



Full wwPDB EM Validation Report ⓘ

Aug 3, 2026 – 03:01 PM EDT

PDB ID : 11FW / pdb_000011fw
EMDB ID : EMD-75669
Title : Cryo-EM structure of the bacteriophage N4 virion RNA polymerase (open plug state)
Authors : Narwal, M.; Shin, Y.; Murakami, K.S.
Deposited on : 2026-02-21
Resolution : 3.35 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.dev133
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) : 2.50

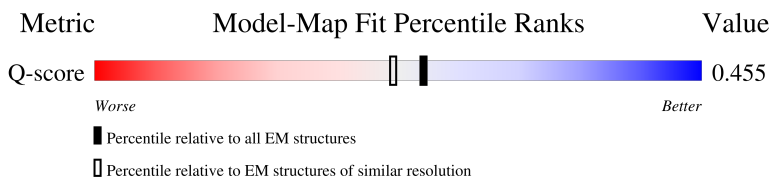
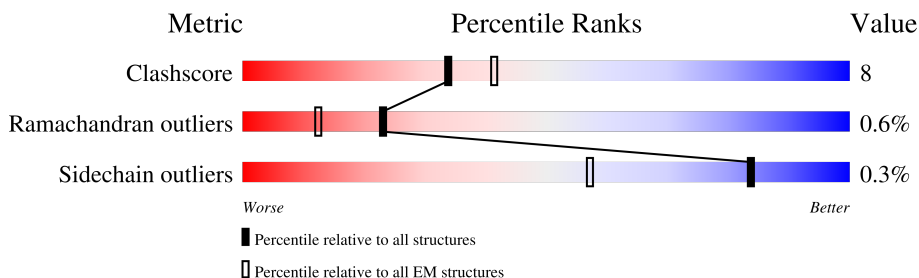
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.35 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	14390 (2.85 - 3.85)

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	2493	 79% 19% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 19054 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.

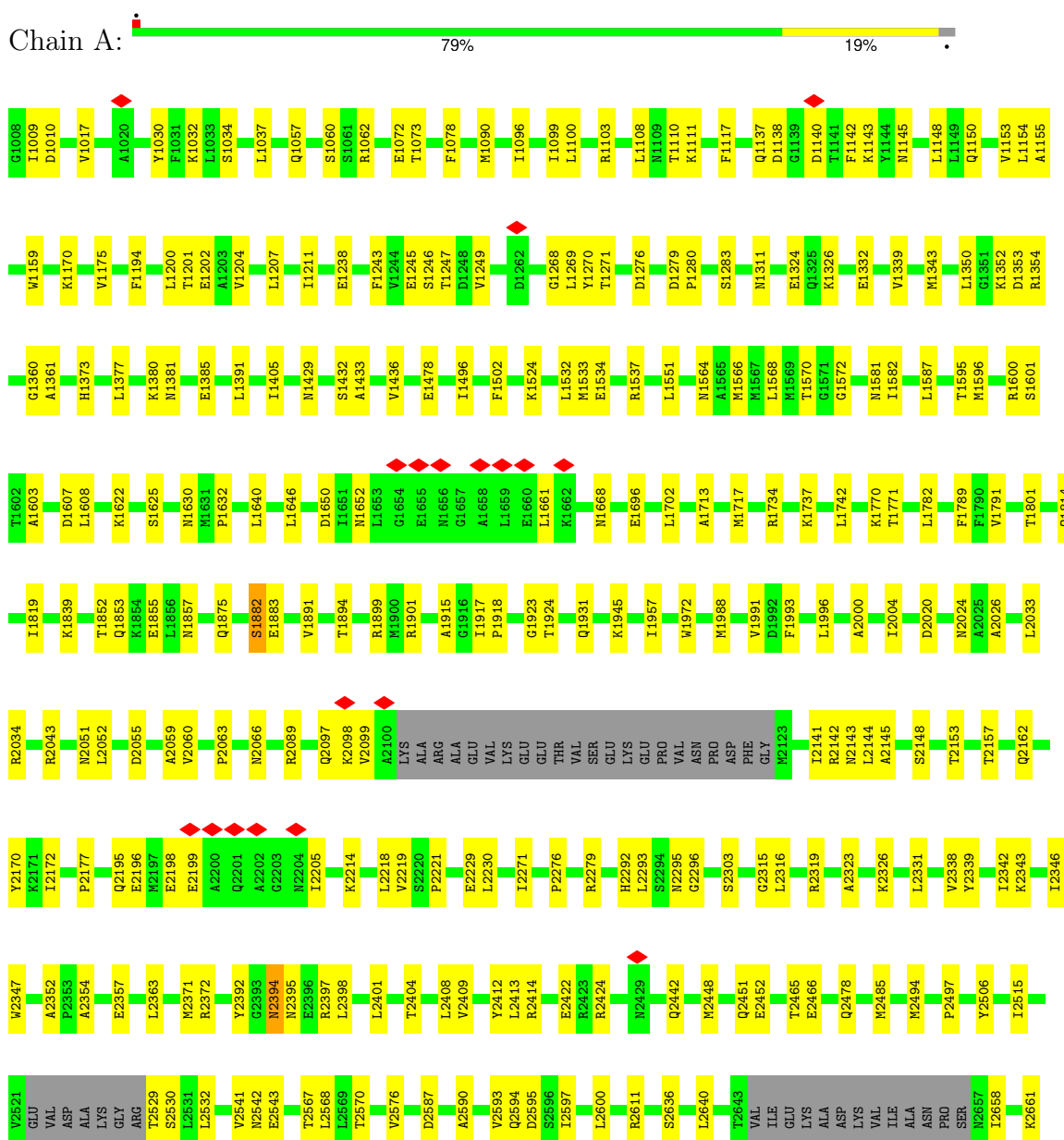
- Molecule 1 is a protein called Virion DNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2451	Total	C	N	O	S	0	0
			19054	11963	3306	3693	92		

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: Virion DNA-directed RNA polymerase



L3394	G3395	Q3396	V3397	T3398	D3405	R3406	L3407	R3410	F3411	R3412	K3432	I3447	V3450	V3451	T3455	G3458	N3459	V3460	G3461	L3477	T3491	L3492	N3493	P3494	L3498	T3499	H3500																		
P3239	Y3257	L3262	R3263	Q3264	I3265	D3266	E3275	L3284	K3285	I3288	T3291	T3292	D3293	S3294	H3295	R3296	R3297	M3298	S3299	I3300	L3303	I3304	E3308	T3317	S3318	R3319	D3320	D3321	K3328	I3329	Y3332	K3339	K3343	V3344	R3345	G3348	R3349	Y3350	Q3364	V3367	R3385				
I3085	E3095	K3096	D3097	I3098	Y3108	D3117	L3120	I3124	N3125	L3126	K3134	D3142	E3143	L3144	V3145	R3148	N3152	Y3157	R3158	A3159	L3185	G3189	A3192	Y3193	N3198	I3203	Q3204	N3205	L3206	V3207	K3211	T3212	V3213	I3214	V3215	V3219	P3222	N3225	V3238						
F2939	Q2954	Q2965	Y2966	S2969	R2974	A2975	P2976	Y2977	S2978	Q2979	Q2980	I2981	L2982	Q2983	N2984	V2985	R2986	A2989	I2994	G2995	T2996	R3028	E3029	P3030	S3047	V3048	D3049	P3050	N3051	K3052	L3053	N3057	H3061	F3062	A3063	K3064	N3065	V3066	G3067	V3068	W3069	R3070	K3078	R3081	D3084
N2830	L2831	L2832	R2833	N2834	A2835	H2836	S2839	R2840	L2841	E2844	R2845	L2846	T2847	A2852	I2857	I2861	Y2864	S2865	L2866	E2867	M2869	L2877	S2878	E2879	L2880	S2891	Y2894	M2895	V2896	G2897	Q2898	E2901	E2902	L2913	H2916	F2917	K2918	I2921	P2922	Q2923	V2924	E2925	Q2926	A2934	
L2669	V2682	V2686	G2693	K2694	V2695	W2696	F2699	W2703	I2706	L2719	D2730	L2738	L2750	T2751	E2754	Q2761	T2765	R2771	E2772	T2773	W2774	S2775	E2778	L2782	L2783	S2784	S2785	E2797	R2806	K2814	S2815	K2816	Q2817	L2818	I2823	G2828	N2829								

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57669	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.598	Depositor
Minimum map value	-0.275	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.102	Depositor
Map size (Å)	256.80002, 256.80002, 256.80002	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	0.25	0/19356	0.40	1/26159 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2394	ASN	CA-C-O	5.25	120.98	117.94

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	19054	0	19155	315	0
All	All	19054	0	19155	315	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 8.

All (315) 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:2413:LEU:HD11	1:A:2594:GLN:HE22	1.29	0.97
1:A:2818:LEU:HD23	1:A:2840:ARG:HH21	1.40	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2986:ARG:NH1	1:A:3491:THR:OG1	2.13	0.79
1:A:3262:LEU:HD12	1:A:3319:ARG:HG2	1.65	0.77
1:A:1702:LEU:HD11	1:A:1770:LYS:HA	1.68	0.76
1:A:2996:THR:HG22	1:A:3126:LEU:HD13	1.69	0.75
1:A:1339:VAL:HG11	1:A:1405:ILE:HG22	1.67	0.74
1:A:3211:LYS:O	1:A:3339:LYS:NZ	2.20	0.73
1:A:2924:GLU:HG3	1:A:3065:MET:HE1	1.69	0.73
1:A:2730:ASP:OD2	1:A:3078:LYS:NZ	2.20	0.72
1:A:2966:TYR:OH	1:A:3029:GLU:OE2	2.07	0.72
1:A:1324:GLU:OE1	1:A:1931:GLN:NE2	2.23	0.72
1:A:2778:GLU:O	1:A:2782:LEU:N	2.23	0.71
1:A:3364:GLN:NE2	1:A:3405:ASP:OD1	2.23	0.71
1:A:2686:VAL:N	1:A:2901:GLU:OE2	2.21	0.69
1:A:2761:GLY:HA2	1:A:2869:MET:HE1	1.73	0.69
1:A:2895:MET:HE3	1:A:3062:PHE:HE1	1.58	0.69
1:A:2840:ARG:HH12	1:A:2861:ILE:HD11	1.57	0.69
1:A:1603:ALA:O	1:A:3412:ARG:NH2	2.25	0.68
1:A:2934:ALA:HB3	1:A:2939:PHE:HE2	1.59	0.67
1:A:2835:ALA:O	1:A:2918:LYS:N	2.28	0.67
1:A:2818:LEU:HD21	1:A:2835:ALA:HA	1.76	0.67
1:A:2343:LYS:NZ	1:A:2354:ALA:O	2.24	0.66
1:A:1622:LYS:O	1:A:2414:ARG:NH2	2.28	0.66
1:A:2422:GLU:HB3	1:A:2424:ARG:HH12	1.60	0.66
1:A:3264:GLN:HB2	1:A:3291:ILE:HG21	1.77	0.66
1:A:2529:THR:OG1	1:A:2530:SER:N	2.29	0.66
1:A:3214:ILE:HB	1:A:3339:LYS:NZ	2.10	0.65
1:A:2831:LEU:HD11	1:A:2845:ARG:HG3	1.77	0.65
1:A:3460:VAL:HG12	1:A:3461:GLY:H	1.61	0.64
1:A:1770:LYS:HG3	1:A:1771:THR:HG23	1.80	0.64
1:A:2773:THR:OG1	1:A:2778:GLU:OE1	2.11	0.64
1:A:3029:GLU:OE2	1:A:3049:ASP:N	2.31	0.64
1:A:1155:ALA:HB3	1:A:1211:ILE:HD13	1.80	0.64
1:A:2413:LEU:HD11	1:A:2594:GLN:NE2	2.07	0.64
1:A:2841:LEU:HD22	1:A:2852:ALA:HB3	1.79	0.63
1:A:3192:ALA:HB2	1:A:3332:TYR:HB2	1.80	0.63
1:A:1090:MET:HE1	1:A:1154:LEU:HD21	1.80	0.63
1:A:2034:ARG:NH1	1:A:2199:GLU:OE2	2.31	0.63
1:A:2797:GLU:OE2	1:A:2864:TYR:OH	2.10	0.63
1:A:2292:HIS:O	1:A:2303:SER:OG	2.15	0.63
1:A:2404:THR:HG23	1:A:2408:LEU:HD12	1.80	0.62
1:A:1062:ARG:HG2	1:A:1078:PHE:HD2	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1110:THR:HG22	1:A:1111:LYS:HG3	1.80	0.62
1:A:2983:GLN:HB3	1:A:2985:VAL:HG23	1.82	0.62
1:A:2902:GLU:OE2	1:A:3069:TRP:NE1	2.28	0.62
1:A:2198:GLU:HG3	1:A:2199:GLU:HG3	1.82	0.61
1:A:2020:ASP:O	1:A:2024:ASN:ND2	2.34	0.61
1:A:1853:GLN:NE2	1:A:1857:ASN:OD1	2.34	0.61
1:A:3257:TYR:HB2	1:A:3298:MET:HE1	1.82	0.60
1:A:3215:VAL:HG23	1:A:3339:LYS:HZ2	1.67	0.60
1:A:3239:PRO:HD2	1:A:3385:ARG:CZ	2.31	0.60
1:A:1391:LEU:HD13	1:A:1436:VAL:HG23	1.84	0.60
1:A:3117:ASP:HB3	1:A:3120:LEU:HB2	1.84	0.60
1:A:1502:PHE:HE2	1:A:1533:MET:HE1	1.67	0.59
1:A:1478:GLU:N	1:A:1478:GLU:OE1	2.35	0.59
1:A:2926:GLN:OE1	1:A:3057:ASN:ND2	2.33	0.58
1:A:2636:SER:OG	1:A:3410:ARG:NH2	2.29	0.58
1:A:1280:PRO:O	1:A:1283:SER:OG	2.18	0.57
1:A:2098:LYS:HG3	1:A:2099:VAL:HG22	1.85	0.57
1:A:2339:TYR:OH	1:A:2357:GLU:O	2.22	0.57
1:A:3204:GLN:OE1	1:A:3349:ARG:NH2	2.37	0.57
1:A:2823:ILE:HD11	1:A:2868:LEU:HB3	1.86	0.57
1:A:1534:GLU:OE2	1:A:1537:ARG:NH1	2.38	0.57
1:A:2834:ASN:O	1:A:2836:HIS:N	2.38	0.56
1:A:3225:ASN:HD22	1:A:3367:VAL:HG13	1.70	0.56
1:A:2784:SER:HA	1:A:2878:SER:OG	2.06	0.56
1:A:1894:THR:OG1	1:A:1899:ARG:O	2.22	0.56
1:A:3295:HIS:HA	1:A:3298:MET:HE2	1.87	0.56
1:A:3303:LEU:HD22	1:A:3308:GLU:HG3	1.87	0.56
1:A:1057:GLN:O	1:A:1060:SER:OG	2.22	0.55
1:A:2485:MET:HE1	1:A:2515:ILE:HG22	1.88	0.55
1:A:3084:ASP:HB3	1:A:3134:LYS:HE2	1.88	0.55
1:A:2682:VAL:HG11	1:A:2894:TYR:CE1	2.41	0.55
1:A:3328:LYS:HG3	1:A:3329:ILE:HG22	1.87	0.55
1:A:1159:TRP:CG	1:A:1207:LEU:HD13	2.41	0.55
1:A:2372:ARG:N	1:A:3343:LYS:HZ1	2.05	0.55
1:A:3143:GLU:OE2	1:A:3145:TRP:NE1	2.31	0.55
1:A:2773:THR:OG1	1:A:2774:MET:N	2.38	0.55
1:A:3215:VAL:N	1:A:3339:LYS:HZ1	2.05	0.55
1:A:2771:ARG:HG2	1:A:2896:VAL:HG21	1.88	0.55
1:A:2465:THR:HG21	1:A:2600:LEU:HD22	1.88	0.55
1:A:1882:SER:OG	1:A:1883:GLU:N	2.37	0.55
1:A:2422:GLU:HB3	1:A:2424:ARG:NH1	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3238:VAL:HA	1:A:3385:ARG:HH12	1.73	0.54
1:A:2177:PRO:HB3	1:A:2205:ILE:HD11	1.89	0.54
1:A:2218:LEU:HD21	1:A:2229:GLU:HG3	1.89	0.54
1:A:2989:ALA:HA	1:A:2994:ILE:HG13	1.91	0.53
1:A:1243:PHE:HB3	1:A:1249:VAL:HG12	1.91	0.53
1:A:1595:THR:HG22	1:A:2063:PRO:HD3	1.90	0.53
1:A:1819:ILE:HD12	1:A:2004:ILE:HG23	1.90	0.53
1:A:2409:VAL:HA	1:A:2412:TYR:CZ	2.43	0.53
1:A:3214:ILE:HB	1:A:3339:LYS:HZ1	1.72	0.53
1:A:1096:ILE:O	1:A:1100:LEU:HG	2.08	0.53
1:A:1496:ILE:HD11	1:A:1532:LEU:HD22	1.89	0.53
1:A:2833:ARG:NH2	1:A:2844:GLU:O	2.42	0.53
1:A:3148:ARG:HG2	1:A:3152:ASN:HD21	1.74	0.53
1:A:2669:LEU:HB3	1:A:2695:VAL:HG12	1.91	0.52
1:A:1875:GLN:NE2	1:A:1923:GLY:O	2.29	0.52
1:A:1072:GLU:HG2	1:A:1073:THR:HG23	1.92	0.52
1:A:2894:TYR:O	1:A:2898:GLN:HG2	2.10	0.51
1:A:1646:LEU:HD13	1:A:1734:ARG:HH21	1.74	0.51
1:A:3238:VAL:HG12	1:A:3385:ARG:HH12	1.75	0.51
1:A:2814:LYS:HE3	1:A:2833:ARG:HE	1.75	0.51
1:A:3207:VAL:HG23	1:A:3212:THR:HB	1.93	0.51
1:A:2703:VAL:HG12	1:A:3085:ILE:HG21	1.91	0.50
1:A:1373:HIS:NE2	1:A:1696:GLU:HG2	2.26	0.50
1:A:2442:GLN:HE21	1:A:2448:MET:HB2	1.76	0.50
1:A:3406:ARG:HB3	1:A:3407:LEU:HD12	1.94	0.50
1:A:3394:LEU:HA	1:A:3397:VAL:HG12	1.94	0.50
1:A:1607:ASP:OD1	1:A:1608:LEU:N	2.43	0.50
1:A:1622:LYS:HD2	1:A:2414:ARG:NE	2.27	0.50
1:A:1814:GLN:HB2	1:A:1917:ILE:HD11	1.94	0.49
1:A:3455:THR:HB	1:A:3491:THR:HA	1.94	0.49
1:A:2145:ALA:O	1:A:2148:SER:OG	2.29	0.49
1:A:2640:LEU:HG	1:A:3407:LEU:HD11	1.94	0.49
1:A:2738:LEU:HD23	1:A:3067:GLY:HA2	1.94	0.49
1:A:1993:PHE:HA	1:A:1996:LEU:HD23	1.94	0.49
1:A:3117:ASP:OD2	1:A:3158:ARG:NH2	2.45	0.49
1:A:1170:LYS:NZ	1:A:1202:GLU:OE1	2.46	0.49
1:A:1072:GLU:OE1	1:A:1072:GLU:N	2.40	0.49
1:A:2089:ARG:NE	1:A:2196:GLU:OE2	2.42	0.49
1:A:2346:ILE:HG22	1:A:2347:TRP:CD1	2.48	0.49
1:A:2448:MET:HB3	1:A:2452:GLU:HB2	1.95	0.49
1:A:2829:ASN:HA	1:A:3030:PRO:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3030:PRO:O	1:A:3047:SER:OG	2.22	0.48
1:A:2921:ILE:HG13	1:A:2922:PRO:HD2	1.95	0.48
1:A:1103:ARG:HH22	1:A:1245:GLU:HG2	1.78	0.48
1:A:1566:MET:O	1:A:1570:THR:OG1	2.29	0.48
1:A:3293:ASP:HB3	1:A:3297:ARG:HH12	1.78	0.48
1:A:1433:ALA:HA	1:A:1661:LEU:HD22	1.95	0.48
1:A:3157:TYR:O	1:A:3159:ALA:N	2.39	0.48
1:A:3450:VAL:HG13	1:A:3451:VAL:HG23	1.96	0.48
1:A:2895:MET:HE3	1:A:3062:PHE:CE1	2.45	0.48
1:A:2170:TYR:CZ	1:A:2214:LYS:HD2	2.49	0.48
1:A:2319:ARG:HH21	1:A:2338:VAL:HG12	1.78	0.48
1:A:2000:ALA:O	1:A:2004:ILE:HG12	2.14	0.47
1:A:2783:LEU:O	1:A:2784:SER:OG	2.31	0.47
1:A:1096:ILE:O	1:A:1099:ILE:HG22	2.14	0.47
1:A:1249:VAL:HG23	1:A:1271:THR:C	2.40	0.47
1:A:1891:VAL:HG21	1:A:1901:ARG:HH21	1.77	0.47
1:A:2097:GLN:HA	1:A:2097:GLN:NE2	2.30	0.47
1:A:2593:VAL:O	1:A:2597:ILE:HG12	2.15	0.47
1:A:1175:VAL:HG13	1:A:1194:PHE:CE2	2.50	0.47
1:A:1343:MET:HE3	1:A:1343:MET:HB3	1.78	0.47
1:A:1429:ASN:OD1	1:A:1429:ASN:N	2.47	0.47
1:A:2295:ASN:OD1	1:A:2296:GLY:N	2.48	0.47
1:A:2342:ILE:O	1:A:2346:ILE:HG12	2.14	0.47
1:A:1581:ASN:ND2	1:A:1801:THR:O	2.47	0.47
1:A:3239:PRO:HD2	1:A:3385:ARG:NH2	2.30	0.47
1:A:1201:THR:HA	1:A:1204:VAL:HG22	1.96	0.47
1:A:1789:PHE:O	1:A:1791:VAL:N	2.42	0.47
1:A:1988:MET:HE1	1:A:2026:ALA:O	2.15	0.47
1:A:2198:GLU:OE1	1:A:2199:GLU:N	2.42	0.47
1:A:2323:ALA:O	1:A:2326:LYS:HE3	2.15	0.47
1:A:1030:TYR:O	1:A:1034:SER:OG	2.26	0.46
1:A:1596:MET:N	1:A:2055:ASP:OD2	2.41	0.46
1:A:2276:PRO:HA	1:A:2279:ARG:HG2	1.96	0.46
1:A:2835:ALA:HB3	1:A:2917:PHE:HA	1.97	0.46
1:A:2894:TYR:HD2	1:A:3066:VAL:HG11	1.80	0.46
1:A:3219:VAL:O	1:A:3222:PRO:HD2	2.15	0.46
1:A:1276:ASP:HB3	1:A:1279:ASP:HB2	1.97	0.46
1:A:1352:LYS:HD2	1:A:1385:GLU:CD	2.41	0.46
1:A:1640:LEU:HA	1:A:1742:LEU:HD11	1.98	0.46
1:A:3142:ASP:OD1	1:A:3142:ASP:N	2.49	0.46
1:A:2319:ARG:HH22	1:A:2342:ILE:HD12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2835:ALA:CB	1:A:2918:LYS:H	2.27	0.46
1:A:1650:ASP:OD1	1:A:1652:ASN:ND2	2.49	0.46
1:A:2401:LEU:HD21	1:A:2611:ARG:HH12	1.81	0.46
1:A:2975:ALA:O	1:A:2978:SER:OG	2.25	0.46
1:A:1140:ASP:OD1	1:A:1140:ASP:N	2.48	0.46
1:A:1713:ALA:HB1	1:A:1717:MET:HE2	1.98	0.46
1:A:1917:ILE:HB	1:A:1918:PRO:HD3	1.98	0.45
1:A:2750:LEU:HD21	1:A:2880:LEU:HD11	1.97	0.45
1:A:2954:GLN:OE1	1:A:3028:ARG:NH2	2.49	0.45
1:A:1852:THR:N	1:A:1855:GLU:OE1	2.44	0.45
1:A:2319:ARG:NH2	1:A:2339:TYR:HA	2.31	0.45
1:A:2394:ASN:ND2	1:A:2543:GLU:OE2	2.41	0.45
1:A:2424:ARG:NE	1:A:2595:ASP:HB3	2.31	0.45
1:A:2898:GLN:HA	1:A:2901:GLU:OE1	2.16	0.45
1:A:2898:GLN:OE1	1:A:3070:ARG:NH2	2.37	0.45
1:A:1432:SER:OG	1:A:1433:ALA:N	2.49	0.45
1:A:1899:ARG:HH11	1:A:1899:ARG:HA	1.80	0.45
1:A:2891:SER:HB3	1:A:3062:PHE:HE2	1.81	0.45
1:A:1353:ASP:OD1	1:A:1354:ARG:N	2.49	0.45
1:A:2567:THR:O	1:A:2570:THR:HG22	2.17	0.45
1:A:3203:ILE:HG21	1:A:3477:LEU:HD22	1.99	0.45
1:A:1017:VAL:HG21	1:A:1117:PHE:HE2	1.82	0.45
1:A:3185:LEU:HD13	1:A:3193:TYR:CD2	2.52	0.45
1:A:1405:ILE:HD12	1:A:1405:ILE:H	1.82	0.45
1:A:3300:ILE:HD12	1:A:3304:ILE:HD11	1.98	0.45
1:A:1100:LEU:HD22	1:A:1238:GLU:OE1	2.16	0.45
1:A:2693:GLY:O	1:A:2695:VAL:N	2.49	0.45
1:A:2782:LEU:HA	1:A:2782:LEU:HD23	1.75	0.45
1:A:2218:LEU:HB3	1:A:2221:PRO:HG3	1.99	0.44
1:A:2699:PHE:CD2	1:A:3081:ARG:HD2	2.51	0.44
1:A:2836:HIS:O	1:A:2839:SER:OG	2.35	0.44
1:A:3097:ASP:OD2	1:A:3108:TYR:OH	2.36	0.44
1:A:1138:ASP:OD2	1:A:1143:LYS:HB2	2.17	0.44
1:A:2343:LYS:HE2	1:A:2352:ALA:HB1	2.00	0.44
1:A:2969:SER:OG	1:A:2974:ARG:NH2	2.50	0.44
1:A:1150:GLN:HA	1:A:1153:VAL:HG12	1.98	0.44
1:A:1137:GLN:HG3	1:A:1142:PHE:CD1	2.53	0.44
1:A:2466:GLU:HG2	1:A:2576:VAL:HG13	1.99	0.44
1:A:1652:ASN:HB3	1:A:1668:ASN:HD21	1.83	0.44
1:A:1373:HIS:CD2	1:A:1696:GLU:HG2	2.52	0.44
1:A:3318:SER:HB2	1:A:3321:ASP:OD2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3343:LYS:O	1:A:3345:ARG:N	2.51	0.44
1:A:1145:ASN:ND2	1:A:1148:LEU:HD13	2.32	0.44
1:A:1988:MET:HA	1:A:1991:VAL:HG12	2.00	0.44
1:A:2696:TRP:HA	1:A:3081:ARG:NH1	2.33	0.44
1:A:1009:ILE:HD12	1:A:1037:LEU:HD13	1.99	0.44
1:A:1010:ASP:OD1	1:A:1032:LYS:NZ	2.43	0.44
1:A:2316:LEU:HD12	1:A:2363:LEU:O	2.18	0.44
1:A:2506:TYR:CD2	1:A:3051:ASN:HB3	2.52	0.44
1:A:3455:THR:O	1:A:3491:THR:OG1	2.24	0.44
1:A:1433:ALA:HB3	1:A:1436:VAL:HG12	1.99	0.43
1:A:1625:SER:HB3	1:A:2414:ARG:CZ	2.48	0.43
1:A:1625:SER:HB3	1:A:2414:ARG:NH2	2.32	0.43
1:A:3262:LEU:HA	1:A:3262:LEU:HD13	1.69	0.43
1:A:2141:ILE:HA	1:A:2144:LEU:HD12	2.01	0.43
1:A:2319:ARG:HD3	1:A:2339:TYR:CD1	2.54	0.43
1:A:3265:ILE:HG23	1:A:3319:ARG:NH2	2.33	0.43
1:A:2841:LEU:HD21	1:A:2857:ILE:HD13	1.99	0.43
1:A:1332:GLU:OE2	1:A:1945:LYS:HE2	2.19	0.43
1:A:2033:LEU:HD23	1:A:2033:LEU:HA	1.79	0.43
1:A:2986:ARG:CZ	1:A:3458:GLY:HA3	2.49	0.43
1:A:1246:SER:O	1:A:1247:THR:HG22	2.19	0.43
1:A:1360:GLY:HA3	1:A:1381:ASN:ND2	2.34	0.43
1:A:2836:HIS:CD2	1:A:2916:HIS:CE1	3.07	0.43
1:A:2833:ARG:HH12	1:A:2844:GLU:CD	2.27	0.43
1:A:1564:ASN:O	1:A:1568:LEU:HB2	2.19	0.43
1:A:1737:LYS:HE3	1:A:1737:LYS:HB3	1.83	0.43
1:A:2784:SER:OG	1:A:2785:SER:N	2.52	0.43
1:A:1350:LEU:HA	1:A:1350:LEU:HD23	1.77	0.42
1:A:2142:ARG:NH1	1:A:2162:GLN:OE1	2.52	0.42
1:A:2658:ILE:HA	1:A:2661:LYS:HE2	2.01	0.42
1:A:3498:LEU:HD23	1:A:3498:LEU:HA	1.88	0.42
1:A:3499:THR:OG1	1:A:3500:HIS:N	2.51	0.42
1:A:1380:LYS:HB2	1:A:1380:LYS:HE3	1.79	0.42
1:A:3284:LEU:O	1:A:3288:ILE:HG12	2.19	0.42
1:A:2806:ARG:NH2	1:A:2847:THR:OG1	2.50	0.42
1:A:3215:VAL:HG23	1:A:3339:LYS:NZ	2.32	0.42
1:A:1524:LYS:HB3	1:A:1524:LYS:HE2	1.75	0.42
1:A:1587:LEU:HD12	1:A:1972:TRP:CZ3	2.55	0.42
1:A:2861:ILE:HD13	1:A:2861:ILE:HA	1.70	0.42
1:A:3124:ILE:HD12	1:A:3124:ILE:HA	1.87	0.42
1:A:2409:VAL:HA	1:A:2412:TYR:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2771:ARG:NE	1:A:2775:SER:HB2	2.35	0.42
1:A:2817:GLN:NE2	1:A:2828:GLY:HA3	2.34	0.42
1:A:2965:GLY:O	1:A:2966:TYR:HB2	2.19	0.42
1:A:1891:VAL:HG21	1:A:1901:ARG:NH2	2.35	0.42
1:A:2424:ARG:CZ	1:A:2595:ASP:HB3	2.50	0.42
1:A:3157:TYR:C	1:A:3159:ALA:H	2.25	0.42
1:A:3345:ARG:HA	1:A:3345:ARG:CZ	2.50	0.42
1:A:2293:LEU:HD23	1:A:2293:LEU:HA	1.86	0.42
1:A:2397:ARG:NH1	1:A:2541:VAL:HB	2.35	0.42
1:A:2398:LEU:HD21	1:A:2451:GLN:HE21	1.84	0.42
1:A:2751:THR:HG22	1:A:2754:GLU:OE1	2.20	0.42
1:A:1200:LEU:HD13	1:A:1270:TYR:CZ	2.55	0.42
1:A:1601:SER:O	1:A:1603:ALA:N	2.53	0.42
1:A:3317:ILE:HD12	1:A:3317:ILE:HA	1.89	0.42
1:A:1361:ALA:HB2	1:A:1377:LEU:HD22	2.02	0.42
1:A:2818:LEU:CD2	1:A:2835:ALA:HA	2.47	0.42
1:A:2913:LEU:O	1:A:2916:HIS:ND1	2.53	0.42
1:A:3189:GLY:HA2	1:A:3329:ILE:HG12	2.02	0.42
1:A:2587:ASP:OD1	1:A:2590:ALA:HB3	2.20	0.41
1:A:2765:THR:HG21	1:A:2866:LEU:HD13	2.02	0.41
1:A:3049:ASP:OD1	1:A:3050:PRO:HD2	2.19	0.41
1:A:1551:LEU:HD12	1:A:1551:LEU:HA	1.86	0.41
1:A:1915:ALA:O	1:A:1918:PRO:HD2	2.20	0.41
1:A:1311:ASN:OD1	1:A:1326:LYS:NZ	2.32	0.41
1:A:1957:ILE:HB	1:A:2060:VAL:HG21	2.01	0.41
1:A:1268:GLY:O	1:A:1269:LEU:HD22	2.20	0.41
1:A:1582:ILE:HD12	1:A:1582:ILE:HA	1.89	0.41
1:A:1622:LYS:HA	1:A:2414:ARG:HE	1.85	0.41
1:A:3345:ARG:HA	1:A:3345:ARG:NE	2.35	0.41
1:A:1608:LEU:HD12	1:A:1608:LEU:HA	1.88	0.41
1:A:2172:ILE:HD11	1:A:2230:LEU:HD21	2.03	0.41
1:A:2315:GLY:O	1:A:2319:ARG:HG3	2.20	0.41
1:A:2153:THR:O	1:A:2157:THR:HG23	2.21	0.41
1:A:2397:ARG:HH22	1:A:2542:ASN:HA	1.85	0.41
1:A:2478:GLN:HA	1:A:2532:LEU:HD11	2.02	0.41
1:A:2774:MET:HB3	1:A:2775:SER:H	1.61	0.41
1:A:3198:ASN:HD22	1:A:3206:LEU:HD11	1.85	0.41
1:A:2371:MET:HB3	1:A:3343:LYS:NZ	2.35	0.41
1:A:3095:GLU:HA	1:A:3098:ILE:HG22	2.02	0.41
1:A:3348:GLY:C	1:A:3350:TYR:H	2.28	0.41
1:A:1154:LEU:HD23	1:A:1154:LEU:HA	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2143:ASN:C	1:A:2143:ASN:OD1	2.63	0.41
1:A:2271:ILE:HG23	1:A:2331:LEU:HD11	2.02	0.41
1:A:2706:ILE:HD11	1:A:2719:LEU:HB3	2.02	0.41
1:A:2986:ARG:HD3	1:A:3493:ASN:HD22	1.86	0.41
1:A:3263:ARG:NH1	1:A:3266:ASP:OD2	2.54	0.41
1:A:3395:GLY:O	1:A:3398:THR:HG22	2.21	0.41
1:A:1137:GLN:HG3	1:A:1142:PHE:HD1	1.86	0.41
1:A:1600:ARG:HA	1:A:1600:ARG:HD3	1.83	0.41
1:A:2761:GLY:HA3	1:A:2877:LEU:HD11	2.03	0.41
1:A:3265:ILE:HG23	1:A:3319:ARG:HH21	1.85	0.41
1:A:2815:SER:HB3	1:A:2861:ILE:HD11	2.03	0.40
1:A:2818:LEU:HD23	1:A:2840:ARG:NH2	2.20	0.40
1:A:3432:LYS:HB3	1:A:3432:LYS:HE2	1.88	0.40
1:A:1108:LEU:HA	1:A:1108:LEU:HD23	1.86	0.40
1:A:1572:GLY:O	1:A:2043:ARG:HD2	2.21	0.40
1:A:2052:LEU:HB2	1:A:2066:ASN:ND2	2.36	0.40
1:A:2494:MET:HE3	1:A:2497:PRO:HA	2.02	0.40
1:A:1630:ASN:OD1	1:A:1632:PRO:HD2	2.21	0.40
1:A:2051:ASN:OD1	1:A:2051:ASN:N	2.54	0.40
1:A:2636:SER:HB3	1:A:3407:LEU:HD23	2.03	0.40
1:A:3053:LEU:HD23	1:A:3053:LEU:HA	1.84	0.40
1:A:1360:GLY:HA3	1:A:1381:ASN:HD21	1.86	0.40
1:A:1839:LYS:HD2	1:A:1839:LYS:HA	1.79	0.40
1:A:2398:LEU:HD23	1:A:2398:LEU:HA	1.86	0.40
1:A:3061:HIS:O	1:A:3065:MET:HG2	2.21	0.40
1:A:3447:ILE:HA	1:A:3450:VAL:HG12	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	2443/2493 (98%)	2295 (94%)	134 (6%)	14 (1%)	21 49

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1882	SER
1	A	2059	ALA
1	A	2392	TYR
1	A	2835	ALA
1	A	2978	SER
1	A	3329	ILE
1	A	2773	THR
1	A	2395	ASN
1	A	3063	ALA
1	A	3344	VAL
1	A	2976	PRO
1	A	3158	ARG
1	A	3494	PRO
1	A	3460	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	2053/2088 (98%)	2047 (100%)	6 (0%)	86 84

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1782	LEU
1	A	1924	THR
1	A	2195	GLN
1	A	2219	VAL
1	A	2568	LEU
1	A	3262	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1373	HIS
1	A	1597	ASN
1	A	1610	GLN
1	A	1778	GLN
1	A	1812	GLN
1	A	1820	GLN
1	A	1965	ASN
1	A	1979	ASN
1	A	2044	HIS
1	A	2188	ASN
1	A	2195	GLN
1	A	2453	GLN
1	A	2478	GLN
1	A	2542	ASN
1	A	2594	GLN
1	A	2737	HIS
1	A	2759	HIS
1	A	3152	ASN
1	A	3198	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 ⓘ

There are no ligands in this entry.

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.

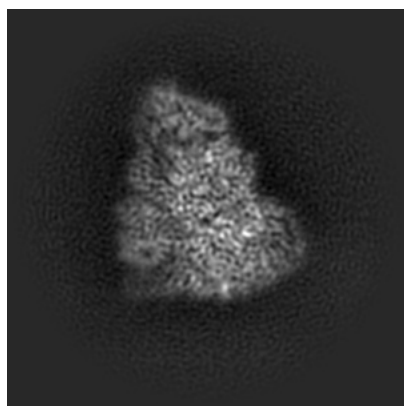
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75669. These allow visual inspection of the internal detail of the map and identification of artifacts.

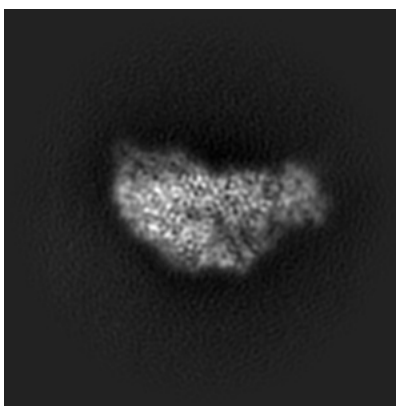
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

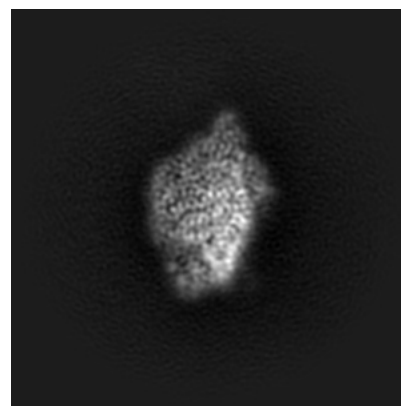
6.1.1 Primary map



X

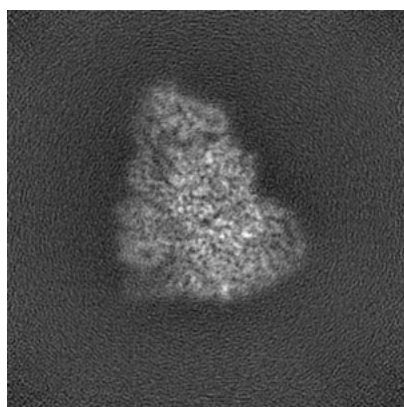


Y

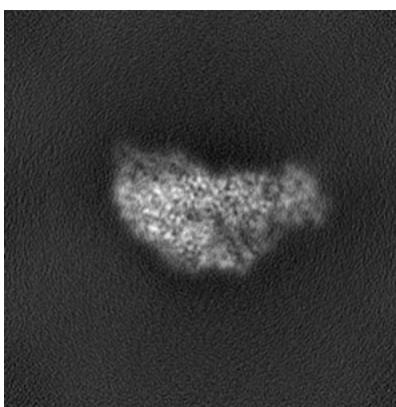


Z

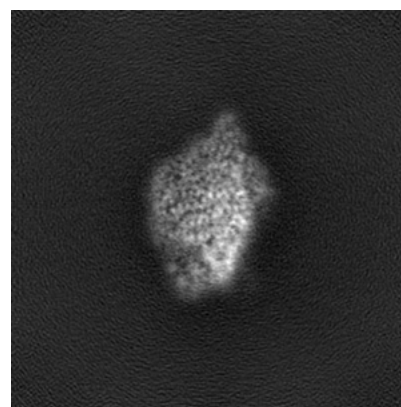
6.1.2 Raw map



X



Y

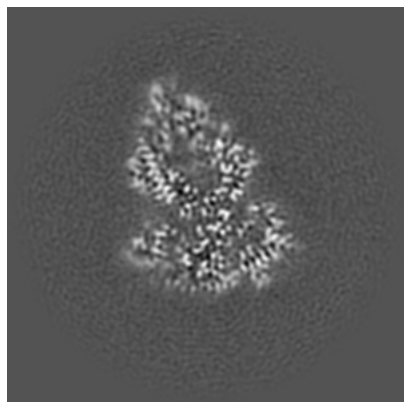


Z

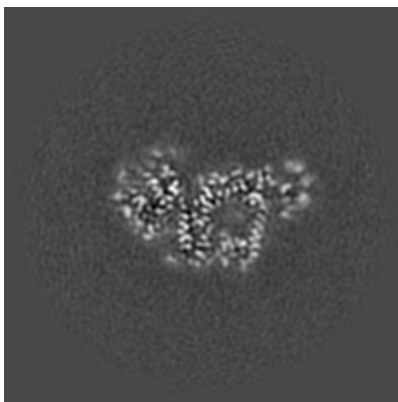
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

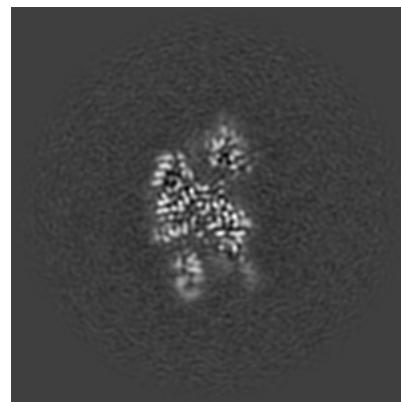
6.2.1 Primary map



X Index: 120

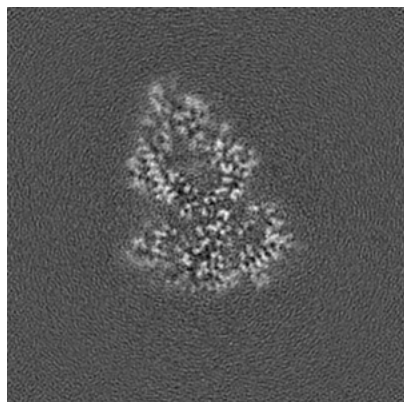


Y Index: 120

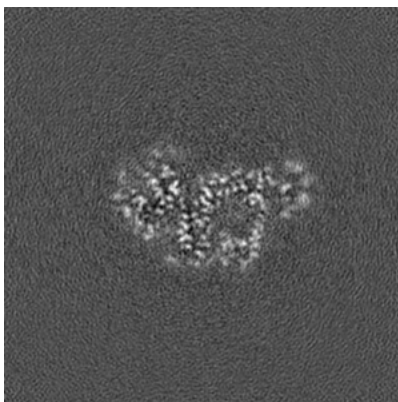


Z Index: 120

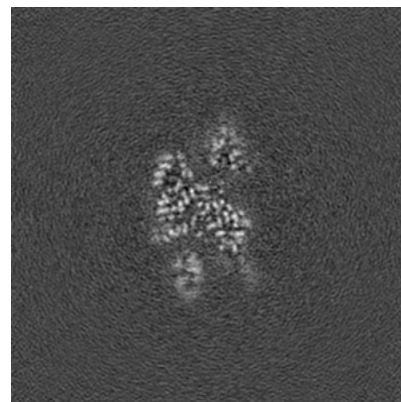
6.2.2 Raw map



X Index: 120



Y Index: 120

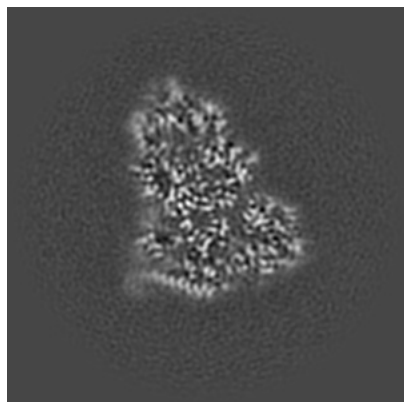


Z Index: 120

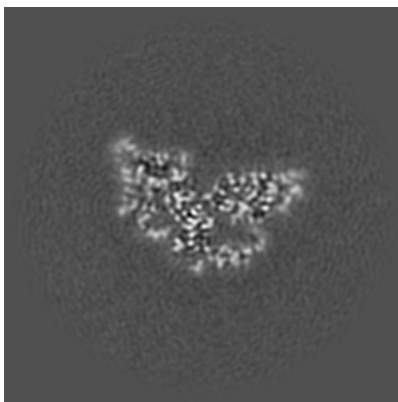
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

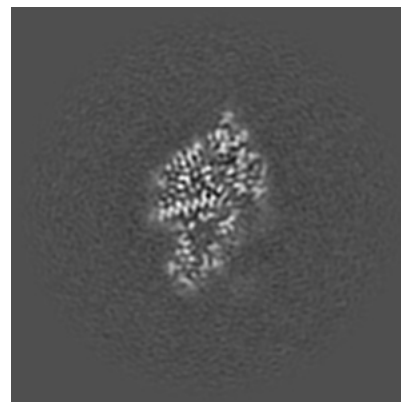
6.3.1 Primary map



X Index: 125

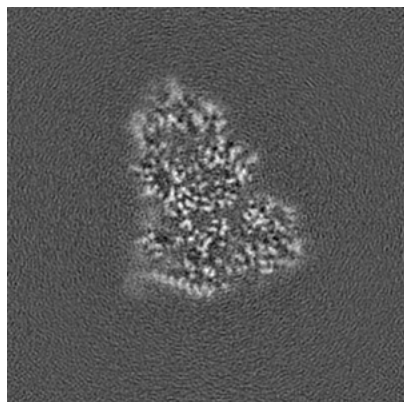


Y Index: 129

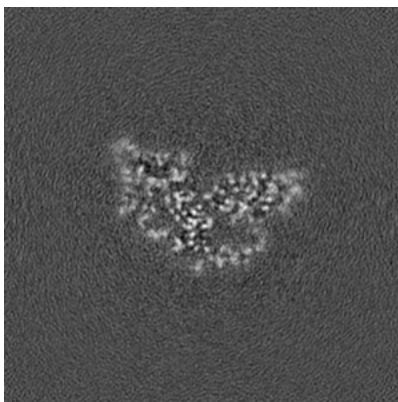


Z Index: 107

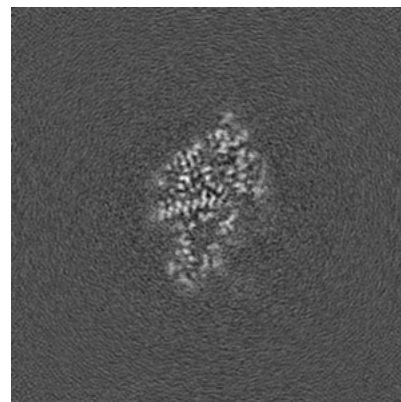
6.3.2 Raw map



X Index: 125



Y Index: 129

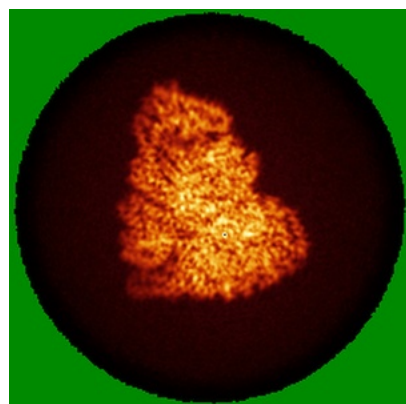


Z Index: 107

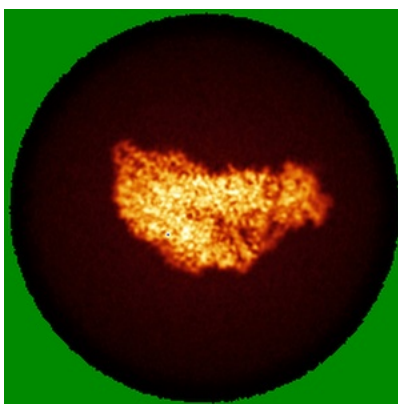
The images above show the largest variance slices of the map in three orthogonal directions.

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

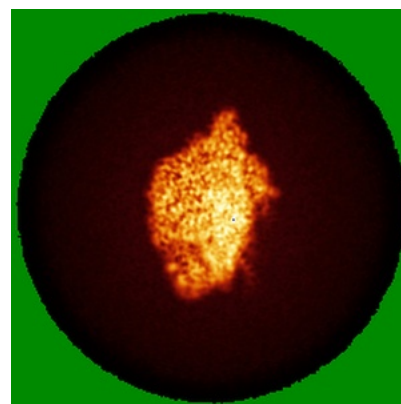
6.4.1 Primary map



X

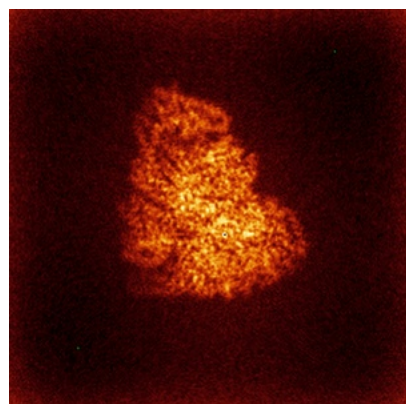


Y

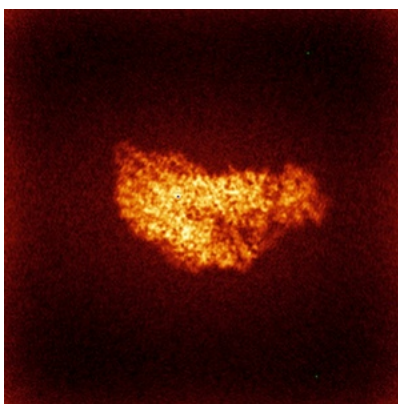


Z

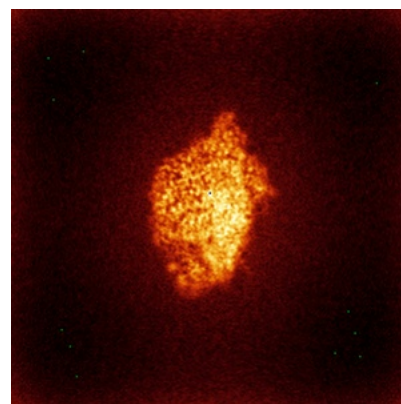
6.4.2 Raw map



X



Y

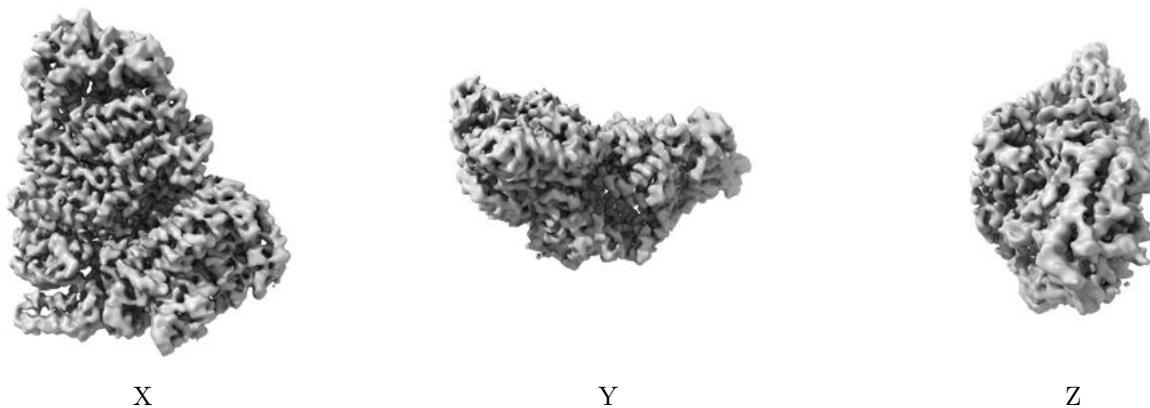


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

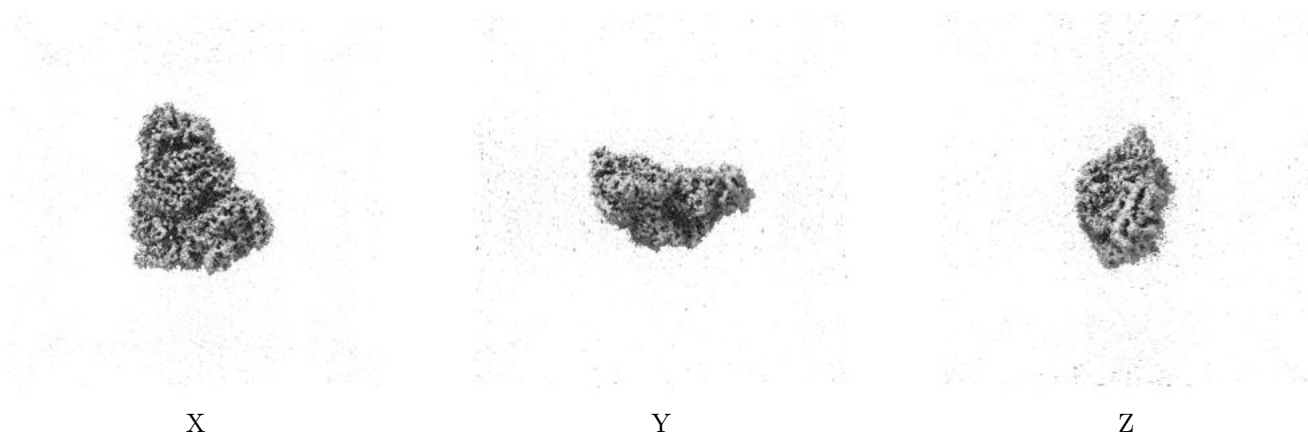
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.102. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

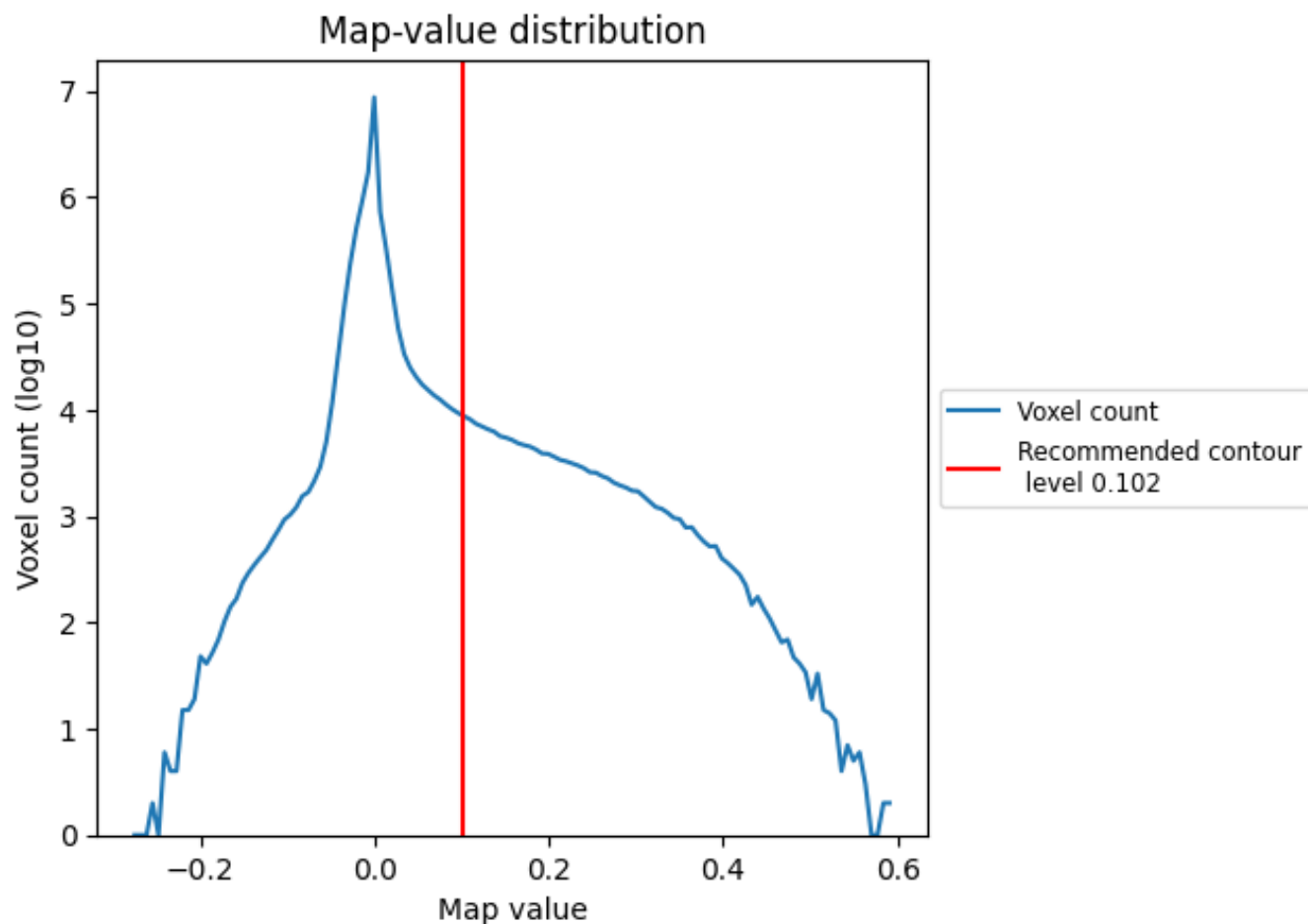
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

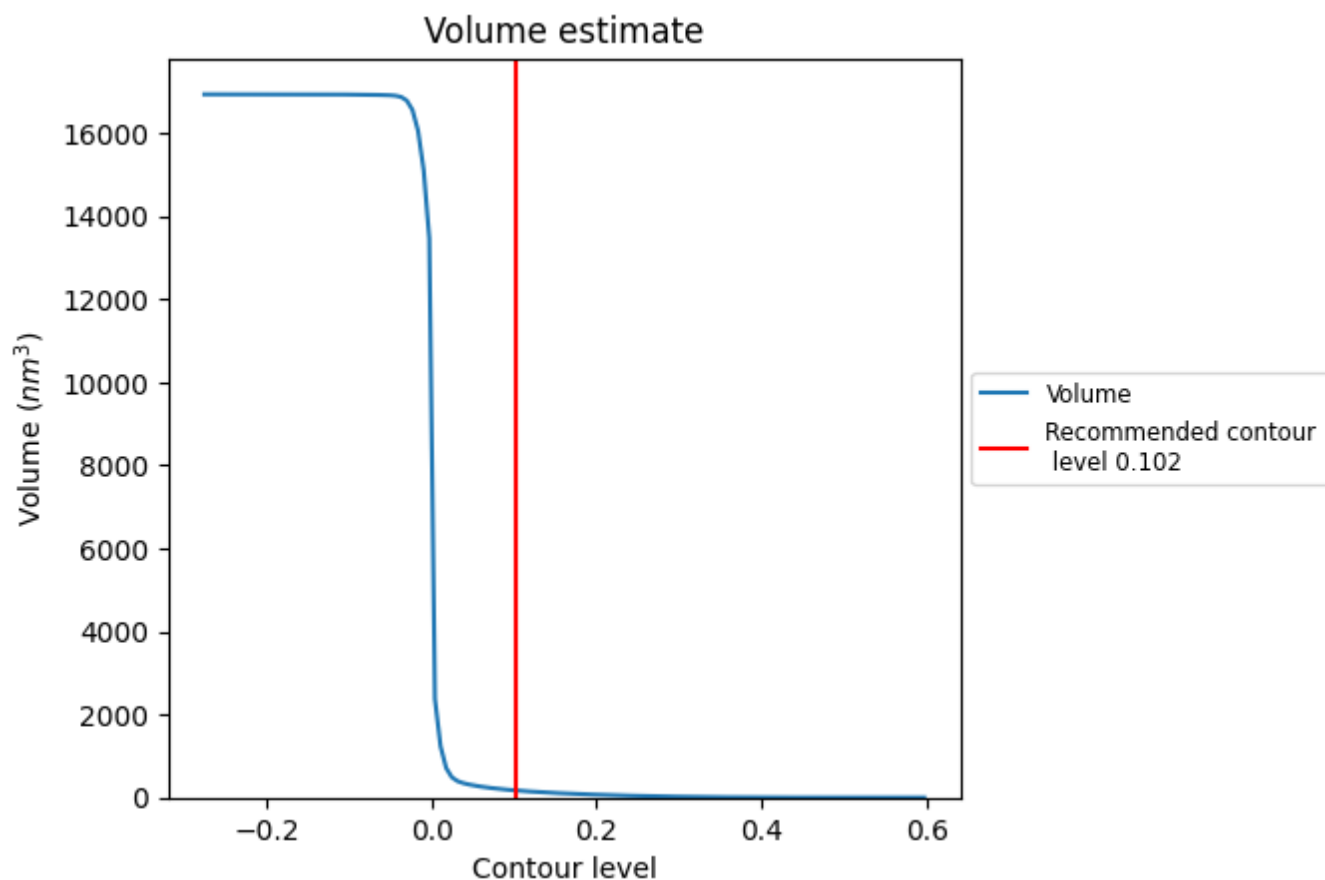
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

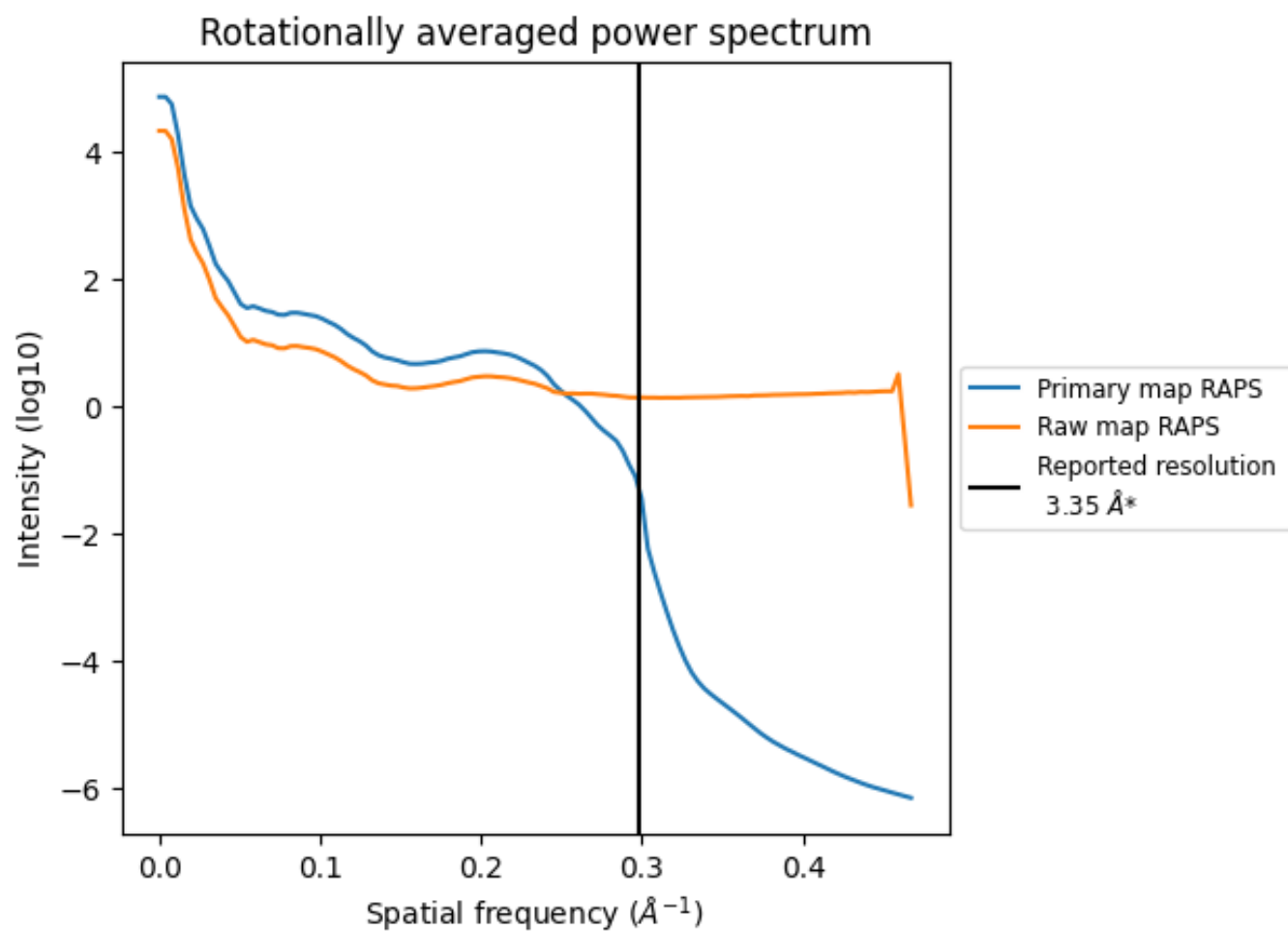
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 172 nm³; this corresponds to an approximate mass of 155 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 ⓘ

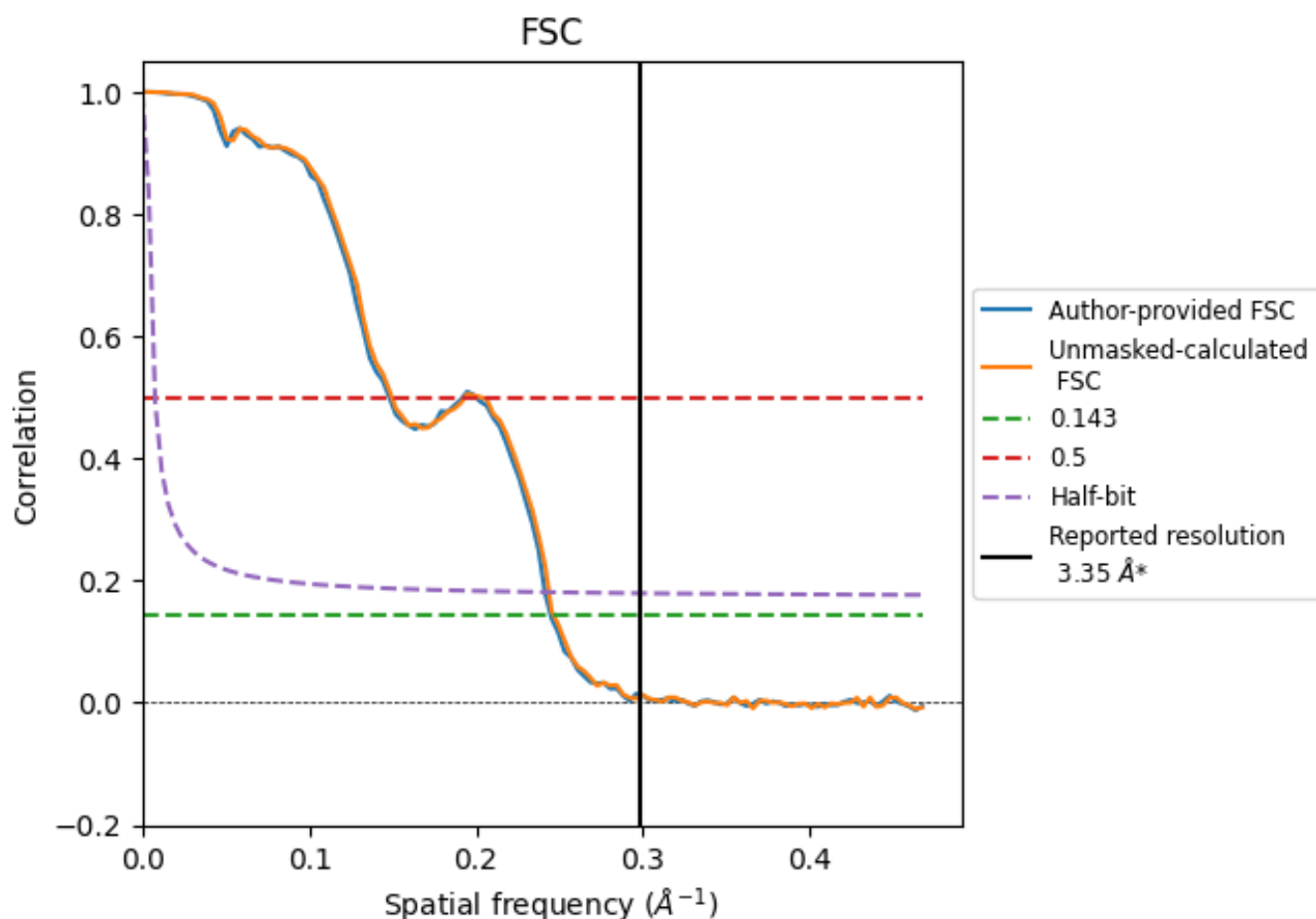


*Reported resolution corresponds to spatial frequency of 0.299 Å⁻¹

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 0.299 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	4.08	6.75	4.14
Unmasked-calculated*	4.06	6.69	4.10

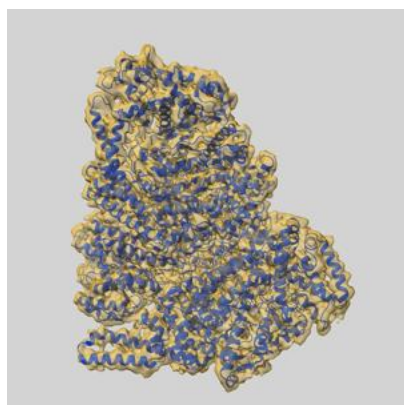
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.08 differs from the reported value 3.35 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.06 differs from the reported value 3.35 by more than 10 %

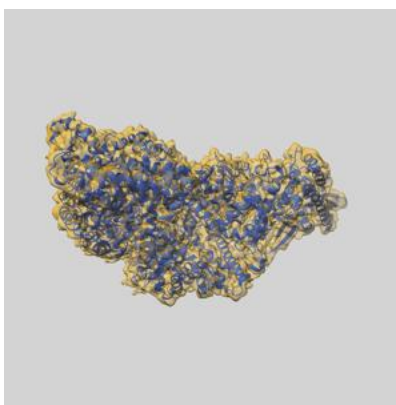
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75669 and PDB model 11FW. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

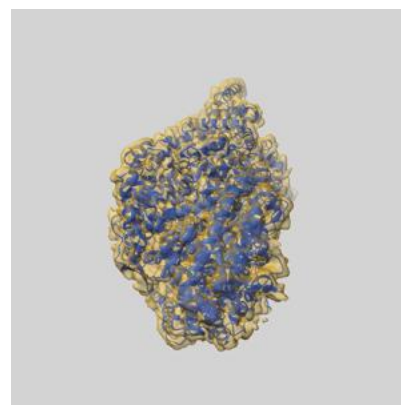
9.1 Map-model overlay [i](#)



X



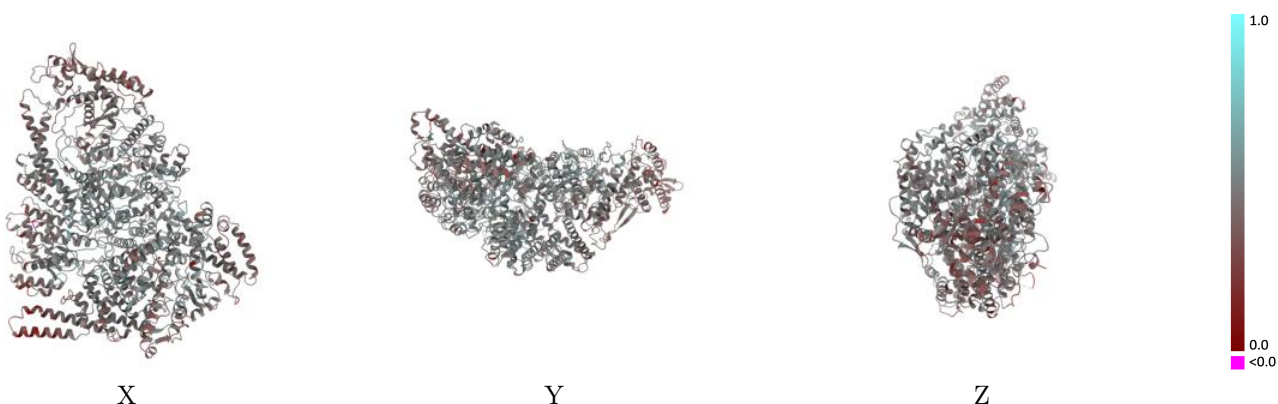
Y



Z

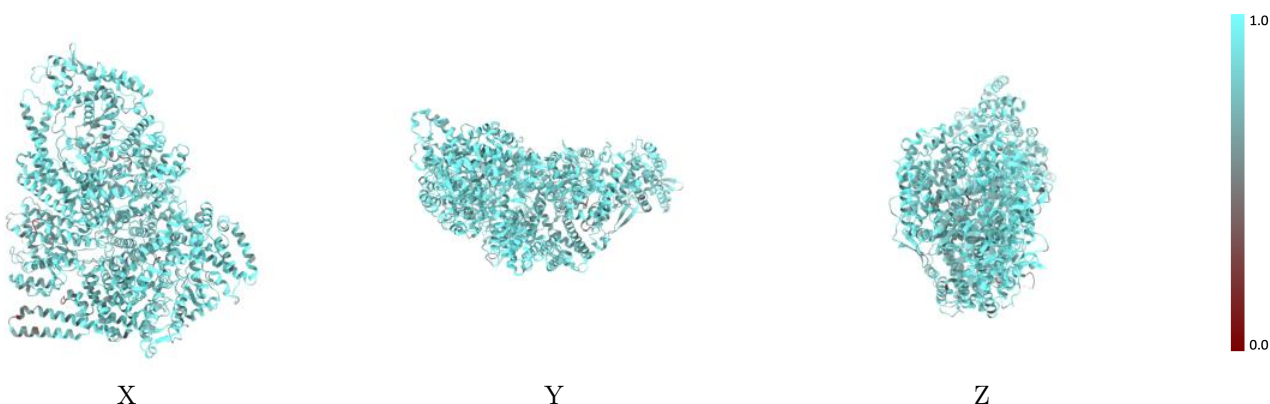
The images above show the 3D surface view of the map at the recommended contour level 0.102 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



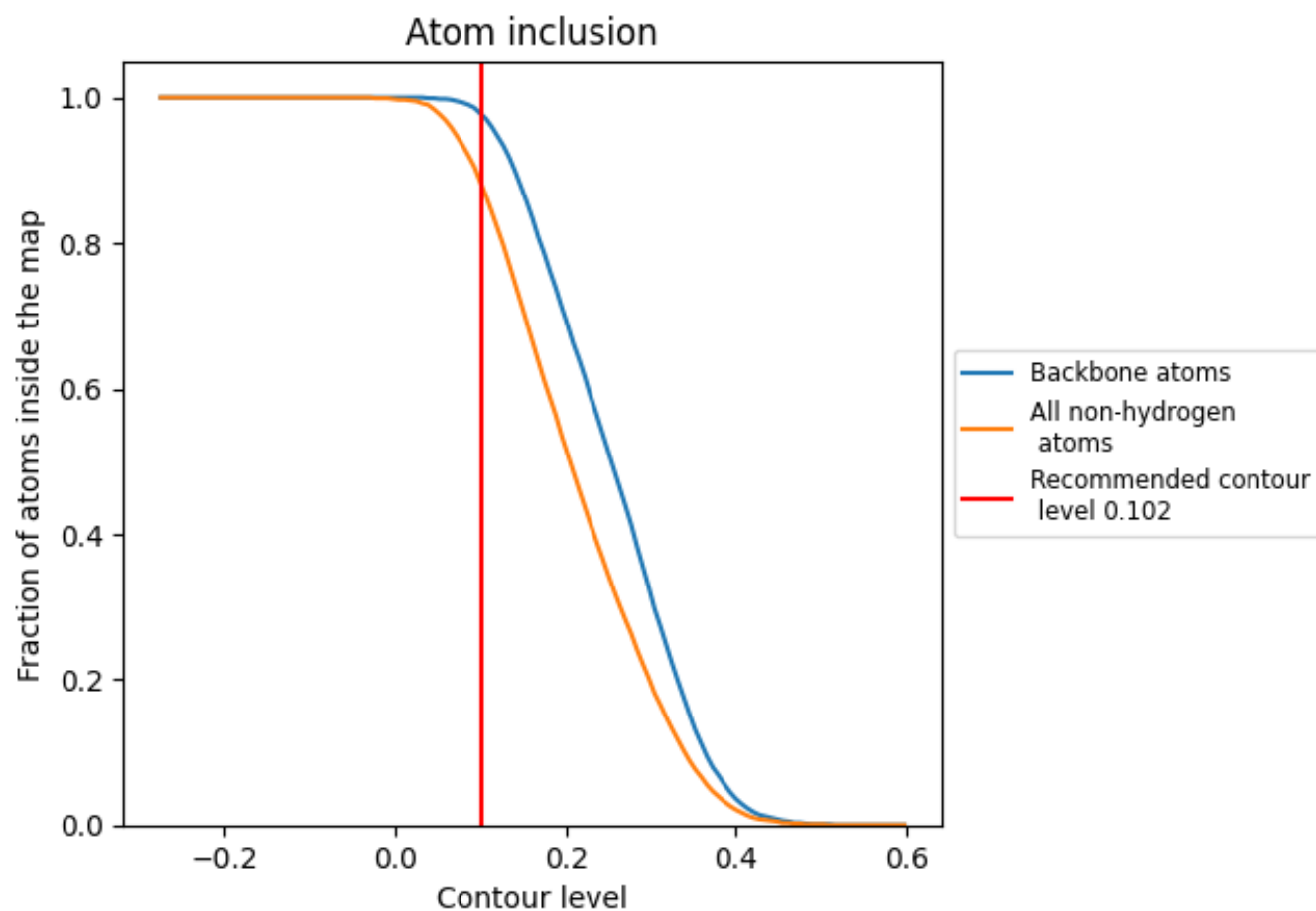
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.102).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 88% 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 (0.102) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8780	0.4550
A	0.8780	0.4550

