



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:53 PM UTC

PDB ID : 8ATO / pdb_00008ato
EMDB ID : EMD-15654
Title : Structure of the giant inhibitor of apoptosis, BIRC6 bound to the regulator SMAC
Authors : Dietz, L.; Elliott, P.R.
Deposited on : 2022-08-23
Resolution : 3.00 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

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<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

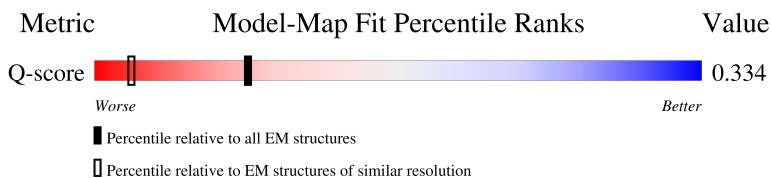
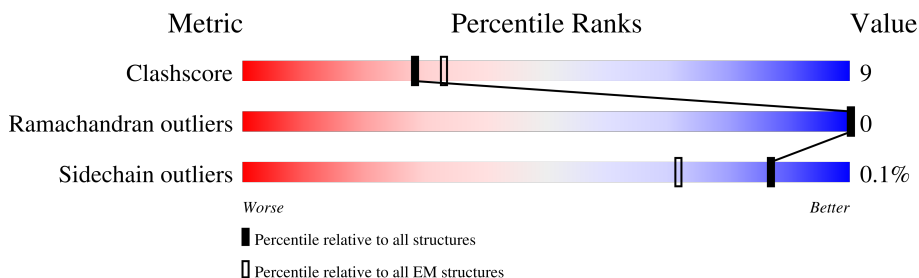
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	4859	20% 47% 12% 41%
1	B	4859	17% 45% 15% 40%
2	C	184	68% 61% 20% 18%
2	D	184	71% 67% 14% 18%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 46909 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 Baculoviral IAP repeat-containing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2871	Total	C	N	O	S	0	0
			22195	14154	3782	4102	157		
1	B	2892	Total	C	N	O	S	0	0
			22348	14249	3807	4135	157		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9NR09
A	0	PRO	-	expression tag	UNP Q9NR09
B	-1	GLY	-	expression tag	UNP Q9NR09
B	0	PRO	-	expression tag	UNP Q9NR09

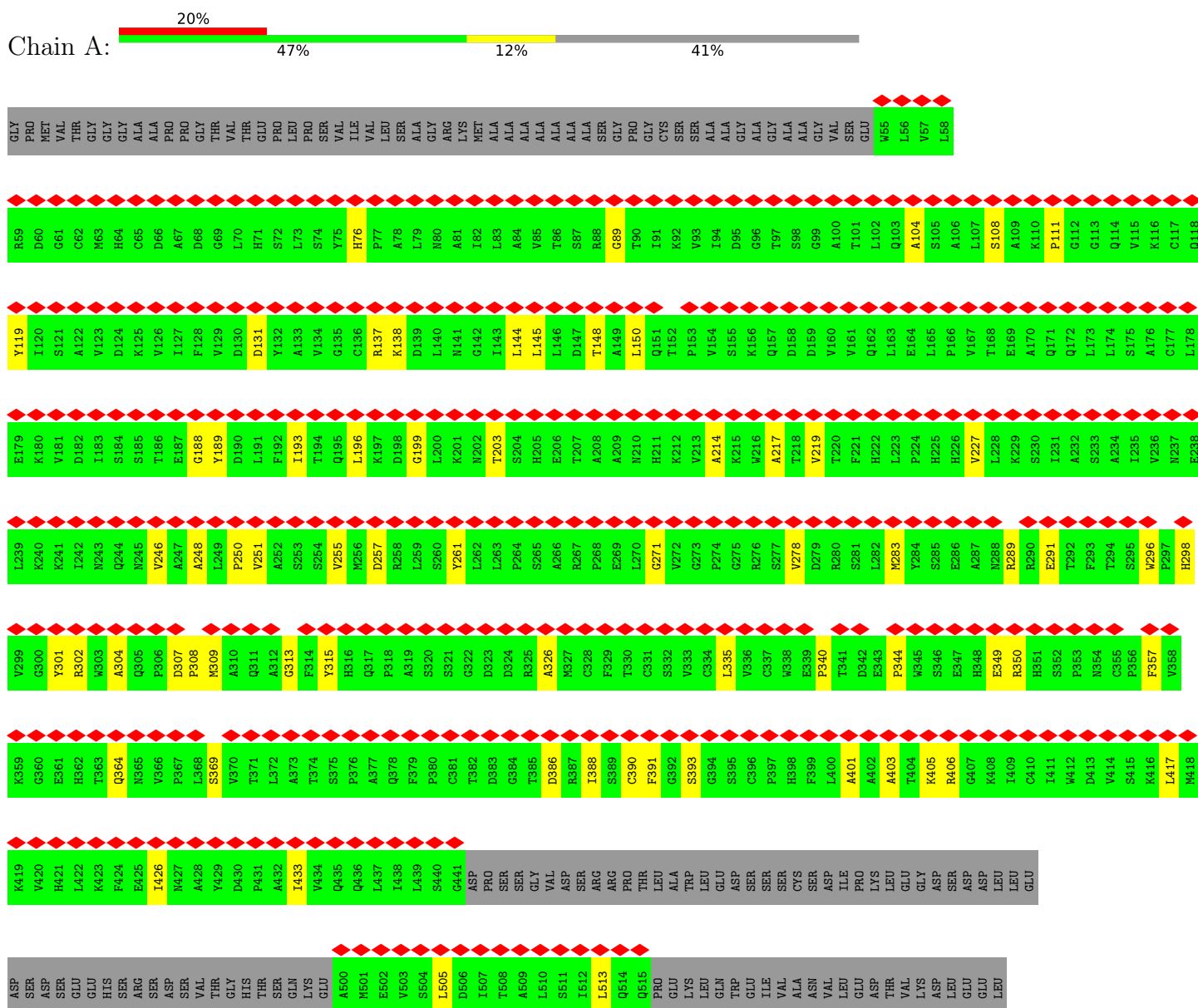
- Molecule 2 is a protein called Diablo IAP-binding mitochondrial protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	150	Total	C	N	O	S	0	0
			1183	739	198	241	5		
2	D	150	Total	C	N	O	S	0	0
			1183	739	198	241	5		

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: Baculoviral IAP repeat-containing protein 6









Y119	I120	S121	A122	V123	K125	V126	I127	F128	V129	D130	D131	Y132	A133	V134	G135	C136	R137	K138	D139	L140	N141	G142	I143	L144	L145	L146	D147	T148	A149	L150	Q151	T152	P153	V154	S155	K156	Q157	D158	D159	V160	V161	Q162	L163	E164	L165	P166	V167	T168	E169	A170	Q171	Q172	L173	L174	S175	A176	C177	L178
E179	K180	V181	D182	I183	S184	S185	T186	E187	G188	Y189	D190	L191	F192	I193	T194	Q195	L196	K197	D198	G199	L200	K201	N202	T203	S204	H205	P206	T207	A208	A209	N210	H211	K212	V213	A214	K215	V216	A217	T218	V219	T220	F221	H222	L223	P224	H225	H226	V227	S230	T231	A232	S233	A234	T235	V236	N237	E238	L239
K240	K241	I242	N243	Q244	N245	V246	A247	A248	L249	P250	V251	A252	S253	S254	D257	R258	L259	S260	Y261	L262	L263	P264	S265	A266	R267	E269	L270	G271	V272	G273	P274	G275	R276	S277	V278	D279	R280	S281	L282	M283	Y284	R289	R290	E291	T292	F293	T294	S295	V296	P297	H298	V299	G300	Y301	R302	W303		
A304	Q305	P306	D307	P308	W309	A310	Q311	F314	G315	H316	Q317	P318	A319	S320	S321	Q322	D323	D324	R325	C328	F329	T330	C331	S332	V333	L335	V336	C337	W338	E339	P340	T341	W345	S346	E347	H348	E349	R350	H351	S352	P353	N354	C355	V358	K359	G360	E361	H362	T363	Q364	N365	V366	P367	L368				
S369	V370	T371	L372	A373	T374	S375	P376	Q377	Q378	F379	P380	C381	T382	D383	G384	T385	D386	R387	I388	S389	C390	F391	G392	S393	G394	S395	C396	P397	H398	F399	A400	A401	A402	A403	T404	K405	R406	G407	K408	L409	C410	L411	W412	D413	V414	S415	G416	L417	W418	K419	V420	H421	L422	K423	F424	T426	N427	A428
Y429	D430	P431	A432	T433	V434	Q435	Q436	L437	T438	L439	S440	G441	ASP	PRO	SER	SER	GLY	ASP	SER	ARG	PRO	THR	LEU	ALA	TRP	LEU	GLU	GLU	SER	GLN	ASP	ALA	ASN	PRO	LEU	GLU	GLY	ASP	LEU	LEU	GLU	ASP	SER	ALA	ASN	PRO	GLY	THR	LEU	GLY	THR	SER	LEU	GLY	THR			
ASP	SER	VAL	THR	GLY	HIS	THR	SER	GLN	LYS	GLU	A500	M501	E502	V503	S504	L505	D506	I507	T508	A509	L510	S511	I512	L513	Q514	Q515	PRO	GLU	LYS	LEU	GLN	THR	GLY	ILE	VAL	ASN	VAL	LEU	GLU	GLY	THR	ASP	THR	VAL	LEU	GLY	THR	LEU	GLY	THR	LEU	GLY	THR					
SER	GLU	LYS	THR	LYS	GLY	THR	HIS	GLN	GLU	HIS	M561	I562	P563	F564	P565	C566	L567	L568	A569	G570	G571	L572	L573	T574	Y575	K576	S577	P578	A579	THR	SER	PRO	GLY	ILE	SER	ASN	VAL	ASN	THR	GLN	ARG	LEU	ASP	LEU	GLY	THR	LEU	GLY	THR	LEU	GLY	THR						
ASP	ASN	GLU	SER	CYS	THR	ASN	SER	GLU	LEU	ASN	P621	L622	V623	R624	R625	T626	L627	P628	V629	L630	L631	L632	V633	S634	L635	K636	E637	P638	D639	GLY	LYS	ALA	GLY	ILE	ASN	GLY	ASN	ASN	MET	ILE	LYS	SER	THR	LEU	GLY	THR	LEU	GLY	THR	LEU	GLY	THR						
GLU	MET	GLU	LEU	ASP	SER	GLN	GLU	GLN	LEU	ASN	P621	L622	V623	R624	R625	T626	L627	P628	V629	L630	L631	L632	V633	S634	L635	K636	E637	P638	D639	GLY	LYS	ALA	GLY	ILE	ASN	GLY	ASN	ASN	MET	ILE	LYS	SER	THR	LEU	GLY	THR	LEU	GLY	THR	LEU	GLY	THR						
E729	N730	L731	G732	D733	Y734	S735	T736	T737	P738	C739	A740	D741	G742	T743	H744	L745	L746	V747	G748	L749	R750	T751	C752	P753	VAL	GLU	GLU	SER	GLU	LEU	ALA	ILE	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728				
E729	N730	L731	G732	D733	Y734	S735	T736	T737	P738	C739	A740	D741	G742	T743	H744	L745	L746	V747	G748	L749	R750	T751	C752	P753	VAL	GLU	GLU	SER	GLU	LEU	ALA	ILE	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728				
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
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ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU	GLY	ASN	GLN	VAL	PHE	P711	K712	P713	G714	T715	L716	V717	Q718	C719	L720	R721	L722	P723	K724	T725	A726	E727	E728						
ALA	VAL	VAL	ASN	GLY	ALA	ASN	ILE	SER	VAL	GLN	HIS	GLU	SER	PRO	PRO	PRO	PHE	ALA	ASP	ALA	ALA	ALA	ASN	LEU	THR	SER	PRO	ASP	GLU																													







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36872	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 ($e^-/\text{\AA}^2$)	47.27	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.429	Depositor
Minimum map value	-0.750	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.144	Depositor
Map size (Å)	248.7, 248.7, 248.7	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.829, 0.829, 0.829	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	0.11	0/22620	0.28	1/30734 (0.0%)
1	B	0.12	0/22774	0.31	4/30945 (0.0%)
2	C	0.14	0/1197	0.31	0/1620
2	D	0.15	0/1197	0.29	0/1620
All	All	0.12	0/47788	0.29	5/64919 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3132	PHE	N-CA-C	-8.47	99.60	110.53
1	B	3128	THR	N-CA-C	-6.45	105.43	113.55
1	B	3133	LEU	N-CA-C	-5.80	103.91	111.74
1	B	3132	PHE	CA-C-O	-5.28	115.87	121.94
1	A	1847	LEU	CB-CA-C	-5.06	109.77	115.79

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	22195	0	22593	394	0
1	B	22348	0	22749	485	0
2	C	1183	0	1185	23	0
2	D	1183	0	1185	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	46909	0	47712	896	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 9.

The worst 5 of 896 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:B:1818:ASP:HB2	1:B:1857:LYS:HB3	1.62	0.81
1:A:283:MET:HE1	1:A:289:ARG:HG3	1.67	0.77
1:B:1032:GLU:HB3	1:B:1307:LYS:HG3	1.66	0.76
1:A:1052:GLU:OE1	1:A:1056:ARG:NH1	2.17	0.76
1:A:1103:HIS:O	1:A:1305:ARG:NH2	2.18	0.76

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	2799/4859 (58%)	2712 (97%)	87 (3%)	0	100	100
1	B	2820/4859 (58%)	2741 (97%)	79 (3%)	0	100	100
2	C	148/184 (80%)	146 (99%)	2 (1%)	0	100	100
2	D	148/184 (80%)	147 (99%)	1 (1%)	0	100	100
All	All	5915/10086 (59%)	5746 (97%)	169 (3%)	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	2517/4217 (60%)	2517 (100%)	0	100	100
1	B	2534/4217 (60%)	2529 (100%)	5 (0%)	87	92
2	C	128/157 (82%)	128 (100%)	0	100	100
2	D	128/157 (82%)	128 (100%)	0	100	100
All	All	5307/8748 (61%)	5302 (100%)	5 (0%)	87	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	3002	ASN
1	B	3129	ILE
1	B	3131	LYS
1	B	3133	LEU
1	B	3134	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1053	GLN
1	B	4332	ASN
1	B	2651	GLN
1	B	4072	GLN
1	B	3754	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.

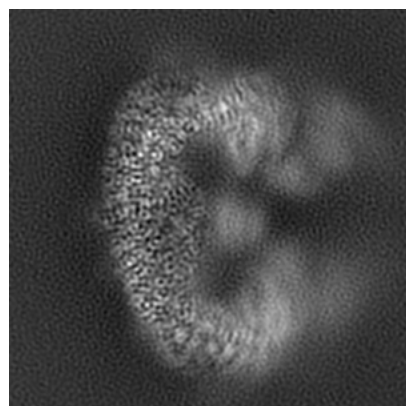
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15654. These allow visual inspection of the internal detail of the map and identification of artifacts.

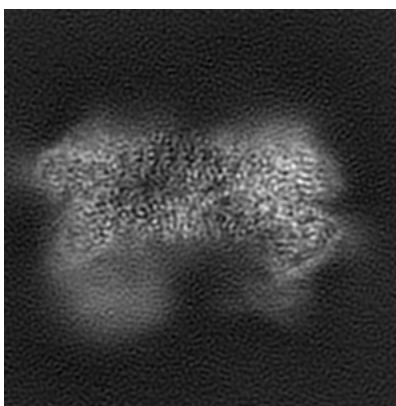
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

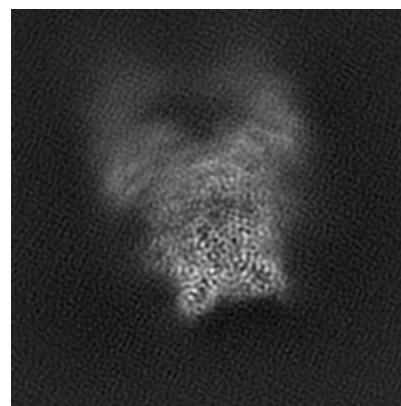
6.1.1 Primary map



X

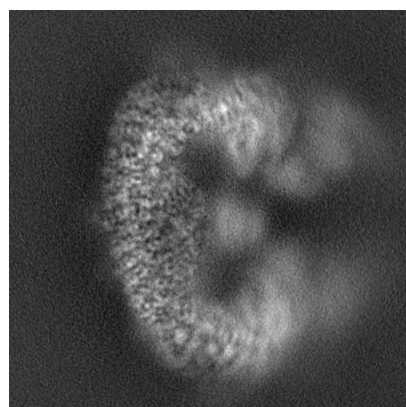


Y

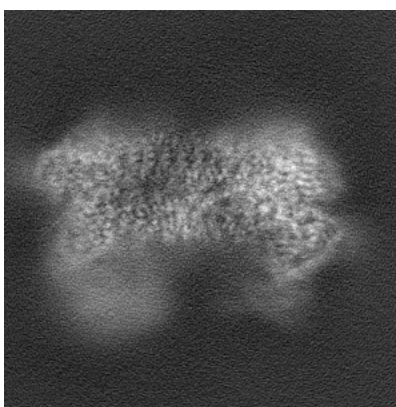


Z

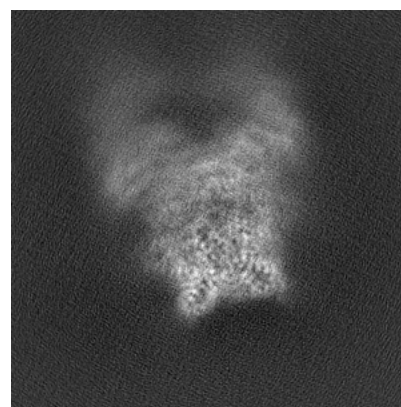
6.1.2 Raw map



X



Y

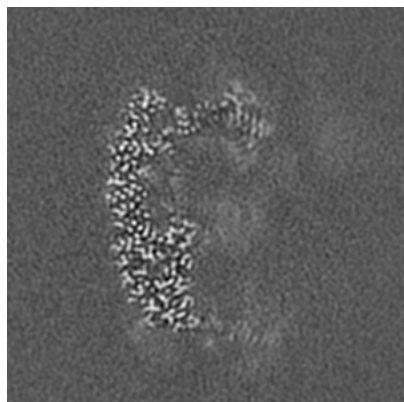


Z

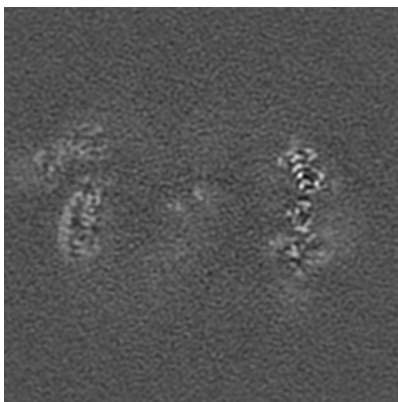
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

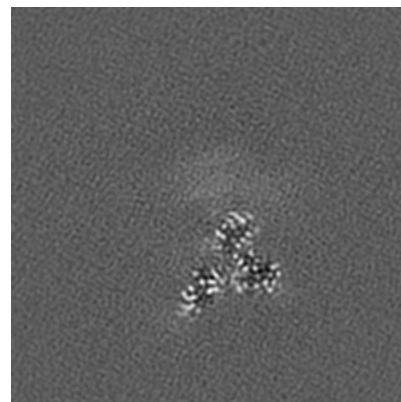
6.2.1 Primary map



X Index: 150

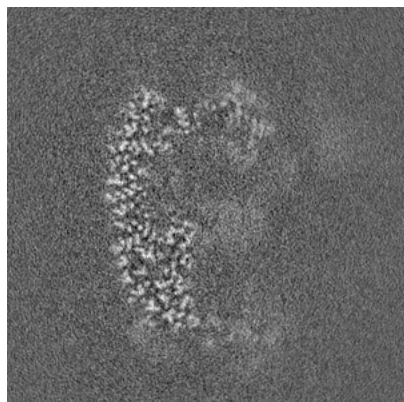


Y Index: 150

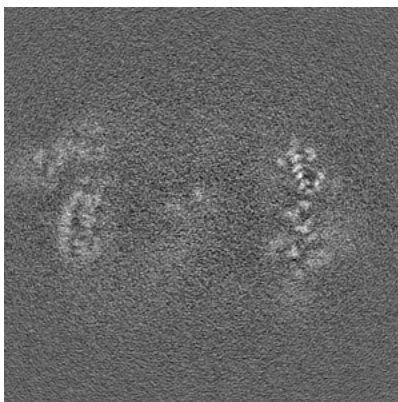


Z Index: 150

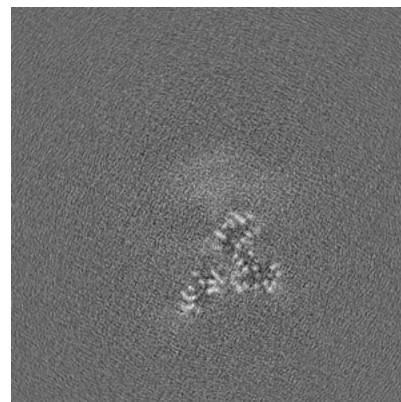
6.2.2 Raw map



X Index: 150



Y Index: 150

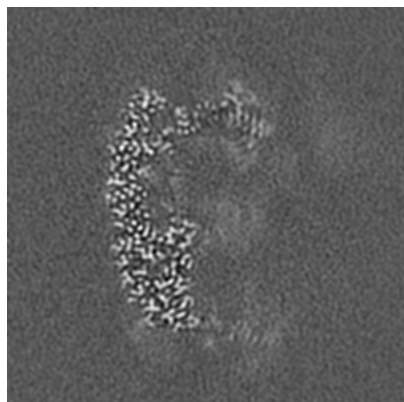


Z Index: 150

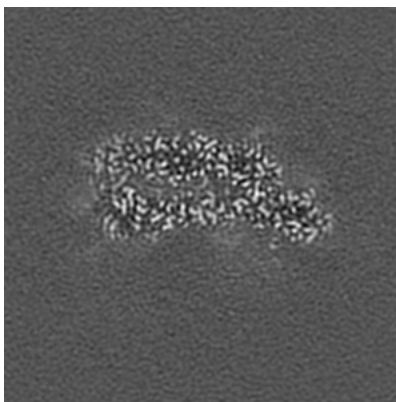
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

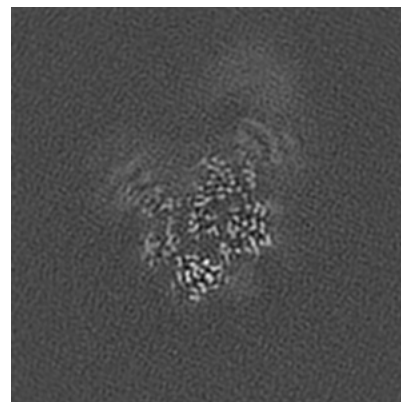
6.3.1 Primary map



X Index: 150

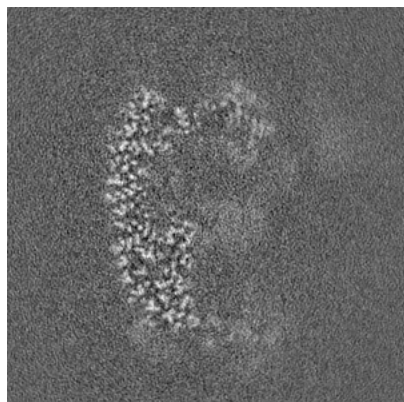


Y Index: 99

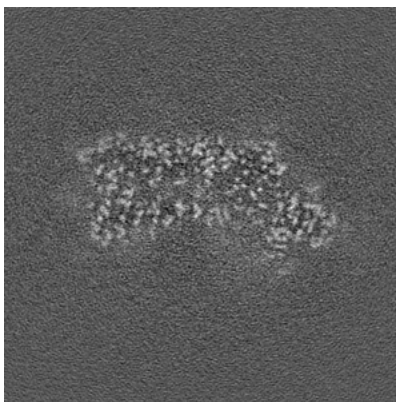


Z Index: 217

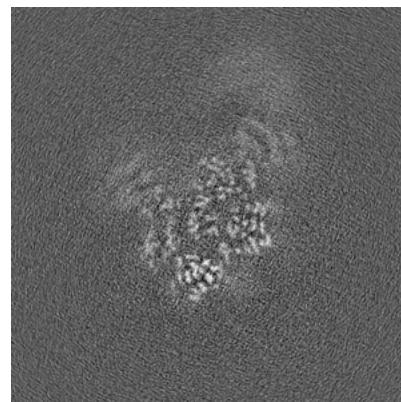
6.3.2 Raw map



X Index: 150



Y Index: 104

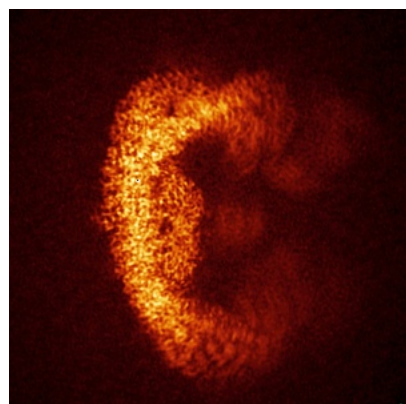


Z Index: 217

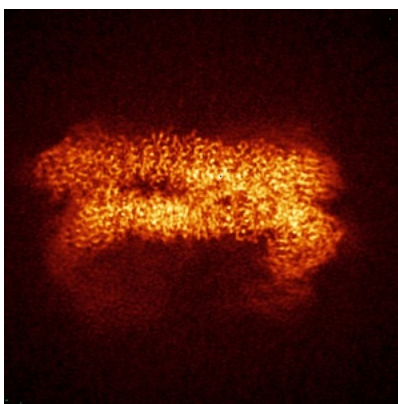
The images above show the largest variance slices of the map in three orthogonal directions.

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

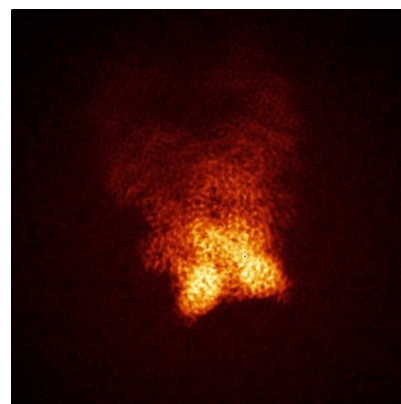
6.4.1 Primary map



X

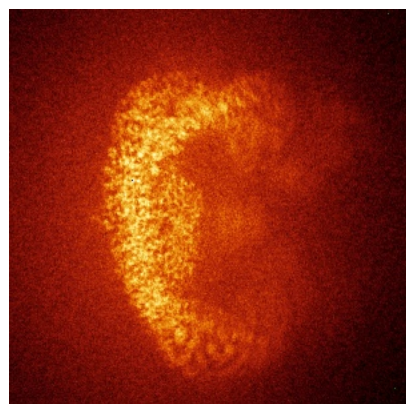


Y

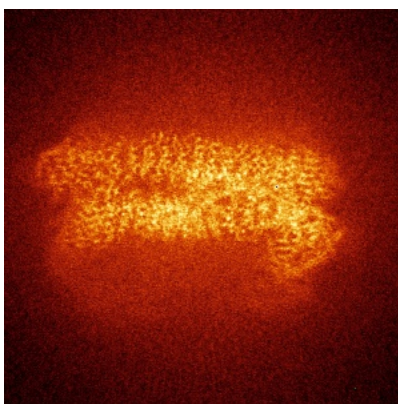


Z

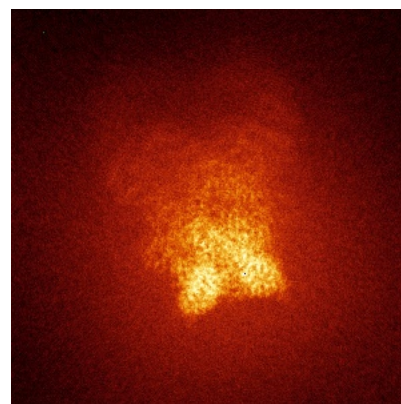
6.4.2 Raw map



X



Y

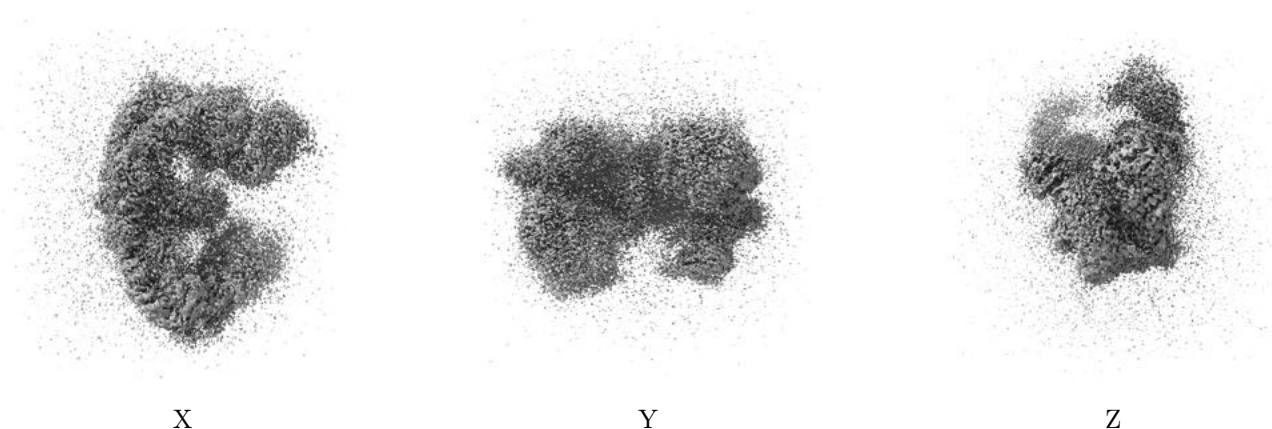


Z

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.

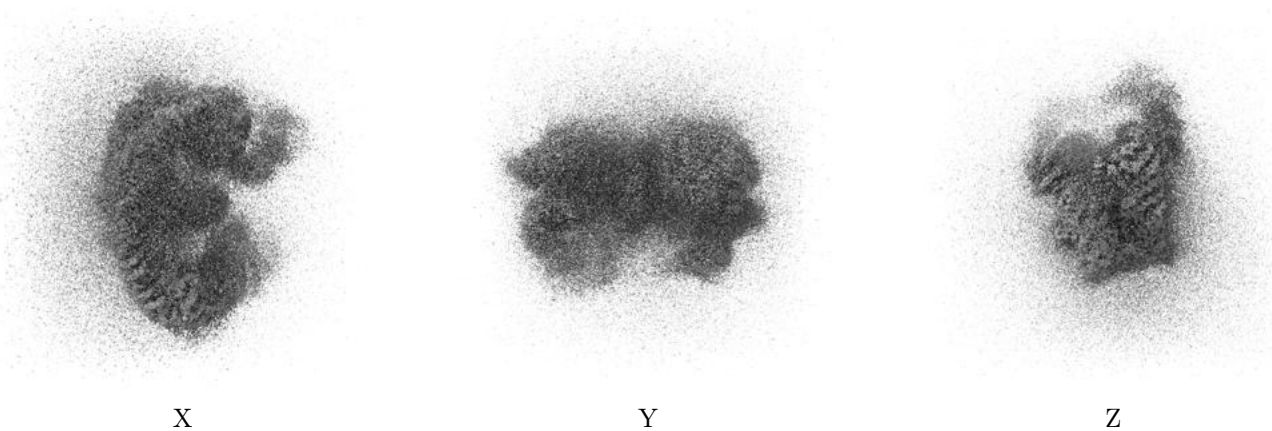
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.144. 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.

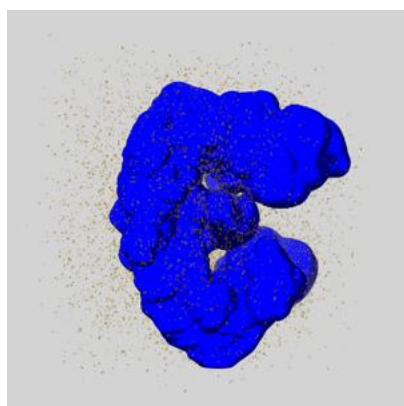
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

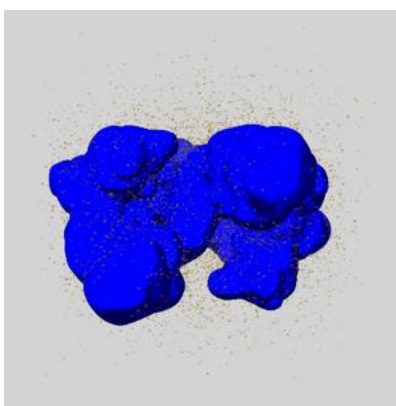
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

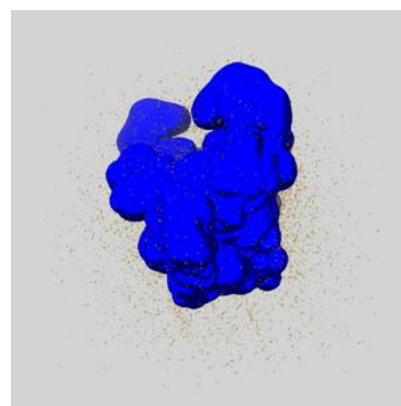
6.6.1 emd_15654_msk_1.map [i](#)



X



Y

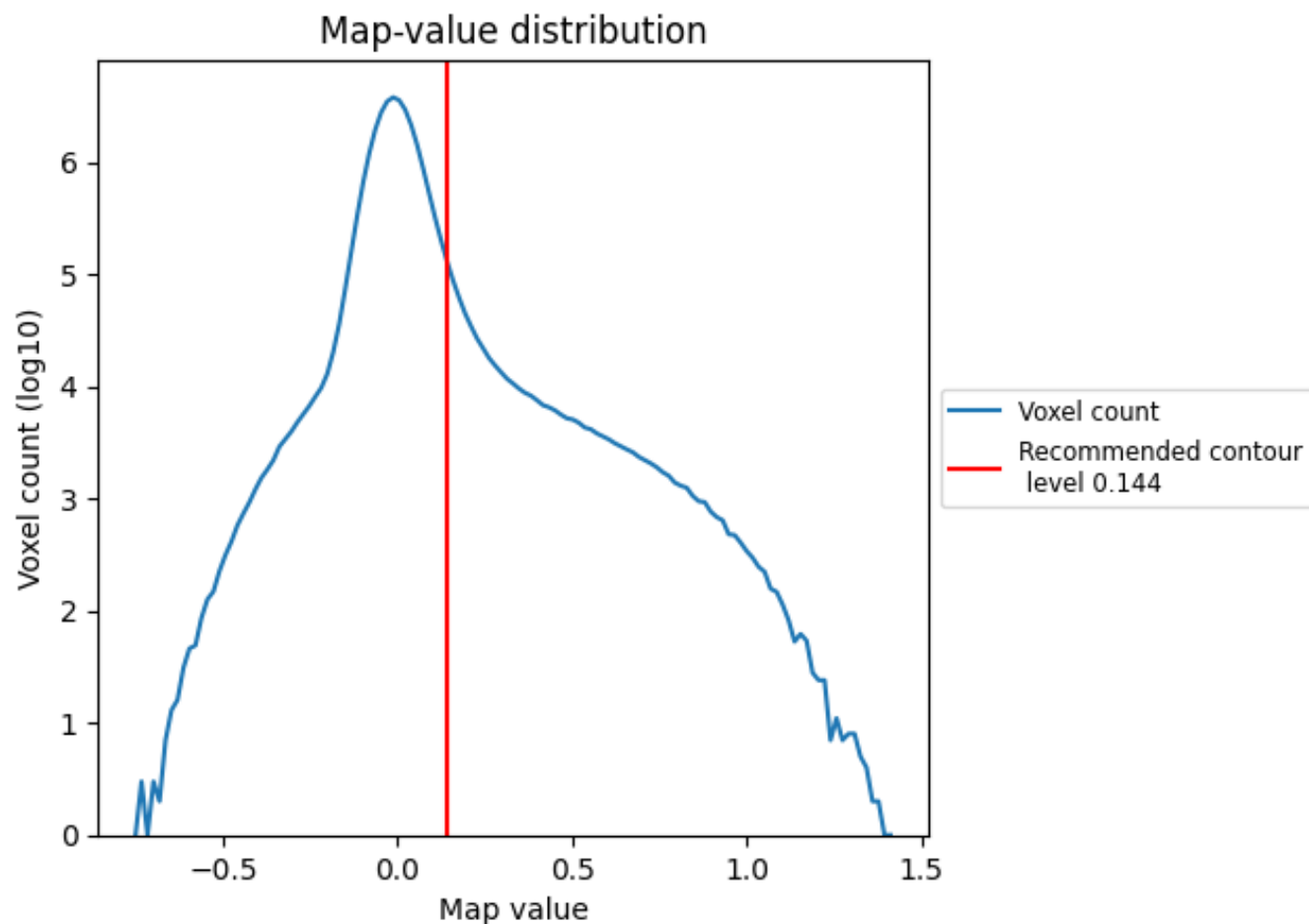


Z

7 Map analysis [i](#)

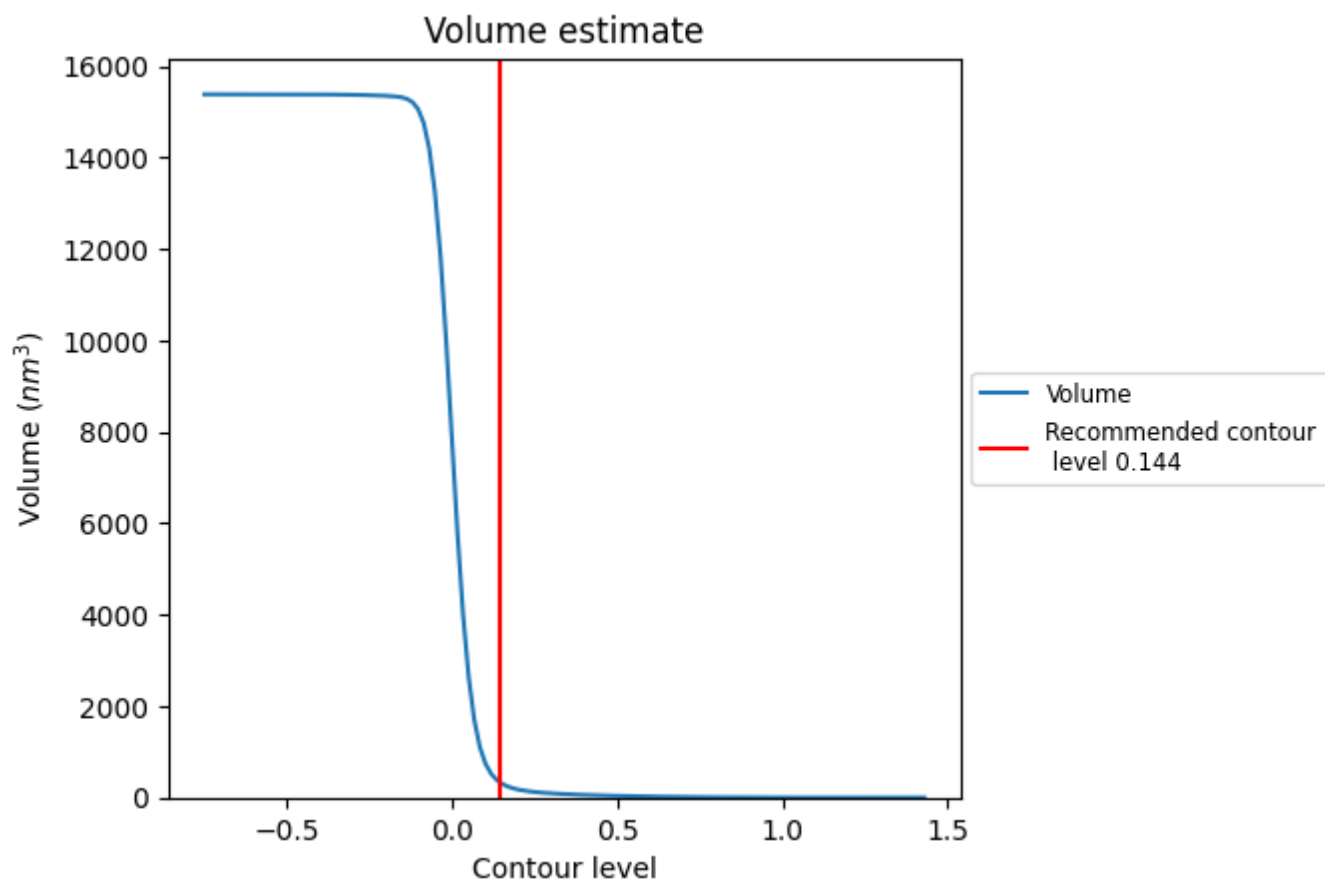
This section contains the results of statistical analysis of the map.

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.

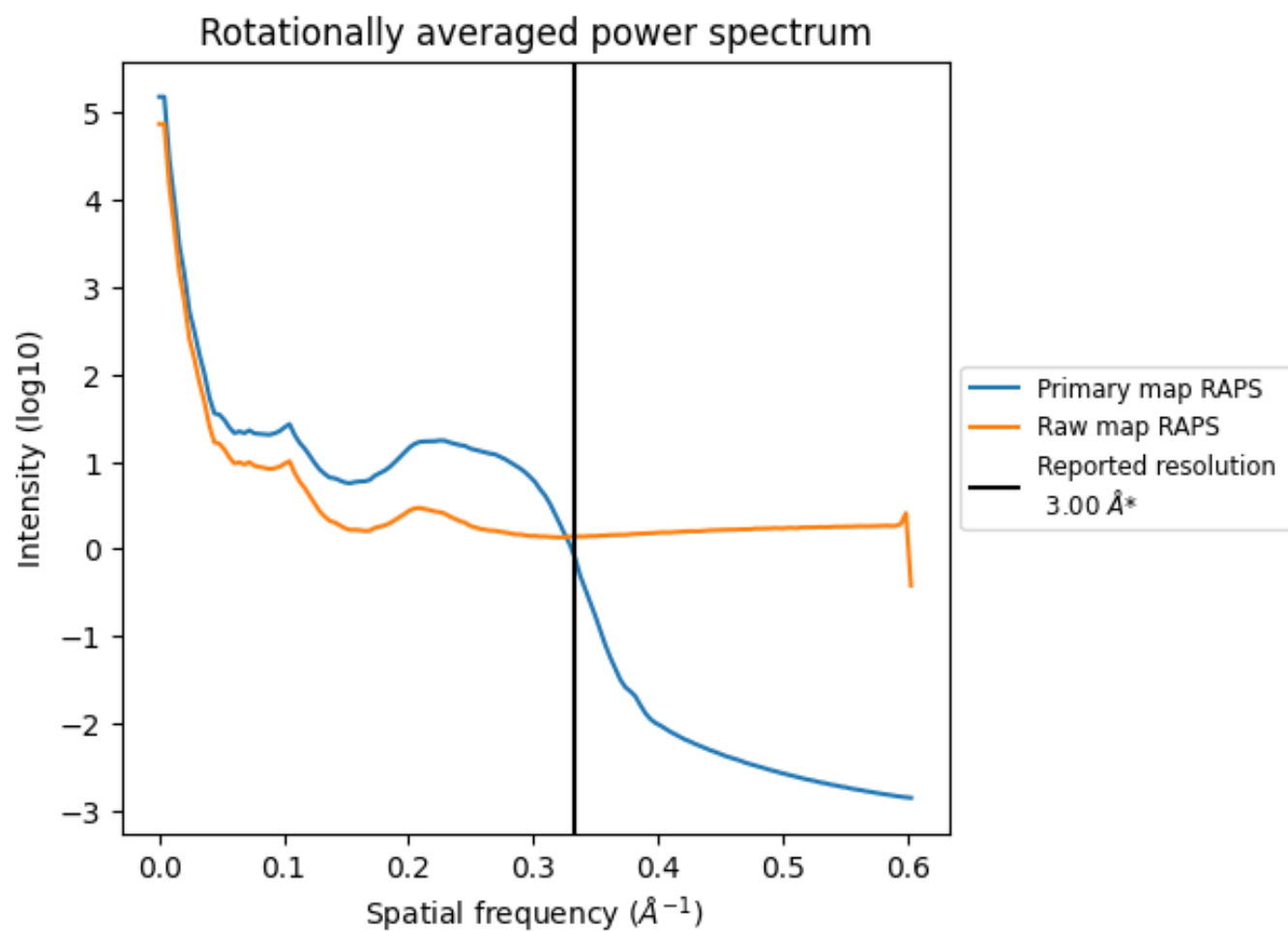
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 339 nm³; this corresponds to an approximate mass of 307 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 ⓘ

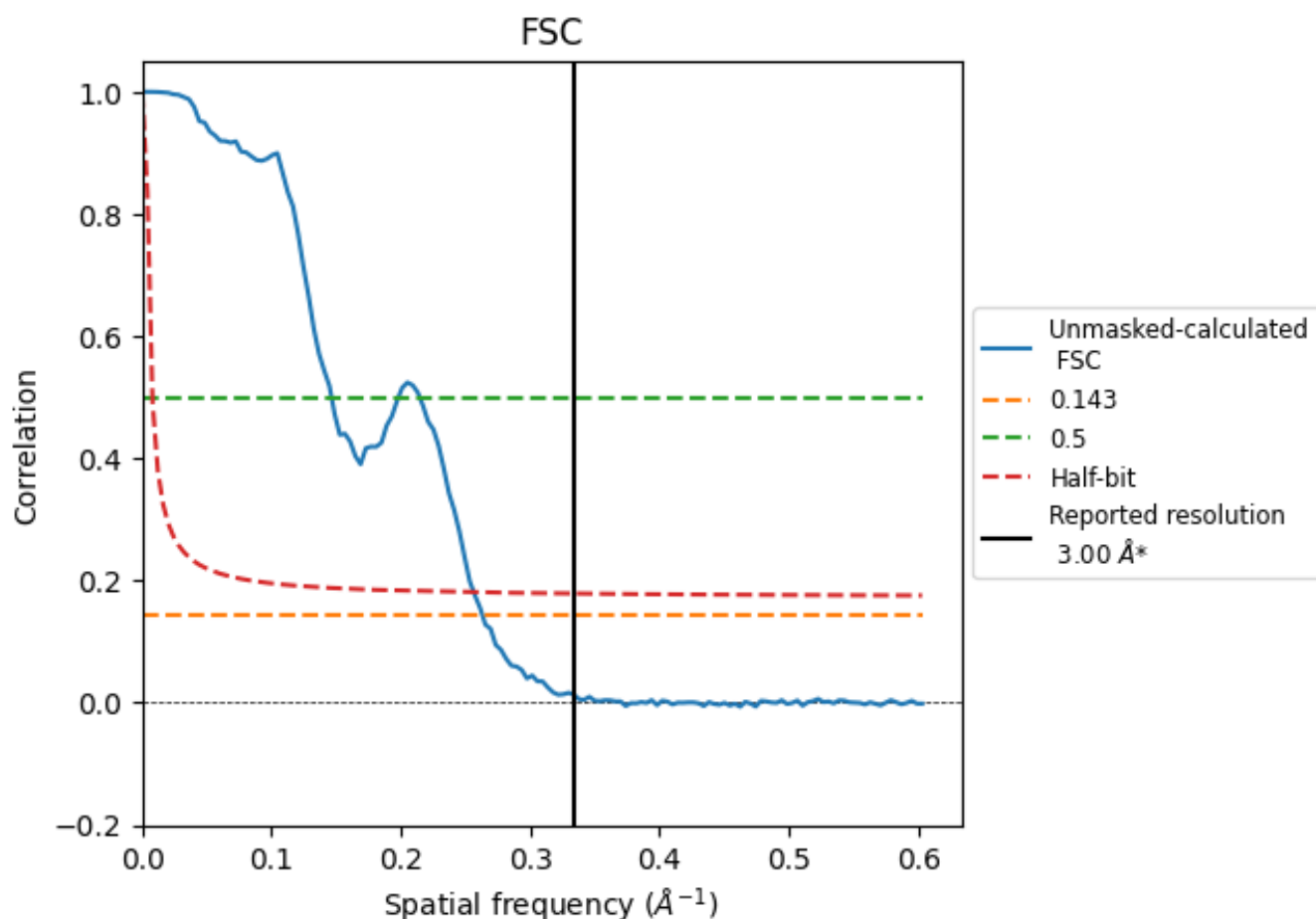


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

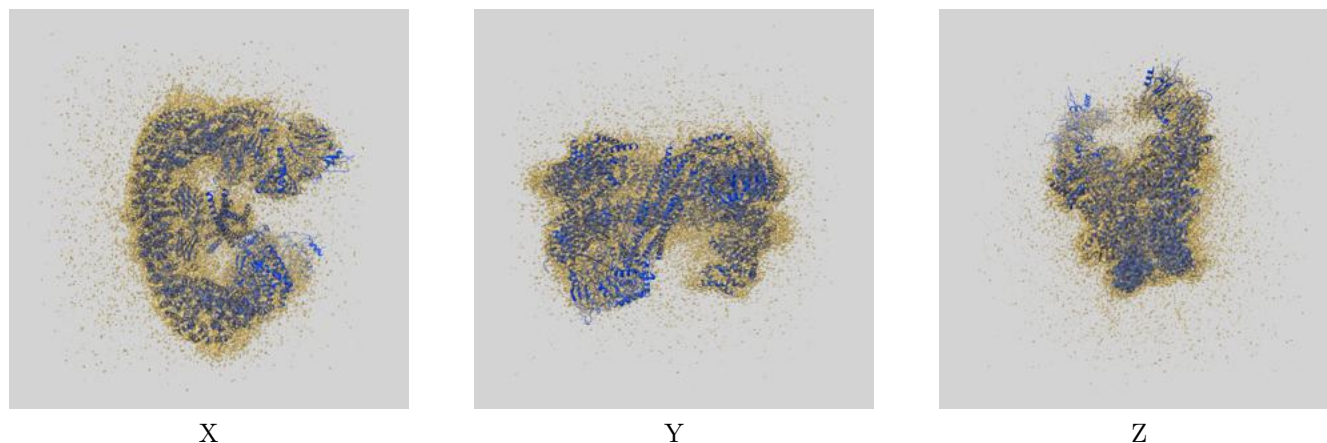
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.80	6.83	3.90

*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 3.80 differs from the reported value 3.0 by more than 10 %

9 Map-model fit [i](#)

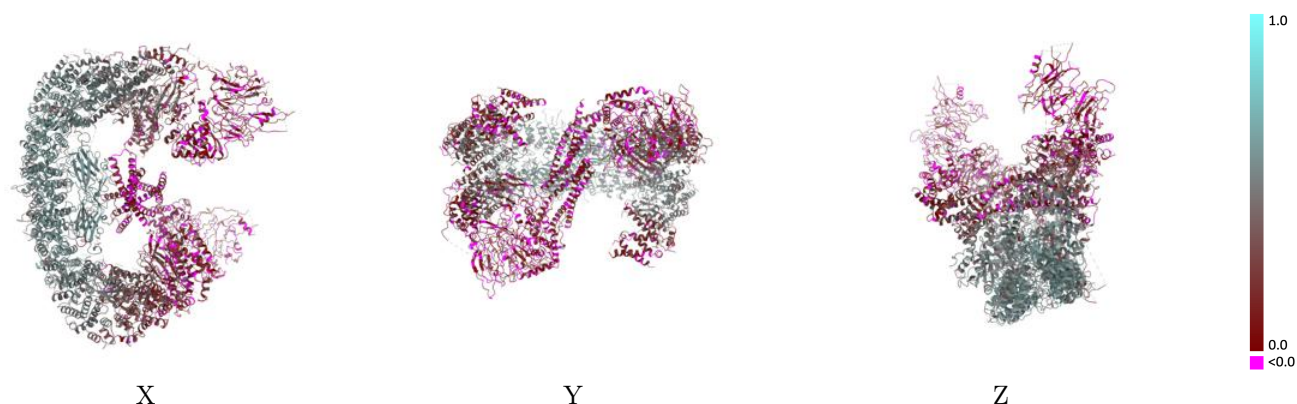
This section contains information regarding the fit between EMDB map EMD-15654 and PDB model 8ATO. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



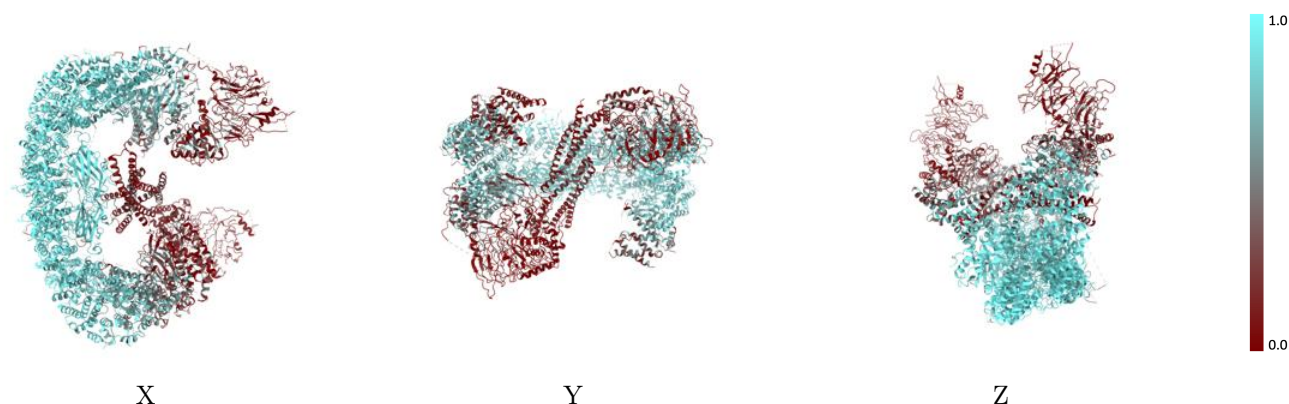
The images above show the 3D surface view of the map at the recommended contour level 0.144 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



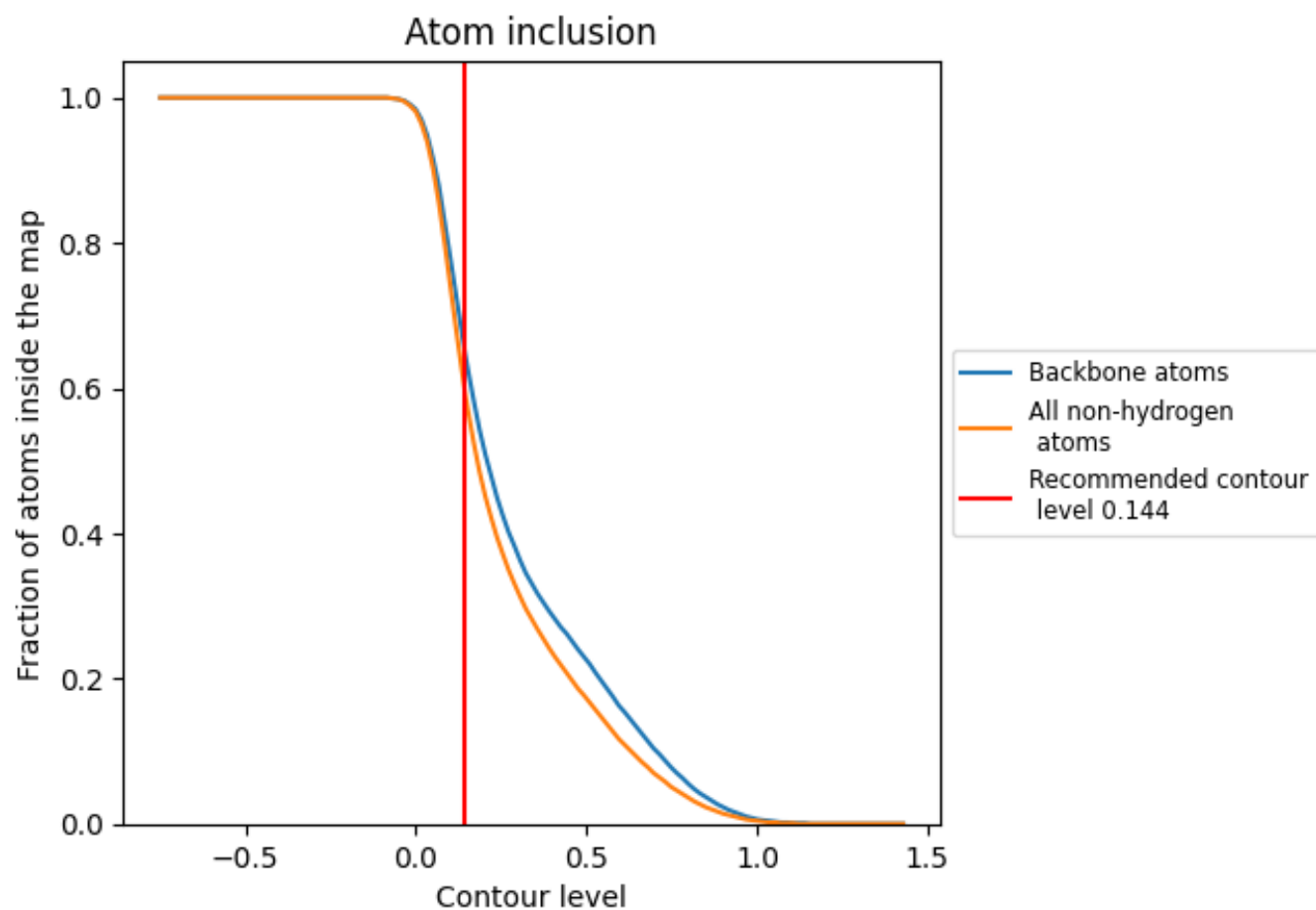
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.144).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 59% 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 (0.144) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5930	0.3340
A	0.5920	0.3390
B	0.6390	0.3550
C	0.1930	0.0830
D	0.1490	0.0780

