



# wwPDB EM Validation Summary Report ⓘ

Jan 1, 2025 – 07:36 PM EST

PDB ID : 8ZJJ  
EMDB ID : EMD-60147  
Title : Structure of DOCK5/ELMO1/Rac1 core (RhoG/DOCK5/ELMO1/Rac1 dataset, class 2)  
Authors : Kukimoto-Niino, M.; Katsura, K.; Ishizuka-Katsura, Y.; Mishima-Tsumagari, C.; Yonemochi, M.; Inoue, M.; Nakagawa, R.; Kaushik, R.; Zhang, K.Y.J.; Shirouzu, M.  
Deposited on : 2024-05-15  
Resolution : 4.23 Å(reported)  
Based on initial model : 7DPA

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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) : 2.40

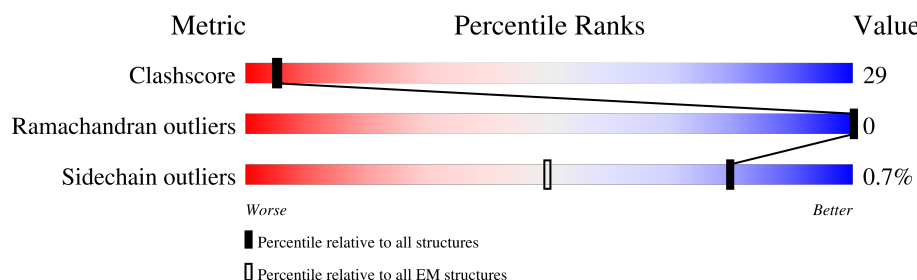
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.23 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  $\geq 3$ , 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	733	
1	D	733	
2	B	1648	
2	E	1648	
3	C	184	
3	F	184	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32858 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 Engulfment and cell motility protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	198	Total	C	N	O	S	0	0
			1608	1018	277	303	10		
1	D	198	Total	C	N	O	S	0	0
			1608	1018	277	303	10		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q92556
A	-4	GLY	-	expression tag	UNP Q92556
A	-3	SER	-	expression tag	UNP Q92556
A	-2	GLY	-	expression tag	UNP Q92556
A	-1	GLY	-	expression tag	UNP Q92556
A	0	SER	-	expression tag	UNP Q92556
D	-5	GLY	-	expression tag	UNP Q92556
D	-4	GLY	-	expression tag	UNP Q92556
D	-3	SER	-	expression tag	UNP Q92556
D	-2	GLY	-	expression tag	UNP Q92556
D	-1	GLY	-	expression tag	UNP Q92556
D	0	SER	-	expression tag	UNP Q92556

- Molecule 2 is a protein called Deducator of cytokinesis protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1642	Total	C	N	O	S	0	0
			13436	8618	2264	2484	70		
2	E	1642	Total	C	N	O	S	0	0
			13436	8618	2264	2484	70		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	GLY	-	expression tag	UNP Q9H7D0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	GLY	-	expression tag	UNP Q9H7D0
B	-3	SER	-	expression tag	UNP Q9H7D0
B	-2	GLY	-	expression tag	UNP Q9H7D0
B	-1	GLY	-	expression tag	UNP Q9H7D0
B	0	SER	-	expression tag	UNP Q9H7D0
B	1285	ARG	LYS	variant	UNP Q9H7D0
E	-5	GLY	-	expression tag	UNP Q9H7D0
E	-4	GLY	-	expression tag	UNP Q9H7D0
E	-3	SER	-	expression tag	UNP Q9H7D0
E	-2	GLY	-	expression tag	UNP Q9H7D0
E	-1	GLY	-	expression tag	UNP Q9H7D0
E	0	SER	-	expression tag	UNP Q9H7D0
E	1285	ARG	LYS	variant	UNP Q9H7D0

- Molecule 3 is a protein called Ras-related C3 botulinum toxin substrate 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	177	Total	C	N	O	S	0	0
			1385	890	228	259	8		
3	F	177	Total	C	N	O	S	0	0
			1385	890	228	259	8		

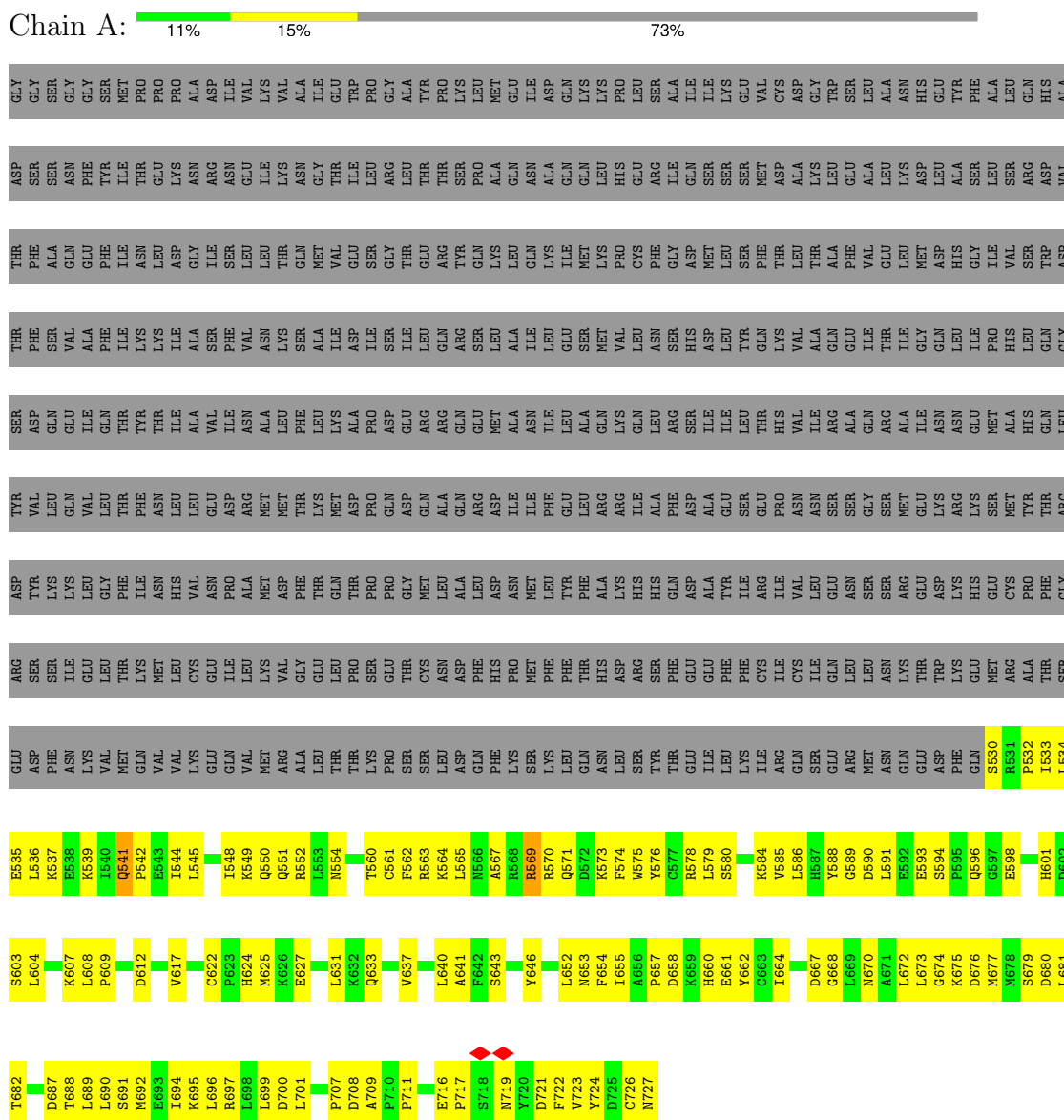
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	GLY	-	expression tag	UNP P63000
C	-5	SER	-	expression tag	UNP P63000
C	-4	SER	-	expression tag	UNP P63000
C	-3	GLY	-	expression tag	UNP P63000
C	-2	SER	-	expression tag	UNP P63000
C	-1	SER	-	expression tag	UNP P63000
C	0	GLY	-	expression tag	UNP P63000
C	15	ALA	GLY	engineered mutation	UNP P63000
F	-6	GLY	-	expression tag	UNP P63000
F	-5	SER	-	expression tag	UNP P63000
F	-4	SER	-	expression tag	UNP P63000
F	-3	GLY	-	expression tag	UNP P63000
F	-2	SER	-	expression tag	UNP P63000
F	-1	SER	-	expression tag	UNP P63000
F	0	GLY	-	expression tag	UNP P63000
F	15	ALA	GLY	engineered mutation	UNP P63000

### 3 Residue-property plots

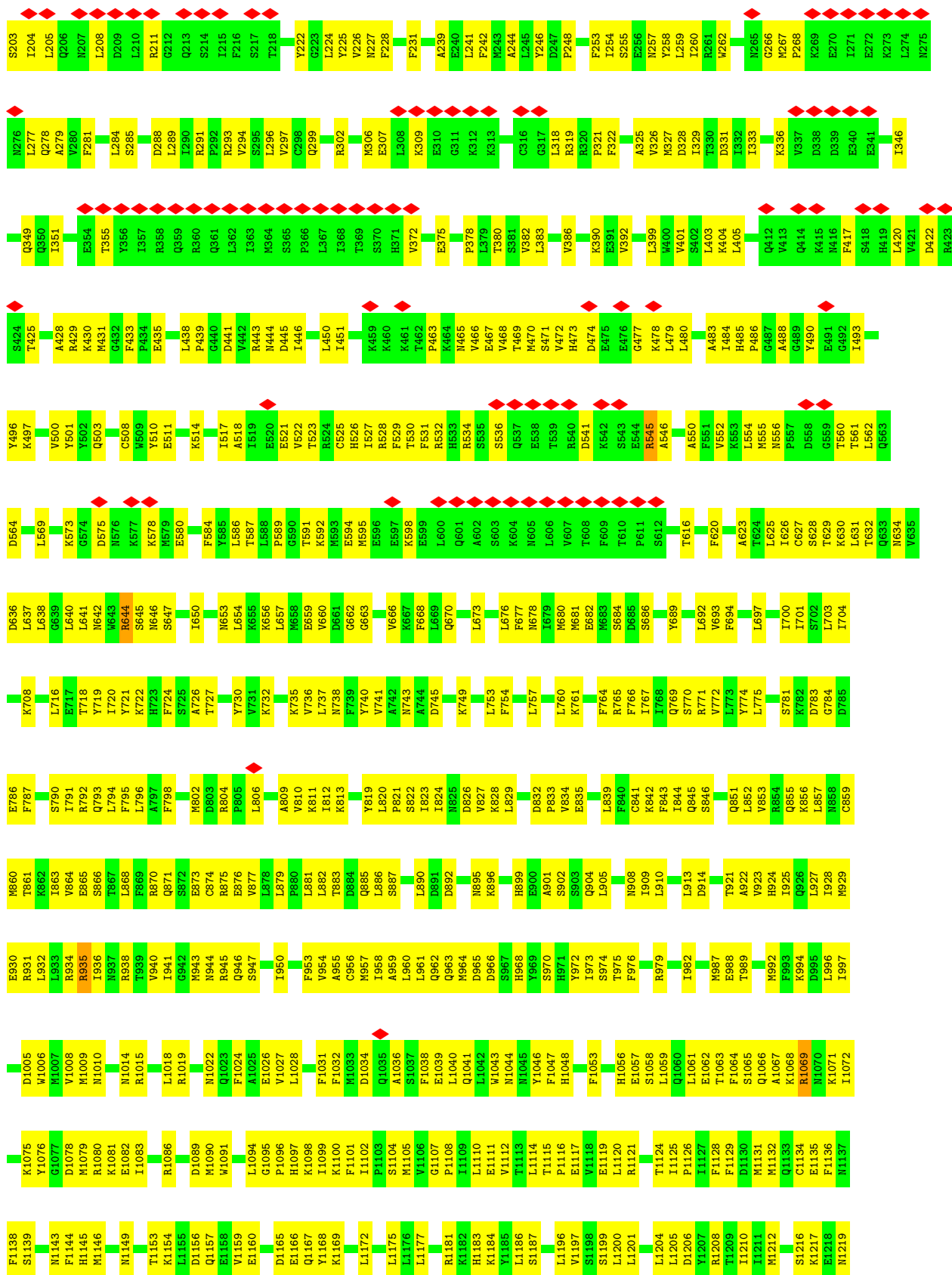
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

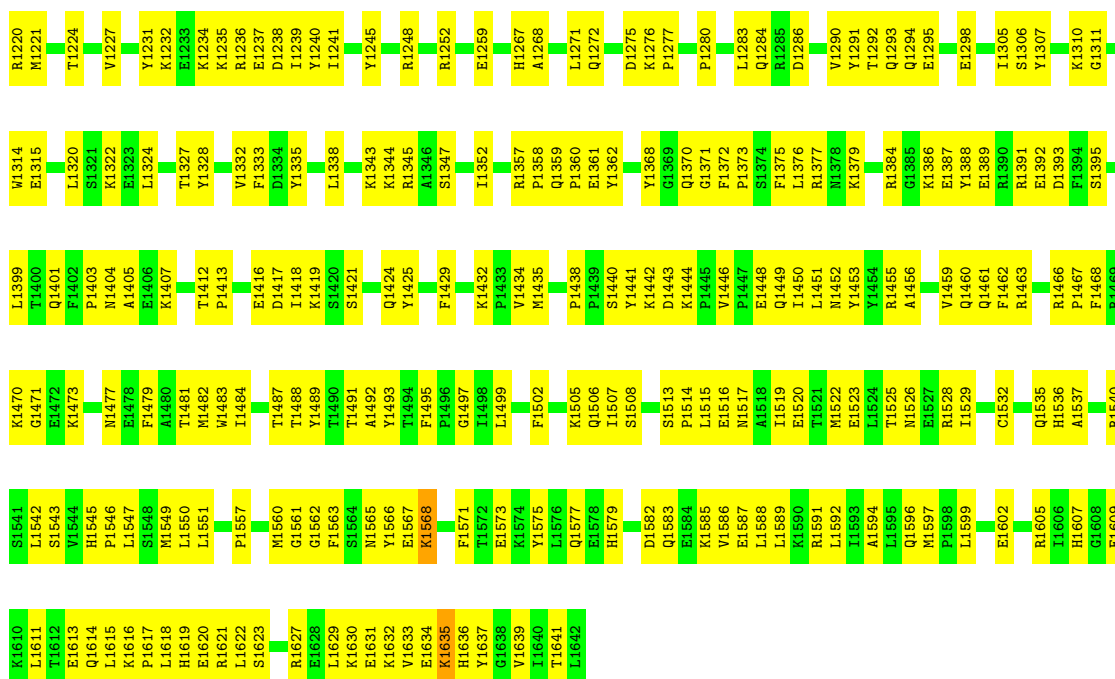
- Molecule 1: Engulfment and cell motility protein 1



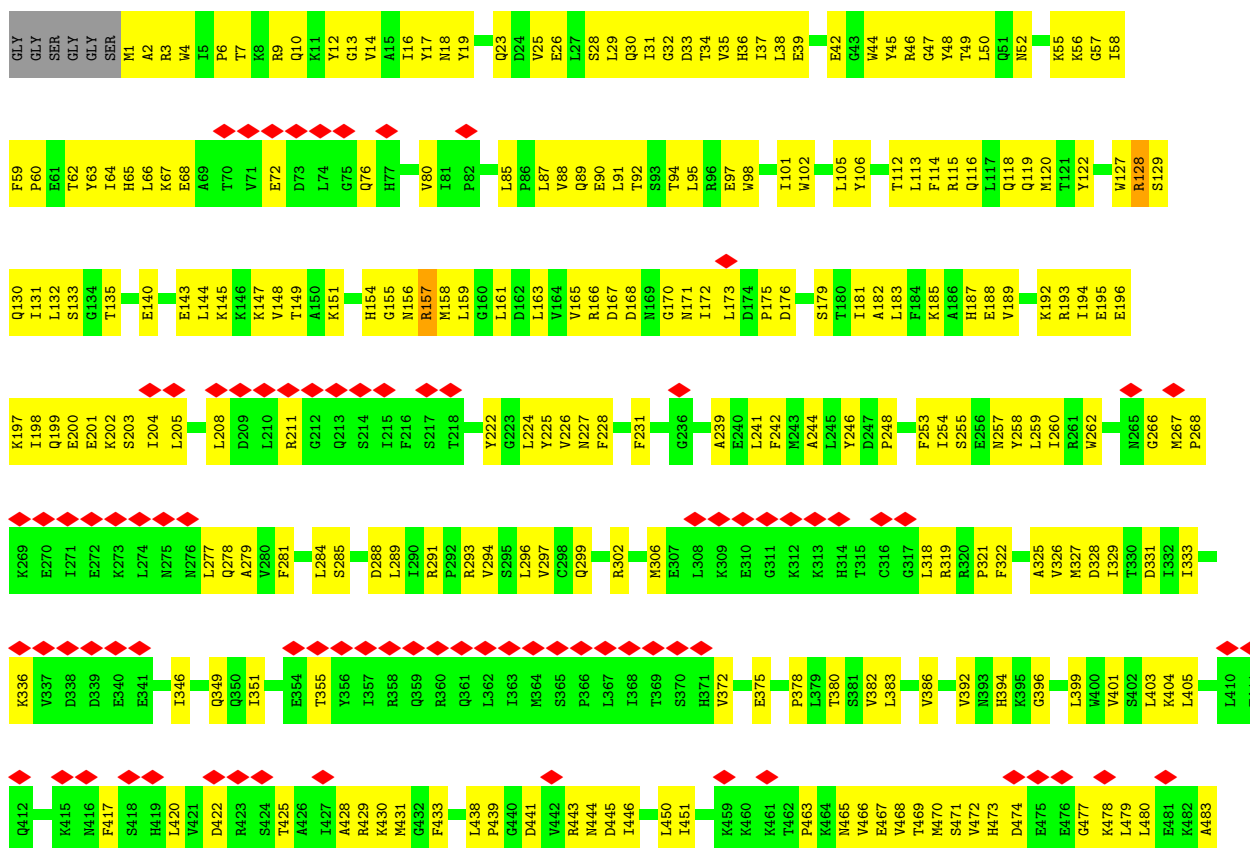
- Molecule 1: Engulfment and cell motility protein 1





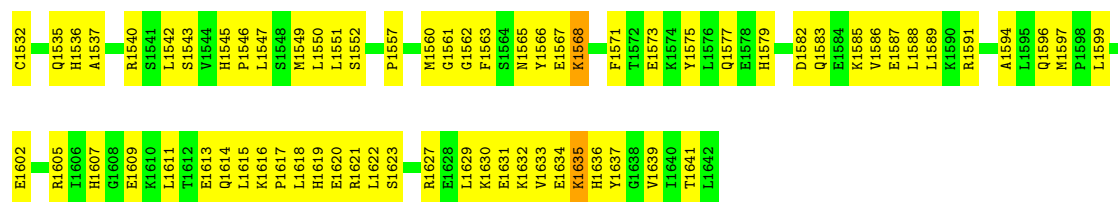


• Molecule 2: Dedicator of cytokinesis protein 5



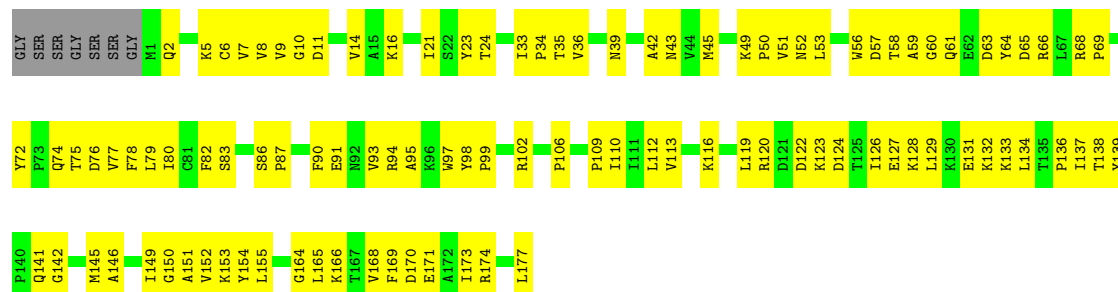


V1459	K1386	Y1301	T1209	F1129	F1064	H992	H924	V853	F694	I626	G553	I484
Q1460	E1387	Y1388	I1210	D1130	S1065	F993	I925	R854	L697	C627	L554	H485
F1461	Y1389	T1305	S1216	M1131	Q1066	K994	Q926	K855	L697	S628	M555	G486
R1462	R1390	S1306	K1217	Q1133	A1067	D995	L927	K856	I700	T629	N556	G487
R1463	R1391	S1306	K1217	Q1133	K1068	L996	I928	N857	I701	K630	A488	A488
Y1464	E1392	Y1307	N1219	E1135	R1069	I997	N929	C859	S702	L631	G489	G489
S1465	D1393	K1310	R1220	E1135	N1070	D1005	E330	M860	L703	T632	T560	Y490
R1466	F1394	G1311	M1221	F1137	K1071	M1006	R931	T861	L704	Q633	T561	E491
F1467	S1395	Y1388	M1221	F1137	I1072	Y1007	L932	K862	I704	L562	G492	G492
F1468	Y1314	E1315	T1224	S1139	K1075	M1008	L933	E786	L716	L637	Q563	I493
R1469	E1400	E1400	Y1227	N1143	Y1076	M1009	R935	R864	E717	L638	Q564	Y496
K1470	Q1401	L1320	Y1227	F1144	G1077	M1010	I936	E865	L638	L638	L569	K497
N1477	F1402	S1321	Y1231	D1078	D1078	N1014	R937	T867	I718	L640	G573	Y500
E1478	P1403	K1322	K1232	M1079	M1079	R1015	T939	T867	I719	L641	K574	Y501
F1479	N1404	E1323	K1232	K1080	K1080	F1024	R945	R875	I720	N642	G574	Y502
A1480	A1405	L1324	K1235	I1081	I1081	A1025	I941	R870	H723	R644	D575	Y503
T1481	E1406	K1407	K1236	I1082	I1083	R1019	G942	Q871	H724	S645	N576	Q503
M1482	K1407	T1327	E1237	I1083	I1083	R1019	M943	S872	S725	N646	K577	C508
W1483	T1412	Y1328	I1239	K1154	R1086	M1022	N944	E873	A726	S647	K578	W509
E1485	P1413	V1332	Y1240	D1089	D1089	Q1023	R945	C874	T727	I650	M579	Y510
R1486	F1413	F1333	I1241	M1090	M1090	A1025	Q946	R875	Y730	N653	E580	E511
T1487	E1416	D1334	Y1245	W1091	W1091	V1027	S947	E876	Y731	L854	F584	K514
D1417	D1417	Y1335	Y1245	Y1159	L1094	V1027	I950	L879	K732	L854	Y585	I517
T1488	K1418	L1338	R1248	E1160	G1095	L1028	F953	P880	K735	K655	L586	I517
Y1489	K1419	S1420	R1248	E1160	P1096	F1031	V954	L881	V736	K656	T587	A518
T1490	S1421	K1343	R1252	D1165	M1097	F1032	A955	T883	L737	L657	L588	I519
A1492	S1421	K1344	E1259	Q1167	K1098	M1033	C956	K884	N738	E659	P589	E520
Y1493	Q1424	R1345	E1259	Y1168	I1099	D1034	M957	Q885	F739	V660	G590	E521
T1494	Y1425	A1346	H1267	K1169	K1100	Q1035	A959	L886	Y740	D661	T591	V522
F1495	F1429	S1347	A1287	F1101	F1101	A1036	L960	S887	A742	G662	K592	T523
G1497	K1432	I1352	L1271	P1103	P1103	S1037	L961	L890	N743	G663	M593	R524
F1502	P1433	R1357	Q1272	S1104	S1104	E1039	Q962	D891	A744	V666	E594	C525
K1505	V1434	P1358	Q1272	M1105	M1105	E1039	Q963	D892	D745	K667	E596	H526
Q1506	M1435	Q1359	D1275	V1106	V1106	Q1041	M964	N825	D746	F668	E597	I527
I1507	P1438	P1360	K1276	G1107	G1107	L1042	D965	K896	S747	L669	K598	R528
S1508	P1438	E1361	P1277	R1181	P1108	W1043	D966	K896	S748	Q670	E599	F529
S1513	S1439	Y1362	P1280	K1183	I1109	W1044	S967	H898	K749	L673	L600	T530
P1514	S1440	Y1367	P1280	K1184	I1110	M1045	Y969	E900	L752	Q601	Q602	F531
L1515	K1442	Y1368	L1283	L1186	E1111	Y1046	S970	A901	L753	R533	A602	R532
E1516	D1443	G1369	Q1284	S1187	V1112	F1047	H971	S902	F754	S903	S535	R534
N1517	K1444	Q1370	R1285	G1107	T1114	Y972	H972	S903	N678	K604	S536	S536
A1518	P1445	G1371	D1286	R1181	T1115	I973	S974	Q904	L757	N605	Q537	Q537
I1519	V1446	F1372	D1287	L1196	P1116	T975	T975	L905	L760	L606	L606	E538
E1520	P1447	P1373	Y1288	S1198	V1117	F1053	F976	N908	L760	M681	V607	T539
E1523	E1448	S1374	Y1289	S1199	E1119	T1055	R979	I909	F764	M683	T508	R540
L1524	Q1449	F1375	Y1290	L1200	H1056	H1056	R979	L910	R765	S684	F609	D541
T1525	L1451	R1377	Y1291	L1201	E1057	E1057	I982	L913	F766	D685	T510	K542
N1526	N1452	R1377	T1292	L1204	S1058	S1058	I982	D914	I768	S686	P611	S543
E1527	Y1453	K1379	Q1293	L1205	L1059	L1059	M987	T921	Q769	Y689	S512	E544
R1528	Y1454	R1384	Q1294	L1206	Q1060	Q1060	E988	A922	S770	L692	R545	A546
I1529	E1455	E1295	E1295	Y1207	L1061	E1062	T989	S946	R771	V693	T616	F550
	G1385	G1385	E1298	R1208	F1128	T1063		V923	V772		F620	A550
											A623	F551
											T624	V552
											L625	



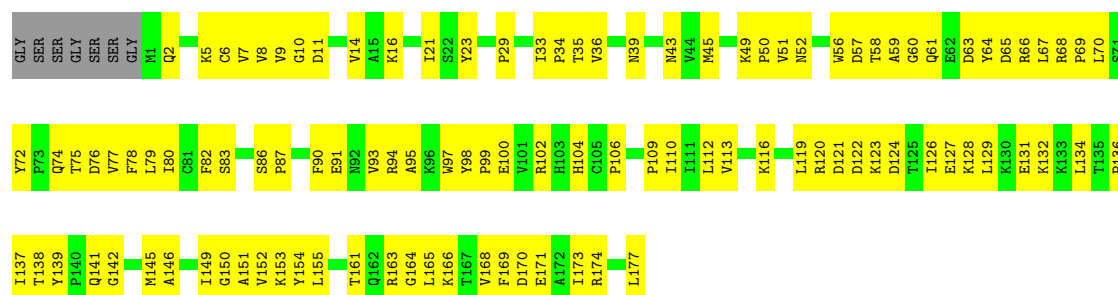
• Molecule 3: Ras-related C3 botulinum toxin substrate 1

Chain C: 40% 56%



• Molecule 3: Ras-related C3 botulinum toxin substrate 1

Chain F: 38% 58%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	128824	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	452.2, 452.2, 452.2	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.33, 1.33, 1.33	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	0.28	0/1641	0.49	0/2218
1	D	0.28	0/1641	0.49	0/2218
2	B	0.31	0/13722	0.49	0/18514
2	E	0.31	0/13722	0.49	0/18514
3	C	0.31	0/1415	0.47	0/1924
3	F	0.31	0/1415	0.47	0/1924
All	All	0.31	0/33556	0.49	0/45312

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	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	541	GLN	Peptide
1	D	541	GLN	Peptide

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1608	0	1617	111	0
1	D	1608	0	1617	109	0
2	B	13436	0	13516	771	0
2	E	13436	0	13516	775	0
3	C	1385	0	1407	86	0
3	F	1385	0	1407	90	0
All	All	32858	0	33080	1889	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 1889 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)
2:B:95:LEU:HA	2:B:98:TRP:HD1	1.38	0.89
2:E:144:LEU:HD13	2:E:147:LYS:HE2	1.55	0.89
2:B:1526:ASN:OD1	2:B:1596:GLN:NE2	2.07	0.88
2:E:1526:ASN:OD1	2:E:1596:GLN:NE2	2.07	0.87
2:B:144:LEU:HD13	2:B:147:LYS:HE2	1.55	0.87

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	196/733 (27%)	180 (92%)	16 (8%)	0	100	100
1	D	196/733 (27%)	180 (92%)	16 (8%)	0	100	100
2	B	1640/1648 (100%)	1530 (93%)	110 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	1640/1648 (100%)	1529 (93%)	111 (7%)	0	100	100
3	C	175/184 (95%)	165 (94%)	10 (6%)	0	100	100
3	F	175/184 (95%)	165 (94%)	10 (6%)	0	100	100
All	All	4022/5130 (78%)	3749 (93%)	273 (7%)	0	100	100

There are no Ramachandran outliers to report.

### 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	183/664 (28%)	182 (100%)	1 (0%)	86	90
1	D	183/664 (28%)	182 (100%)	1 (0%)	86	90
2	B	1495/1497 (100%)	1486 (99%)	9 (1%)	84	88
2	E	1495/1497 (100%)	1486 (99%)	9 (1%)	84	88
3	C	153/157 (98%)	151 (99%)	2 (1%)	65	77
3	F	153/157 (98%)	151 (99%)	2 (1%)	65	77
All	All	3662/4636 (79%)	3638 (99%)	24 (1%)	80	87

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	157	ARG
2	E	811	LYS
2	E	644	ARG
2	E	935	ARG
2	B	935	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	1526	ASN
2	E	1577	GLN
3	F	2	GLN
2	B	1526	ASN
2	B	1517	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 [i](#)

There are no chain breaks in this entry.

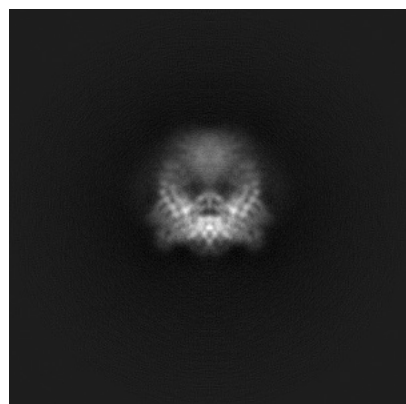
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60147. These allow visual inspection of the internal detail of the map and identification of artifacts.

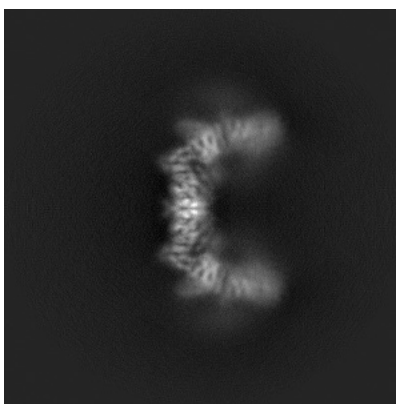
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

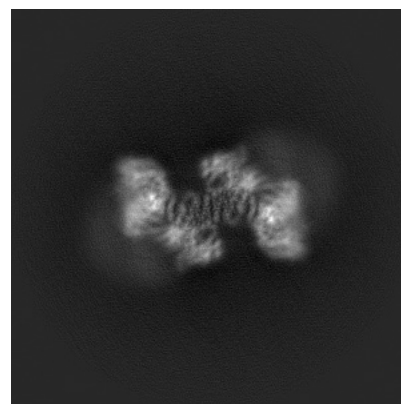
#### 6.1.1 Primary map



X

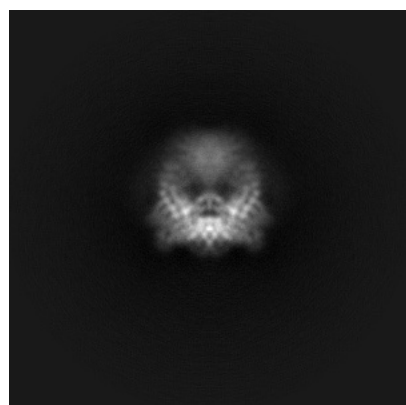


Y

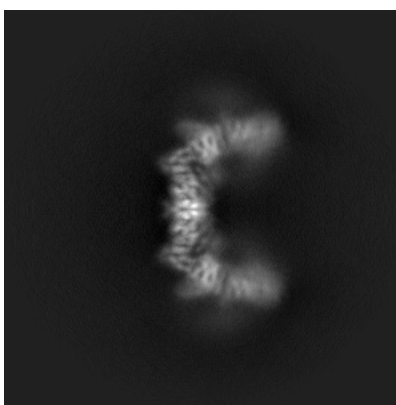


Z

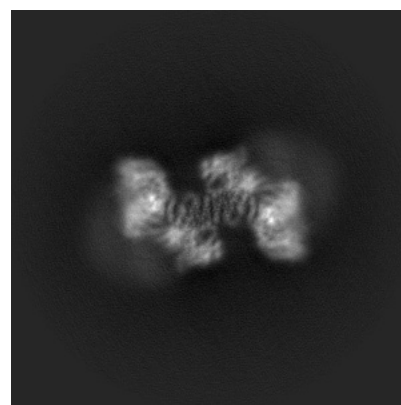
#### 6.1.2 Raw map



X



Y



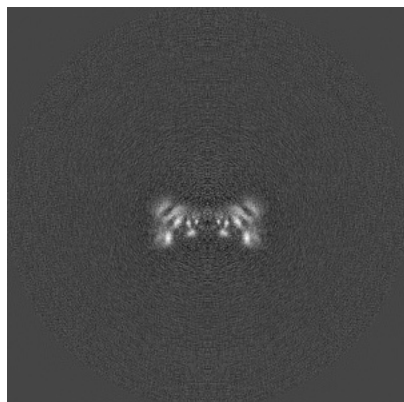
Z

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

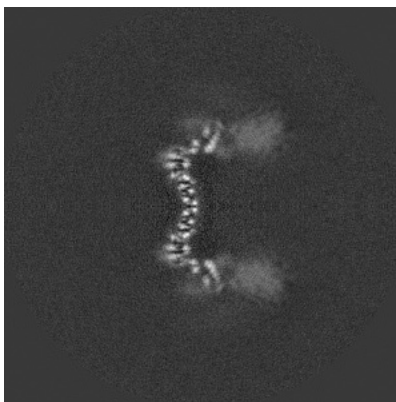


## 6.2 Central slices [i](#)

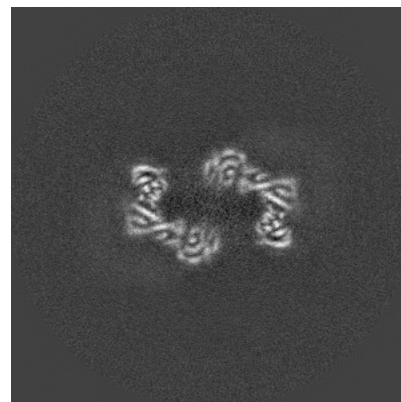
### 6.2.1 Primary map



X Index: 170

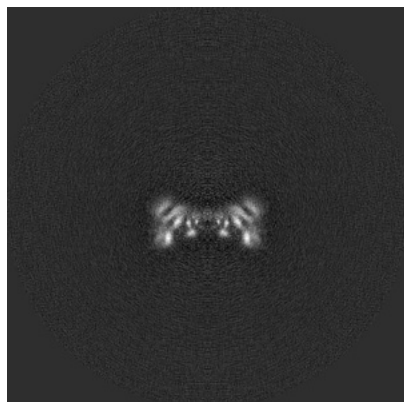


Y Index: 170

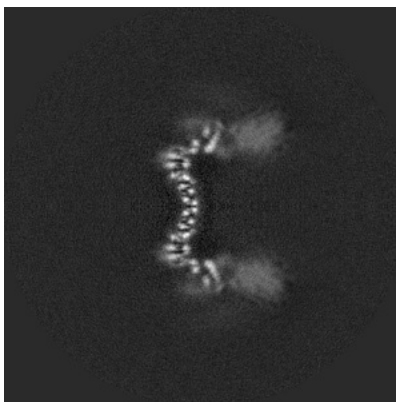


Z Index: 170

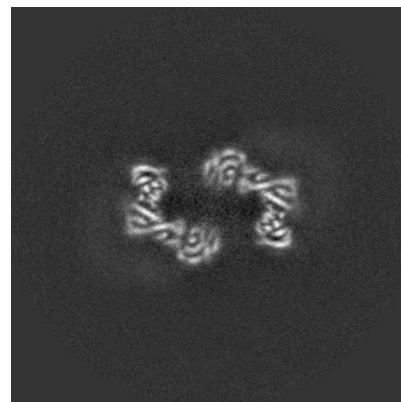
### 6.2.2 Raw map



X Index: 170



Y Index: 170

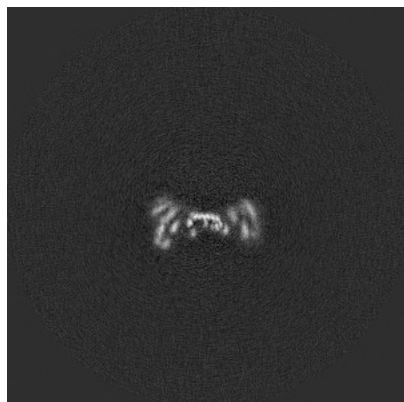


Z Index: 170

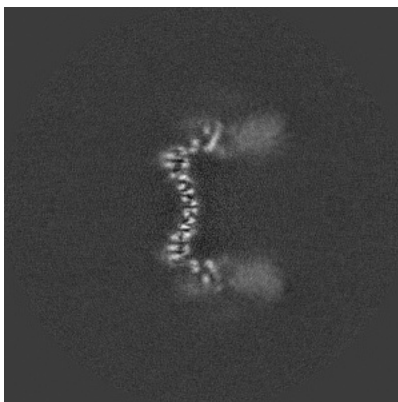
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

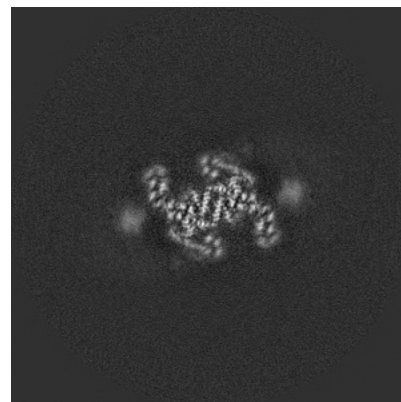
### 6.3.1 Primary map



X Index: 167

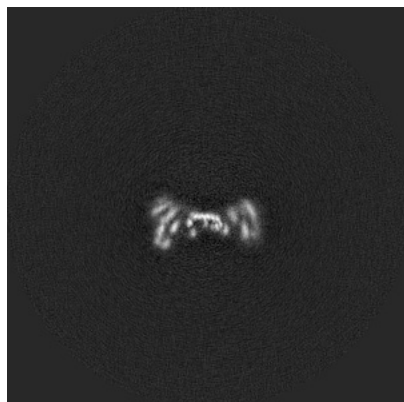


Y Index: 169

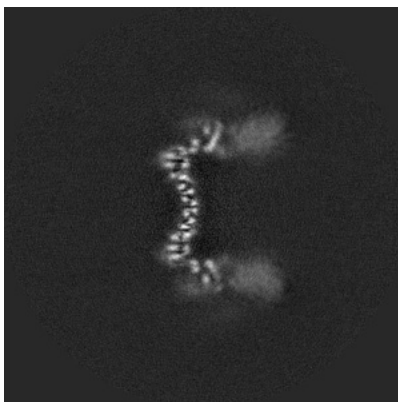


Z Index: 154

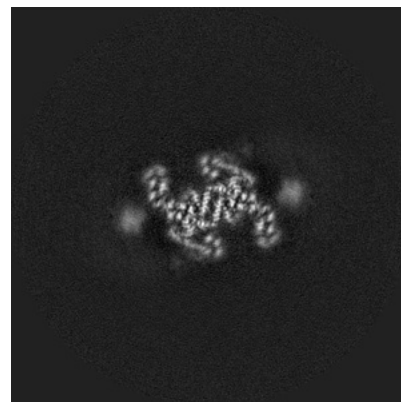
### 6.3.2 Raw map



X Index: 167



Y Index: 169

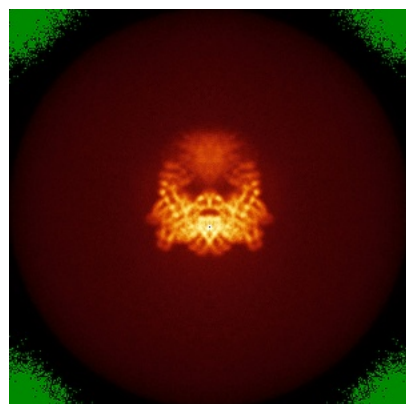


Z Index: 154

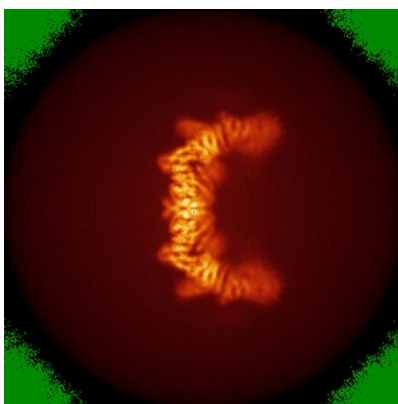
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



X



Y

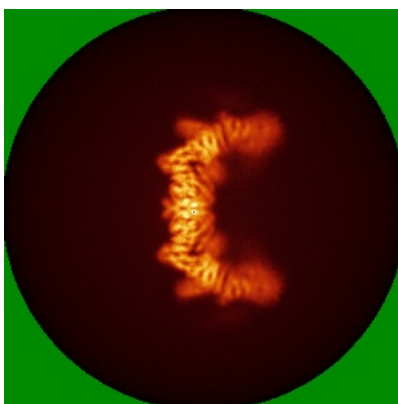


Z

### 6.4.2 Raw map



X



Y

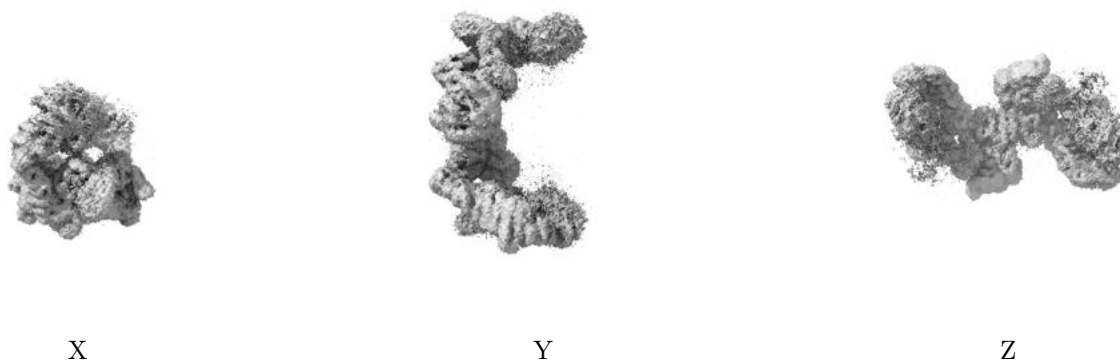


Z

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.

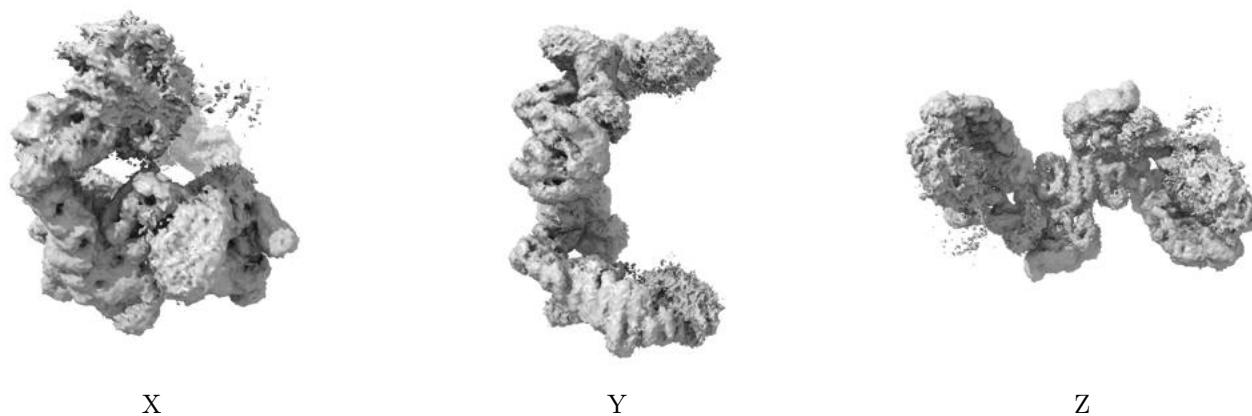
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

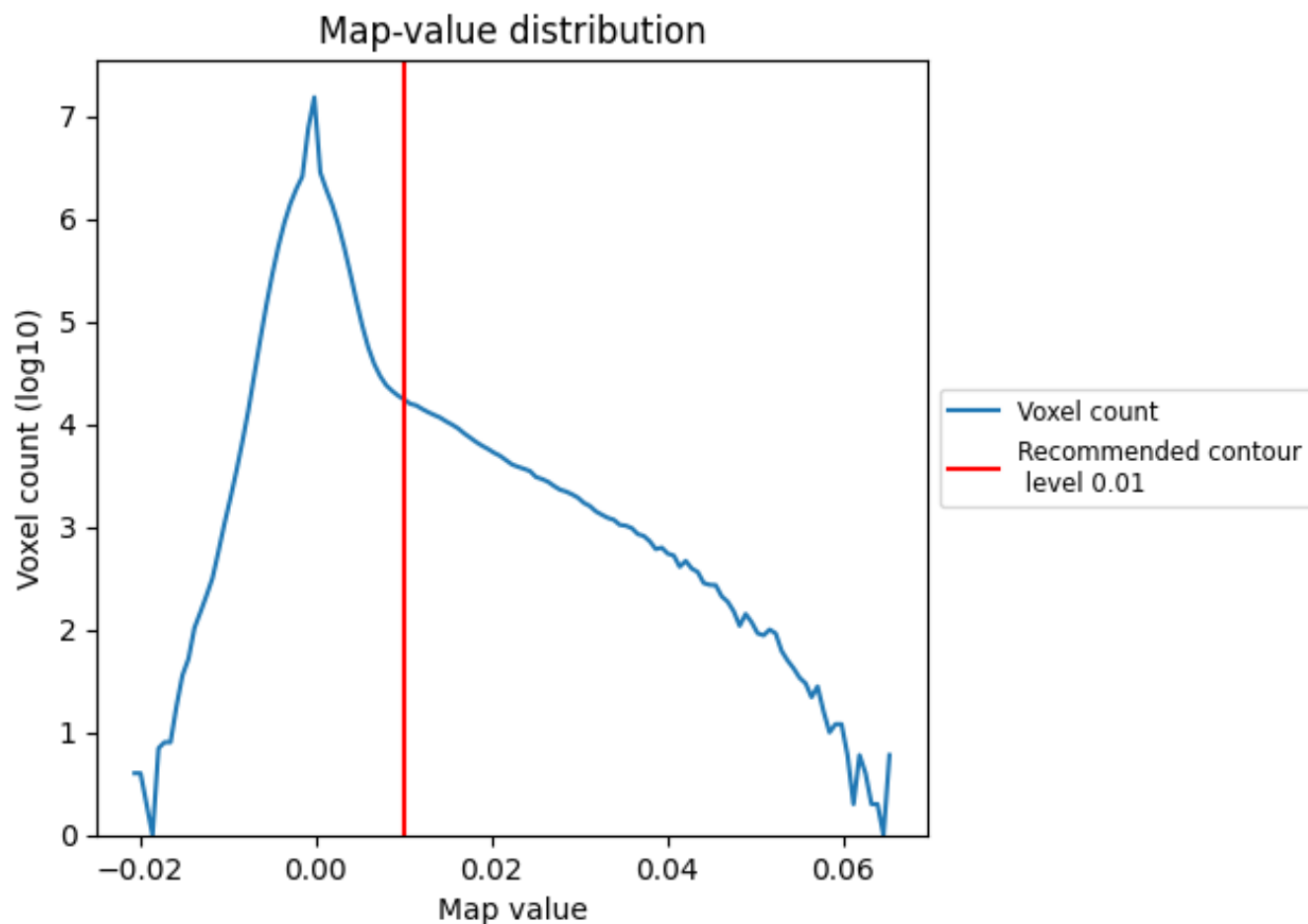
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

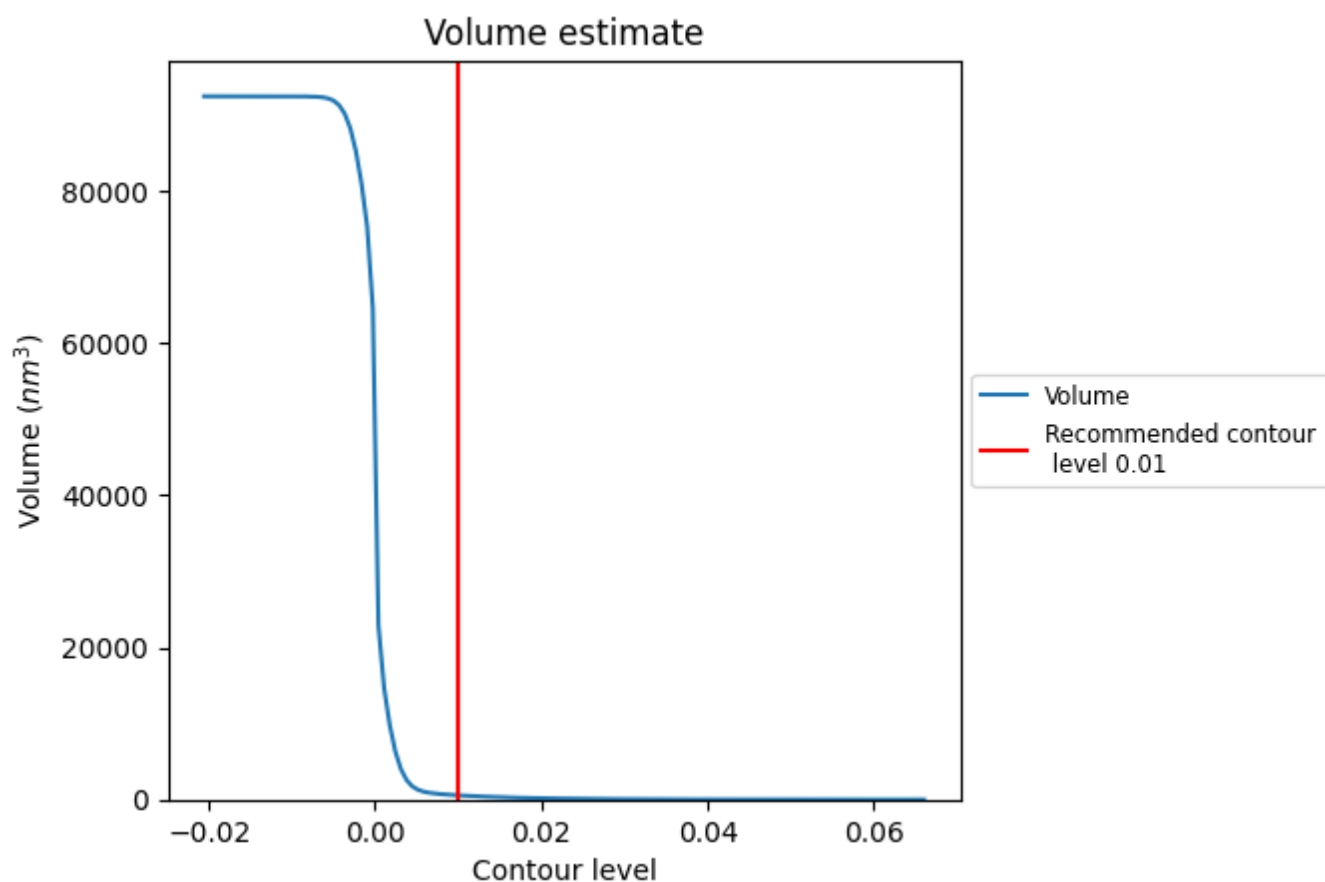
This section contains the results of statistical analysis of the map.

### 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.

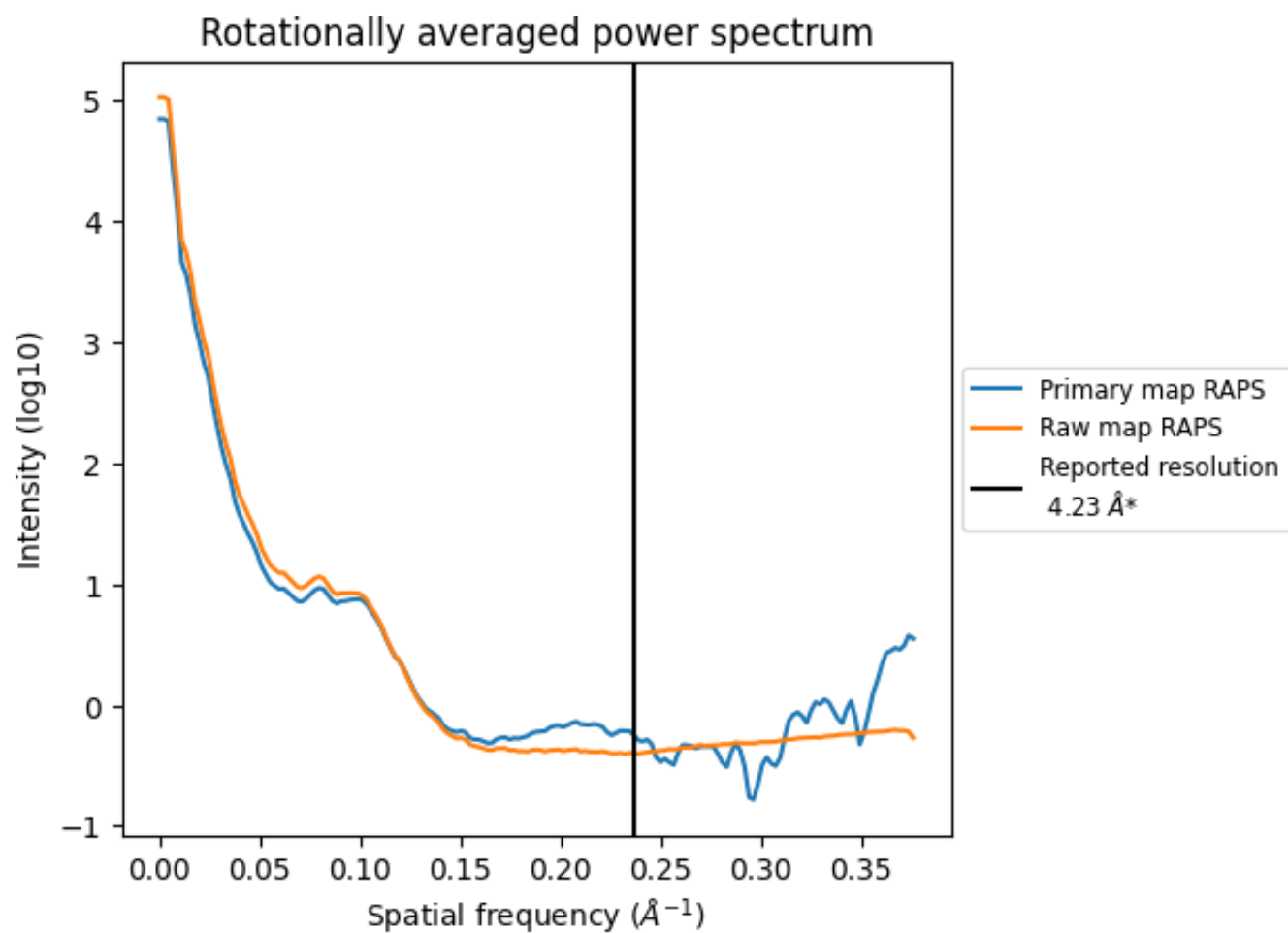
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 555  $\text{nm}^3$ ; this corresponds to an approximate mass of 502 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 ⓘ



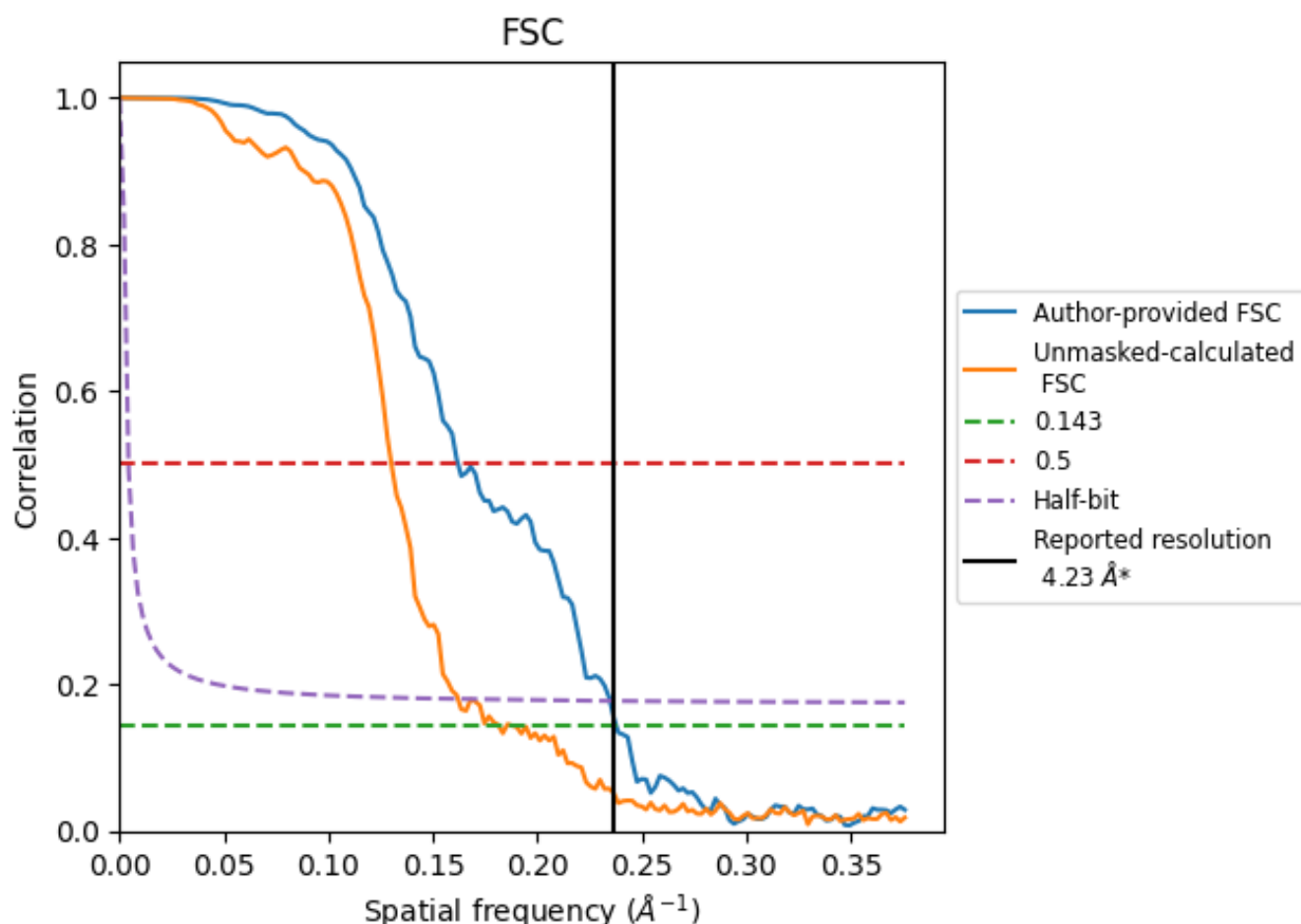
\*Reported resolution corresponds to spatial frequency of 0.236 Å<sup>-1</sup>



## 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 0.236  $\text{\AA}^{-1}$



## 8.2 Resolution estimates [i](#)

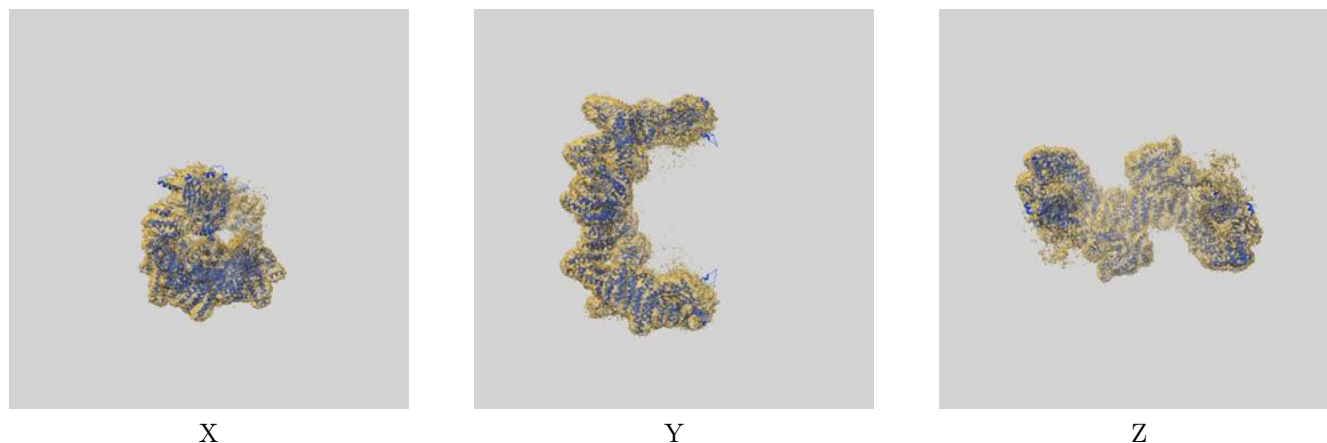
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.23	-	-
Author-provided FSC curve	4.21	6.17	4.26
Unmasked-calculated*	5.51	7.68	6.17

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.51 differs from the reported value 4.23 by more than 10 %

## 9 Map-model fit [i](#)

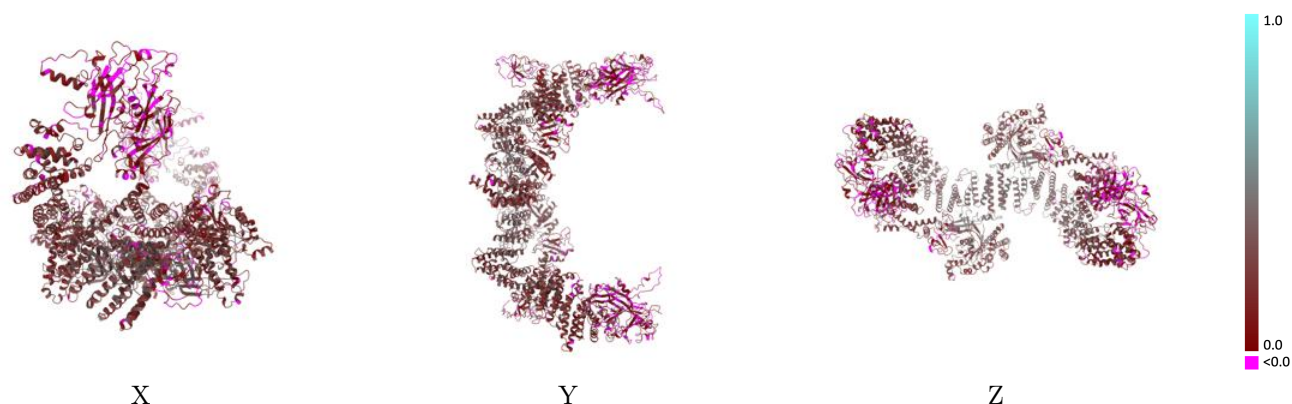
This section contains information regarding the fit between EMDB map EMD-60147 and PDB model 8ZJJ. Per-residue inclusion information can be found in section [3](#) on page [5](#).

### 9.1 Map-model overlay [i](#)



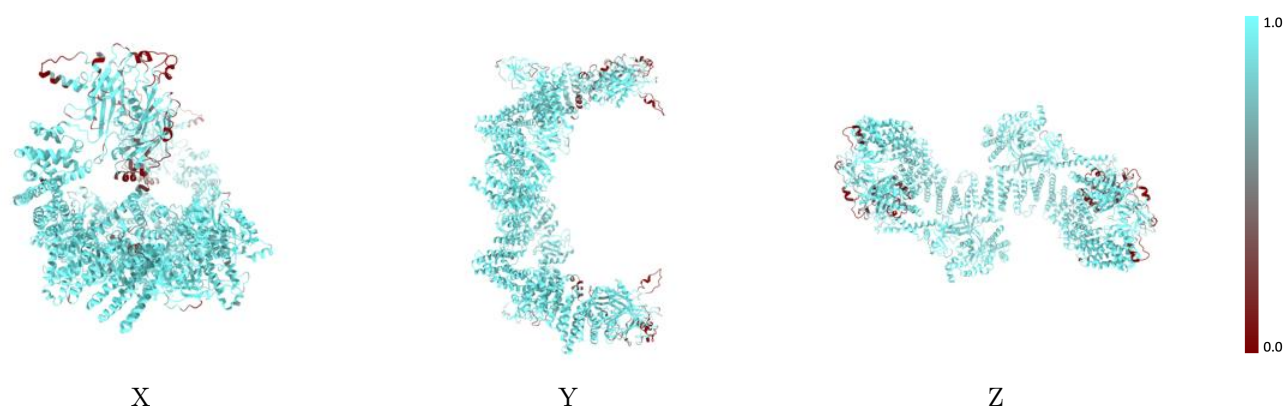
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



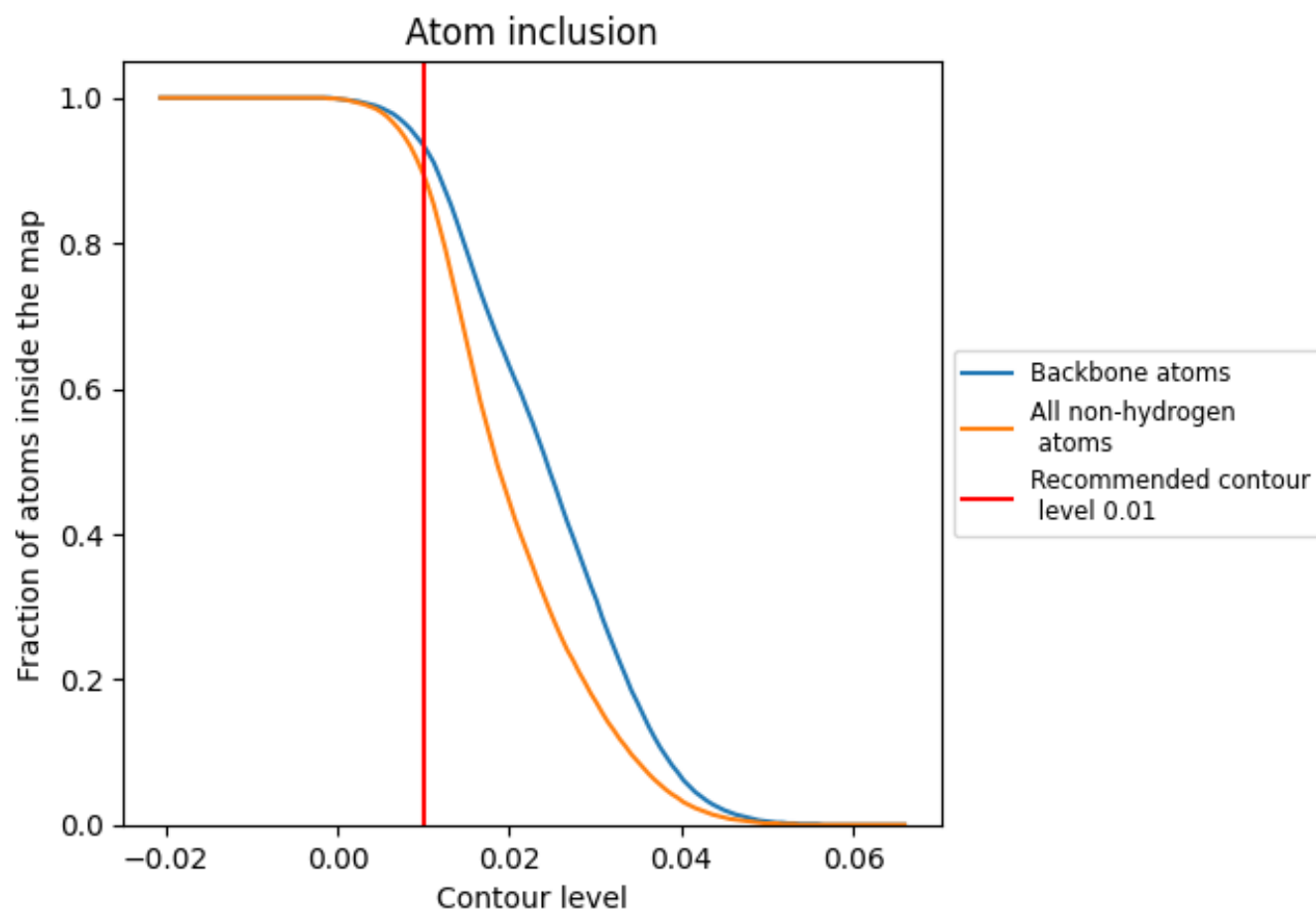
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

## 9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8950	<div><div></div></div> 0.2110
A	<div><div></div></div> 0.9390	<div><div></div></div> 0.1680
B	<div><div></div></div> 0.8870	<div><div></div></div> 0.2120
C	<div><div></div></div> 0.9630	<div><div></div></div> 0.2610
D	<div><div></div></div> 0.9160	<div><div></div></div> 0.1650
E	<div><div></div></div> 0.8810	<div><div></div></div> 0.2100
F	<div><div></div></div> 0.9640	<div><div></div></div> 0.2600

1.0

0.0

<0.0