



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 11:13 PM UTC

PDB ID : 6KG7 / pdb_00006kg7
EMDB ID : EMD-9975
Title : Cryo-EM Structure of the Mammalian Tactile Channel Piezo2
Authors : Wang, L.; Zhou, H.; Zhang, M.; Liu, W.; Deng, T.; Zhao, Q.; Li, Y.; Lei, J.;
Li, X.; Xiao, B.
Deposited on : 2019-07-11
Resolution : 3.80 Å(reported)

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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

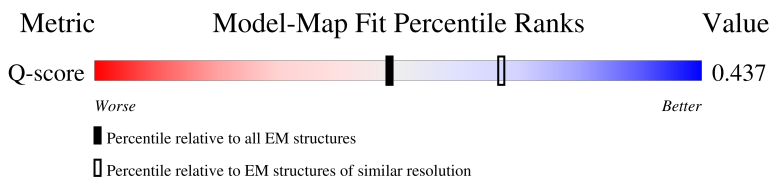
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	2822	 50% 14% 36%
1	B	2822	 50% 14% 36%
1	C	2822	 50% 15% 36%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 44892 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 Piezo-type mechanosensitive ion channel component 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1817	Total	C	N	O	S	1	0
			14908	9922	2377	2508	101		
1	B	1817	Total	C	N	O	S	1	0
			14908	9922	2377	2508	101		
1	C	1817	Total	C	N	O	S	1	0
			14908	9922	2377	2508	101		

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	A	1	Total	C	N	O	0
			14	8	1	5	

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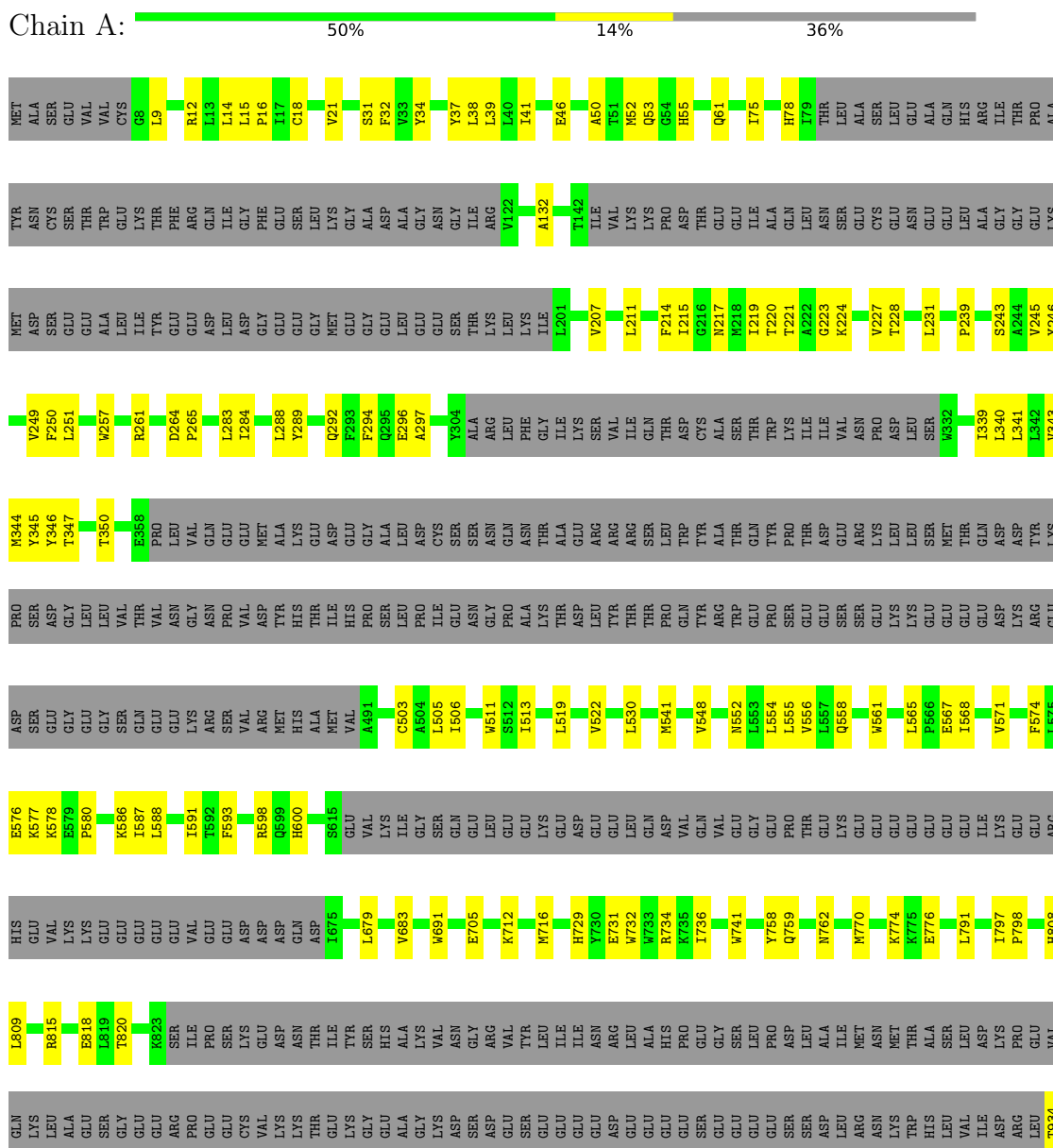
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Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	B	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	
2	C	1	Total	C	N	O	0
			14	8	1	5	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Piezo-type mechanosensitive ion channel component 2

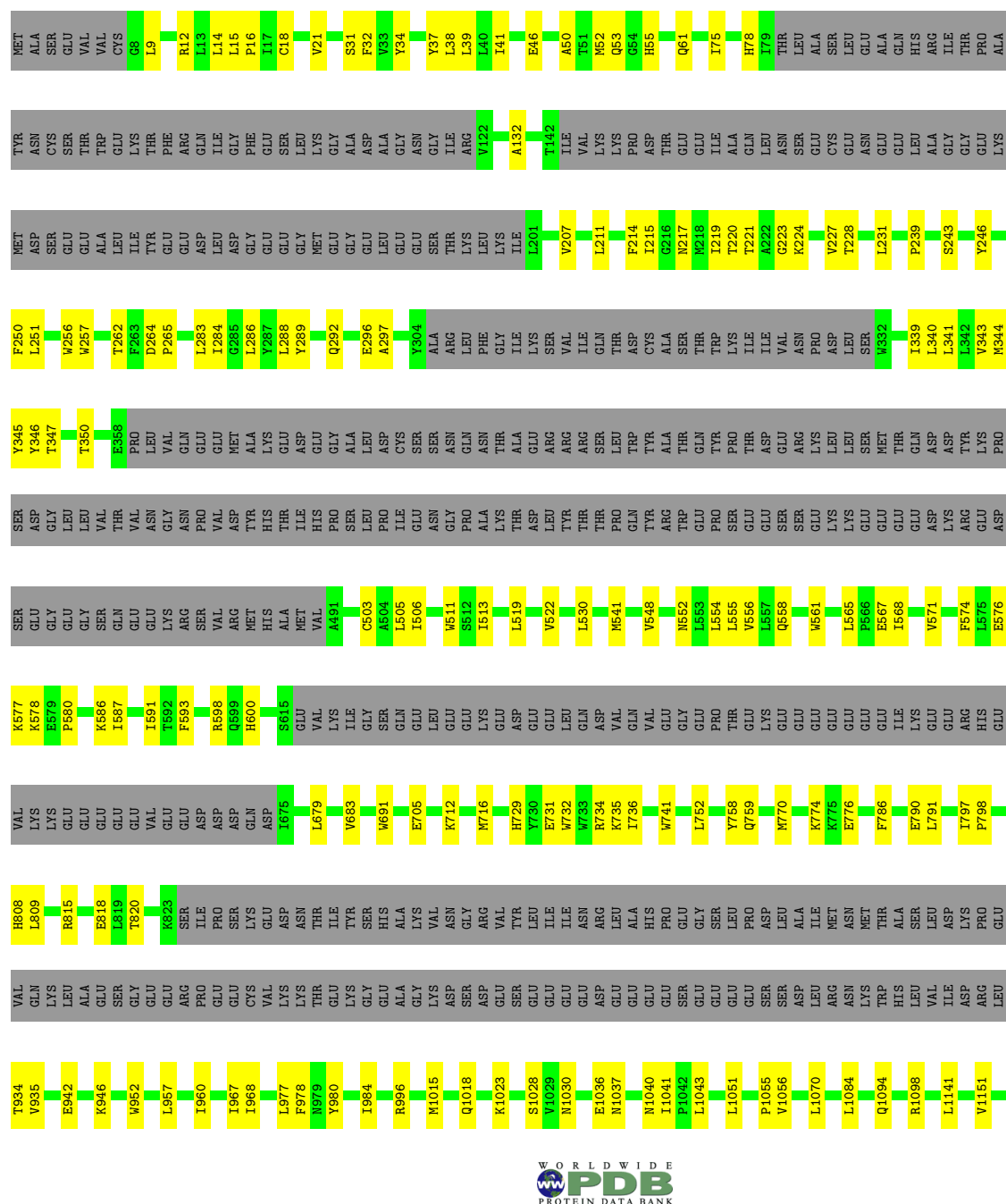




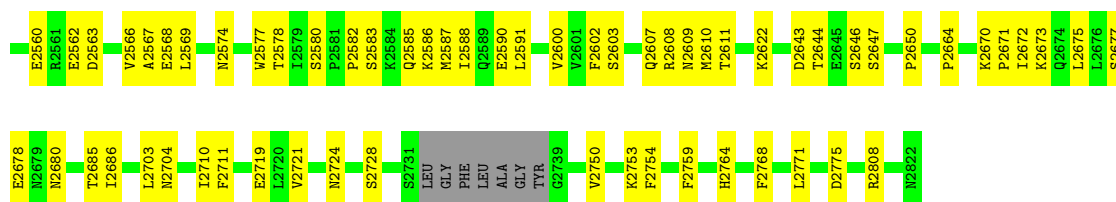


● Molecule 1: Piezo-type mechanosensitive ion channel component 2

Chain B: 50% 14% 36%

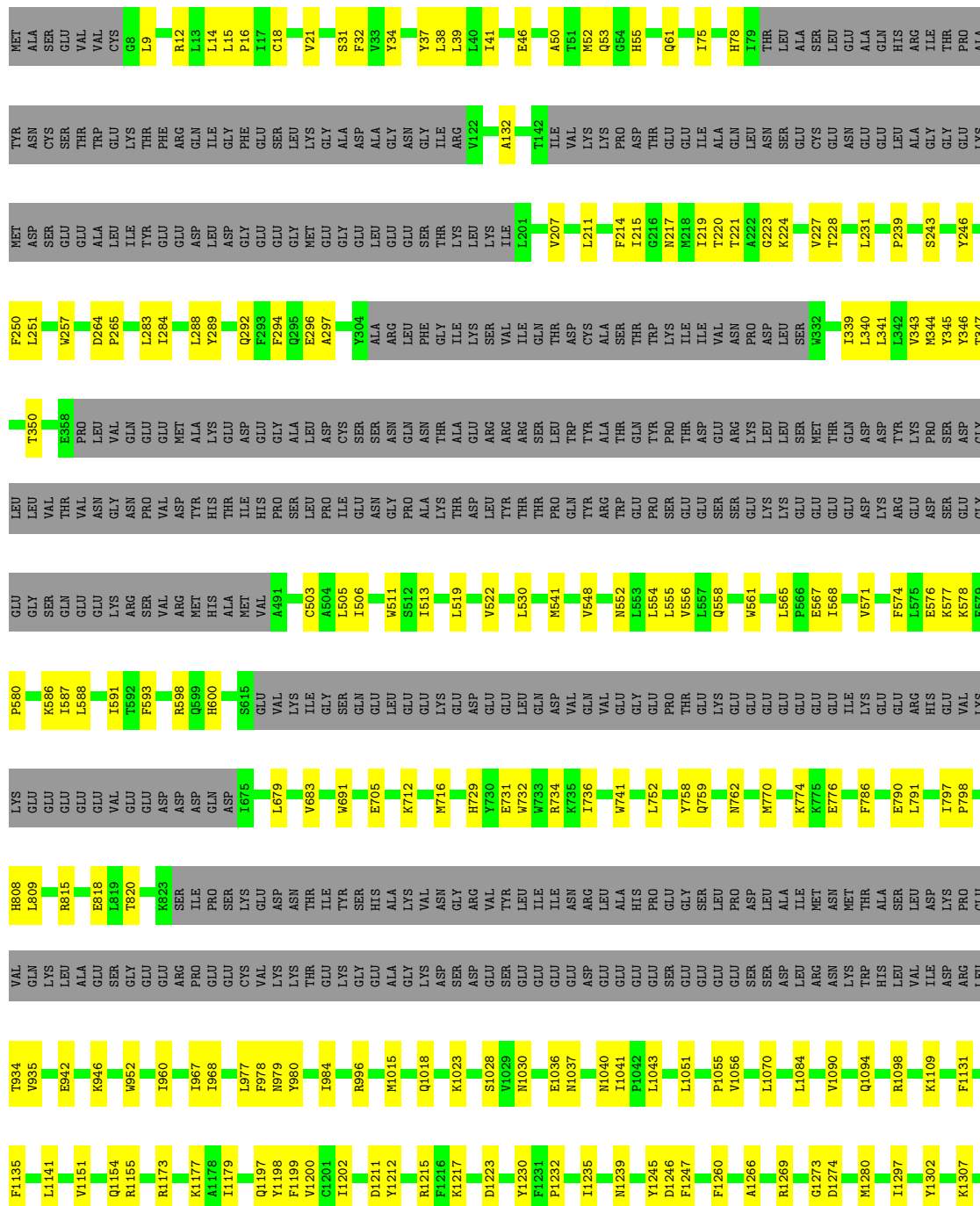


L2491	Q2310	GLU	VAL	ILE	M1955	SER	LEU	GLU	R1707	ARG	TRP	GLY	Q1154
F2492	T2313	LEU	HIS	TTR	M1956	THR	TYR	THR	E1708	ARG	GLY	GLU	R1156
MET	T2316	TYR	VAL	GLY	K1957	ASP	ARG	THR	I1709	GLY	ASP	LYS	D1157
SER	V2316	MET	PHE	ARG	M1958	ASP	GLN	GLY	G1712	SER	R1563	GLY	F1158
ILE	V2330	GLY	PRO	PRO	F1959	CYS	GLY	THR	G1716	GLY	R1564	ASP	Y1159
LYS	V2337	LEU	GLU	TYR	H1960	ALA	THR	SER	T1716	ASP	D1574	C1435	H1163
SER	V2337	GLN	GLN	PHE	D1961	PRO	THR	THR	R1717	GLY	E1577	L1439	R1173
VAL	V2337	PRO	PRO	PRO	D1962	SER	GLU	GLN	S1719	VAL	GLU	PRO	I1179
ALA	I2340	ALA	ALA	N2075	L1964	TYR	ILE	THR	I1720	GLU	GLU	D1457	Q1197
G2501	I2344	ILE	ILE	K2082	E1968	SER	GLU	LEU	H1721	THR	GLU	Q1473	Y1198
N2504	N2344	LYS	ARG	Y1982	K1969	LYS	GLU	ASP	M1722	ASP	GLU	Y1477	F1199
Q2505	I2348	ALA	ARG	M1986	F1970	ALA	VAL	ASP	Y1723	ARG	LEU	A1368	V1200
L2507	L2348	LYS	LYS	T1987	Y1971	VAL	GLA	LEU	I1727	GLY	ASP	R1483	C1201
D2508	E2353	ALA	ARG	L1988	V1972	SER	ALA	ASP	GLY	GLU	PRO	R1514	I1202
V2509	E2353	THR	SER	V1989	V1972	PHE	GLU	GLY	ILE	GLU	ASP	GLY	D1211
G2513	L2364	ILE	CYS	A1990	Y1982	GLU	ALA	GLU	ASN	PRO	VAL	ALA	Y1212
T2514	N2365	LYS	SER	E2111	Y1982	HIS	GLU	GLU	MET	VAL	LEU	LEU	R1215
L2515	V2368	LYS	SER	ASP	M1986	LEU	GLU	GLU	ASN	VAL	CYS	GLY	F1216
G2516	V2368	THR	ILE	ILE	T1987	SER	VAL	VAL	ASN	GLY	PRO	TYR	K1217
C2517	K2369	LEU	ILE	VAL	L1988	PHE	VAL	VAL	SER	ASP	LYS	ILE	D1223
Y2518	C2370	LEU	PRO	ASP	V1989	SER	GLY	THR	GLU	GLY	ARG	GLY	W1228
Q2519	Q2379	I2237	ARG	ASN	A1990	GLN	GLY	GLY	ILE	ASP	LYS	GLN	Y1229
Y2520	I2380	I2237	ARG	ASN	R1991	ASP	LEU	GLU	ASP	GLY	VAL	GLY	Y1230
I2521	I2383	V2256	SER	THR	S1992	ASP	LEU	ARG	GLU	ILE	THR	ASP	F1232
M2524	G2383	V2261	PHE	LYS	E1993	GLY	PRO	ALA	THR	ILE	PHE	GLY	P1232
S2525	N2391	L2262	LYS	GLY	M1994	ALA	LEU	PRO	ILE	ILE	ASN	GLN	I1235
A2526	T2394	D2270	SER	GLY	V1995	ALA	HIS	ARG	ASP	ILE	VAL	ALA	N1239
Q2527	E2416	F2271	ARG	ASP	C1996	ASN	ASP	LEU	GLU	LYS	THR	GLU	Y1245
S2529	E2416	I2274	LYS	ASP	F1998	HIS	ALA	ARG	HIS	ARG	LYS	ASP	D1246
Q2530	L2430	G2282	ARG	GLY	V1999	MET	GLU	GLU	GLY	ILE	ALA	GLY	F1247
L2531	L2430	LYS	GLY	LEU	S2009	VAL	LYS	TYR	ALA	ASN	LEU	VAL	F1260
V2532	S2434	HIS	SER	LEU	I2010	PRO	SER	LEU	ARG	LYS	GLN	VAL	A1266
M2534	K2449	THR	THR	GLN	L2014	ASP	ALA	ASP	MET	THR	LYS	GLY	R1269
D2535	K2449	ALA	ARG	GLY	F2020	SER	GLU	GLU	GLY	THR	ALA	ASP	G1273
N2536	R2452	ALA	ASN	ARG	L2021	ARG	TYR	SER	ALA	ALA	GLY	GLY	D1274
S2537	R2452	ASP	ASN	ARG	V2027	THR	GLU	ALA	SER	THR	ARG	VAL	M1280
K2538	P2461	ILE	SER	GLY	P2028	ASP	GLY	ALA	ALA	GLY	LEU	ALA	I1297
Y2539	R2462	THR	GLN	SER	Y2041	LEU	VAL	ASP	ARG	ARG	GLN	ALA	Y1302
N2540	Q2463	SER	LYS	ASP	Q2053	GLY	GLY	GLY	ASP	LYS	LYS	PRO	F1323
E2541	Q2464	SER	GLY	SER	G2055	SER	GLY	GLY	ASP	ARG	GLY	GLY	SER
K2544	K2465	SER	SER	LEU	F2054	THR	ILE	ILE	THR	GLY	LYS	GLY	GLY
S2545	V2480	SER	SER	LYS	G2055	LEU	SER	SER	ASP	GLY	LYS	GLY	GLY
F2546	L2481	GLU	VAL	SER	PHE	LEU	THR	LEU	ARG	ASP	LYS	GLY	GLY
G2547	L2481	ASP	ILE	ILE	PHE	PRO	THR	PRO	ASP	ASP	LYS	GLY	GLY
G2551	I2483	V2299	SER	ASN	PHE	LEU	LEU	PRO	ASP	ASP	LYS	GLY	GLY
A2552	I2483	P2300	LYS	ALA	PHE	LEU	LEU	PRO	ASP	ASP	LYS	GLY	GLY
M2553	V2486	LYS	LYS	ALA	G2055	THR	GLY	THR	ASP	ASP	LYS	GLY	GLY
Q2554	N2487	LYS	GLN	ALA	G2055	ASN	GLY	THR	ASP	ASP	LYS	GLY	GLY
P2555	F2488	VAL	LYS	SER	LYS	LYS	LEU	GLN	ASP	ASP	LYS	GLY	GLY
L2556	P2489	M2306	SER	VAL	ASP	GLU	LEU	LEU	ASP	ASP	LYS	GLY	GLY
E2557	L2490	ARG	ARG	SER	GLU	GLU	GLU	GLU	THR	THR	GLY	GLY	GLY



• Molecule 1: Piezo-type mechanosensitive ion channel component 2

Chain C: 50% 15% 36%



P2664	K2670	I2672	K2673	Q2674	L2675	L2676	S2677	K2678	N2679	N2680	T2685	I2686	L2703	N2704	I2710	F2711	E2719	N2724	S2728	S2731	LEU	PHE	LEU	ALA	GLY	TYR	G2739	V2750	K2753	F2754	F2759	H2764	S2765	F2768	L2771	D2775	R2808	N2822													
G2547	G2561	K2562	M2563	Q2564	L2565	L2566	E2567	E2568	E2569	E2570	N2574	W2577	T2578	I2579	S2580	F2581	P2582	S2583	K2584	G2585	K2586	M2587	I2588	Q2589	E2590	L2591	V2600	I2601	F2602	S2603	Q2607	R2608	N2609	M2610	T2611	K2622	D2643	T2644	E2645	S2646	S2647	P2650									
V2480	L2481	I2482	I2483	V2486	I2487	F2488	P2489	L2490	L2491	F2492	MET	SER	ILE	LYS	VAL	ALA	G2501	N2504	Q2505	L2506	L2507	D2508	V2509	T2513	T2514	L2515	G2516	G2517	V2518	Q2519	F2520	I2521	N2524	S2525	Q2527	Q2528	S2529	Q2530	L2531	K2532	V2533	M2534	D2535	N2536	S2537	K2538	V2539	N2540	E2541	F2542	L2543
ASP	GLN	P2300	L2304	V2305	M2306	Q2310	T2313	V2316	V2330	V2337	I2340	M2344	L2348	E2353	L2364	W2365	L2368	K2369	C2370	Q2379	I2380	G2383	N2391	T2394	K2395	E2416	L2430	S2434	K2449	R2452	P2461	R2462	Q2463	Q2464	K2465	GLU	VAL	SER	ASN	ALA	ALA	ASP	ILE	THR	SER	GLN	LYS	GLY	SER	SER	
LYS	SER	ASN	LEU	ALA	ALA	SER	VAL	GLU	SER	VAL	HIS	THR	THR	PHE	PRO	GLN	PRO	ALA	VAL	PHE	GLN	LYS	ALA	VAL	SER	PHE	GLY	ALA	LYS	ASN	ASP	THR	LYS	ARG	GLY	LEU	SER	LEU	THR	PRO	GLY	THR	SER	VAL	GLN	THR	GLN	GLY	SER	SER	SER
ILE	PRO	PHE	PRO	THR	ASN	HIS	GLU	L1948	D1952	M1955	S1956	K1957	M1958	F1959	H1960	D1961	D1962	E1963	L1964	E1968	K1969	F1970	Y1971	V1972	Y1982	M1986	T1987	L1988	V1989	A1990	R1991	S1992	E1993	M1994	V1995	C1996	Y1997	F1998	V1999	S2009	I2010	L2014	F2020	L2021	V2027	P2028	L2041	N2045	G2052		
F2054	G2055	PHE	PRO	TRP	ASN	LYS	ASP	LEU	LEU	ILE	TYR	LYS	GLU	ARG	PRO	PHE	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
VAL	ALA	SER	SER	GLU	THR	GLU	THR	GLN	CYS	THR	MET	LEU	LEU	ALA	THR	THR	GLU	GLU	GLU	VAL	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	
ASP	SER	ARG	ASP	ILE	SER	SER	CYS	GLU	GLU	GLU	THR	SER	ARG	GLN	GLN	THR	GLU	ASP	ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
L1684	M1685	S1686	I1687	S1688	R1689	D1693	T1706	R1707	E1708	I1709	K1710	G1711	G1712	T1716	R1717	E1718	S1719	H1720	H1721	M1722	Y1723	Y1724	H1727	ILE	MET	ASN	LEU	PRO	VAL	LEU	LEU	PRO	ARG	ASP	GLU	GLY	THR	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE
LYS	LYS	LEU	ALA	ARG	GLU	GLN	LYS	GLU	ARG	LYS	GLY	SER	GLY	PRO	VAL	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU
CYS	LYS	LEU	PRO	SER	GLY	GLU	A1427	G1428	I1429	C1435	L1439	L1440	D1457	S1466	Q1473	V1477	R1483	I1484	E1485	R1514	GLY	MET	GLY	LEU	SER	LEU	VAL	THR	GLN	ASN	GLY	SER	CYS	TRP	LEU	ILE	GLN	ALA	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	2721959	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	49.744	Depositor
Minimum map value	-19.493	Depositor
Average map value	0.078	Depositor
Map value standard deviation	1.367	Depositor
Recommended contour level	5.69	Depositor
Map size ($\text{\AA}$)	448.32, 448.32, 448.32	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.401, 1.401, 1.401	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.16	0/15321	0.35	0/20784
1	B	0.16	0/15321	0.35	0/20784
1	C	0.16	0/15321	0.35	0/20784
All	All	0.16	0/45963	0.35	0/62352

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	14908	0	15077	289	0
1	B	14908	0	15077	285	0
1	C	14908	0	15077	295	0
2	A	56	0	52	5	0
2	B	56	0	52	5	0
2	C	56	0	52	5	0
All	All	44892	0	45387	840	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 840 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2650:PRO:HB2	1:B:2685:THR:HG22	1.33	1.11
1:C:2650:PRO:HB2	1:C:2685:THR:HG22	1.33	1.08
1:A:2650:PRO:HB2	1:A:2685:THR:HG22	1.33	1.06
1:A:2650:PRO:HB2	1:A:2685:THR:CG2	1.89	1.02
1:C:2650:PRO:HB2	1:C:2685:THR:CG2	1.89	1.02

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	1786/2822 (63%)	1683 (94%)	103 (6%)	0	100	100
1	B	1786/2822 (63%)	1684 (94%)	102 (6%)	0	100	100
1	C	1786/2822 (63%)	1684 (94%)	102 (6%)	0	100	100
All	All	5358/8466 (63%)	5051 (94%)	307 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1626/2541 (64%)	1626 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	1561/2541 (61%)	1561 (100%)	0	100	100
1	C	1626/2541 (64%)	1626 (100%)	0	100	100
All	All	4813/7623 (63%)	4813 (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 80 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	292	GLN
1	C	2053	GLN
1	C	558	GLN
1	C	1076	ASN
1	C	2519	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](#)

12 ligands 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
2	NAG	A	3002	1	14,14,15	1.29	2 (14%)	17,19,21	0.82	0
2	NAG	A	3003	1	14,14,15	1.30	2 (14%)	17,19,21	0.68	0
2	NAG	B	3004	1	14,14,15	1.31	2 (14%)	17,19,21	0.58	0
2	NAG	B	3001	1	14,14,15	0.34	0	17,19,21	0.72	1 (5%)
2	NAG	C	3003	1	14,14,15	1.29	2 (14%)	17,19,21	0.68	0
2	NAG	B	3003	1	14,14,15	1.30	2 (14%)	17,19,21	0.68	0
2	NAG	A	3004	1	14,14,15	1.32	2 (14%)	17,19,21	0.58	0
2	NAG	C	3002	1	14,14,15	1.29	2 (14%)	17,19,21	0.82	0
2	NAG	C	3004	1	14,14,15	1.32	2 (14%)	17,19,21	0.58	0
2	NAG	C	3001	1	14,14,15	0.33	0	17,19,21	0.72	1 (5%)
2	NAG	B	3002	1	14,14,15	1.30	2 (14%)	17,19,21	0.82	0
2	NAG	A	3001	1	14,14,15	0.33	0	17,19,21	0.73	1 (5%)

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
2	NAG	A	3002	1	-	5/6/23/26	0/1/1/1
2	NAG	A	3003	1	-	3/6/23/26	0/1/1/1
2	NAG	B	3004	1	-	2/6/23/26	0/1/1/1
2	NAG	B	3001	1	-	4/6/23/26	0/1/1/1
2	NAG	C	3003	1	-	3/6/23/26	0/1/1/1
2	NAG	B	3003	1	-	3/6/23/26	0/1/1/1
2	NAG	A	3004	1	-	2/6/23/26	0/1/1/1
2	NAG	C	3002	1	-	5/6/23/26	0/1/1/1
2	NAG	C	3004	1	-	2/6/23/26	0/1/1/1
2	NAG	C	3001	1	-	4/6/23/26	0/1/1/1
2	NAG	B	3002	1	-	5/6/23/26	0/1/1/1
2	NAG	A	3001	1	-	4/6/23/26	0/1/1/1

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3004	NAG	O5-C1	4.27	1.50	1.43
2	C	3004	NAG	O5-C1	4.26	1.50	1.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3004	NAG	O5-C1	4.25	1.50	1.43
2	B	3003	NAG	O5-C1	4.16	1.50	1.43
2	B	3002	NAG	O5-C1	4.15	1.50	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3001	NAG	C1-O5-C5	2.14	115.06	112.19
2	C	3001	NAG	C1-O5-C5	2.12	115.03	112.19
2	B	3001	NAG	C1-O5-C5	2.11	115.02	112.19

There are no chirality outliers.

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3002	NAG	C1-C2-N2-C7
2	A	3002	NAG	C8-C7-N2-C2
2	A	3003	NAG	C1-C2-N2-C7
2	B	3002	NAG	C1-C2-N2-C7
2	B	3002	NAG	C8-C7-N2-C2

There are no ring outliers.

6 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3002	NAG	4	0
2	A	3003	NAG	1	0
2	C	3003	NAG	1	0
2	B	3003	NAG	1	0
2	C	3002	NAG	4	0
2	B	3002	NAG	4	0

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.

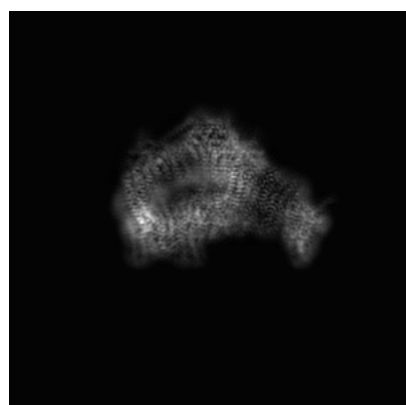
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9975. These allow visual inspection of the internal detail of the map and identification of artifacts.

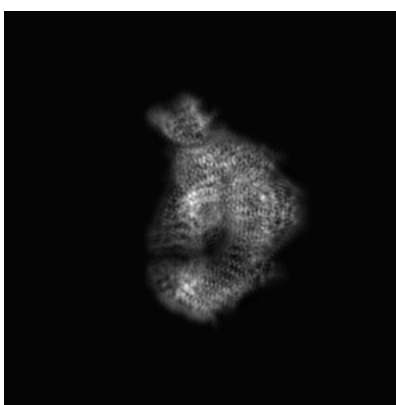
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

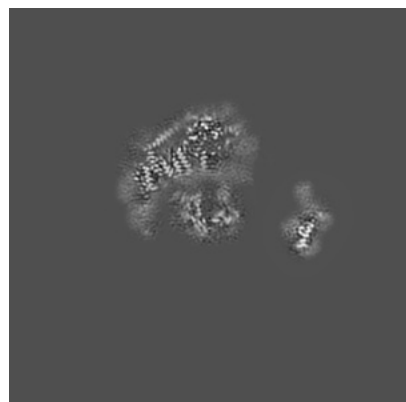


Z

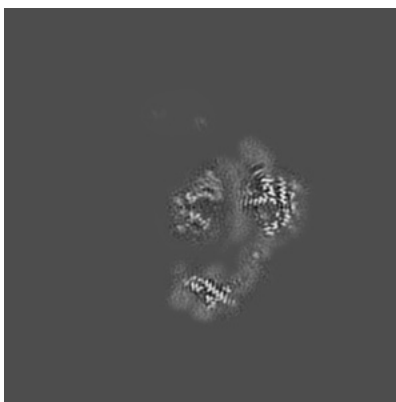
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

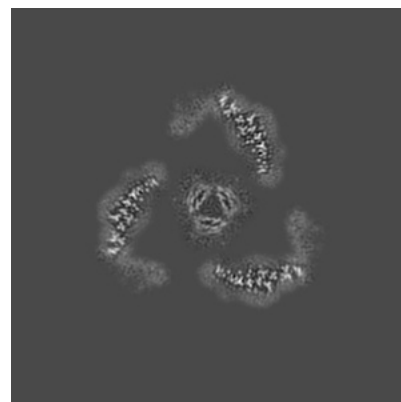
6.2.1 Primary map



X Index: 160



Y Index: 160

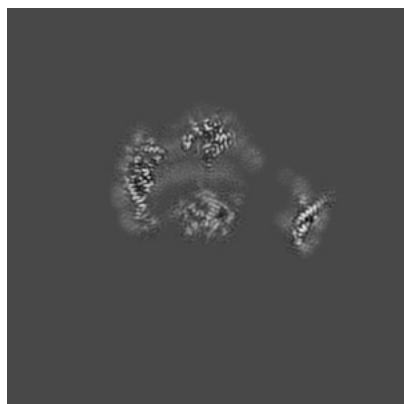


Z Index: 160

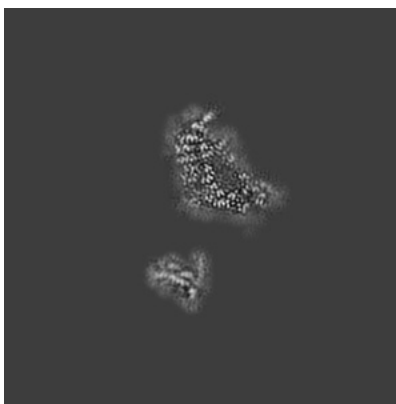
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

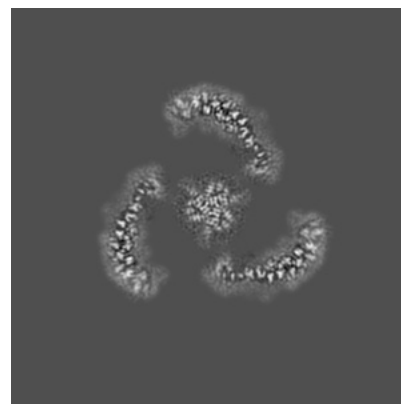
6.3.1 Primary map



X Index: 168



Y Index: 107

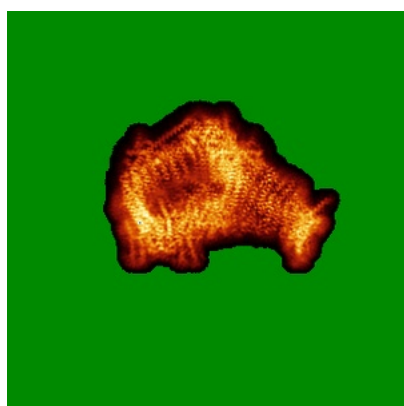


Z Index: 150

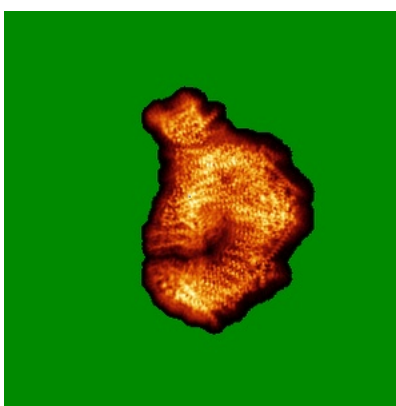
The images above show the largest variance slices of the map in three orthogonal directions.

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

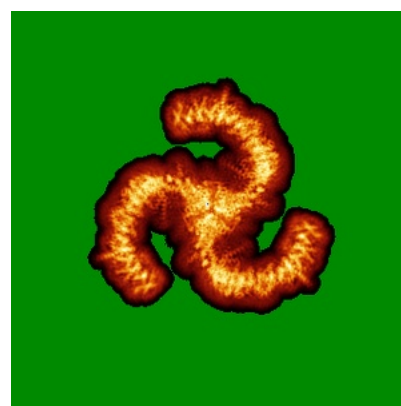
6.4.1 Primary map



X



Y

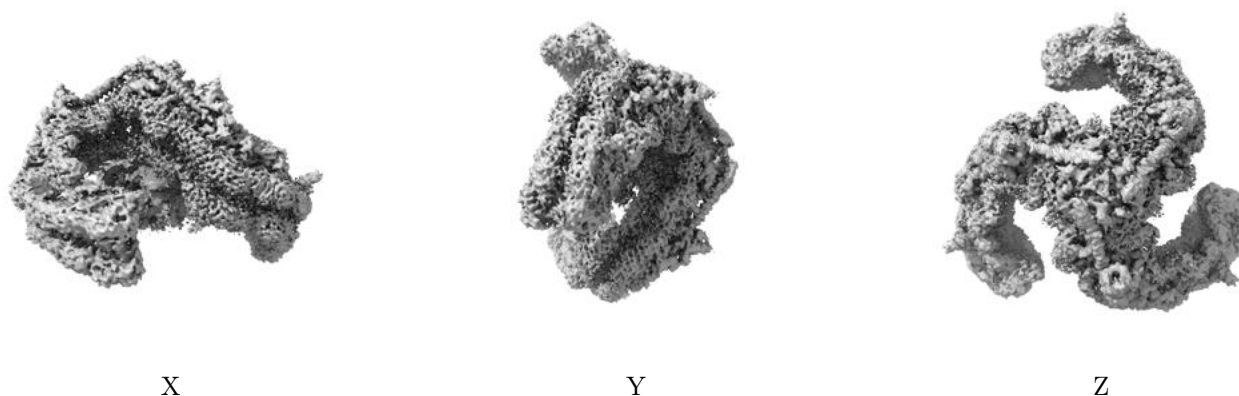


Z

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 5.69. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

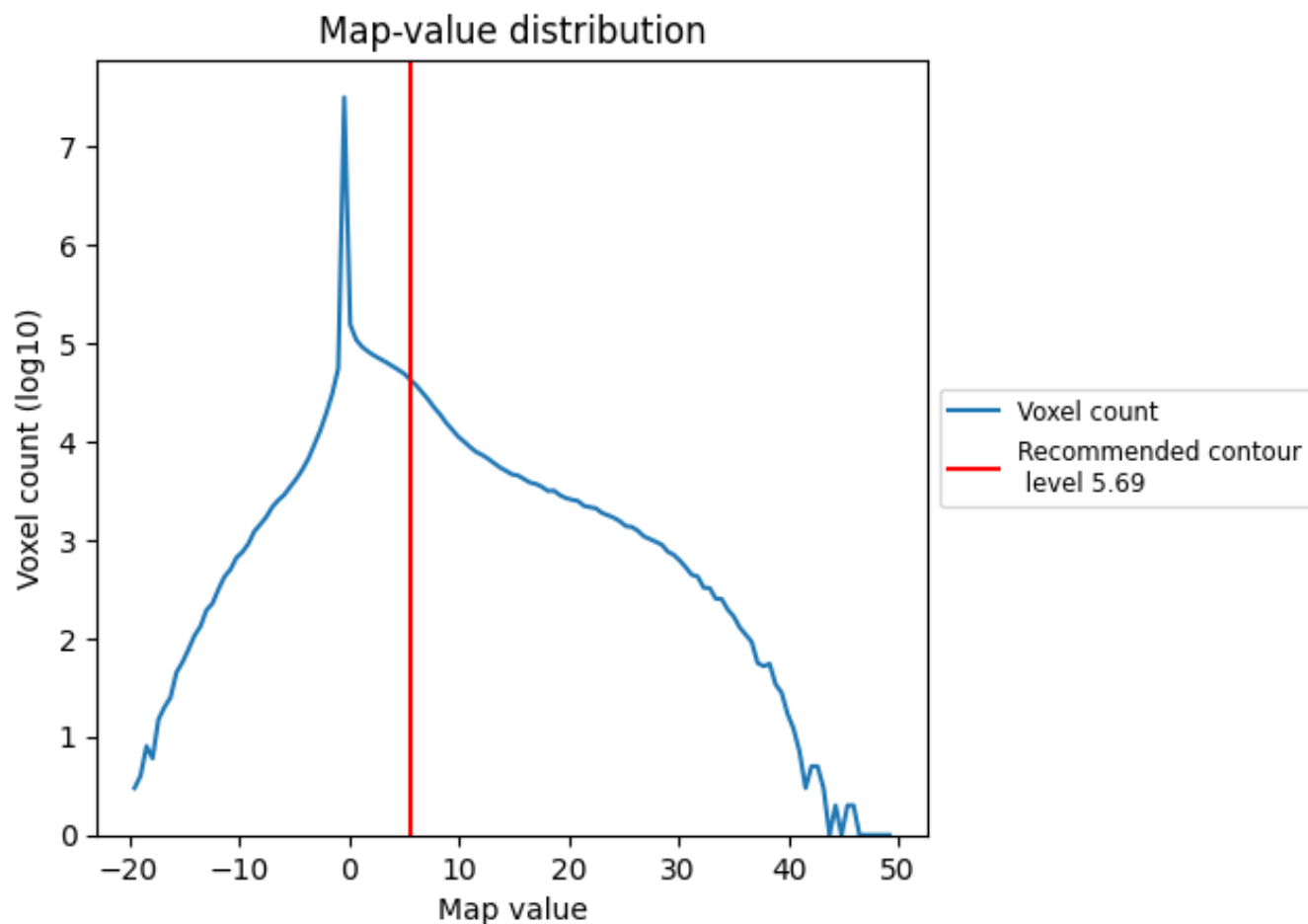
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

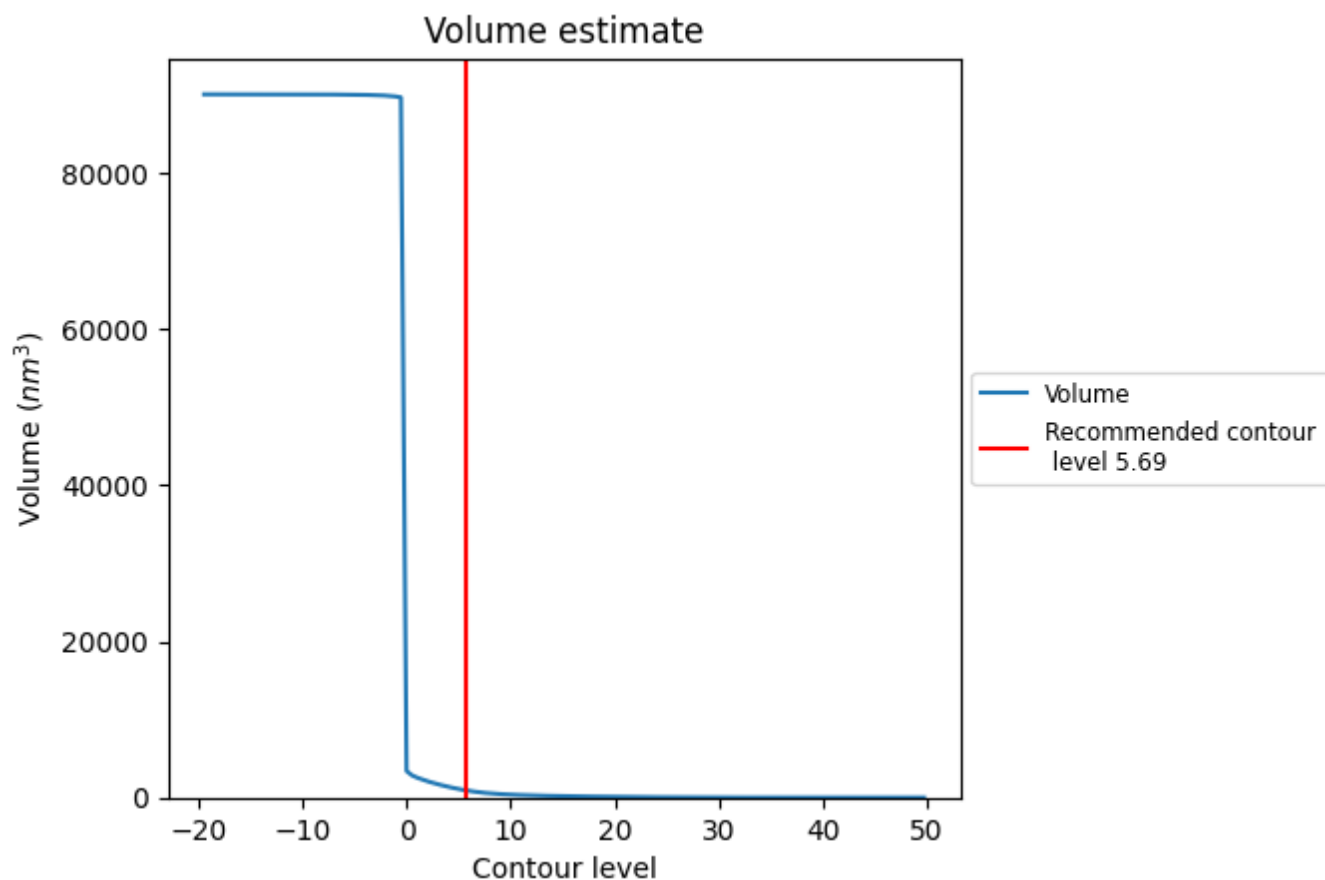
This section contains the results of statistical analysis of the map.

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.

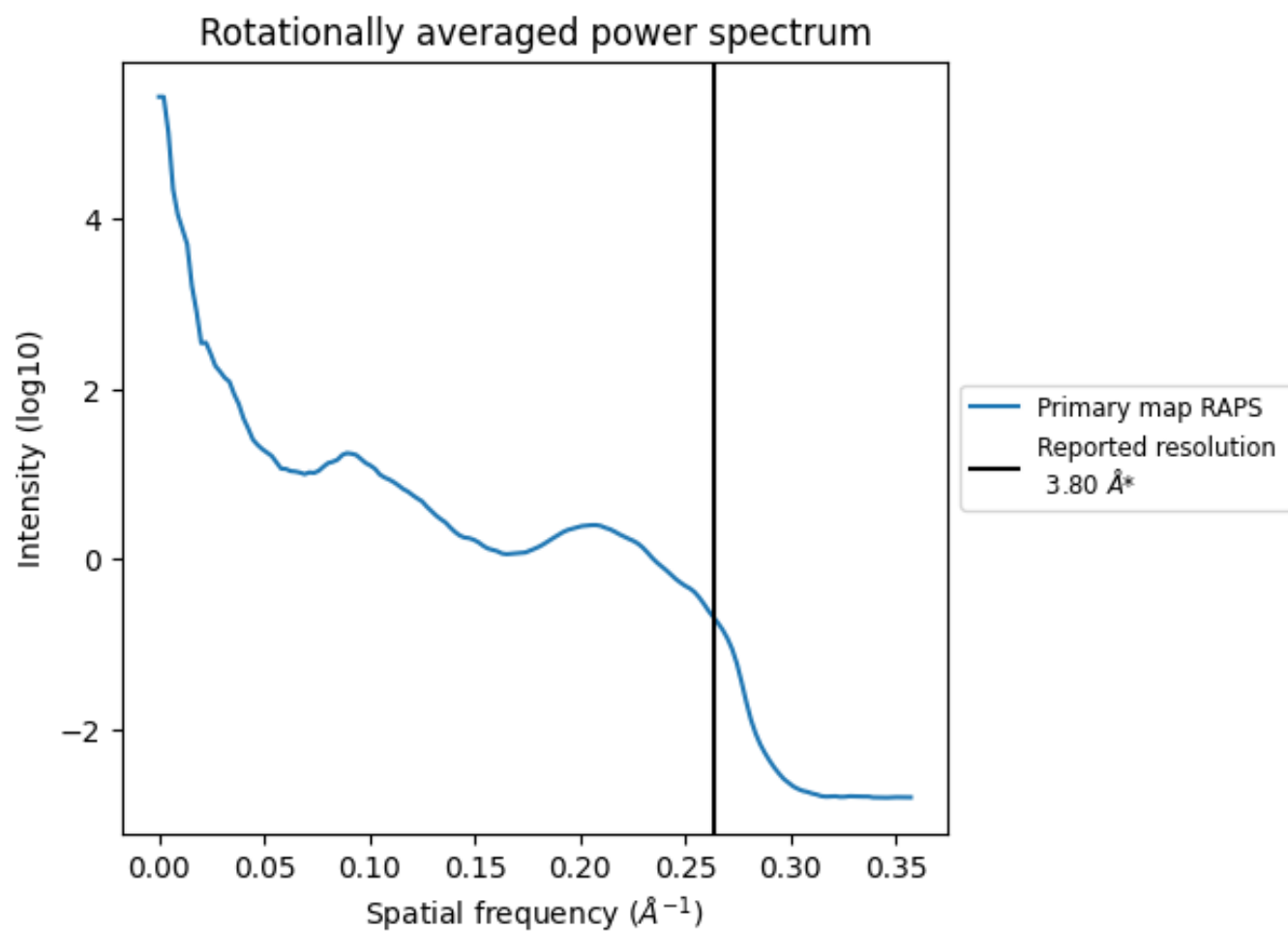
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 925 nm^3 ; this corresponds to an approximate mass of 836 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 0.263 Å⁻¹

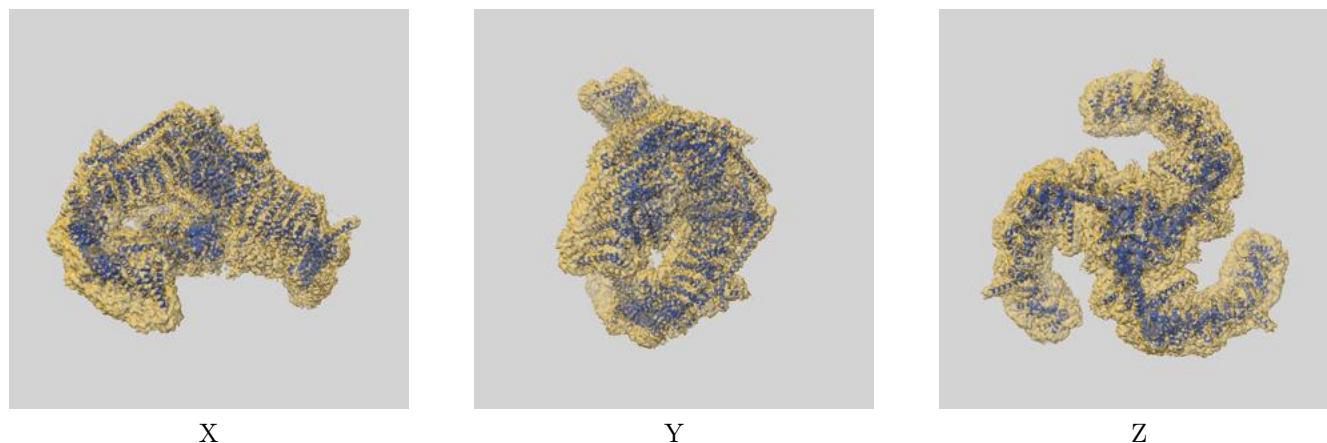
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

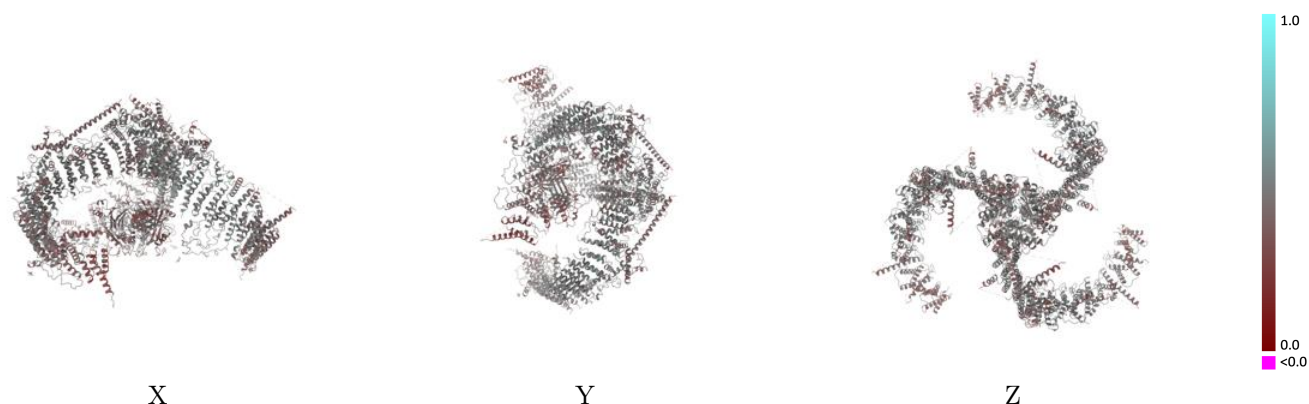
This section contains information regarding the fit between EMDB map EMD-9975 and PDB model 6KG7. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 5.69 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](#)

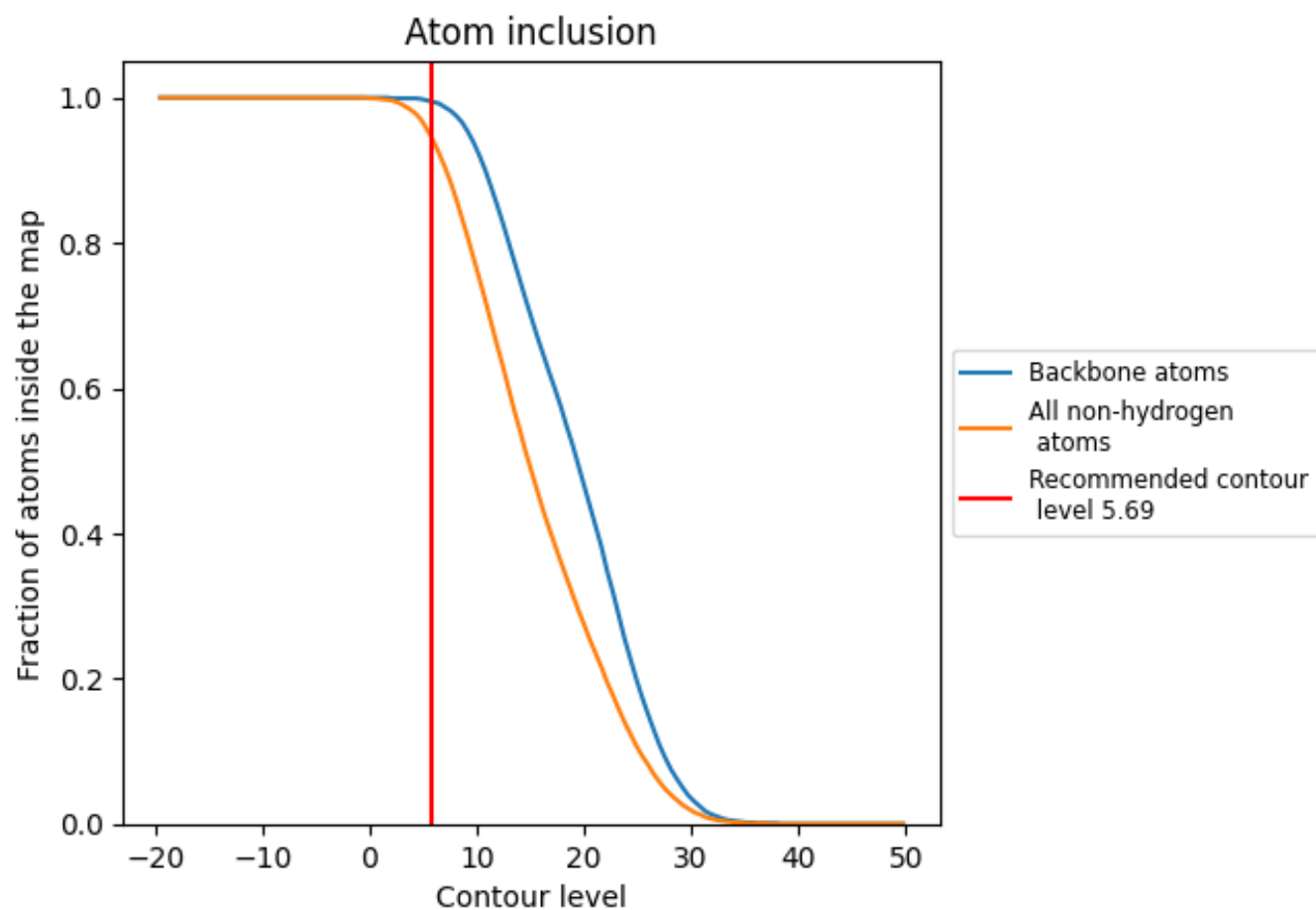


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 100% of all backbone atoms, 95% 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 (5.69) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9480	0.4370
A	0.9460	0.4410
B	0.9490	0.4370
C	0.9480	0.4320

