



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 09:11 PM UTC

PDB ID : 8X4B / pdb_00008x4b
EMDB ID : EMD-38045
Title : Cryo-EM structure of Ryanodine receptor 1 (TM helix S0,100 nM Ca²⁺, open state)
Authors : Chen, Q.; Hu, H.
Deposited on : 2023-11-15
Resolution : 4.20 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:

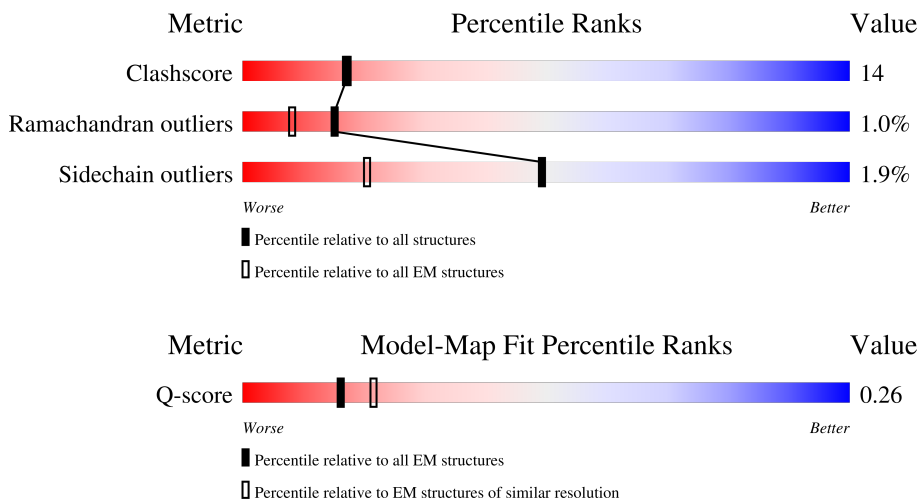
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.20 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	5410 (3.70 - 4.70)

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	5037	10% 66% 16% • 17%
1	B	5037	10% 65% 16% • 17%
1	C	5037	10% 66% 16% • 17%
1	D	5037	10% 66% 16% • 17%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 110456 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4173	Total	C	N	O	S	0	0
			27613	17058	5114	5292	149		
1	B	4173	Total	C	N	O	S	0	0
			27613	17058	5114	5292	149		
1	C	4173	Total	C	N	O	S	0	0
			27613	17058	5114	5292	149		
1	D	4173	Total	C	N	O	S	0	0
			27613	17058	5114	5292	149		

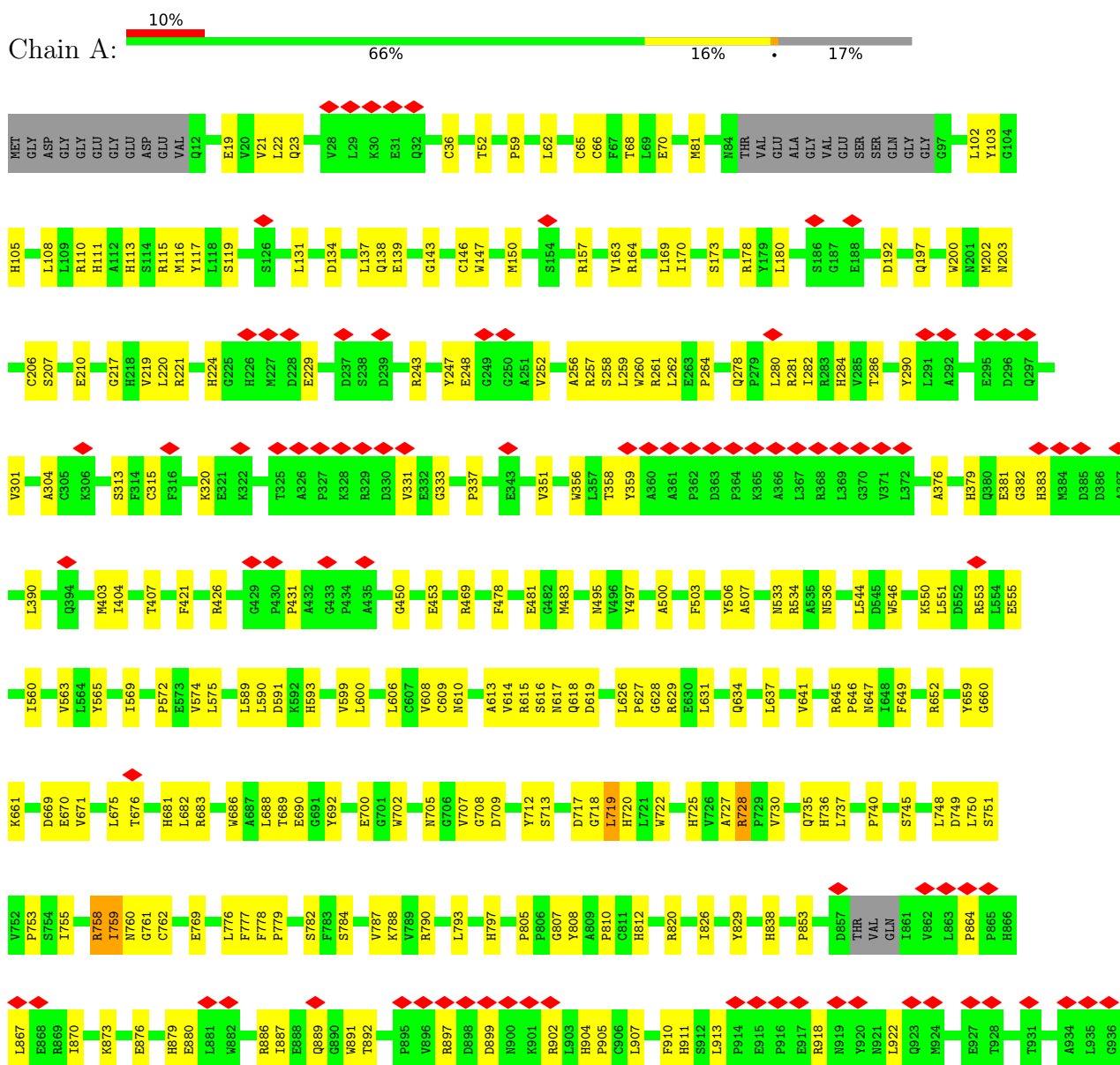
- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

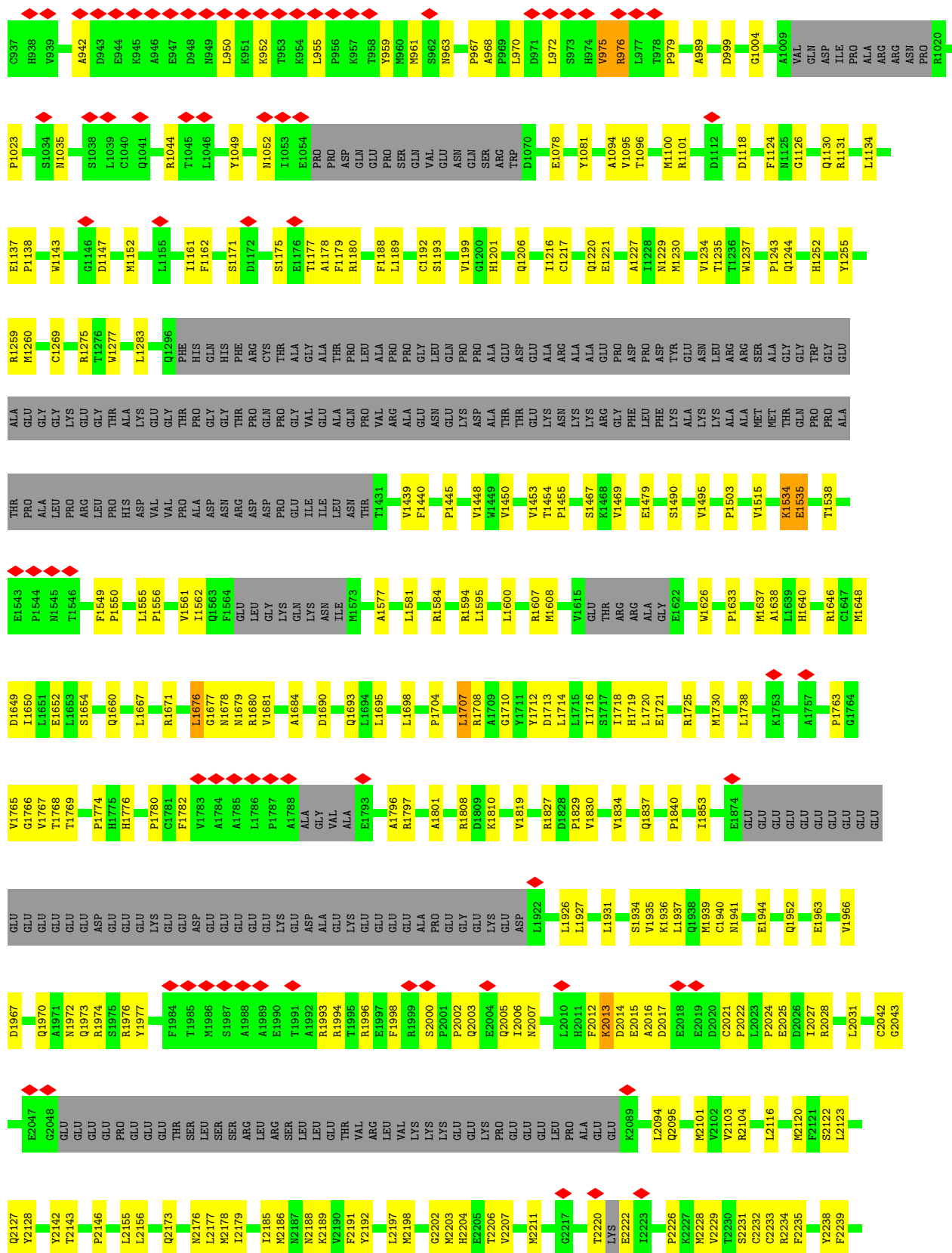
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	Ca	0
			1	1	
2	B	1	Total	Ca	0
			1	1	
2	C	1	Total	Ca	0
			1	1	
2	D	1	Total	Ca	0
			1	1	

3 Residue-property plots

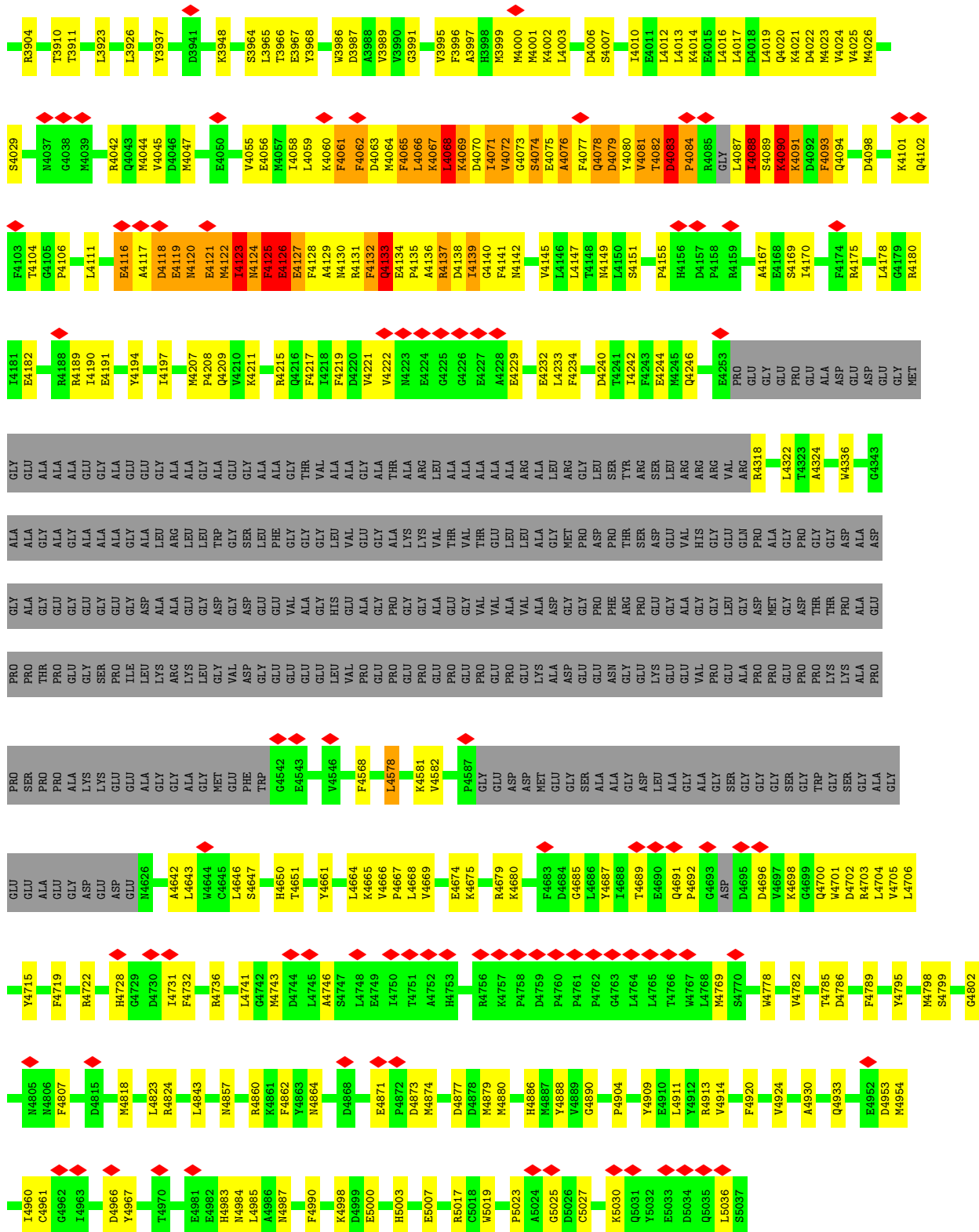
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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









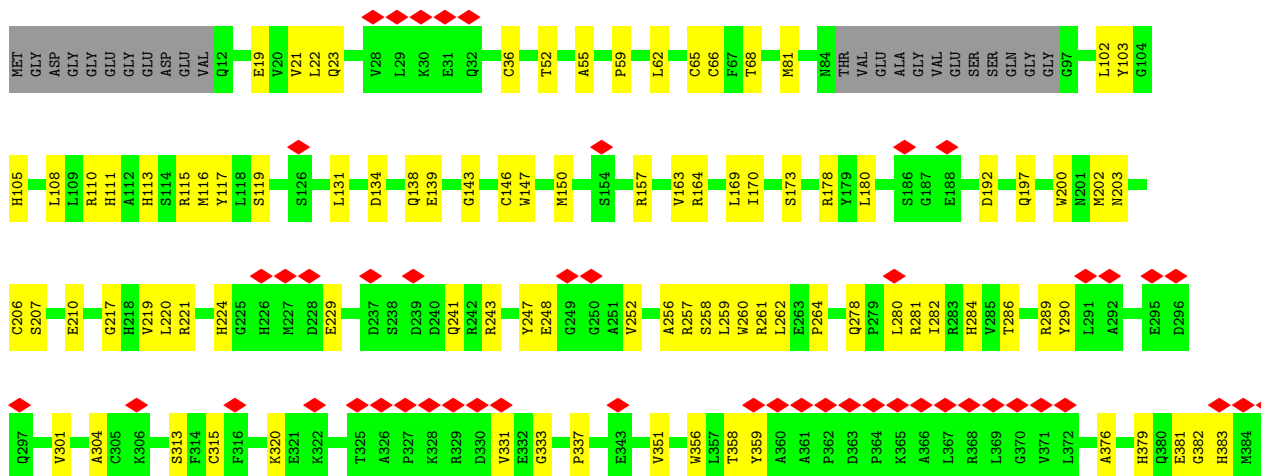
• Molecule 1: Ryanodine receptor 1

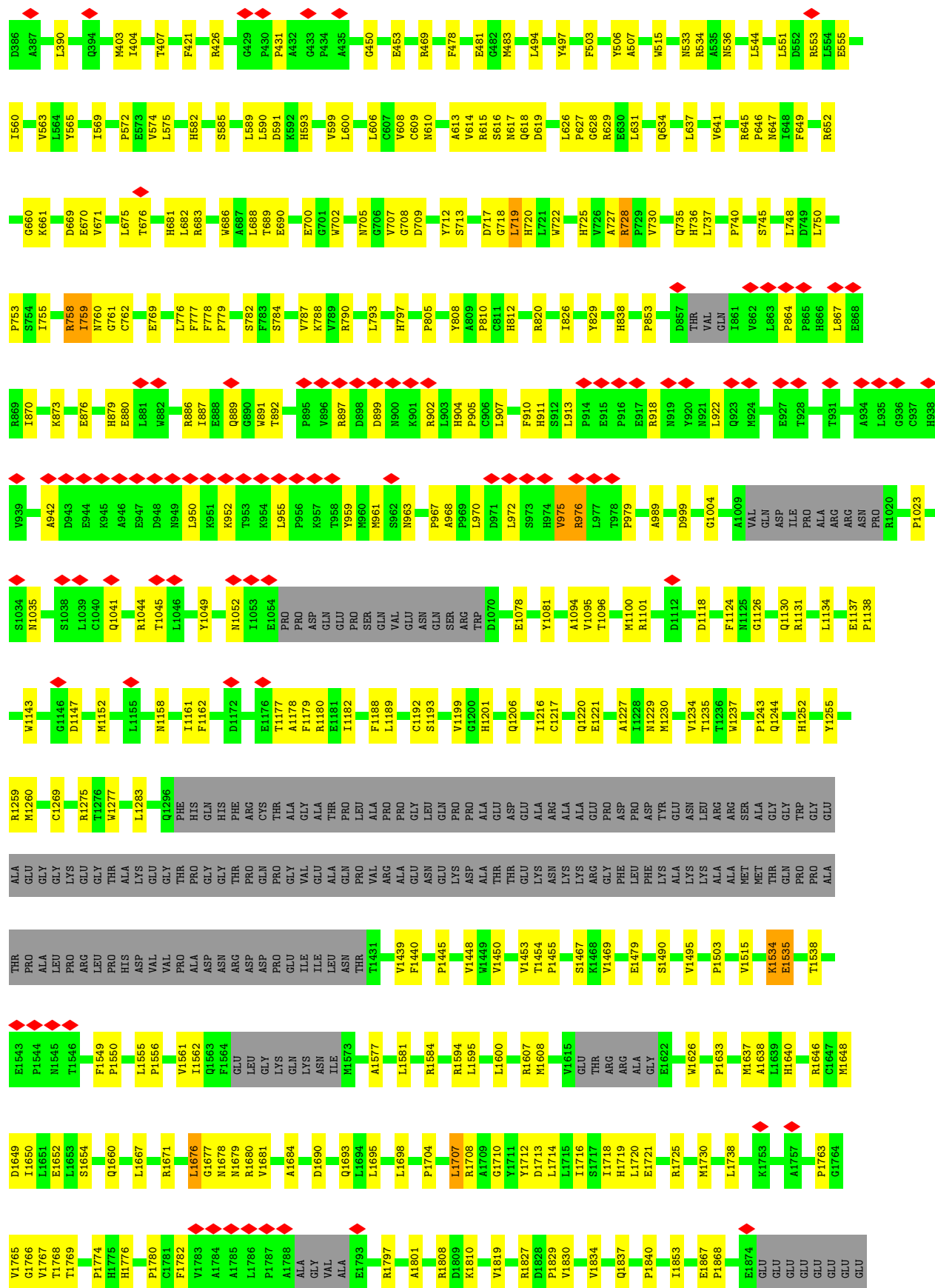






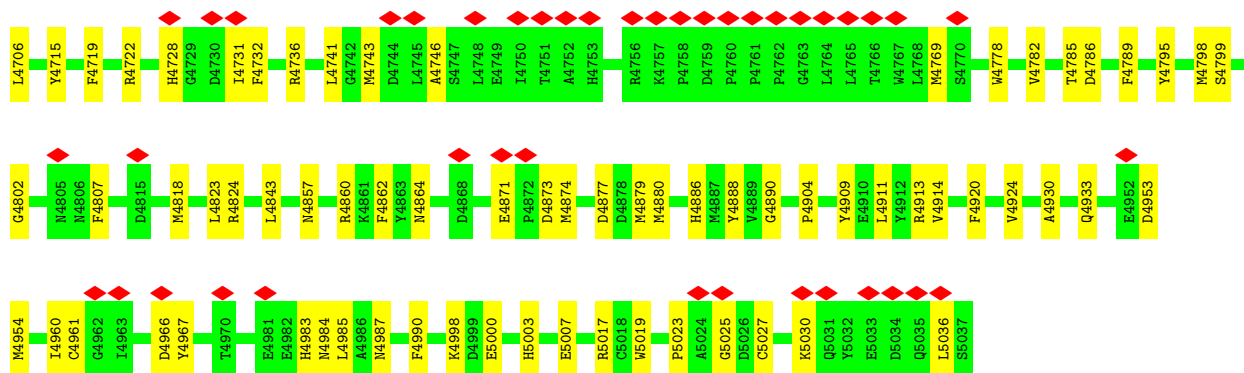




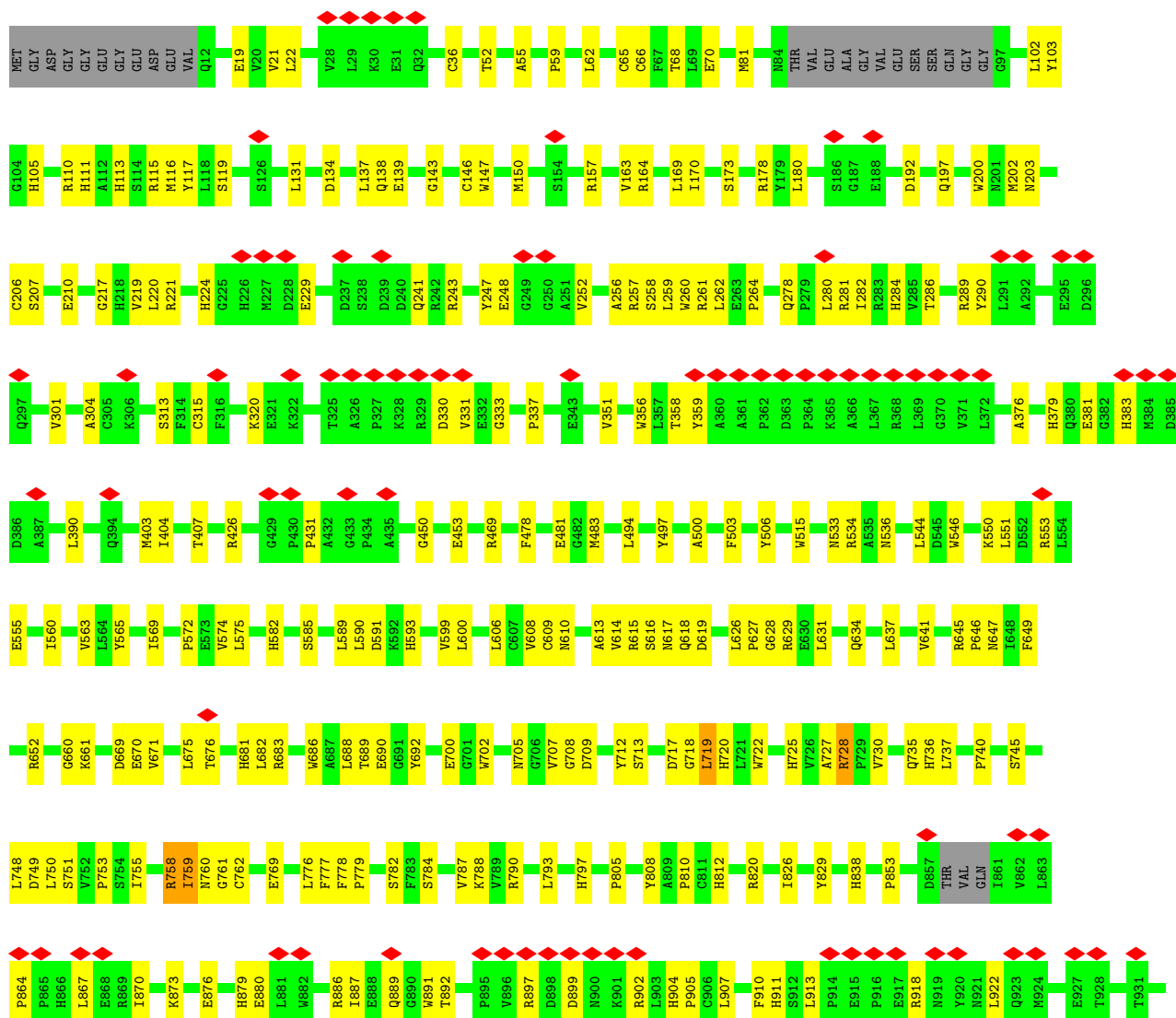








• Molecule 1: Ryanodine receptor 1



L2116	L2027	E1944	E1757	R1646	E1535	THR	ALA	R1259	L1134	PRO	A934
M2120	R2028	Q1952	P1763	C1647	T1538	PRO	GLU	M1260	E1137	R1020	L935
S2122	L2031	E1963	G1764	D1649	E1543	ALA	GLY	C1269	P1138	P1023	G936
L2123	C2042	V1966	V1765	I1650	P1544	ARG	LYS	R1275	W1143	S1034	C937
Q2127	G2043	D1967	V1767	L1651	M1545	LEU	GLY	T1276	W1277	N1035	H938
Y2128	E2047	Q1970	T1768	E1652	T1546	PRO	THR	L1283	G1146	S1038	V939
Y2142	G2048	P1774	P1774	S1654	F1549	HIS	ALA	Q1296	D1147	L1039	A942
T2143	GLU	H1775	H1775	Q1660	P1550	VAL	GLY	PHE	M1152	C1040	D943
P2146	GLU	H1776	H1776	L1667	L1555	PRO	THR	HIS	L1155	Q1041	E944
L2155	ASP	P1780	P1780	L1671	P1556	ALA	PRO	GLN	I1161	R1044	K945
L2156	GLU	F1781	F1781	R1671	V1561	ASN	GLY	HIS	F1162	T1045	A946
Q2173	GLU	E1782	E1782	L1676	V1562	ARG	THR	ARG	T1046	D948	E947
L2177	THR	V1783	V1783	G1677	Q1563	ASP	PRO	CYS	S1171	Y1049	H949
M2178	SER	A1784	A1784	N1678	F1564	PRO	PRO	THR	D1172	N1052	L950
I2179	SER	L1785	L1785	N1679	GLU	GLY	GLY	ALA	S1175	I1053	K951
I2179	SER	V1681	V1681	I1680	LEU	ILE	VAL	ALA	E1176	E1054	K952
T2185	SER	A1684	A1684	L1695	LYS	LEU	ALA	ALA	T1177	PRO	T953
M2186	ARG	D1690	D1690	L1698	GLN	ASN	GLN	PRO	A1178	PRO	K954
M2187	ARG	Q1693	Q1693	L1699	ILE	THR	VAL	ALA	F1179	ASP	L955
N2188	SER	L1694	L1694	L1695	M1573	ASN	ASN	GLY	R1180	GLN	P956
K2189	LEU	L1695	L1695	L1698	A1577	GLY	GLY	LEU	T1199	GLN	K957
V2190	LEU	P1704	P1704	L1698	L1581	GLY	GLY	GLN	G1200	VAL	T958
F2191	GLU	Q1704	Q1704	L1698	R1584	LEU	GLY	GLN	H1201	GLU	K960
Y2192	THR	L1707	L1707	L1698	R1584	GLY	THR	GLN	Q1206	ASN	K961
M2198	VAL	R1708	R1708	L1698	R1594	THR	THR	ASP	I1216	GLN	S962
M2203	LYS	D1809	D1809	L1698	L1595	GLY	GLY	ASP	C1217	GLN	K963
T2206	LYS	K1810	K1810	L1698	L1600	LYS	LYS	GLU	Q1220	TRP	P967
V2207	GLY	V1819	V1819	L1698	L1607	ASN	ASN	GLY	E1221	ARG	A968
M2211	LYS	R1827	R1827	L1698	M1608	GLY	GLY	GLY	A1227	LYS	P969
G2217	ASP	D1828	D1828	L1698	V1615	GLY	PHE	ASP	I1228	PRO	L970
T2220	LEU	P1829	P1829	L1698	THR	THR	LEU	ASP	N1229	E1078	D971
LYS	PRO	V1830	V1830	L1698	ARG	ARG	GLY	PRO	M1230	Y1081	L972
E2222	ALA	V1834	V1834	L1698	ALA	ALA	ALA	LYS	V1234	A1084	H973
I2223	GLU	Q1837	Q1837	L1698	E1622	GLY	LYS	ASN	T1235	V1095	H974
P2226	LEU	P1840	P1840	L1698	E1622	GLY	LYS	LEU	W1237	T1096	R975
K2227	PRO	I1853	I1853	L1698	GLY	GLY	LYS	ARG	V1243	M1100	R976
V2229	ALA	L1853	L1853	L1698	GLY	GLY	LYS	ALA	Q1244	R1101	L977
T2230	GLU	E1867	E1867	L1698	GLY	GLY	LYS	ALA	H1252	D1112	T978
S2231	GLU	P1868	P1868	L1698	GLY	GLY	LYS	ALA	Y1255	D1118	T978
C2232	GLU	E1874	E1874	L1698	GLY	GLY	LYS	ALA	F1124	D1118	A989
R2234	GLU	GLU	GLU	L1698	GLY	GLY	LYS	ALA	N1125	D1118	D999
F2235	GLU	GLU	GLU	L1698	GLY	GLY	LYS	ALA	G1126	D1118	G1004
											A1009
											VAL
											GLN
											ASP
											ILE
											PRO
											ALA
											ALA
											ARG
											ARG
											ASN





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	52414	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	1.049	Depositor
Minimum map value	-0.431	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.237	Depositor
Map size (Å)	523.2, 523.2, 523.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	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: CA

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	0.22	1/28107 (0.0%)	0.46	11/37709 (0.0%)
1	B	0.22	1/28107 (0.0%)	0.46	11/37709 (0.0%)
1	C	0.22	1/28107 (0.0%)	0.46	11/37709 (0.0%)
1	D	0.22	1/28107 (0.0%)	0.46	11/37709 (0.0%)
All	All	0.22	4/112428 (0.0%)	0.46	44/150836 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4125	PHE	C-O	5.61	1.31	1.24
1	B	4125	PHE	C-O	5.61	1.31	1.24
1	C	4125	PHE	C-O	5.61	1.31	1.24
1	D	4125	PHE	C-O	5.61	1.31	1.24

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4062	PHE	N-CA-C	-9.52	100.86	111.14
1	B	4062	PHE	N-CA-C	-9.52	100.86	111.14
1	C	4062	PHE	N-CA-C	-9.52	100.86	111.14
1	D	4062	PHE	N-CA-C	-9.52	100.86	111.14
1	A	4126	GLU	N-CA-C	-8.51	102.66	112.87

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	27613	0	23271	731	0
1	B	27613	0	23271	744	0
1	C	27613	0	23271	731	0
1	D	27613	0	23271	726	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	110456	0	93084	2812	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 14.

The worst 5 of 2812 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:A:4324:ALA:CB	1:B:4880:MET:HE3	1.39	1.53
1:B:4324:ALA:CB	1:C:4880:MET:HE3	1.39	1.52
1:A:4880:MET:HE3	1:D:4324:ALA:CB	1.39	1.48
1:C:4324:ALA:CB	1:D:4880:MET:HE3	1.39	1.46
1:C:1963:GLU:HA	1:C:3650:CYS:SG	1.69	1.32

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	4107/5037 (82%)	3689 (90%)	378 (9%)	40 (1%)	12	47
1	B	4107/5037 (82%)	3689 (90%)	378 (9%)	40 (1%)	12	47
1	C	4107/5037 (82%)	3689 (90%)	378 (9%)	40 (1%)	12	47
1	D	4107/5037 (82%)	3689 (90%)	378 (9%)	40 (1%)	12	47
All	All	16428/20148 (82%)	14756 (90%)	1512 (9%)	160 (1%)	15	47

5 of 160 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1455	PRO
1	A	1490	SER
1	A	1495	VAL
1	A	1503	PRO
1	A	1549	PHE

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	2310/4276 (54%)	2267 (98%)	43 (2%)	50	66
1	B	2310/4276 (54%)	2267 (98%)	43 (2%)	50	66
1	C	2310/4276 (54%)	2267 (98%)	43 (2%)	50	66
1	D	2310/4276 (54%)	2267 (98%)	43 (2%)	50	66
All	All	9240/17104 (54%)	9068 (98%)	172 (2%)	49	66

5 of 172 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4088	ILE
1	D	3639	THR
1	C	4116	GLU
1	D	728	ARG
1	D	4068	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 127 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	4109	GLN
1	D	2036	GLN
1	C	904	HIS
1	D	2005	GLN
1	D	3960	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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

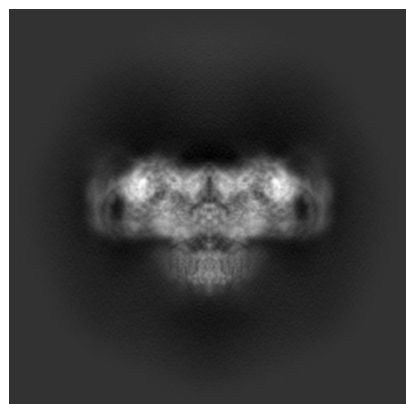
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38045. These allow visual inspection of the internal detail of the map and identification of artifacts.

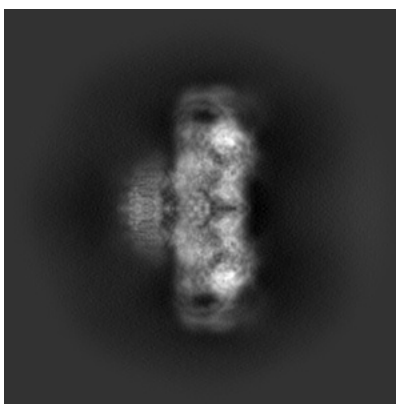
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

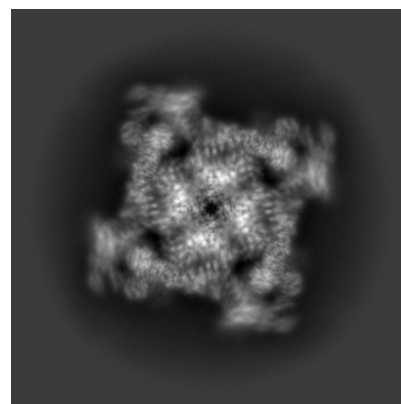
6.1.1 Primary map



X

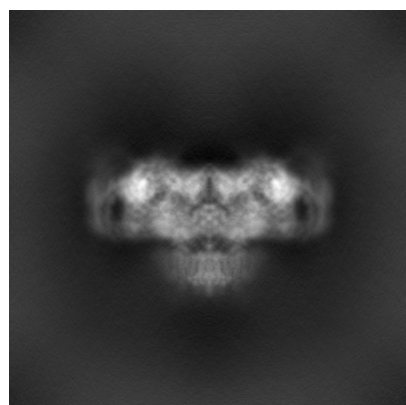


Y

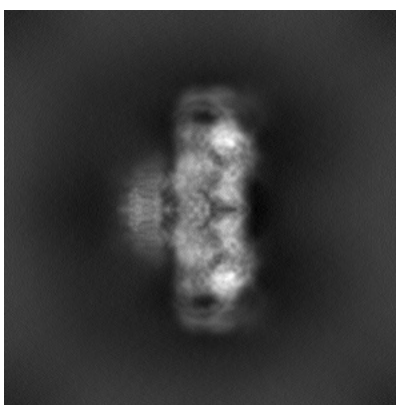


Z

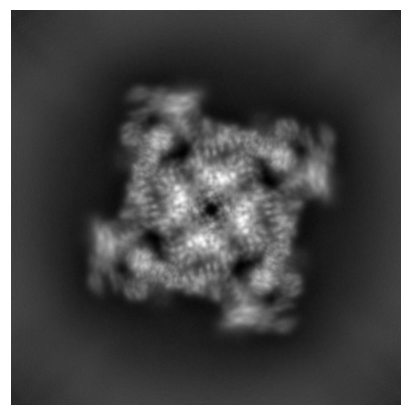
6.1.2 Raw map



X



Y

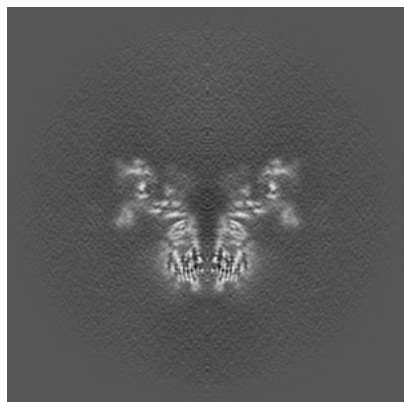


Z

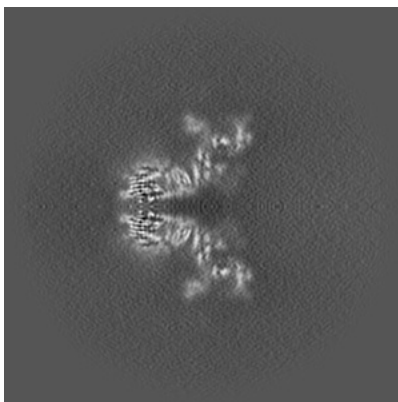
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

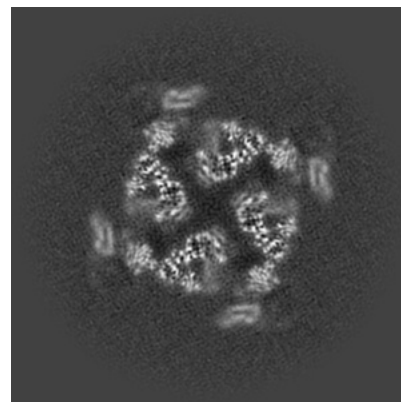
6.2.1 Primary map



X Index: 240

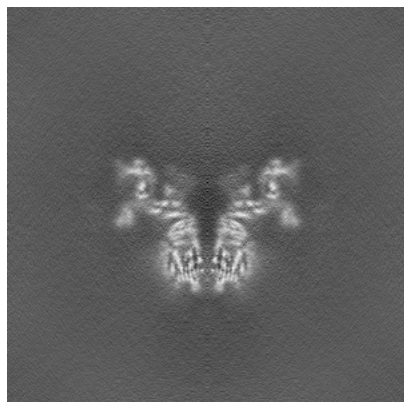


Y Index: 240

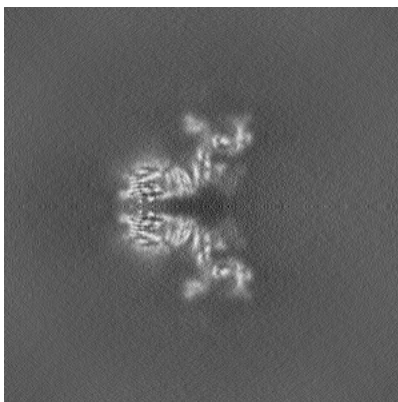


Z Index: 240

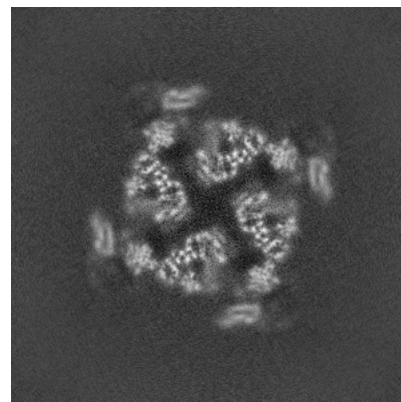
6.2.2 Raw map



X Index: 240



Y Index: 240

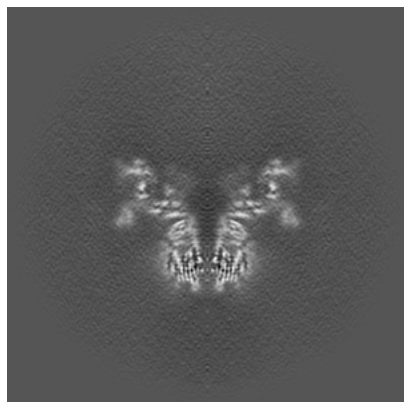


Z Index: 240

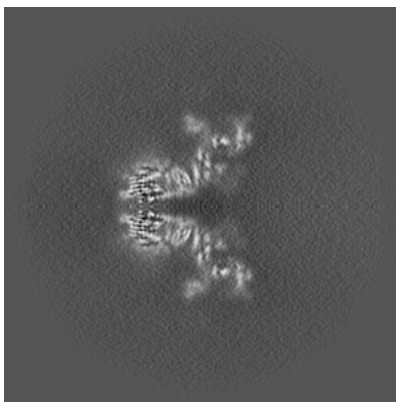
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

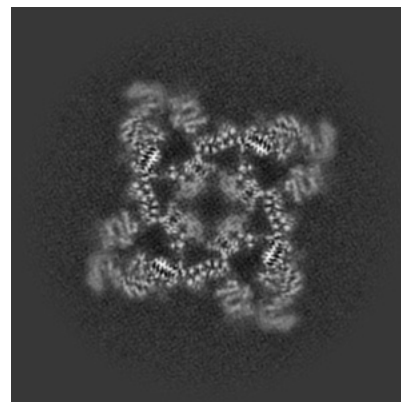
6.3.1 Primary map



X Index: 240

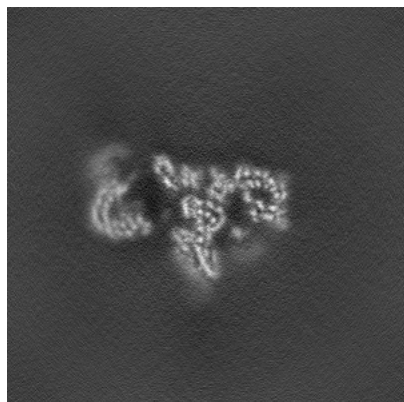


Y Index: 240

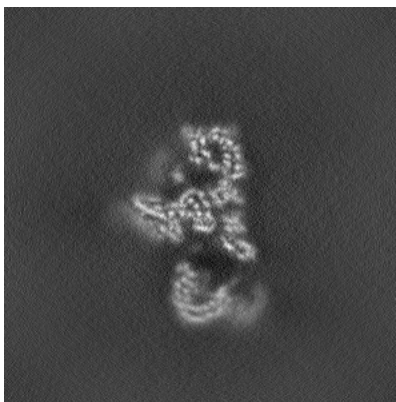


Z Index: 262

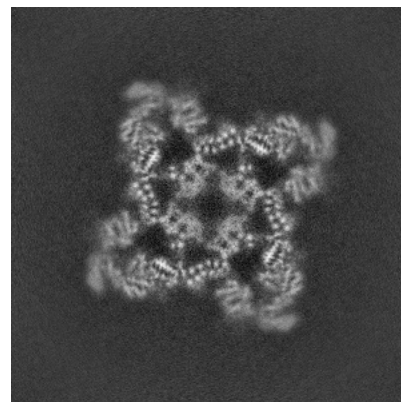
6.3.2 Raw map



X Index: 281



Y Index: 199

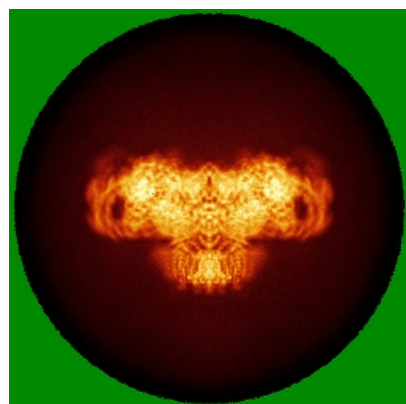


Z Index: 262

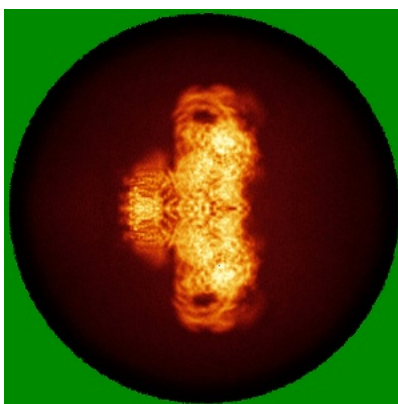
The images above show the largest variance slices of the map in three orthogonal directions.

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

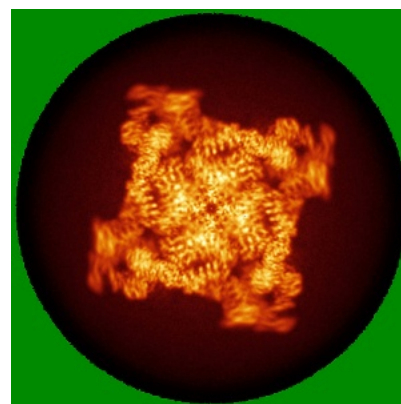
6.4.1 Primary map



X

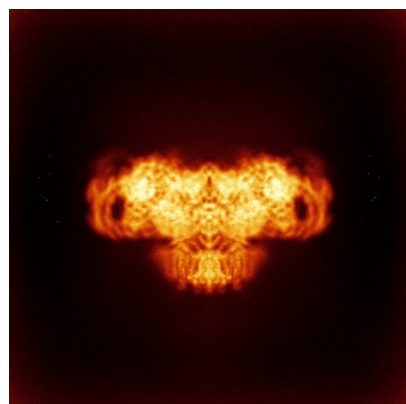


Y

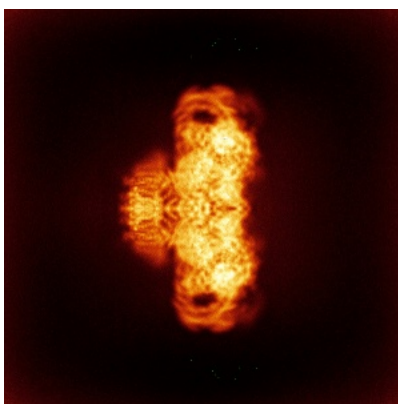


Z

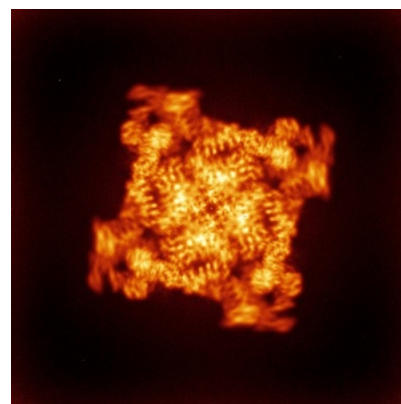
6.4.2 Raw map



X



Y

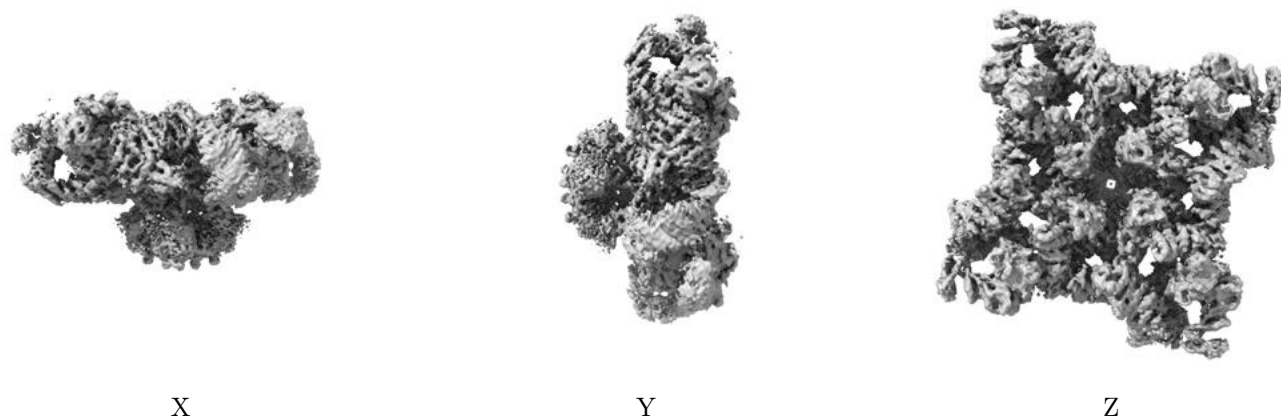


Z

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.

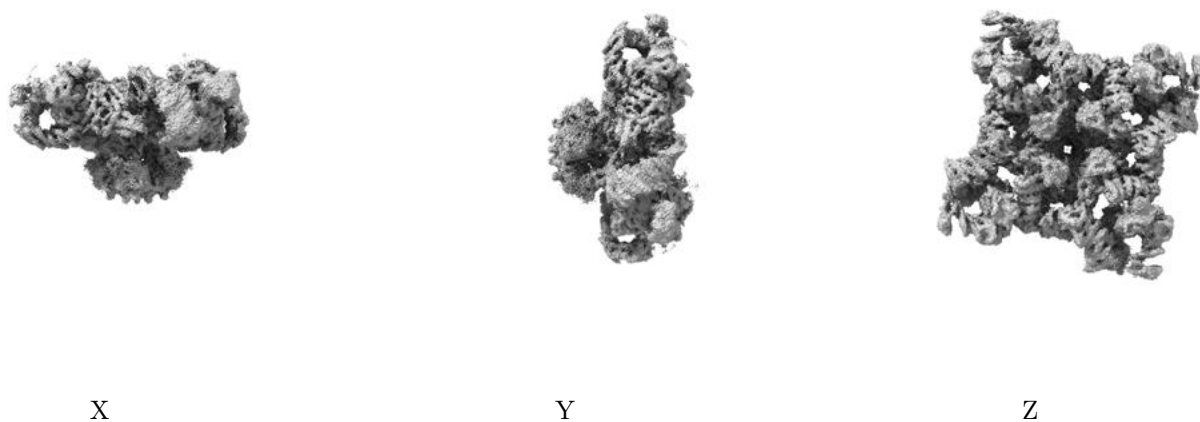
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.237. 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.

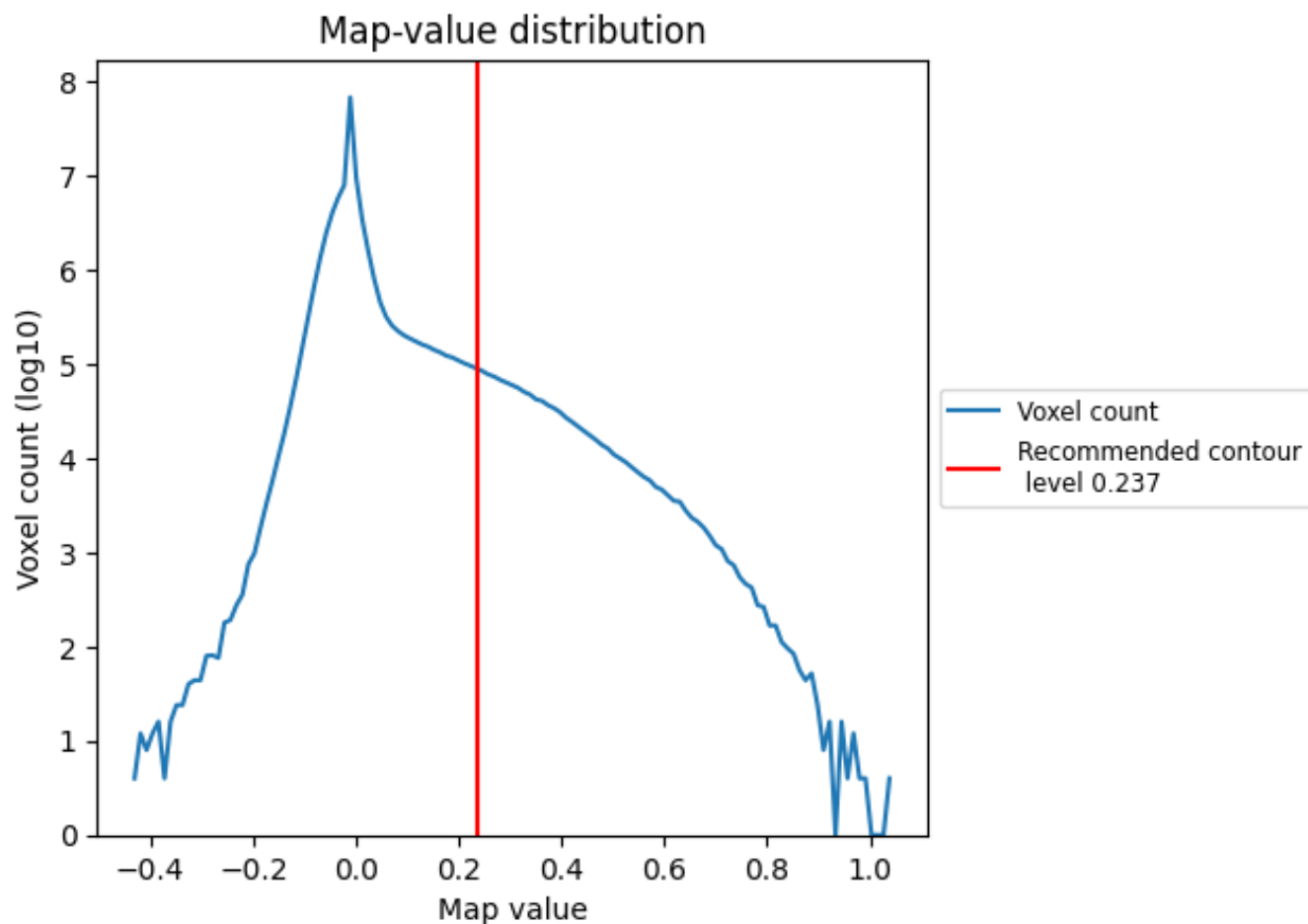
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

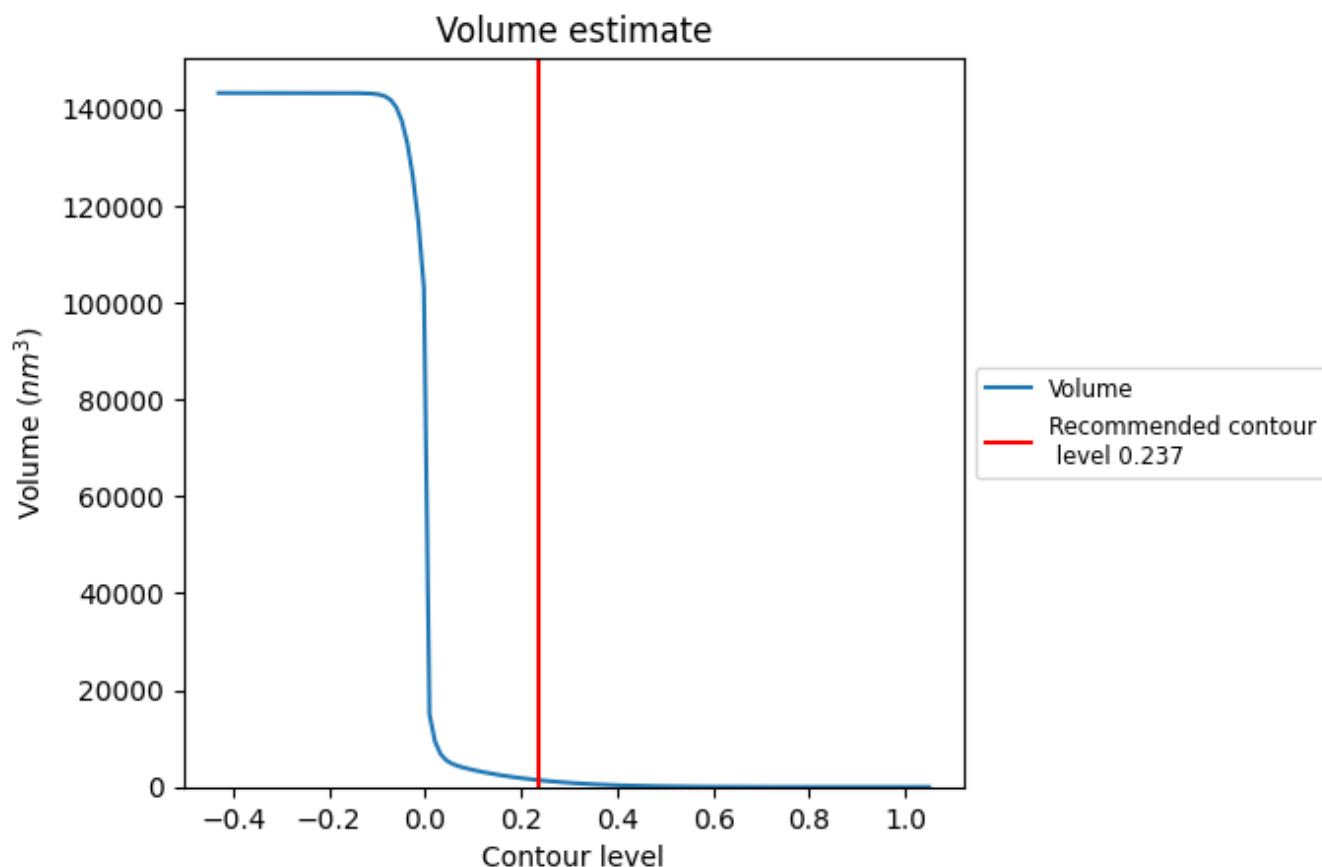
This section contains the results of statistical analysis of the map.

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.

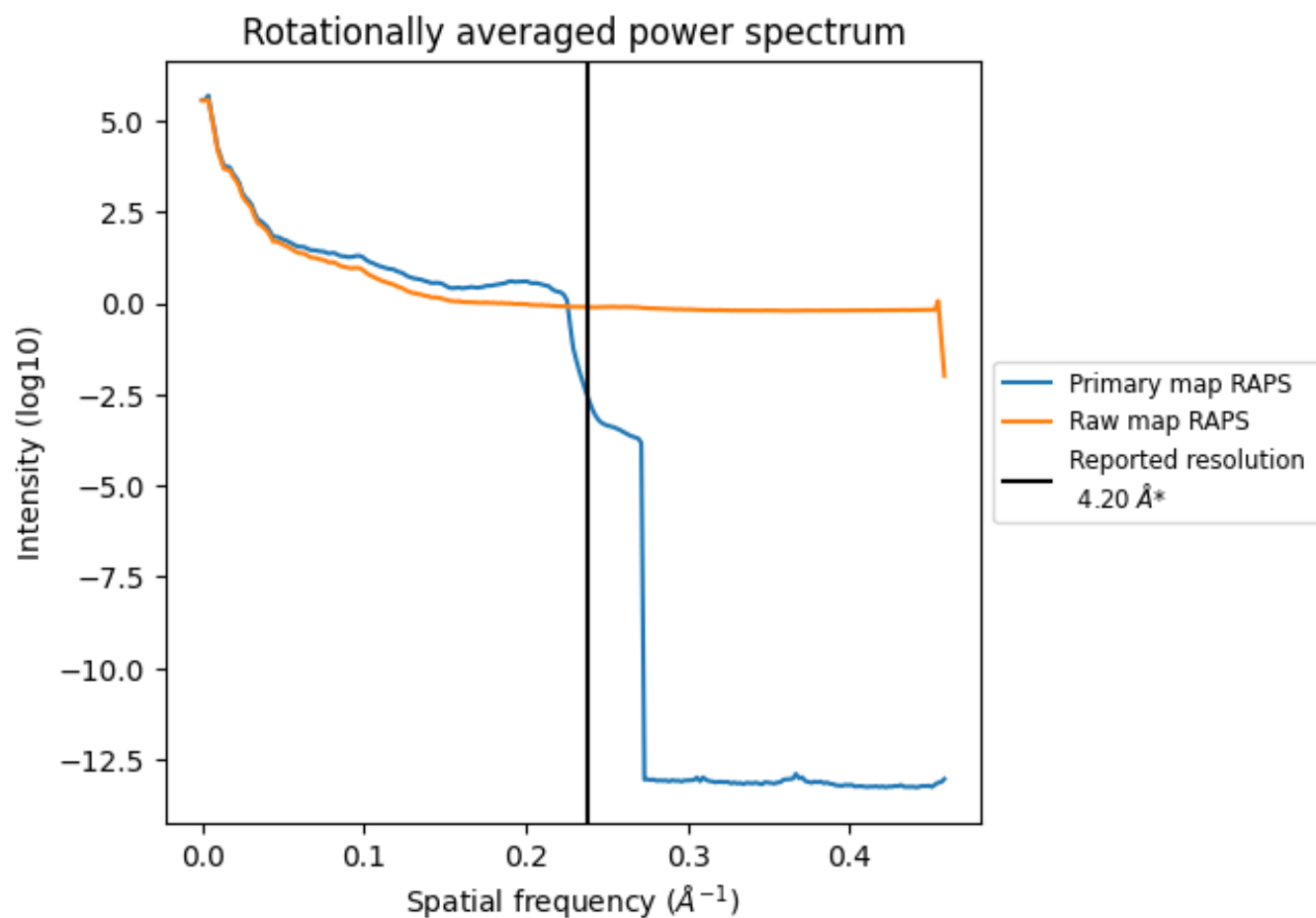
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1401 nm³; this corresponds to an approximate mass of 1265 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 ⓘ

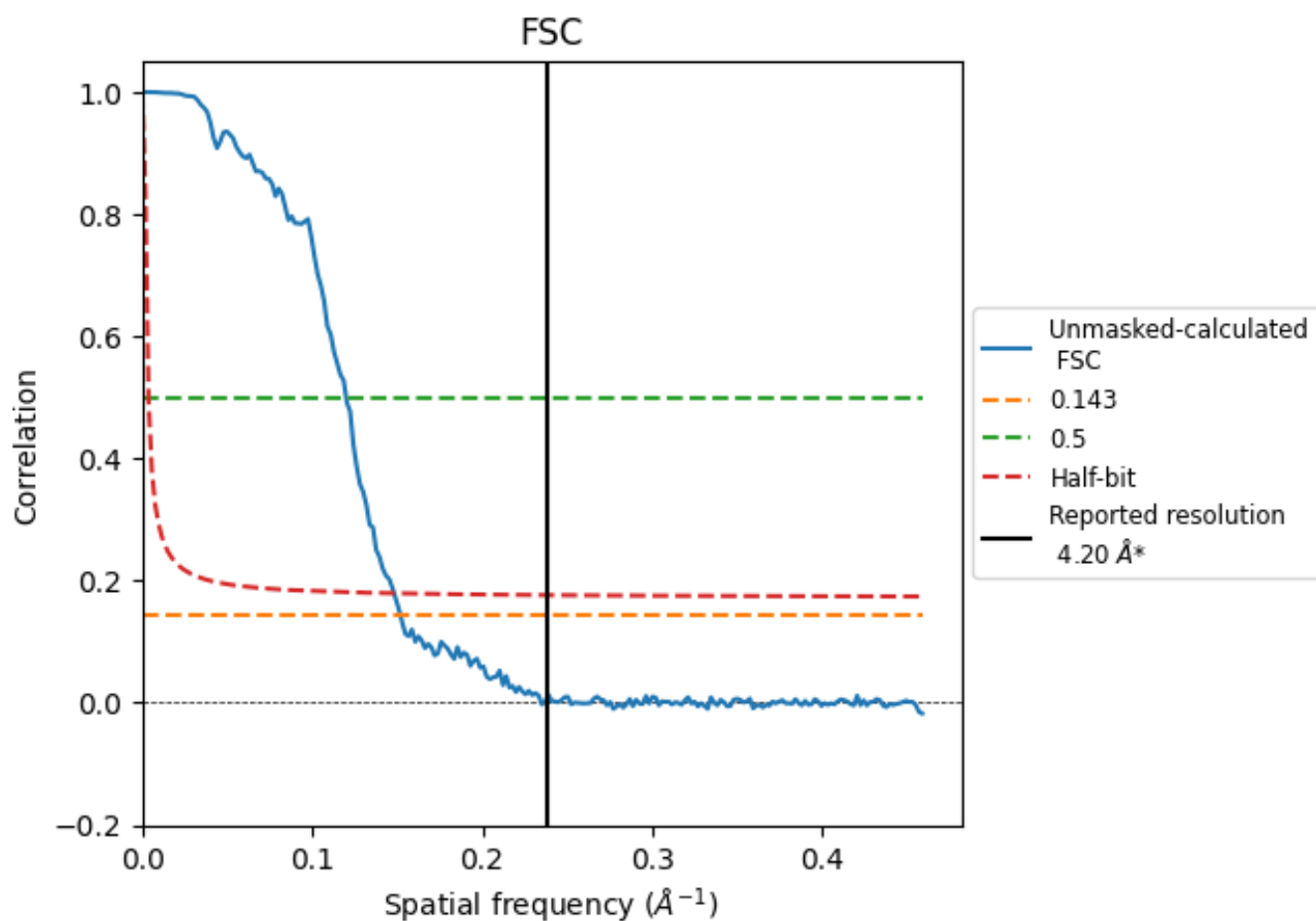


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

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 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

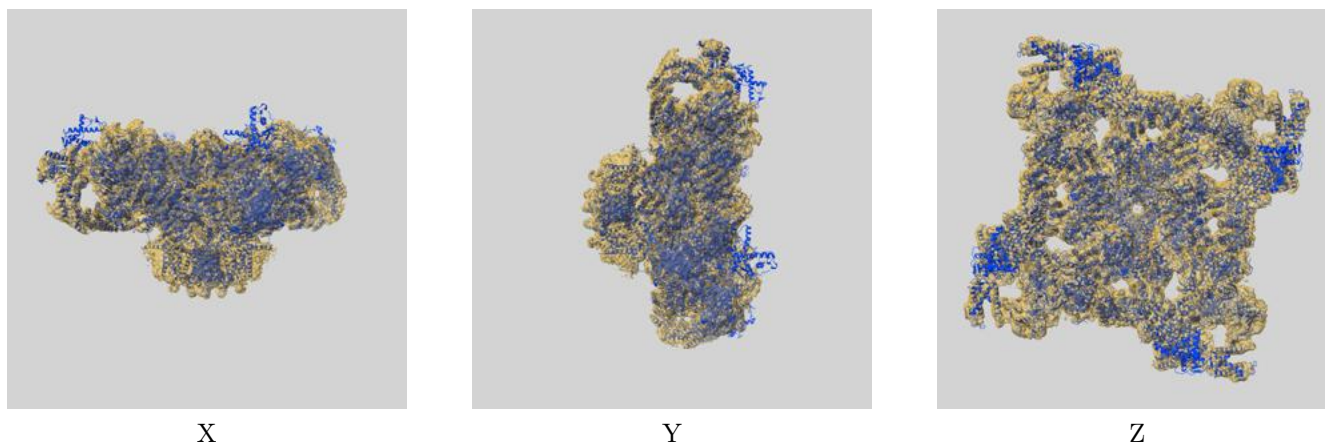
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.58	8.33	6.75

*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 6.58 differs from the reported value 4.2 by more than 10 %

9 Map-model fit [i](#)

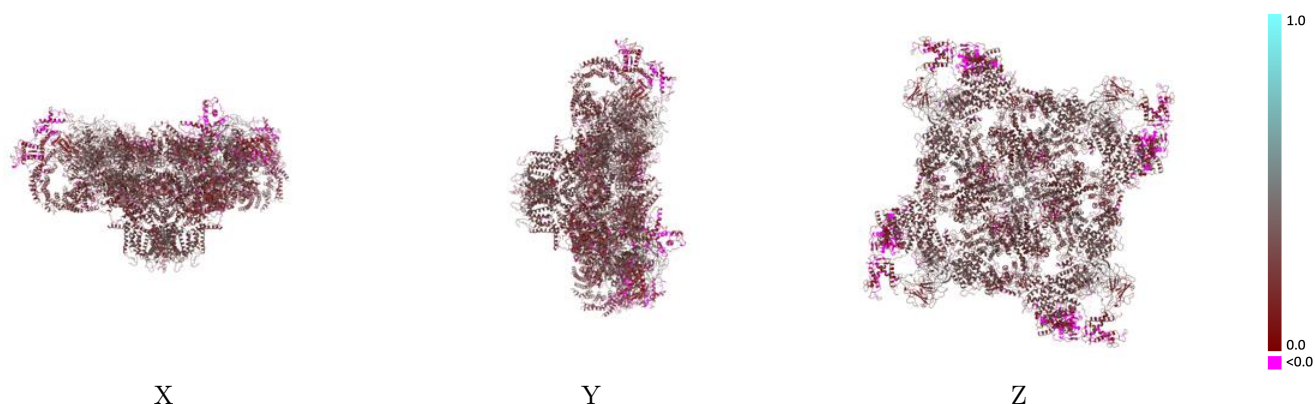
This section contains information regarding the fit between EMDB map EMD-38045 and PDB model 8X4B. Per-residue inclusion information can be found in section [3](#) on page [4](#).

9.1 Map-model overlay [i](#)



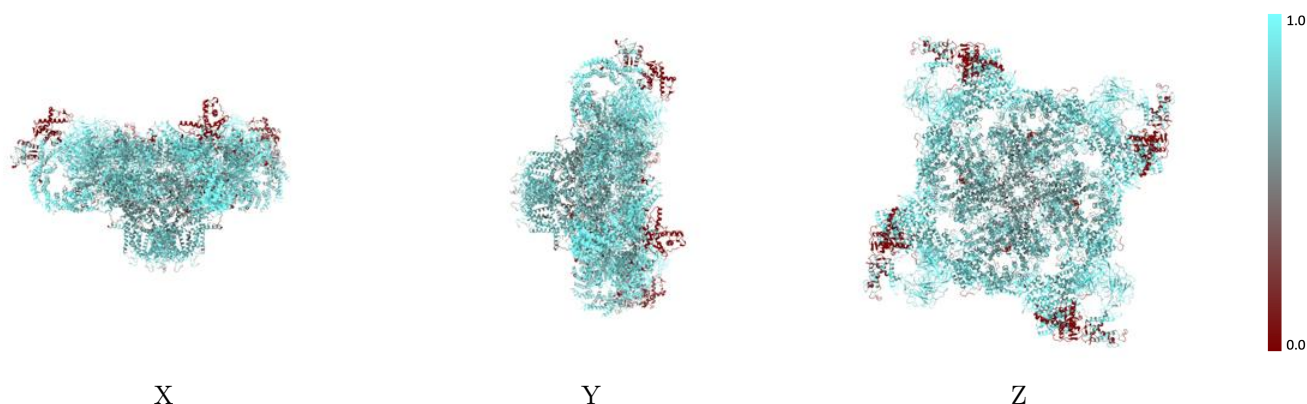
The images above show the 3D surface view of the map at the recommended contour level 0.237 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



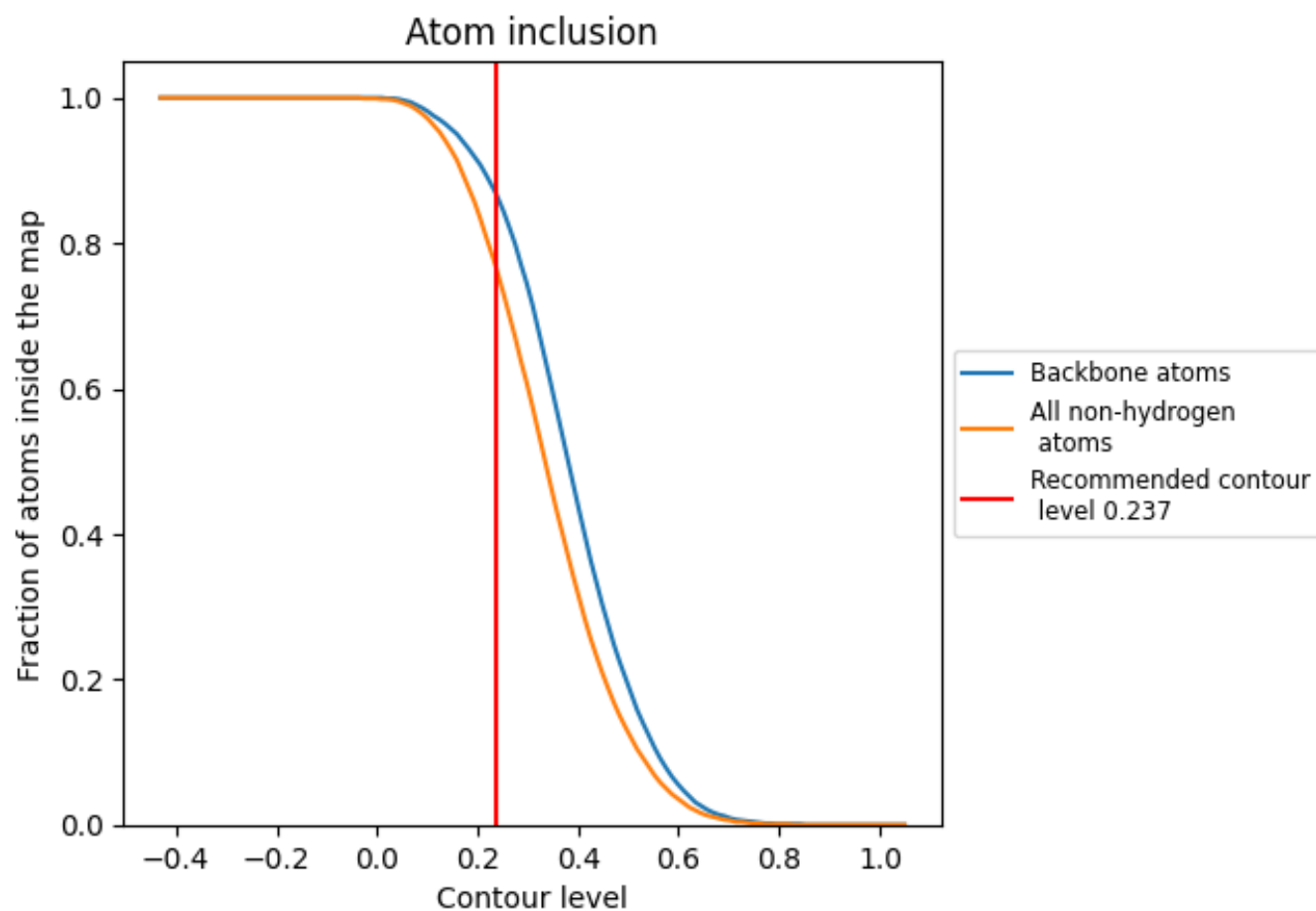
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.237).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 77% 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 (0.237) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7670	0.2600
A	0.7670	0.2600
B	0.7670	0.2600
C	0.7670	0.2600
D	0.7670	0.2600

