



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:04 PM UTC

PDB ID : 6JXC / pdb_00006jxc
EMDB ID : EMD-9893
Title : Tel1 kinase butterfly symmetric dimer
Authors : Xin, J.
Deposited on : 2019-04-23
Resolution : 4.10 Å(reported)

This is a Full wwPDB EM Validation 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

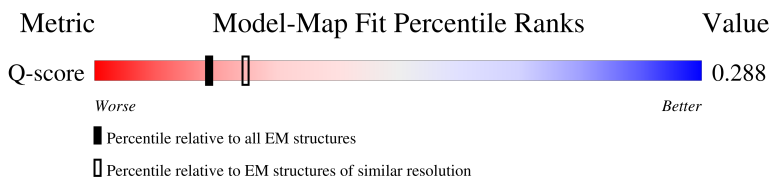
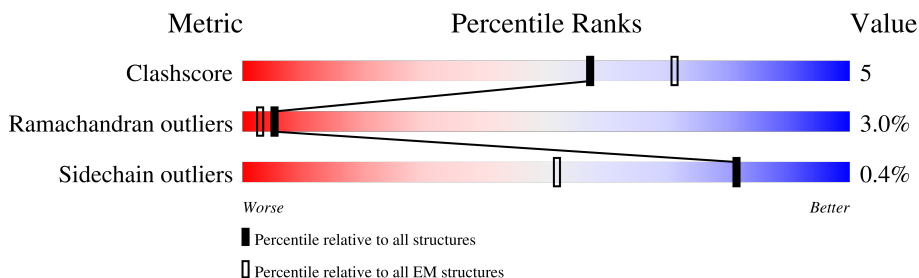
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 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	6458 (3.60 - 4.60)

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	2787	

2 Entry composition

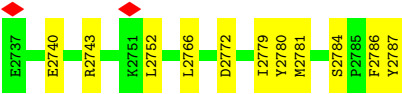
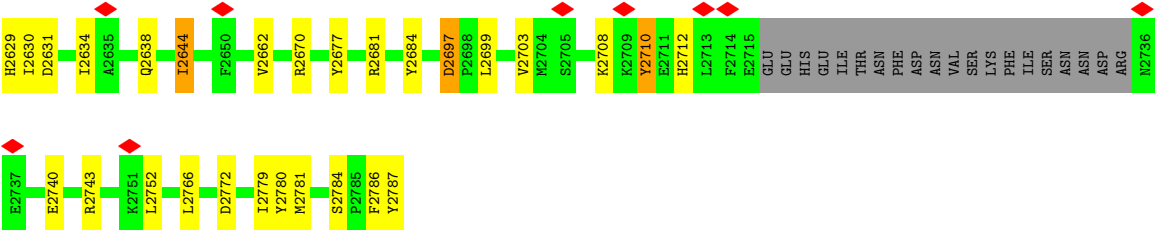
There is only 1 type of molecule in this entry. The entry contains 15270 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase TEL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2345	15270	9560	2758	2911	41	0	0





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83185	Depositor
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.237	Depositor
Minimum map value	-0.151	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	345.6, 345.6, 345.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.35, 1.35, 1.35	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1.08	8/15437 (0.1%)	1.23	127/21079 (0.6%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2278	LYS	CA-C	-8.26	1.49	1.53
1	A	1530	HIS	CB-CG	-6.09	1.41	1.50
1	A	1973	HIS	CB-CG	-5.87	1.42	1.50
1	A	1965	HIS	CB-CG	-5.86	1.42	1.50
1	A	2629	HIS	CB-CG	-5.69	1.42	1.50
1	A	1930	ILE	CB-CG1	-5.45	1.42	1.53
1	A	2062	GLU	CA-C	-5.32	1.48	1.53
1	A	2230	HIS	CB-CG	-5.28	1.42	1.50

All (127) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1369	SER	N-CA-C	-10.28	102.90	114.62
1	A	1986	GLU	N-CA-C	-8.73	101.85	111.36
1	A	1724	LEU	N-CA-C	-8.61	103.29	113.88
1	A	2644	ILE	CA-C-N	7.88	127.83	120.03
1	A	2644	ILE	C-N-CA	7.88	127.83	120.03
1	A	287	PRO	N-CA-CB	7.76	111.87	103.33
1	A	2014	ALA	CA-C-N	7.51	128.18	119.47
1	A	2014	ALA	C-N-CA	7.51	128.18	119.47
1	A	1025	PRO	N-CA-CB	7.45	110.31	103.08
1	A	40	PRO	N-CA-CB	7.45	111.19	103.00
1	A	1262	PRO	N-CA-CB	7.41	110.89	103.48
1	A	2428	PRO	N-CA-CB	7.39	110.87	103.48
1	A	1601	PRO	N-CA-CB	7.30	111.61	103.44
1	A	1263	LEU	N-CA-C	7.19	121.45	111.74
1	A	1747	PHE	CA-CB-CG	-7.16	106.64	113.80
1	A	1705	LEU	N-CA-C	7.14	120.11	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	397	PRO	N-CA-CB	7.12	110.72	103.25
1	A	2491	ASP	CA-CB-CG	-7.02	105.58	112.60
1	A	1258	PRO	N-CA-CB	7.02	110.50	103.48
1	A	2510	GLY	CA-C-N	7.01	127.16	119.87
1	A	2510	GLY	C-N-CA	7.01	127.16	119.87
1	A	1779	ASP	N-CA-C	-6.96	102.60	111.92
1	A	1888	LEU	CA-C-N	6.85	127.30	120.52
1	A	1888	LEU	C-N-CA	6.85	127.30	120.52
1	A	2038	ASP	CA-C-N	6.72	127.27	119.47
1	A	2038	ASP	C-N-CA	6.72	127.27	119.47
1	A	2697	ASP	CA-C-N	6.69	127.14	120.52
1	A	2697	ASP	C-N-CA	6.69	127.14	120.52
1	A	2493	VAL	N-CA-C	6.67	117.46	110.72
1	A	1643	PRO	N-CA-CB	6.64	109.52	103.08
1	A	2779	ILE	N-CA-C	6.56	117.50	109.30
1	A	1026	PRO	N-CA-CB	6.56	110.79	103.44
1	A	948	PRO	N-CA-CB	6.54	110.11	103.25
1	A	1049	PRO	N-CA-CB	6.53	110.51	103.33
1	A	2488	LEU	N-CA-C	-6.52	104.96	113.17
1	A	2598	VAL	N-CA-C	-6.49	104.70	111.58
1	A	1177	PRO	N-CA-CB	6.45	110.42	103.33
1	A	321	PRO	N-CA-CB	6.43	110.41	103.33
1	A	2097	PRO	N-CA-CB	6.41	109.94	102.76
1	A	1622	PRO	N-CA-CB	6.41	110.31	103.39
1	A	1257	TYR	CA-C-N	6.40	126.09	119.56
1	A	1257	TYR	C-N-CA	6.40	126.09	119.56
1	A	493	PRO	N-CA-CB	6.39	110.03	103.00
1	A	2413	SER	CB-CA-C	-6.37	109.22	116.54
1	A	1237	PRO	N-CA-CB	6.28	109.85	103.25
1	A	2274	ILE	CA-C-N	6.28	126.82	120.04
1	A	2274	ILE	C-N-CA	6.28	126.82	120.04
1	A	1528	GLN	CA-C-N	6.19	126.31	119.87
1	A	1528	GLN	C-N-CA	6.19	126.31	119.87
1	A	1650	PRO	N-CA-CB	6.13	110.07	103.33
1	A	115	PRO	N-CA-CB	6.11	110.05	103.33
1	A	2554	SER	CB-CA-C	-6.06	109.58	116.54
1	A	1644	PRO	N-CA-CB	6.04	110.20	103.44
1	A	1929	PHE	CA-CB-CG	5.96	119.76	113.80
1	A	2286	ILE	N-CA-C	-5.96	106.01	111.67
1	A	1262	PRO	CA-C-N	5.95	130.57	122.19
1	A	1262	PRO	C-N-CA	5.95	130.57	122.19
1	A	1163	GLY	CA-C-N	5.93	130.10	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1163	GLY	C-N-CA	5.93	130.10	120.60
1	A	1243	PRO	N-CA-CB	5.93	109.86	103.33
1	A	2456	ASP	CA-C-N	5.93	128.12	120.64
1	A	2456	ASP	C-N-CA	5.93	128.12	120.64
1	A	2699	LEU	CA-C-N	5.93	129.13	120.71
1	A	2699	LEU	C-N-CA	5.93	129.13	120.71
1	A	1801	ASP	N-CA-C	5.92	119.13	109.24
1	A	1767	THR	N-CA-C	-5.92	105.32	112.54
1	A	1194	PRO	N-CA-CB	5.90	109.91	103.30
1	A	2427	ARG	CA-C-N	5.85	125.52	119.56
1	A	2427	ARG	C-N-CA	5.85	125.52	119.56
1	A	2505	LYS	N-CA-C	-5.83	98.39	110.80
1	A	1477	VAL	N-CA-C	5.81	121.44	108.88
1	A	1572	SER	CA-C-N	-5.79	112.52	120.28
1	A	1572	SER	C-N-CA	-5.79	112.52	120.28
1	A	1699	GLU	N-CA-C	5.78	119.59	112.54
1	A	1699	GLU	CA-C-N	-5.75	115.60	122.22
1	A	1699	GLU	C-N-CA	-5.75	115.60	122.22
1	A	2506	VAL	N-CA-C	5.73	121.27	109.34
1	A	1417	PHE	N-CA-C	5.73	120.28	112.04
1	A	1743	LYS	N-CA-C	-5.71	105.06	111.28
1	A	2784	SER	CA-C-N	5.69	126.95	119.84
1	A	2784	SER	C-N-CA	5.69	126.95	119.84
1	A	1373	LEU	N-CA-C	-5.68	105.12	112.68
1	A	2583	ASP	CA-C-N	5.68	126.94	119.84
1	A	2583	ASP	C-N-CA	5.68	126.94	119.84
1	A	1264	ALA	N-CA-C	-5.68	105.18	111.71
1	A	1552	PHE	CA-CB-CG	-5.66	108.14	113.80
1	A	2365	PRO	N-CA-CB	5.60	109.72	103.44
1	A	1723	CYS	N-CA-C	-5.58	106.51	113.38
1	A	2279	PHE	CA-C-N	5.58	127.06	120.09
1	A	2279	PHE	C-N-CA	5.58	127.06	120.09
1	A	2670	ARG	CB-CA-C	-5.58	101.53	110.79
1	A	2772	ASP	CA-C-N	5.53	125.62	119.87
1	A	2772	ASP	C-N-CA	5.53	125.62	119.87
1	A	1617	LEU	CB-CA-C	-5.51	110.20	116.54
1	A	1377	ILE	CB-CA-C	-5.51	104.81	112.02
1	A	2447	PRO	N-CA-CB	5.51	109.03	103.25
1	A	1002	SER	N-CA-C	-5.49	102.21	110.06
1	A	1746	LYS	CA-C-N	5.48	132.00	121.54
1	A	1746	LYS	C-N-CA	5.48	132.00	121.54
1	A	1525	HIS	CA-C-N	5.47	126.67	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1525	HIS	C-N-CA	5.47	126.67	119.84
1	A	1802	SER	N-CA-C	5.40	122.30	110.80
1	A	1590	PRO	N-CA-CB	5.39	109.26	103.33
1	A	1936	PRO	N-CA-C	-5.33	107.48	114.03
1	A	2456	ASP	N-CA-C	-5.32	105.64	111.82
1	A	2712	HIS	CA-CB-CG	-5.31	108.49	113.80
1	A	1929	PHE	CB-CA-C	-5.30	101.84	110.85
1	A	2752	LEU	N-CA-C	-5.30	102.64	110.48
1	A	2296	GLU	N-CA-C	-5.29	103.63	110.19
1	A	2517	GLU	N-CA-C	5.25	118.88	111.52
1	A	175	MET	N-CA-C	-5.22	102.32	110.42
1	A	2445	SER	CB-CA-C	-5.21	110.55	116.54
1	A	2710	TYR	N-CA-C	-5.21	106.70	113.16
1	A	1021	SER	N-CA-C	-5.14	102.71	110.06
1	A	2340	ILE	CB-CA-C	-5.12	105.42	111.97
1	A	1264	ALA	CA-C-N	5.11	127.13	120.28
1	A	1264	ALA	C-N-CA	5.11	127.13	120.28
1	A	2507	VAL	CA-C-N	5.10	125.55	120.14
1	A	2507	VAL	C-N-CA	5.10	125.55	120.14
1	A	1987	ASN	CA-CB-CG	-5.07	107.53	112.60
1	A	2129	ASP	CA-C-N	-5.06	116.04	122.37
1	A	2129	ASP	C-N-CA	-5.06	116.04	122.37
1	A	1040	MET	N-CA-C	-5.05	102.80	110.28
1	A	1475	HIS	CA-CB-CG	-5.03	108.78	113.80
1	A	751	ARG	CB-CA-C	-5.02	110.80	116.63
1	A	1935	ILE	CA-C-N	5.02	125.09	119.87
1	A	1935	ILE	C-N-CA	5.02	125.09	119.87

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	15270	0	12008	130	0
All	All	15270	0	12008	130	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 5.

All (130) 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:2504:TYR:OH	1:A:2630:ILE:HA	1.43	1.15
1:A:1747:PHE:HE2	1:A:1749:TYR:CE1	1.66	1.12
1:A:2505:LYS:HB3	1:A:2517:GLU:OE2	1.66	0.96
1:A:1747:PHE:CE2	1:A:1749:TYR:CE1	2.58	0.91
1:A:2505:LYS:CB	1:A:2517:GLU:OE2	2.22	0.87
1:A:1747:PHE:CE2	1:A:1749:TYR:CD1	2.64	0.86
1:A:2504:TYR:HB3	1:A:2506:VAL:HG13	1.57	0.86
1:A:1479:LYS:HD3	1:A:1486:PHE:CE2	2.11	0.85
1:A:2504:TYR:OH	1:A:2630:ILE:CA	2.26	0.82
1:A:1747:PHE:HE2	1:A:1749:TYR:CD1	1.99	0.81
1:A:1747:PHE:HE2	1:A:1749:TYR:HE1	1.31	0.79
1:A:2677:TYR:CE2	1:A:2681:ARG:HD2	2.19	0.78
1:A:2504:TYR:HE2	1:A:2631:ASP:OD1	1.67	0.77
1:A:1932:ILE:HD11	1:A:1942:PHE:CE1	2.20	0.76
1:A:2247:ILE:HB	1:A:2282:TRP:HH2	1.51	0.75
1:A:2504:TYR:CE2	1:A:2631:ASP:OD1	2.45	0.68
1:A:2243:ASP:OD2	1:A:2278:LYS:NZ	2.31	0.64
1:A:2740:GLU:OE2	1:A:2743:ARG:NH2	2.30	0.63
1:A:1819:TYR:O	1:A:1820:THR:C	2.40	0.63
1:A:2482:GLN:HG2	1:A:2503:THR:HG21	1.83	0.61
1:A:2504:TYR:HB3	1:A:2517:GLU:OE1	2.02	0.58
1:A:825:TYR:O	1:A:826:LEU:C	2.45	0.58
1:A:555:GLN:O	1:A:556:TYR:C	2.46	0.58
1:A:2588:PHE:CE2	1:A:2592:LYS:HE2	2.39	0.58
1:A:2398:TYR:N	1:A:2398:TYR:HD1	2.02	0.58
1:A:1479:LYS:CD	1:A:1486:PHE:CE2	2.86	0.57
1:A:2504:TYR:OH	1:A:2630:ILE:CB	2.52	0.56
1:A:1410:LYS:NZ	1:A:1414:ASP:OD2	2.37	0.56
1:A:1479:LYS:CE	1:A:1486:PHE:HE2	2.17	0.56
1:A:1914:ILE:HG22	1:A:1919:TRP:HE1	1.70	0.56
1:A:1942:PHE:CE2	1:A:1946:LEU:HD11	2.40	0.56
1:A:2398:TYR:N	1:A:2398:TYR:CD1	2.73	0.56
1:A:2243:ASP:N	1:A:2243:ASP:OD1	2.35	0.56
1:A:909:GLU:O	1:A:910:ALA:C	2.48	0.55
1:A:1293:THR:HG1	1:A:1553:PHE:HE1	1.55	0.55
1:A:2289:LYS:NZ	1:A:2697:ASP:OD2	2.37	0.55
1:A:2606:TYR:CE1	1:A:2766:LEU:HD21	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:THR:O	1:A:48:ALA:C	2.50	0.55
1:A:1722:ASN:OD1	1:A:1728:SER:HB3	2.07	0.55
1:A:2420:SER:OG	1:A:2421:ALA:N	2.41	0.54
1:A:1914:ILE:HG22	1:A:1919:TRP:NE1	2.23	0.54
1:A:2115:GLU:HB3	1:A:2116:PRO:CD	2.38	0.54
1:A:2505:LYS:HB2	1:A:2517:GLU:OE2	2.04	0.53
1:A:2419:SER:OG	1:A:2420:SER:N	2.40	0.53
1:A:1288:PHE:CE1	1:A:1334:ARG:NH1	2.70	0.52
1:A:2376:LEU:CB	1:A:2398:TYR:OH	2.58	0.52
1:A:399:ILE:O	1:A:400:LEU:C	2.53	0.51
1:A:1747:PHE:CZ	1:A:1749:TYR:HD1	2.28	0.51
1:A:2506:VAL:HG13	1:A:2517:GLU:OE1	2.11	0.51
1:A:1293:THR:HA	1:A:1553:PHE:CE1	2.45	0.51
1:A:1932:ILE:CD1	1:A:1942:PHE:CE1	2.92	0.51
1:A:1940:THR:OG1	1:A:1941:SER:N	2.42	0.51
1:A:175:MET:O	1:A:176:VAL:CB	2.59	0.50
1:A:216:SER:O	1:A:217:LYS:C	2.53	0.50
1:A:1985:ASP:OD1	1:A:1985:ASP:N	2.42	0.50
1:A:602:GLY:O	1:A:603:ASN:C	2.55	0.50
1:A:1483:SER:OG	1:A:1484:LYS:N	2.44	0.50
1:A:1479:LYS:HD3	1:A:1486:PHE:CD2	2.47	0.49
1:A:1820:THR:OG1	1:A:1821:THR:N	2.43	0.49
1:A:1465:SER:OG	1:A:1466:LYS:N	2.44	0.49
1:A:1786:VAL:O	1:A:1787:PRO:C	2.56	0.49
1:A:2677:TYR:CZ	1:A:2681:ARG:HD2	2.48	0.49
1:A:1747:PHE:CE2	1:A:1749:TYR:HE1	2.18	0.48
1:A:1479:LYS:CE	1:A:1486:PHE:CE2	2.97	0.48
1:A:1747:PHE:CZ	1:A:1749:TYR:CD1	3.01	0.48
1:A:1942:PHE:HB3	1:A:1943:PRO:HD3	1.95	0.48
1:A:2119:ALA:O	1:A:2120:ILE:C	2.58	0.47
1:A:1853:SER:OG	1:A:1854:SER:N	2.48	0.46
1:A:1441:ASP:OD1	1:A:1441:ASP:N	2.48	0.46
1:A:2065:ALA:HB3	1:A:2066:PRO:HD3	1.97	0.46
1:A:1019:ILE:O	1:A:1020:LYS:C	2.59	0.46
1:A:1786:VAL:O	1:A:1788:HIS:N	2.48	0.46
1:A:2786:PHE:O	1:A:2787:TYR:C	2.56	0.46
1:A:782:THR:O	1:A:783:GLY:C	2.59	0.45
1:A:1737:GLN:O	1:A:1739:SER:N	2.49	0.45
1:A:2280:LEU:N	1:A:2281:PRO:CD	2.79	0.45
1:A:2478:GLU:HG2	1:A:2504:TYR:HB2	1.98	0.45
1:A:1367:GLU:N	1:A:1368:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2539:THR:OG1	1:A:2540:PHE:N	2.50	0.45
1:A:2634:ILE:O	1:A:2638:GLN:NE2	2.50	0.45
1:A:534:LEU:O	1:A:535:SER:C	2.58	0.45
1:A:1268:THR:O	1:A:1269:LEU:C	2.59	0.45
1:A:1569:ASN:O	1:A:1570:SER:C	2.60	0.44
1:A:1370:LEU:N	1:A:1371:PRO:HD2	2.33	0.44
1:A:2482:GLN:CG	1:A:2503:THR:HG21	2.47	0.44
1:A:1300:THR:OG1	1:A:1301:TYR:N	2.50	0.44
1:A:2067:VAL:HG21	1:A:2113:ARG:HD2	2.00	0.44
1:A:2115:GLU:HB3	1:A:2116:PRO:HD3	1.99	0.44
1:A:2467:SER:OG	1:A:2468:ASN:N	2.41	0.44
1:A:2504:TYR:CZ	1:A:2630:ILE:HA	2.44	0.44
1:A:1173:TYR:O	1:A:1177:PRO:N	2.51	0.44
1:A:1930:ILE:O	1:A:1931:LYS:HB2	2.18	0.44
1:A:944:THR:O	1:A:945:GLY:C	2.61	0.43
1:A:1876:SER:H	1:A:1879:LYS:HB2	1.82	0.43
1:A:2247:ILE:HD12	1:A:2282:TRP:CZ3	2.53	0.43
1:A:19:LYS:O	1:A:20:GLU:C	2.62	0.43
1:A:31:ILE:O	1:A:32:LEU:C	2.62	0.43
1:A:1848:SER:OG	1:A:1849:ARG:N	2.47	0.43
1:A:2114:LEU:O	1:A:2115:GLU:C	2.60	0.43
1:A:2278:LYS:C	1:A:2280:LEU:H	2.25	0.43
1:A:2536:ASP:HB3	1:A:2569:ILE:HG21	2.00	0.43
1:A:1363:THR:O	1:A:1364:PHE:C	2.62	0.43
1:A:1891:ASP:O	1:A:1892:VAL:C	2.60	0.43
1:A:2136:GLU:OE2	1:A:2241:ARG:NH1	2.45	0.43
1:A:2535:ASN:OD1	1:A:2535:ASN:N	2.45	0.43
1:A:2354:ASP:O	1:A:2355:ARG:CB	2.67	0.43
1:A:998:ASN:O	1:A:999:SER:C	2.62	0.42
1:A:2554:SER:OG	1:A:2555:ASN:N	2.52	0.42
1:A:2622:CYS:O	1:A:2624:THR:N	2.52	0.42
1:A:2540:PHE:CD2	1:A:2540:PHE:C	2.96	0.42
1:A:1572:SER:O	1:A:1573:GLU:C	2.61	0.42
1:A:1866:TRP:HH2	1:A:1978:VAL:HG22	1.84	0.42
1:A:2005:TYR:CD2	1:A:2005:TYR:C	2.97	0.42
1:A:1374:PHE:O	1:A:1375:CYS:C	2.60	0.42
1:A:1786:VAL:N	1:A:1787:PRO:CD	2.82	0.42
1:A:1479:LYS:NZ	1:A:1486:PHE:HE2	2.17	0.42
1:A:1367:GLU:N	1:A:1368:PRO:HD2	2.34	0.42
1:A:1475:HIS:ND1	1:A:1475:HIS:N	2.66	0.41
1:A:2428:PRO:O	1:A:2429:TYR:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1944:GLN:OE1	1:A:1944:GLN:N	2.53	0.41
1:A:1722:ASN:OD1	1:A:1728:SER:CB	2.69	0.41
1:A:2329:GLN:O	1:A:2330:SER:C	2.64	0.41
1:A:1686:PHE:CD2	1:A:1686:PHE:C	2.97	0.41
1:A:2630:ILE:O	1:A:2631:ASP:C	2.62	0.41
1:A:1692:LEU:O	1:A:1694:HIS:N	2.53	0.41
1:A:1777:ASP:CG	1:A:1779:ASP:H	2.29	0.40
1:A:1875:ASP:O	1:A:1919:TRP:CH2	2.74	0.40
1:A:2708:LYS:O	1:A:2710:TYR:N	2.53	0.40
1:A:2780:TYR:O	1:A:2781:MET:C	2.61	0.40
1:A:2121:TYR:CD1	1:A:2121:TYR:C	3.00	0.40

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	2287/2787 (82%)	2006 (88%)	212 (9%)	69 (3%)	3	25

All (69) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	VAL
1	A	397	PRO
1	A	1000	ILE
1	A	1236	PHE
1	A	1237	PRO
1	A	1261	ILE
1	A	1693	LEU
1	A	1820	THR
1	A	2355	ARG
1	A	2447	PRO

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Mol	Chain	Res	Type
1	A	2468	ASN
1	A	2515	ILE
1	A	2568	GLU
1	A	326	VAL
1	A	755	VAL
1	A	1039	ALA
1	A	1181	ILE
1	A	1787	PRO
1	A	2119	ALA
1	A	2132	VAL
1	A	2505	LYS
1	A	2644	ILE
1	A	2662	VAL
1	A	2684	TYR
1	A	174	SER
1	A	759	VAL
1	A	1019	ILE
1	A	1076	ASN
1	A	1428	ASN
1	A	1476	HIS
1	A	1639	SER
1	A	1892	VAL
1	A	2100	GLN
1	A	2120	ILE
1	A	2313	PRO
1	A	2442	THR
1	A	2455	SER
1	A	2516	ILE
1	A	2623	SER
1	A	244	ASP
1	A	1176	ILE
1	A	1421	VAL
1	A	1610	SER
1	A	1747	PHE
1	A	1765	ILE
1	A	1960	ILE
1	A	2454	ILE
1	A	2703	VAL
1	A	274	PHE
1	A	753	ILE
1	A	769	VAL
1	A	964	ASP

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Mol	Chain	Res	Type
1	A	1015	ILE
1	A	1239	SER
1	A	1526	PRO
1	A	1776	ASN
1	A	1874	VAL
1	A	1984	LEU
1	A	2135	HIS
1	A	2411	PRO
1	A	1738	ILE
1	A	1890	GLN
1	A	2101	ILE
1	A	2467	SER
1	A	1760	ILE
1	A	948	PRO
1	A	1425	ILE
1	A	2096	VAL
1	A	2437	VAL

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	1046/2569 (41%)	1042 (100%)	4 (0%)	84 83

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1704	MET
1	A	2114	LEU
1	A	2133	GLU
1	A	2398	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1525	HIS
1	A	1540	ASN
1	A	1764	ASN
1	A	1788	HIS
1	A	2044	GLN
1	A	2240	ASN
1	A	2489	GLN
1	A	2638	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](#)

There are no ligands in this entry.

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.

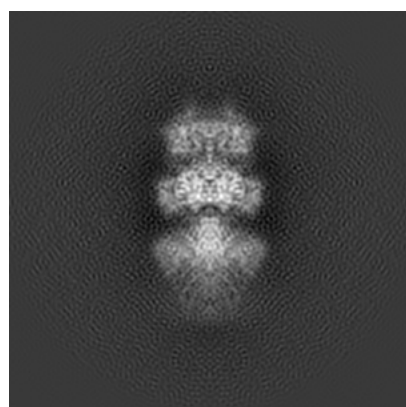
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9893. These allow visual inspection of the internal detail of the map and identification of artifacts.

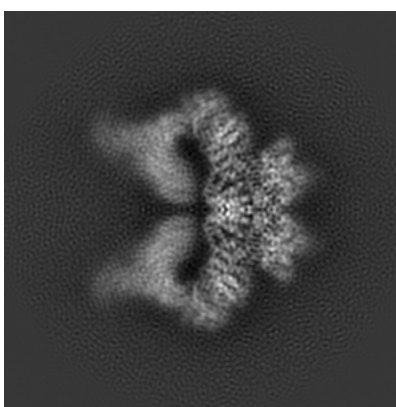
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

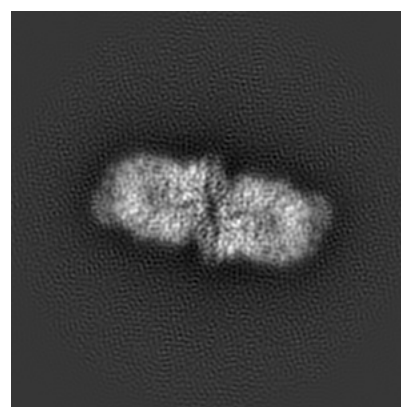
6.1.1 Primary map



X



Y

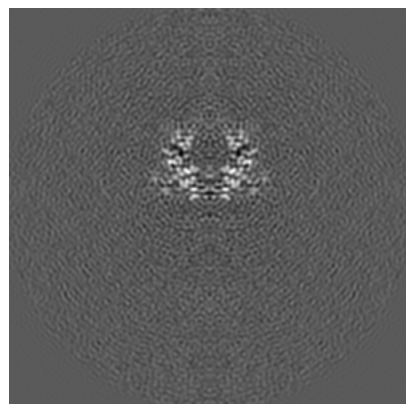


Z

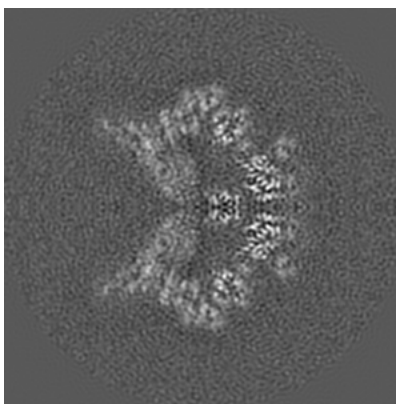
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

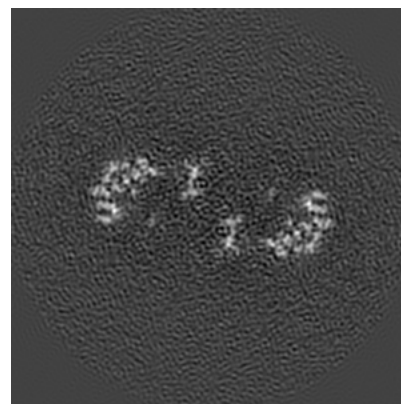
6.2.1 Primary map



X Index: 128



Y Index: 128

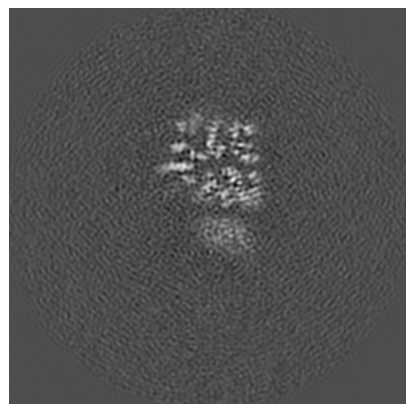


Z Index: 128

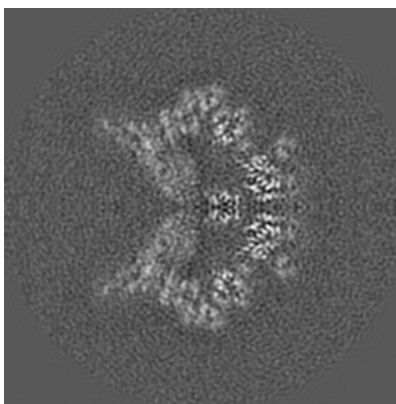
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

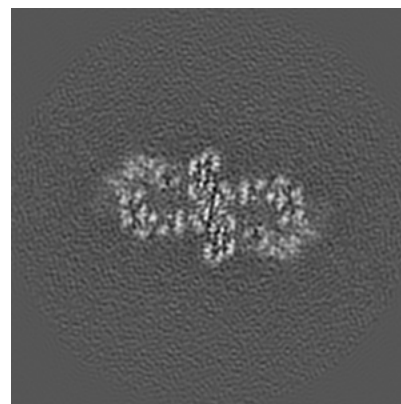
6.3.1 Primary map



X Index: 121



Y Index: 128

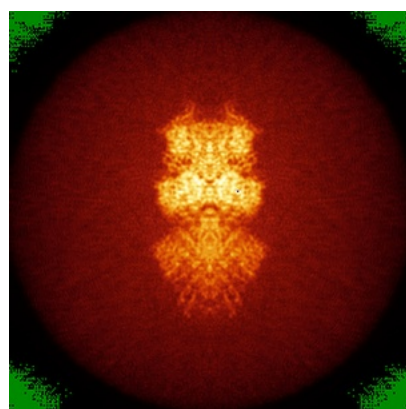


Z Index: 145

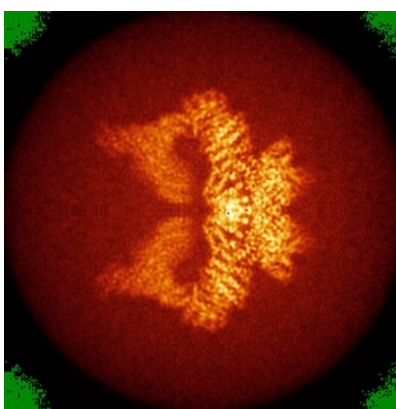
The images above show the largest variance slices of the map in three orthogonal directions.

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

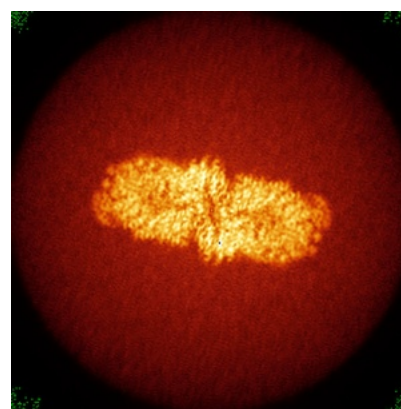
6.4.1 Primary map



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.

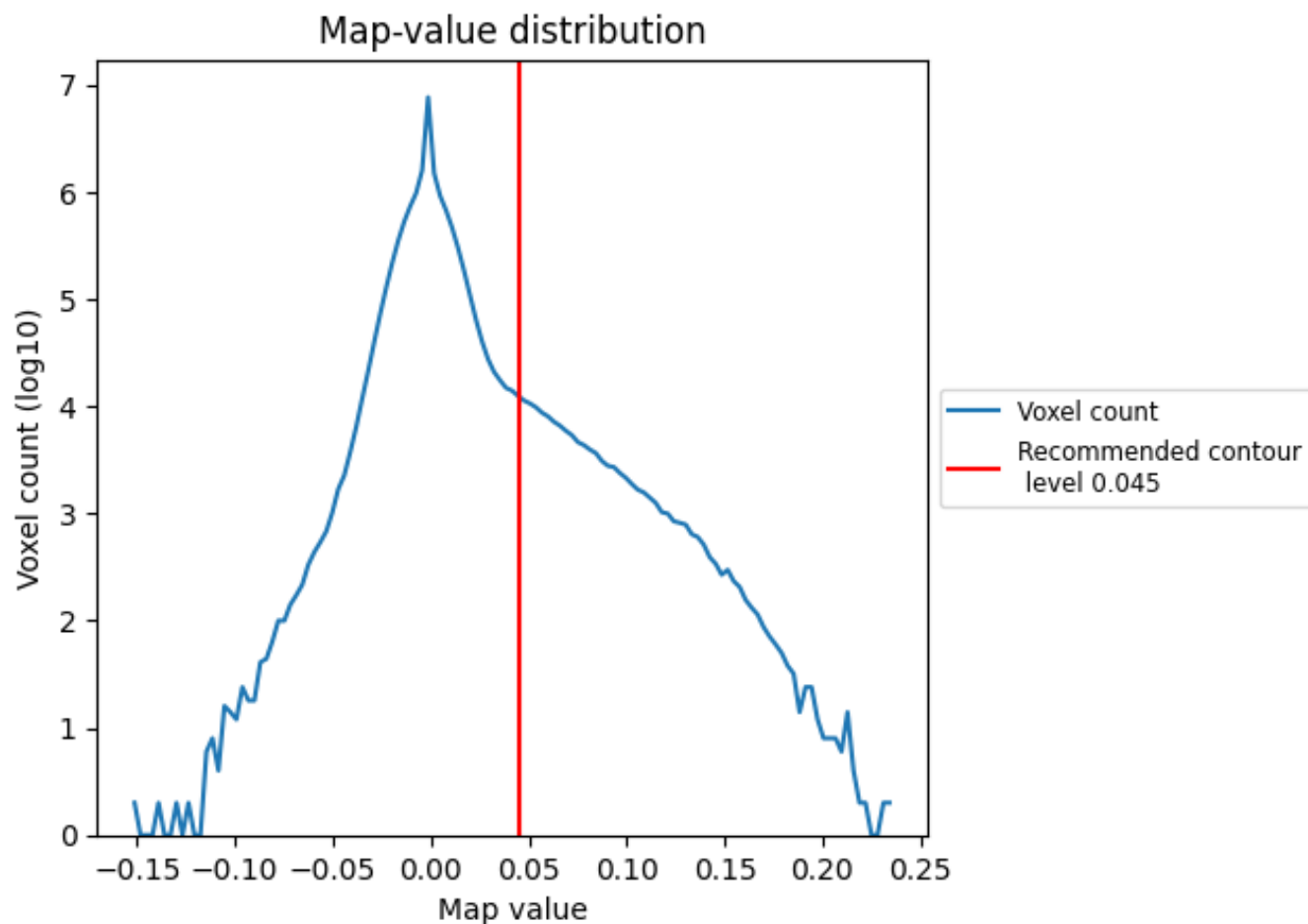
6.6 Mask visualisation

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

7 Map analysis [i](#)

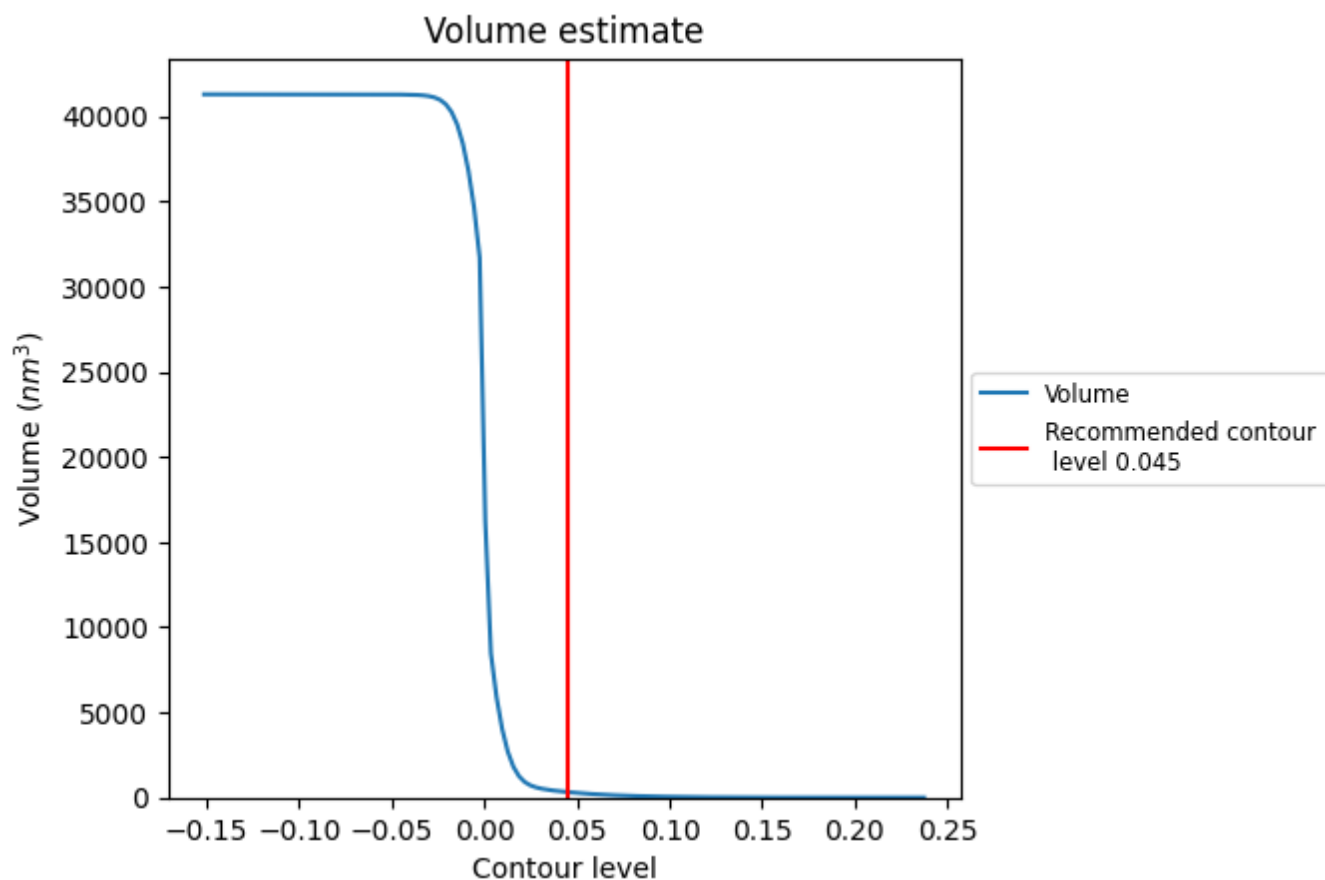
This section contains the results of statistical analysis of the map.

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.

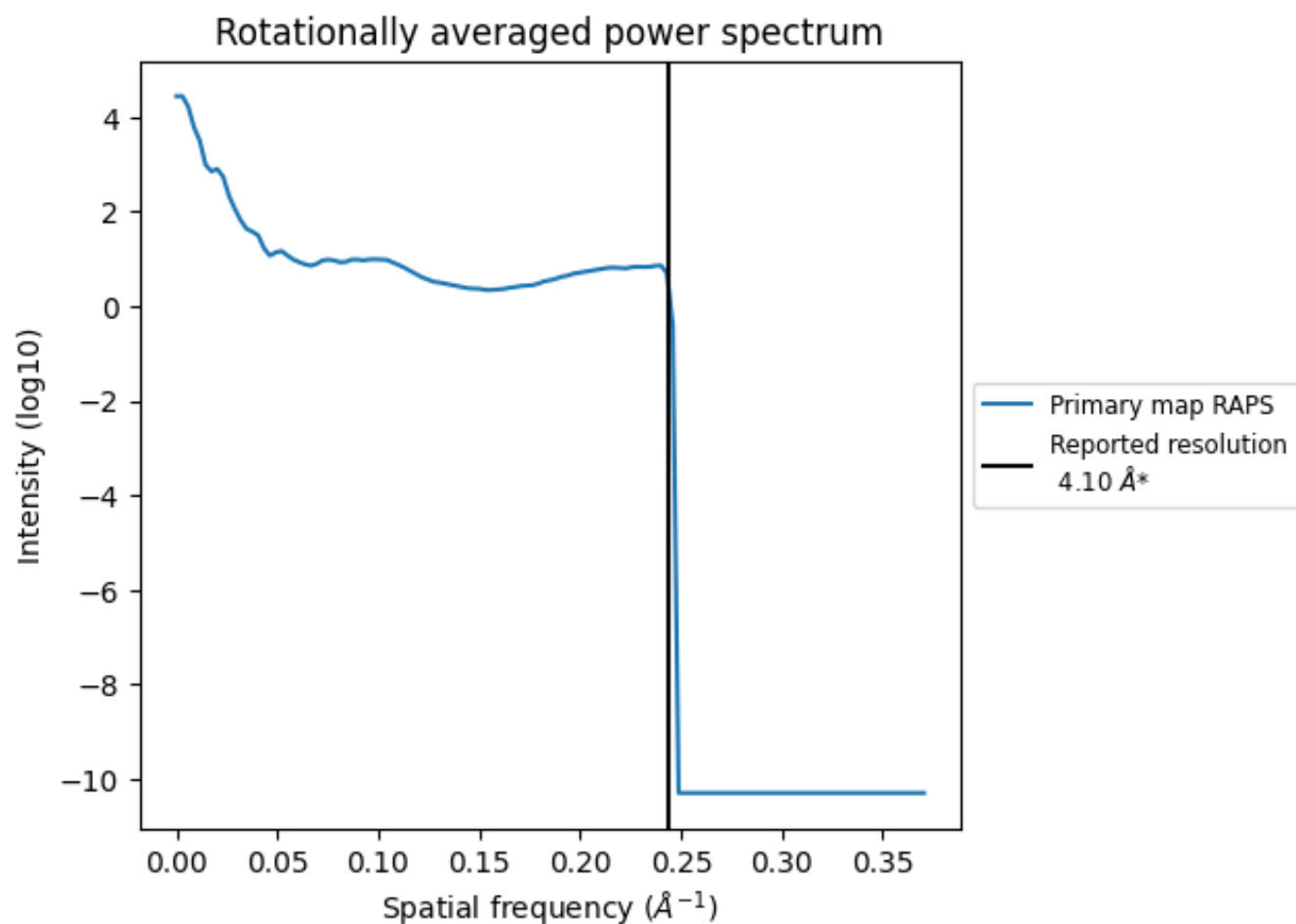
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 321 nm³; this corresponds to an approximate mass of 290 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 0.244 $\text{\AA}^{-1}$

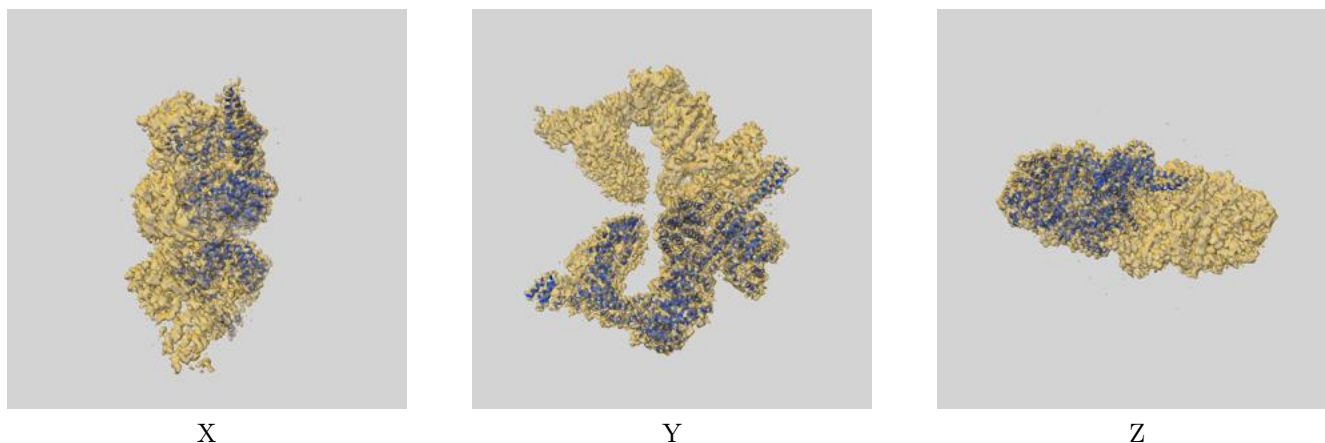
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

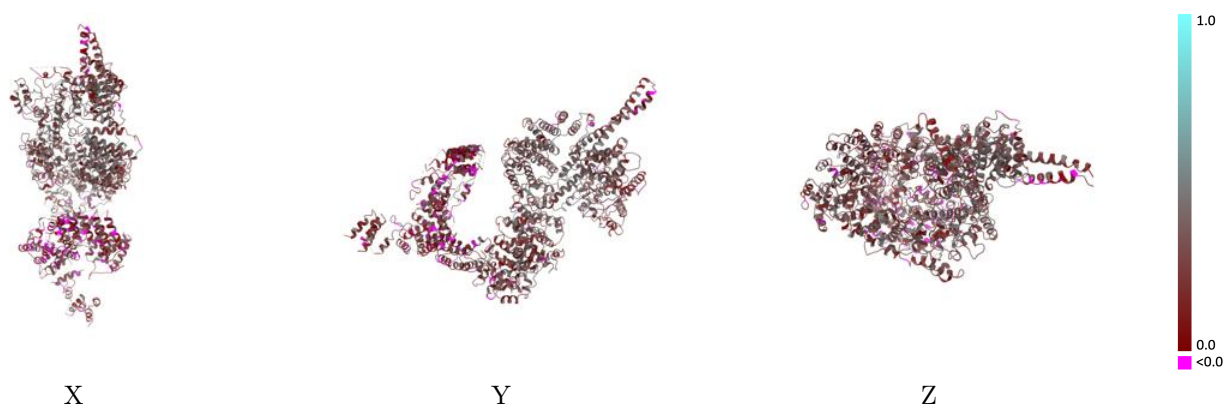
This section contains information regarding the fit between EMDB map EMD-9893 and PDB model 6JXC. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



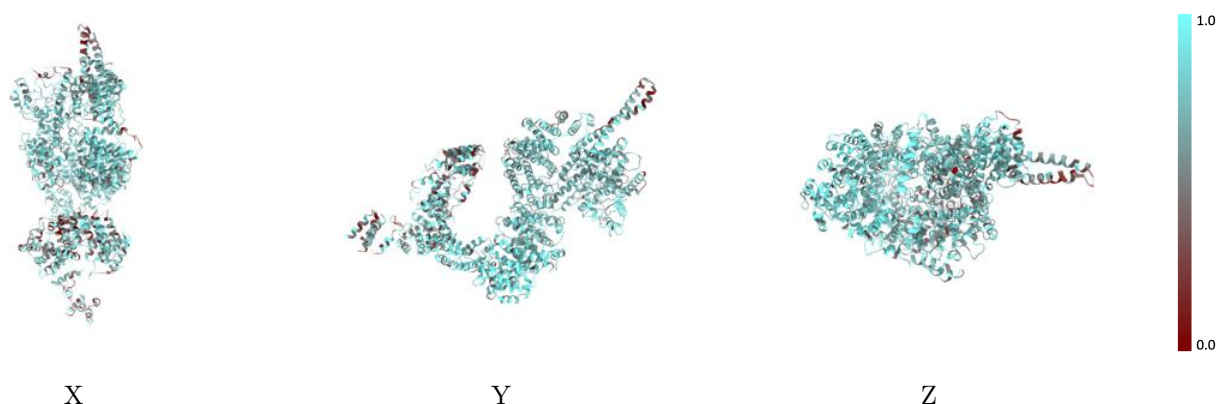
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



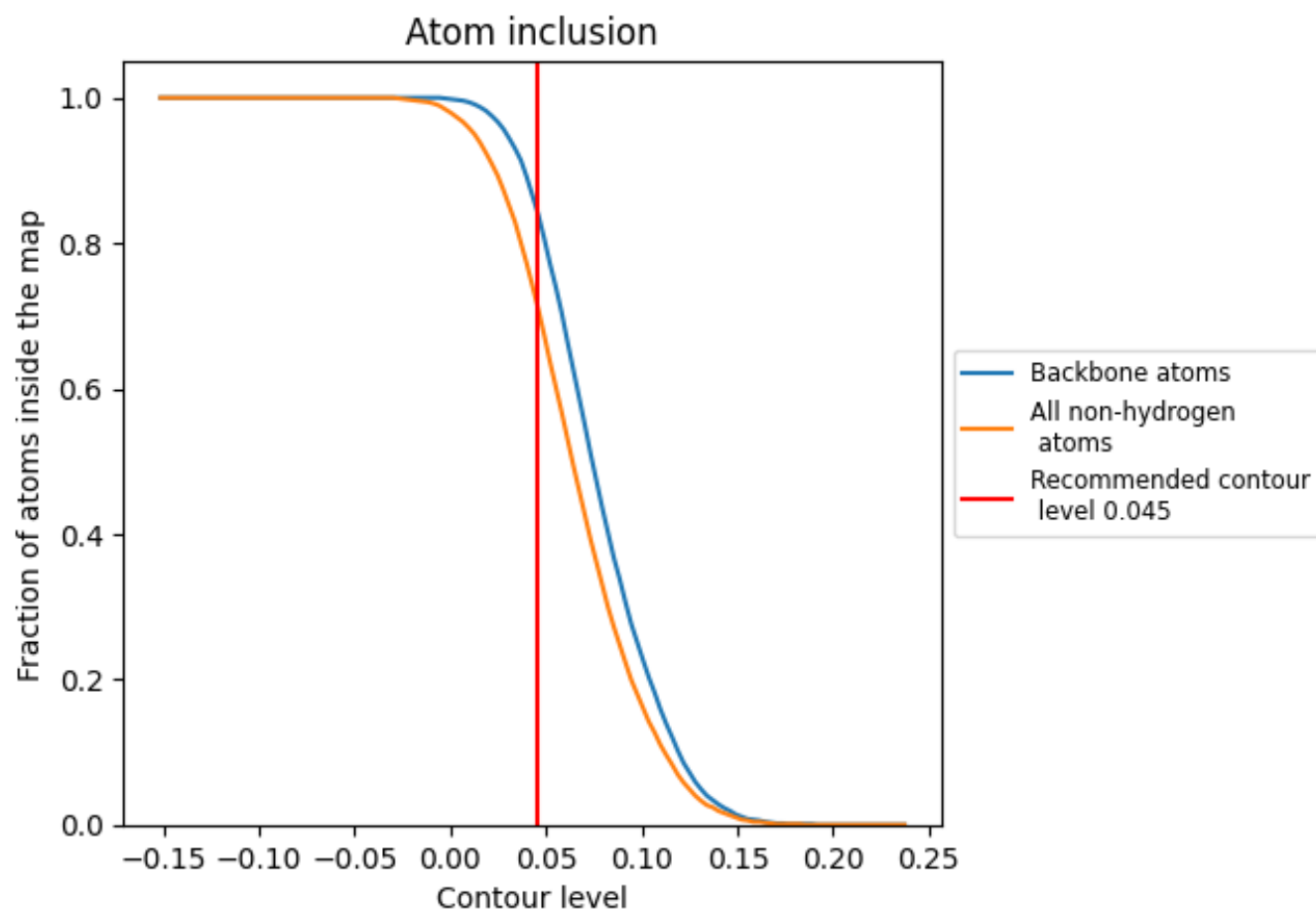
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 72% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7200	0.2880
A	0.7200	0.2880

