



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:34 AM UTC

PDB ID : 8J0O / pdb_00008j0o
EMDB ID : EMD-35907
Title : cryo-EM structure of human EMC and VDAC
Authors : Li, M.; Zhang, C.; Wu, J.; Lei, M.
Deposited on : 2023-04-11
Resolution : 3.32 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
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

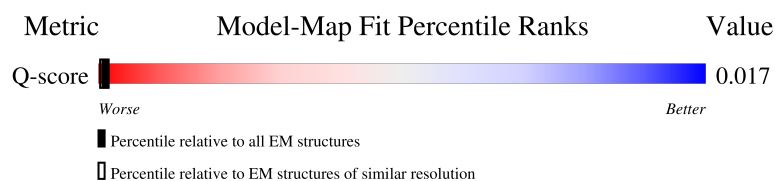
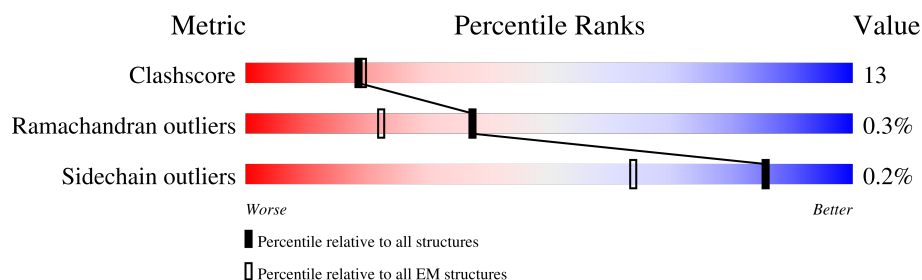
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.32 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	14518 (2.82 - 3.82)

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	993	18% 72% 23% ..
2	B	297	31% 73% 26%
3	C	261	29% 75% 23% ..
4	D	183	18% 61% 25% 15%

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Mol	Chain	Length	Quality of chain
5	E	131	
6	F	110	
7	G	242	
8	H	210	
9	J	207	
10	K	283	
11	L	3	
11	M	3	
11	N	3	

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 20986 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 ER membrane protein complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	949	Total	C	N	O	S	0	0
			7544	4839	1290	1390	25		

- Molecule 2 is a protein called ER membrane protein complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	296	Total	C	N	O	S	0	0
			2438	1530	431	463	14		

- Molecule 3 is a protein called ER membrane protein complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	258	Total	C	N	O	S	0	0
			2086	1353	340	378	15		

- Molecule 4 is a protein called ER membrane protein complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	156	Total	C	N	O	S	0	0
			1222	798	197	212	15		

- Molecule 5 is a protein called ER membrane protein complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	103	Total	C	N	O	S	0	0
			817	528	142	144	3		

- Molecule 6 is a protein called ER membrane protein complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	100	Total	C	N	O	S	0	0
			781	526	127	126	2		

- Molecule 7 is a protein called ER membrane protein complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	139	Total	C	N	O	S	0	0
			1114	729	186	192	7		

- Molecule 8 is a protein called ER membrane protein complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	195	Total	C	N	O	S	0	0
			1559	984	272	291	12		

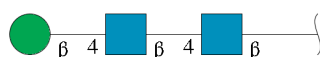
- Molecule 9 is a protein called ER membrane protein complex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	149	Total	C	N	O	S	0	0
			1146	710	209	224	3		

- Molecule 10 is a protein called Voltage-dependent anion-selective channel protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	282	Total	C	N	O	S	0	0
			2162	1367	365	426	4		

- Molecule 11 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

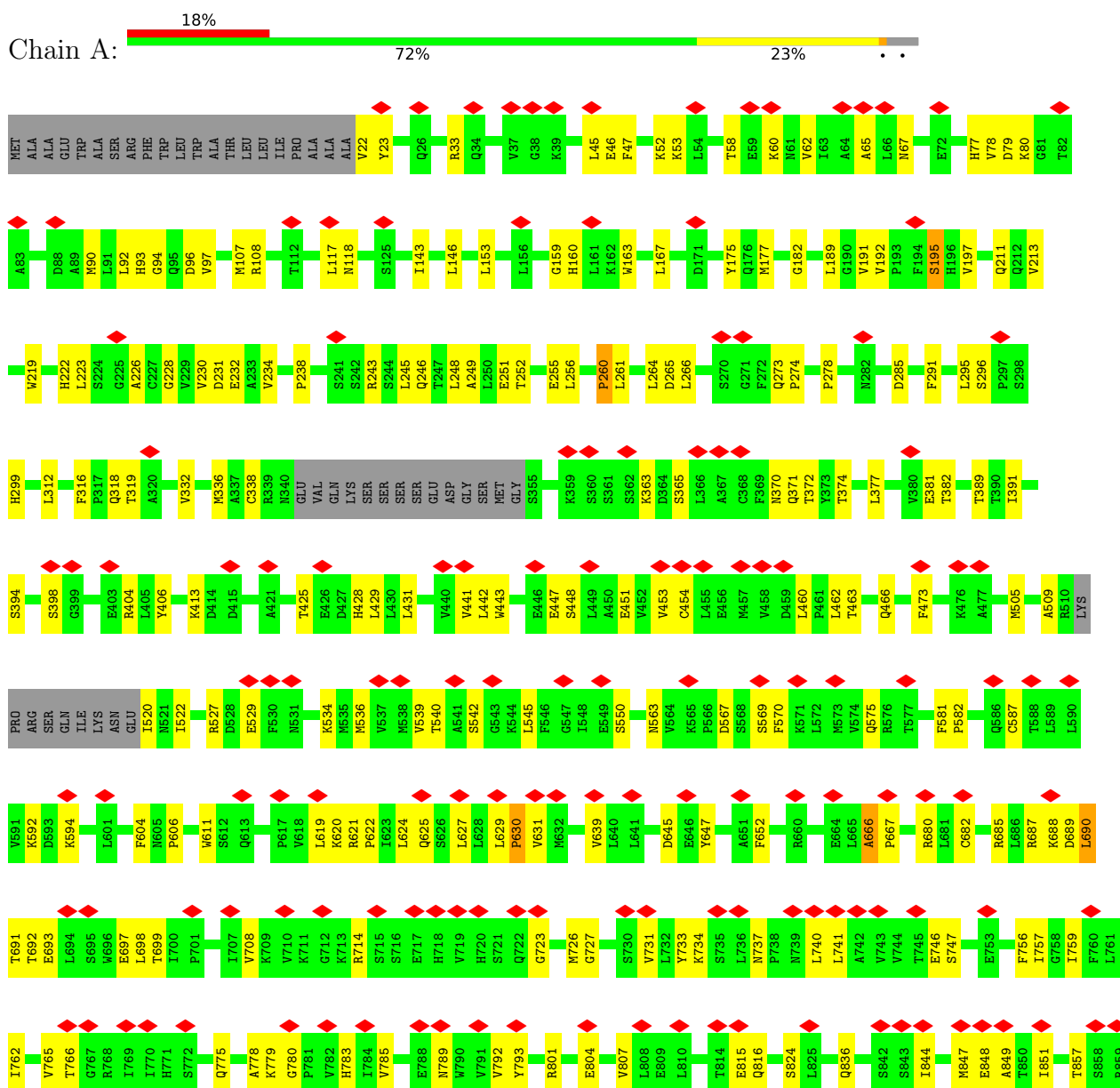


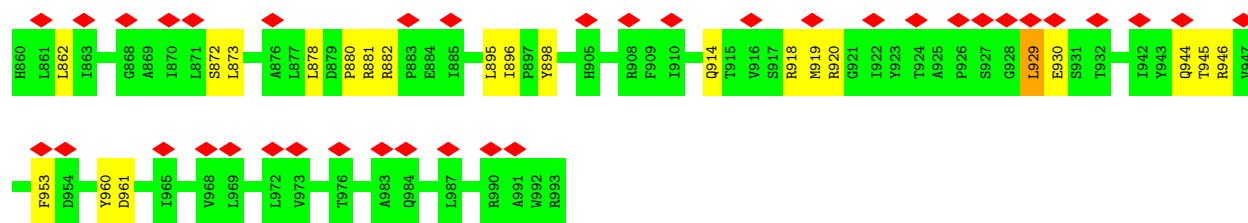
Mol	Chain	Residues	Atoms				AltConf	Trace
11	L	3	Total	C	N	O	0	0
			39	22	2	15		
11	M	3	Total	C	N	O	0	0
			39	22	2	15		
11	N	3	Total	C	N	O	0	0
			39	22	2	15		

3 Residue-property plots

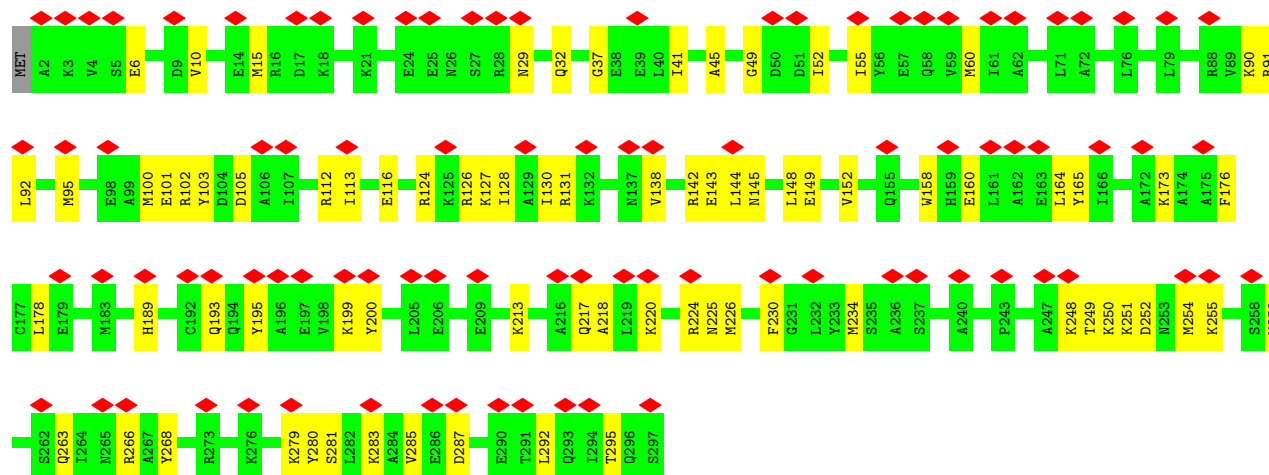
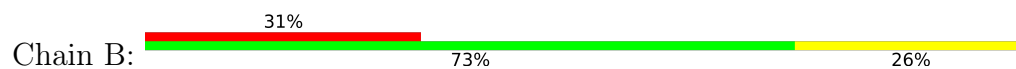
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: ER membrane protein complex subunit 1

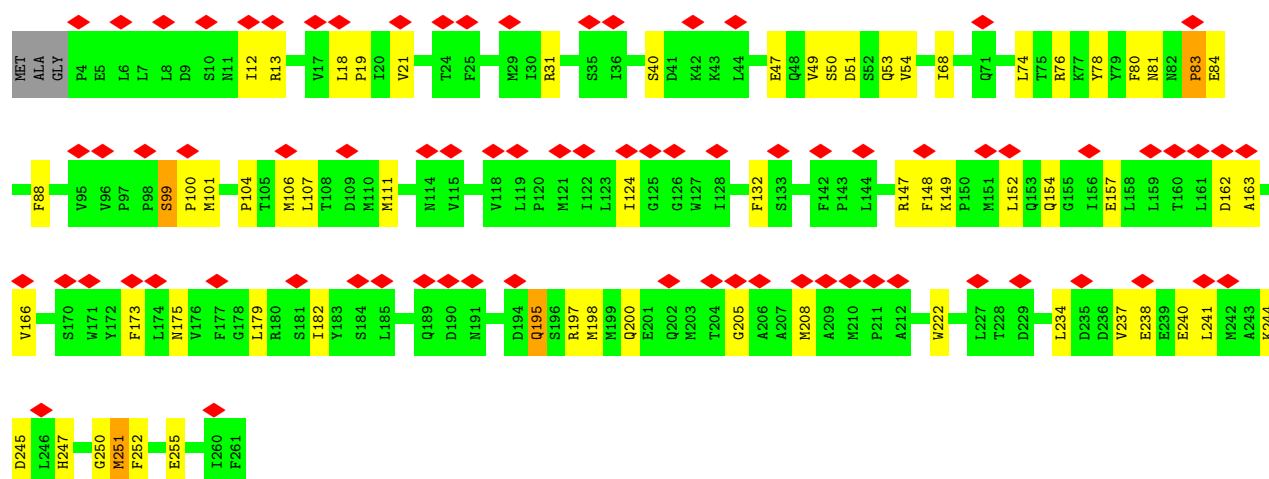
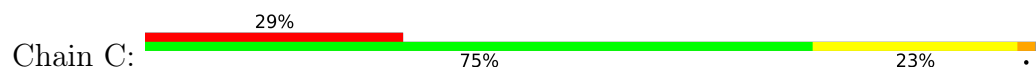




• Molecule 2: ER membrane protein complex subunit 2

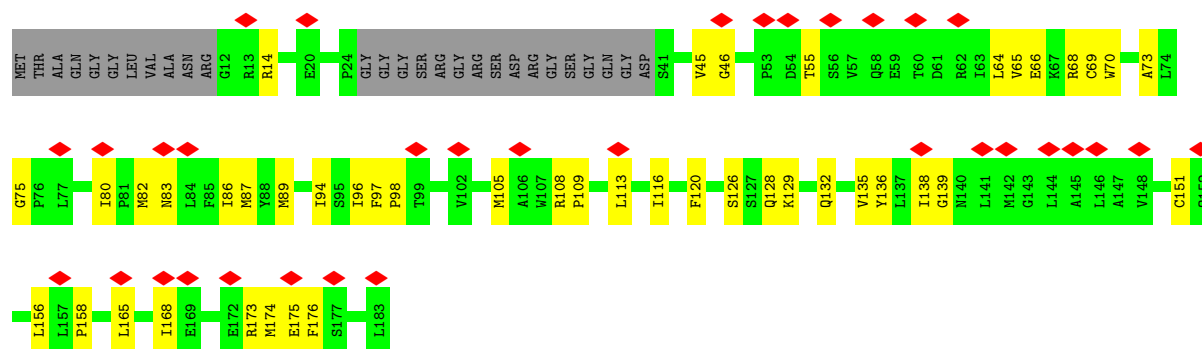


• Molecule 3: ER membrane protein complex subunit 3

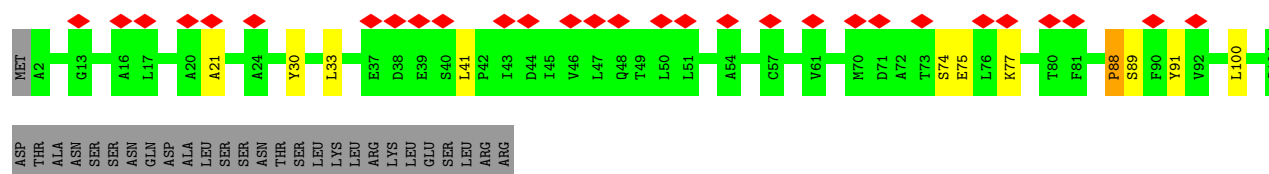


• Molecule 4: ER membrane protein complex subunit 4

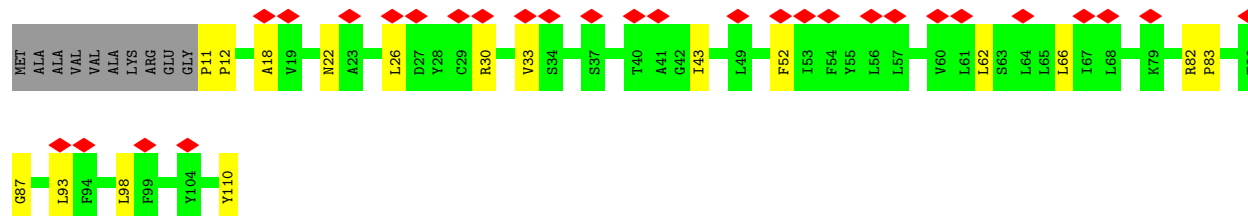
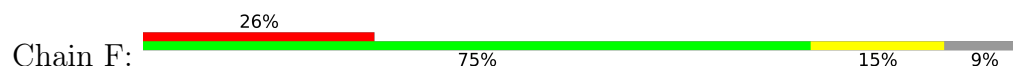




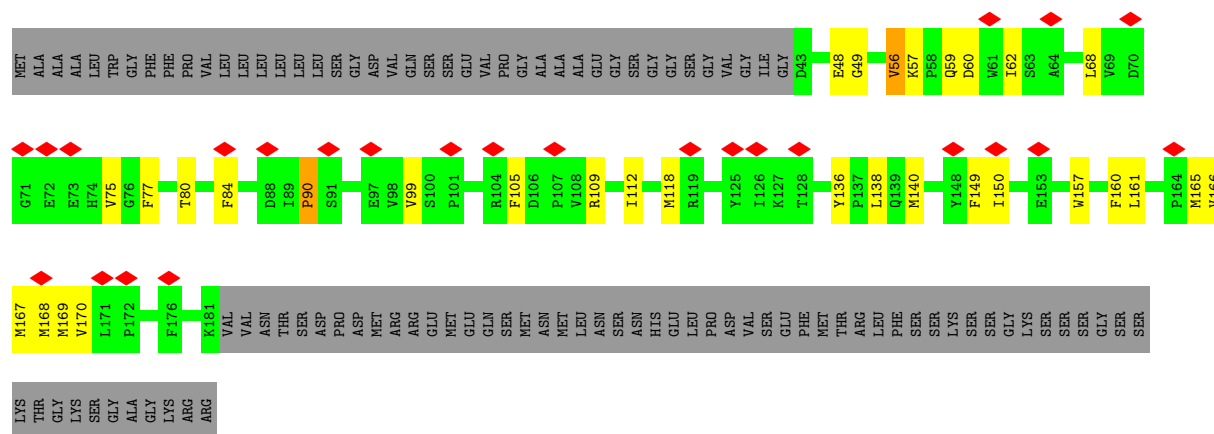
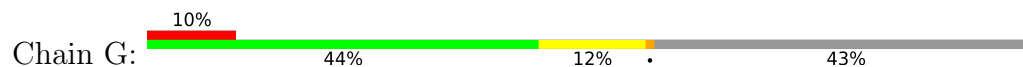
• Molecule 5: ER membrane protein complex subunit 5



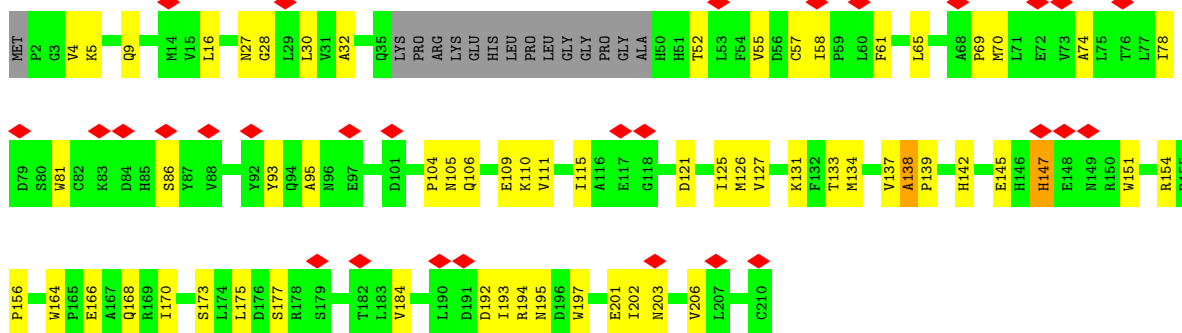
• Molecule 6: ER membrane protein complex subunit 6



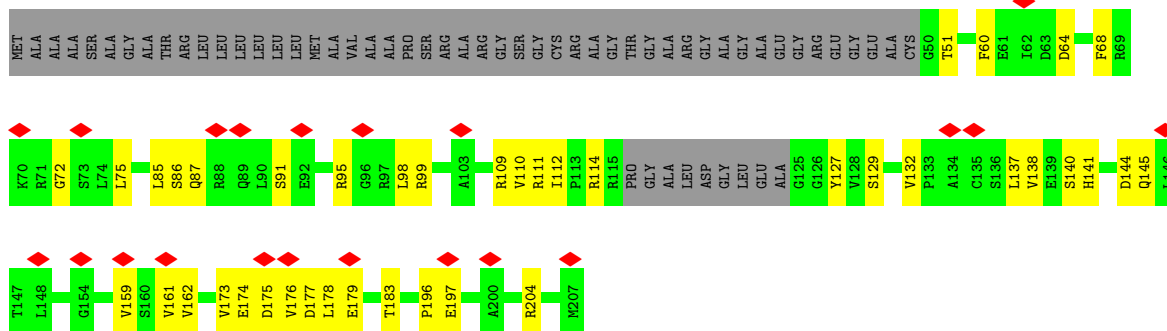
• Molecule 7: ER membrane protein complex subunit 7



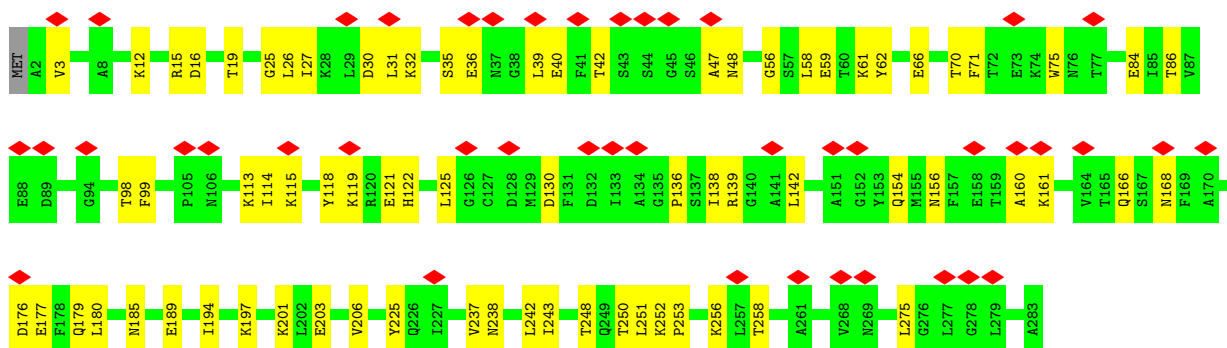
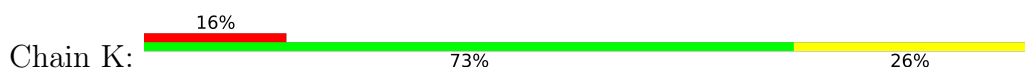
• Molecule 8: ER membrane protein complex subunit 8



• Molecule 9: ER membrane protein complex subunit 10



• Molecule 10: Voltage-dependent anion-selective channel protein 1



• Molecule 11: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 11: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 11: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	455504	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)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.334	Depositor
Minimum map value	-0.526	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.154	Depositor
Map size (Å)	383.68002, 383.68002, 383.68002	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA

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	1.10	3/7716 (0.0%)	0.62	5/10479 (0.0%)
2	B	0.16	0/2482	0.40	0/3336
3	C	2.11	1/2135 (0.0%)	0.95	3/2889 (0.1%)
4	D	0.19	0/1251	0.45	0/1691
5	E	0.58	1/838 (0.1%)	0.51	1/1134 (0.1%)
6	F	0.15	0/803	0.35	0/1089
7	G	0.49	1/1146 (0.1%)	0.53	1/1556 (0.1%)
8	H	0.18	0/1600	0.44	1/2179 (0.0%)
9	J	0.16	0/1165	0.41	0/1580
10	K	0.16	0/2203	0.43	0/2976
All	All	0.96	6/21339 (0.0%)	0.58	11/28909 (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

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	83	PRO	N-CD	96.78	2.83	1.47
1	A	630	PRO	N-CD	91.85	2.76	1.47
1	A	260	PRO	N-CD	23.58	1.80	1.47
5	E	88	PRO	N-CD	16.07	1.70	1.47
7	G	90	PRO	N-CD	14.97	1.68	1.47

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	83	PRO	N-CD-CG	-32.79	54.01	103.20
3	C	83	PRO	CA-N-CD	-31.23	68.27	112.00
1	A	630	PRO	CA-N-CD	-31.06	68.51	112.00
1	A	630	PRO	N-CD-CG	-27.02	62.67	103.20
1	A	260	PRO	CA-N-CD	-14.99	91.02	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	929	LEU	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	7544	0	7597	192	0
2	B	2438	0	2391	86	0
3	C	2086	0	2115	96	0
4	D	1222	0	1254	53	0
5	E	817	0	812	18	0
6	F	781	0	810	13	0
7	G	1114	0	1139	30	0
8	H	1559	0	1493	50	0
9	J	1146	0	1121	34	0
10	K	2162	0	2133	57	0
11	L	39	0	34	0	0
11	M	39	0	34	0	0
11	N	39	0	34	1	0
All	All	20986	0	20967	546	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 13.

The worst 5 of 546 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)
7:G:90:PRO:N	7:G:90:PRO:CD	1.68	1.49
2:B:251:LYS:HA	2:B:254:MET:CE	1.43	1.45
5:E:88:PRO:N	5:E:88:PRO:CD	1.70	1.38
2:B:251:LYS:CA	2:B:254:MET:HE3	1.52	1.35
2:B:224:ARG:NH1	3:C:251:MET:SD	1.99	1.35

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	943/993 (95%)	835 (88%)	104 (11%)	4 (0%)	30	60
2	B	294/297 (99%)	280 (95%)	14 (5%)	0	100	100
3	C	256/261 (98%)	234 (91%)	21 (8%)	1 (0%)	30	60
4	D	152/183 (83%)	142 (93%)	10 (7%)	0	100	100
5	E	101/131 (77%)	98 (97%)	3 (3%)	0	100	100
6	F	98/110 (89%)	95 (97%)	3 (3%)	0	100	100
7	G	137/242 (57%)	122 (89%)	14 (10%)	1 (1%)	18	49
8	H	191/210 (91%)	172 (90%)	18 (9%)	1 (0%)	24	56
9	J	145/207 (70%)	136 (94%)	9 (6%)	0	100	100
10	K	280/283 (99%)	259 (92%)	21 (8%)	0	100	100
All	All	2597/2917 (89%)	2373 (91%)	217 (8%)	7 (0%)	37	66

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	226	ALA
1	A	666	ALA
3	C	99	SER

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Mol	Chain	Res	Type
8	H	138	ALA
1	A	195	SER

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	837/872 (96%)	834 (100%)	3 (0%)	84	83
2	B	254/255 (100%)	254 (100%)	0	100	100
3	C	234/235 (100%)	233 (100%)	1 (0%)	84	83
4	D	133/149 (89%)	133 (100%)	0	100	100
5	E	86/112 (77%)	86 (100%)	0	100	100
6	F	79/85 (93%)	79 (100%)	0	100	100
7	G	125/207 (60%)	125 (100%)	0	100	100
8	H	171/182 (94%)	171 (100%)	0	100	100
9	J	127/158 (80%)	127 (100%)	0	100	100
10	K	229/230 (100%)	229 (100%)	0	100	100
All	All	2275/2485 (92%)	2271 (100%)	4 (0%)	85	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	222	HIS
1	A	563	ASN
1	A	625	GLN
3	C	195	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	242	ASN

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Mol	Chain	Res	Type
8	H	17	HIS
4	D	128	GLN
8	H	27	ASN
1	A	634	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

9 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
11	NAG	L	1	1,11	14,14,15	0.29	0	17,19,21	0.47	0
11	NAG	L	2	11	14,14,15	0.24	0	17,19,21	0.37	0
11	BMA	L	3	11	11,11,12	0.53	0	15,15,17	0.70	0
11	NAG	M	1	1,11	14,14,15	0.64	1 (7%)	17,19,21	0.84	1 (5%)
11	NAG	M	2	11	14,14,15	0.25	0	17,19,21	0.40	0
11	BMA	M	3	11	11,11,12	0.54	0	15,15,17	0.74	0
11	NAG	N	1	9,11	14,14,15	0.41	0	17,19,21	0.66	1 (5%)
11	NAG	N	2	11	14,14,15	0.43	0	17,19,21	1.33	2 (11%)
11	BMA	N	3	11	11,11,12	0.55	0	15,15,17	0.69	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	L	1	1,11	-	0/6/23/26	0/1/1/1
11	NAG	L	2	11	-	0/6/23/26	0/1/1/1
11	BMA	L	3	11	-	0/2/19/22	0/1/1/1
11	NAG	M	1	1,11	-	2/6/23/26	0/1/1/1
11	NAG	M	2	11	-	1/6/23/26	0/1/1/1
11	BMA	M	3	11	-	0/2/19/22	0/1/1/1
11	NAG	N	1	9,11	-	2/6/23/26	0/1/1/1
11	NAG	N	2	11	-	6/6/23/26	0/1/1/1
11	BMA	N	3	11	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	M	1	NAG	C1-C2	2.10	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	N	2	NAG	C2-N2-C7	4.59	129.05	122.90
11	M	1	NAG	C1-O5-C5	2.63	115.71	112.19
11	N	2	NAG	C1-C2-N2	2.10	113.74	110.43
11	N	1	NAG	C1-O5-C5	2.03	114.91	112.19

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

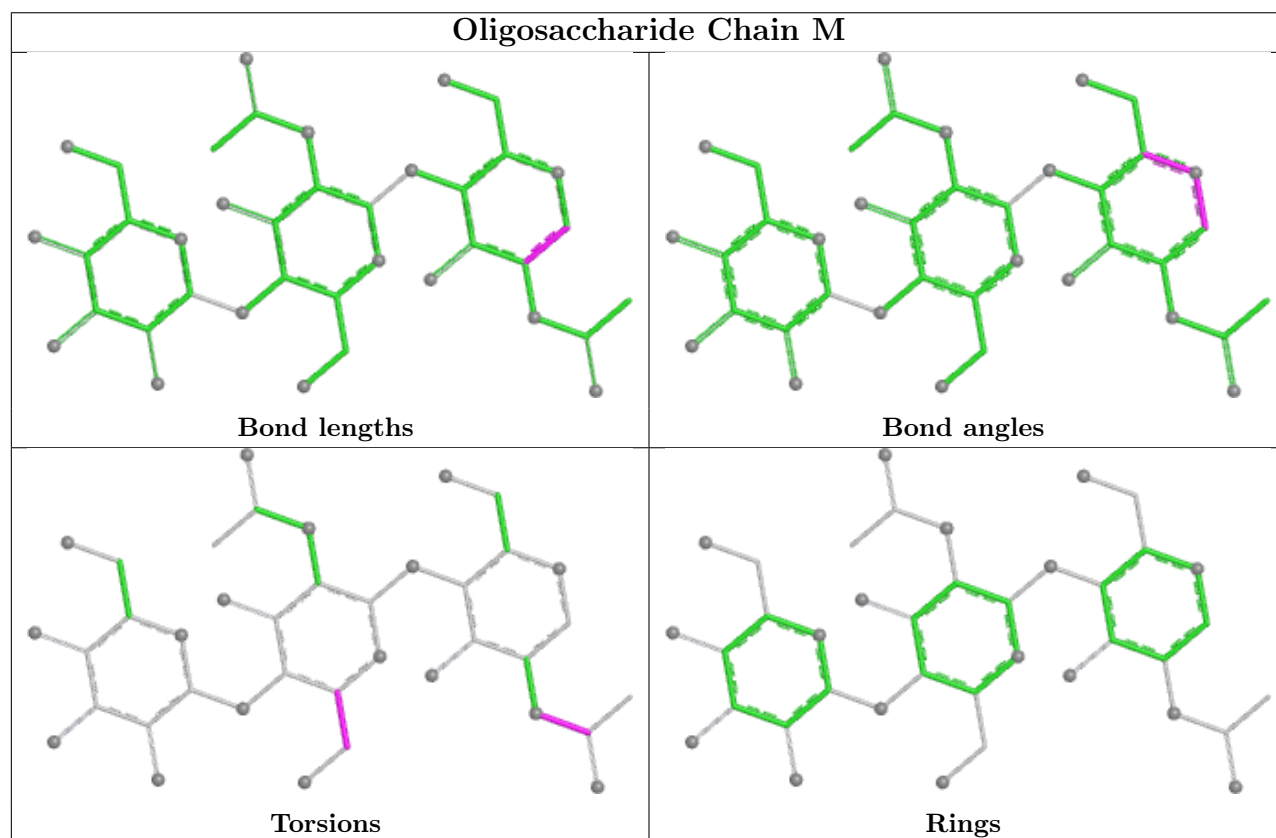
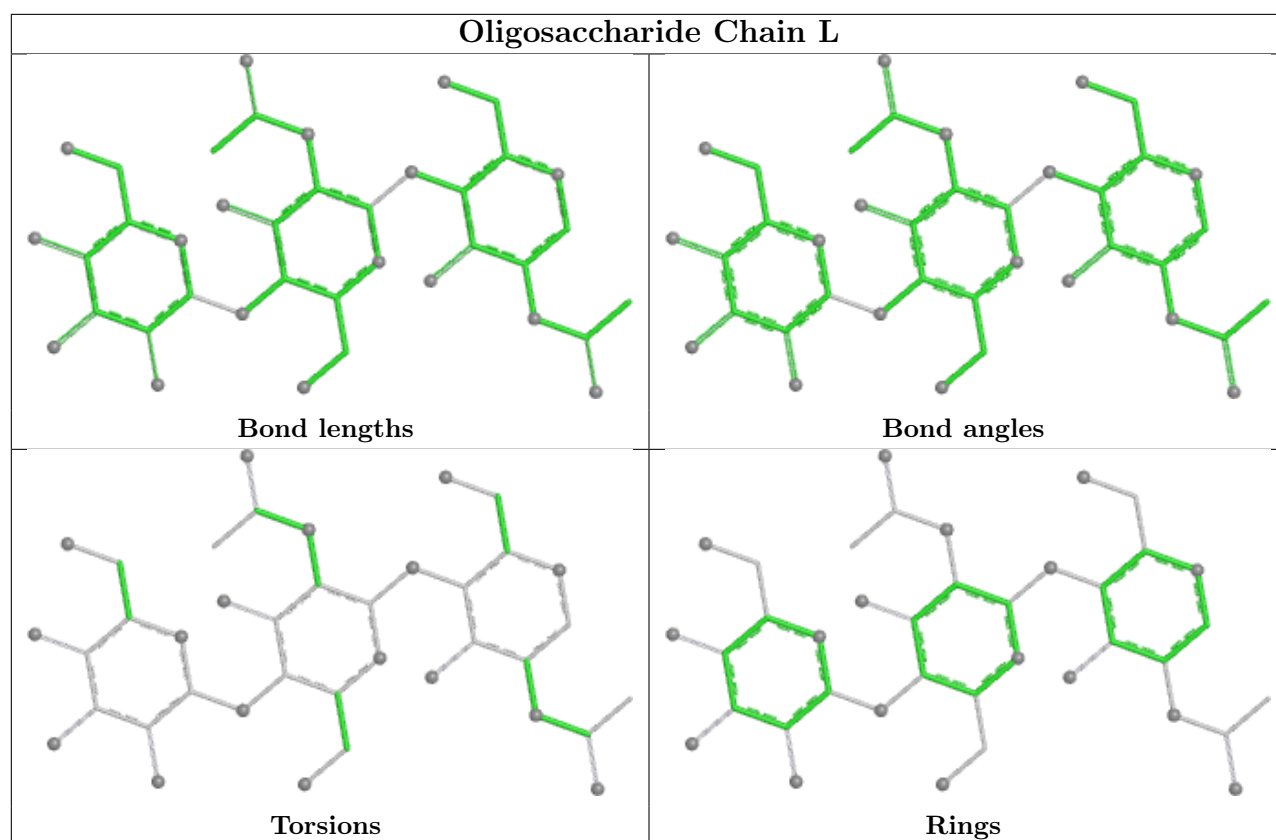
Mol	Chain	Res	Type	Atoms
11	N	2	NAG	O5-C5-C6-O6
11	N	2	NAG	C4-C5-C6-O6
11	M	1	NAG	C8-C7-N2-C2
11	M	1	NAG	O7-C7-N2-C2
11	N	2	NAG	C8-C7-N2-C2

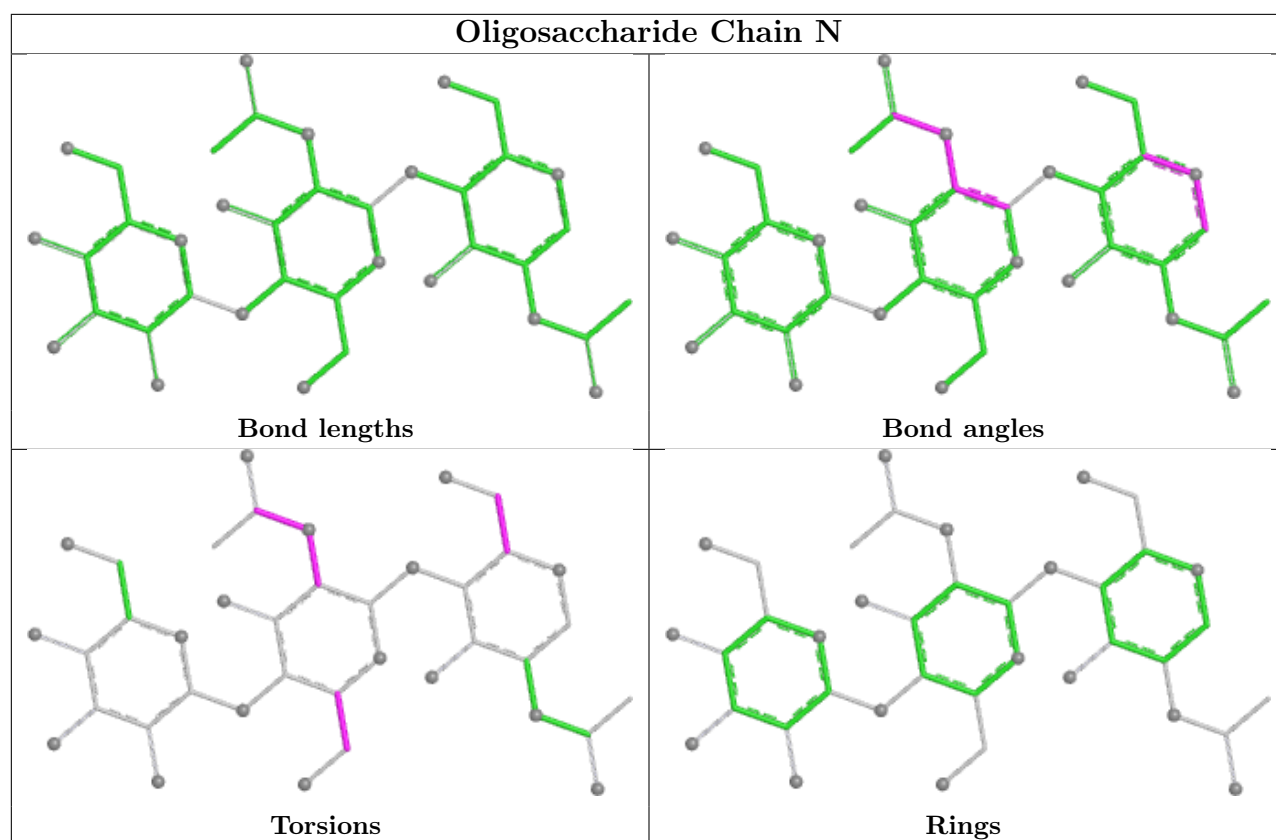
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	N	2	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





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.

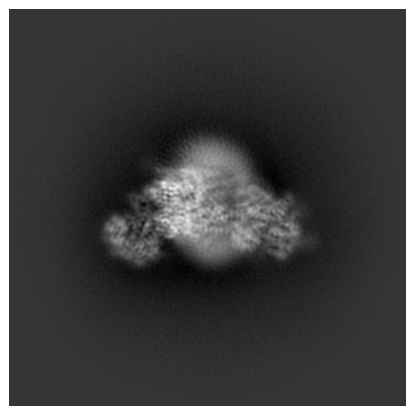
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35907. These allow visual inspection of the internal detail of the map and identification of artifacts.

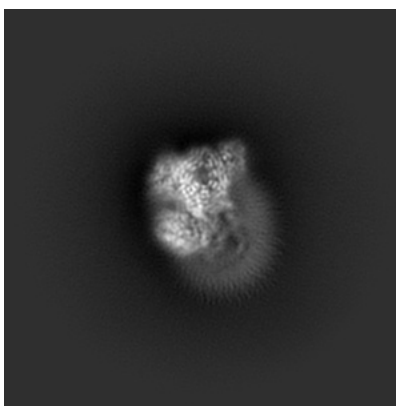
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

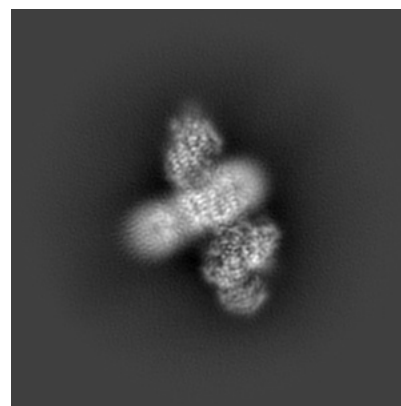
6.1.1 Primary map



X

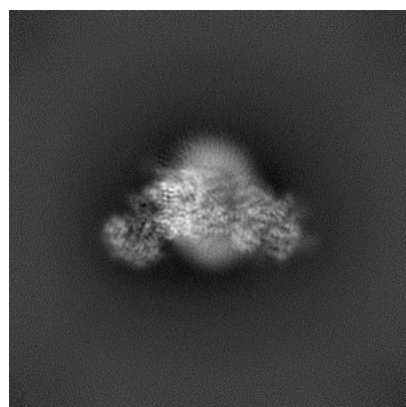


Y

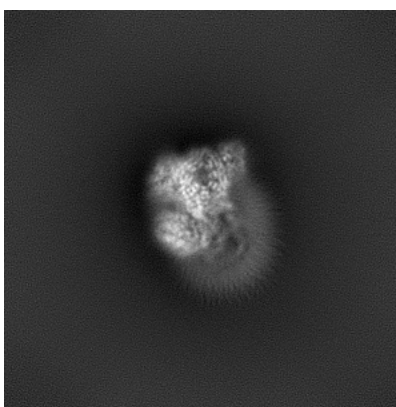


Z

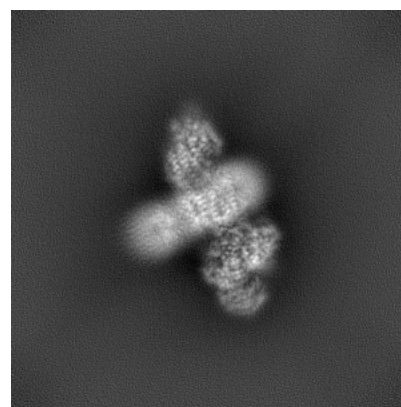
6.1.2 Raw map



X



Y

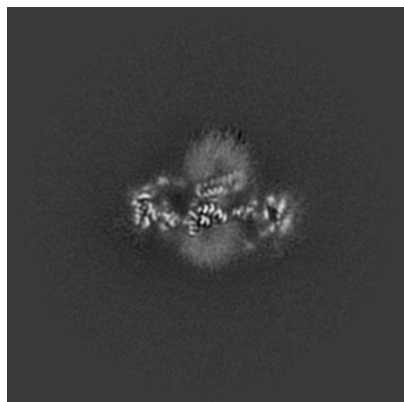


Z

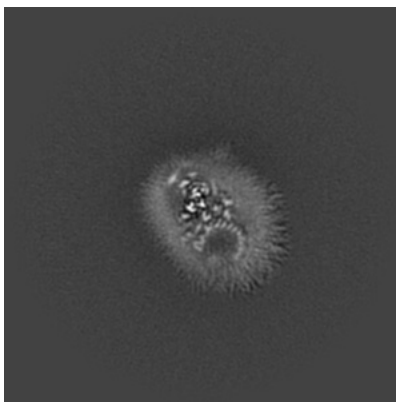
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

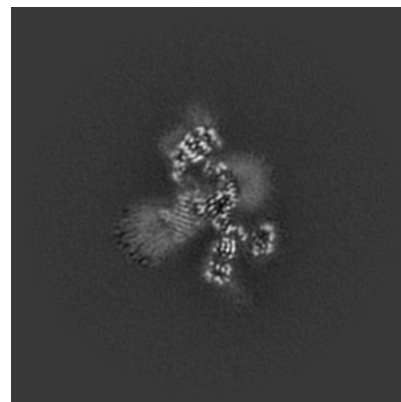
6.2.1 Primary map



X Index: 176

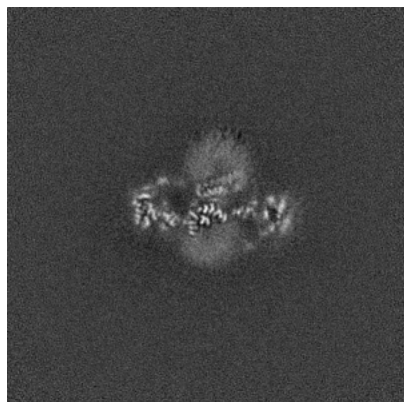


Y Index: 176

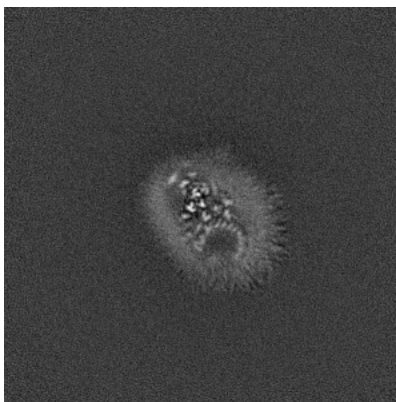


Z Index: 176

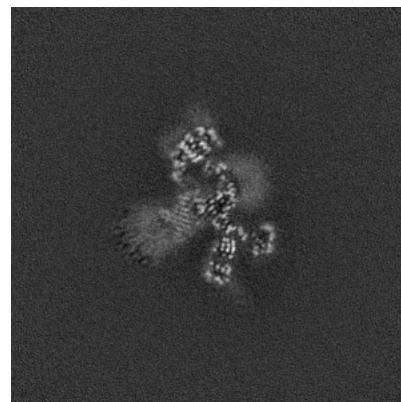
6.2.2 Raw map



X Index: 176



Y Index: 176

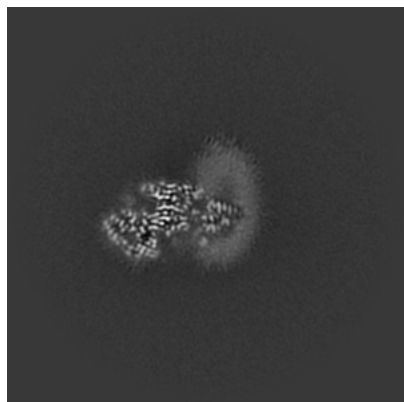


Z Index: 176

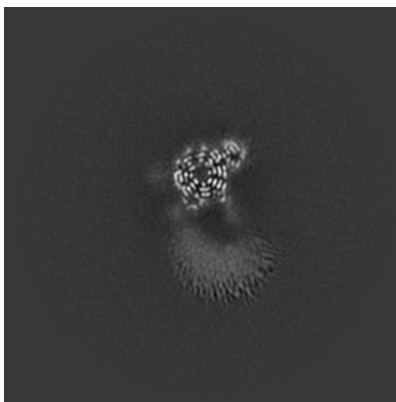
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

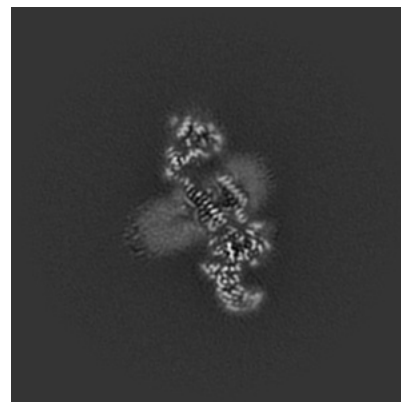
6.3.1 Primary map



X Index: 195

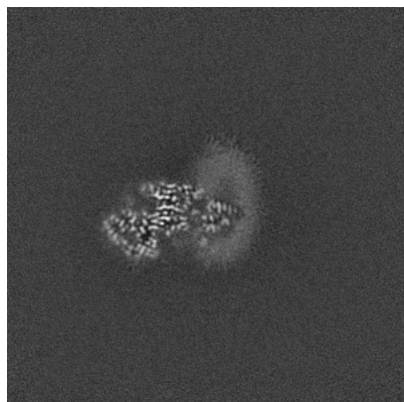


Y Index: 142

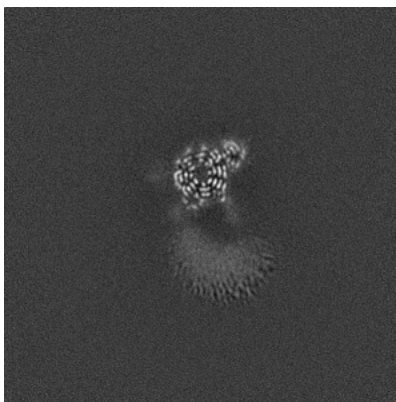


Z Index: 162

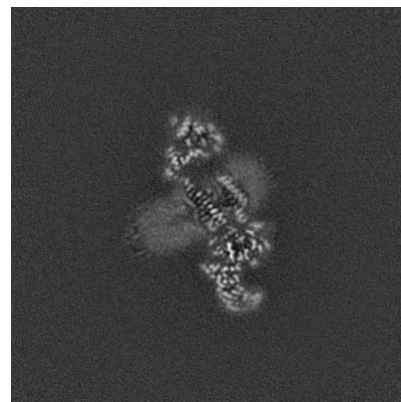
6.3.2 Raw map



X Index: 195



Y Index: 142

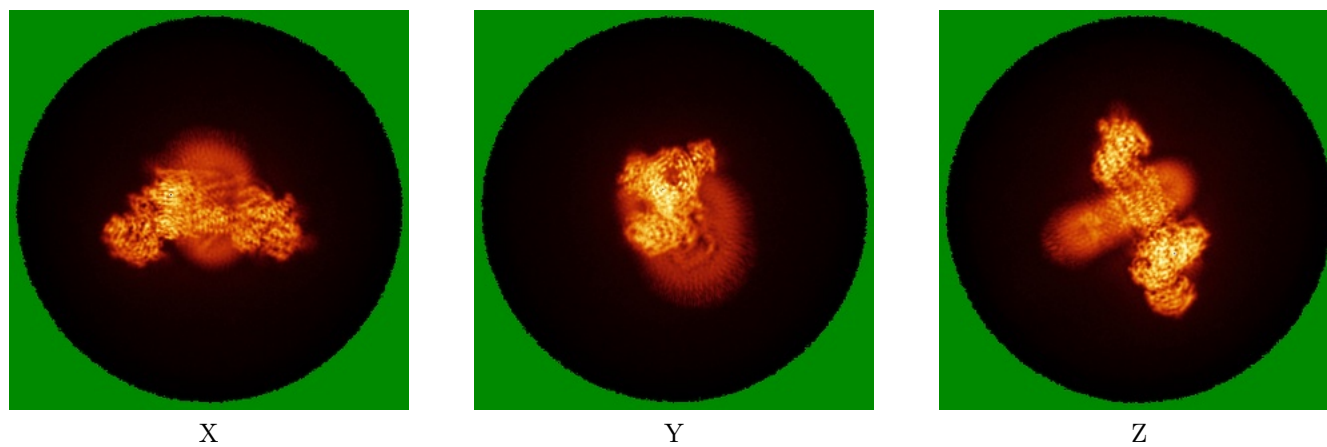


Z Index: 162

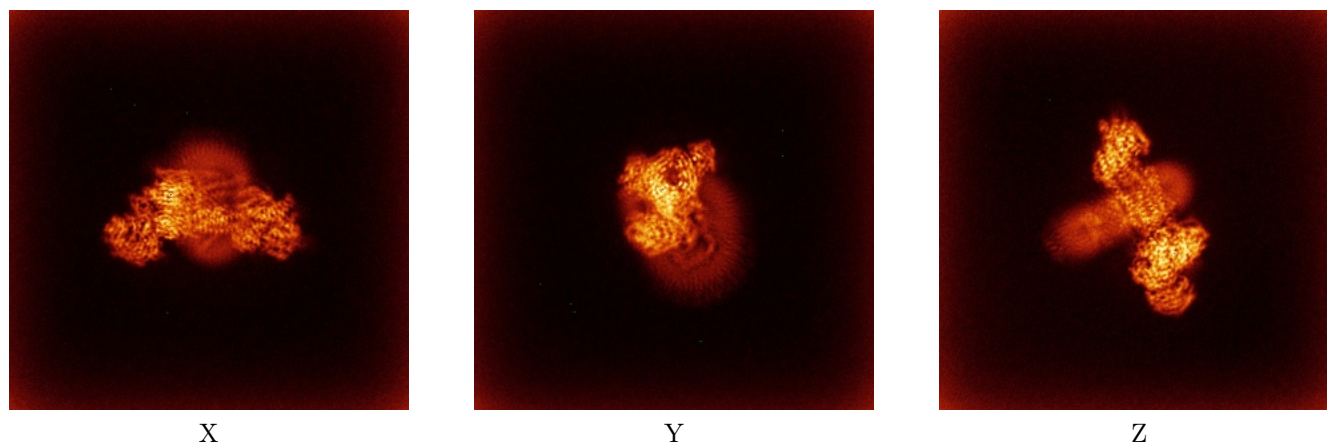
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

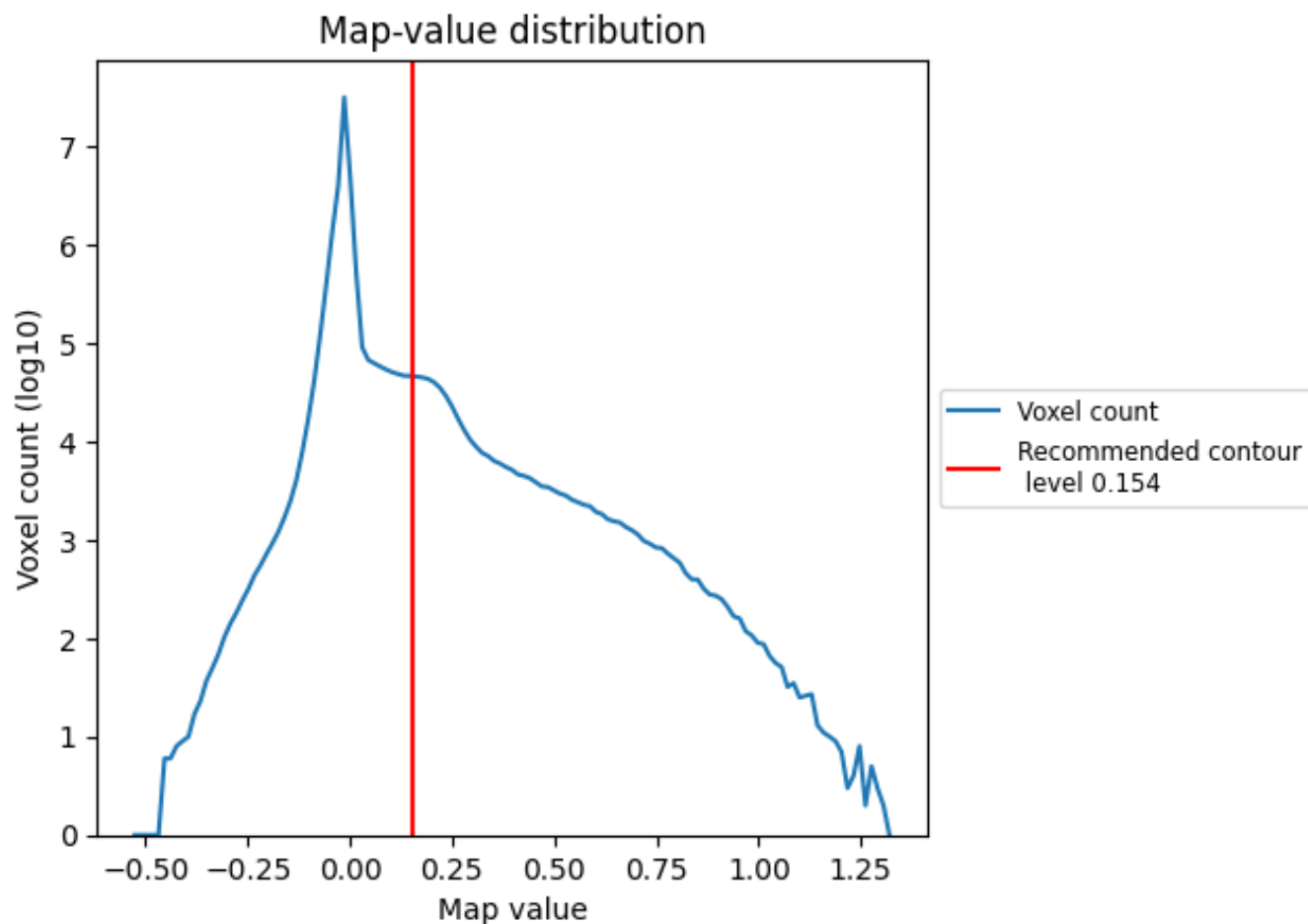
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

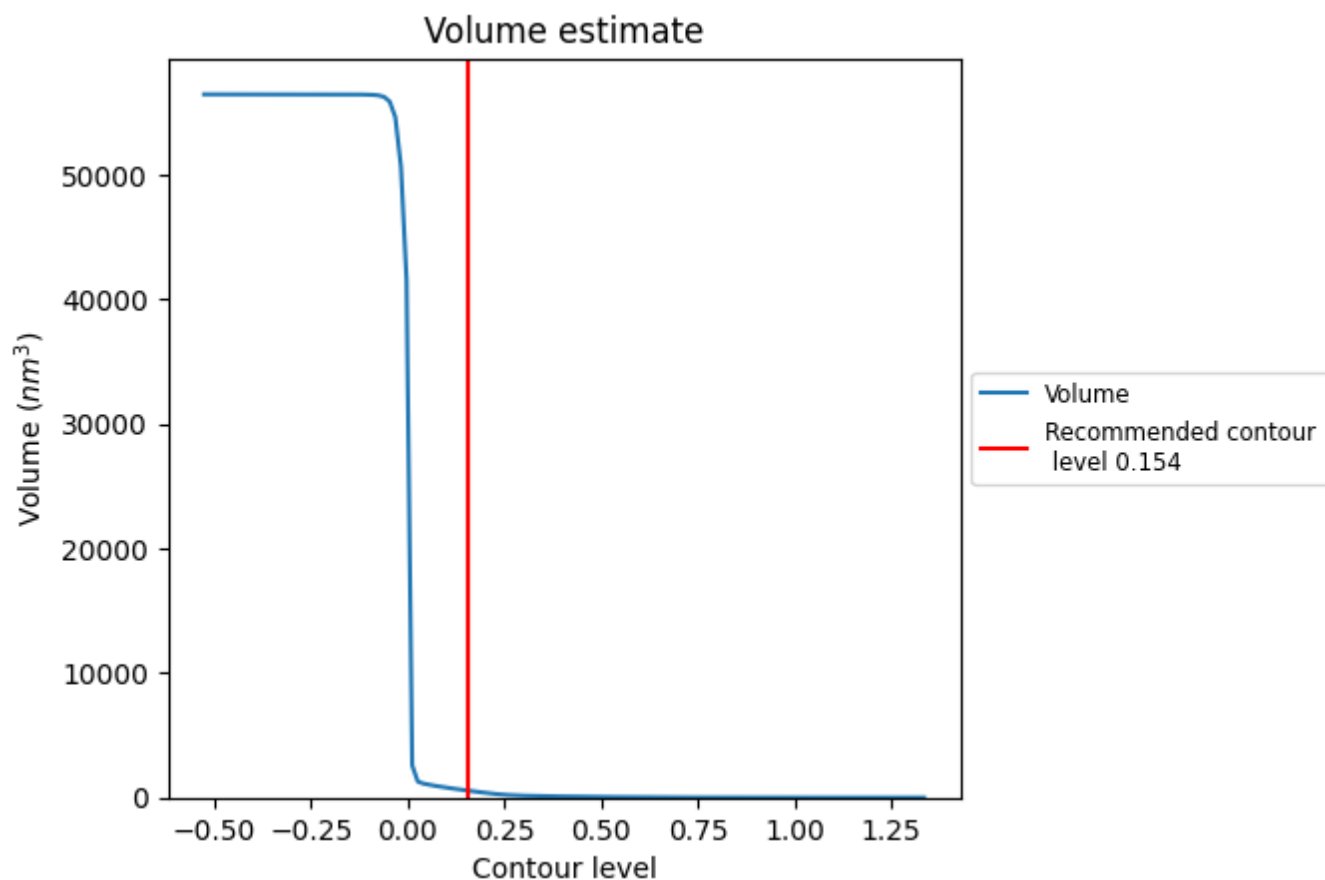
This section contains the results of statistical analysis of the map.

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.

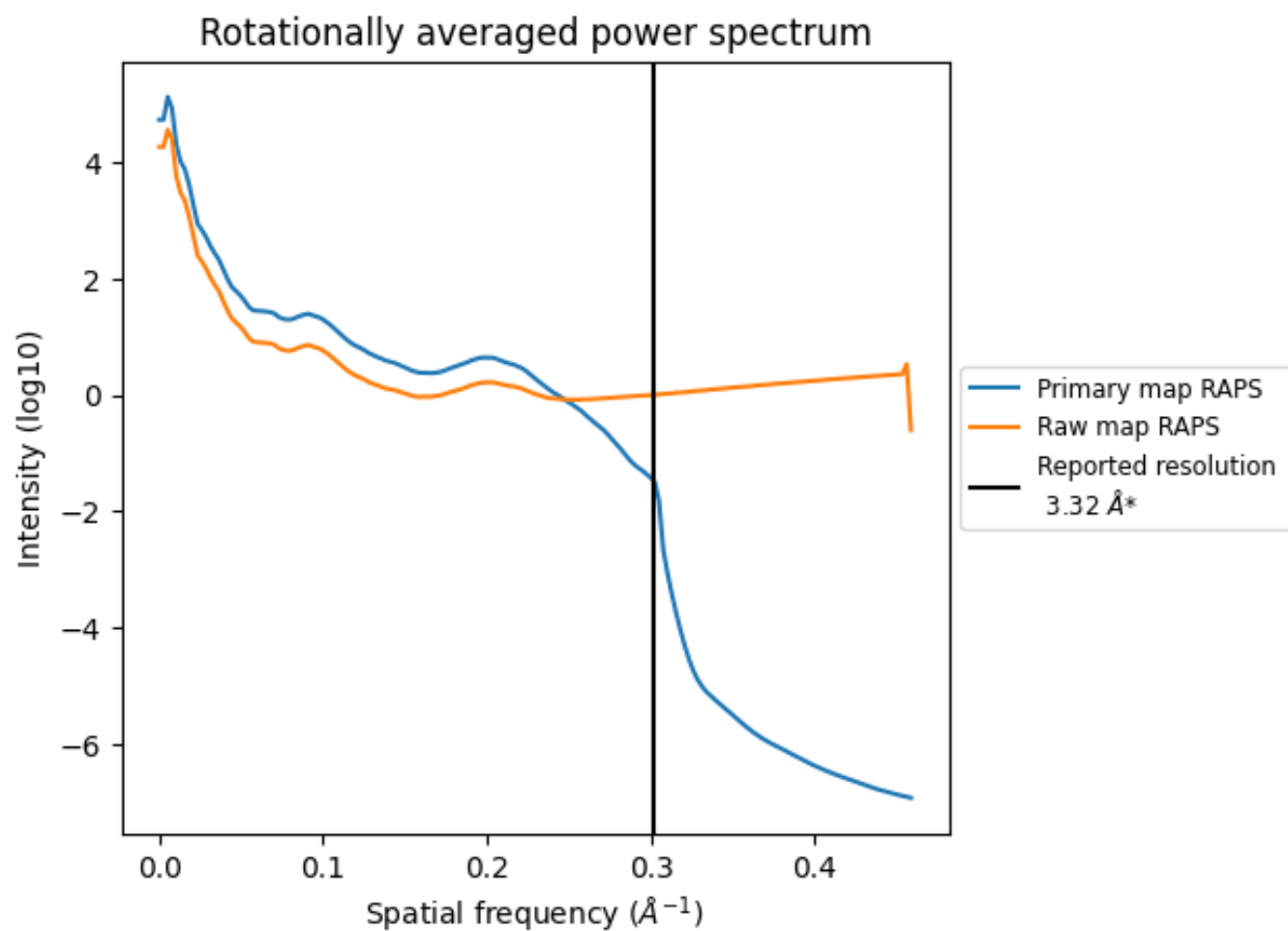
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 566 nm^3 ; this corresponds to an approximate mass of 511 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 ⓘ

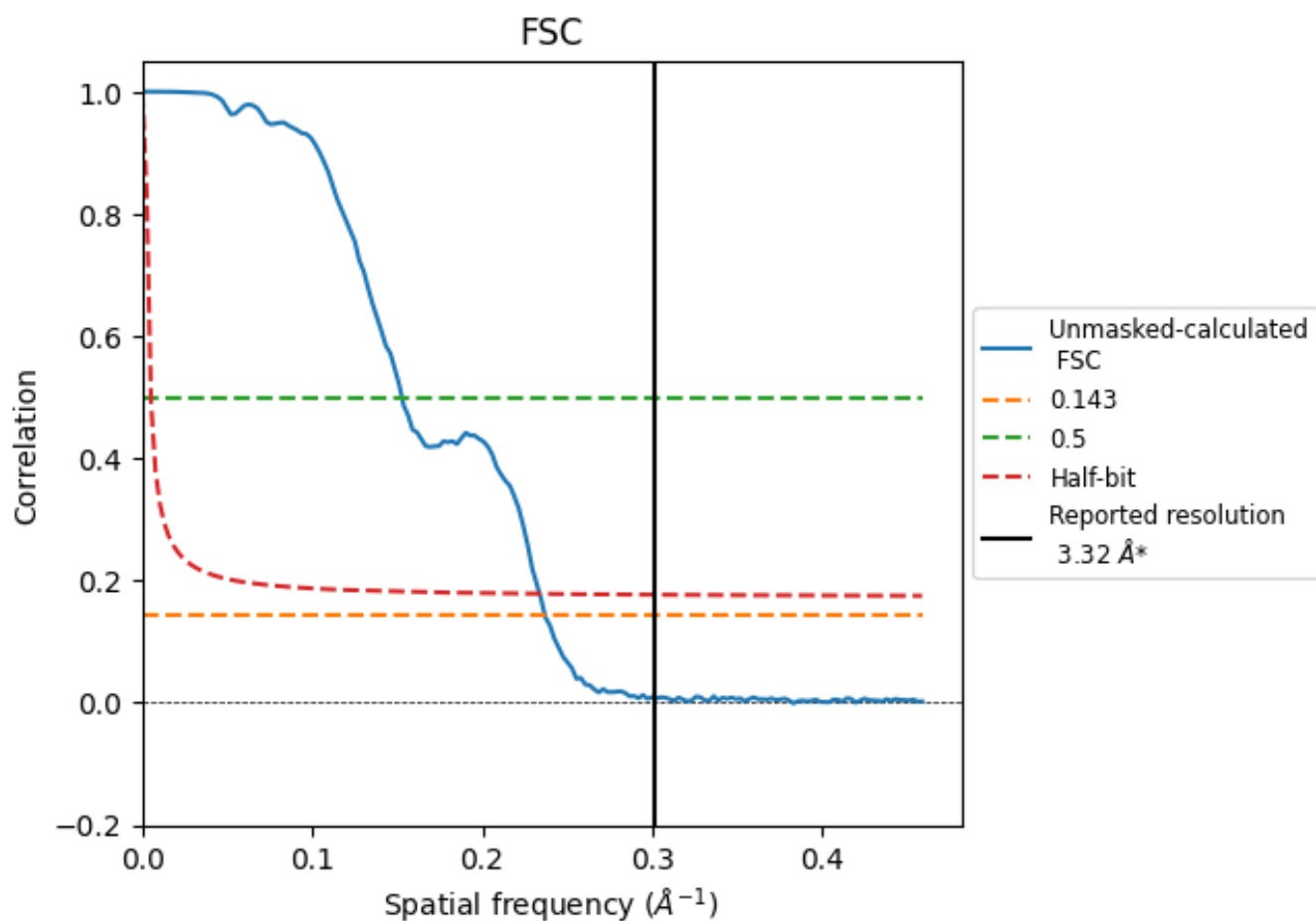


*Reported resolution corresponds to spatial frequency of 0.301 Å⁻¹

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 0.301 Å⁻¹

8.2 Resolution estimates [i](#)

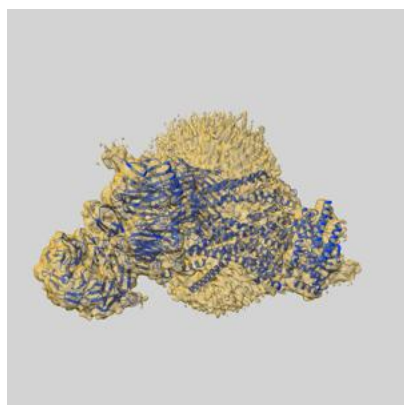
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.32	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.22	6.55	4.28

*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 4.22 differs from the reported value 3.32 by more than 10 %

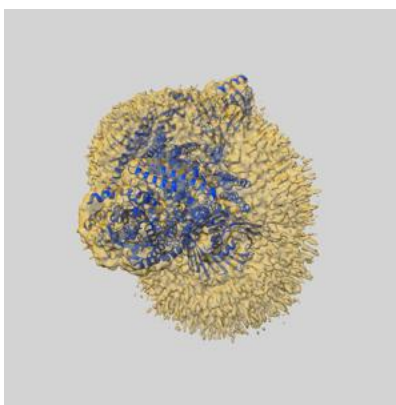
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35907 and PDB model 8J0O. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

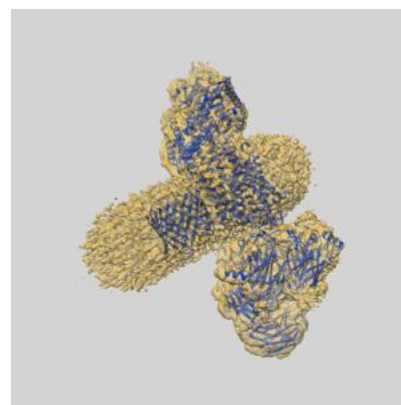
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.154 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](#)

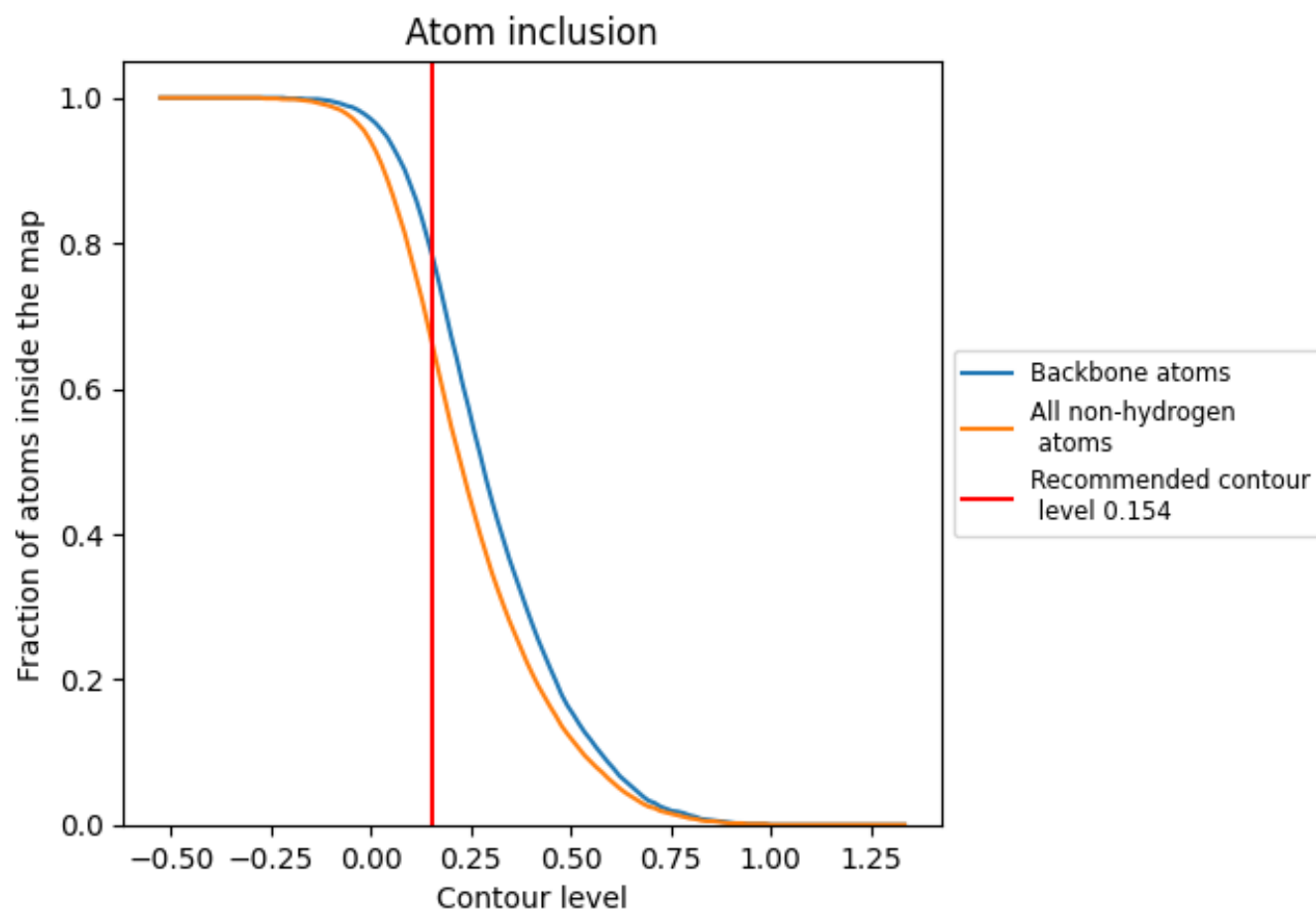


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 66% 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 (0.154) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6600	 0.0170
A	 0.6730	 0.0280
B	 0.6050	 -0.0060
C	 0.6120	 0.0220
D	 0.6930	 0.0220
E	 0.5970	 -0.0050
F	 0.5580	 -0.0270
G	 0.6750	 0.0490
H	 0.6980	 0.0140
J	 0.7130	 0.0180
K	 0.7080	 0.0010
L	 0.6410	 0.0670
M	 0.6410	 0.1080
N	 0.4100	 0.0200

