



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 03:27 AM EST

PDB ID : 7S64
EMDB ID : EMD-24849
Title : Intermediate-form oocyte/egg Alpha-2-Macroglobulin (A2Moo) tetramer
Authors : Arimura, Y.; Funabiki, H.
Deposited on : 2021-09-13
Resolution : 6.43 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

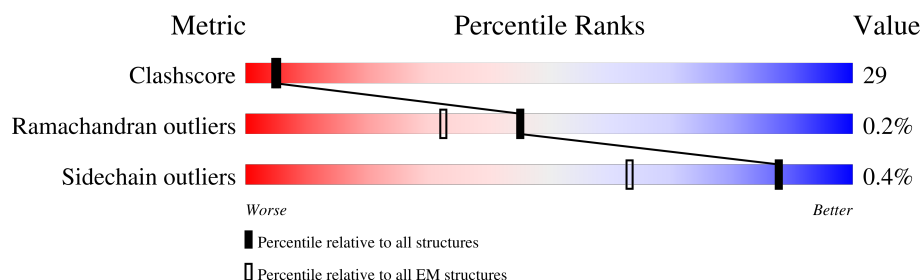
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.43 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	1441	
1	B	1441	
1	C	1441	
1	D	1441	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 44067 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.

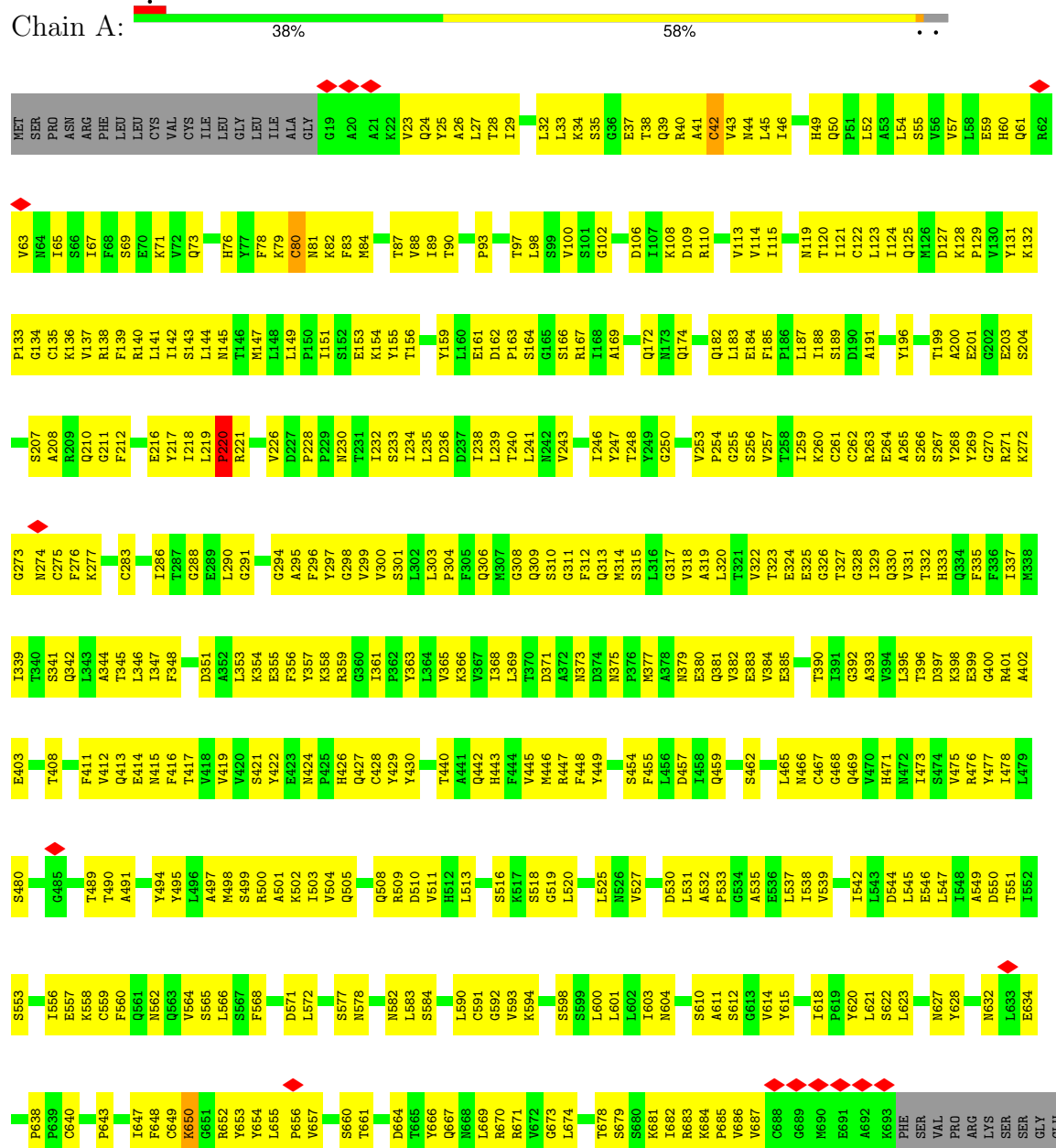
- Molecule 1 is a protein called Alpha 2-macroglobulin.

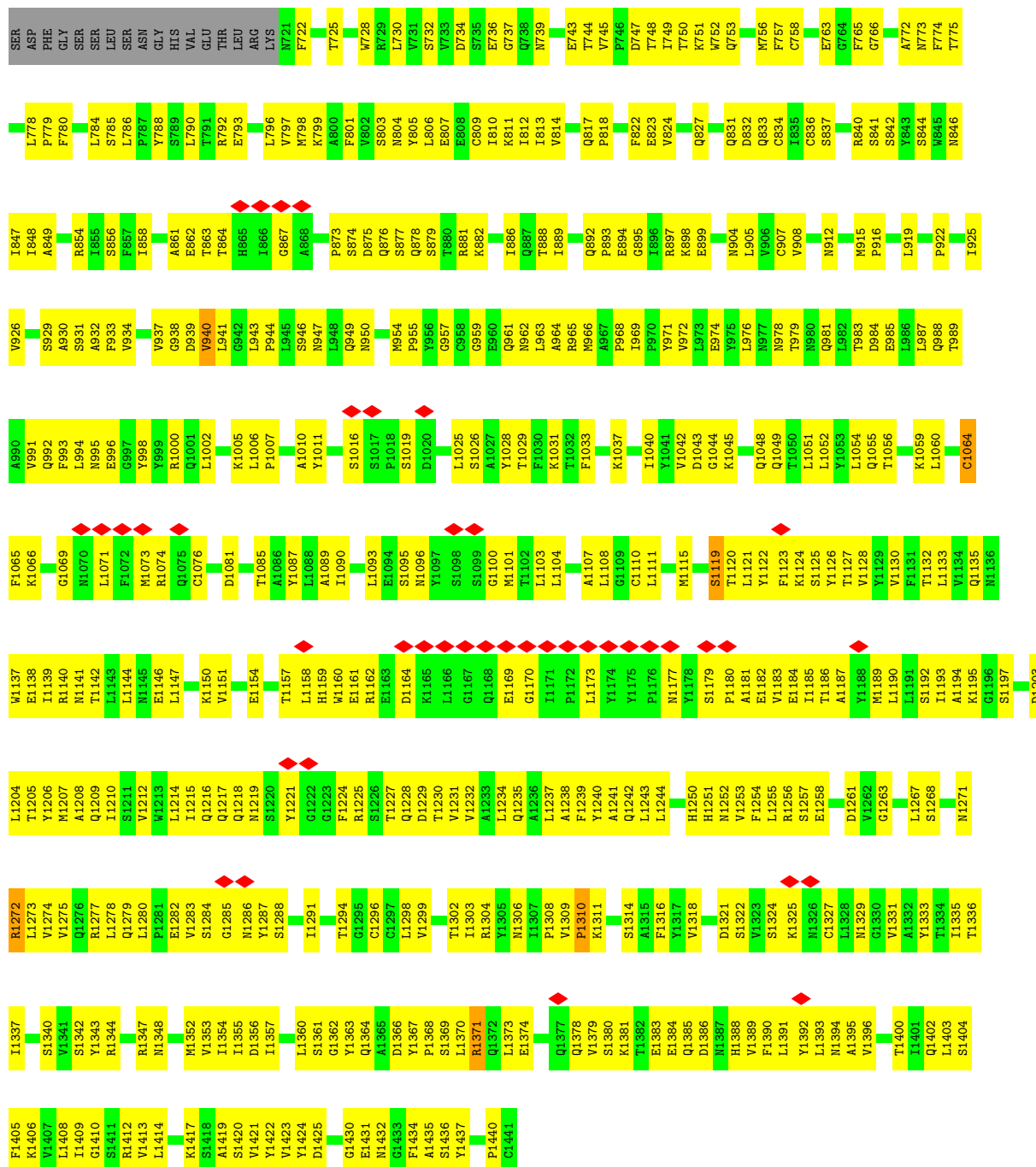
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1396	Total	C	N	O	S	0	0
			10875	6924	1772	2124	55		
1	B	1420	Total	C	N	O	S	0	0
			11064	7040	1806	2163	55		
1	C	1420	Total	C	N	O	S	0	0
			11064	7040	1806	2163	55		
1	D	1420	Total	C	N	O	S	0	0
			11064	7040	1806	2163	55		

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.

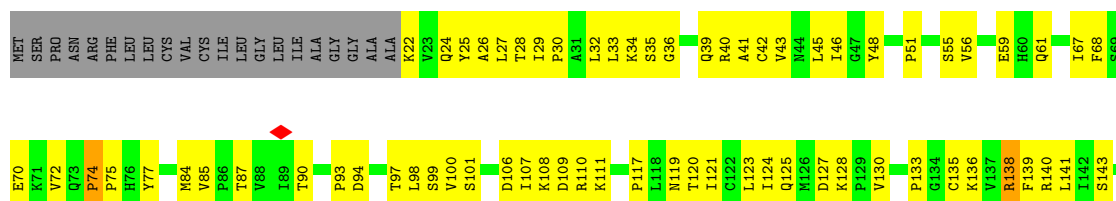
• Molecule 1: Alpha 2-macroglobulin



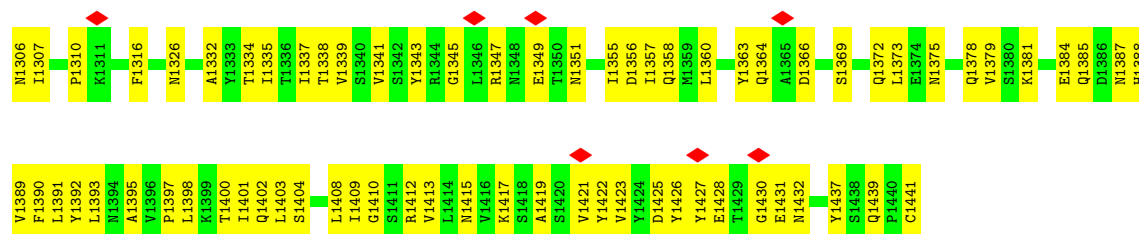


• Molecule 1: Alpha 2-macroglobulin

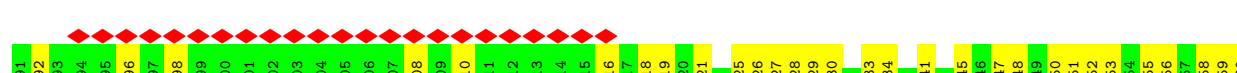
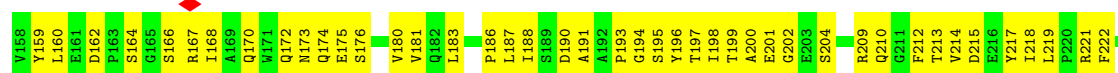
Chain B: 6% 52% 46%







• Molecule 1: Alpha 2-macroglobulin



L1403	S1404	F1405	K1406	V1407	L1408	T1409	G1410	S1411	V1339	S1340	V1341	V1342	V1413	L1414	N1415	V1416	K1417	S1418	A1419	S1420	V1421	V1422	V1423	D1424	Y1425	V1426	V1427	E1428	E1431	N1432	A1435	S1436	Y1437	C1441	N1376	A1382	K1406	T1334	I1335	V1339	S1340	V1341	V1342	V1343	V1344	G1345	L1346	R1347	T1350	N1351	M1352	V1353	I1354	I1355	D1356	I1357	Q1358	M1359	L1360	Y1363	Q1364	A1365	D1366	Y1367	P1368	S1369	N1375	S1376	Q1377	Q1378	V1379	S1380	K1381	N1387	H1388	F1389	V1390	L1391	L1392	L1393	P1394	V1395	P1396	K1397	T1400	L1401	Q1402	V1152	S1153	E1154	R1155	G1156	T1157	E1161	R1162	K1165	L1166	Q1167	Q1168	E1169	G1170	L1171	P1172	L1173	Y1174	Y1175	A1181	E1182	I1185	L1190	L1191	S1192	I1193	G1196	S1197	D1198	P1199	T1200	H1201	D1202	D1203	L1204	M1207	V1212	W1213	L1214	I1215	Q1216	Q1217	Q1218	M1219	G1222	S1226	D1229	V1232	D1061	C1064	F1065	K1066	A1067	E1068	L1071	F1072	M1073	R1074	Q1075	R1080	D1081	F1084	T1085	A1086	Y1087	I1090	A1091	L1092	S1099	G1100	M1101	L1102	L1103	L1104	M1115	S1119	T1120	L1121	K1124	S1125	Y1126	T1127	Y1128	Y1129	V1130	F1131	T1132	L1133	V1134	Q1135	N1136	W1137	E1138	T1139	R1140	N1141	T1142	L1143	E923	N924	V925	I926	S927	A930	S931	A932	F933	E934	T935	F936	V937	L941	G942	L943	P944	N947	Q949	N950	L951	L952	Q953	M954	R955	Y956	G957	C958	G959	E960	K1031	N962	L963	A964	R965	M966	I969	P970	Y971	V972	E974	S975	L976	T979	N980	Q981	D984	E985	T989	L1052	Y1053	L1054	Q1055	Q1058	F993	L994	N995	E996	G997	Y998	Y999	R1000	Q1001	F933	E962	T963	T935	F936	V937	L941	G942	L943	P944	N947	Q949	N950	L951	L952	Q953	M954	R955	Y956	G957	C958	G959	E960	K1031	N962	L963	A964	R965	M966	I969	P970	Y971	V972	E974	S975	L976	T979	N980	Q981	D984	E985	T989	L1052	Y1053	L1054	Q1055	Q1058	L852	S856	F857	I858	V859	S860	A861	E862	T863	T864	H865	I866	G867	S869	G872	P873	S874	Q877	S878	S879	T880	K881	W1024	K882	Y956	D883	T884	V885	I886	Q887	T888	I889	E894	G895	I896	R897	K898	E899	N900	T901	S902	N904	L905	V908	S911	N912	V913	E914	I917	N918	L919	K693	F694	S695	I618	L623	Y626	N627	Y628	S701	G702	E703	S704	D705	F706	G707	S708	S709	L710	S711	N712	G713	H714	K799	S659	E662	G663	D664	T665	Y666	Q667	N668	L669	R670	K671	V672	G673	L674	V675	L676	G677	T678	S679	S680	K681	L682	R683	K684	P685	C688	G689	M690	E691	V692	S760	E761	K762	E763	G764	F765	Y615	Y616	S617	I618	L623	Y626	N627	Y628	S701	G702	E703	S704	D705	F706	G707	S708	S709	L710	S711	N712	G713	H714	K799	S659	E662	G663	D664	T665	Y666	Q667	N668	L669	R670	K671	V672	G673	L674	V675	L676	G677	T678	S679	S680	K681	L682	R683	K684	P685	C688	G689	M690	E691	V692	S760	E761	K762	E763	G764	F765	T370	D371	A372	N373	D374	N375	P376	M377	A378	N379	E380	Q381	L382	E383	V384	E385	L386	T390	L391	G392	A393	V394	L395	T396	D397	K398	E399	G400	R401	A402	E403	S410	F411	V412	F416	T417	V418	V419	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466	C467	V470	H471	R476	Y477	L478	L479	S480	G483	M484	T489	Y494	Y495	T575	Y576	S577	L581	S499	R500	A501	K502	L503	V504	R509	D510	L513	I523	L525	T528	S529	L530	L531	A532	P533	F444	V445	M446	E536	L537	I538	V539	Y540	C541	I542	L543	D544	L545	E546	L547	I548	E464	L465	N466
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11170	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	33.11, 38.34, 35.27, 34.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k), GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	20.991	Depositor
Minimum map value	-11.364	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4	Depositor
Map size (Å)	384.0, 384.0, 384.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.5, 1.5, 1.5	Depositor

5 Model quality

5.1 Standard geometry

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	0.32	0/11104	0.58	3/15099 (0.0%)
1	B	0.30	0/11298	0.54	2/15359 (0.0%)
1	C	0.32	1/11298 (0.0%)	0.57	4/15359 (0.0%)
1	D	0.32	0/11298	0.56	0/15359
All	All	0.32	1/44998 (0.0%)	0.56	9/61176 (0.0%)

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	1
1	B	0	1
1	C	0	1
1	D	0	2
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	916	PRO	CG-CD	-9.07	1.20	1.50

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	916	PRO	N-CD-CG	-11.71	85.63	103.20
1	A	80	CYS	CA-CB-SG	11.09	133.97	114.00
1	C	916	PRO	CA-N-CD	-9.80	97.78	111.50
1	A	42	CYS	CA-CB-SG	9.71	131.47	114.00
1	A	1310	PRO	CA-N-CD	-6.35	102.61	111.50

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	220	PRO	Peptide
1	B	757	PHE	Peptide
1	C	590	LEU	Peptide
1	D	139	PHE	Peptide
1	D	652	ARG	Sidechain

5.2 Too-close contacts ⓘ

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	10875	0	10684	775	0
1	B	11064	0	10871	550	0
1	C	11064	0	10871	575	0
1	D	11064	0	10871	690	0
All	All	44067	0	43297	2546	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 29.

The worst 5 of 2546 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:358:LYS:HE3	1:C:448:PHE:HB3	1.40	1.03
1:A:23:VAL:HA	1:A:46:ILE:O	1.62	0.98
1:D:381:GLN:HE21	1:D:393:ALA:HA	1.32	0.94
1:D:356:PHE:HA	1:D:446:MET:O	1.67	0.93
1:A:1251:HIS:HB3	1:A:1267:LEU:HB3	1.48	0.93

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	1392/1441 (97%)	1152 (83%)	235 (17%)	5 (0%)	30	68
1	B	1418/1441 (98%)	1257 (89%)	158 (11%)	3 (0%)	44	78
1	C	1418/1441 (98%)	1246 (88%)	170 (12%)	2 (0%)	48	83
1	D	1418/1441 (98%)	1239 (87%)	177 (12%)	2 (0%)	48	83
All	All	5646/5764 (98%)	4894 (87%)	740 (13%)	12 (0%)	45	78

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	PRO
1	A	1119	SER
1	B	74	PRO
1	C	74	PRO
1	D	74	PRO

5.3.2 Protein sidechains ⓘ

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	1220/1259 (97%)	1215 (100%)	5 (0%)	89	91
1	B	1244/1259 (99%)	1240 (100%)	4 (0%)	91	92
1	C	1244/1259 (99%)	1236 (99%)	8 (1%)	84	88
1	D	1244/1259 (99%)	1240 (100%)	4 (0%)	91	92
All	All	4952/5036 (98%)	4931 (100%)	21 (0%)	88	91

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	792	ARG
1	D	652	ARG
1	D	1256	ARG
1	D	1140	ARG
1	C	1101	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	313	GLN
1	D	375	ASN
1	C	753	GLN
1	D	39	GLN
1	D	424	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.

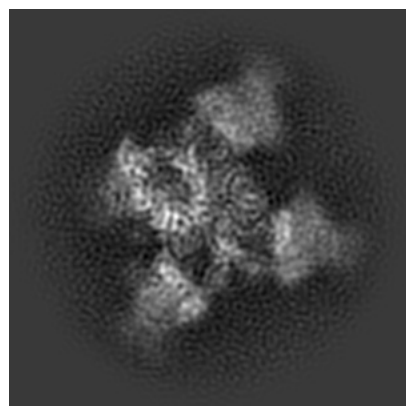
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24849. These allow visual inspection of the internal detail of the map and identification of artifacts.

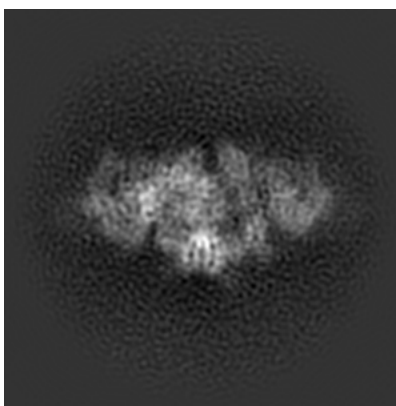
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

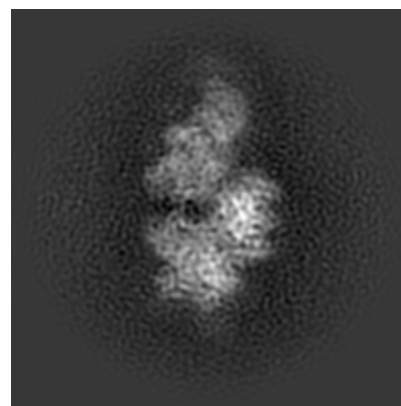
6.1.1 Primary map



X

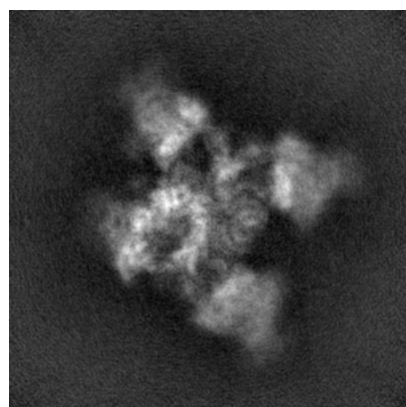


Y

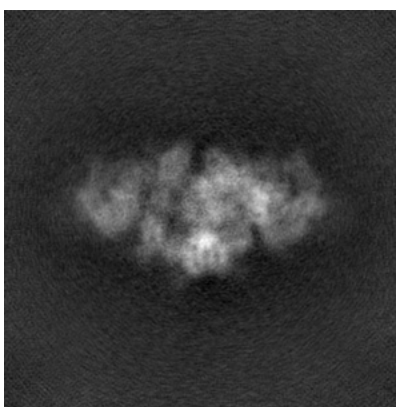


Z

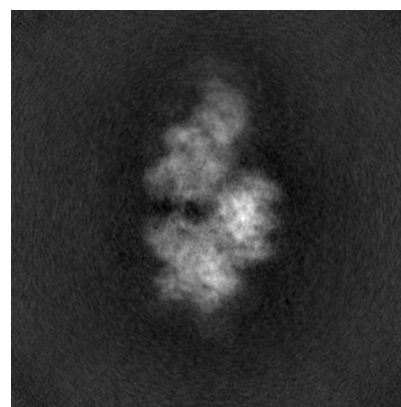
6.1.2 Raw map



X



Y

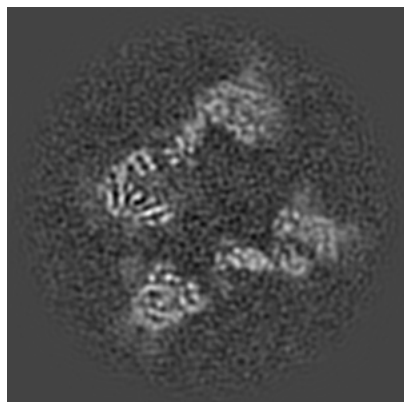


Z

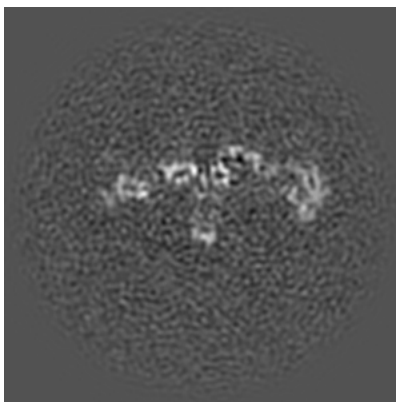
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

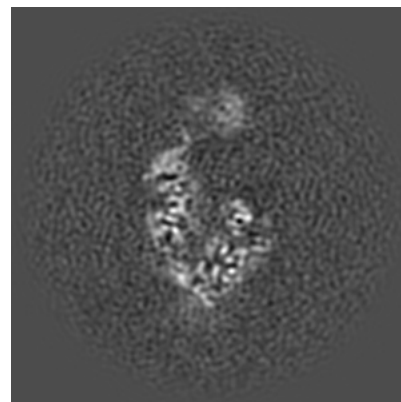
6.2.1 Primary map



X Index: 128

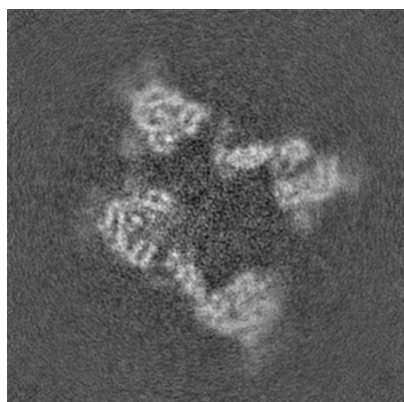


Y Index: 128

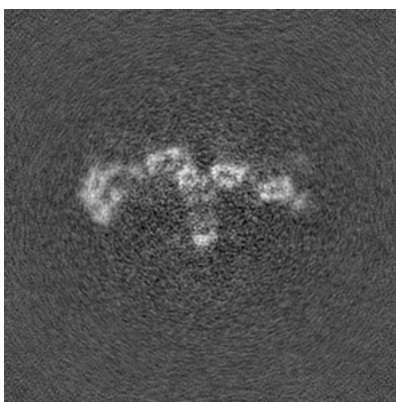


Z Index: 128

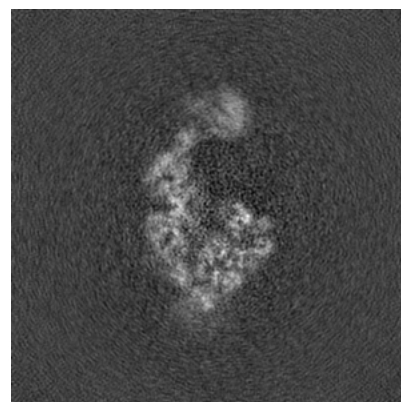
6.2.2 Raw map



X Index: 128



Y Index: 128

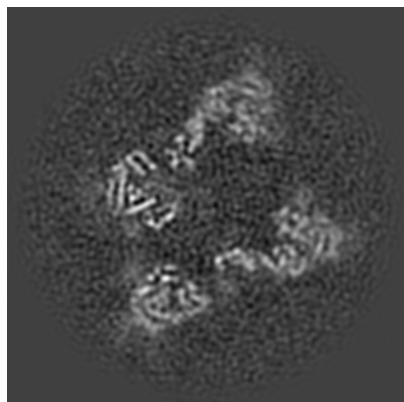


Z Index: 128

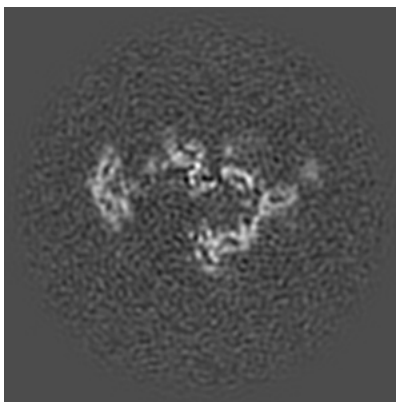
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

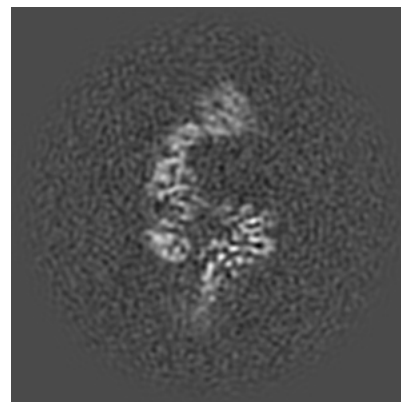
6.3.1 Primary map



X Index: 130

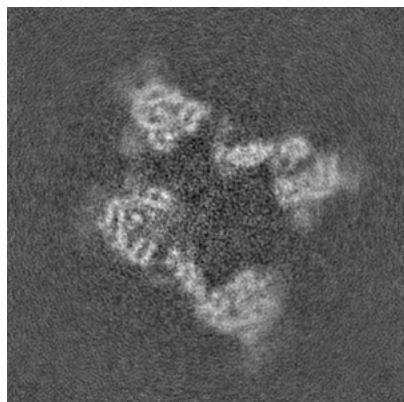


Y Index: 118

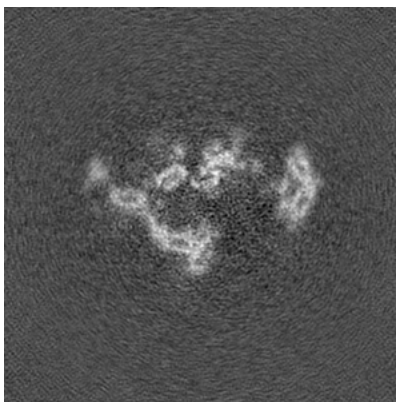


Z Index: 123

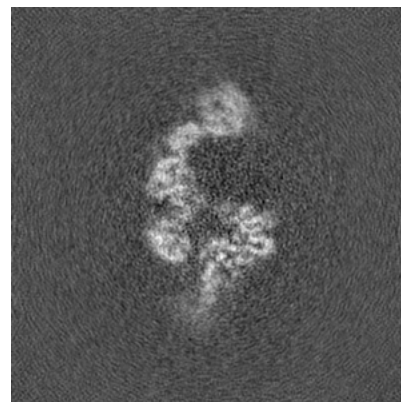
6.3.2 Raw map



X Index: 128



Y Index: 119

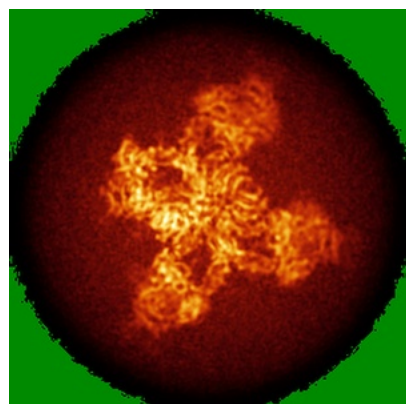


Z Index: 132

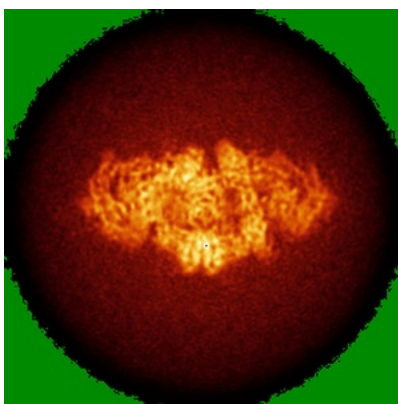
The images above show the largest variance slices of the map in three orthogonal directions.

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

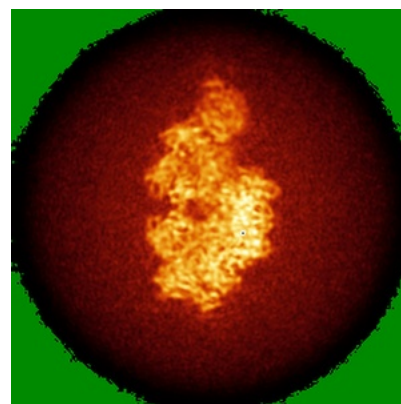
6.4.1 Primary map



X

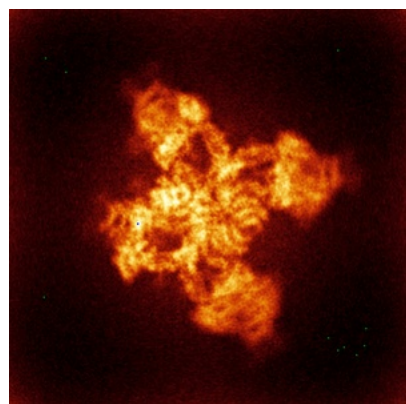


Y

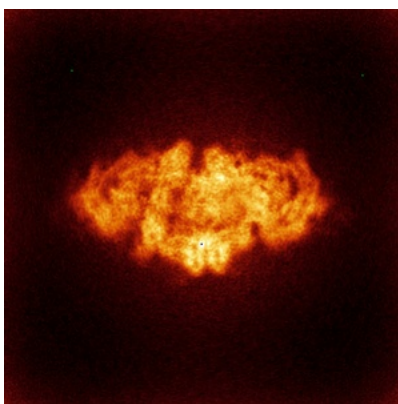


Z

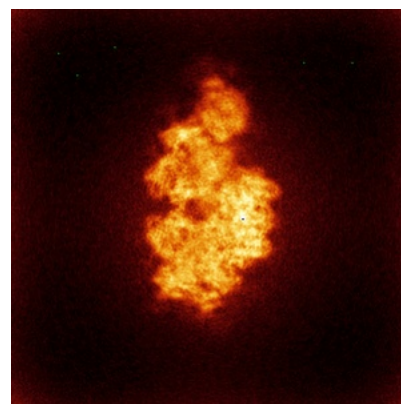
6.4.2 Raw map



X



Y

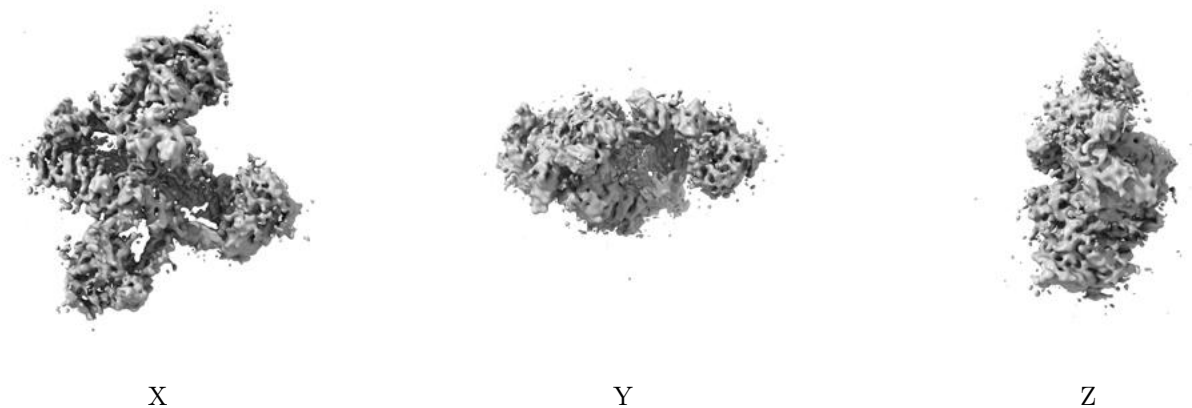


Z

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.

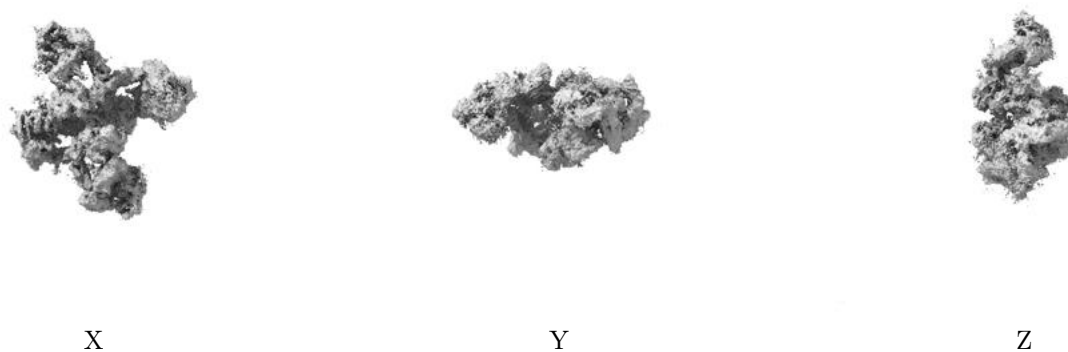
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

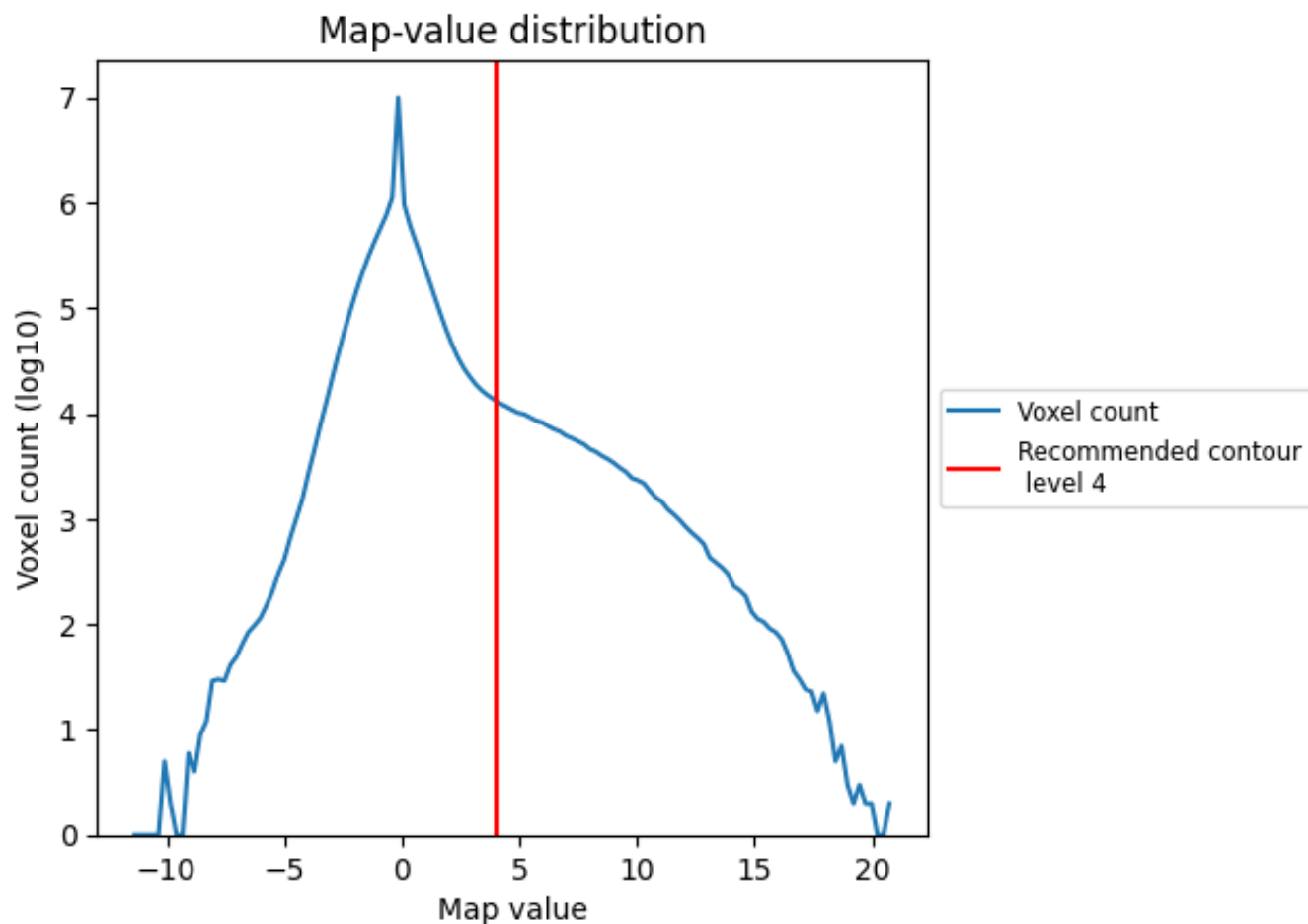
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

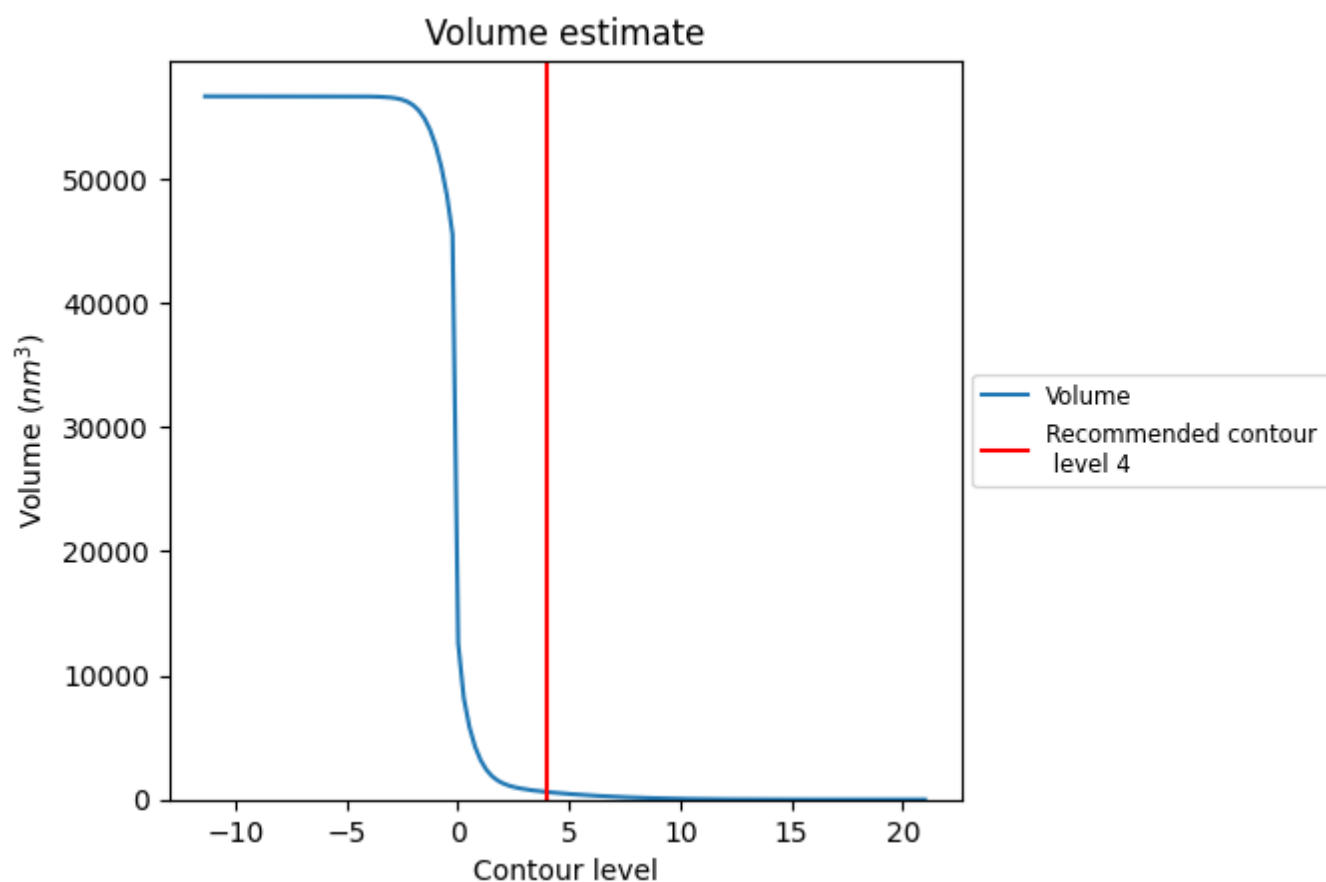
This section contains the results of statistical analysis of the map.

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.

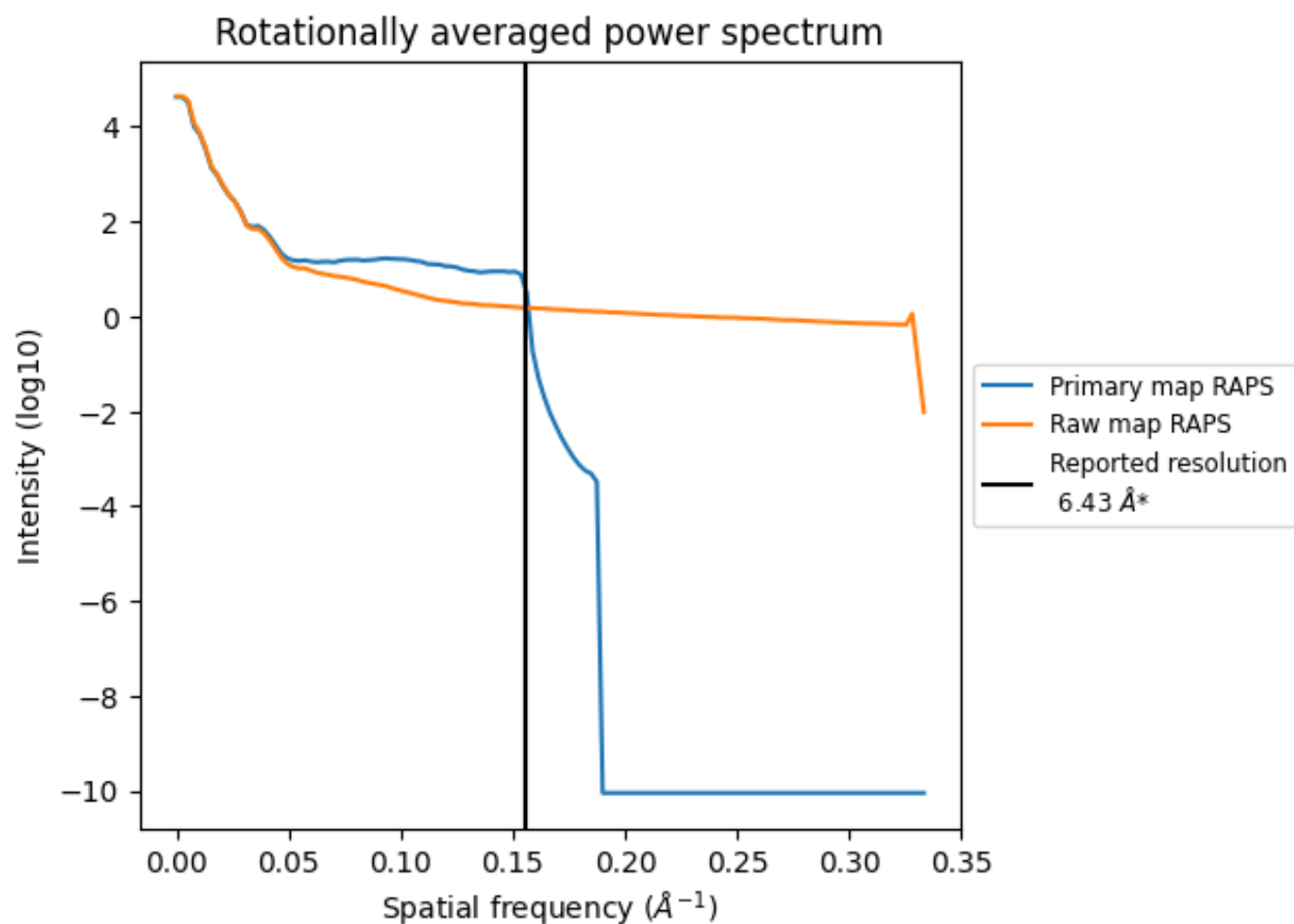
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 608 nm³; this corresponds to an approximate mass of 550 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 ⓘ

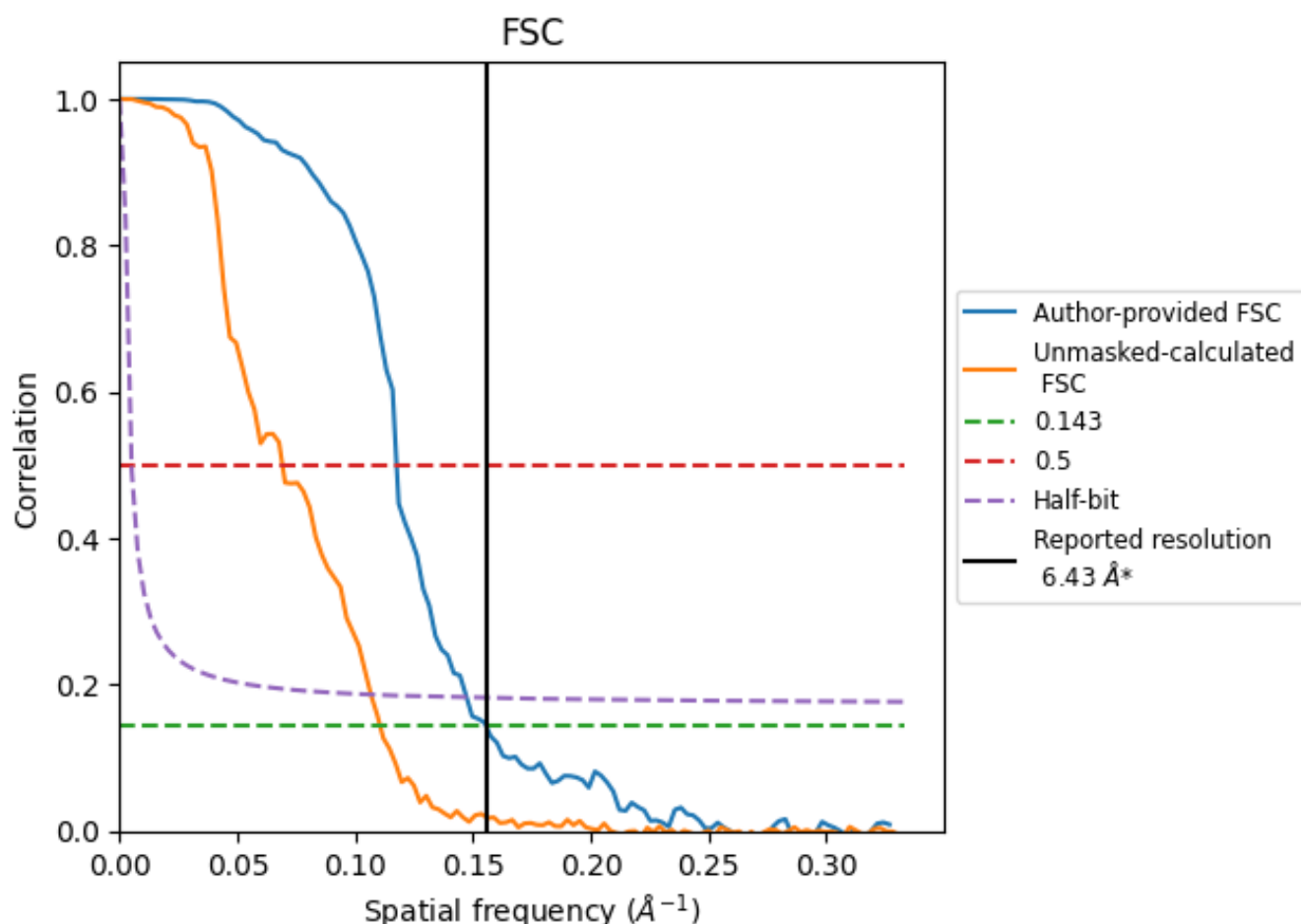


*Reported resolution corresponds to spatial frequency of 0.156 Å⁻¹

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 0.156 Å⁻¹

8.2 Resolution estimates [i](#)

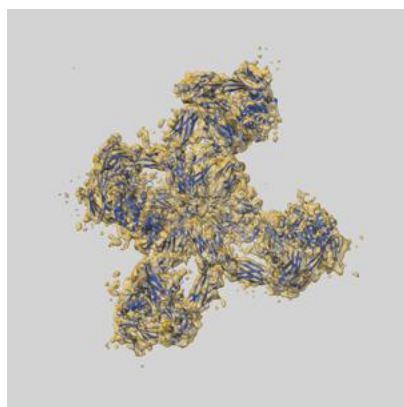
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.43	-	-
Author-provided FSC curve	6.43	8.50	6.78
Unmasked-calculated*	9.04	14.45	9.37

*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 9.04 differs from the reported value 6.43 by more than 10 %

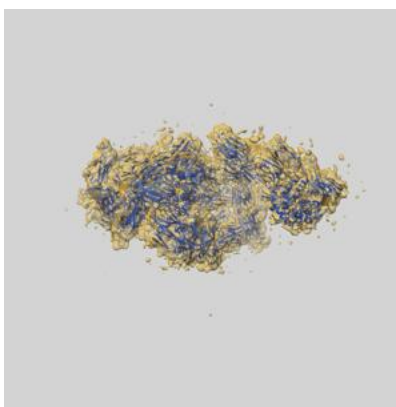
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24849 and PDB model 7S64. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

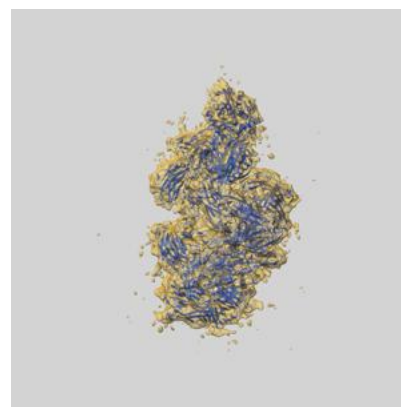
9.1 Map-model overlay [i](#)



X



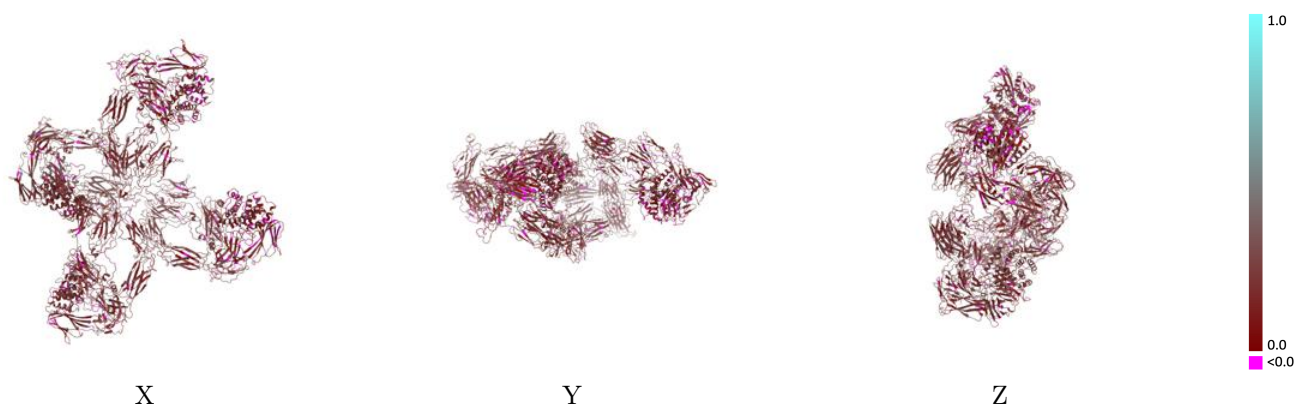
Y



Z

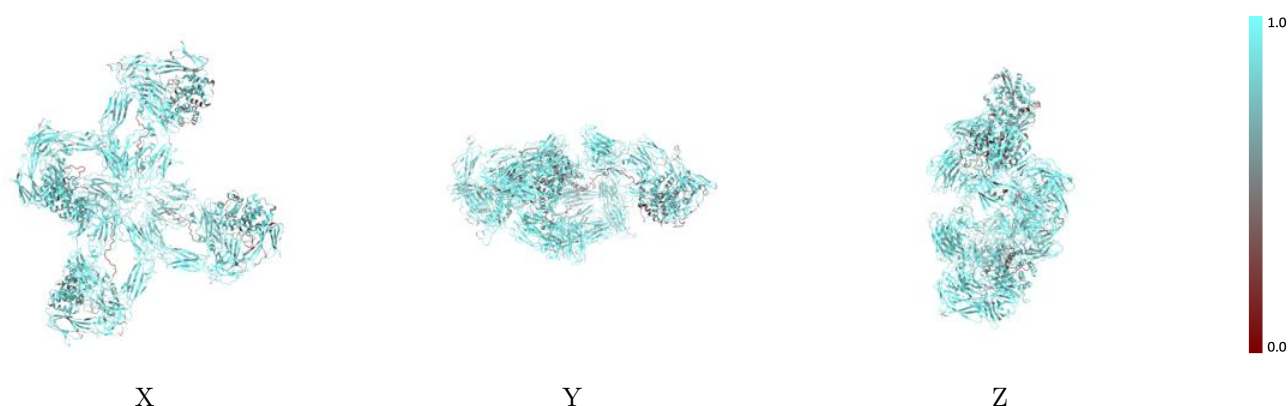
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



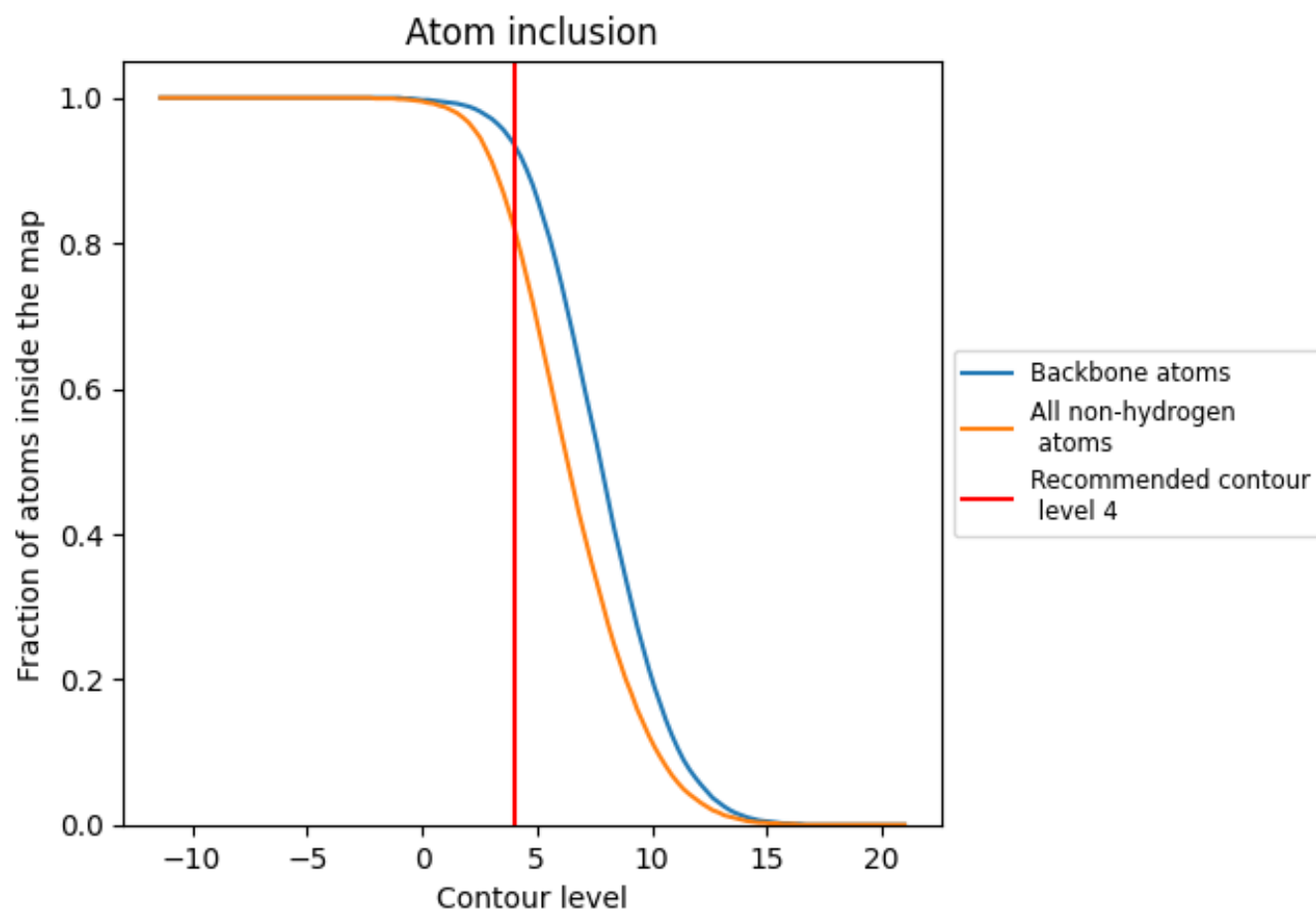
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 82% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8230	<div></div> 0.2090
A	<div></div> 0.8380	<div></div> 0.2310
B	<div></div> 0.8260	<div></div> 0.1990
C	<div></div> 0.7980	<div></div> 0.1950
D	<div></div> 0.8290	<div></div> 0.2120

