



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:11 PM UTC

PDB ID : 6JGZ / pdb_00006jgz
EMDB ID : EMD-9824
Title : Structure of RyR2 (F/P/Ca2+ dataset)
Authors : Chi, X.M.; Gong, D.S.; Ren, K.; Zhou, G.W.; Huang, G.X.Y.; Lei, J.L.; Zhou, Q.; Yan, N.
Deposited on : 2019-02-16
Resolution : 4.60 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

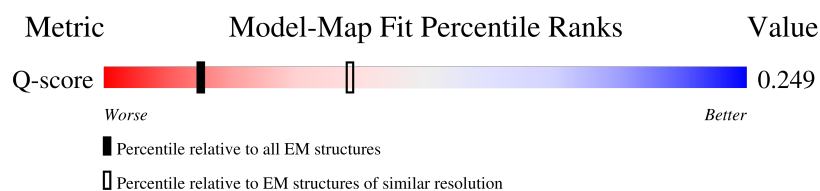
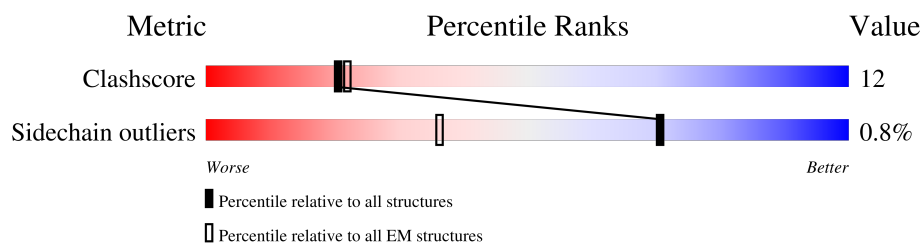
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 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.



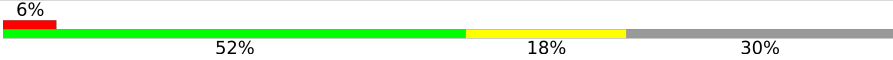
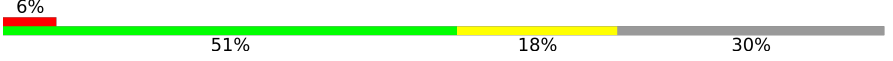
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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	108	
1	C	108	
1	E	108	
1	G	108	
2	B	4968	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	4968	
2	F	4968	
2	H	4968	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 109824 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 Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	C	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	E	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
1	G	107	Total	C	N	O	S	0	0
			819	516	144	155	4		

- Molecule 2 is a protein called RyR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		
2	D	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		
2	F	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		
2	H	3485	Total	C	N	O	S	0	0
			26636	16958	4556	4964	158		

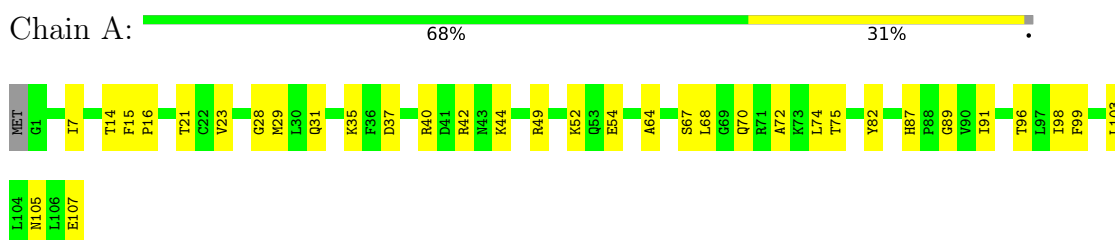
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	
3	F	1	Total	Zn	0
			1	1	
3	H	1	Total	Zn	0
			1	1	

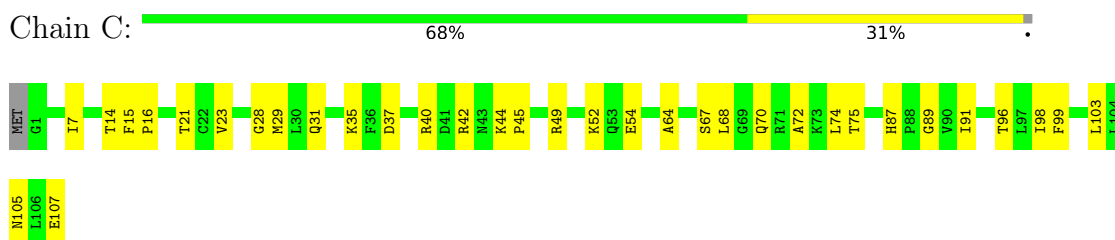
3 Residue-property plots [i](#)

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.

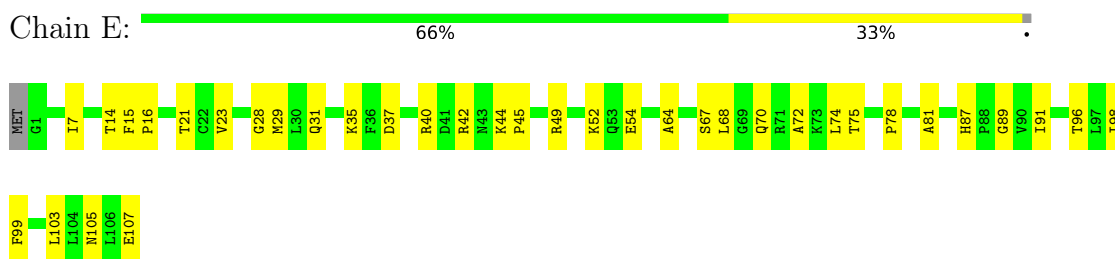
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



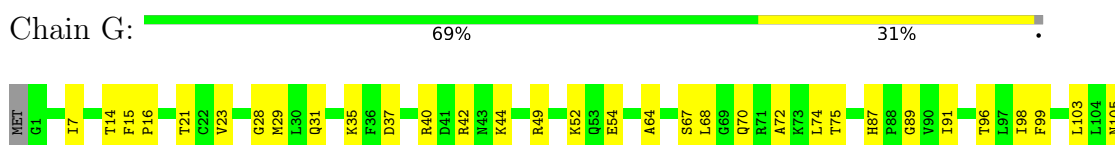
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

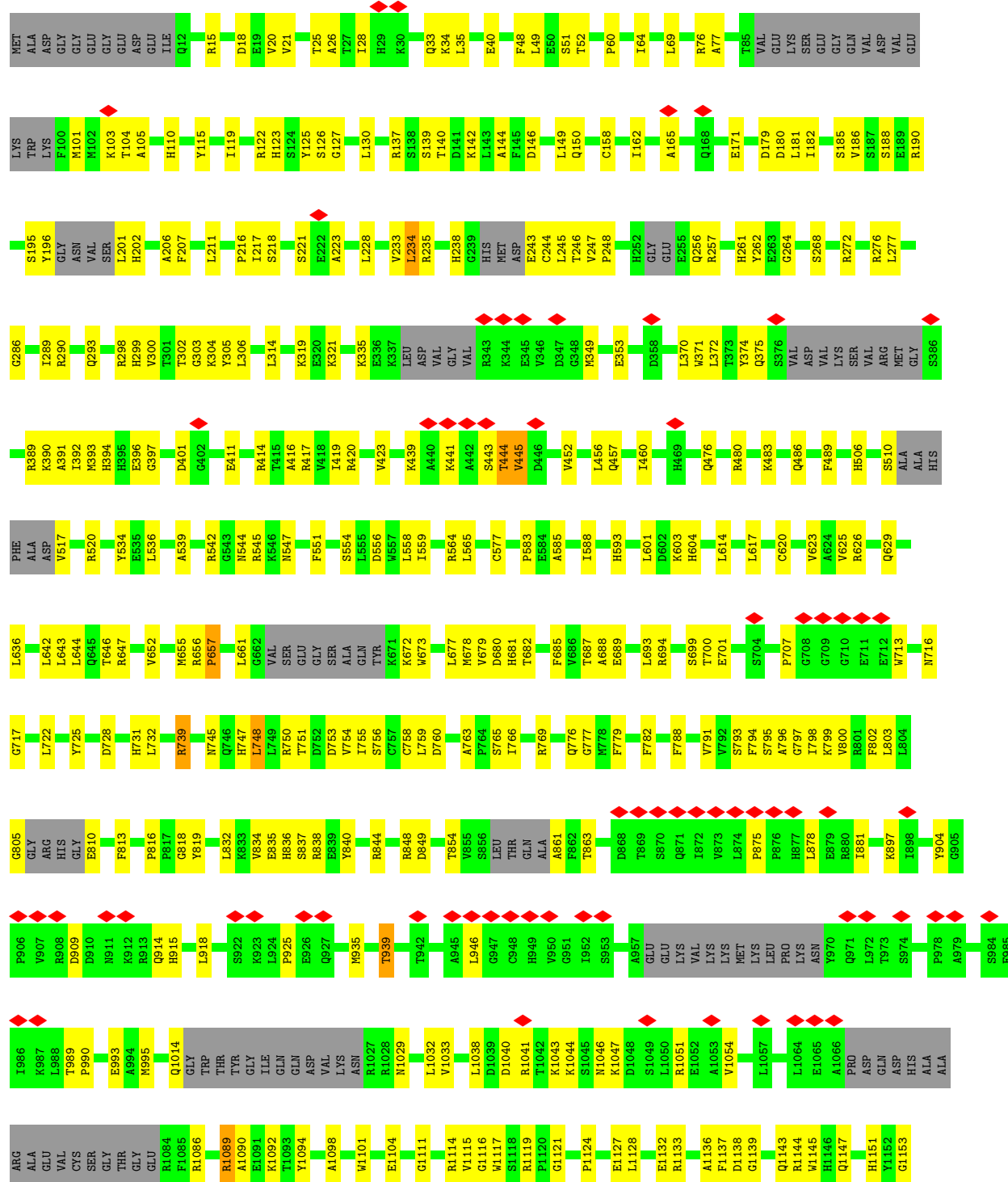


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



L106
E107

• Molecule 2: RyR2





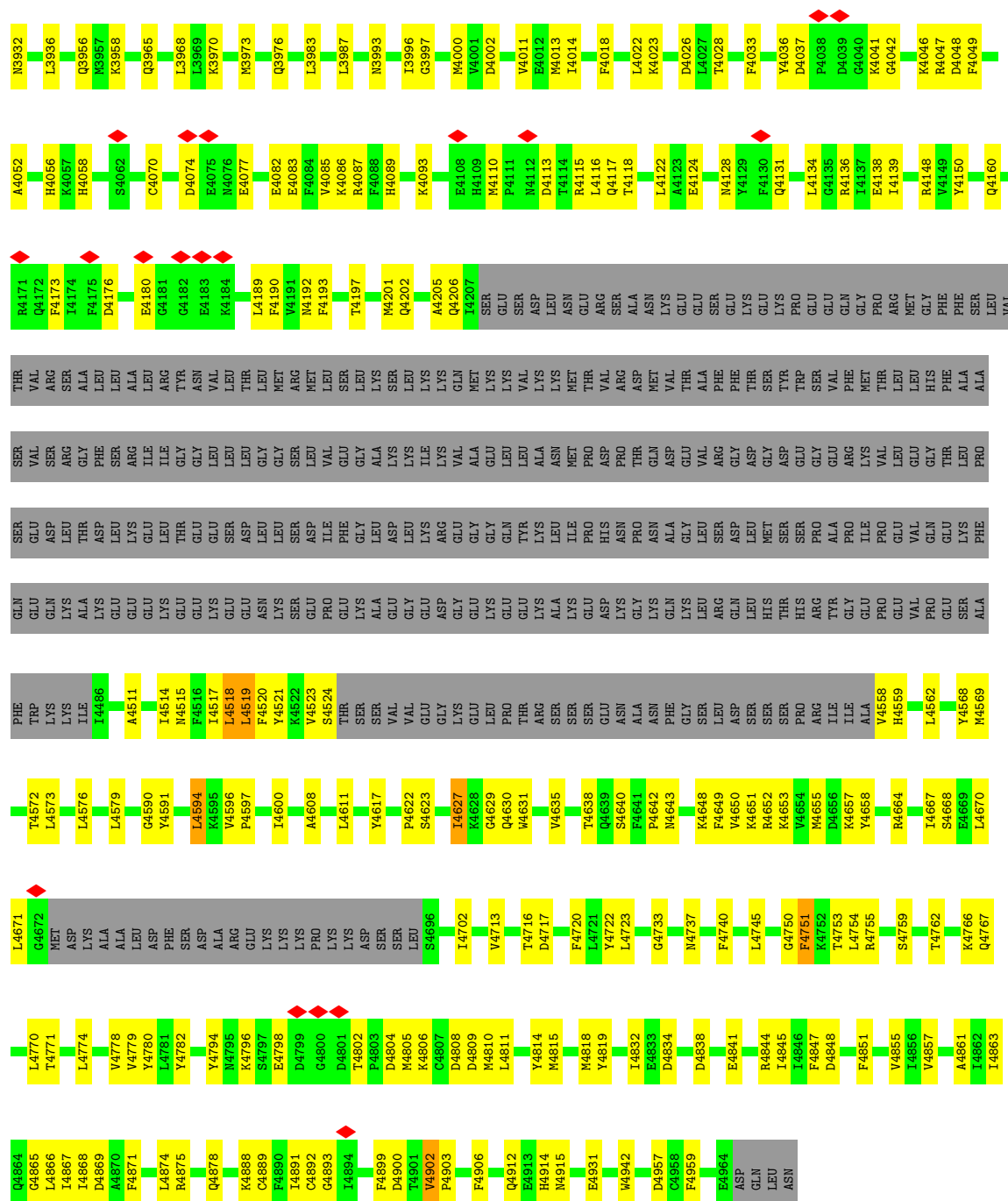


- Molecule 2: RyR2

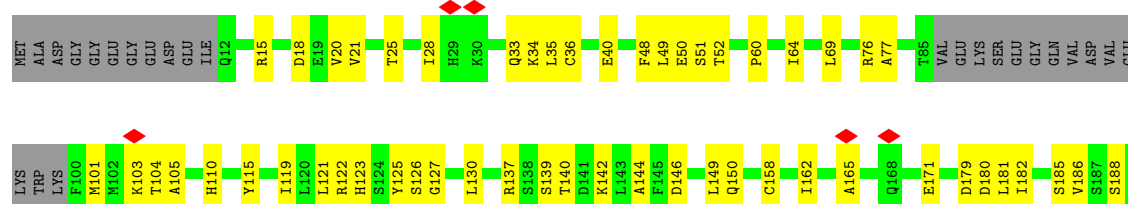


V2476	ASP	THR	GLY	TRP	Y2157	SER	LYS	GLU	F1816	T1716	I1611	S1536	W1445	PRO	ILE	T1238
Y2477	THR	ILE	ASN	P2293	P2160	T2068	SER	G1893	L1817	T1716	S1612	L1539	D1449	GLY	PRO	L1232
GLY	ILE	GLY	GLY	G2181	GLY	Q2060	GLU	L1894	P1820	L1719	E1613	L1539	GLY	ALA	GLY	E1237
GLY	GLY	GLY	GLY	G2296	GLY	T2063	PRO	M1907	L1821	I1726	Q1615	F1543	ARG	LEU	PHE	N1242
L2488	PRO	GLY	GLY	Y2299	GLY	W2067	GLU	L1910	T1827	E1732	Q1620	T1548	ASP	GLY	GLY	R1245
L2489	PRO	GLY	GLY	L2300	SER	A2071	GLU	Q1912	I1830	S1735	C1621	ARG	VAL	PRO	PRO	M1249
VAL	MET	GLY	GLY	D2301	LYS	Q2072	ILE	Q1911	H1835	I1736	L1622	V1552	ARG	ASN	ASN	L1250
G2492	HIS	ILE	THR	R2304	ILE	V2075	PRO	H1921	L1843	I1737	L1738	F1566	THR	THR	ASP	L1251
L2503	ILE	ILE	T2326	T2326	THR	T2076	GLU	R1922	VAL	L1738	F1627	LEU	LEU	LEU	GLU	S1252
L2503	HIS	ALA	E2330	E2330	ALA	R2083	GLU	I1926	I1846	F1739	M1628	GLY	THR	ASP	ASP	K1253
ALA	ALA	ALA	CYS	PHE	ALA	A2084	ALA	L1998	E1847	P1740	S1629	ARG	VAL	THR	ASP	R1254
ALA	LYS	GLY	GLY	GLY	GLY	W2085	ASP	F1929	P1848	GLU	H1631	ILE	GLY	ASP	ASP	L1255
GLY	GLY	PRO	PRO	C2197	GLY	L2088	LEU	V1934	VAL	LYS	P1633	ASN	THR	ALA	ALA	P1256
ALA	GLY	ALA	ALA	C2198	GLY	L2088	ASP	Q1938	PHE	LYS	E1634	VAL	SER	SER	ASP	Q1257
T2511	R2421	ARG	LEU	F2200	ARG	Q2092	GLY	R1942	GLU	HIS	E1635	MET	K1474	ASP	ASP	F1258
L2423	S2422	ARG	GLY	L2201	GLY	Q2092	SER	R1942	ALA	L1748	S1638	PRO	K1475	ASP	PHE	V1261
T2523	L2423	GLY	GLY	C2202	GLY	T2096	LEU	V1943	ALA	P1749	V1639	SER	R1482	VAL	GLU	R1272
L2529	LEU	LEU	GLY	F2204	GLY	W2100	ASP	MET	GLY	L1753	D1640	SER	S1483	LEU	LEU	T1273
THR	ILE	ASN	ASN	I2207	ASN	R2101	ASN	GLN	PRO	L1642	I1641	G1569	CYS	THR	MET	D1274
CYS	PRO	GLY	GLY	A2102	CYS	L2103	S2022	LEU	GLU	S1756	E1643	F1570	Y1486	ALA	THR	GLY
ALA	LEU	GLY	GLY	L2344	GLY	L2103	D2023	ASN	SER	L1757	L1644	K1572	V1488	HIS	ALA	ILE
P2534	G2431	GLY	GLY	Q2212	GLY	T2106	L2024	MET	ASP	R1758	T1645	F1574	C1489	GLY	SER	SER
L2535	G2442	THR	GLY	Q2212	GLY	T2106	L2024	SER	THR	M1761	E1648	H1575	A1490	HIS	SER	SER
F2536	PRO	THR	GLY	Y2221	ALA	D2116	ALA	ALA	LEU	S1764	L1651	V1579	GLY	LEU	PRO	PRO
A2537	PRO	THR	ALA	L2222	GLY	T2117	ALA	ALA	GLU	S1765	L1651	V1579	GLU	VAL	VAL	VAL
L2549	ILE	ILE	ASP	S2226	GLY	T2118	THR	THR	GLU	P1766	H1654	P1584	SER	ASP	ARG	ARG
V2553	ALA	ALA	PRO	S2232	PRO	L2121	ARG	ALA	CYS	M1772	A1666	H1587	PRO	VAL	VAL	VAL
TYR	LYS	LYS	SER	S2232	SER	R2122	LYS	LYS	ALA	H1773	L1667	V1588	GLY	ASP	ASP	ASP
ARG	ASP	ASP	ARG	S2123	GLN	R2122	THR	THR	SER	E1774	Q1668	Q1589	GLN	MET	LYS	LYS
LEU	GLY	GLY	GLY	D2250	ALA	Q2126	LYS	GLU	GLU	G1775	M1669	F1590	ARG	GLY	ASP	ASP
K2558	VAL	VAL	PRO	L2256	GLY	T2127	PHE	GLU	ASP	Y1776	H1670	L1591	THR	THR	LYS	LYS
L2562	VAL	VAL	SER	G2274	PRO	T2133	ARG	ARG	ARG	Y1778	R1671	S1592	N1501	GLU	GLU	ALA
S2576	PRO	THR	LEU	LEU	LEU	W2133	SER	SER	LEU	S1779	E1682	H1593	L1505	ALA	ALA	S1306
ILE	ASP	THR	GLN	GLN	GLN	R2134	PRO	PRO	GLY	A1789	Q1683	V1596	C1509	THR	THR	M1300
CYS	MET	GLY	SER	SER	SER	W2135	LYS	LYS	GLY	L1789	Q1684	S1597	GLY	LYS	LYS	F1301
GLY	ALA	SER	GLN	GLN	GLN	G2136	GLU	GLU	PRO	I1792	L1685	R1598	V1510	ASP	ASP	Y1302
GLN	GLY	SER	GLN	GLN	GLN	L2142	GLU	GLU	ALA	I1792	L1686	V1599	V1511	ASP	LYS	R1303
R2582	GLY	MET	LEU	LEU	LEU	W2143	LYS	ILE	GLU	A1797	Y1687	V1599	ASP	GLY	ALA	L1304
N2601	PRO	PRO	VAL	VAL	VAL	T2144	VAL	ASN	GLU	E1798	A1688	P1600	ALA	ALA	VAL	HIS
GLY	THR	THR	SER	SER	SER	R2145	GLU	LEU	SER	V1799	I1689	Q1602	SER	GLY	GLN	PHE
GLY	GLY	GLY	LYS	LYS	LYS	G2148	SER	LEU	GLY	S1803	K1692	F1603	G1516	PRO	TYR	SER
V2470	TYR	GLY	GLY	GLY	GLY	W2152	ASP	ASN	GLY	G1696	G1696	V1606	F1520	ALA	ALA	THR
ALA	PRO	GLY	GLY	GLY	GLY	N2153	SER	PHE	LYS	R1807	D1607	V1608	N1523	GLN	GLN	SER
L2473	ASP	GLU	GLU	GLU	GLU	K2154	LYS	ASP	ARG	P1809	R1699	V1608	Y1531	GLY	GLY	ALA
	ASP	ASP	ASP	ASP	ASP		SER	ASP	PRO		Y1703	R1610		PRO	PRO	GLY





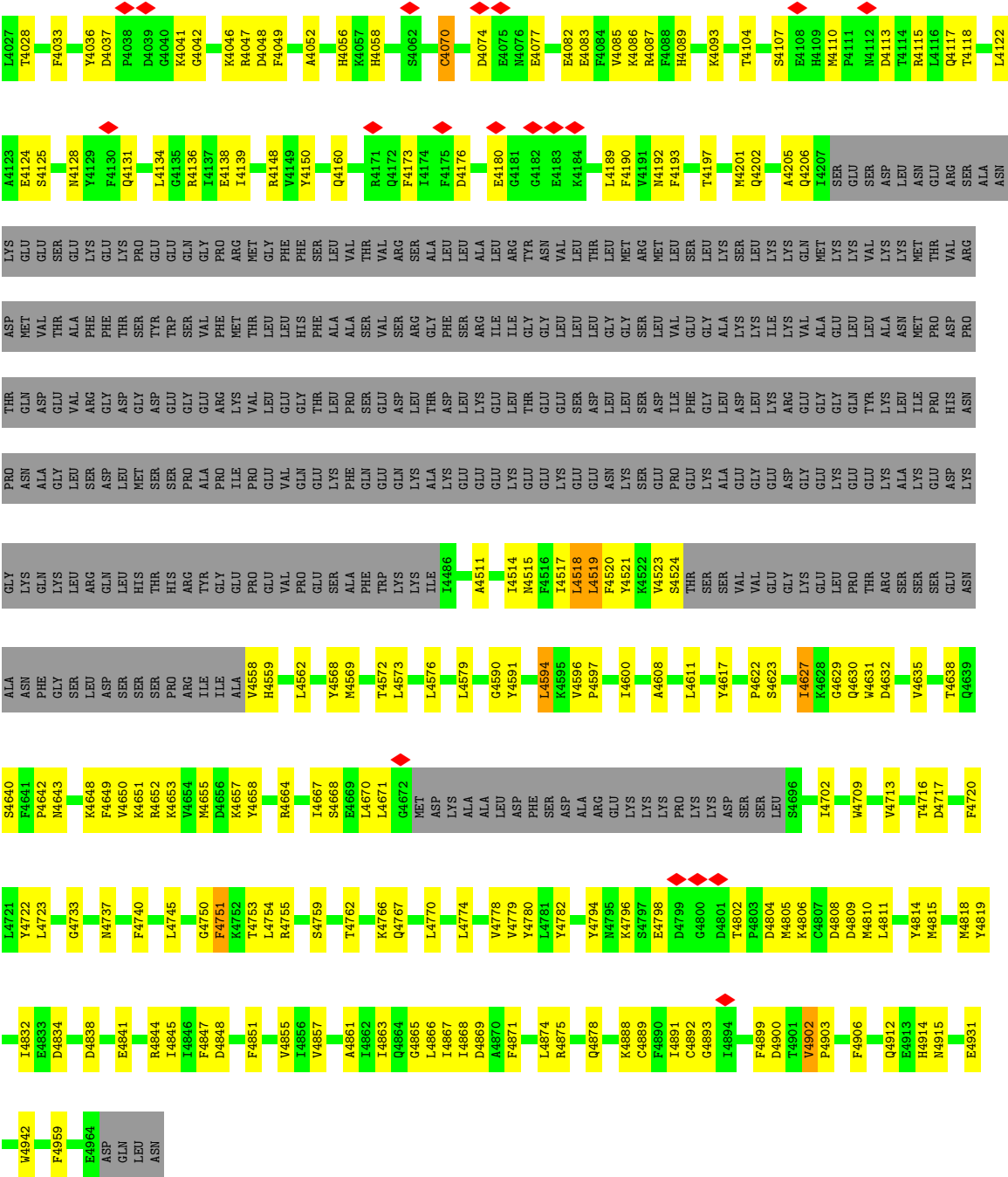
• Molecule 2: RyR2



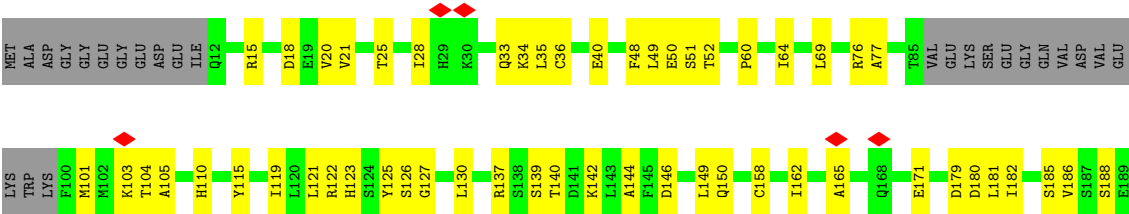








● Molecule 2: RyR2











4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	60287	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 ($e^-/\text{\AA}^2$)	48.6	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	0.085	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	522.616, 522.616, 522.616	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.30654, 1.30654, 1.30654	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.28	0/835	0.55	0/1123
1	C	0.28	0/835	0.55	0/1123
1	E	0.28	0/835	0.55	0/1123
1	G	0.28	0/835	0.55	0/1123
2	B	0.33	0/27132	0.66	21/36687 (0.1%)
2	D	0.33	0/27132	0.66	21/36687 (0.1%)
2	F	0.33	0/27132	0.66	21/36687 (0.1%)
2	H	0.33	0/27132	0.66	21/36687 (0.1%)
All	All	0.33	0/111868	0.65	84/151240 (0.1%)

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
2	B	0	29
2	D	0	29
2	F	0	29
2	H	0	29
All	All	0	116

There are no bond length outliers.

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2039	TYR	N-CA-C	8.41	123.22	113.38
2	B	2039	TYR	N-CA-C	8.39	123.19	113.38
2	F	2039	TYR	N-CA-C	8.38	123.18	113.38
2	H	2039	TYR	N-CA-C	8.36	123.16	113.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2039	TYR	CA-C-N	7.22	134.69	121.70

There are no chirality outliers.

5 of 116 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	105	ALA	Peptide
2	B	142	LYS	Peptide
2	B	221	SER	Peptide
2	B	321	LYS	Peptide
2	B	657	PRO	Peptide

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	819	0	824	25	0
1	C	819	0	824	25	0
1	E	819	0	824	26	0
1	G	819	0	824	24	0
2	B	26636	0	25174	691	0
2	D	26636	0	25174	687	0
2	F	26636	0	25174	695	0
2	H	26636	0	25174	703	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
All	All	109824	0	103992	2593	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 12.

The worst 5 of 2593 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:F:4520:PHE:CD1	2:F:4562:LEU:HD21	1.50	1.47
2:B:4520:PHE:CD1	2:B:4562:LEU:HD21	1.50	1.47
2:D:4520:PHE:CD1	2:D:4562:LEU:HD21	1.50	1.46
2:H:4520:PHE:CD1	2:H:4562:LEU:HD21	1.50	1.44
2:B:4808:ASP:HB3	2:D:4523:VAL:CG2	1.55	1.36

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	88/89 (99%)	88 (100%)	0	100	100
1	C	88/89 (99%)	88 (100%)	0	100	100
1	E	88/89 (99%)	88 (100%)	0	100	100
1	G	88/89 (99%)	88 (100%)	0	100	100
2	B	2688/4355 (62%)	2666 (99%)	22 (1%)	73	77
2	D	2688/4355 (62%)	2666 (99%)	22 (1%)	73	77
2	F	2688/4355 (62%)	2666 (99%)	22 (1%)	73	77
2	H	2689/4355 (62%)	2666 (99%)	23 (1%)	70	76
All	All	11105/17776 (62%)	11016 (99%)	89 (1%)	70	77

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	2118	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	H	925	PRO
2	F	4139	ILE
2	F	4902	VAL
2	H	990	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 272 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	1589	GLN
2	H	1836	ASN
2	H	3954	HIS
2	D	1722	ASN
2	D	1602	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 [i](#)

There are no chain breaks in this entry.

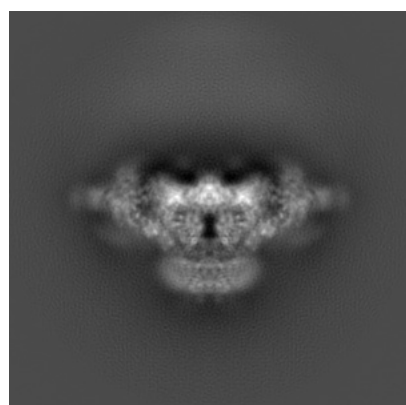
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9824. These allow visual inspection of the internal detail of the map and identification of artifacts.

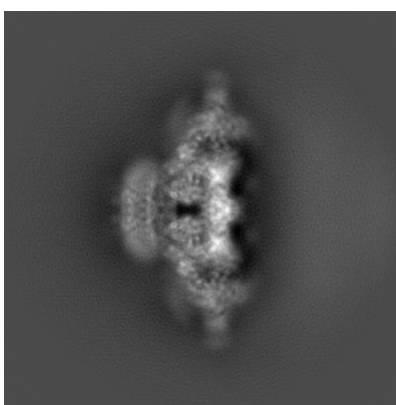
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

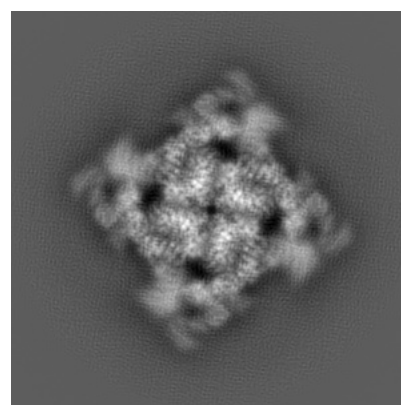
6.1.1 Primary map



X



Y

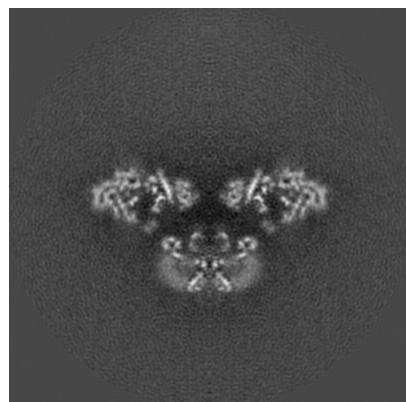


Z

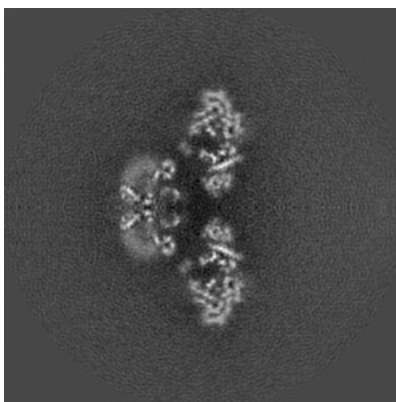
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

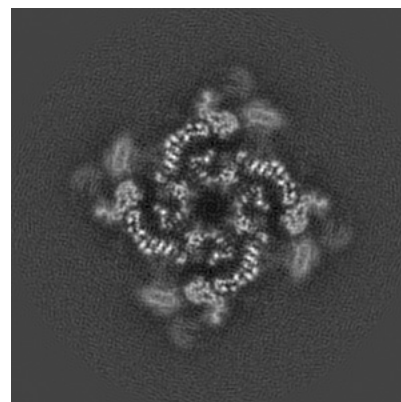
6.2.1 Primary map



X Index: 200



Y Index: 200

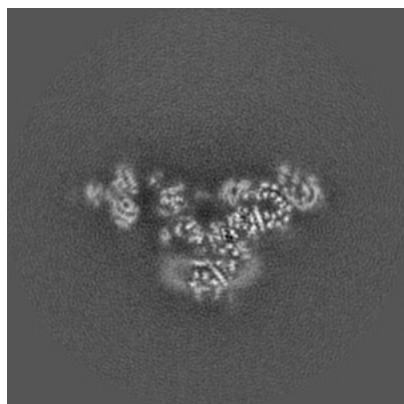


Z Index: 200

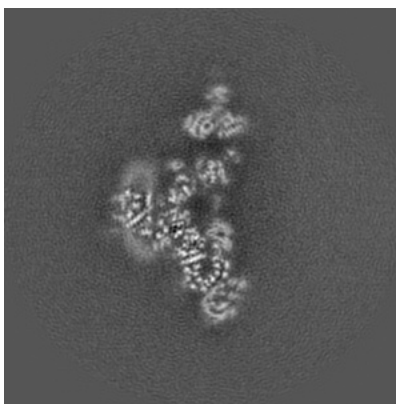
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

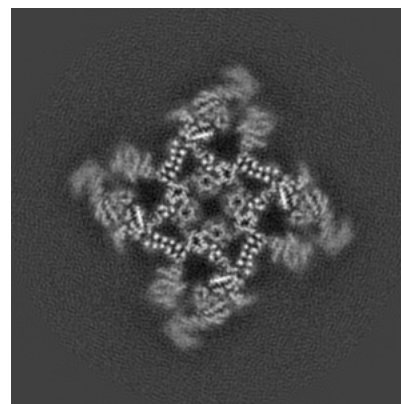
6.3.1 Primary map



X Index: 189



Y Index: 189

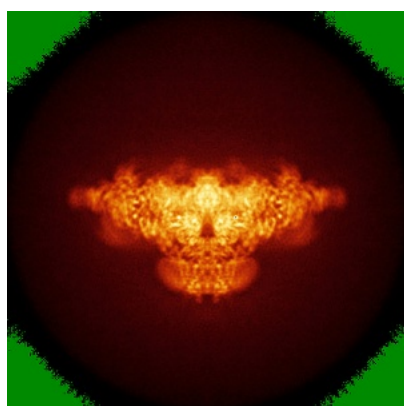


Z Index: 209

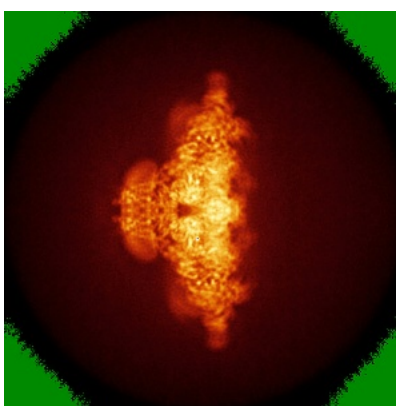
The images above show the largest variance slices of the map in three orthogonal directions.

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

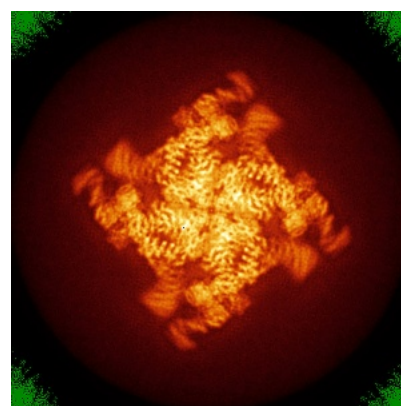
6.4.1 Primary map



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

This section was not generated.

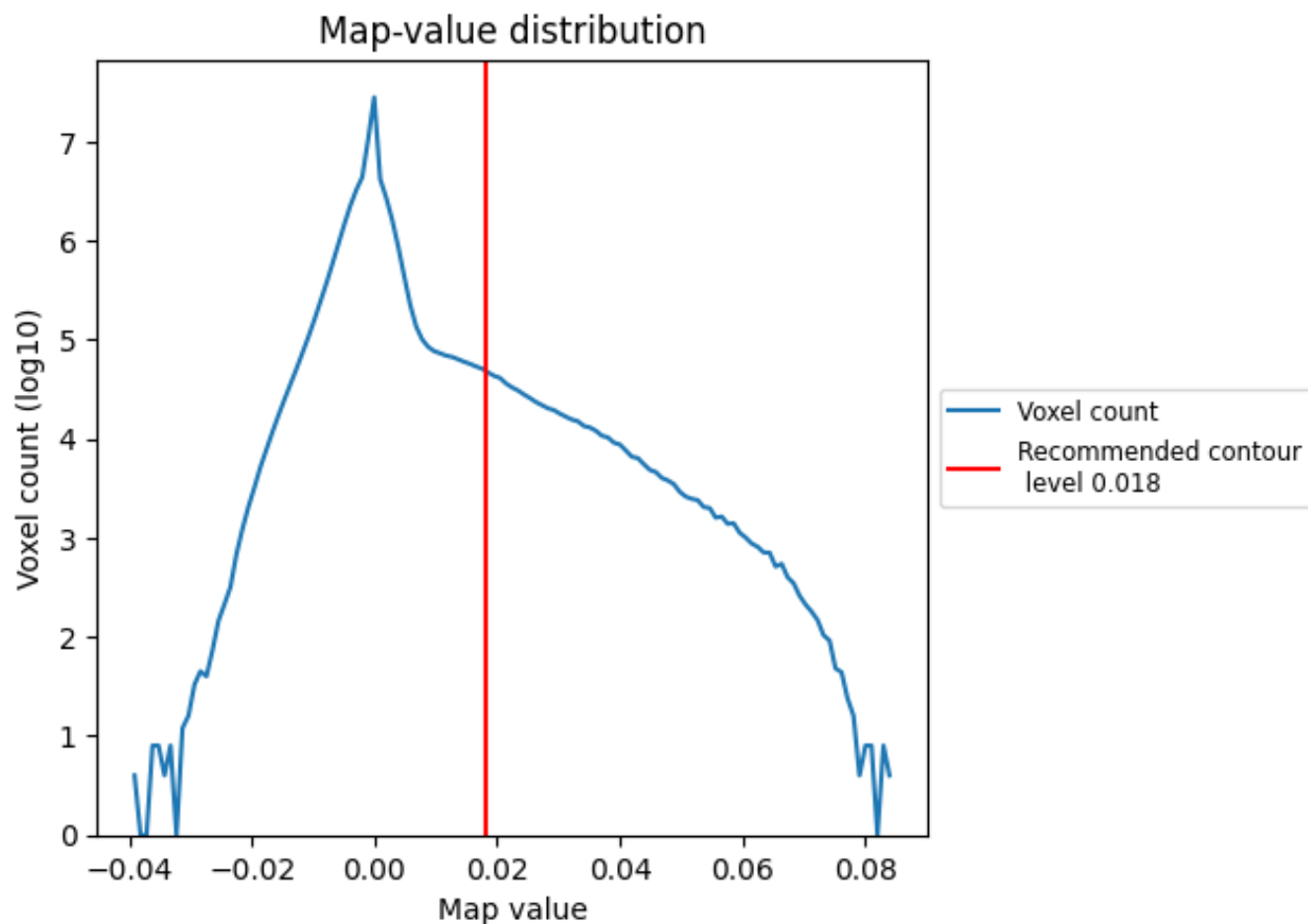
6.6 Mask visualisation

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

7 Map analysis [i](#)

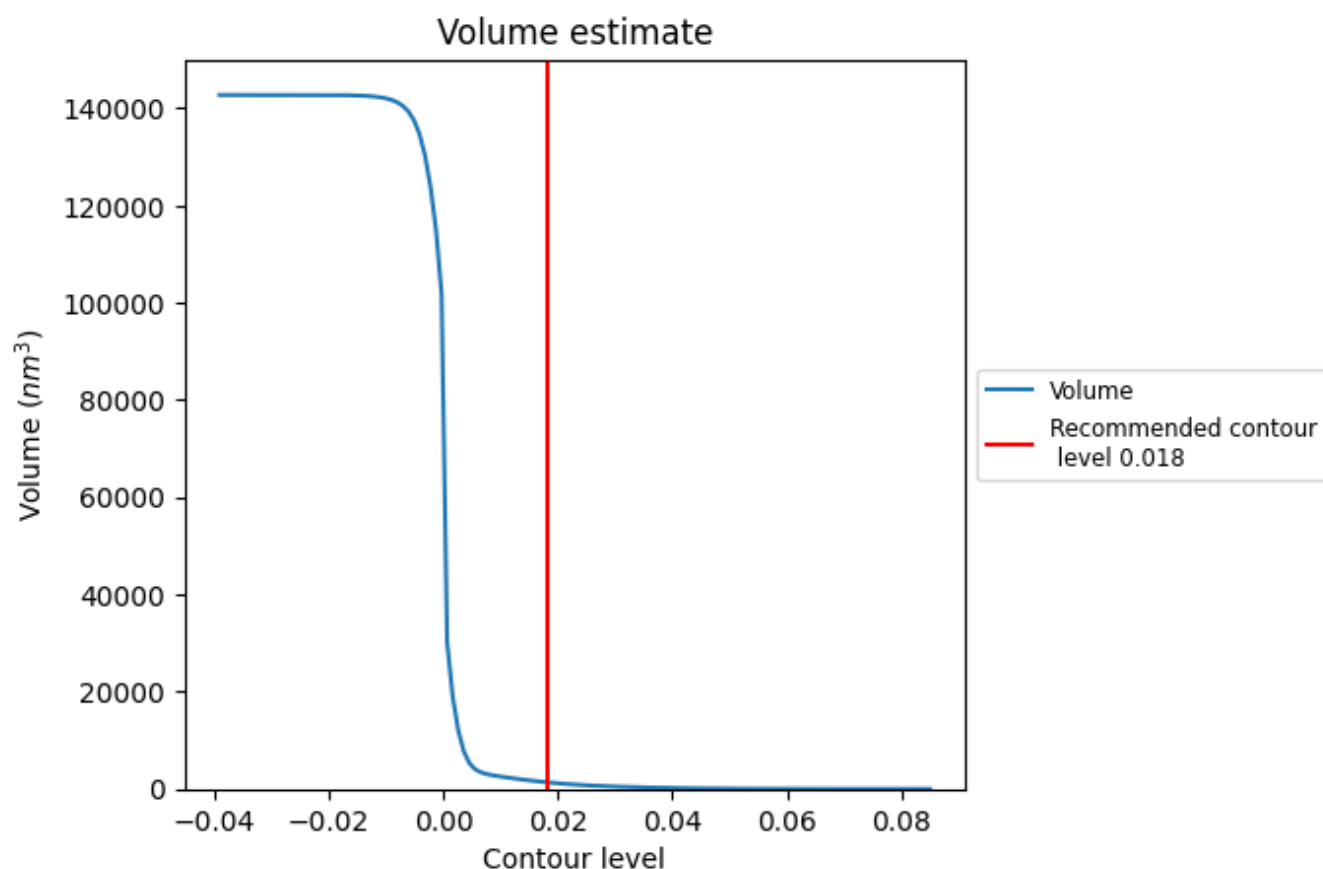
This section contains the results of statistical analysis of the map.

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.

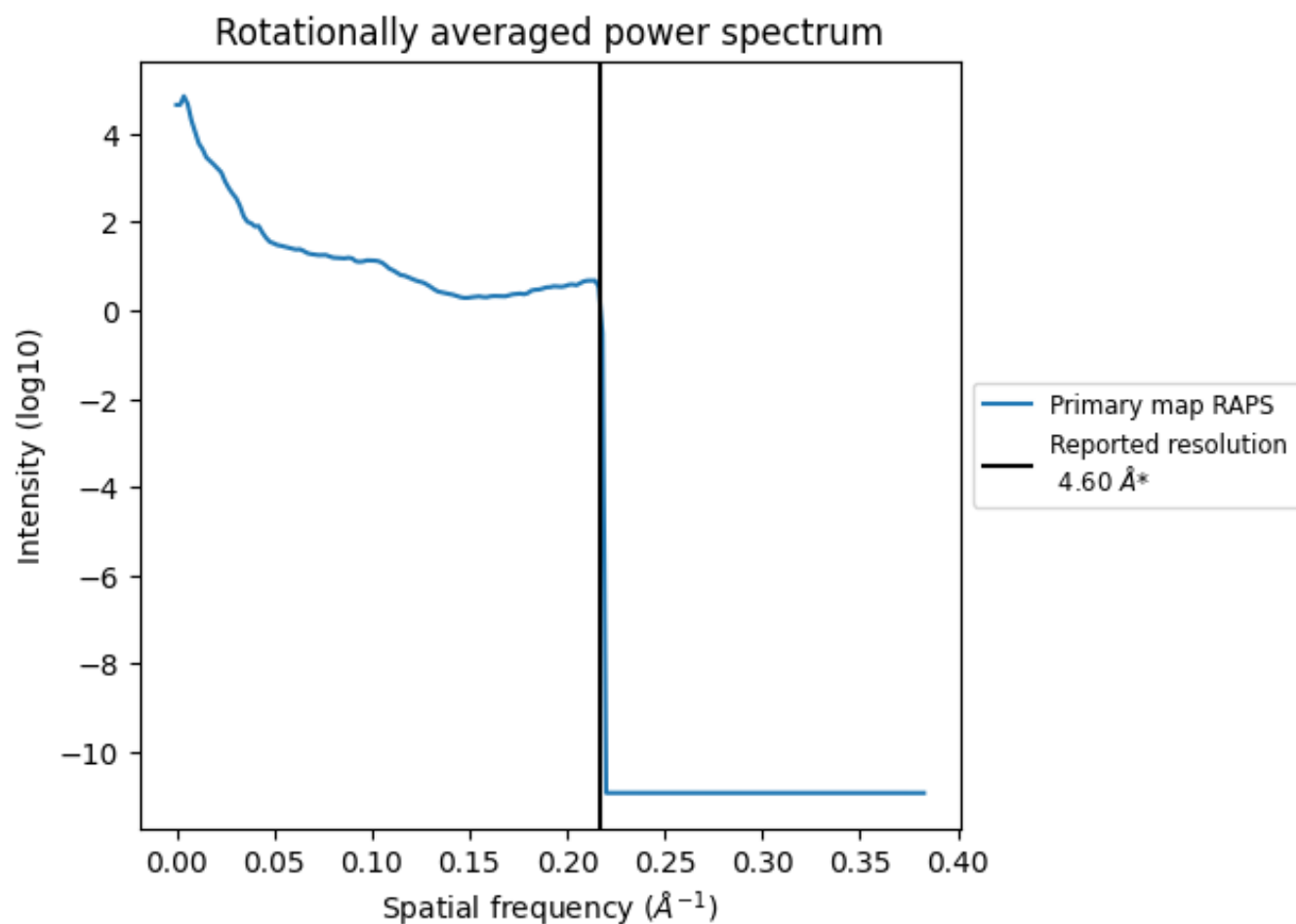
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1373 nm^3 ; this corresponds to an approximate mass of 1240 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 [i](#)

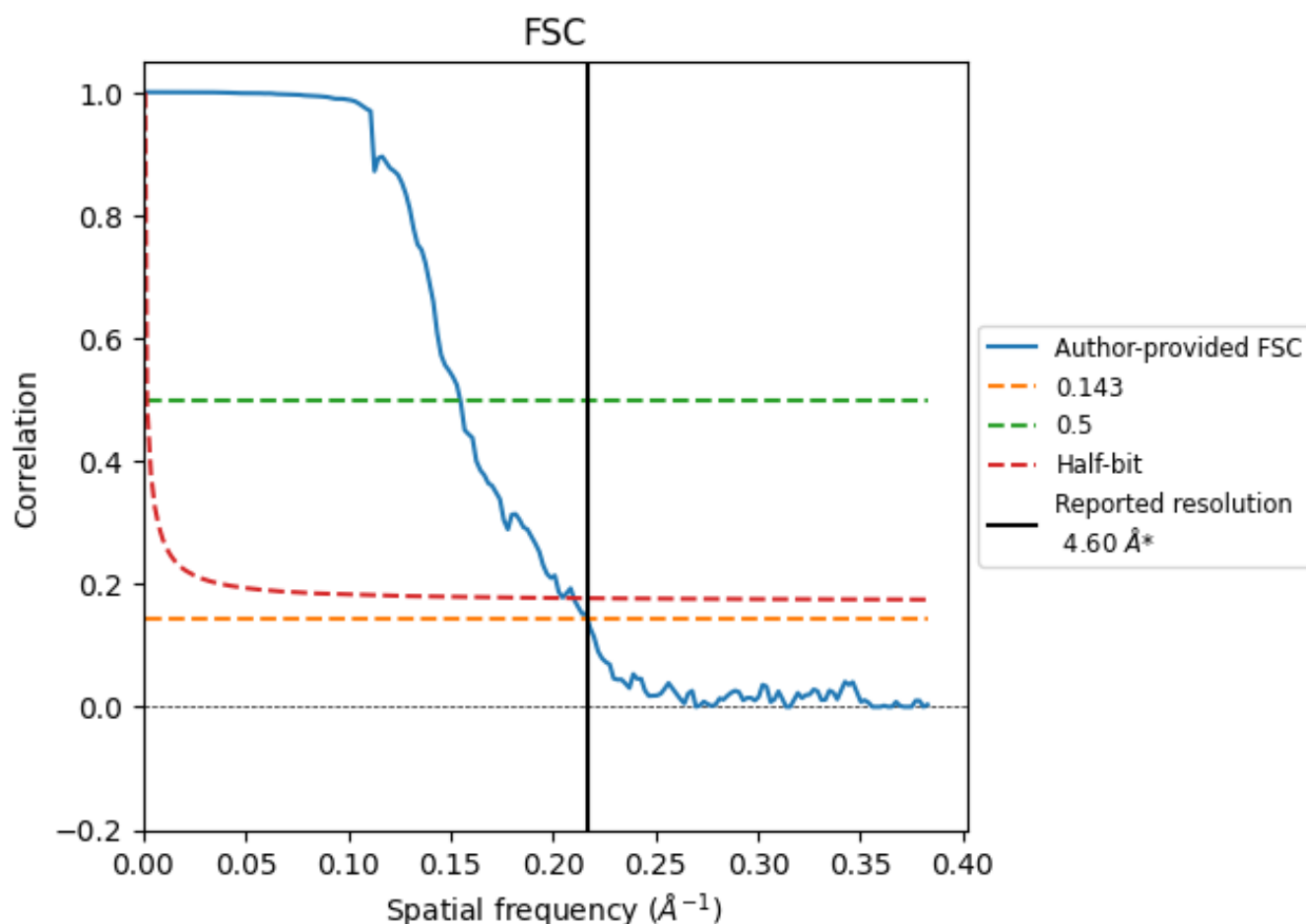


*Reported resolution corresponds to spatial frequency of 0.217 $\text{\AA}^{-1}$

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 0.217 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.61	6.46	4.76
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

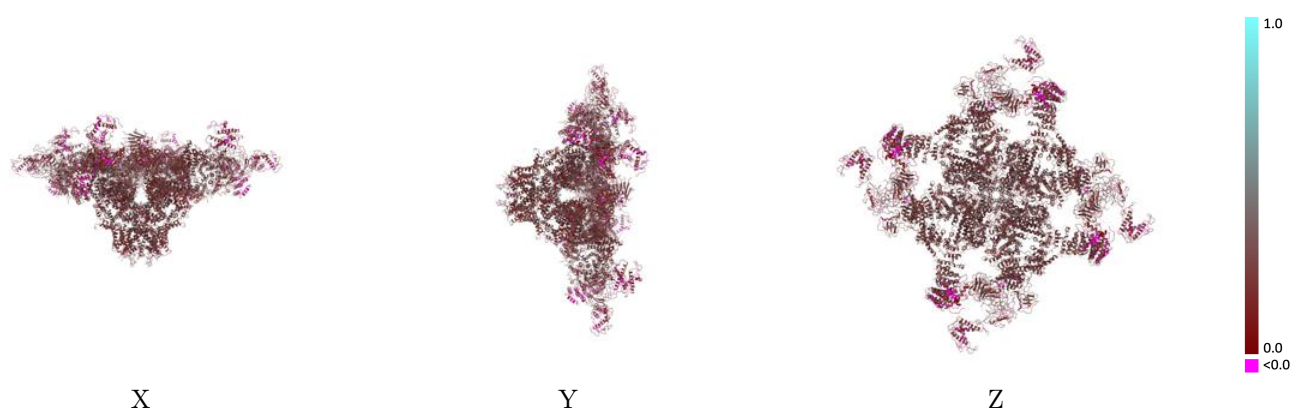
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9824 and PDB model 6JGZ. 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](#)

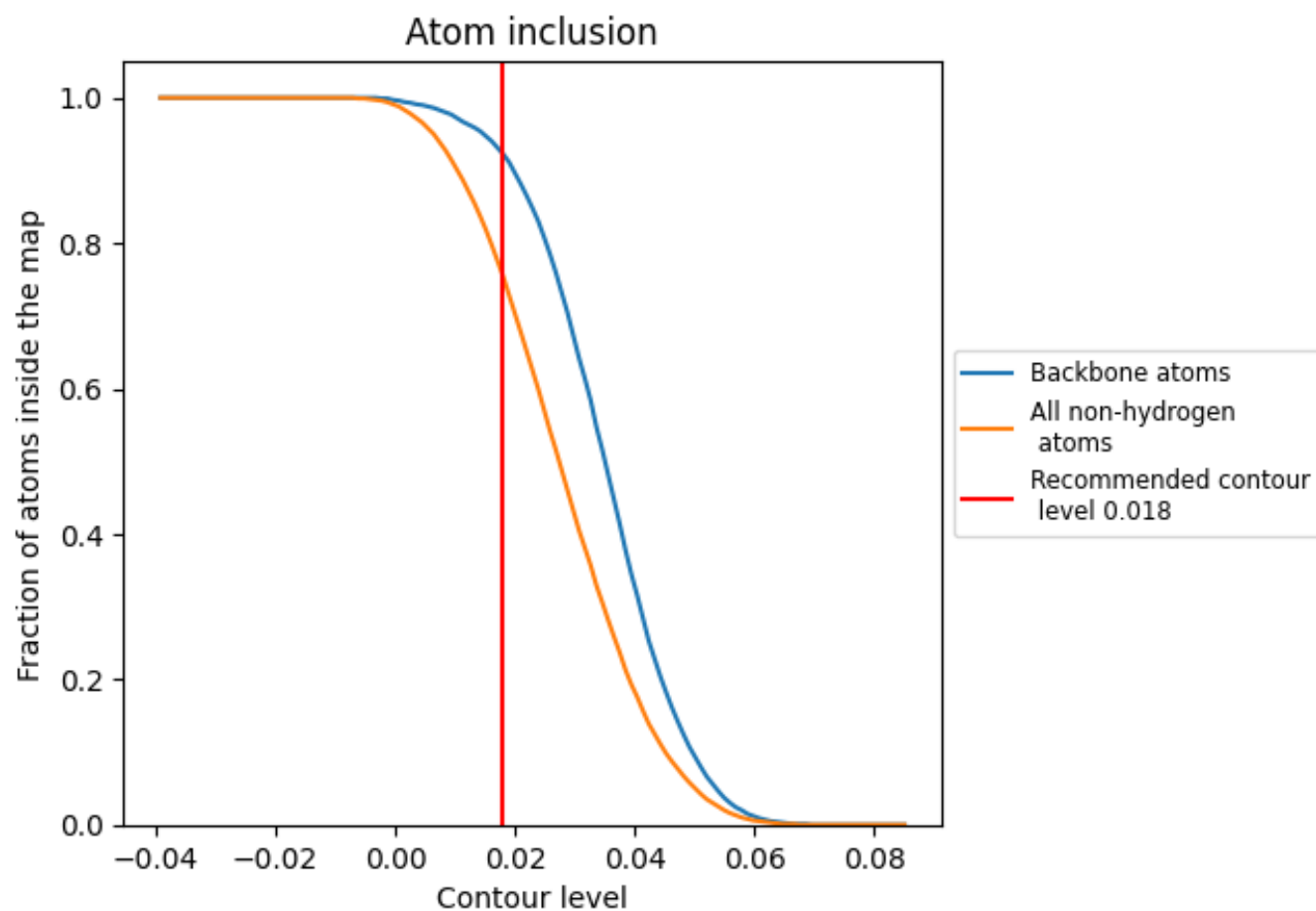


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 76% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7550	0.2490
A	0.8170	0.2650
B	0.7530	0.2480
C	0.8190	0.2650
D	0.7530	0.2490
E	0.8170	0.2650
F	0.7530	0.2480
G	0.8140	0.2650
H	0.7530	0.2480

1.0

0.0

<0.0