



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 12:17 PM UTC

PDB ID : 7W7G / pdb_00007w7g
EMDB ID : EMD-32344
Title : Structure of Mammalian NALCN-FAM155A-UNC79-UNC80 quaternary complex
Authors : Chen, L.; Kang, Y.
Deposited on : 2021-12-04
Resolution : 3.20 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

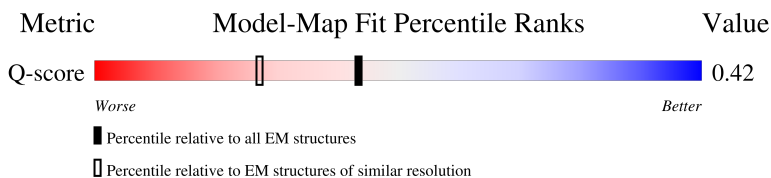
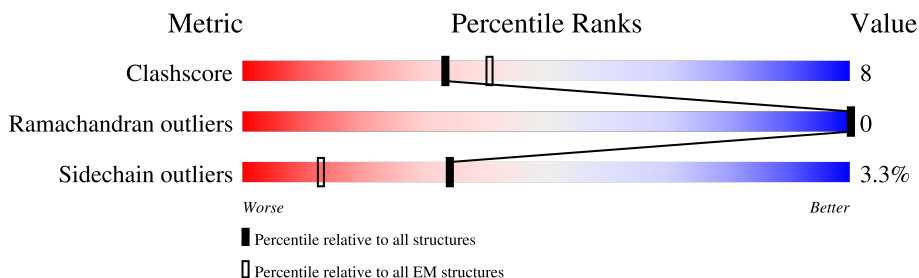
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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	2654	11% 43% 13% 42%
2	B	3326	6% 39% 12% 49%
3	C	1738	15% 63% 14% 23%
4	D	467	9% 28% 8% 63%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 38143 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 Protein unc-79 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1528	Total	C	N	O	S	0	0
			12097	7833	1998	2161	105		

- Molecule 2 is a protein called Protein unc-80 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1711	Total	C	N	O	S	0	0
			13777	8900	2351	2430	96		

- Molecule 3 is a protein called Sodium leak channel non-selective protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	1346	Total	C	N	O	S	0	0
			10847	7164	1777	1821	85		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	52	SER	PRO	conflict	UNP Q6Q760
C	748	ALA	THR	conflict	UNP Q6Q760

- Molecule 4 is a protein called Transmembrane protein FAM155A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	173	Total	C	N	O	S	0	0
			1378	875	212	275	16		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

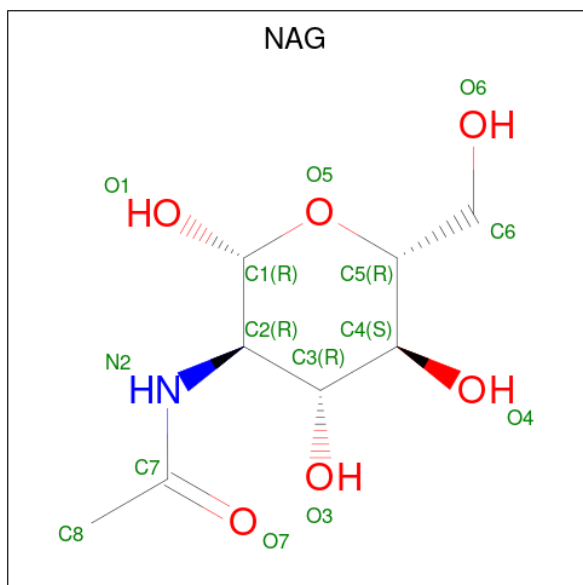
Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
5	B	1	Total	Zn	0
			1	1	

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$) (labeled as "Ligand of Interest" by depositor).



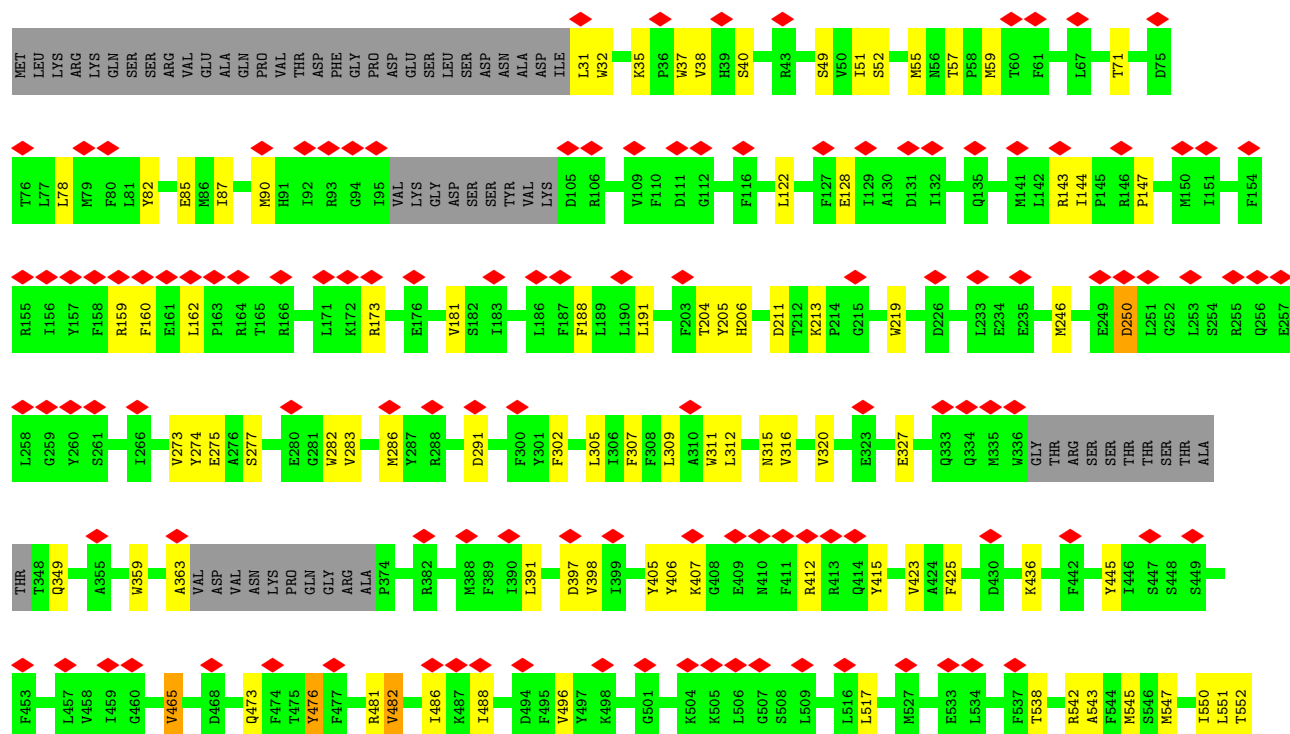
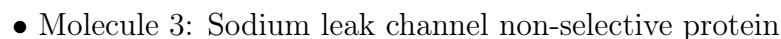
Mol	Chain	Residues	Atoms				AltConf
6	C	1	Total	C	N	O	0
			14	8	1	5	
6	C	1	Total	C	N	O	0
			14	8	1	5	
6	C	1	Total	C	N	O	0
			14	8	1	5	

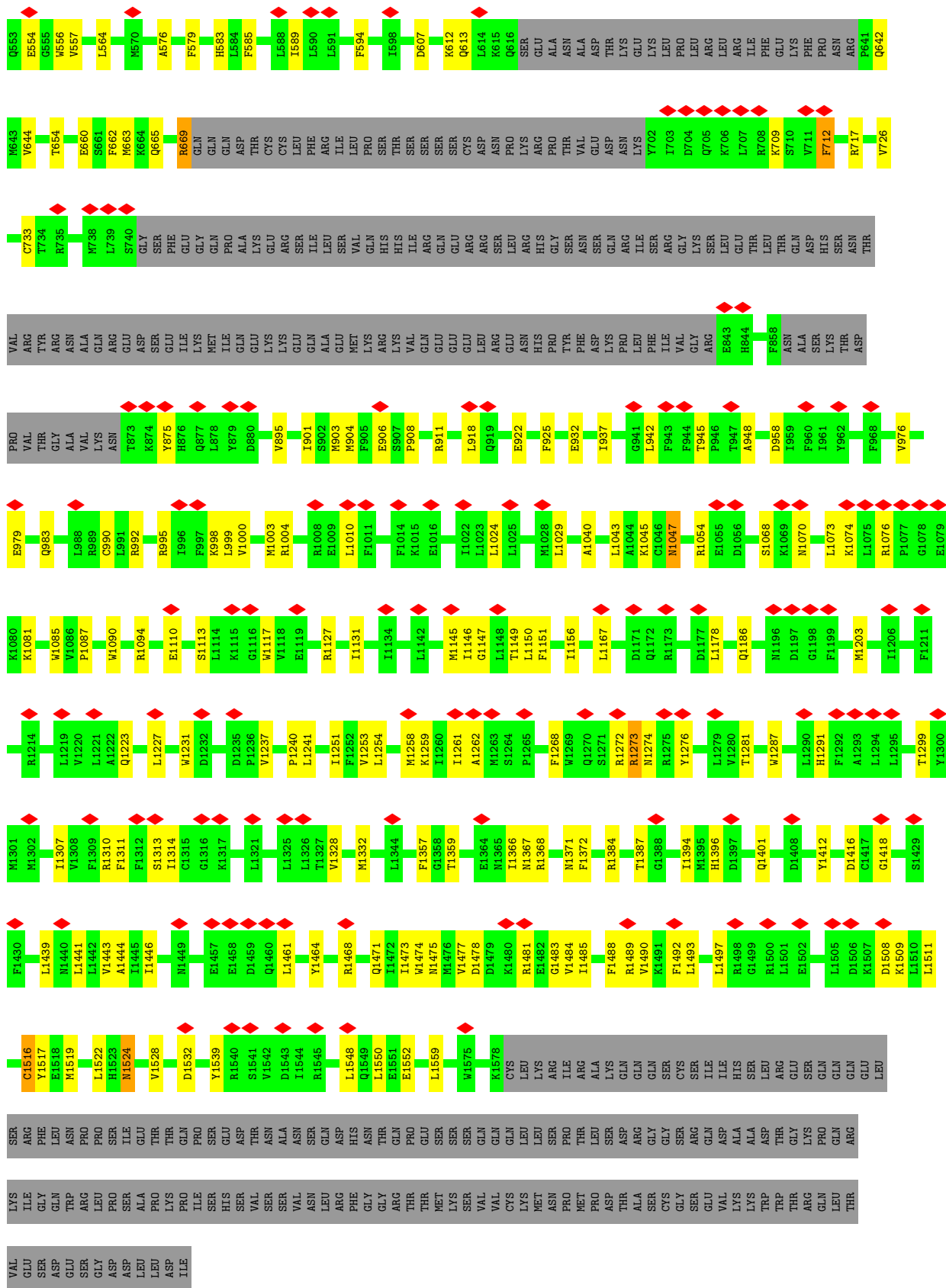




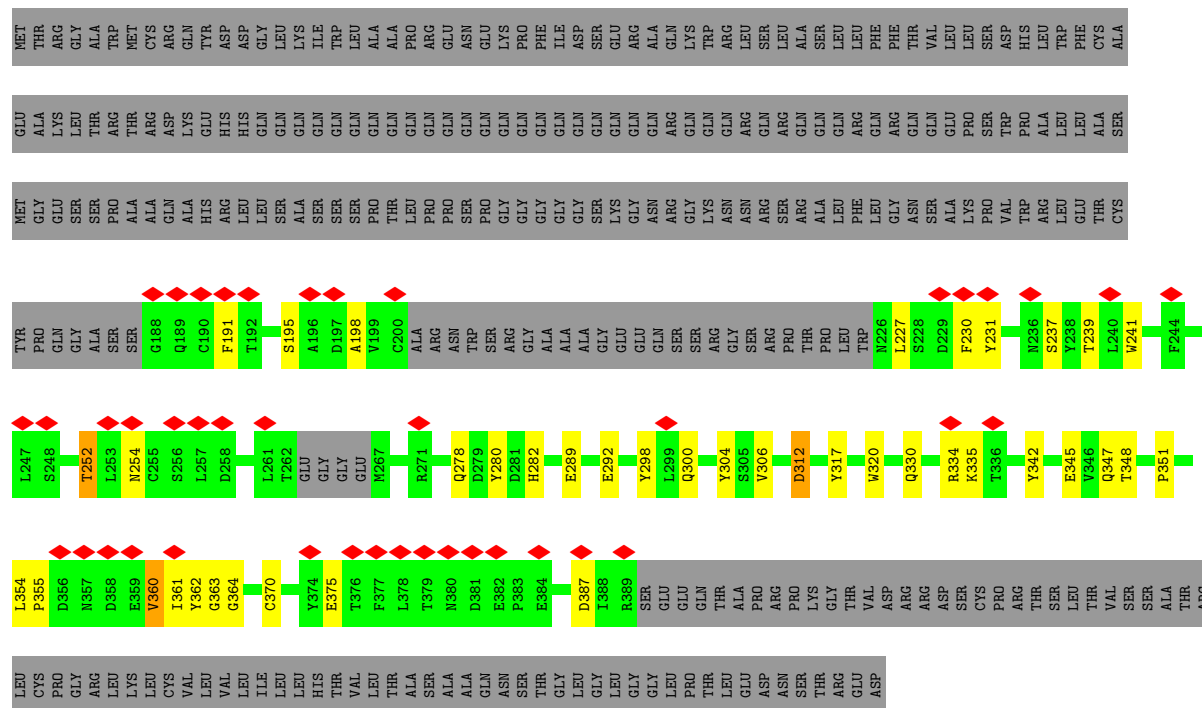


C2687	L2585	MET	L2302	E2164	K2042	M1926	VAL	SER	S1752	GLY	ASP
L2688	A2586	SER	P2303	L2170	M2045	E1927	SER	PHE	THR	THR	THR
T2689	G2587	GLY	L2306	F2171	E2048	D1928	ALA	ALA	VAL	VAL	VAL
Q2693	E2588	VAL	Q2307	L2172	E2048	G1929	CYS	ARG	ALA	ASP	LEU
L2696	P2589	ASN	V2308	T2176	E2051	E1930	THR	ALA	SER	GLU	LEU
R2590	A2414	THR	D2311	T2179	K2052	D1934	SER	SER	SER	ASN	GLY
V2591	L2415	ARG	Y2312	T2179	K2052	V1941	THR	ARG	ARG	HIS	SER
T2592	K2416	PRO	E2313	H2187	L2054	L1946	SER	SER	GLN	TRP	SER
A2593	L2417	GLU	S2314	H2187	L2055	L1946	HIS	HIS	ASN	VAL	ALA
L2594	V2421	GLN	N2315	M2190	V2056	L1950	ASN	ARG	ALA	SER	ALA
E2595	E2427	GLY	L2318	L2195	M2060	I1951	TYR	ALA	ALA	ALA	SER
L2596	R2430	ALA	R2319	L2195	T2063	E1952	SER	GLU	GLU	LEU	GLU
L2597	S2431	LYS	R2320	F2201	T2063	D1953	PHE	HIS	PRO	PRO	GLU
S2601	L2432	HIS	F2324	P2202	T2065	P1954	ARG	ILE	ILE	GLY	SER
S2611	L2438	ILE	Q2328	T2206	V2067	H1960	GLY	K1804	L1803	LYS	LYS
P2619	R2451	ARG	F2329	D2207	V2068	F1961	SER	N1805	L1806	GLN	GLN
R2626	Q2452	ASN	Y2330	E2209	Q2087	L1962	VAL	Q1807	L1806	LYS	LYS
G2627	T2453	LEU	H2333	E2209	E2088	E1963	THR	Q1807	L1806	CYS	LEU
R2630	S2454	HIS	R2334	E2221	E2089	K1964	VAL	E1809	L1806	SER	ASN
R2633	Q2455	LEU	K2335	L2222	L2096	L1965	SER	E1810	L1806	LYS	ALA
E2634	V2456	GLU	L2339	F2223	S2104	N1969	ALA	E1811	L1806	THR	GLY
E2635	E2457	GLY	Q2340	L2228	Q2105	R1970	VAL	E1733	L1806	GLY	THR
L2639	T2458	GLN	L2341	Q2229	Q2105	Q1971	SER	G1734	L1806	ARG	LEU
T2640	A2461	GLY	F2342	K2230	H2108	L1974	ASP	A1735	L1806	THR	THR
R2647	A2462	LEU	F2351	T2234	Y2109	M1977	GLU	Q1736	L1806	PRO	PRO
P2648	R2463	PRO	P2351	E2238	Y2121	N1977	GLU	E1737	L1806	SER	SER
R2656	E2464	ARG	ALA	E2238	N2122	I1986	HIS	G1744	L1806	LEU	LEU
L2657	E2465	ALA	ALA	L2256	K2123	G1986	ALA	S1745	L1806	LYS	LYS
M2660	L2466	ASN	ASN	L2256	T2124	D1987	THR	I1746	L1806	ARG	ARG
K2663	Q2477	THR	GLY	A2264	Y2125	F1988	GLU	S1752	L1806	VAL	VAL
L2664	T2487	SER	SER	L2267	P2131	Q1991	HIS	P1753	L1806	SER	SER
M2665	A2492	GLN	K2361	E2270	R2132	Y1999	THR	M1757	L1806	ASN	ASN
K2666	P2493	MET	Q2366	L2274	S2137	L2000	PRO	F1763	L1806	LEU	LEU
M2667	D2370	SER	D2370	Q2277	L2140	G2002	VAL	Q1770	L1806	GLY	GLY
P2668	L2371	ARG	L2372	T2281	N2141	V2001	PRO	CYS	L1806	ASP	ASP
R2671	E2392	ASN	E2392	N2284	V2143	L2003	GLN	SER	L1806	LYS	LYS
R2672	S2397	GLY	S2397	F2283	M2144	V2008	GLU	GLY	L1806	ASP	ASP
Q2673	L2398	HIS	L2398	S2294	R2145	R2009	GLU	SER	L1806	GLY	GLY
V2674	D2399	LYS	D2399	L2295	L2153	S2020	GLU	VAL	L1806	VAL	VAL
V2787	Y2402	THR	Y2402	S2296	Q2157	A2021	VAL	ASP	L1806	ASP	ASP
L2788	G2403	THR	G2403	G2297	V2158	T2023	ALA	ILE	L1806	ASN	ASN
G2791	N2582	ALA	N2404	W2300	R2161	T2024	ASN	GLU	L1806	GLY	GLY
S2792	Q2583	ASN	E2405	I2301	R2161	G2035	THR	ASP	L1806	ASP	ASP
S2793	N2584	HIS	E2405	I2301	R2161	L2041	LEU	GLN	L1806	GLN	GLN
S2794		THR					SER	LYS	L1806	LYS	LYS





- Molecule 4: Transmembrane protein FAM155A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	275170	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	8.606	Depositor
Minimum map value	-0.139	Depositor
Average map value	0.087	Depositor
Map value standard deviation	0.155	Depositor
Recommended contour level	0.95	Depositor
Map size ($\text{\AA}$)	370.72, 370.72, 370.72	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.324, 1.324, 1.324	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, ZN

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	0.17	0/12360	0.27	0/16769
2	B	0.18	0/14084	0.29	0/19082
3	C	0.11	0/11121	0.23	0/15080
4	D	0.10	0/1410	0.21	0/1913
All	All	0.16	0/38975	0.27	0/52844

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	12097	0	12285	244	0
2	B	13777	0	14013	252	0
3	C	10847	0	10959	149	0
4	D	1378	0	1253	23	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	C	42	0	39	1	0
All	All	38143	0	38549	633	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 8.

The worst 5 of 633 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:1545:HIS:HE1	2:B:1553:CYS:SG	1.88	0.97
2:B:2421:VAL:HG22	3:C:663:MET:HE1	1.64	0.79
1:A:1162:ARG:HE	1:A:1231:ILE:HG23	1.49	0.77
3:C:173:ARG:HH21	3:C:327:GLU:HB2	1.54	0.73
2:B:1214:ALA:O	2:B:1219:ARG:NH1	2.22	0.72

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	1492/2654 (56%)	1441 (97%)	51 (3%)	0	100	100
2	B	1671/3326 (50%)	1586 (95%)	85 (5%)	0	100	100
3	C	1330/1738 (76%)	1294 (97%)	36 (3%)	0	100	100
4	D	167/467 (36%)	157 (94%)	10 (6%)	0	100	100
All	All	4660/8185 (57%)	4478 (96%)	182 (4%)	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	1363/2366 (58%)	1313 (96%)	50 (4%)	30	63
2	B	1529/2916 (52%)	1471 (96%)	58 (4%)	29	62
3	C	1174/1572 (75%)	1149 (98%)	25 (2%)	47	71
4	D	157/409 (38%)	151 (96%)	6 (4%)	29	62
All	All	4223/7263 (58%)	4084 (97%)	139 (3%)	34	65

5 of 139 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	654	THR
3	C	875	TYR
3	C	1516	CYS
1	A	2522	PHE
1	A	2477	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	2069	HIS
2	B	2477	GLN
3	C	1392	ASN
2	B	2291	HIS
2	B	2711	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

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
6	NAG	C	2001	3	14,14,15	0.20	0	17,19,21	0.43	0
6	NAG	C	2002	3	14,14,15	0.22	0	17,19,21	0.48	0
6	NAG	C	2003	3	14,14,15	0.22	0	17,19,21	0.47	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
6	NAG	C	2001	3	-	4/6/23/26	0/1/1/1
6	NAG	C	2002	3	-	0/6/23/26	0/1/1/1
6	NAG	C	2003	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

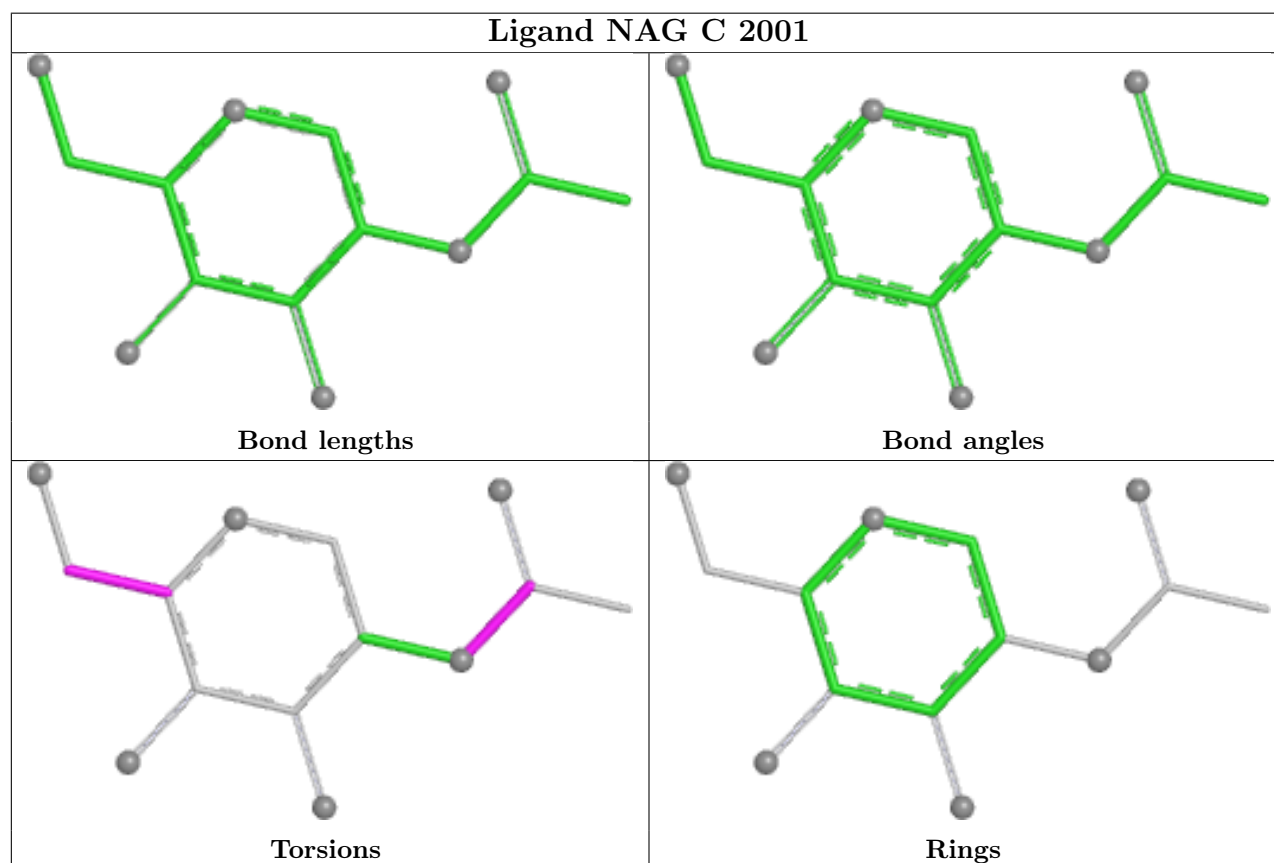
Mol	Chain	Res	Type	Atoms
6	C	2001	NAG	C4-C5-C6-O6
6	C	2001	NAG	O5-C5-C6-O6
6	C	2001	NAG	C8-C7-N2-C2
6	C	2001	NAG	O7-C7-N2-C2

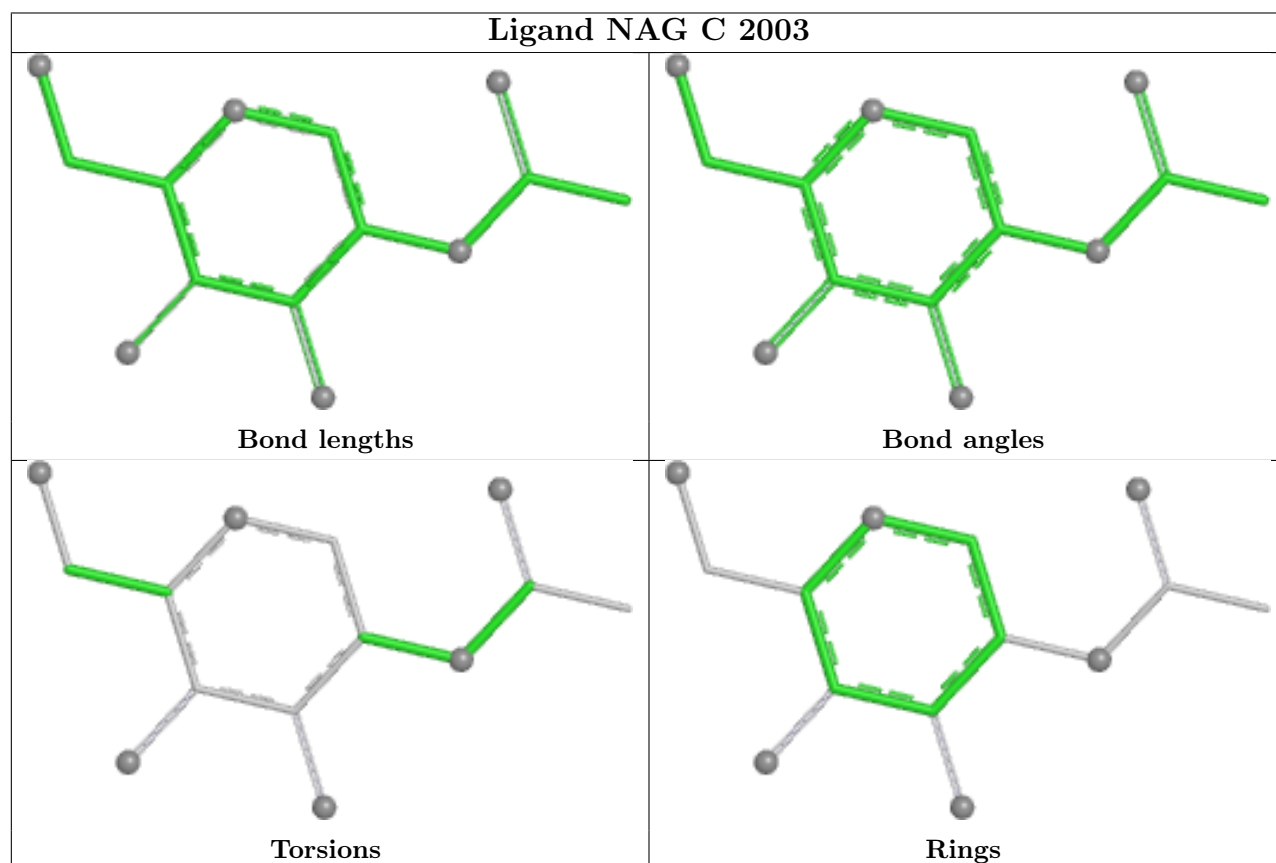
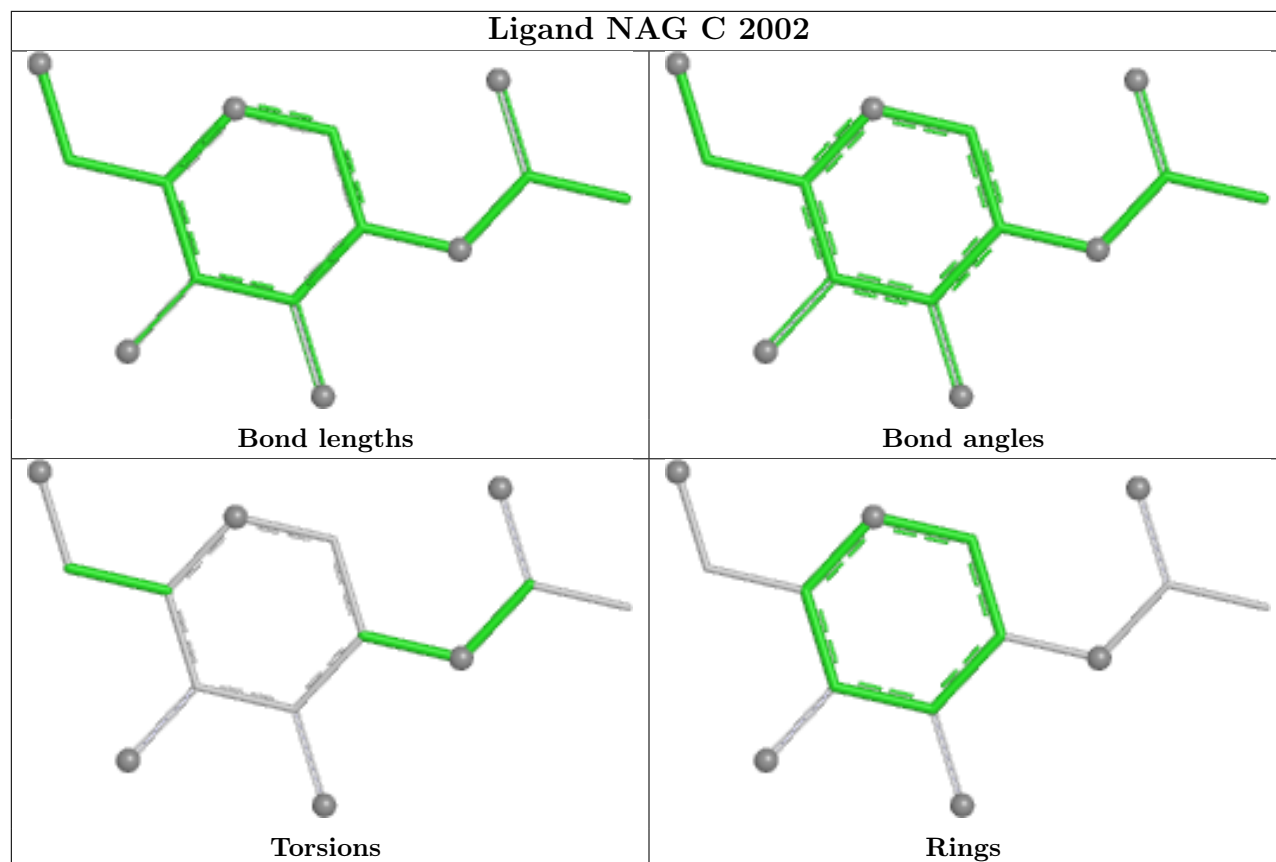
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	2002	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

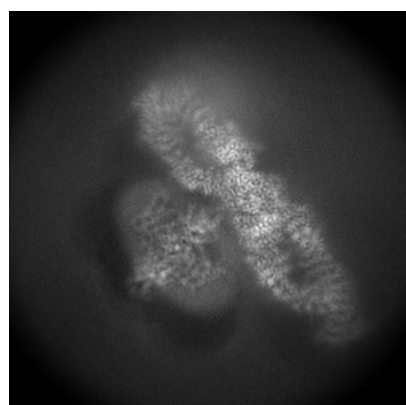
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32344. These allow visual inspection of the internal detail of the map and identification of artifacts.

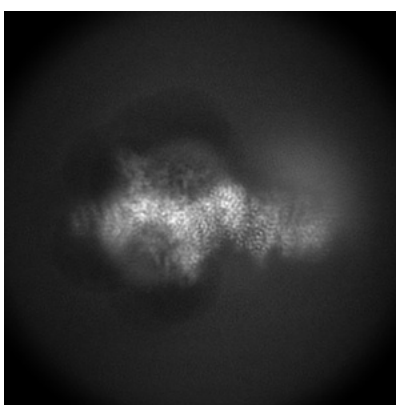
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

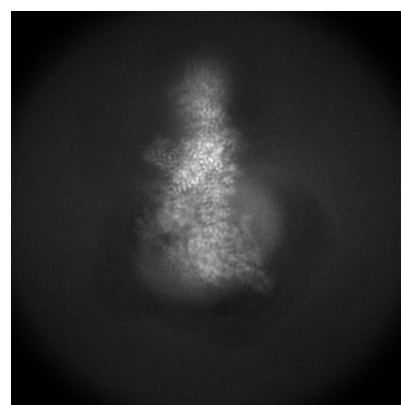
6.1.1 Primary map



X



Y

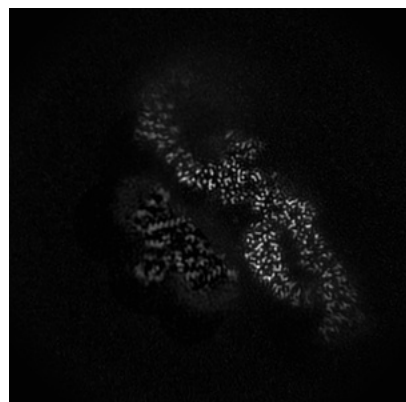


Z

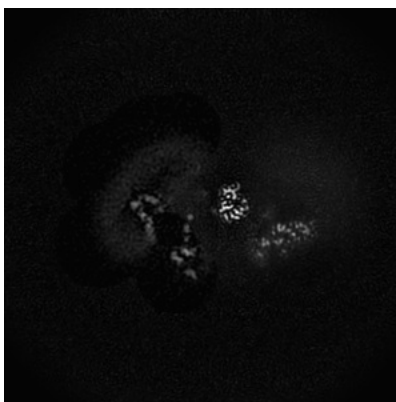
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

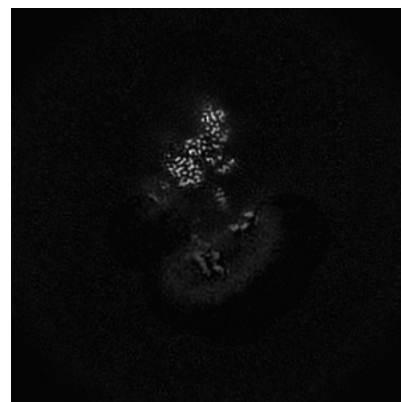
6.2.1 Primary map



X Index: 140



Y Index: 140

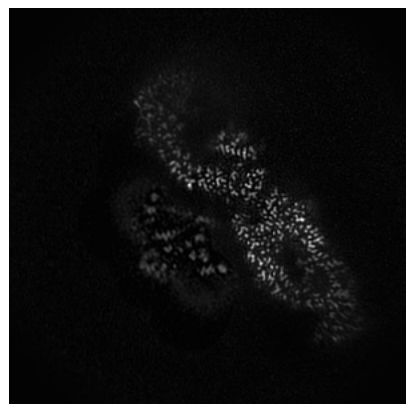


Z Index: 140

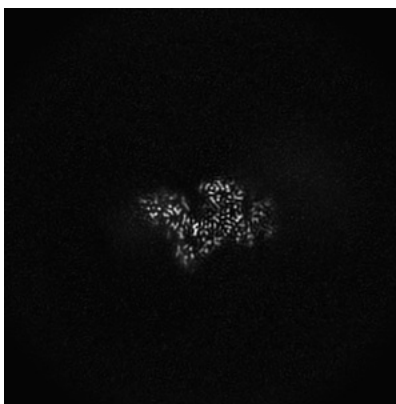
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

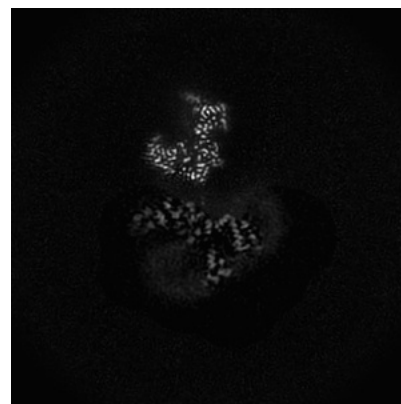
6.3.1 Primary map



X Index: 135



Y Index: 170

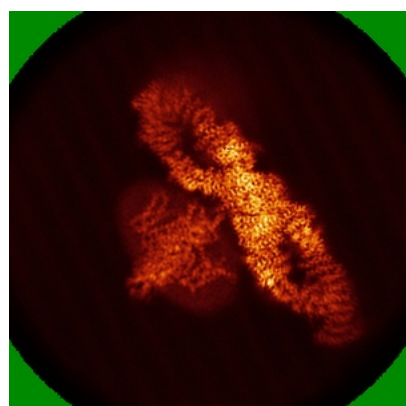


Z Index: 126

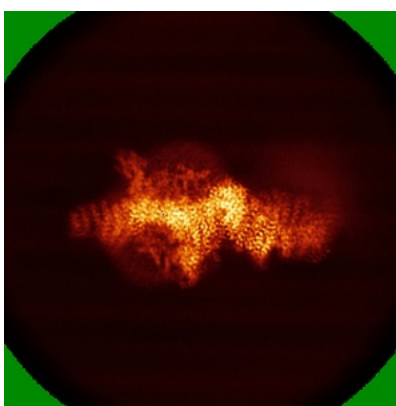
The images above show the largest variance slices of the map in three orthogonal directions.

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

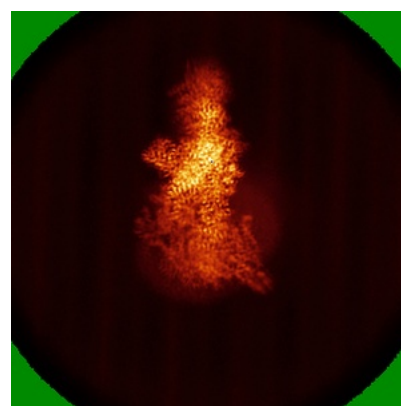
6.4.1 Primary map



X



Y

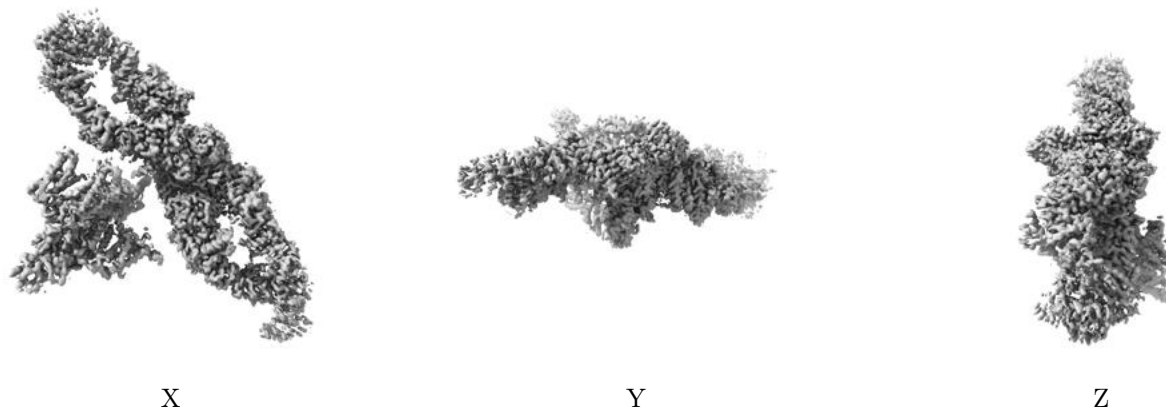


Z

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

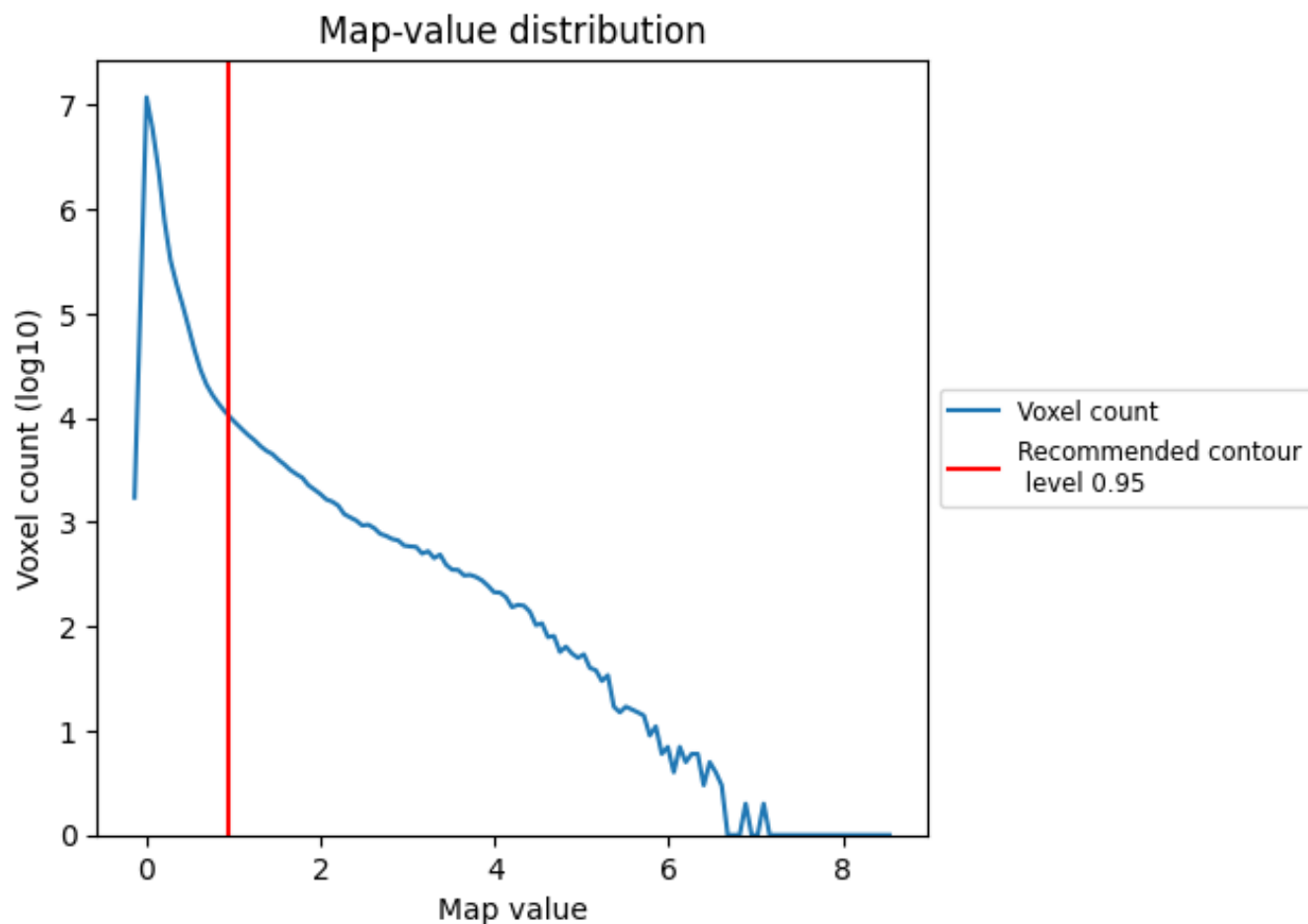
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

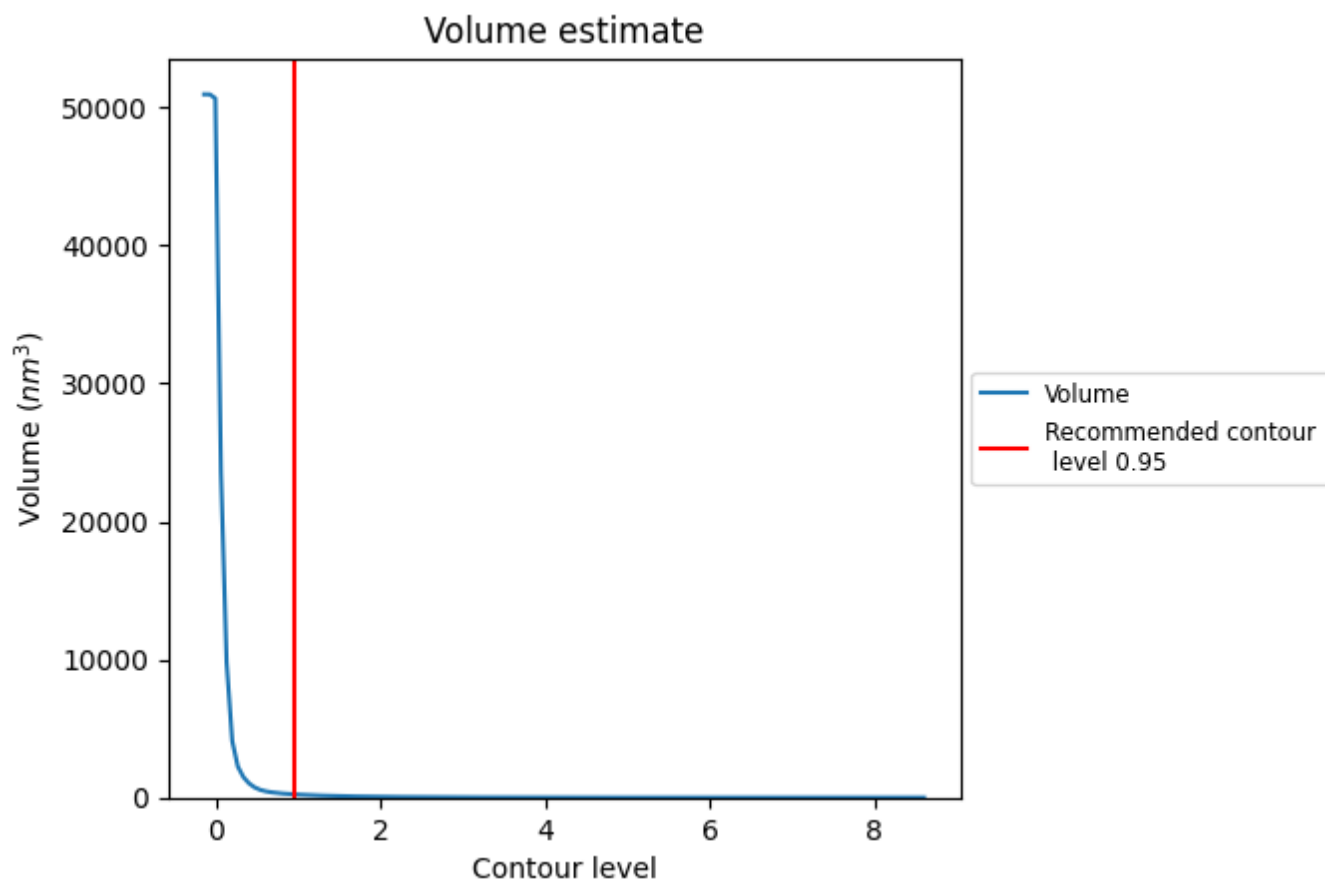
This section contains the results of statistical analysis of the map.

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.

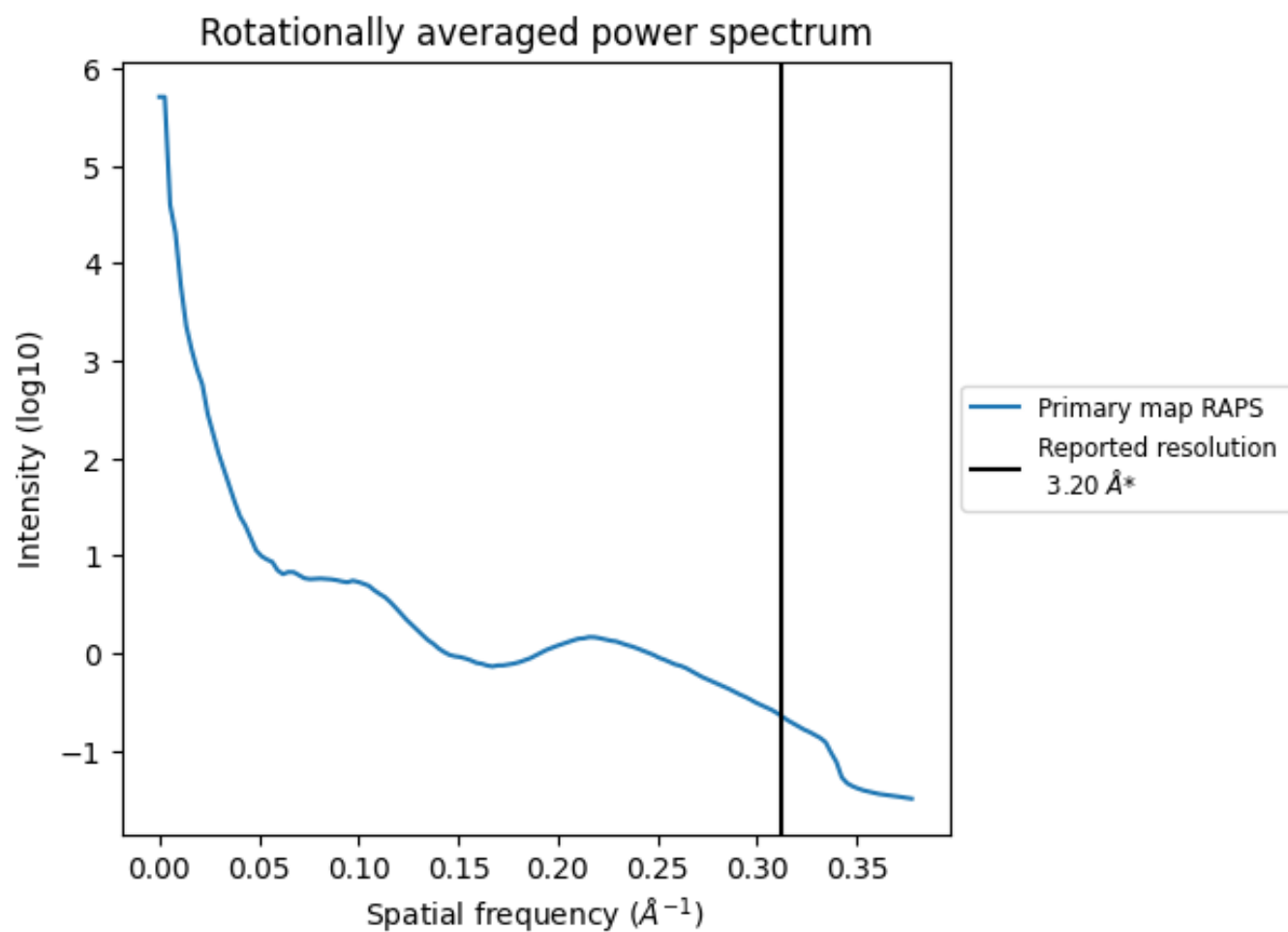
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 234 nm³; this corresponds to an approximate mass of 211 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 0.312 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

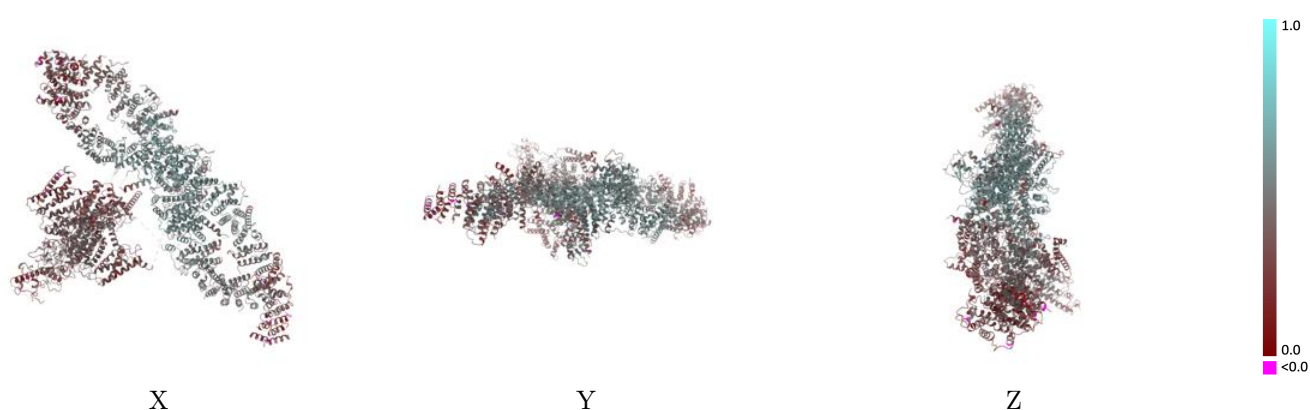
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32344 and PDB model 7W7G. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)

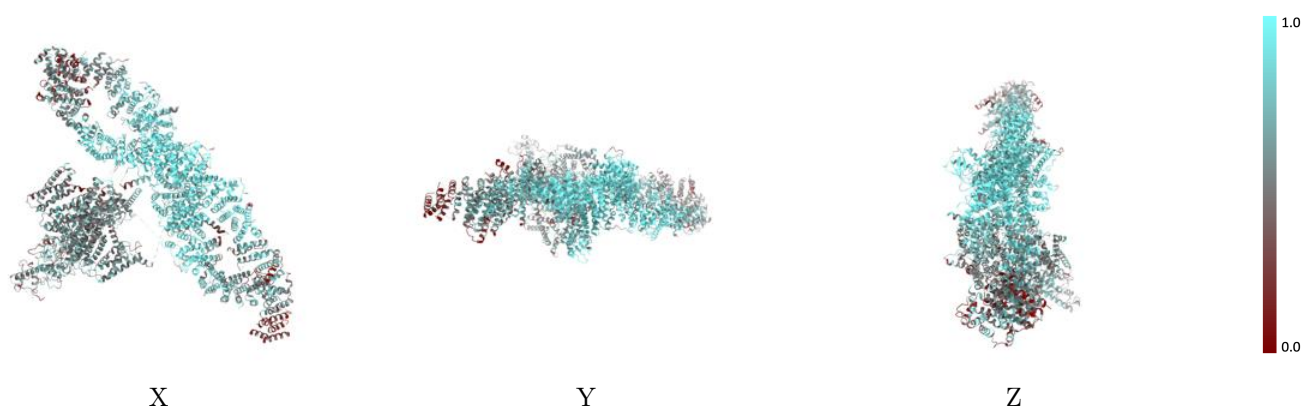
This section was not generated.

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



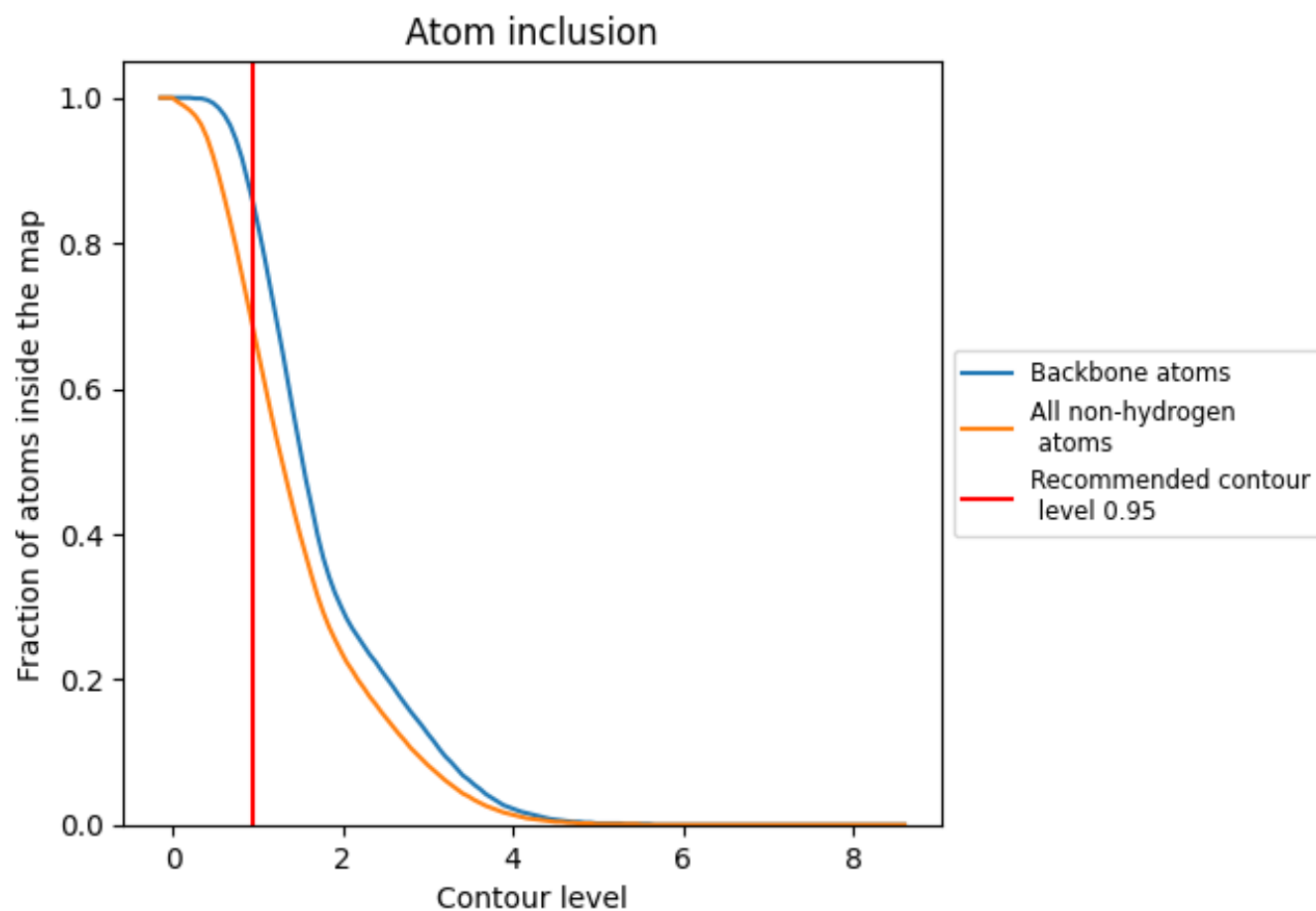
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.95).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 68% 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 (0.95) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6820	0.4200
A	0.7210	0.4400
B	0.7710	0.4660
C	0.5450	0.3520
D	0.5240	0.3220

