



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 08:25 PM UTC

PDB ID : 7S64 / pdb_00007s64
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.

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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

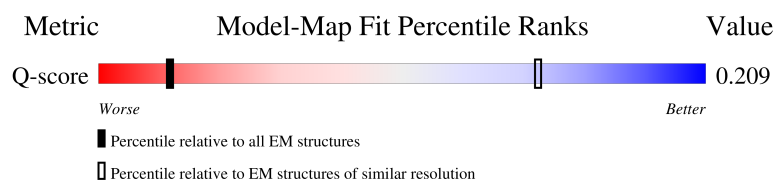
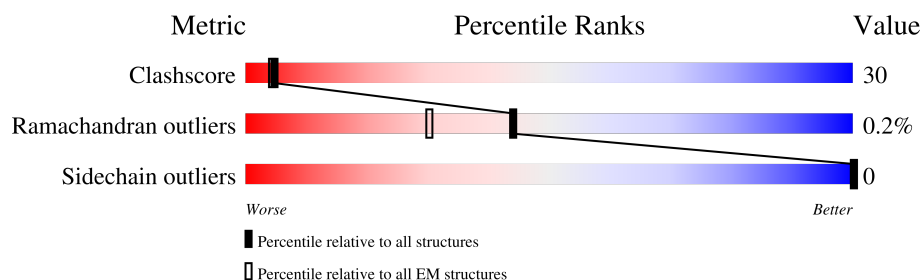
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	500 (5.94 - 6.91)

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.

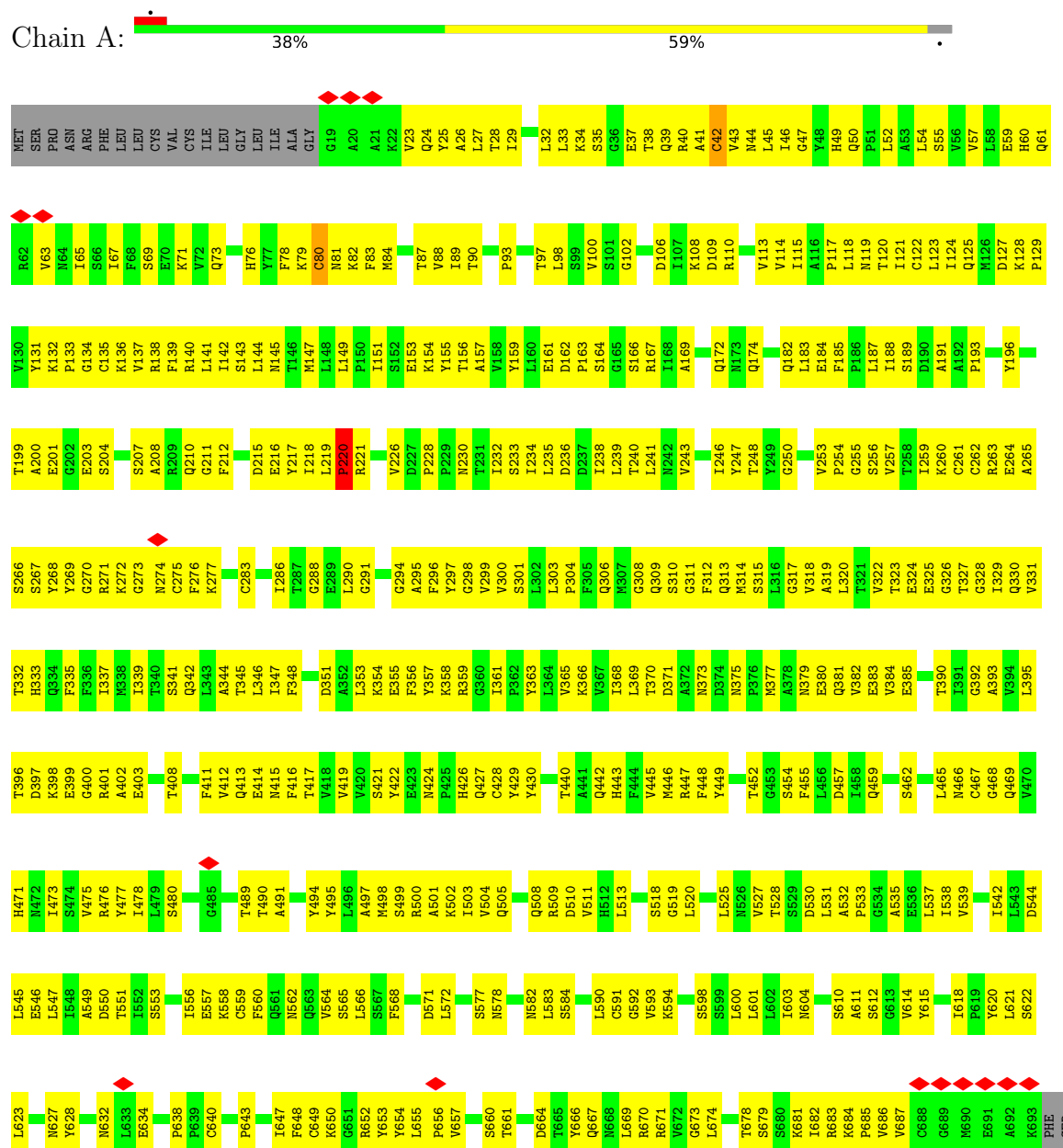
- Molecule 1 is a protein called Alpha 2-macroglobulin.

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		

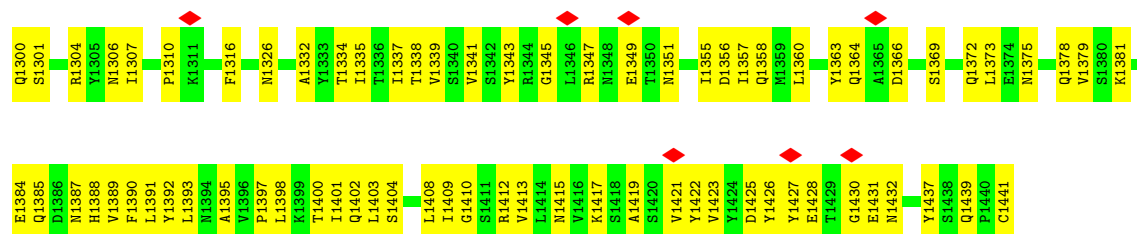
3 Residue-property plots

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.

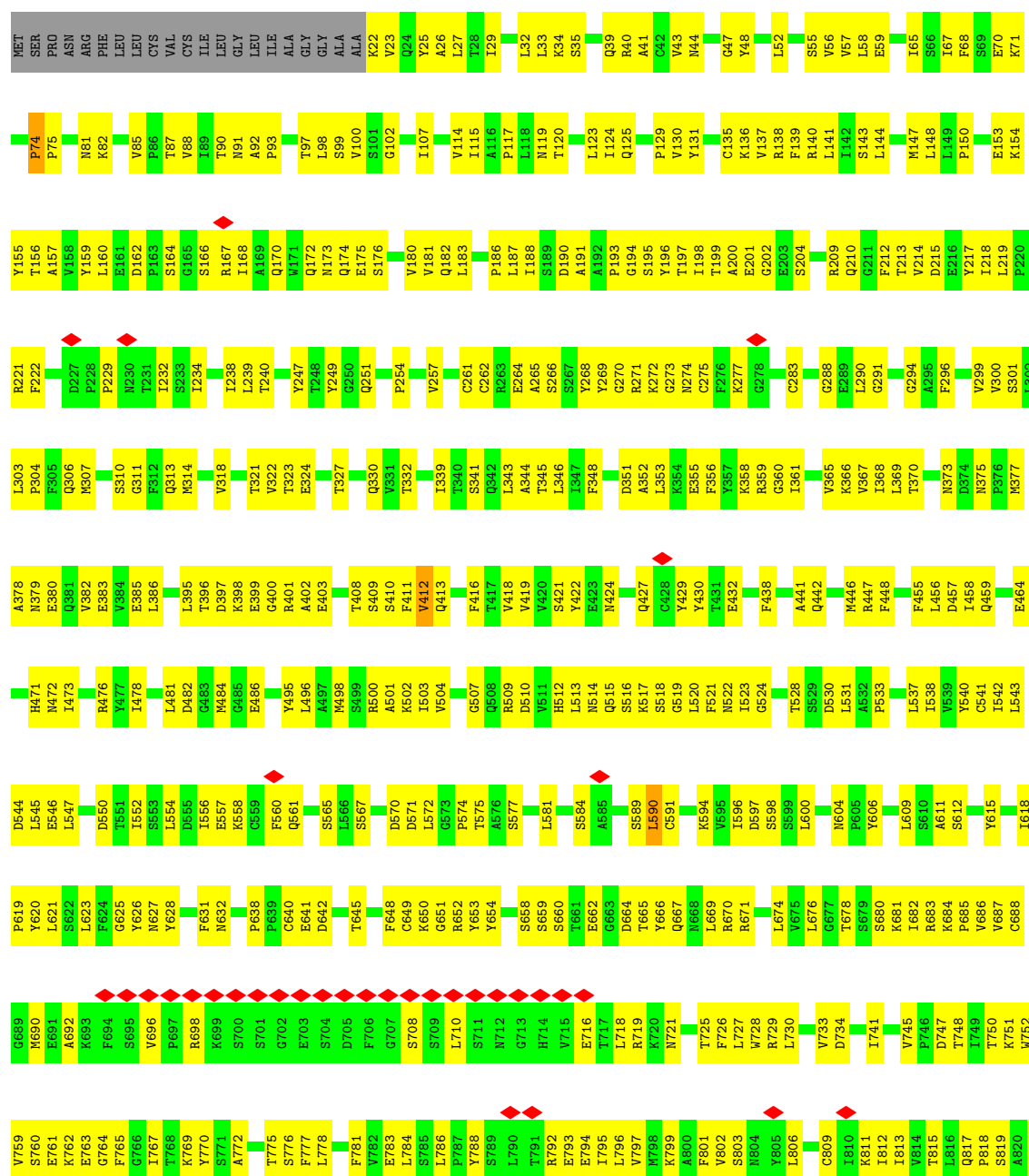
• Molecule 1: Alpha 2-macroglobulin



W1213	M115	S1023	F857	P779	E703	N627	C541	H471	E380	Q313	D215	S143
L1214	S1116	S1023	I858	F780	S704	Y628	I542	H472	Q381	M314	E216	M147
L1215	S1117	T1029	V859	F781	D705	F631	L543	H473	E382	S315	Y217	L148
Q1216	A1118	F1030	S860	V782	D706	N632	D544	S474	V383	L316	L218	L149
Q1217	S1119	K1031	E862	E783	G706	L633	E546	R476	V384	T321	P220	P150
Q1218	T1120	T1032	T863	L784	G707	E634	L547		E385	V322	R221	
N1219	L1121	F1033	T864	L786	S708		I548		L386	T323	R222	E153
		E1034	H865		S709					E324	F223	K154
G1222	K1124	K1035	I866	S789	L710	C640	T551	L479	K389	E325	R224	T156
G1223			G867	L790	S711	V646	I552	S480	T390	E326	I225	Y155
F1224	V1128	T1046	A868	T791	N712	I647	S553	D482	I391			A157
F1225	Y1129	Q1048	S869	R792	G713	F648		M483	G392	Q330	I232	V158
S1226	V1130	Q1049	C870	E793	H714	C649	I566	G485	A393	V331	S233	Y159
T1227	F1131	T1050	D871	I795	H715	R650		E486	V394	T332	S234	Y160
T1230	L1132	K1059	S874	L796	V716	R651	S565	L479	L395	H333	I234	
V1231	L1133	L1060	Q878	L797	T717	R652	S566	S480	T396	Q334		E161
V1232	V1134	A964	Q878	M798	L718	Y654	S567	Y494	K398	F335	S244	D162
		R965	L855	K799	R719		F568	Y495	F399	I337	A245	P163
Q1235	E1138	R966	L855	F801	L727	T572	L572	K502	G400	K338	Y247	G165
A1236	I1139			F802	R728	T575		R670	A402	I337	Y249	R167
				S803	R729			I496	I406	Q342	G250	Q170
S1247	L1143	F1065	V885	V802	V733	D664	L581	L497	I406	L343	Q251	W171
N1248	E1154	K1066	I886	S803	E736	T665	N582	M498	T408	A344	P253	Q172
A1249	Y971	A1067	Q887	L806	V737	Y666	L583	S499	S409	L345	P254	M173
H1250	V972	E1068			G738	L669	S584	Y494	F411	T346		Q174
H1251	L976				R739	R671			Q413	S341	G250	E175
F1264	L982	M1073	R897	C809	T740	L674	V593	Q508	T417	Q342	Q251	Q170
L1265	E985	Q1075	K898	I810	I741	V675	K594	R509	V418	L343	P252	W171
L1266	L986	Q1078	E899	I812	I741	L676	V595	D510	V419	A344	V253	Q172
S1267	L987	E1079	E900	V814			V595	H512	V420	L345	P254	M173
E1268	Q988	Q1080	T901	Q817	V745	G677	I596	H512		T346		Q174
Y1269	S819	R1081	S819	P818	T746	T678	D597	L513		S341	G250	E175
	A990		S802	S819	D747	S679	D597	L513	E423	D349	Y257	
V1262	V991	F1084	N904	A820	T748	S680	S598	N514	M424	Q350	T258	L183
G1263	Q992	T1085	L905	D821	I749	K681	S599	Q515	P425	D351	K260	P186
	F993	A1086			T750	I682	S516	Q516		A352	K261	P186
L1267	L994				K751	R683	L601	L601	Y430	K353	R263	L188
	E995				W752	K684				K354	E264	S189
R1272	E996	I1090	D910	K830	Q753	P685	P605	F521	F444	L354	A265	D190
L1273	R1000	L1093	E914	Q831	Q753	P685	Y606	N522	V445	D351	S267	A191
L1274	P915	E1094	M915	D832	Q753	P685	E607		V445	A352	Y268	A192
V1275	P916		P916	I835	M756	P685	E607		V445	I361	R271	Y196
L1280	R1003	Y1097	E923	I835	F757	P685	S608	L525	M446	Y363	C275	T197
P1281	K1005	S1099	N924	C836	Q757	P685	L609	N526	R447	L364	F276	I198
	P1007			S837	G758	P685	G689		F448	V365	K277	T199
Y1287	L1006	G1100	S929	G838	V759	P685	M690		Y449	V367	C283	A200
S1288	S1008	M1101	S930	S841	E761	P685	A611	D530	S450	L369	N285	E201
L1289	G1009	T1102	A930	S845	G764	P685	I618	L531	G453	T370	I286	C206
S1290	A1010	L1103	S931	N845	F765	P685	P619	A532	S454	D371	T287	E206
S1291	Y1011	L1104	A932	N846	G766	P685	Y620	P533	S454	A372	C275	A208
I1291	F933	D1105	I847	I848	I767	P685	L621	G534	F455	N373	F276	Q209
	D1012	D1106	I848	I848	I767	P685	S622	A535	D457	D374	C283	Q210
	A1013	V934	I848	I848	I767	P685	L623	E536	M307	N375	N285	R209
		T935	I848	I848	I767	P685	L623	E536	M307	N375	I286	Q210
		F936	I848	I848	I767	P685	L623	E536	M307	N375	I286	Q210
G1295	P1018	A1107	L852	L852	A772	K699	G625	F538	Q459	F376	G368	G211
C1296		L1108	S856	S856	N773	F774	G625	F538	Q459	N377	Q309	F212
C1297		G1109	S856	S856	T775	S776	G625	F538	Q459	A378	F312	T213
L1298		L1111	S856	S856	T775	S776	G625	F538	Q459	N379	F312	T213
V1299			S856	S856	T775	S776	G625	F538	Q459	N379	F312	T213



• Molecule 1: Alpha 2-macroglobulin



K1399	F1316	S1226	I1139	Y1053	D984	V913	S842	V759	P685	L609	G534	R447	I368
T1400	Y1317	D1229	R1140	L1054	E985	E914	W845	S760	C688	S610	A535	E451	L369
I1401	M1141	Y1232	M1142	Q1055	T989	I917	N846	E761	G689	A611	E536	T452	T370
L1403	L1143	Y1235	L1144	Q1058	A990	N918	I847	G762	M690	G612	L537	G453	D371
M1326	Y1152	Q1236	Y1153	D1061	V991	L919	I849	E764	G691	G614	V539	S484	N373
A1332	S1153	A1236	S1154	C1064	Q992	E923	A849	F765	A692	G615	Y540	F455	D374
Y1333	C1064	F1065	C1064	F1065	F993	N924	L852	A772	G693	Y616	C541	L456	N375
I1335	T1157	H1250	T1157	K1066	N995	I925	S856	T774	F694	I618	L542	D457	M377
Y1339	E1161	H1251	E1161	A1067	G997	V926	F857	T775	G696	L623	D544	S461	A378
S1340	R1162	Y1254	R1162	E1068	Y998	A930	I858	T776	P697	Y626	E546	V462	N379
V1341	K1165	R1254	K1165	L1071	Y999	S931	V859	F777	R698	Y628	L547	E464	Q381
S1342	L1166	R1256	L1166	F1072	R1000	A932	S860	L778	K699	Y628	I548	L465	V382
Y1343	M1073	E1257	M1073	M1073	Q1001	F933	E861	F779	S700	F631	D550	C467	V384
R1344	G1167	E1258	G1167	R1074	L1002	V934	E862	F780	S700	N632	I552	H470	E385
G1345	Q1168	Q1075	Q1168	Q1075	R1004	T935	T864	F781	S700	N632	I552	H470	E385
L1346	Q1168	Q1075	Q1168	Q1075	K1005	V937	H865	E783	G702	C640	S553	H471	L386
R1347	E1169	G1170	E1169	G1170	G1009	L941	I866	L784	E703	E641	L554	R476	T390
T1350	G1170	I1171	G1170	I1171	A1010	L942	G867	S785	S704	F647	I555	R476	I391
M1351	I1171	P1172	I1171	P1172	Y1011	L943	G868	S785	S704	F647	I555	R476	G392
M1352	L1173	L1173	L1173	L1173	D1012	P944	S869	L786	D705	C649	E557	I478	A393
V1353	Y1174	Y1174	Y1174	Y1174	N947	N947	G872	S789	F706	K650	Q561	S480	L395
I1354	Y1175	Y1175	Y1175	Y1175	R873	R873	G872	S789	F706	K650	Q561	S480	L395
I1355	A1181	E1182	A1181	E1182	S874	S874	G872	S789	F706	K650	Q561	S480	L395
I1357	E1182	E1182	E1182	E1182	S874	S874	G872	S789	F706	K650	Q561	S480	L395
I1358	E1182	E1182	E1182	E1182	S874	S874	G872	S789	F706	K650	Q561	S480	L395
M1359	E1182	E1182	E1182	E1182	S874	S874	G872	S789	F706	K650	Q561	S480	L395
L1360	E1182	E1182	E1182	E1182	S874	S874	G872	S789	F706	K650	Q561	S480	L395
Y1363	L1280	P1281	L1280	P1281	G1021	L951	Q878	S789	F706	K650	Q561	S480	L395
Q1364	P1281	E1282	P1281	E1282	S1022	L952	S879	S789	F706	K650	Q561	S480	L395
A1365	E1282	E1282	E1282	E1282	S1023	Q953	S879	S789	F706	K650	Q561	S480	L395
D1366	Y1283	Y1283	Y1283	Y1283	W954	M954	R881	S789	F706	K650	Q561	S480	L395
Y1367	S1284	G1285	S1284	G1285	P955	P955	K882	S789	F706	K650	Q561	S480	L395
P1368	G1285	G1285	G1285	G1285	Y956	Y956	K883	S789	F706	K650	Q561	S480	L395
S1369	N1286	Y1287	N1286	Y1287	C958	C958	T884	S789	F706	K650	Q561	S480	L395
M1375	Y1287	Y1287	Y1287	Y1287	E960	E960	I886	S789	F706	K650	Q561	S480	L395
S1376	S1287	S1287	S1287	S1287	Q961	Q961	Q887	S789	F706	K650	Q561	S480	L395
Q1377	I1289	I1289	I1289	I1289	N962	N962	T888	S789	F706	K650	Q561	S480	L395
Q1378	S1290	S1290	S1290	S1290	L863	L863	I889	S789	F706	K650	Q561	S480	L395
V1379	C1297	C1297	C1297	C1297	A964	A964	E894	S789	F706	K650	Q561	S480	L395
S1380	L1298	L1298	L1298	L1298	R965	R965	G895	S789	F706	K650	Q561	S480	L395
K1381	Q1300	Q1300	Q1300	Q1300	M966	M966	I896	S789	F706	K650	Q561	S480	L395
M1387	T1302	T1302	T1302	T1302	T969	T969	R897	S789	F706	K650	Q561	S480	L395
H1388	L1303	L1303	L1303	L1303	P970	P970	K898	S789	F706	K650	Q561	S480	L395
V1389	R1304	R1304	R1304	R1304	Y971	Y971	E899	S789	F706	K650	Q561	S480	L395
L1391	Y1305	Y1305	Y1305	Y1305	V972	V972	E900	S789	F706	K650	Q561	S480	L395
Y1392	N1306	N1306	N1306	N1306	E974	E974	T901	S789	F706	K650	Q561	S480	L395
L1393	I1307	I1307	I1307	I1307	Y975	Y975	S902	S789	F706	K650	Q561	S480	L395
M1394	P1308	P1308	P1308	P1308	L976	L976	S903	S789	F706	K650	Q561	S480	L395
A1395	Q1217	Q1217	Q1217	Q1217	Q1048	Q1048	N904	S789	F706	K650	Q561	S480	L395
V1396	G1218	G1218	G1218	G1218	Q1049	Q1049	L905	S789	F706	K650	Q561	S480	L395
N1397	N1219	N1219	N1219	N1219	T1050	T1050	V908	S789	F706	K650	Q561	S480	L395
G1222	G1222	G1222	G1222	G1222	L1051	L1051	S911	S789	F706	K650	Q561	S480	L395
					L1052	L1052	N912	S789	F706	K650	Q561	S480	L395

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 [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	0.24	0/11104	0.52	5/15099 (0.0%)
1	B	0.20	0/11298	0.45	2/15359 (0.0%)
1	C	0.23	1/11298 (0.0%)	0.50	4/15359 (0.0%)
1	D	0.24	1/11298 (0.0%)	0.50	0/15359
All	All	0.23	2/44998 (0.0%)	0.49	11/61176 (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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	916	PRO	CG-CD	-8.83	1.20	1.50
1	D	654	TYR	C-N	5.12	1.40	1.33

The worst 5 of 11 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	C	916	PRO	CA-N-CD	-10.16	97.78	112.00
1	A	80	CYS	CA-CB-SG	8.51	133.97	114.40
1	A	42	CYS	N-CA-C	7.56	119.89	107.73
1	A	42	CYS	CA-CB-SG	7.42	131.47	114.40

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	801	0
1	B	11064	0	10871	571	0
1	C	11064	0	10871	598	0
1	D	11064	0	10871	709	0
All	All	44067	0	43297	2634	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 30.

The worst 5 of 2634 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	67
1	B	1418/1441 (98%)	1257 (89%)	158 (11%)	3 (0%)	43	77
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%)	44	77

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%)	1220 (100%)	0	100	100
1	B	1244/1259 (99%)	1244 (100%)	0	100	100
1	C	1244/1259 (99%)	1244 (100%)	0	100	100
1	D	1244/1259 (99%)	1244 (100%)	0	100	100
All	All	4952/5036 (98%)	4952 (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 70 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	578	ASN
1	D	714	HIS
1	D	1075	GLN
1	B	443	HIS
1	B	381	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.

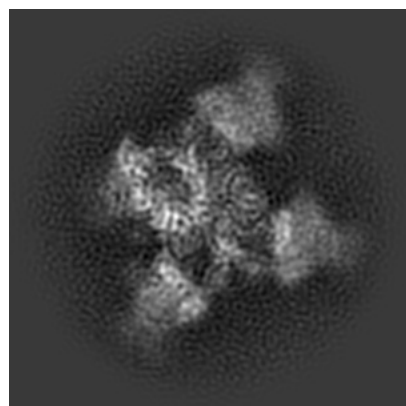
6 Map visualisation [i](#)

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

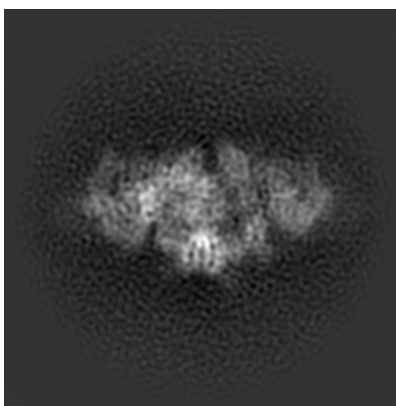
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

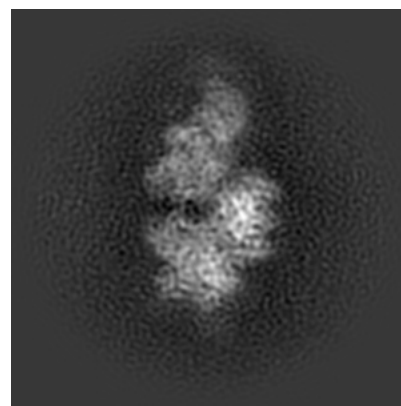
6.1.1 Primary map



X

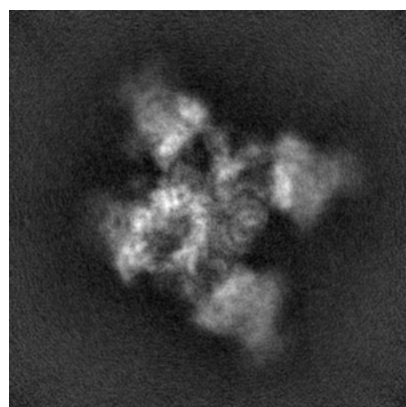


Y

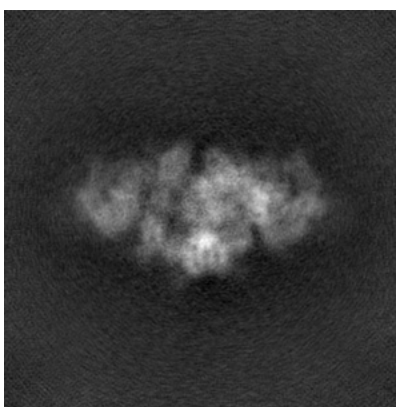


Z

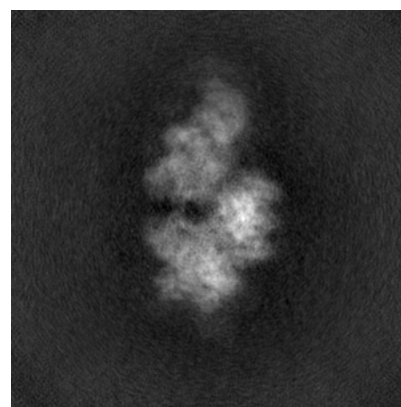
6.1.2 Raw map



X



Y

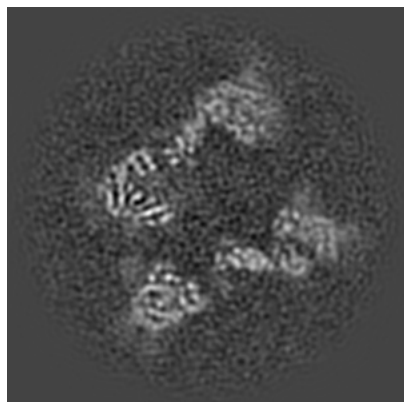


Z

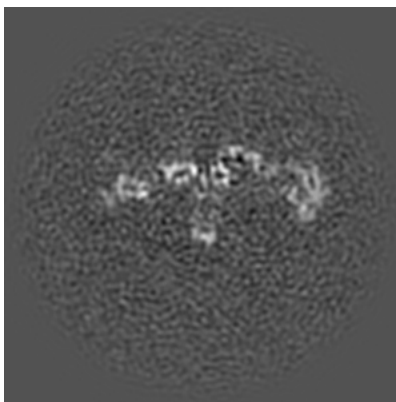
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

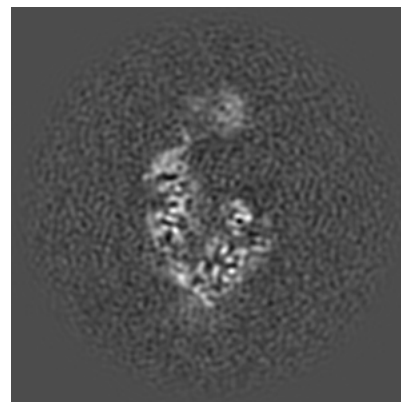
6.2.1 Primary map



X Index: 128

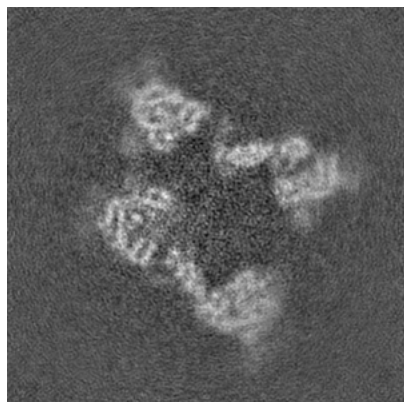


Y Index: 128

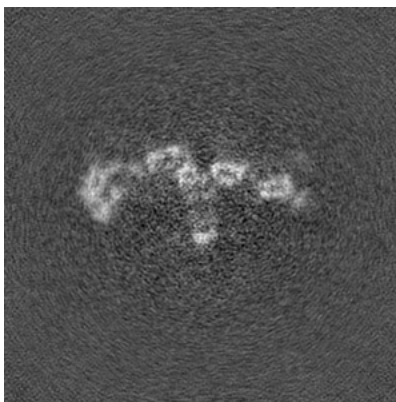


Z Index: 128

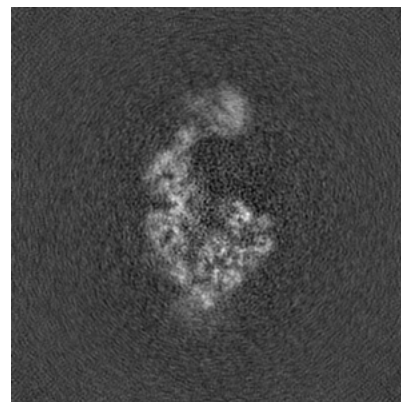
6.2.2 Raw map



X Index: 128



Y Index: 128

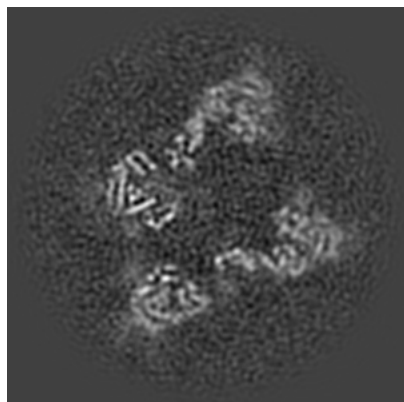


Z Index: 128

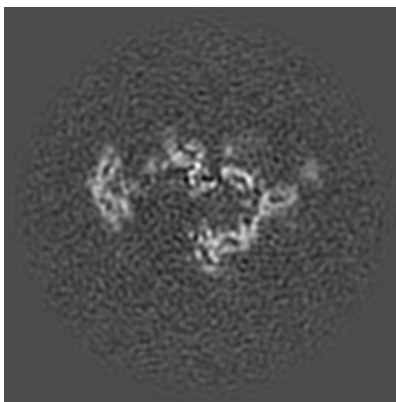
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

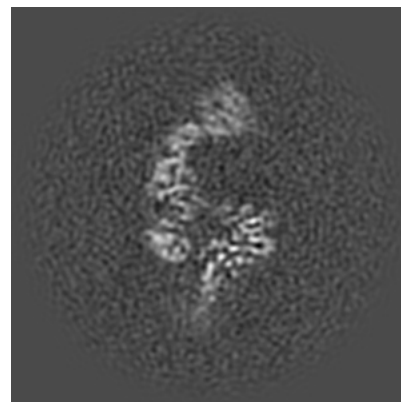
6.3.1 Primary map



X Index: 130

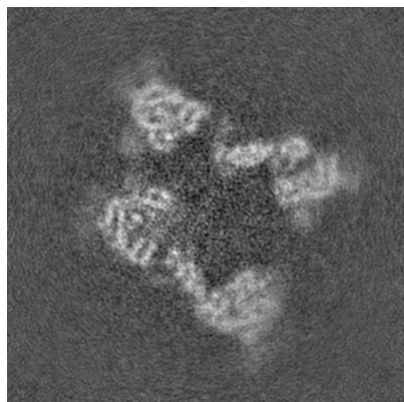


Y Index: 118

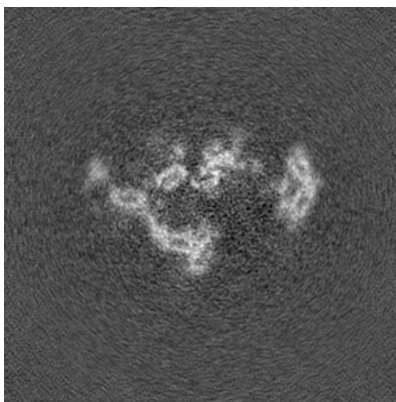


Z Index: 123

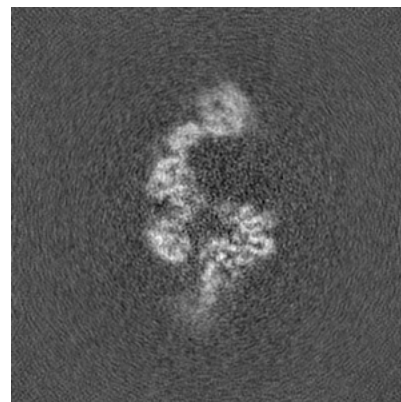
6.3.2 Raw map



X Index: 128



Y Index: 119

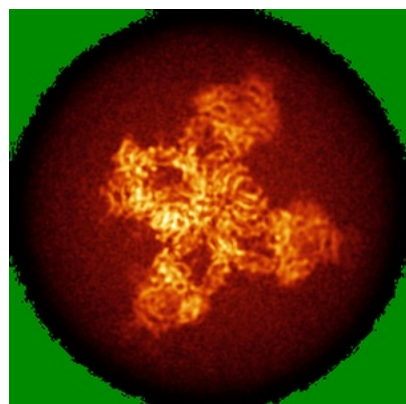


Z Index: 132

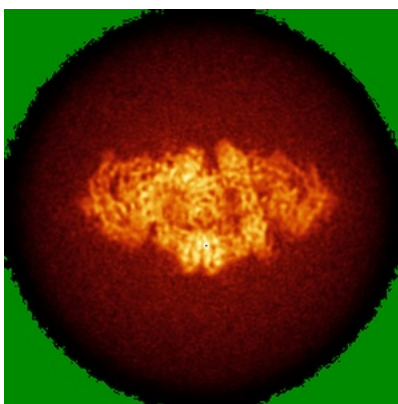
The images above show the largest variance slices of the map in three orthogonal directions.

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

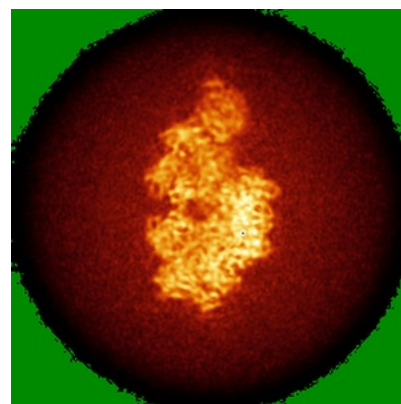
6.4.1 Primary map



X

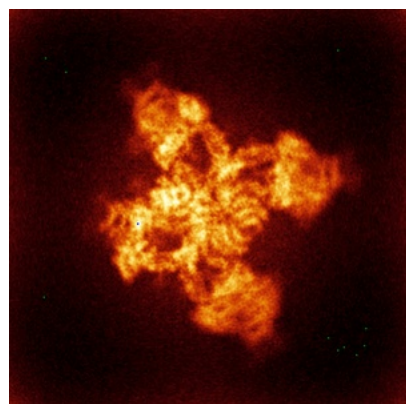


Y

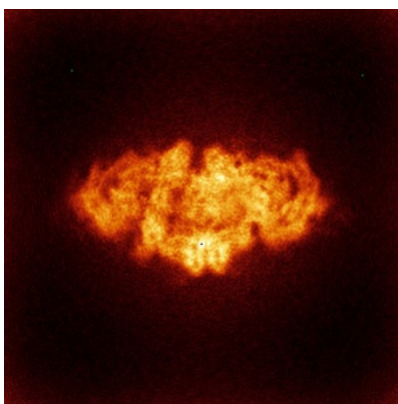


Z

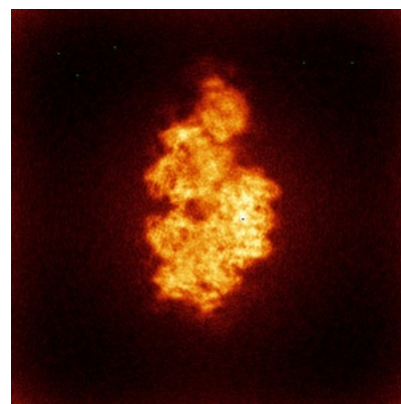
6.4.2 Raw map



X



Y

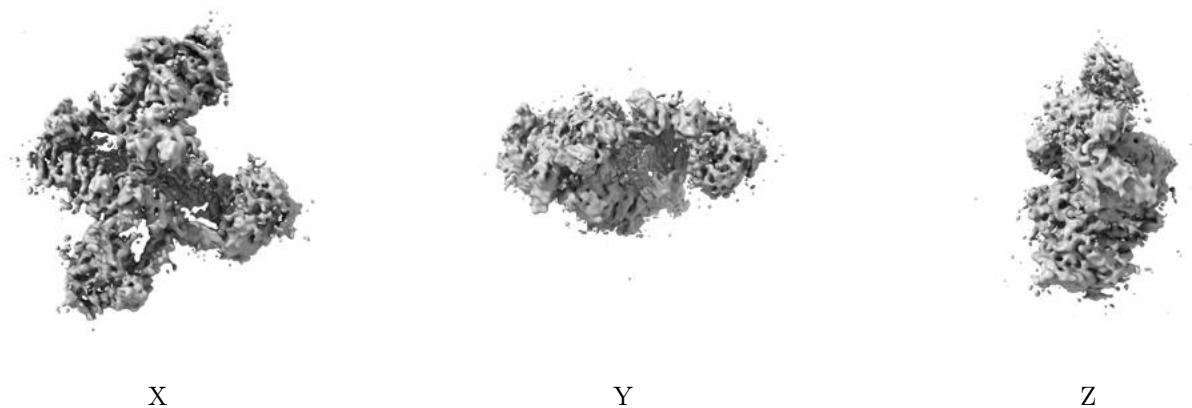


Z

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.

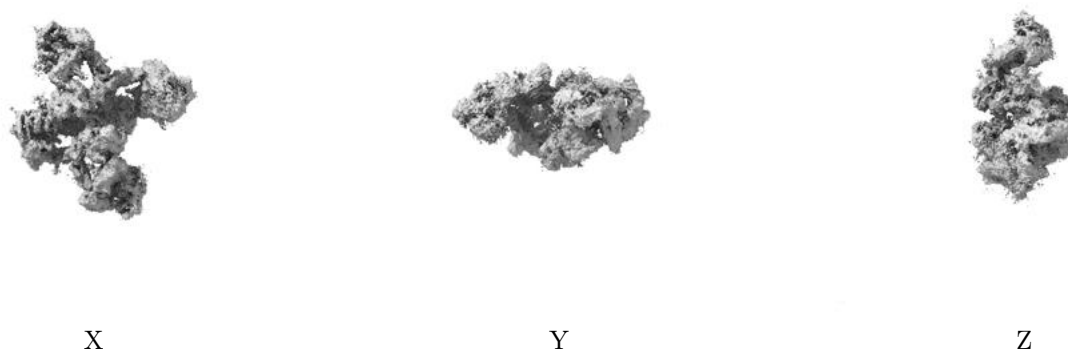
6.5 Orthogonal surface views [i](#)

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.

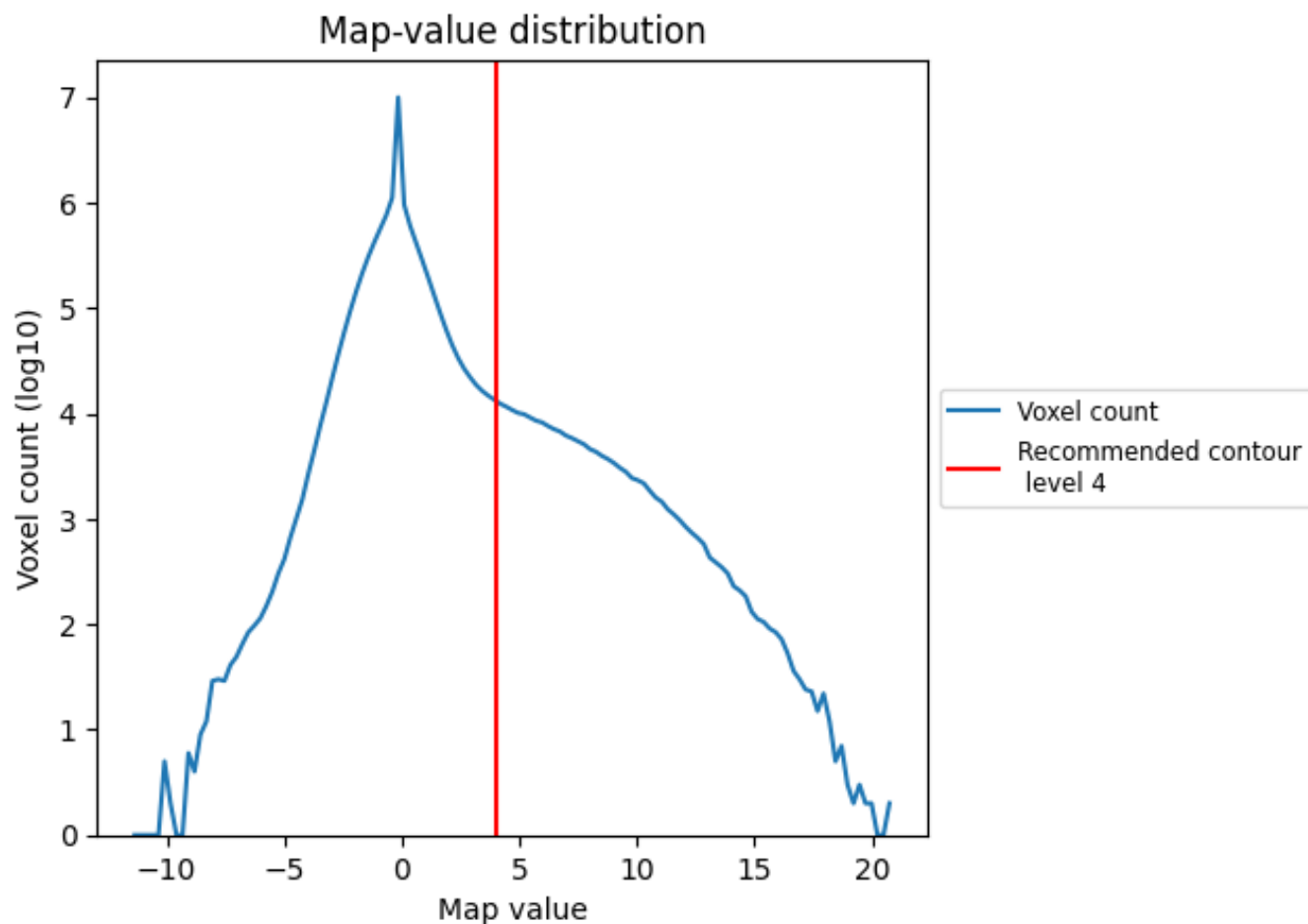
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

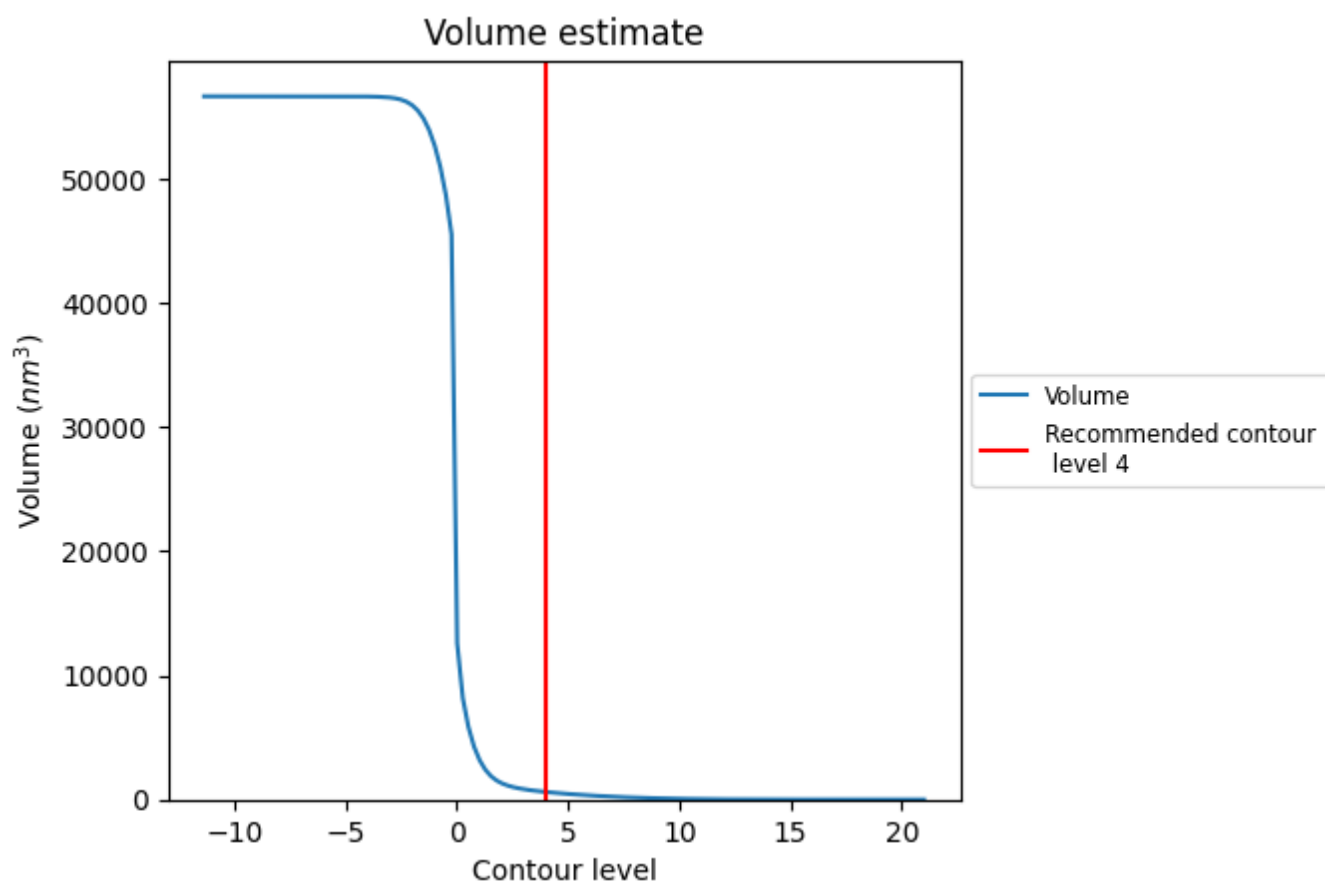
This section contains the results of statistical analysis of the map.

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.

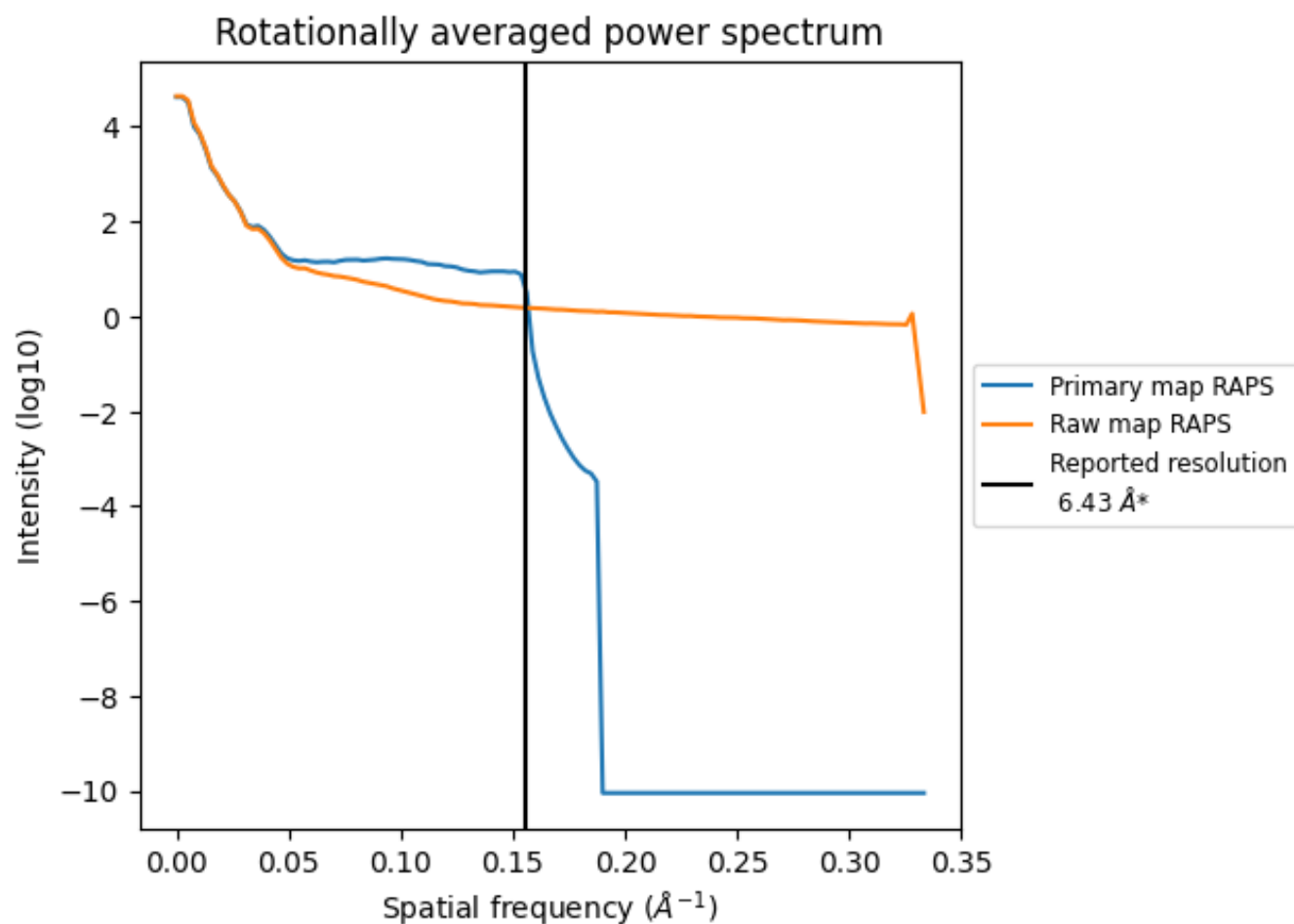
7.2 Volume estimate [i](#)



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 ⓘ

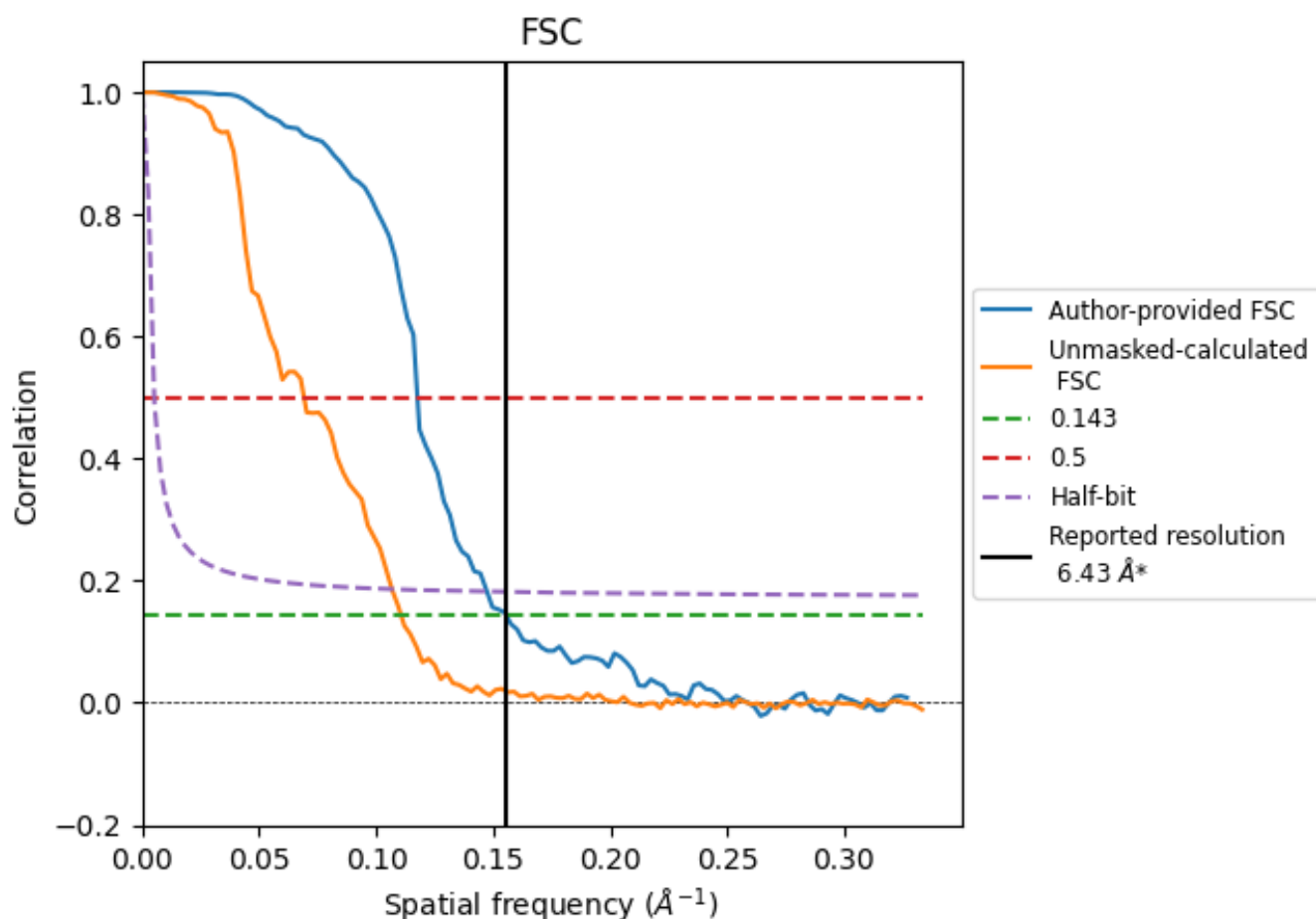


*Reported resolution corresponds to spatial frequency of $0.156 \text{ \AA}^{-1}$

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 0.156 Å⁻¹

8.2 Resolution estimates [i](#)

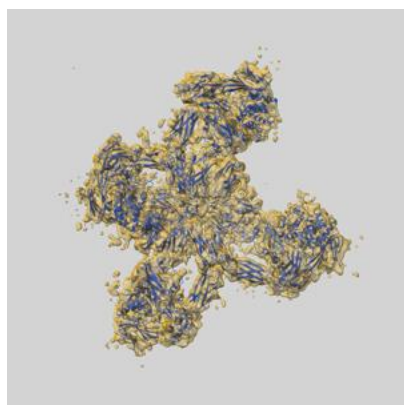
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.43	-	-
Author-provided FSC curve	6.43	8.50	6.78
Unmasked-calculated*	9.04	14.45	9.37

*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 %

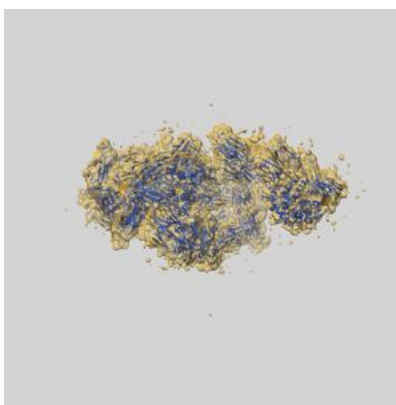
9 Map-model fit [i](#)

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](#).

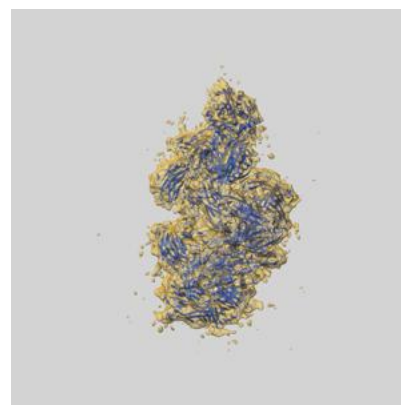
9.1 Map-model overlay [i](#)



X



Y



Z

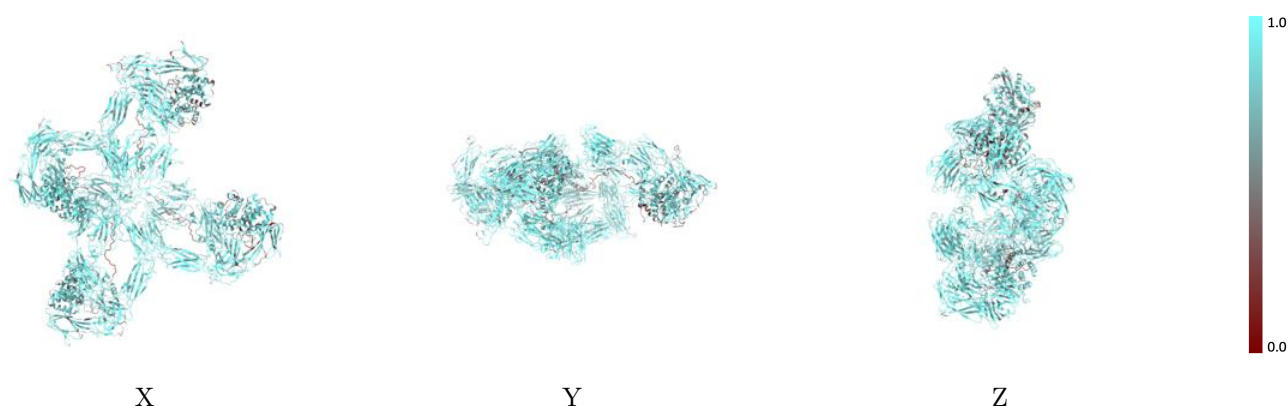
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



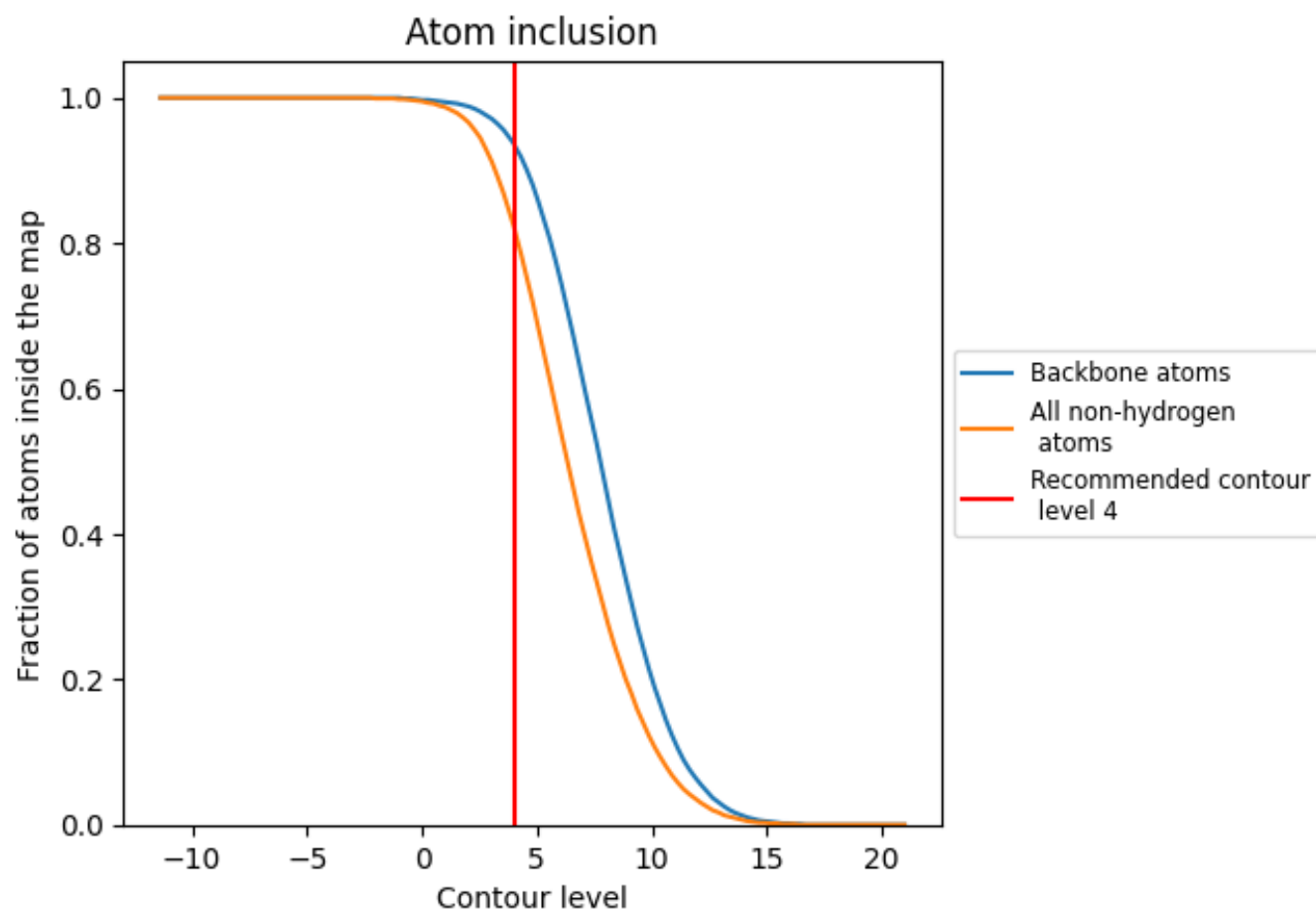
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	0.8230	0.2090
A	0.8380	0.2310
B	0.8260	0.1990
C	0.7980	0.1950
D	0.8290	0.2120

