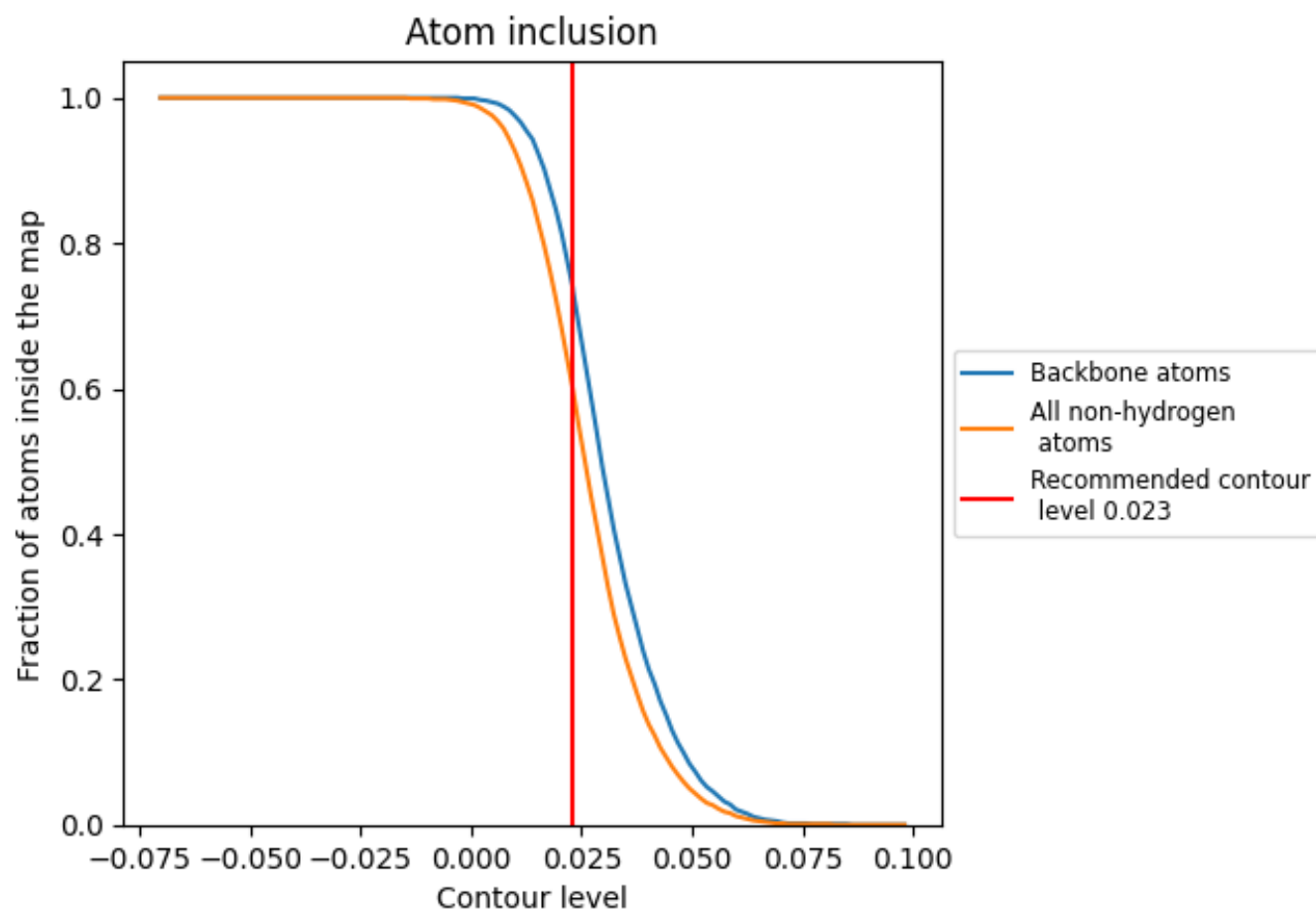
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.023).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 60% 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 (0.023) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6020	0.1830
A	0.6180	0.1890
C	0.5900	0.1740
D	0.6080	0.2270
E	0.5220	0.1820

