



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 01:19 AM UTC

PDB ID : 6JI8 / pdb_00006ji8
EMDB ID : EMD-9833
Title : Structure of RyR2 (F/apoCaM dataset)
Authors : Gong, D.S.; Chi, X.M.; Zhou, G.W.; Huang, G.X.Y.; Lei, J.L.; Yan, N.
Deposited on : 2019-02-20
Resolution : 3.60 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:

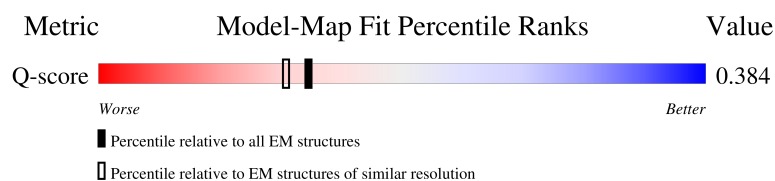
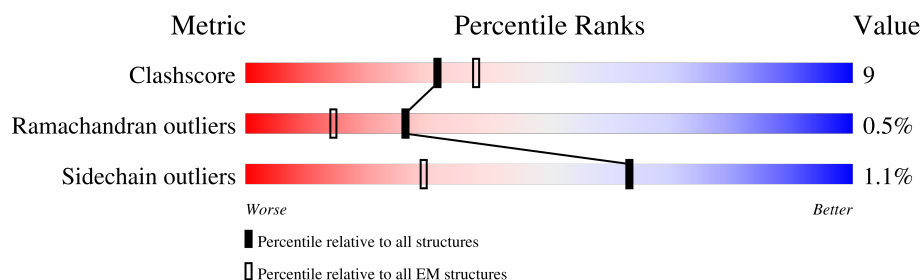
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

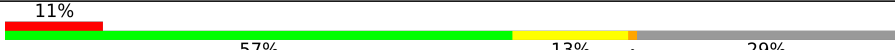
The reported resolution of this entry is 3.60 Å.

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	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	4968	
1	D	4968	
1	G	4968	
1	J	4968	

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Mol	Chain	Length	Quality of chain
2	B	108	 81%17%..
2	E	108	 81%17%..
2	H	108	 84%14%..
2	K	108	 81%17%..
3	C	149	 45%72%19%• 7%
3	F	149	 44%72%20%• 7%
3	I	149	 46%72%19%• 7%
3	L	149	 45%73%19%• 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 115060 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 RyR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3511	Total	C	N	O	S	0	0
			26851	17104	4605	4982	160		
1	D	3511	Total	C	N	O	S	0	0
			26851	17104	4605	4982	160		
1	G	3511	Total	C	N	O	S	0	0
			26851	17104	4605	4982	160		
1	J	3511	Total	C	N	O	S	0	0
			26851	17104	4605	4982	160		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
2	E	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
2	H	107	Total	C	N	O	S	0	0
			819	516	144	155	4		
2	K	107	Total	C	N	O	S	0	0
			819	516	144	155	4		

- Molecule 3 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	138	Total	C	N	O	S	0	0
			1094	676	176	233	9		
3	F	138	Total	C	N	O	S	0	0
			1094	676	176	233	9		
3	I	138	Total	C	N	O	S	0	0
			1094	676	176	233	9		
3	L	138	Total	C	N	O	S	0	0
			1094	676	176	233	9		

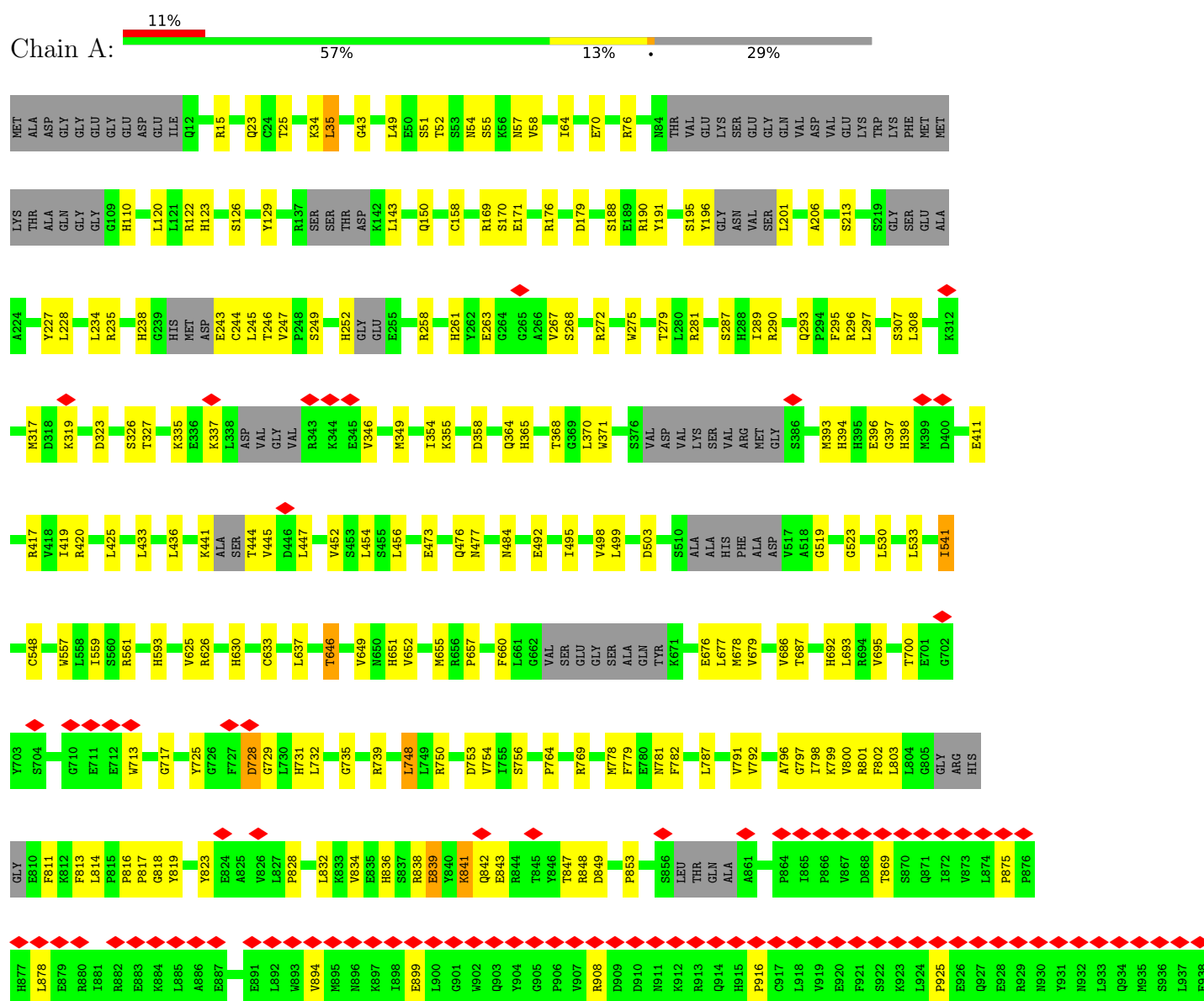
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Zn 1	0
4	D	1	Total 1	Zn 1	0
4	G	1	Total 1	Zn 1	0
4	J	1	Total 1	Zn 1	0

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: RyR2



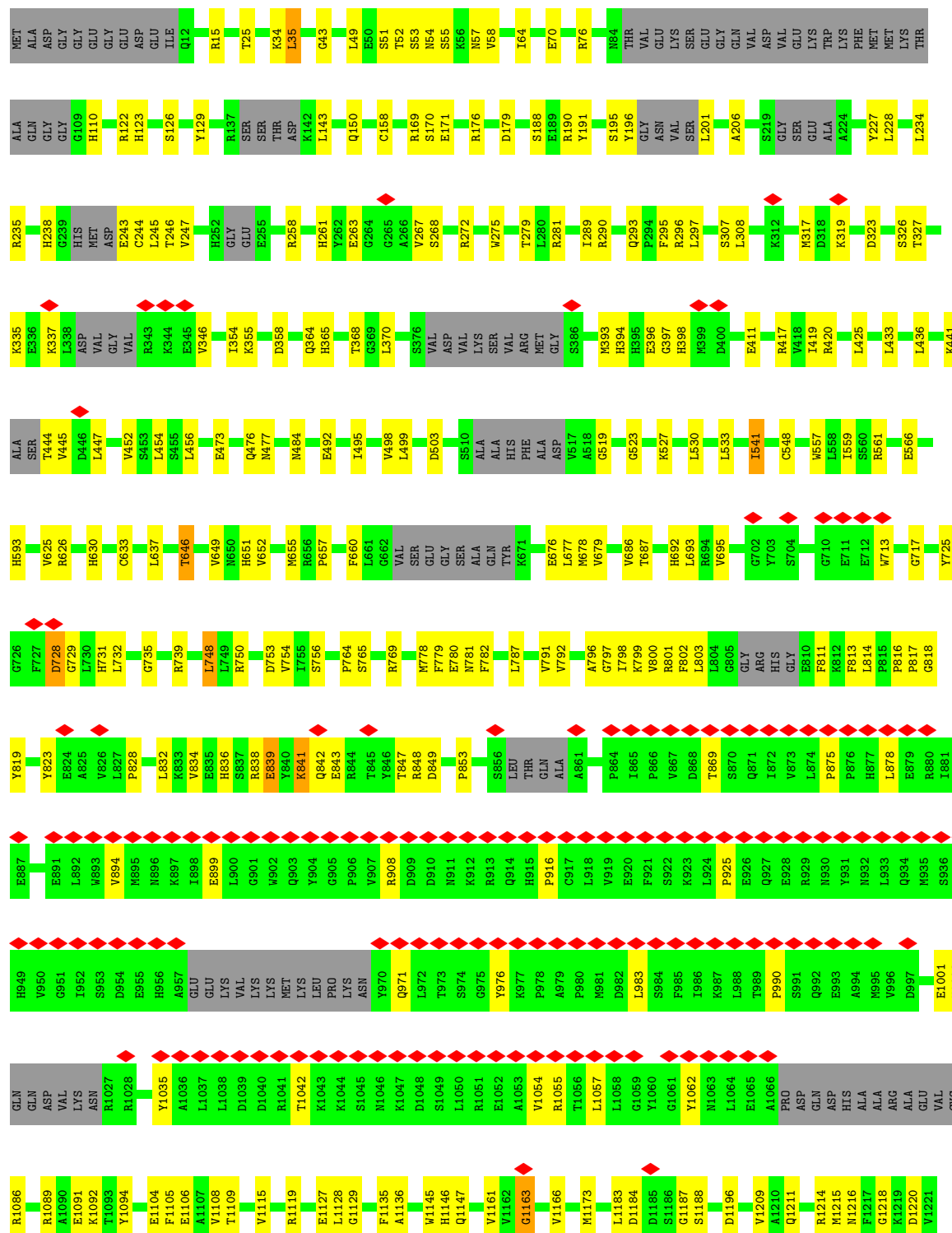
L2241	L2058	L1595	L1501	T1425	D1298	D1196	ARG	L999	T839
E2260	A2071	R1598	L1505	Y1426	R1303	V1209	ALA	A1000	L940
P2261	V2075	M1601	V1510	R1431	L1304	Q1211	GLU	E1001	K941
E2264	L2076	Q1602	V1511	P1434	C1310	Q1214	CYS	M1002	T942
V2267	L2081	F1603	ASP	GLY	ALA	R1214	SER	Q1014	L943
L2275	V2082	L1604	ALA	GLN	GLU	M1215	GLY	GLY	L944
L2088	R2083	R1610	SER	ALA	PHE	M1216	THR	THR	A945
L2088	L2088	I1611	G1516	N1440	SER	F1217	TYR	TYR	L946
T2106	L2088	W1617	L1517	V1441	THR	G1218	GLY	GLY	C947
T2117	L2088	L1618	L1518	W1442	LYS	S1222	ILE	ILE	C948
T2126	L2088	V1619	G1524	V1443	ALA	T1228	GLN	GLN	H949
T2127	L2088	Q1620	K1525	W1445	GLY	L1232	ASP	ASP	V950
L2120	L2088	C1621	S1523	D1449	PRO	A1240	LYS	LYS	I952
L2124	L2088	M1628	Y1531	F1450	GLY	N1242	ASN	ASN	S953
G2125	L2088	L1630	P1535	L1459	ALA	P1256	R1027	R1028	D954
G2126	L2088	E1634	P1541	ASP	SER	T1248	Y1035	Y1036	H956
G2127	L2088	E1635	A1542	VAL	LEU	M1249	A1036	A1037	A957
V2133	L2088	E1635	F1544	ARG	LEU	W1250	L1037	L1038	GLU
ARG	L2088	D1640	F1544	THR	LEU	L1251	D1039	D1039	LYS
MET	L2088	I1641	Q1554	T1466	LEU	P1256	D1040	D1040	LYS
GLY	L2088	T1645	F1555	T1467	GLY	V1261	R1041	R1041	LYS
LYS	L2088	Y1655	E1556	T1468	ASP	E1266	T1042	T1042	MET
LYS	L2088	Y1655	LEU	D1471	TYR	H1267	K1043	K1043	LYS
GLY	L2088	R1659	GLY	E1472	SER	R1272	K1044	K1044	PRO
ASN	L2088	Y1664	ILE	K1475	ALA	D1274	S1045	S1045	LYS
SER	L2088	R1671	LYS	Y1476	SER	GLY	M1046	M1046	ASN
ASP	L2088	L1824	ASN	H1477	PHE	THR	K1047	K1047	Y970
L2024	L2024	Y1826	VAL	E1478	ALA	THR	D1048	D1048	Q971
L2037	L2037	I1830	LEU	S1479	THR	ILE	S1049	S1049	L972
L2039	L2039	V1680	PRO	R1482	LEU	ASP	L1050	L1050	T973
LEU	L2039	D1681	SER	S1483	GLY	SER	R1051	R1051	S974
LYS	L2039	E1682	A1568	N1484	LYS	ASP	E1052	E1052	G975
LYS	L2039	P1683	G1569	CYS	THR	PRO	A1053	A1053	Y976
LYS	L2039	Q1684	L1570	Y1486	ALA	CYS	V1054	V1054	K977
ALA	L2039	L1685	E1574	M1487	HIS	LYS	R1055	R1055	P978
ALA	L2039	I1689	M1577	A1490	ARG	LYS	T1056	T1056	A979
ALA	L2039	E1690	P1578	GLY	VAL	THR	L1057	L1057	P980
ALA	L2039	P1695	V1579	A1490	ASP	ASP	L1058	L1058	M981
ALA	L2039	P1695	P1580	GLY	TYR	ASP	G1059	G1059	D982
ALA	L2039	Q1581	Q1581	SER	ARG	ASP	Y1060	Y1060	L983
ALA	L2039	Y1703	H1587	THR	VAL	ASP	L1061	L1061	S984
ALA	L2039	D1704	V1588	MET	LYS	ASP	Y1062	Y1062	F985
ALA	L2039	L1706	Q1589	SER	LYS	ASP	N1063	N1063	I986
ALA	L2039	L1706	F1590	GLY	THR	ASP	L1064	L1064	K987
ALA	L2039	Y1714	V1594	GLY	SER	ASP	E1065	E1065	L988
ALA	L2039	Y1714	V1594	GLY	SER	ASP	A1066	A1066	T989
ALA	L2039	Y1714	V1594	GLY	SER	ASP	PRO	PRO	P990
ALA	L2039	Y1714	V1594	GLY	SER	ASP	ASP	ASP	S991
ALA	L2039	Y1714	V1594	GLY	SER	ASP	GLN	GLN	Q992
ALA	L2039	Y1714	V1594	GLY	SER	ASP	ASP	ASP	E993
ALA	L2039	Y1714	V1594	GLY	SER	ASP	HIS	HIS	A994
ALA	L2039	Y1714	V1594	GLY	SER	ASP	ALA	ALA	M995
ALA	L2039	Y1714	V1594	GLY	SER	ASP	ALA	ALA	V996
ALA	L2039	Y1714	V1594	GLY	SER	ASP	ALA	ALA	D997
ALA	L2039	Y1714	V1594	GLY	SER	ASP	ALA	ALA	K998



V4777	D4799	K4792	K4796	D4799	G4800	D4801	D4804	F4805	K4806	C4807	D4808	D4809	M4810	L4811	Y4819	R4823	G4826	P4835	D4838	E4841	R4844	D4848	V4857	I4858	A4861	I4862	I4863	Q4864	G4865	L4866	I4867	I4868	E4873	L4874	R4875	M4885	C4889	F4890	D4897	P4903	H4904	
GLY	GLY	LYS	GLY	THR	THR	SER	SER	GLY	GLY	ASP	PHE	SER	GLY	SER	GLY	GLY	ILE	ILE	ALA	SER	SER	LEU	G4733	G4737	F4738	F4739	F4740	Y4617	I4618	Q4621	C4629	R4633	I4634	V4635	V4761	T4762	K4766	Q4767	L4770	P4903	H4904	
GLY	THR	GLY	GLY	ARG	ARG	SER	SER	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	GLY	GLY	GLY	
LEU	LEU	LEU	LEU	PRO	PRO	THR	ASP	VAL	GLY	GLY	GLY	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	
LEU	LEU	ALA	ASN	ASN	ASN	GLN	ASP	VAL	VAL	VAL	PHE	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	
GLN	TYR	LYS	LEU	ILE	PRO	HIS	ASN	ASN	PRO	PRO	ASN	ALA	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	
ASP	LEU	ASN	ARG	ALA	ALA	ASN	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	GLY	GLY	GLY	GLY	
S4069	C4070	A4071	D4074	E4075	N4076	E4077	T4078	V4085	K4086	R4087	F4088	H4089	E4090	P4091	D4094	I4095	G4096	F4097	V4101	R4115	R4136	M4140	I4146	E4147	R4148	E4152	I4153	S4154	E4155	S4156	Q4160	W4161	K4162	P4164	I4174	E4183	K4184	E4188	L4203	I4207	SER	SER
L3936	V3951	K3955	K3956	S3960	K3973	Q3976	K3977	V3980	V3981	K3982	L3983	L3984	S3985	K3986	I3996	M4000	M4003	V4010	V4011	L4014	L4015	F4018	D4019	M4020	F4021	K4034	D4039	K4046	H4050	F4051	A4052	H4056	K4057	H4058	Q4061	T4064	E4065	F4066	L4067	L4068		
L3797	S3800	C3801	S3802	V3803	L3804	D3805	F3809	E3810	R3811	G3817	V3820	VAL	THR	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
E3634	H3635	F3636	F3637	E3638	F3648	GLY	ALA	VAL	PRO	PRO	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
ASP	ILE	ASN	ARG	ASN	VAL	PHE	LEU	LEU	HIS	THR	THR	MET	ILE	ARG	ILE	ARG	ARG	ARG	TYR	SER	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
THR	ASP	THR	LYS	SER	VAL	LEU	THR	VAL	SER	VAL	GLN	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



• Molecule 1: RyR2





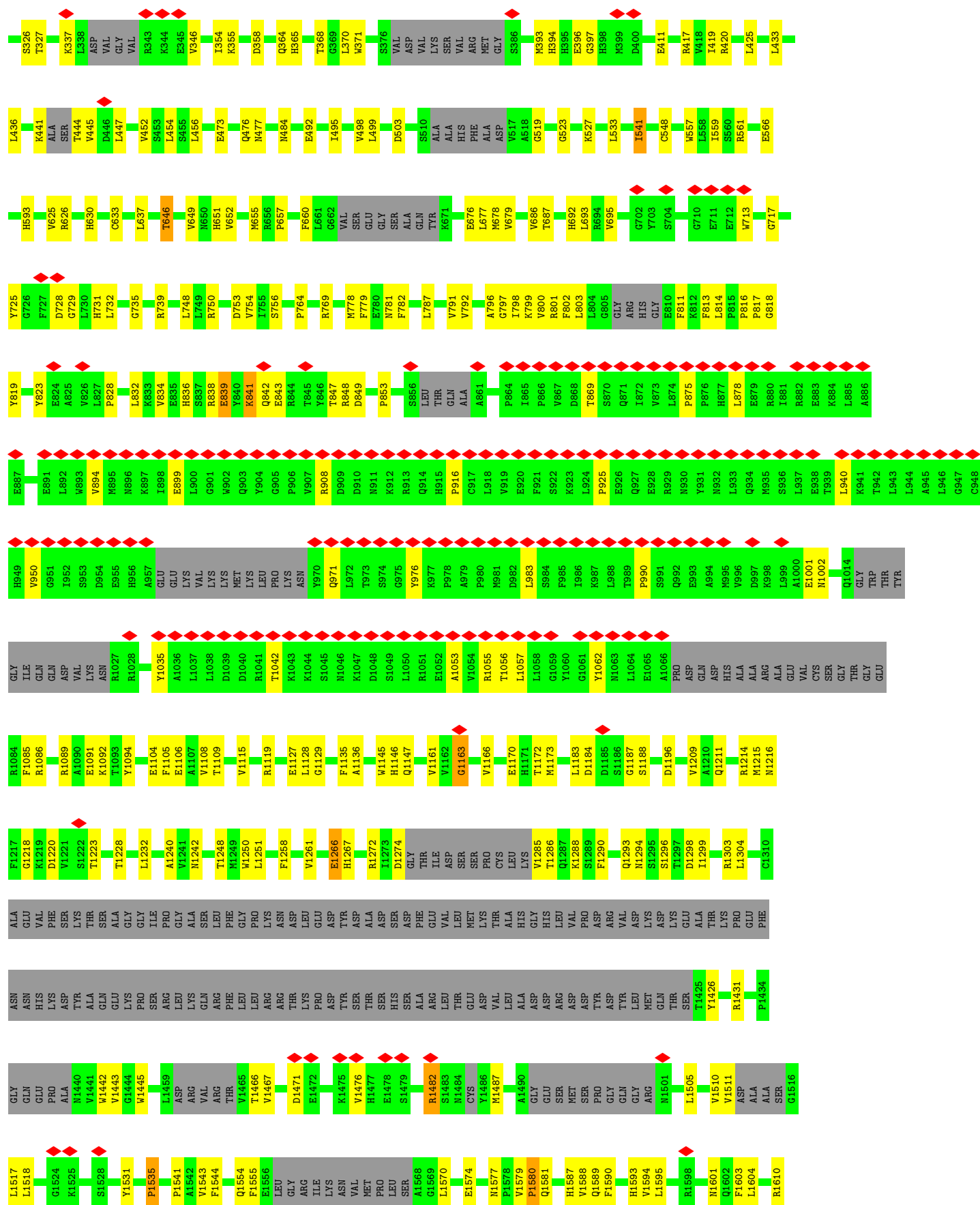








WORLDWIDE
PDB
PROTEIN DATA BANK

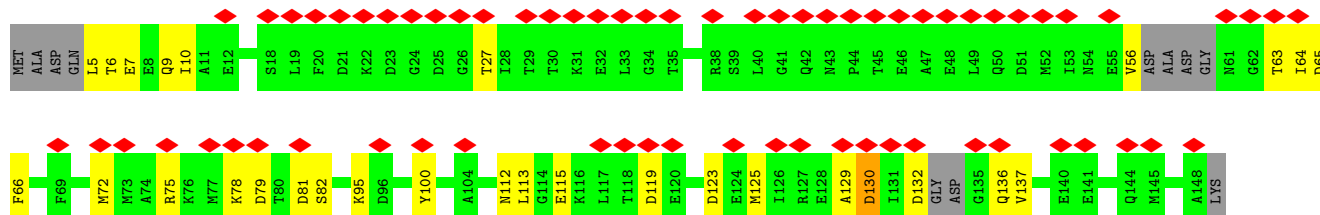
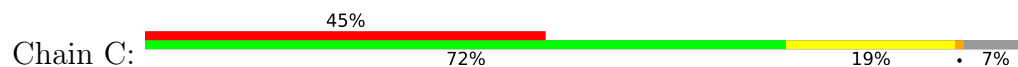




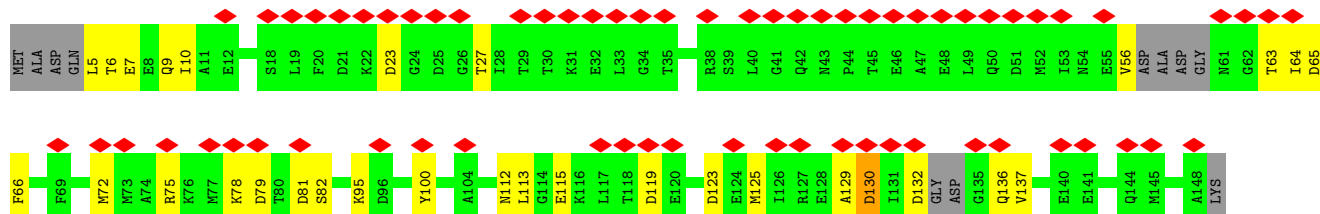
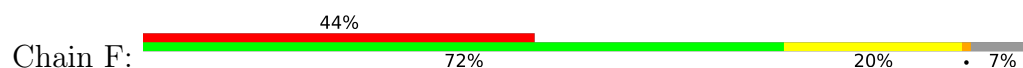




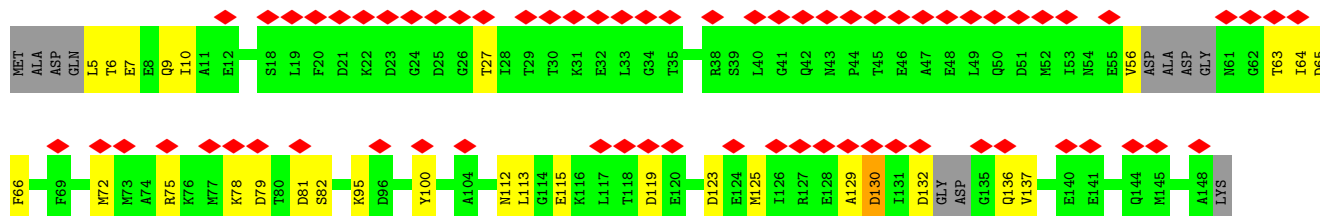
- Molecule 3: Calmodulin-1



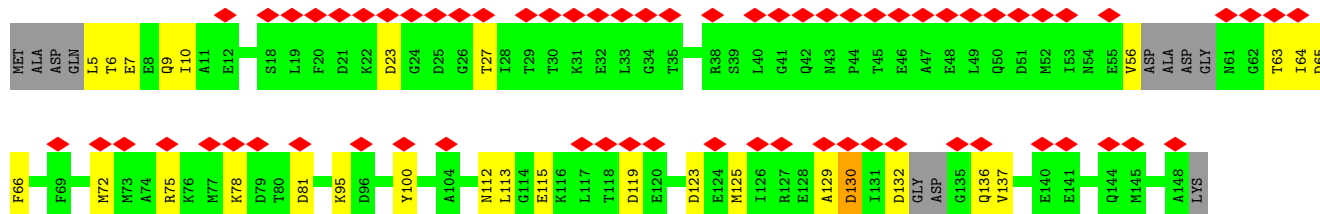
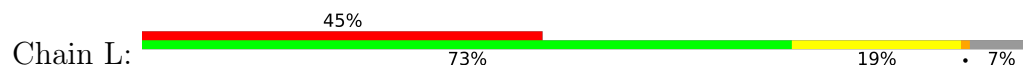
- Molecule 3: Calmodulin-1



- Molecule 3: Calmodulin-1



- Molecule 3: Calmodulin-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	208715	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 ($e^-/\text{\AA}^2$)	45.6	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	0.223	Depositor
Minimum map value	-0.121	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.027	Depositor
Map size (Å)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.338, 1.338, 1.338	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	0.43	1/27354 (0.0%)	0.73	16/36987 (0.0%)
1	D	0.43	1/27354 (0.0%)	0.73	16/36987 (0.0%)
1	G	0.43	1/27354 (0.0%)	0.73	16/36987 (0.0%)
1	J	0.43	1/27354 (0.0%)	0.73	16/36987 (0.0%)
2	B	0.36	0/835	0.62	0/1123
2	E	0.36	0/835	0.62	0/1123
2	H	0.36	0/835	0.62	0/1123
2	K	0.36	0/835	0.62	0/1123
3	C	0.29	0/1104	0.67	2/1479 (0.1%)
3	F	0.29	0/1104	0.67	2/1479 (0.1%)
3	I	0.29	0/1104	0.67	2/1479 (0.1%)
3	L	0.29	0/1104	0.67	2/1479 (0.1%)
All	All	0.43	4/117172 (0.0%)	0.73	72/158356 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	32
1	D	0	32
1	G	0	32
1	J	0	32
All	All	0	128

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1577	ASN	C-N	5.81	1.39	1.33
1	D	1577	ASN	C-N	5.81	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	1577	ASN	C-N	5.81	1.39	1.33
1	J	1577	ASN	C-N	5.77	1.39	1.33

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	687	THR	N-CA-C	-5.71	98.63	110.80
1	A	687	THR	N-CA-C	-5.71	98.64	110.80
1	D	687	THR	N-CA-C	-5.71	98.64	110.80
1	G	687	THR	N-CA-C	-5.69	98.67	110.80
1	J	1163	GLY	N-CA-C	5.66	119.32	112.48

There are no chirality outliers.

5 of 128 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	261	HIS	Peptide
1	A	729	GLY	Peptide
1	A	748	LEU	Peptide
1	A	791	VAL	Peptide
1	A	817	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	26851	0	25388	521	0
1	D	26851	0	25388	518	0
1	G	26851	0	25388	517	0
1	J	26851	0	25388	526	0
2	B	819	0	824	10	0
2	E	819	0	824	10	0
2	H	819	0	824	8	0
2	K	819	0	824	10	0
3	C	1094	0	1036	17	0
3	F	1094	0	1036	18	0
3	I	1094	0	1036	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	1094	0	1036	17	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
4	G	1	0	0	0	0
4	J	1	0	0	0	0
All	All	115060	0	108992	1951	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 1951 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:G:4518:LEU:HD21	1:G:4738:PHE:CE1	1.58	1.39
1:D:4518:LEU:HD21	1:D:4738:PHE:CE1	1.58	1.38
1:A:4518:LEU:HD21	1:A:4738:PHE:CE1	1.58	1.37
1:J:4518:LEU:HD21	1:J:4738:PHE:CE1	1.58	1.36
1:D:4733:GLY:HA3	1:D:4740:PHE:CE1	1.68	1.28

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	3389/4968 (68%)	3012 (89%)	360 (11%)	17 (0%)	24	57
1	D	3389/4968 (68%)	3013 (89%)	359 (11%)	17 (0%)	24	57
1	G	3389/4968 (68%)	3015 (89%)	356 (10%)	18 (0%)	24	57
1	J	3389/4968 (68%)	3012 (89%)	360 (11%)	17 (0%)	24	57
2	B	105/108 (97%)	96 (91%)	9 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	H	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
2	K	105/108 (97%)	96 (91%)	9 (9%)	0	100	100
3	C	132/149 (89%)	119 (90%)	12 (9%)	1 (1%)	16	49
3	F	132/149 (89%)	119 (90%)	12 (9%)	1 (1%)	16	49
3	I	132/149 (89%)	118 (89%)	13 (10%)	1 (1%)	16	49
3	L	132/149 (89%)	119 (90%)	12 (9%)	1 (1%)	16	49
All	All	14504/20900 (69%)	12911 (89%)	1520 (10%)	73 (0%)	26	57

5 of 73 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4916	LEU
1	D	4916	LEU
1	G	4916	LEU
1	J	4916	LEU
1	A	1580	PRO

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	2704/4355 (62%)	2674 (99%)	30 (1%)	65	74
1	D	2704/4355 (62%)	2674 (99%)	30 (1%)	65	74
1	G	2704/4355 (62%)	2673 (99%)	31 (1%)	65	74
1	J	2704/4355 (62%)	2675 (99%)	29 (1%)	65	74
2	B	88/89 (99%)	86 (98%)	2 (2%)	44	64
2	E	88/89 (99%)	86 (98%)	2 (2%)	44	64
2	H	88/89 (99%)	86 (98%)	2 (2%)	44	64
2	K	88/89 (99%)	86 (98%)	2 (2%)	44	64
3	C	119/127 (94%)	119 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	119/127 (94%)	119 (100%)	0	100	100
3	I	119/127 (94%)	119 (100%)	0	100	100
3	L	119/127 (94%)	119 (100%)	0	100	100
All	All	11644/18284 (64%)	11516 (99%)	128 (1%)	63	74

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	4094	ASP
1	J	4521	TYR
1	D	2420	ILE
1	D	2409	LEU
1	J	4738	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 267 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	1267	HIS
1	J	1746	HIS
1	J	4737	ASN
1	D	1620	GLN
1	D	1216	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

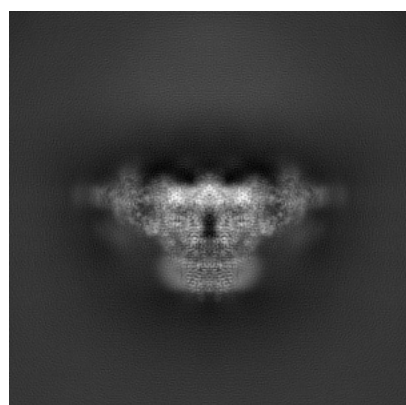
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9833. These allow visual inspection of the internal detail of the map and identification of artifacts.

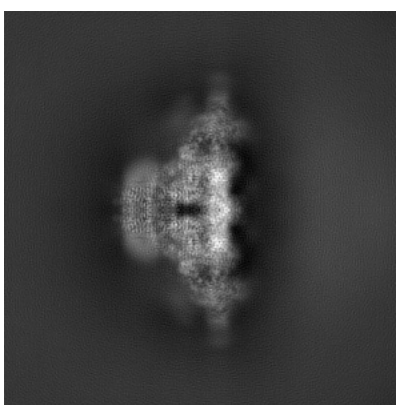
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

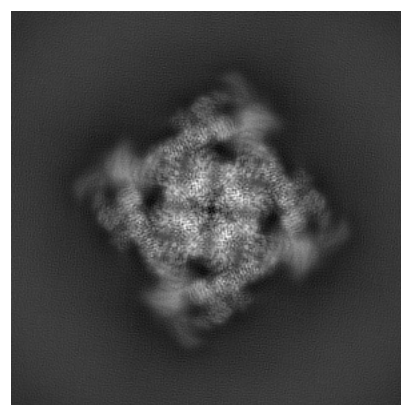
6.1.1 Primary map



X



Y

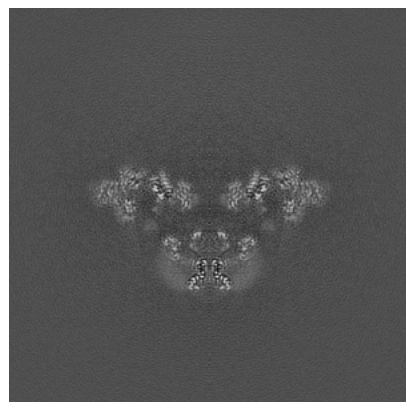


Z

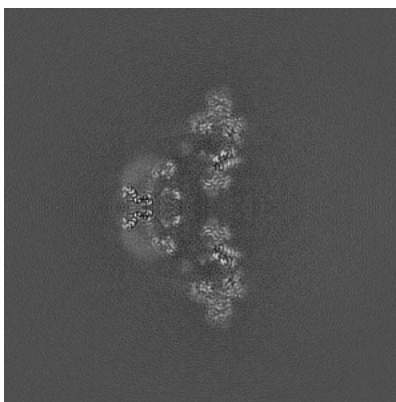
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

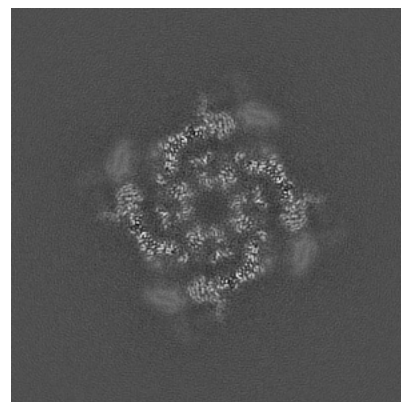
6.2.1 Primary map



X Index: 200



Y Index: 200

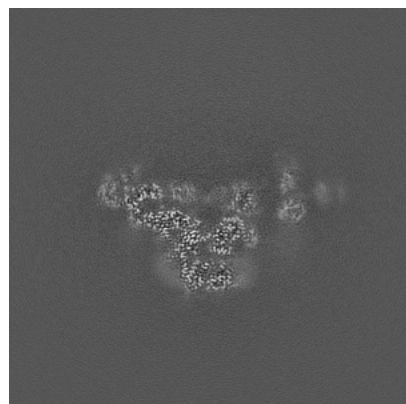


Z Index: 200

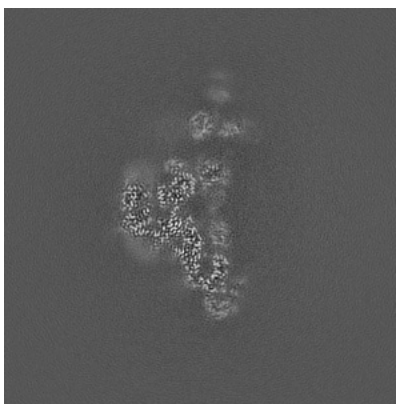
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

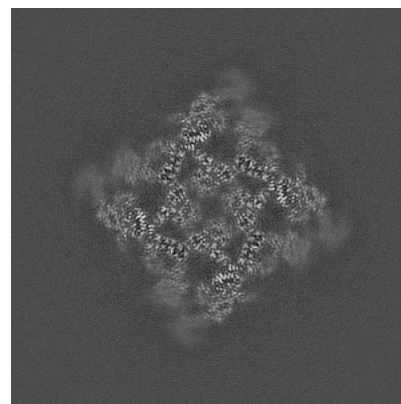
6.3.1 Primary map



X Index: 214



Y Index: 186



Z Index: 209

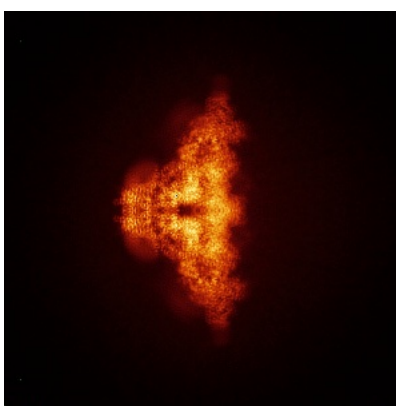
The images above show the largest variance slices of the map in three orthogonal directions.

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

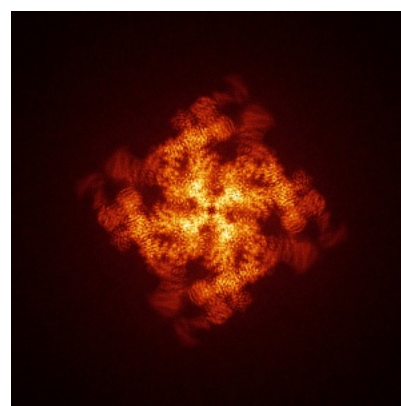
6.4.1 Primary map



X



Y

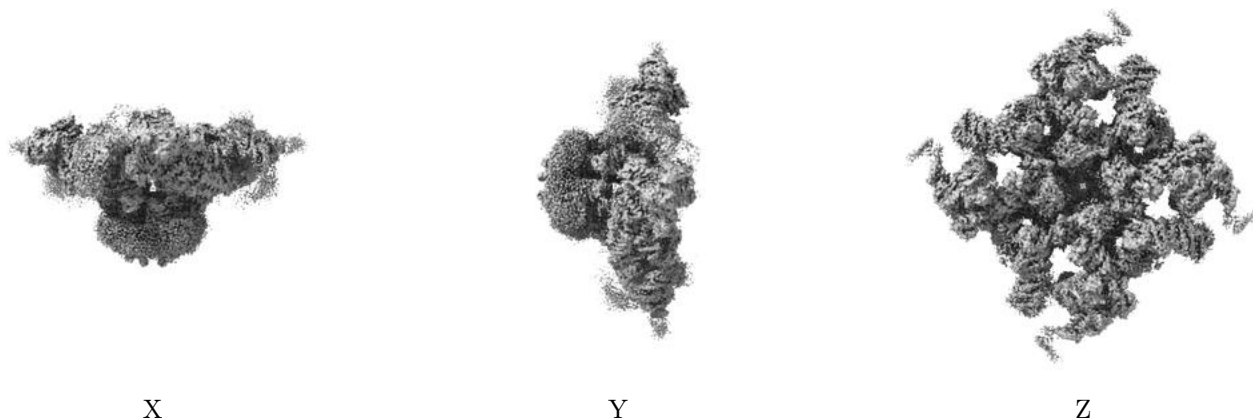


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.027. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

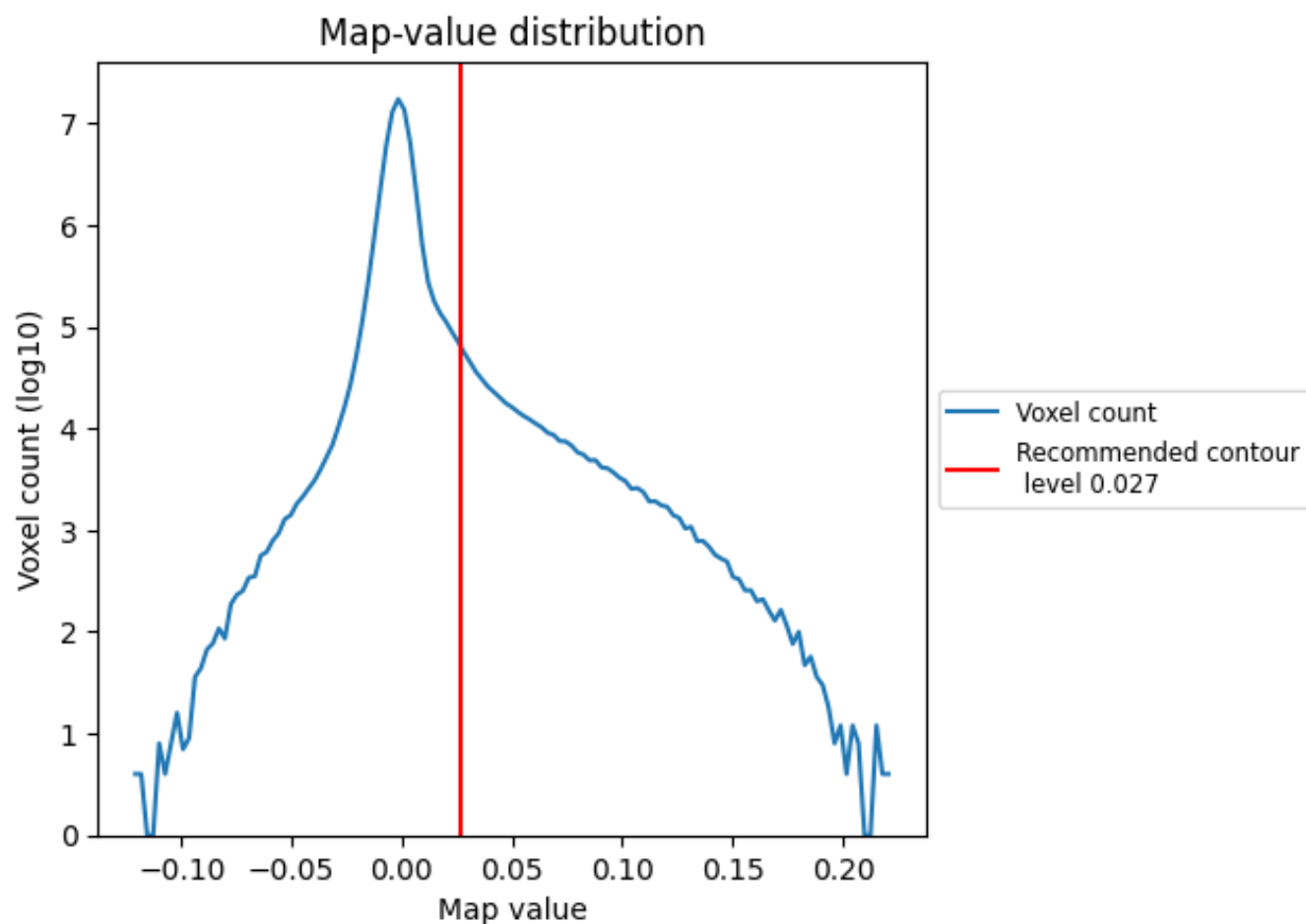
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

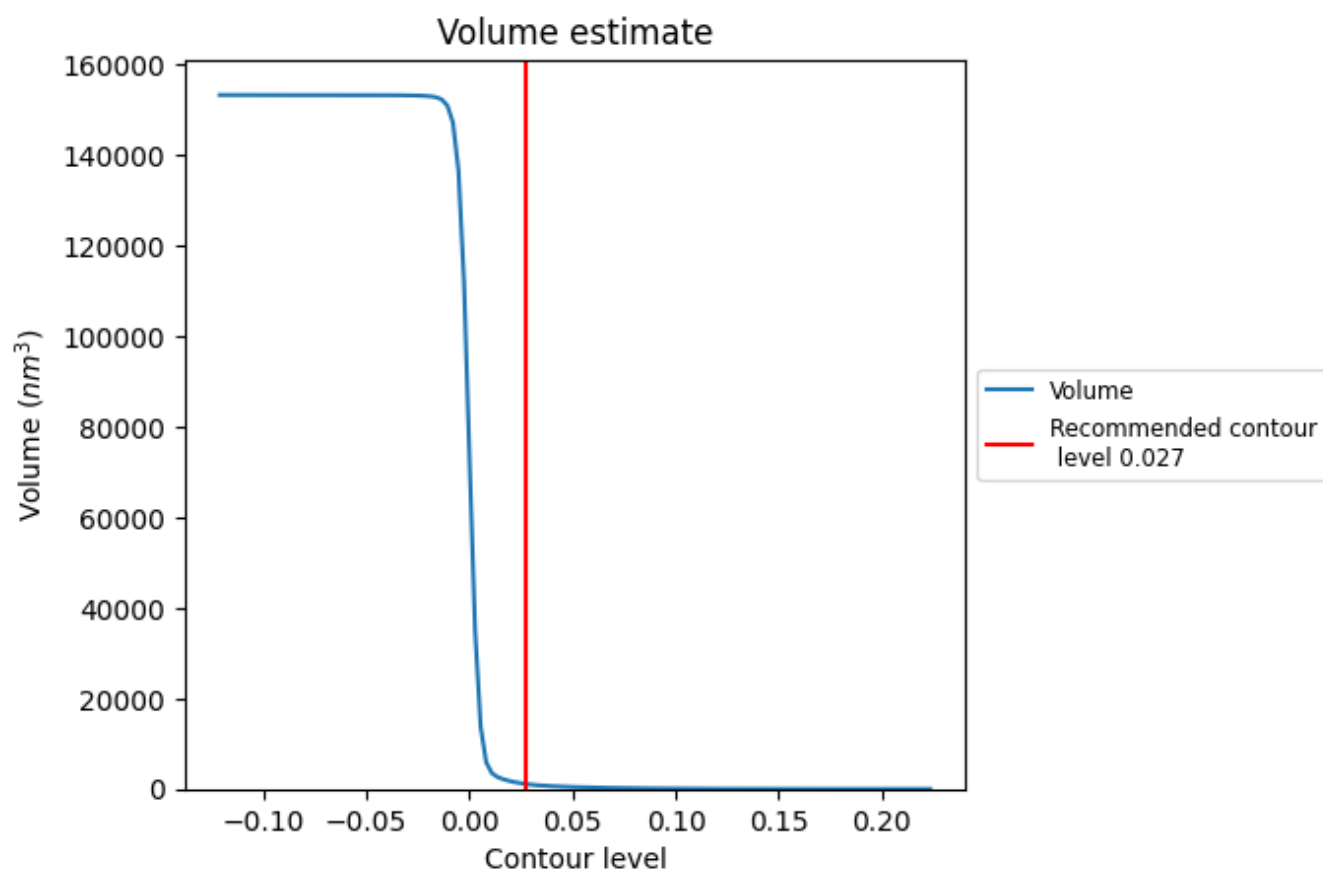
This section contains the results of statistical analysis of the map.

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.

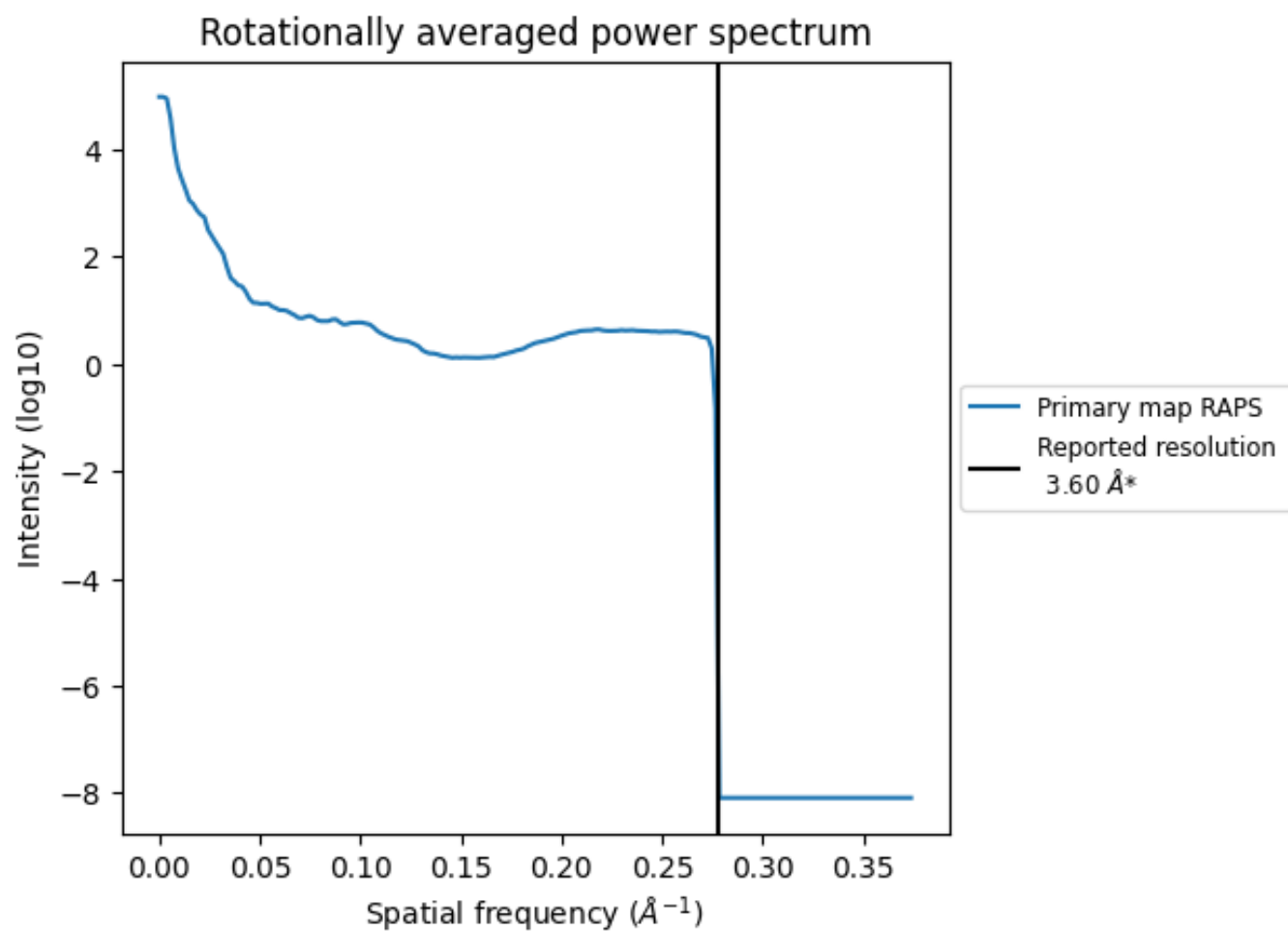
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1114 nm³; this corresponds to an approximate mass of 1007 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 ⓘ

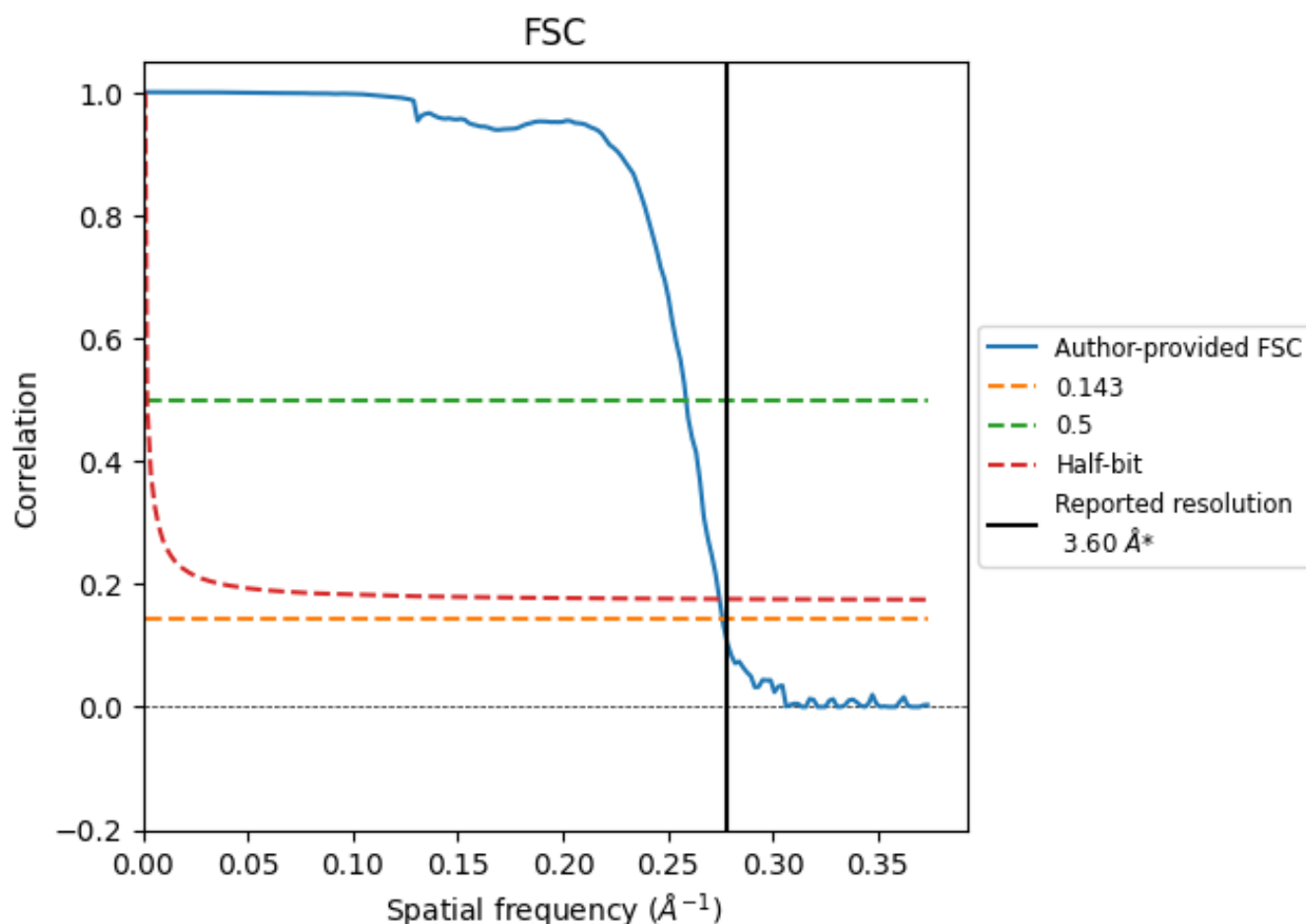


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

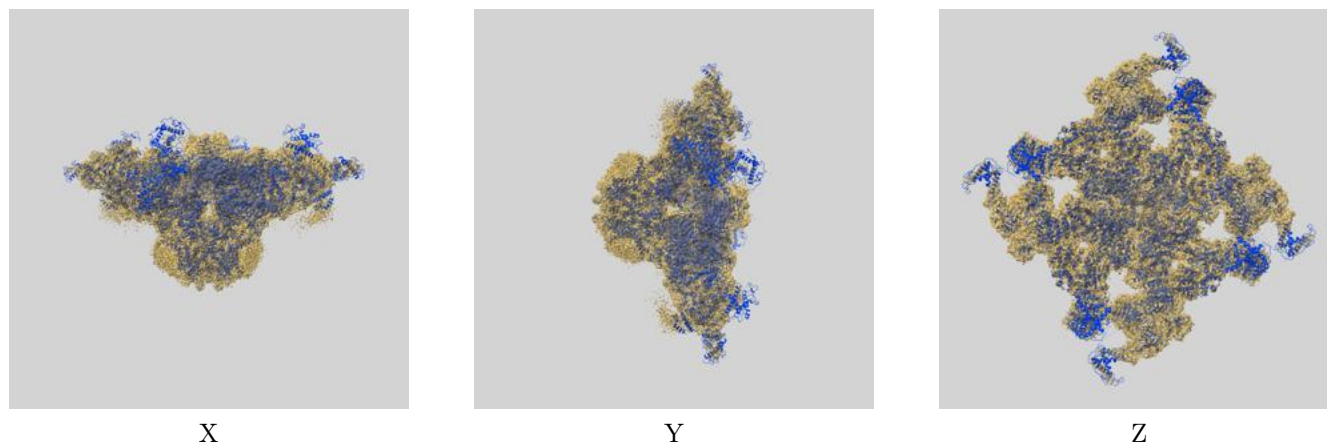
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.62	3.87	3.64
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

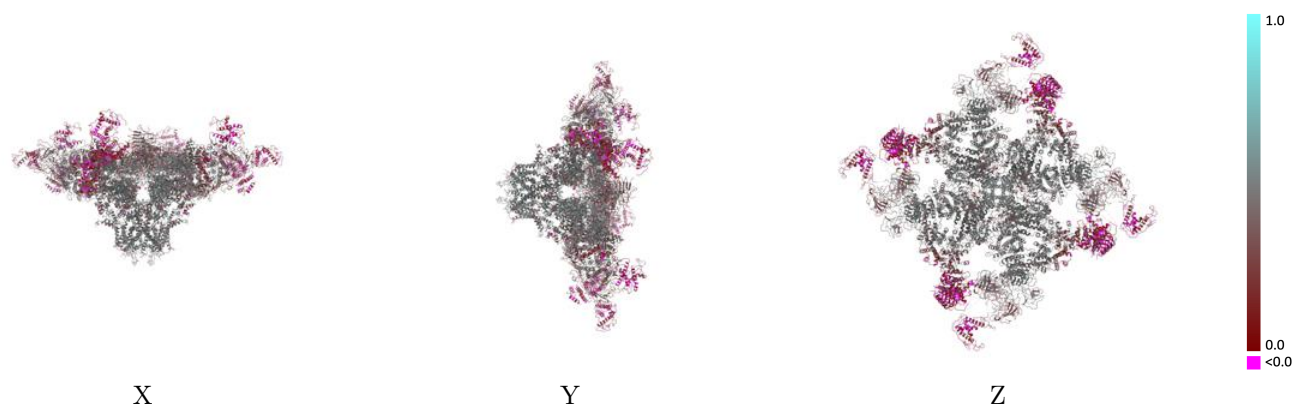
This section contains information regarding the fit between EMDB map EMD-9833 and PDB model 6JI8. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



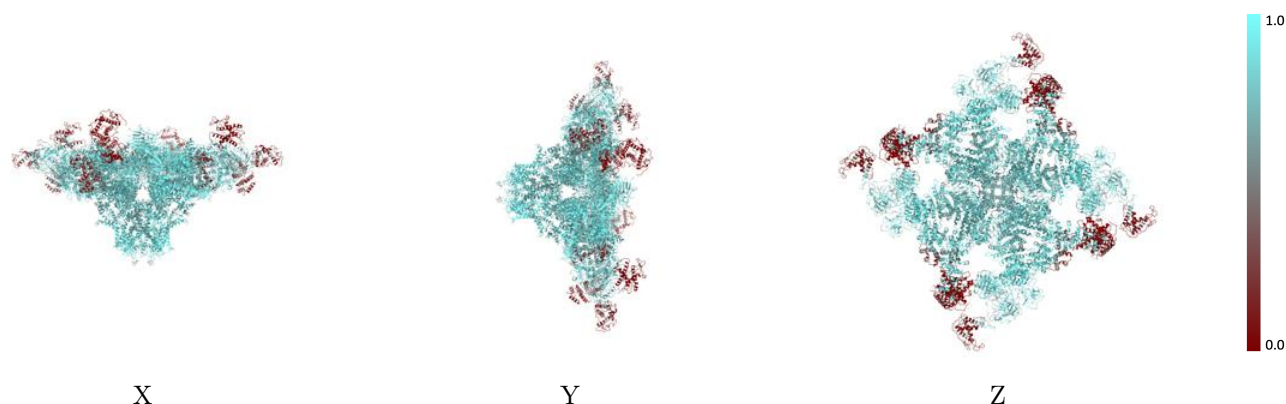
The images above show the 3D surface view of the map at the recommended contour level 0.027 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



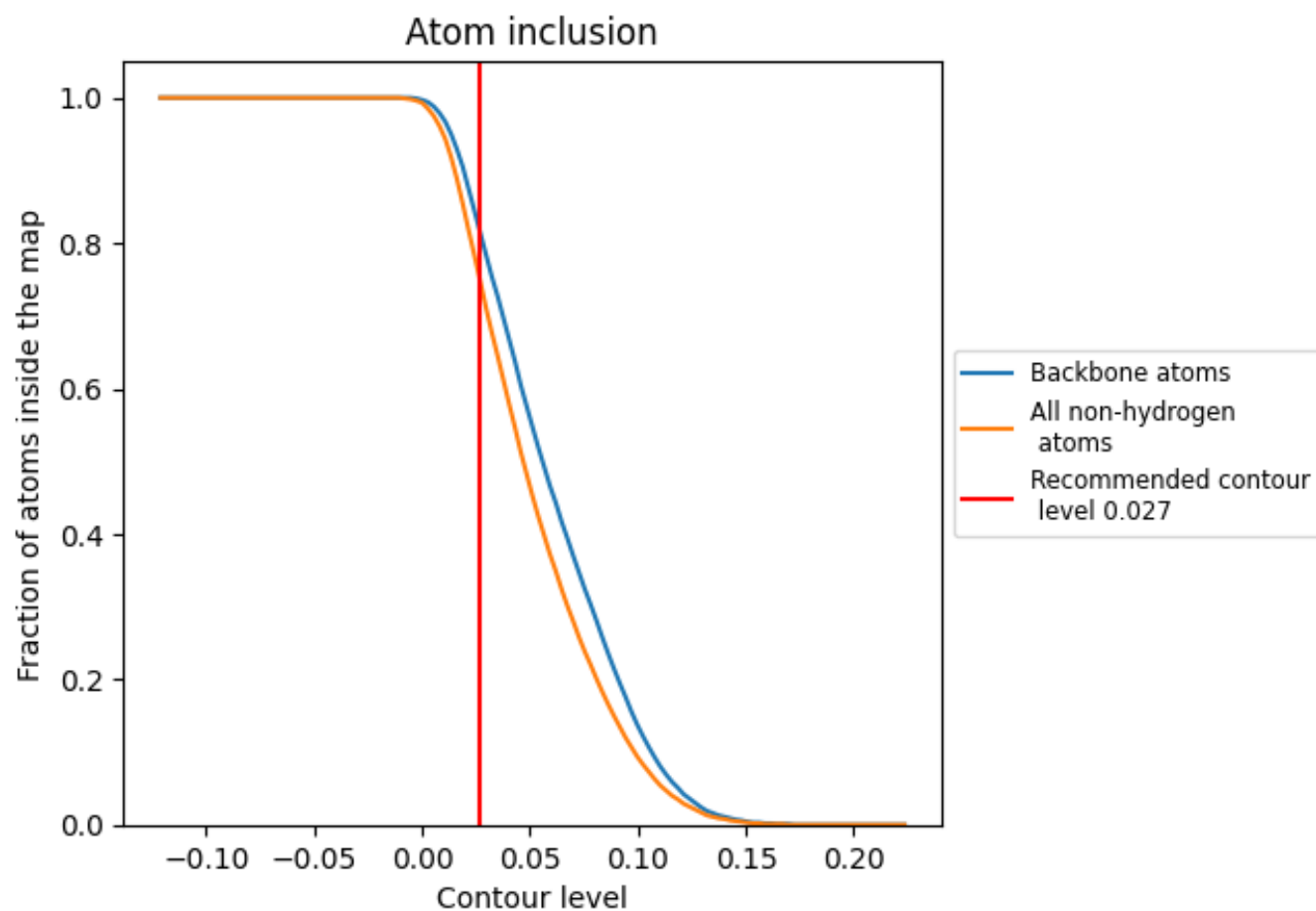
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.027).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 75% 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 (0.027) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7480	0.3840
A	0.7590	0.3880
B	0.8330	0.4310
C	0.4250	0.2340
D	0.7580	0.3880
E	0.8330	0.4310
F	0.4250	0.2340
G	0.7590	0.3880
H	0.8340	0.4320
I	0.4230	0.2350
J	0.7590	0.3880
K	0.8340	0.4310
L	0.4240	0.2360

1.0

0.0

<0.0