



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 02:56 PM UTC

PDB ID : 5I1M / pdb_00005i1m
EMDB ID : EMD-8070
Title : Yeast V-ATPase average of densities, a subunit segment
Authors : Schep, D.G.; Zhao, J.; Rubinstein, J.L.
Deposited on : 2016-02-05
Resolution : 7.00 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

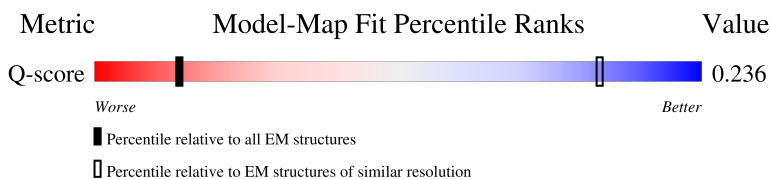
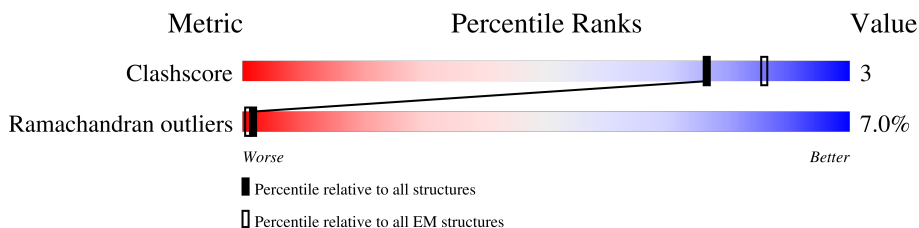
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.00 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	-
Q-score	-	25397	483 (6.50 - 7.50)

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	V	458	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2751 atoms, of which 920 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.

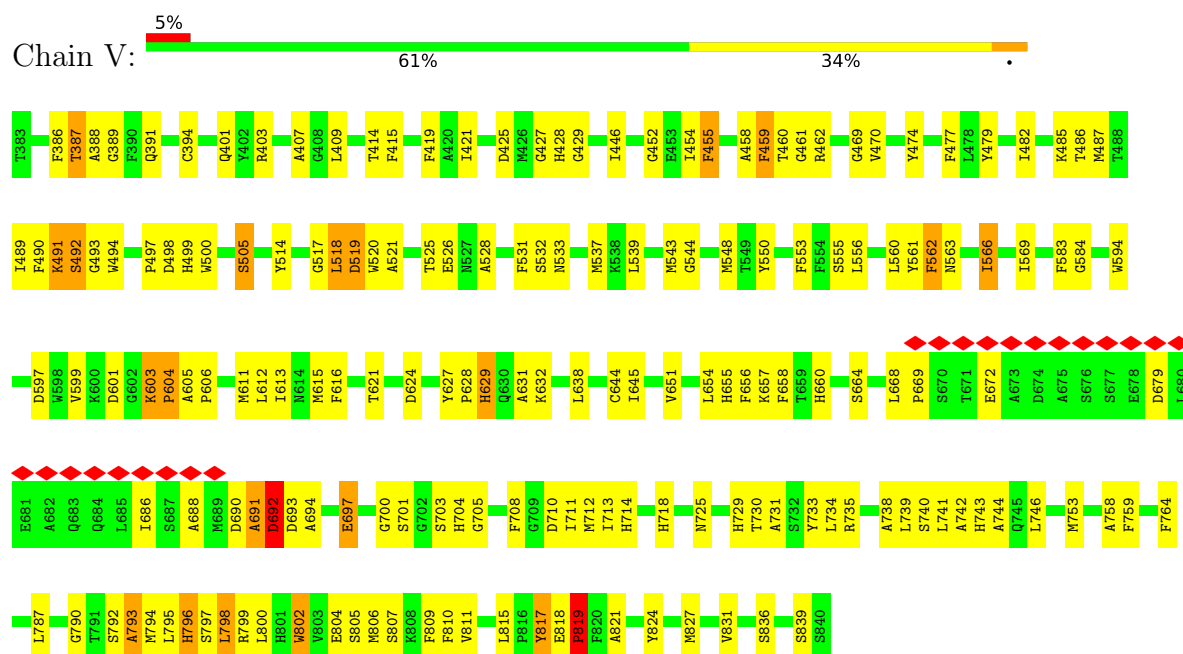
- Molecule 1 is a protein called V-type proton ATPase subunit a, vacuolar isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
1	V	458	2751	916	920	458	457	0	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: V-type proton ATPase subunit a, vacuolar isoform



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	269377	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35.7	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	0.034	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	464.0, 464.0, 464.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.45, 1.45, 1.45	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	V	2.32	71/1830 (3.9%)	2.71	159/2286 (7.0%)

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	V	0	5

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	V	712	MET	N-CA	-8.32	1.36	1.46
1	V	795	LEU	CA-C	-7.82	1.42	1.52
1	V	796	HIS	CA-C	-7.68	1.43	1.52
1	V	793	ALA	CA-C	-7.42	1.42	1.52
1	V	739	LEU	CA-C	-7.42	1.43	1.52
1	V	560	LEU	CA-C	-7.38	1.43	1.52
1	V	794	MET	CA-C	-7.38	1.43	1.52
1	V	550	TYR	CA-C	-7.26	1.43	1.52
1	V	556	LEU	CA-C	-7.18	1.44	1.52
1	V	735	ARG	CA-C	-7.17	1.43	1.52
1	V	528	ALA	CA-C	-6.93	1.44	1.52
1	V	746	LEU	CA-C	-6.73	1.44	1.52
1	V	790	GLY	CA-C	-6.65	1.44	1.52
1	V	798	LEU	CA-C	-6.61	1.44	1.52
1	V	389	GLY	CA-C	-6.51	1.45	1.52
1	V	741	LEU	CA-C	-6.32	1.44	1.52
1	V	718	HIS	CA-C	-6.30	1.45	1.52
1	V	584	GLY	CA-C	-6.25	1.43	1.51
1	V	485	LYS	CA-C	-6.15	1.46	1.53
1	V	733	TYR	CA-C	-6.11	1.44	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	V	414	THR	CA-C	-6.08	1.44	1.52
1	V	539	LEU	CA-C	-6.07	1.45	1.52
1	V	800	LEU	CA-C	-6.04	1.45	1.52
1	V	386	PHE	CA-C	-6.01	1.44	1.52
1	V	793	ALA	N-CA	-6.00	1.38	1.46
1	V	787	LEU	CA-C	-5.96	1.45	1.52
1	V	532	SER	CA-C	-5.95	1.44	1.52
1	V	807	SER	CA-C	-5.94	1.44	1.52
1	V	657	LYS	CA-C	-5.92	1.44	1.52
1	V	792	SER	CA-C	-5.83	1.45	1.52
1	V	740	SER	CA-C	-5.79	1.45	1.52
1	V	690	ASP	CA-C	-5.78	1.45	1.52
1	V	561	TYR	N-CA	-5.78	1.38	1.46
1	V	819	PRO	CA-C	-5.78	1.44	1.52
1	V	562	PHE	CA-C	-5.71	1.45	1.52
1	V	697	GLU	CA-C	-5.68	1.45	1.52
1	V	544	GLY	CA-C	-5.68	1.45	1.52
1	V	800	LEU	N-CA	-5.68	1.39	1.46
1	V	795	LEU	N-CA	-5.67	1.39	1.46
1	V	738	ALA	CA-C	-5.60	1.45	1.52
1	V	691	ALA	N-CA	-5.59	1.39	1.46
1	V	742	ALA	N-CA	-5.58	1.39	1.46
1	V	802	TRP	CA-C	-5.55	1.45	1.52
1	V	744	ALA	CA-C	-5.51	1.45	1.52
1	V	583	PHE	CA-C	-5.50	1.45	1.52
1	V	742	ALA	CA-C	-5.48	1.45	1.52
1	V	555	SER	CA-C	-5.47	1.44	1.52
1	V	631	ALA	N-CA	-5.47	1.40	1.46
1	V	731	ALA	CA-C	-5.46	1.45	1.52
1	V	799	ARG	CA-C	-5.41	1.45	1.52
1	V	611	MET	CA-C	-5.41	1.45	1.52
1	V	734	LEU	CA-C	-5.40	1.45	1.52
1	V	743	HIS	CA-C	-5.39	1.46	1.52
1	V	409	LEU	CA-C	-5.38	1.46	1.52
1	V	655	HIS	CA-C	-5.36	1.46	1.52
1	V	797	SER	N-CA	-5.29	1.39	1.46
1	V	729	HIS	CA-C	-5.26	1.45	1.52
1	V	714	HIS	CA-C	-5.23	1.46	1.52
1	V	690	ASP	N-CA	-5.20	1.39	1.46
1	V	629	HIS	CA-C	-5.19	1.45	1.52
1	V	517	GLY	CA-C	-5.19	1.44	1.51
1	V	806	MET	N-CA	-5.18	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	V	548	MET	CA-C	-5.16	1.46	1.52
1	V	419	PHE	CA-C	-5.14	1.46	1.52
1	V	537	MET	CA-C	-5.13	1.46	1.52
1	V	738	ALA	N-CA	-5.12	1.40	1.46
1	V	493	GLY	N-CA	-5.12	1.40	1.45
1	V	656	PHE	N-CA	-5.03	1.40	1.46
1	V	797	SER	CA-C	-5.03	1.45	1.52
1	V	455	PHE	CA-C	-5.02	1.46	1.52
1	V	612	LEU	CA-C	-5.02	1.45	1.52

All (159) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	V	556	LEU	N-CA-C	-17.81	89.00	112.68
1	V	804	GLU	N-CA-C	15.01	127.72	111.36
1	V	701	SER	N-CA-C	-11.99	99.17	114.04
1	V	460	THR	N-CA-C	-11.67	97.66	113.18
1	V	691	ALA	N-CA-C	-11.66	91.57	108.60
1	V	759	PHE	N-CA-C	10.99	123.26	111.28
1	V	658	PHE	N-CA-C	10.80	123.06	111.28
1	V	827	MET	N-CA-C	-10.75	99.53	111.14
1	V	553	PHE	N-CA-C	10.29	122.58	111.36
1	V	809	PHE	N-CA-C	10.27	122.47	111.28
1	V	389	GLY	N-CA-C	-9.96	100.94	112.50
1	V	831	VAL	CA-C-N	9.71	133.06	120.44
1	V	831	VAL	C-N-CA	9.71	133.06	120.44
1	V	712	MET	N-CA-C	-9.36	101.03	111.14
1	V	599	VAL	N-CA-C	-9.23	104.42	111.90
1	V	494	TRP	N-CA-C	-9.20	94.57	108.46
1	V	644	CYS	CA-C-N	8.84	127.40	120.33
1	V	644	CYS	C-N-CA	8.84	127.40	120.33
1	V	741	LEU	N-CA-C	-8.82	101.61	111.14
1	V	704	HIS	CA-C-N	8.72	138.51	121.41
1	V	704	HIS	C-N-CA	8.72	138.51	121.41
1	V	563	ASN	N-CA-C	-8.71	101.78	111.28
1	V	694	ALA	CA-C-N	8.70	132.64	120.29
1	V	694	ALA	C-N-CA	8.70	132.64	120.29
1	V	710	ASP	N-CA-C	8.67	120.73	111.28
1	V	725	ASN	N-CA-C	-8.66	102.25	113.17
1	V	519	ASP	N-CA-C	-8.65	92.37	110.80
1	V	521	ALA	N-CA-C	-8.59	102.11	112.59
1	V	461	GLY	N-CA-C	-8.49	102.66	112.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	V	569	ILE	N-CA-C	-8.48	95.36	107.75
1	V	613	ILE	N-CA-C	-8.43	100.47	112.35
1	V	606	PRO	N-CA-C	-8.32	95.33	112.47
1	V	664	SER	CA-C-N	8.15	131.21	120.28
1	V	664	SER	C-N-CA	8.15	131.21	120.28
1	V	817	TYR	N-CA-C	-7.85	97.84	109.15
1	V	403	ARG	N-CA-C	-7.77	101.29	111.71
1	V	415	PHE	N-CA-C	-7.74	102.23	112.75
1	V	796	HIS	N-CA-C	-7.62	102.92	111.14
1	V	758	ALA	N-CA-C	7.61	121.06	111.24
1	V	711	ILE	CA-C-O	7.57	128.43	120.25
1	V	474	TYR	N-CA-C	7.56	119.31	111.14
1	V	387	THR	CA-C-N	7.49	131.07	120.28
1	V	387	THR	C-N-CA	7.49	131.07	120.28
1	V	452	GLY	N-CA-C	7.45	120.98	111.37
1	V	604	PRO	N-CA-C	7.44	127.79	112.47
1	V	560	LEU	N-CA-C	-7.42	96.47	108.41
1	V	809	PHE	CA-C-O	-7.37	112.73	120.55
1	V	810	PHE	CA-C-N	7.34	135.18	121.97
1	V	810	PHE	C-N-CA	7.34	135.18	121.97
1	V	645	ILE	CA-C-O	-7.27	113.82	118.69
1	V	603	LYS	CA-C-N	7.25	128.91	119.84
1	V	603	LYS	C-N-CA	7.25	128.91	119.84
1	V	818	GLU	CA-C-N	7.19	128.83	119.84
1	V	818	GLU	C-N-CA	7.19	128.83	119.84
1	V	460	THR	CA-C-N	7.15	127.88	119.94
1	V	460	THR	C-N-CA	7.15	127.88	119.94
1	V	532	SER	N-CA-C	-7.08	103.61	111.82
1	V	492	SER	N-CA-C	-6.94	96.01	110.80
1	V	477	PHE	N-CA-C	-6.91	105.48	114.04
1	V	486	THR	N-CA-C	-6.90	96.10	110.80
1	V	612	LEU	N-CA-C	-6.82	104.53	112.92
1	V	531	PHE	N-CA-C	-6.78	104.13	112.88
1	V	624	ASP	CA-C-N	6.74	130.93	120.75
1	V	624	ASP	C-N-CA	6.74	130.93	120.75
1	V	403	ARG	CA-C-N	6.72	129.28	120.28
1	V	403	ARG	C-N-CA	6.72	129.28	120.28
1	V	632	LYS	N-CA-C	-6.61	104.15	111.82
1	V	729	HIS	N-CA-C	-6.61	104.15	111.82
1	V	660	HIS	CA-C-N	6.54	129.58	120.29
1	V	660	HIS	C-N-CA	6.54	129.58	120.29
1	V	798	LEU	N-CA-C	-6.43	104.19	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	V	517	GLY	N-CA-C	-6.41	97.98	113.18
1	V	594	TRP	N-CA-C	-6.37	105.38	112.57
1	V	597	ASP	N-CA-C	-6.34	97.33	108.23
1	V	764	PHE	CA-C-N	6.32	129.40	120.42
1	V	764	PHE	C-N-CA	6.32	129.40	120.42
1	V	490	PHE	CA-C-N	6.29	133.56	121.54
1	V	490	PHE	C-N-CA	6.29	133.56	121.54
1	V	657	LYS	N-CA-C	6.29	118.94	111.33
1	V	638	LEU	N-CA-C	-6.27	104.53	111.36
1	V	690	ASP	N-CA-C	-6.18	98.18	108.75
1	V	486	THR	CA-C-N	6.17	133.33	121.54
1	V	486	THR	C-N-CA	6.17	133.33	121.54
1	V	672	GLU	N-CA-C	6.08	123.76	110.80
1	V	498	ASP	CA-C-N	6.08	133.15	121.54
1	V	498	ASP	C-N-CA	6.08	133.15	121.54
1	V	407	ALA	N-CA-C	6.07	118.69	111.71
1	V	500	TRP	CA-C-N	6.07	128.70	120.38
1	V	500	TRP	C-N-CA	6.07	128.70	120.38
1	V	429	GLY	N-CA-C	-6.06	98.82	113.18
1	V	668	LEU	CA-C-N	6.04	127.39	119.84
1	V	668	LEU	C-N-CA	6.04	127.39	119.84
1	V	566	ILE	CA-C-N	6.02	133.04	121.54
1	V	566	ILE	C-N-CA	6.02	133.04	121.54
1	V	470	VAL	N-CA-C	6.00	116.78	110.72
1	V	818	GLU	N-CA-C	-5.95	101.46	110.39
1	V	491	LYS	CA-C-N	5.95	132.90	121.54
1	V	491	LYS	C-N-CA	5.95	132.90	121.54
1	V	454	ILE	CA-C-N	5.85	128.04	120.44
1	V	454	ILE	C-N-CA	5.85	128.04	120.44
1	V	469	GLY	N-CA-C	-5.85	105.71	112.73
1	V	708	PHE	N-CA-C	-5.83	100.45	109.14
1	V	806	MET	N-CA-C	-5.79	105.11	111.82
1	V	654	LEU	CA-C-N	5.77	127.94	120.44
1	V	654	LEU	C-N-CA	5.77	127.94	120.44
1	V	711	ILE	CA-C-N	5.77	128.28	120.44
1	V	711	ILE	C-N-CA	5.77	128.28	120.44
1	V	627	TYR	CA-C-N	5.73	127.00	119.84
1	V	627	TYR	C-N-CA	5.73	127.00	119.84
1	V	839	SER	N-CA-C	-5.64	98.78	110.80
1	V	692	ASP	CA-C-O	-5.59	114.77	120.80
1	V	388	ALA	CA-C-N	5.59	126.14	119.94
1	V	388	ALA	C-N-CA	5.59	126.14	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	V	505	SER	N-CA-C	-5.57	98.93	110.80
1	V	836	SER	N-CA-C	-5.56	106.08	112.92
1	V	518	LEU	CA-C-N	5.54	132.12	121.54
1	V	518	LEU	C-N-CA	5.54	132.12	121.54
1	V	482	ILE	O-C-N	-5.51	116.69	122.20
1	V	730	THR	CA-C-N	-5.50	112.42	122.38
1	V	730	THR	C-N-CA	-5.50	112.42	122.38
1	V	679	ASP	CA-C-N	5.46	127.59	120.28
1	V	679	ASP	C-N-CA	5.46	127.59	120.28
1	V	805	SER	N-CA-C	-5.45	104.98	111.03
1	V	703	SER	N-CA-C	-5.44	99.21	110.80
1	V	533	ASN	N-CA-C	-5.43	105.44	111.36
1	V	514	TYR	N-CA-C	-5.42	102.39	110.20
1	V	452	GLY	CA-C-N	5.40	127.97	120.63
1	V	452	GLY	C-N-CA	5.40	127.97	120.63
1	V	805	SER	CA-C-N	5.37	128.47	120.31
1	V	805	SER	C-N-CA	5.37	128.47	120.31
1	V	525	THR	CA-C-N	5.36	127.46	120.28
1	V	525	THR	C-N-CA	5.36	127.46	120.28
1	V	446	ILE	N-CA-C	-5.36	101.93	109.21
1	V	493	GLY	CA-C-N	5.35	133.37	121.81
1	V	493	GLY	C-N-CA	5.35	133.37	121.81
1	V	651	VAL	CA-C-N	5.33	127.39	120.26
1	V	651	VAL	C-N-CA	5.33	127.39	120.26
1	V	686	ILE	N-CA-C	5.31	117.73	111.09
1	V	479	TYR	N-CA-C	-5.30	106.49	113.17
1	V	794	MET	N-CA-C	-5.30	105.58	111.36
1	V	644	CYS	N-CA-C	-5.27	105.67	112.68
1	V	514	TYR	CA-C-O	-5.26	115.09	120.87
1	V	394	CYS	N-CA-C	-5.23	106.16	112.54
1	V	713	ILE	N-CA-C	5.22	115.84	110.36
1	V	693	ASP	N-CA-C	5.21	121.89	110.80
1	V	753	MET	N-CA-C	5.17	116.91	111.28
1	V	497	PRO	N-CA-C	-5.16	104.00	111.22
1	V	604	PRO	CA-C-N	5.11	134.28	121.80
1	V	604	PRO	C-N-CA	5.11	134.28	121.80
1	V	543	MET	CA-C-N	5.11	125.61	119.94
1	V	543	MET	C-N-CA	5.11	125.61	119.94
1	V	601	ASP	N-CA-C	5.11	119.47	112.88
1	V	621	THR	N-CA-C	-5.11	100.37	109.06
1	V	526	GLU	N-CA-C	-5.10	105.72	111.28
1	V	631	ALA	N-CA-C	-5.10	104.85	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	V	427	GLY	CA-C-N	5.02	131.13	121.54
1	V	427	GLY	C-N-CA	5.02	131.13	121.54
1	V	566	ILE	N-CA-C	5.00	119.75	109.34
1	V	712	MET	CA-C-O	-5.00	115.55	120.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	V	421	ILE	Mainchain
1	V	692	ASP	Mainchain
1	V	817	TYR	Mainchain,Peptide
1	V	819	PRO	Mainchain

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	V	1831	920	508	7	0
All	All	1831	920	508	7	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 3.

All (7) 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:V:459:PHE:H	1:V:462:ARG:H	1.17	0.92
1:V:459:PHE:N	1:V:462:ARG:H	1.95	0.58
1:V:387:THR:O	1:V:391:GLN:N	2.49	0.46
1:V:798:LEU:O	1:V:802:TRP:N	2.50	0.44
1:V:455:PHE:C	1:V:458:ALA:H	2.25	0.44
1:V:793:ALA:C	1:V:796:HIS:H	2.29	0.41
1:V:691:ALA:O	1:V:692:ASP:C	2.64	0.41

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	V	456/458 (100%)	375 (82%)	49 (11%)	32 (7%)	1 11

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	V	401	GLN
1	V	492	SER
1	V	505	SER
1	V	519	ASP
1	V	566	ILE
1	V	615	MET
1	V	616	PHE
1	V	811	VAL
1	V	425	ASP
1	V	489	ILE
1	V	491	LYS
1	V	697	GLU
1	V	705	GLY
1	V	824	TYR
1	V	428	HIS
1	V	499	HIS
1	V	518	LEU
1	V	520	TRP
1	V	562	PHE
1	V	688	ALA
1	V	700	GLY
1	V	821	ALA
1	V	459	PHE
1	V	487	MET
1	V	603	LYS
1	V	604	PRO
1	V	628	PRO
1	V	629	HIS

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Mol	Chain	Res	Type
1	V	605	ALA
1	V	819	PRO
1	V	669	PRO
1	V	815	LEU

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.

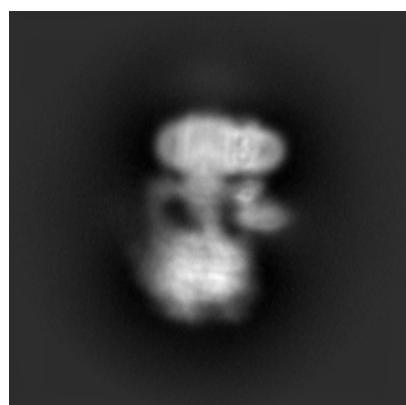
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8070. These allow visual inspection of the internal detail of the map and identification of artifacts.

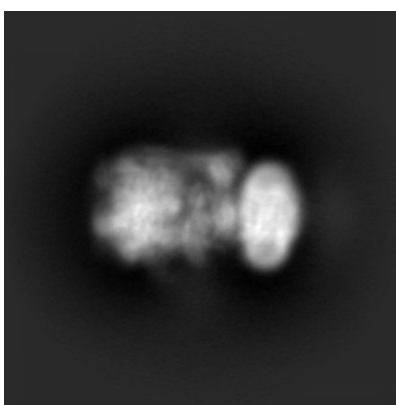
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

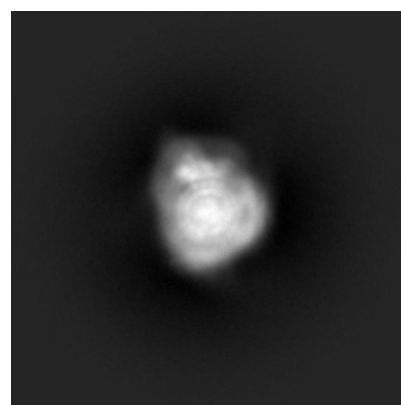
6.1.1 Primary map



X



Y

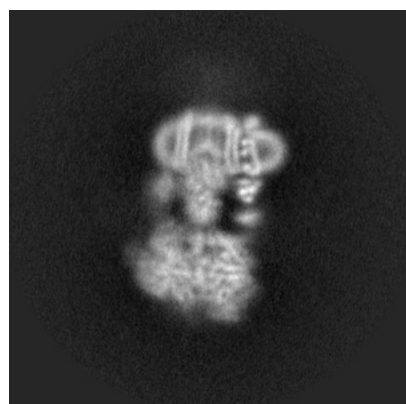


Z

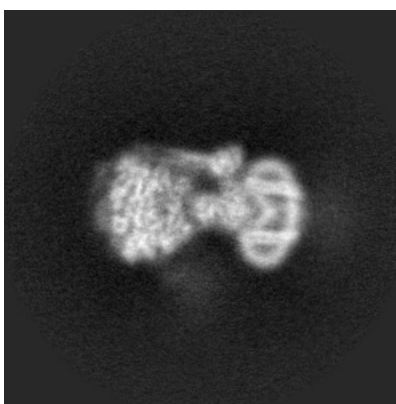
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

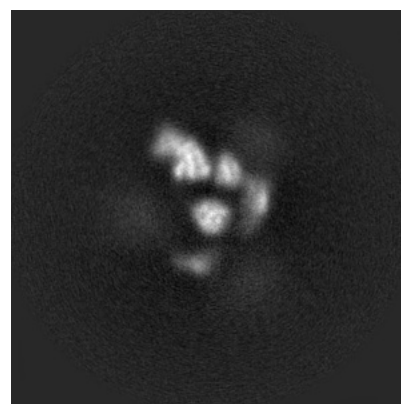
6.2.1 Primary map



X Index: 160



Y Index: 160

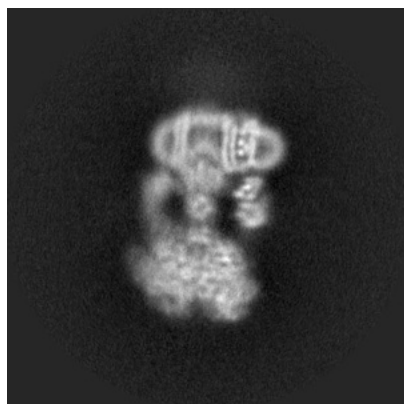


Z Index: 160

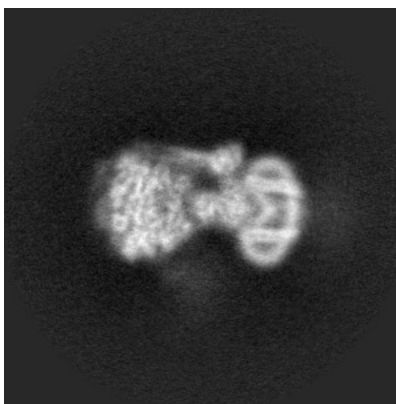
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

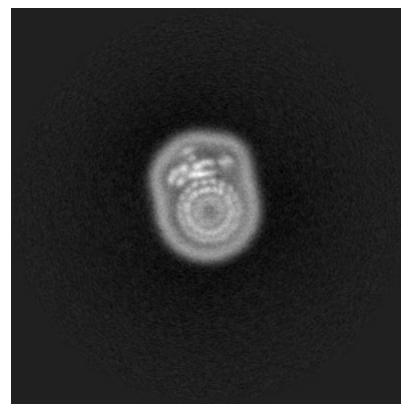
6.3.1 Primary map



X Index: 153



Y Index: 160



Z Index: 204

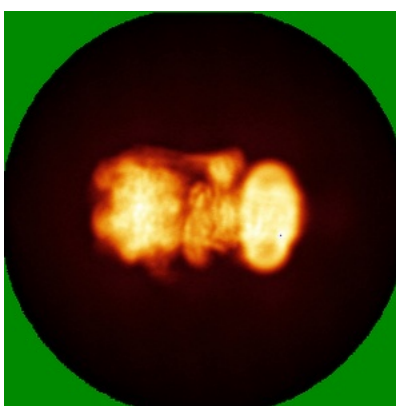
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

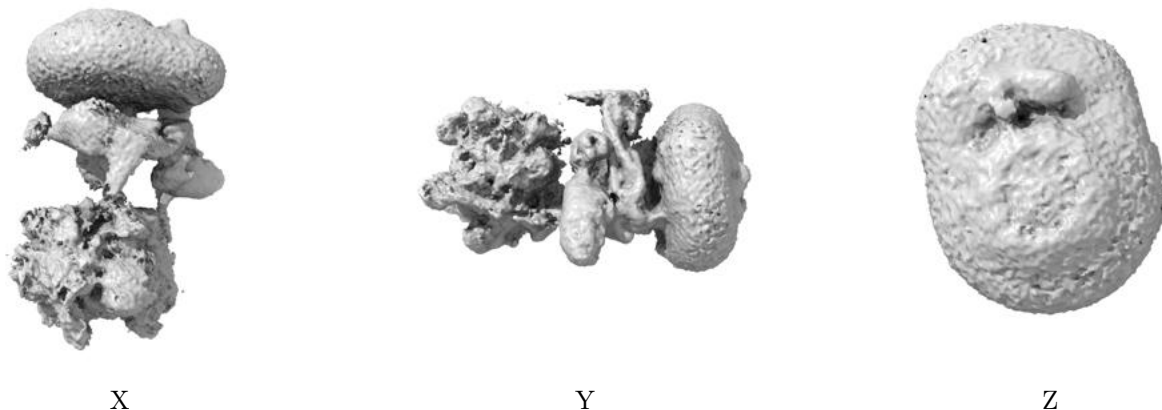


Z

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

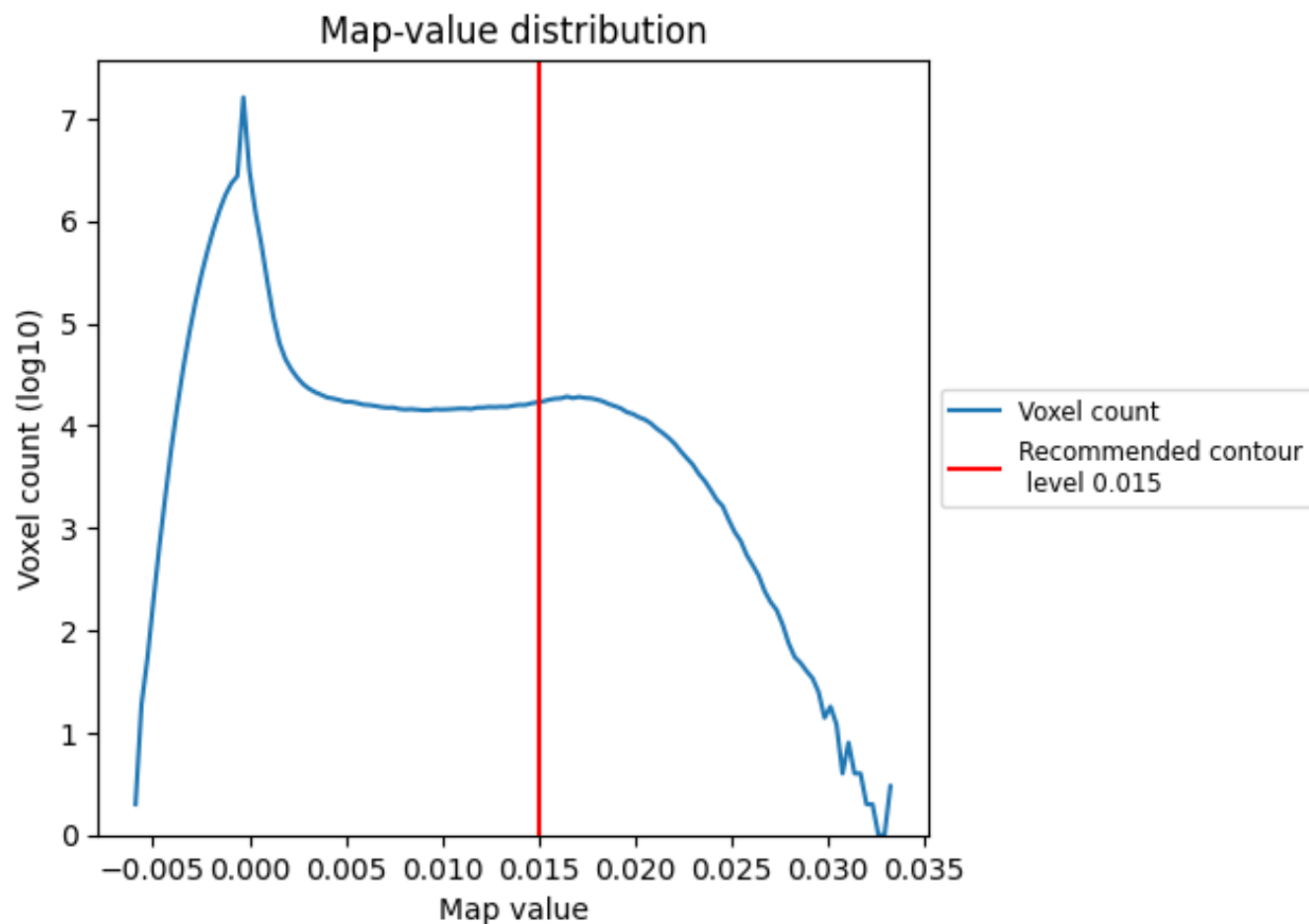
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

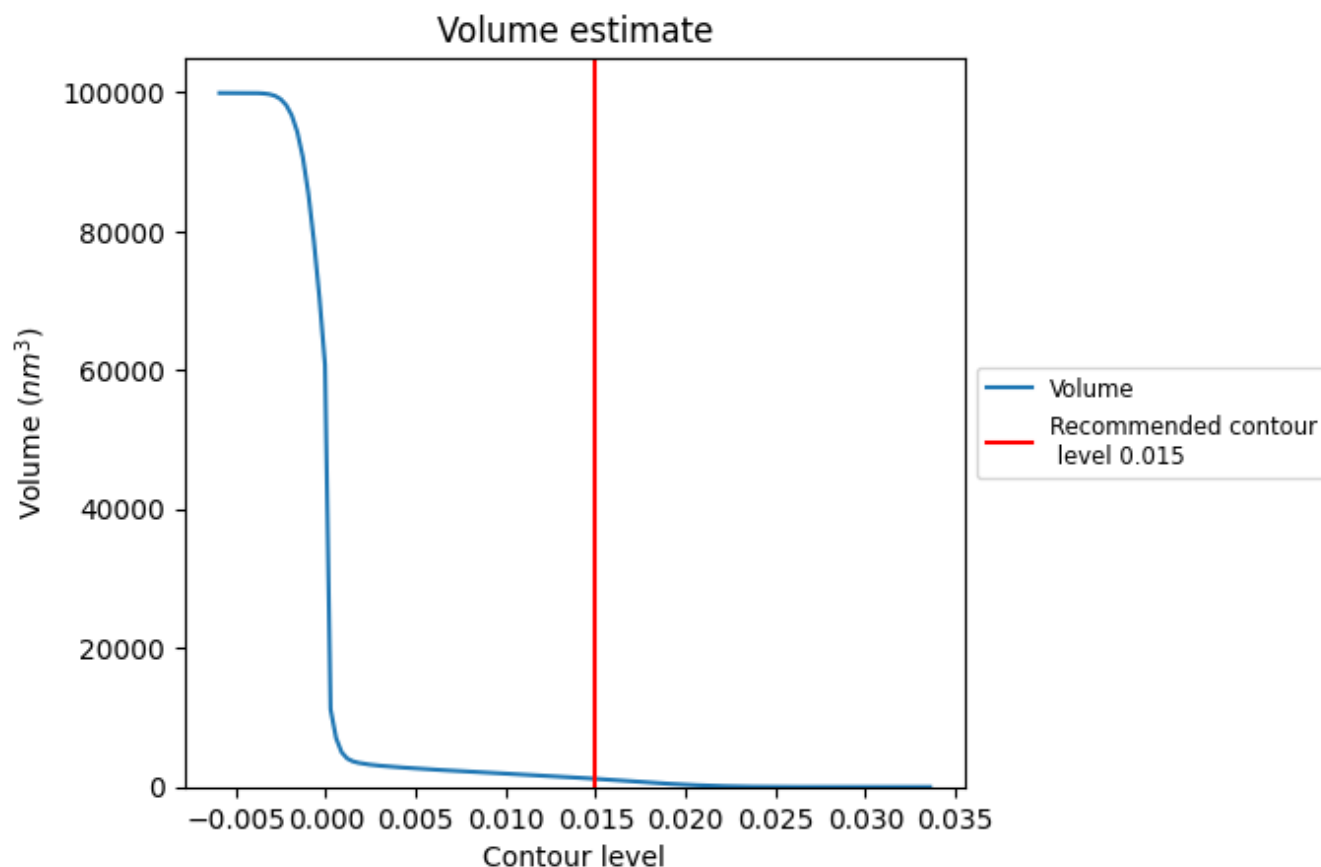
This section contains the results of statistical analysis of the map.

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.

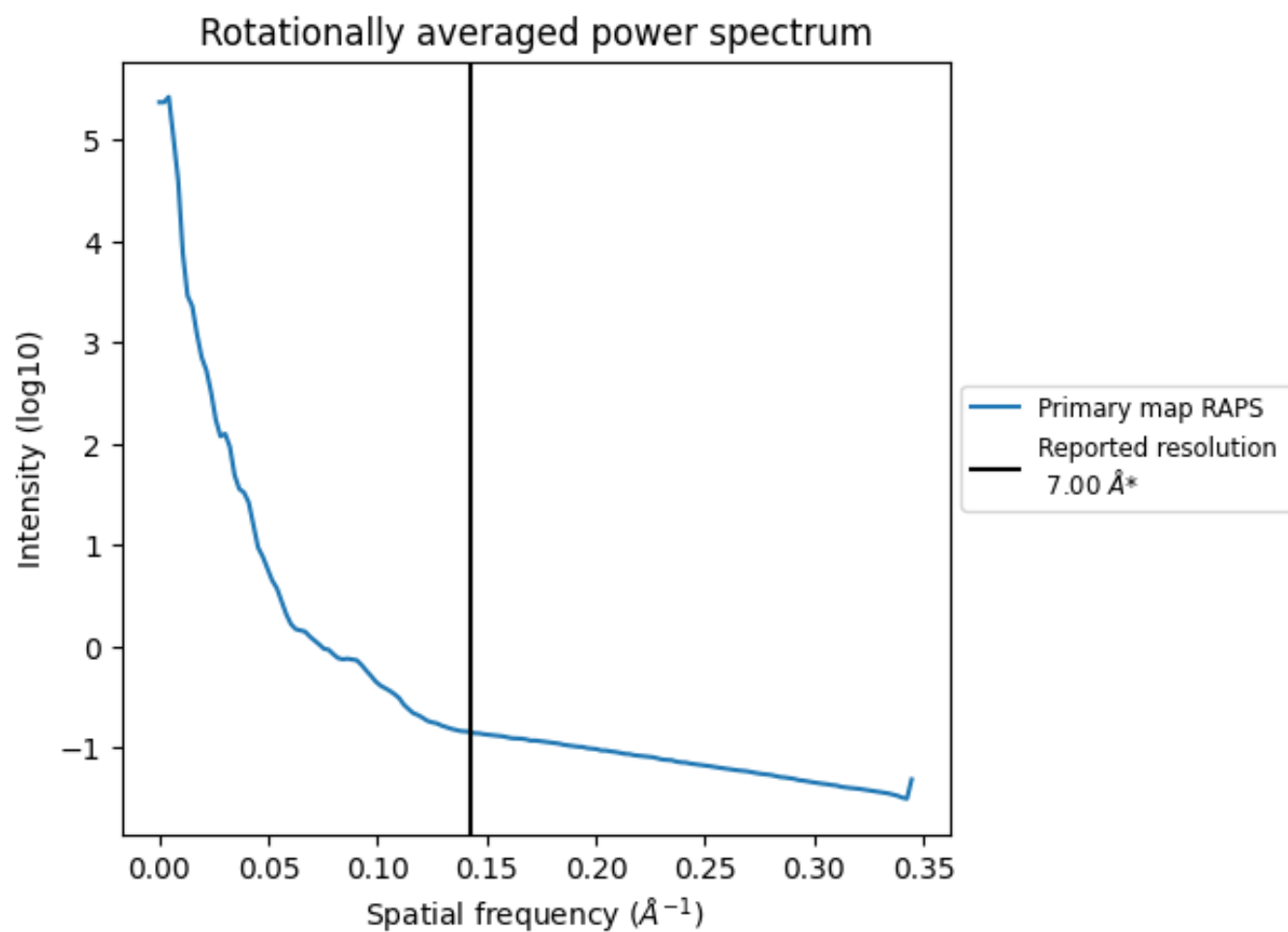
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1178 nm³; this corresponds to an approximate mass of 1064 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 0.143 Å⁻¹

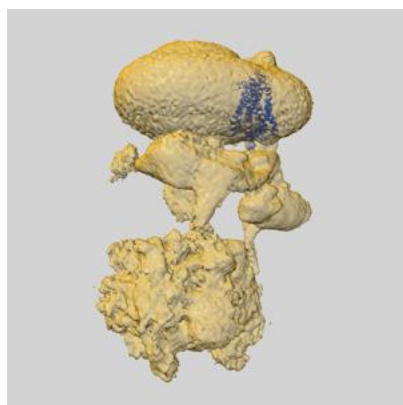
8 Fourier-Shell correlation

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

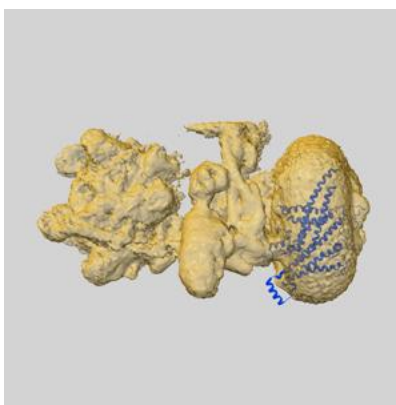
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8070 and PDB model 5I1M. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

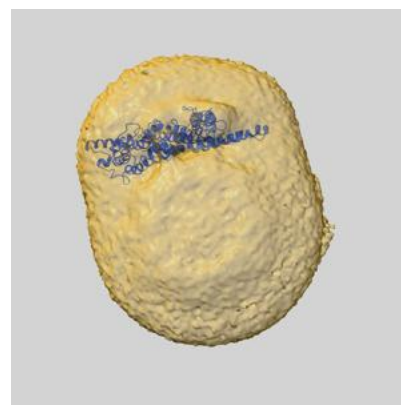
9.1 Map-model overlay [i](#)



X



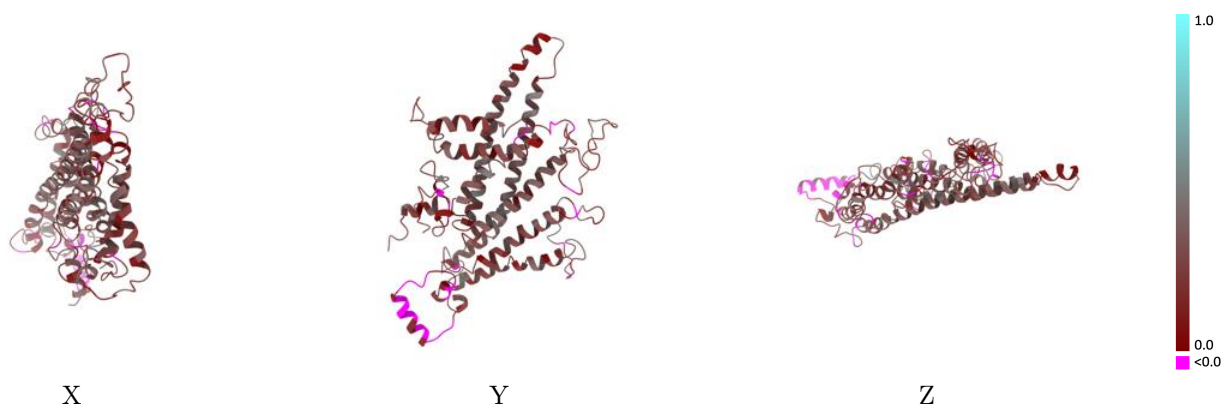
Y



Z

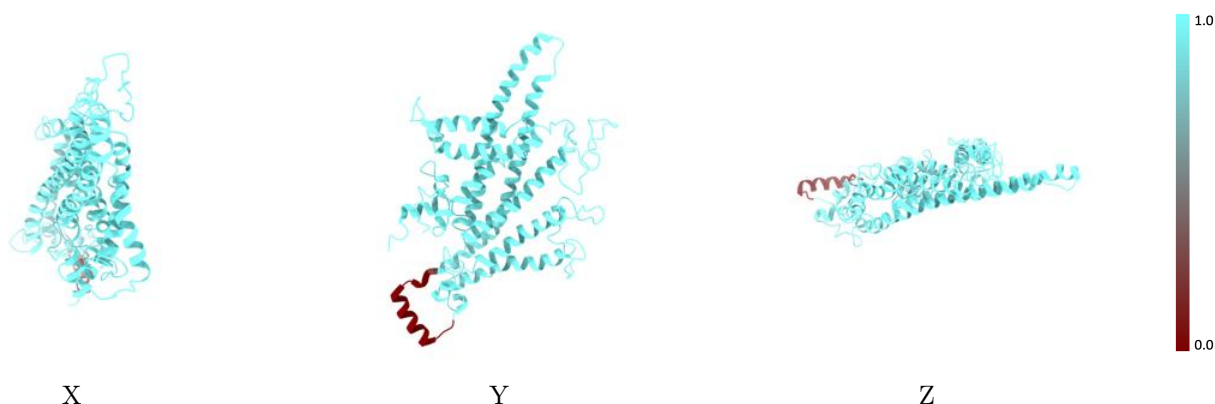
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



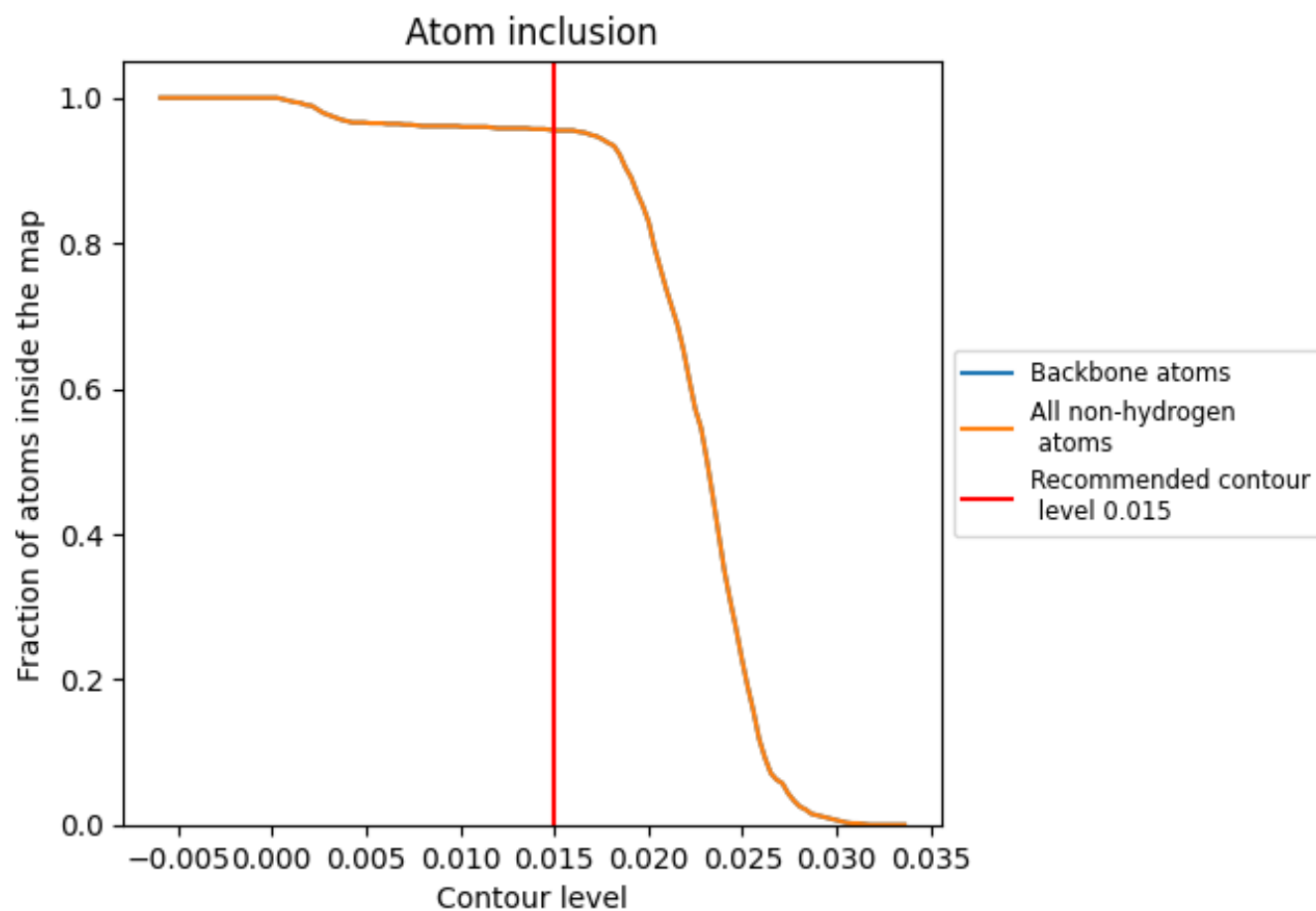
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9550	0.2360
V	0.9550	0.2360

