Full wwPDB EM Validation Report ⓘ

Aug 24, 2026 – 11:38 AM 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:

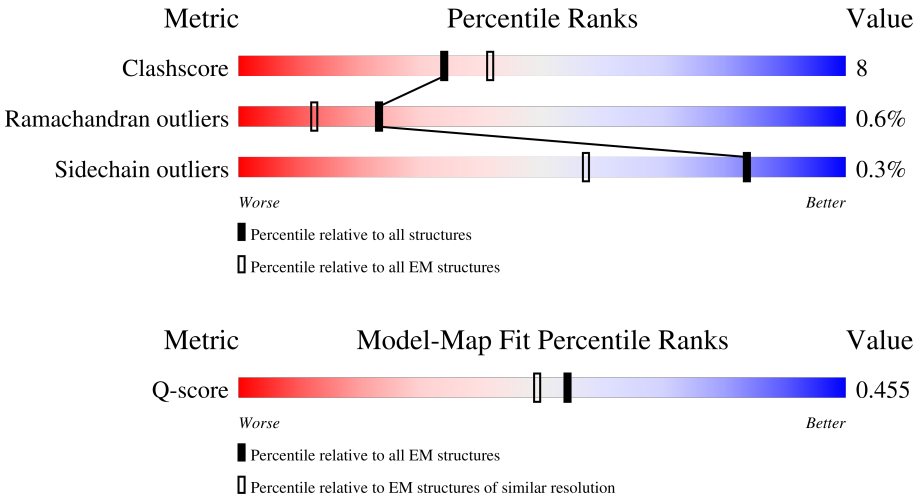
EMDB validation analysis	:	0.0.1.dev133
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & 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 <=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 (i)

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.

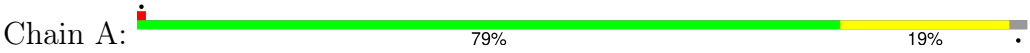
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2451	19054	11963	3306	3693	92	0	0

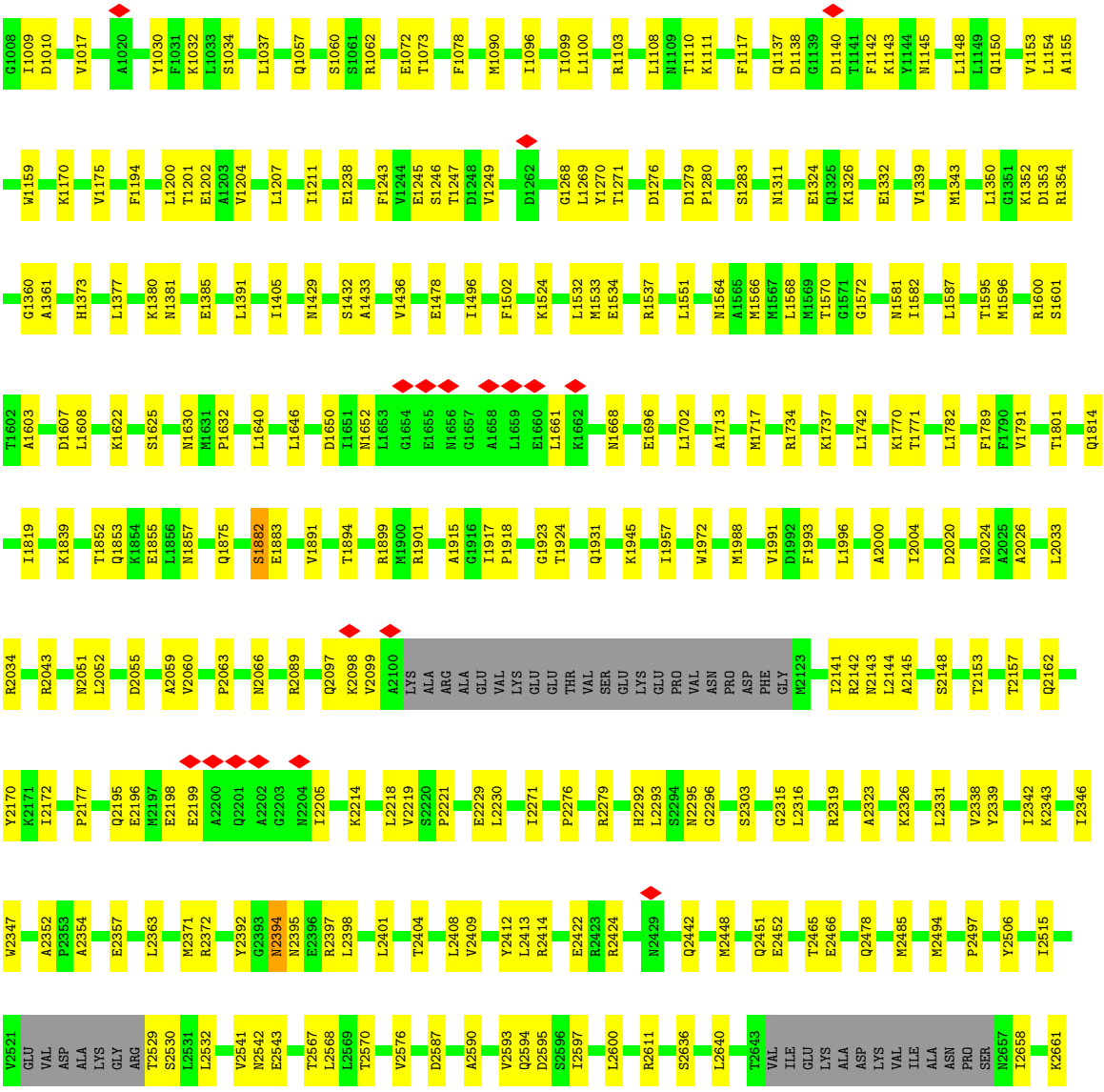
3 Residue-property plots (i)

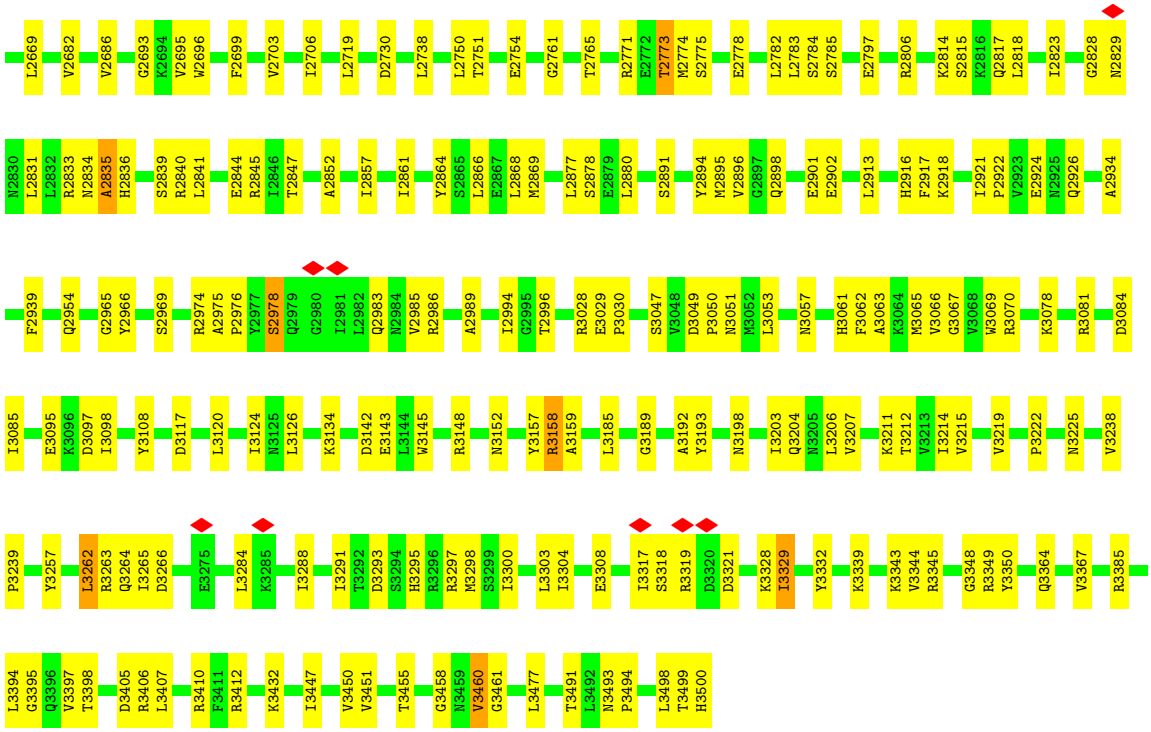
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Virion DNA-directed RNA polymerase

Chain A:






L2669 V2682 V2686 G2693 K2694 V2695 W2696 F2699 V2703 I2706 L2719 D2730 L2738 L2750 T2751 E2754 G2761 T2765 R2771 E2772 T2773 M2774 S2775 E2778 L2782 L2783 S2784 S2785 E2797 R2806 K2814 S2815 K2816 Q2817 L2818 I2823 G2828 N2829
N2830 L2831 L2832 R2833 N2834 A2835 H2836 S2839 R2840 L2841 E2844 R2845 I2846 T2847 A2852 I2857 I2861 Y2864 S2865 L2866 E2867 L2868 M2869 L2877 S2878 E2879 L2880 S2891 Y2894 M2895 V2896 G2897 Q2898 E2901 E2902 L2913 H2916 F2917 K2918 I2921 P2922 V2923 E2924 N2925 Q2926 A2934
F2939 Q2954 G2965 Y2966 S2969 R2974 A2975 P2976 Y2977 S2978 Q2979 G2980 I2981 L2982 Q2983 N2984 V2985 R2986 A2989 I2994 G2995 T2996 R3028 E3029 P3030 S3047 V3048 D3049 P3050 N3051 M3052 L3053 N3057 H3061 F3062 A3063 K3064 M3065 V3066 G3067 V3068 W3069 R3070 K3078 R3081 D3084
I3085 E3095 K3096 D3097 I3098 Y3108 D3117 L3120 I3124 N3125 L3126 K3134 D3142 E3143 L3144 W3145 R3148 N3152 Y3157 R3158 A3159 L3185 G3189 A3192 Y3193 N3198 I3203 Q3204 N3205 L3206 V3207 K3211 T3212 V3213 I3214 V3215 V3219 P3222 N3225 V3238
P3239 Y3257 L3262 R3263 Q3264 I3265 D3266 E3275 L3284 K3285 I3288 I3291 T3292 D3293 S3294 H3295 R3296 R3297 M3298 S3299 I3300 L3303 I3304 E3308 I3317 S3318 R3319 D3320 D3321 K3328 I3329 Y3332 K3339 K3343 V3344 R3345 G3348 R3349 Y3350 Q3364 V3367 R3385
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

4 Experimental information (i)

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 ($e^-/Å^2$)	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

5.1 Standard geometry

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(^{o})	Ideal(^{o})
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

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 (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	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 (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	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 (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.

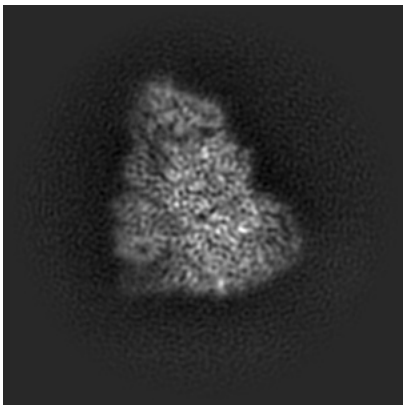
6 Map visualisation

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.

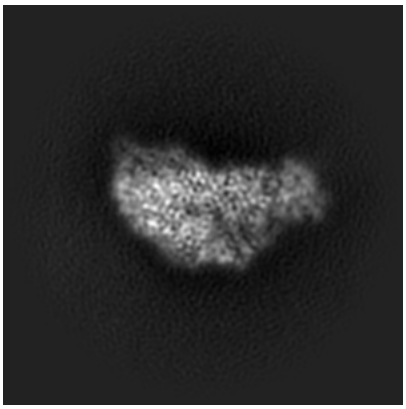
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

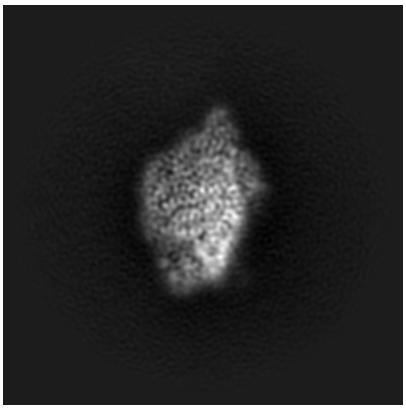
6.1.1 Primary map



X

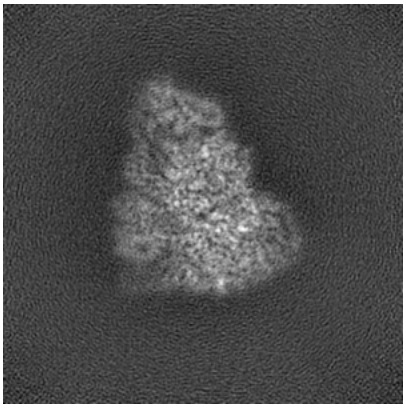


Y

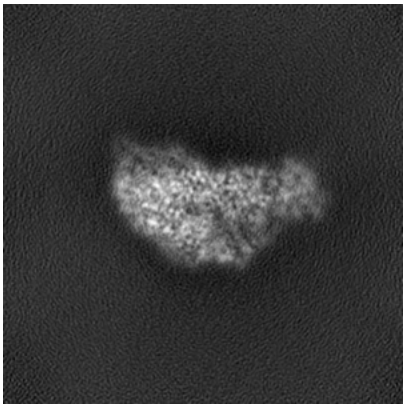


Z

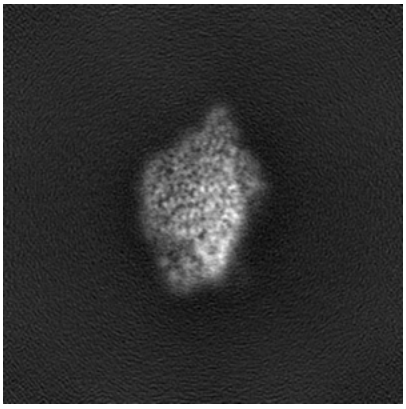
6.1.2 Raw map



X



Y

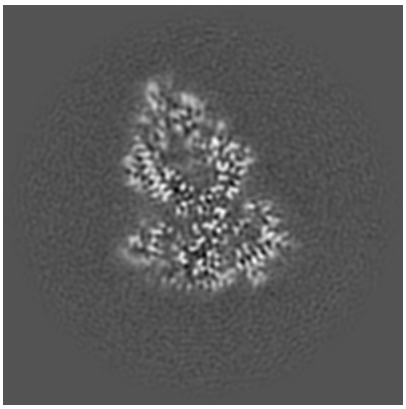


Z

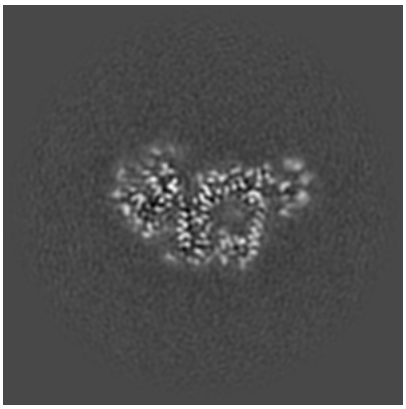
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

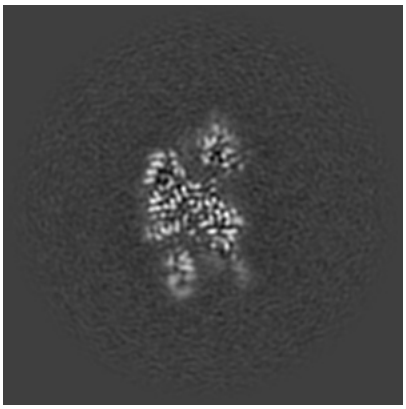
6.2.1 Primary map



X Index: 120

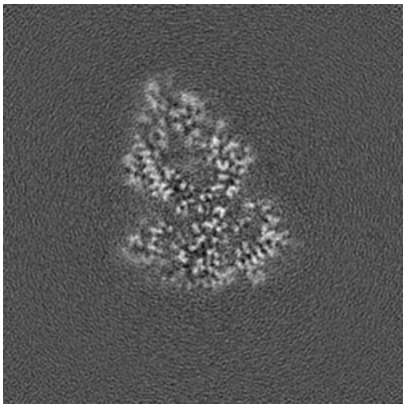


Y Index: 120

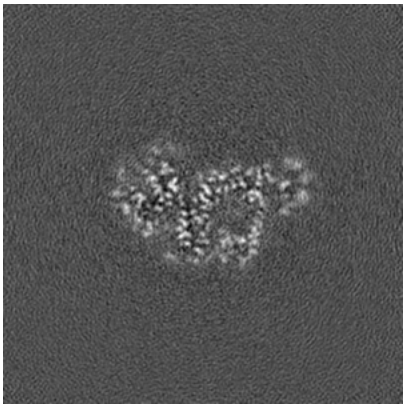


Z Index: 120

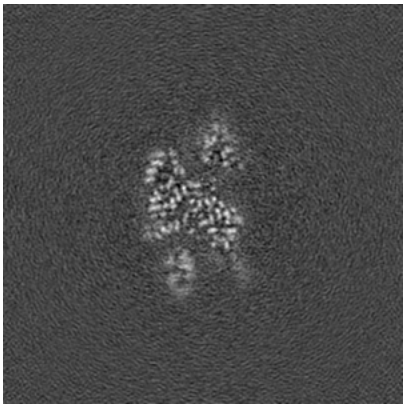
6.2.2 Raw map



X Index: 120



Y Index: 120

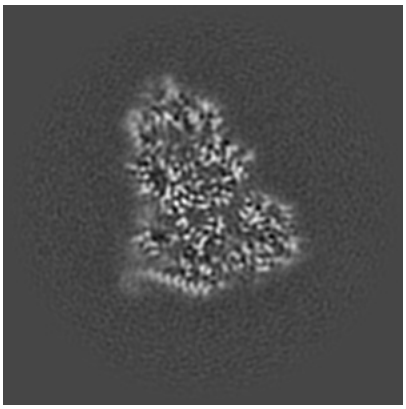


Z Index: 120

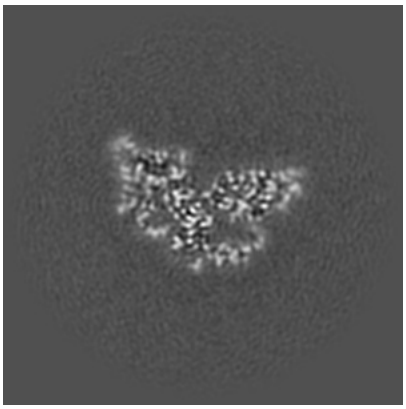
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

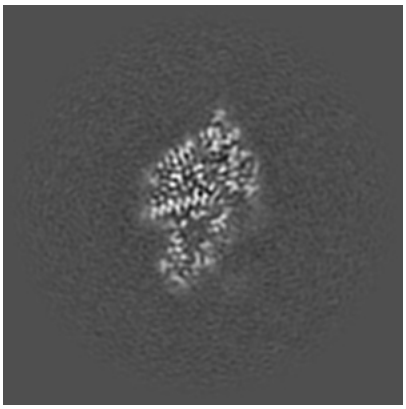
6.3.1 Primary map



X Index: 125

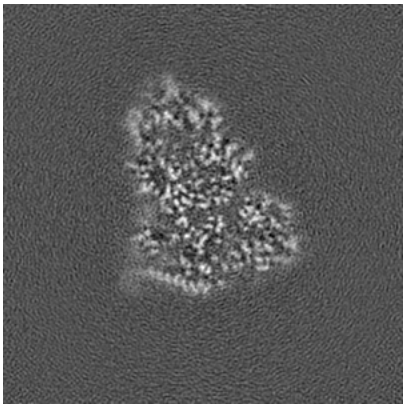


Y Index: 129

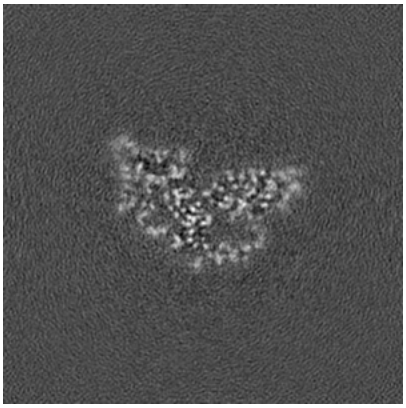


Z Index: 107

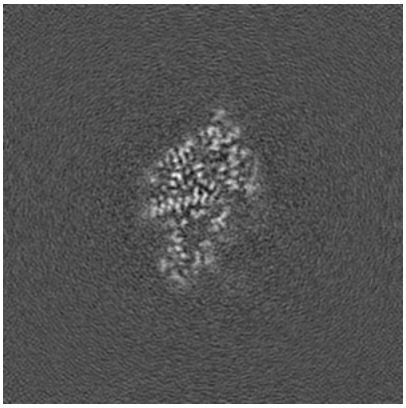
6.3.2 Raw map



X Index: 125



Y Index: 129

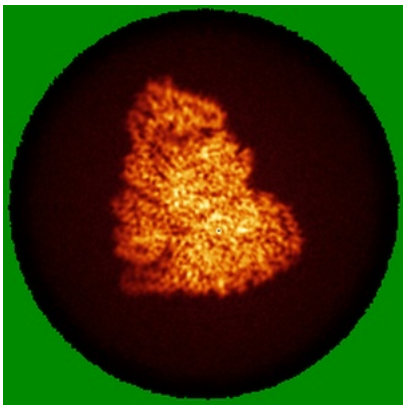


Z Index: 107

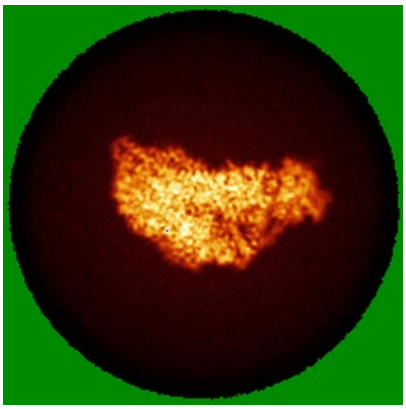
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

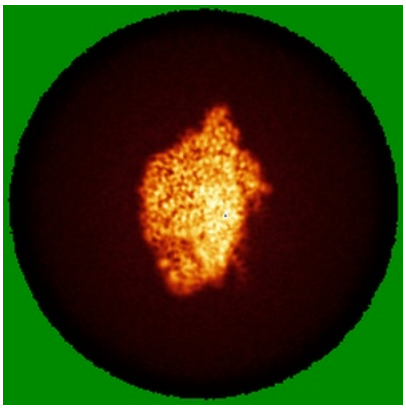
6.4.1 Primary map



X

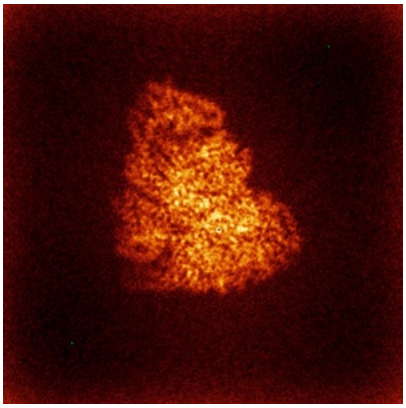


Y

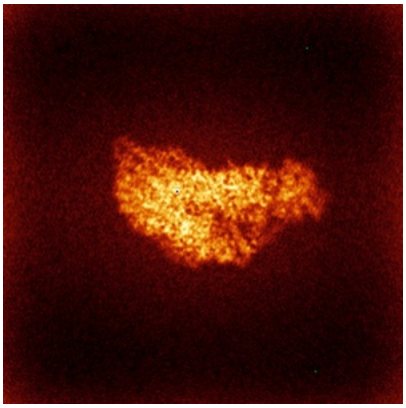


Z

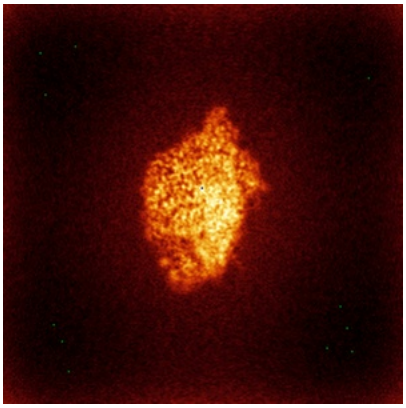
6.4.2 Raw map



X



Y

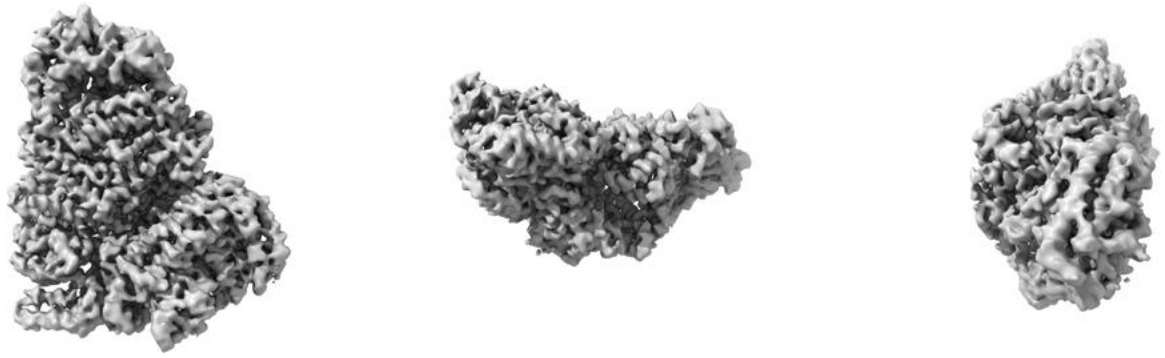


Z

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)

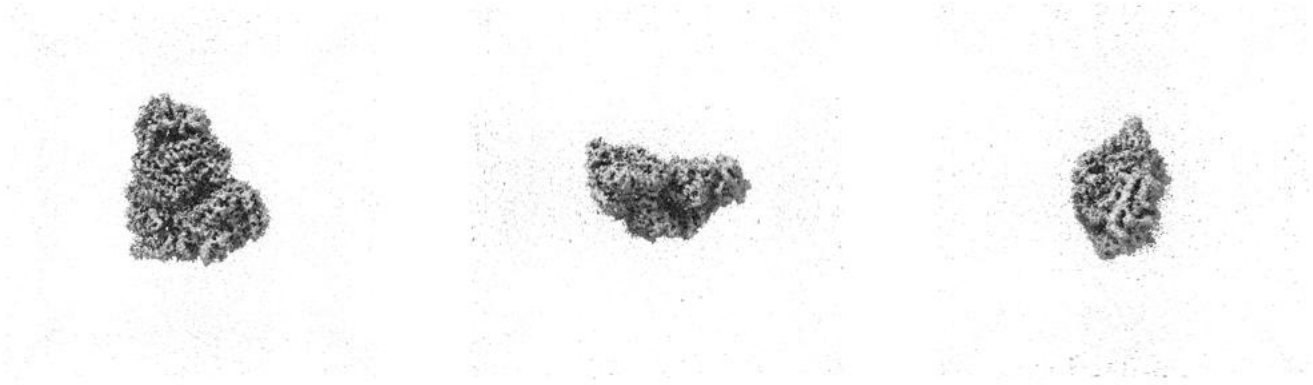
6.5.1 Primary map



X Y Z

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



X Y Z

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.

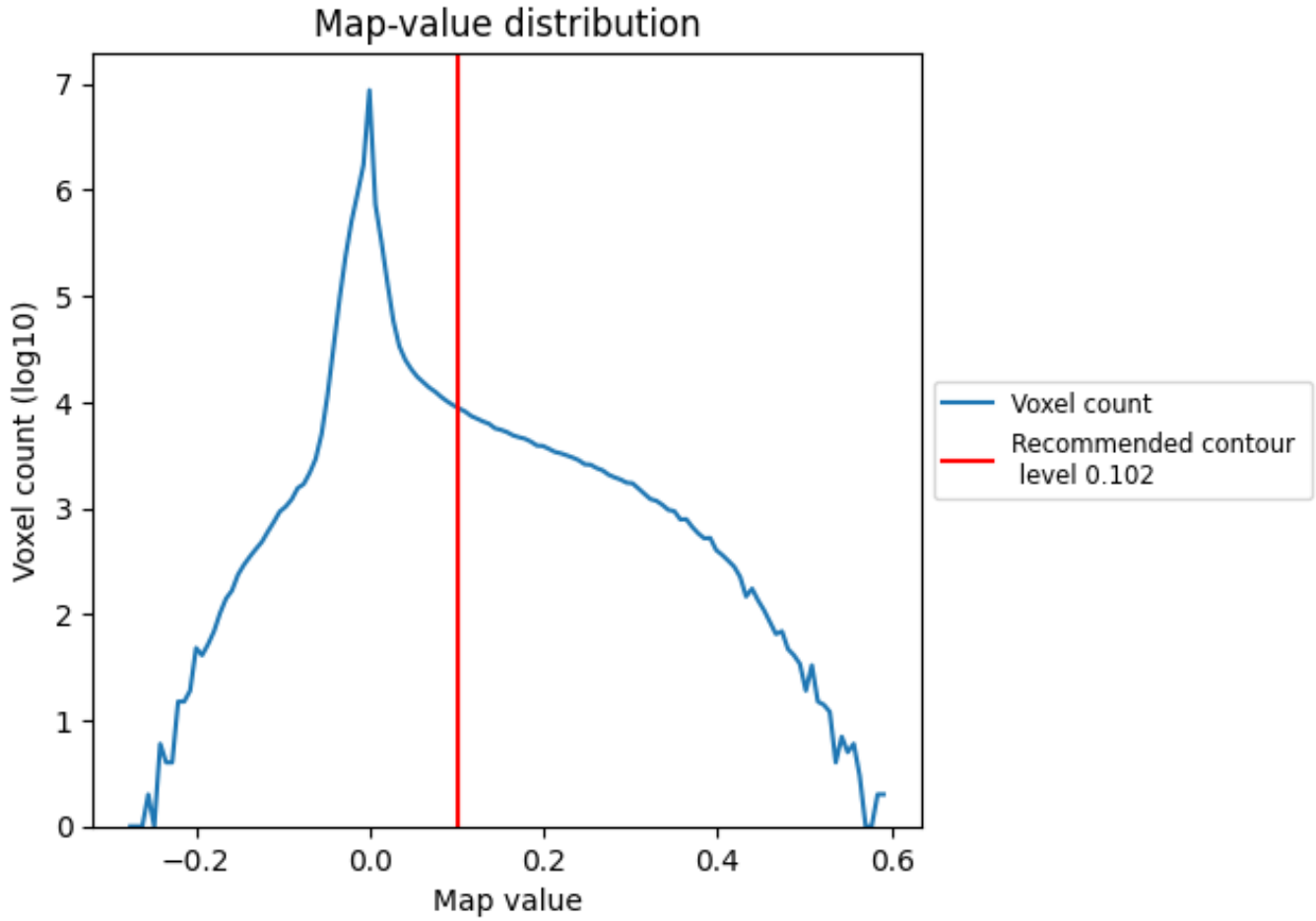
6.6 Mask visualisation (i)

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

7 Map analysis

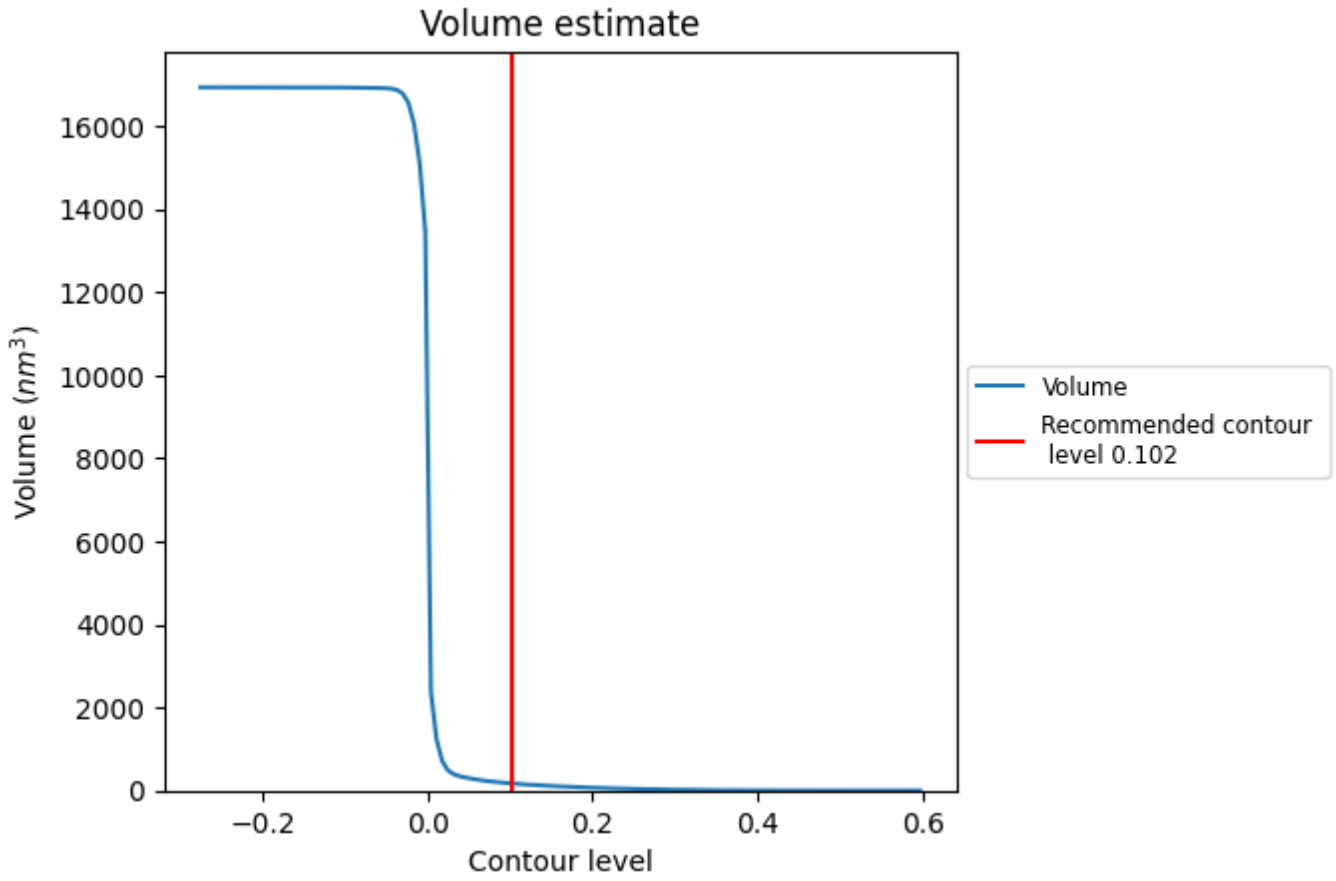
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

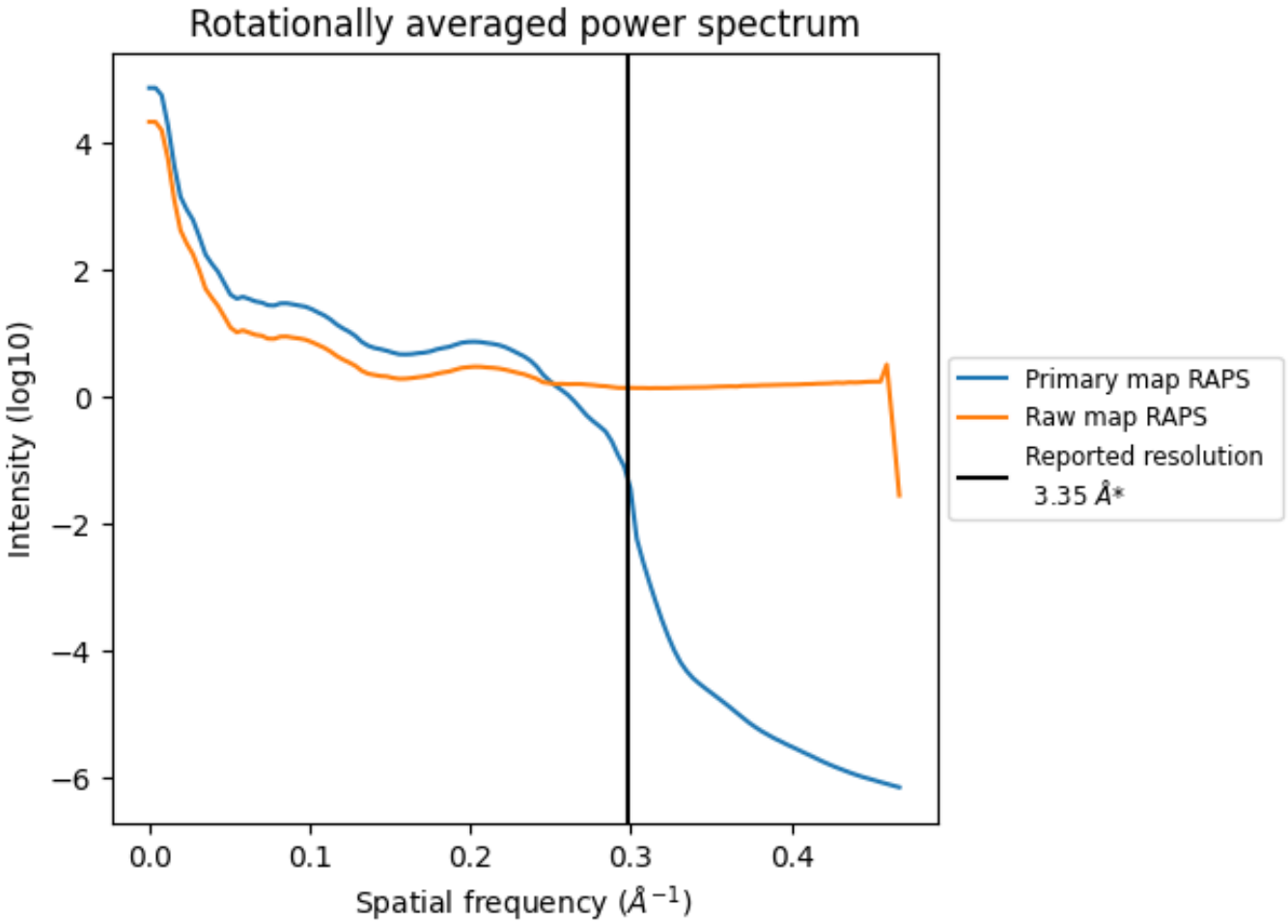
7.2 Volume estimate



The volume at the recommended contour level is 172 nm^3; 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 (i)

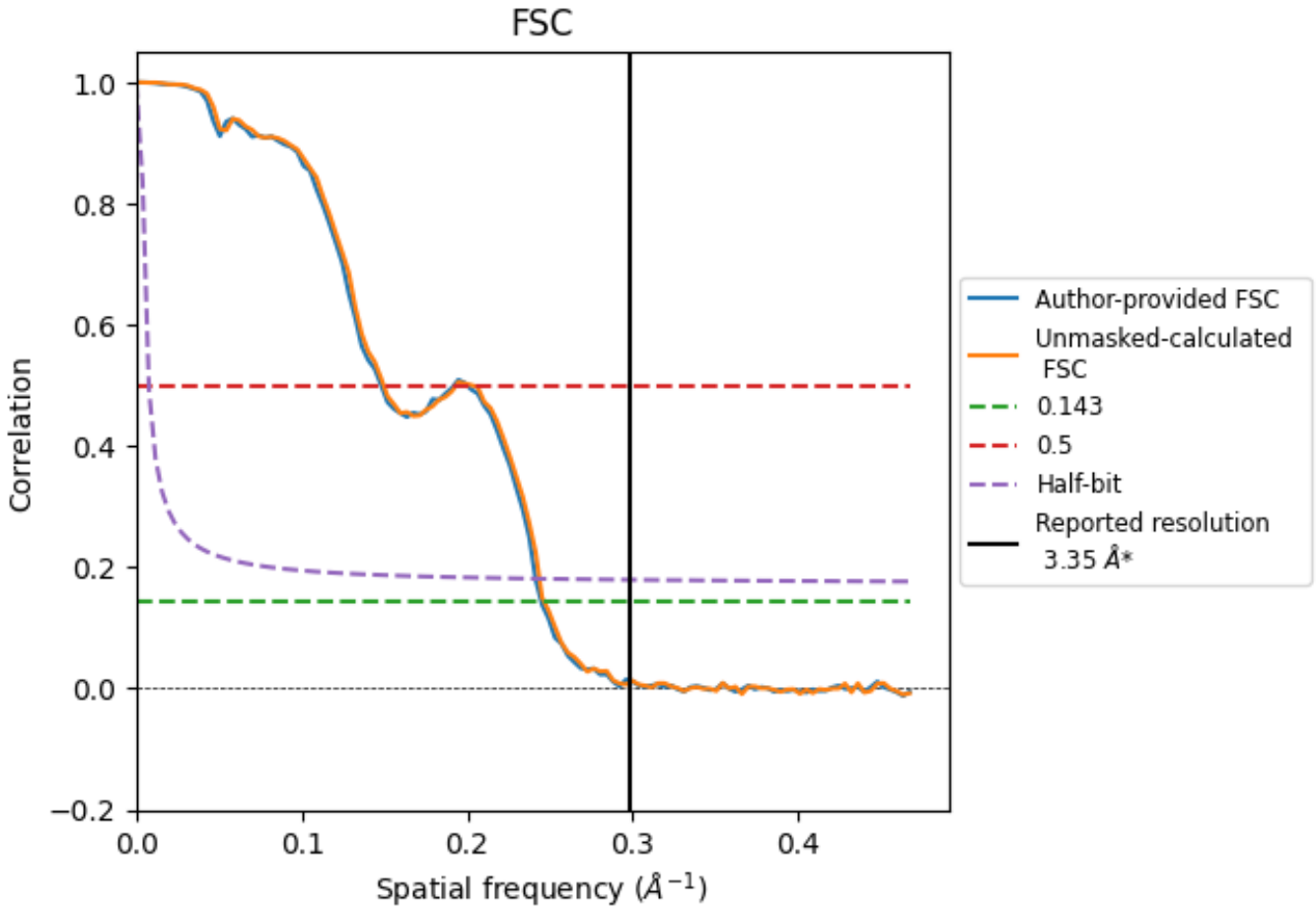


*Reported resolution corresponds to spatial frequency of 0.299 Å^{-1}

8 Fourier-Shell correlation

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



*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

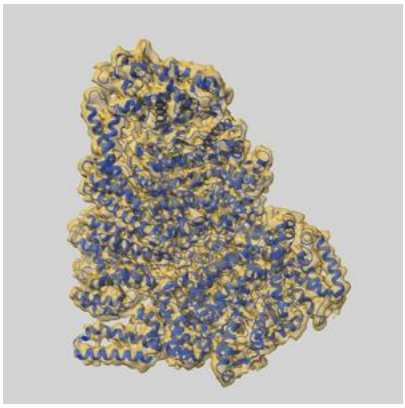
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.08 differs from the reported value 3.35 by more than 10 %

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 %

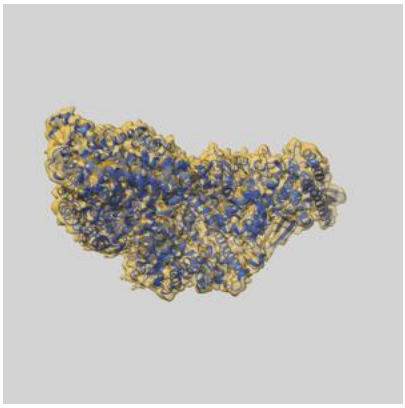
9 Map-model fit

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.

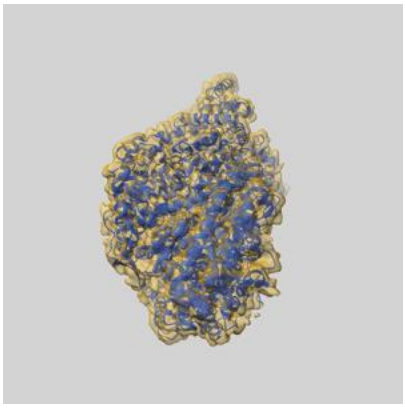
9.1 Map-model overlay



X



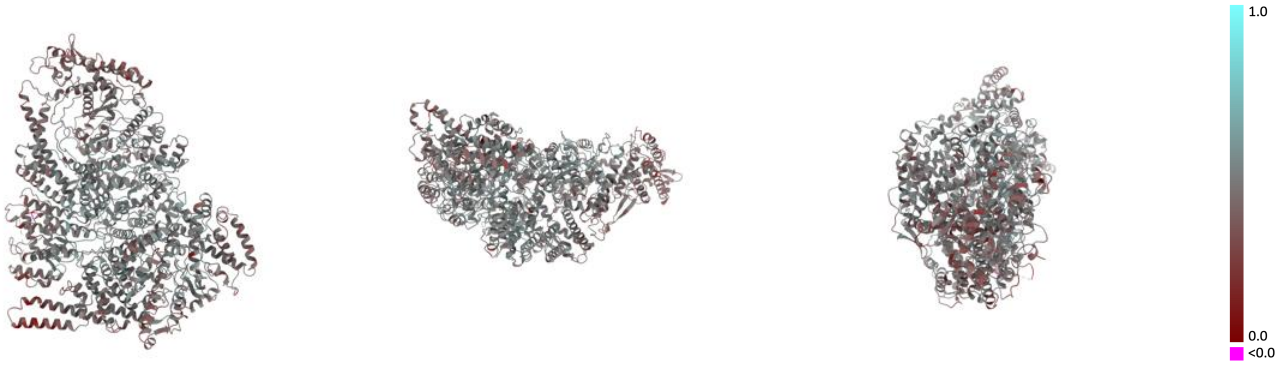
Y



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.

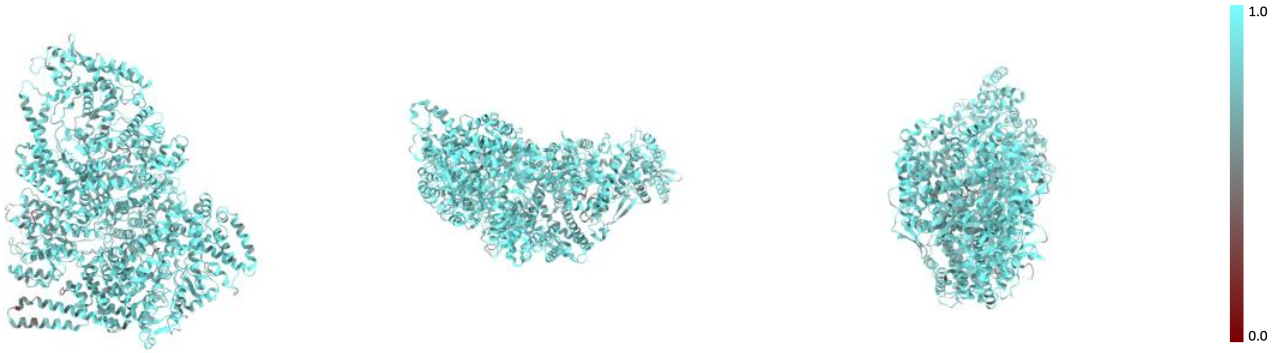
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

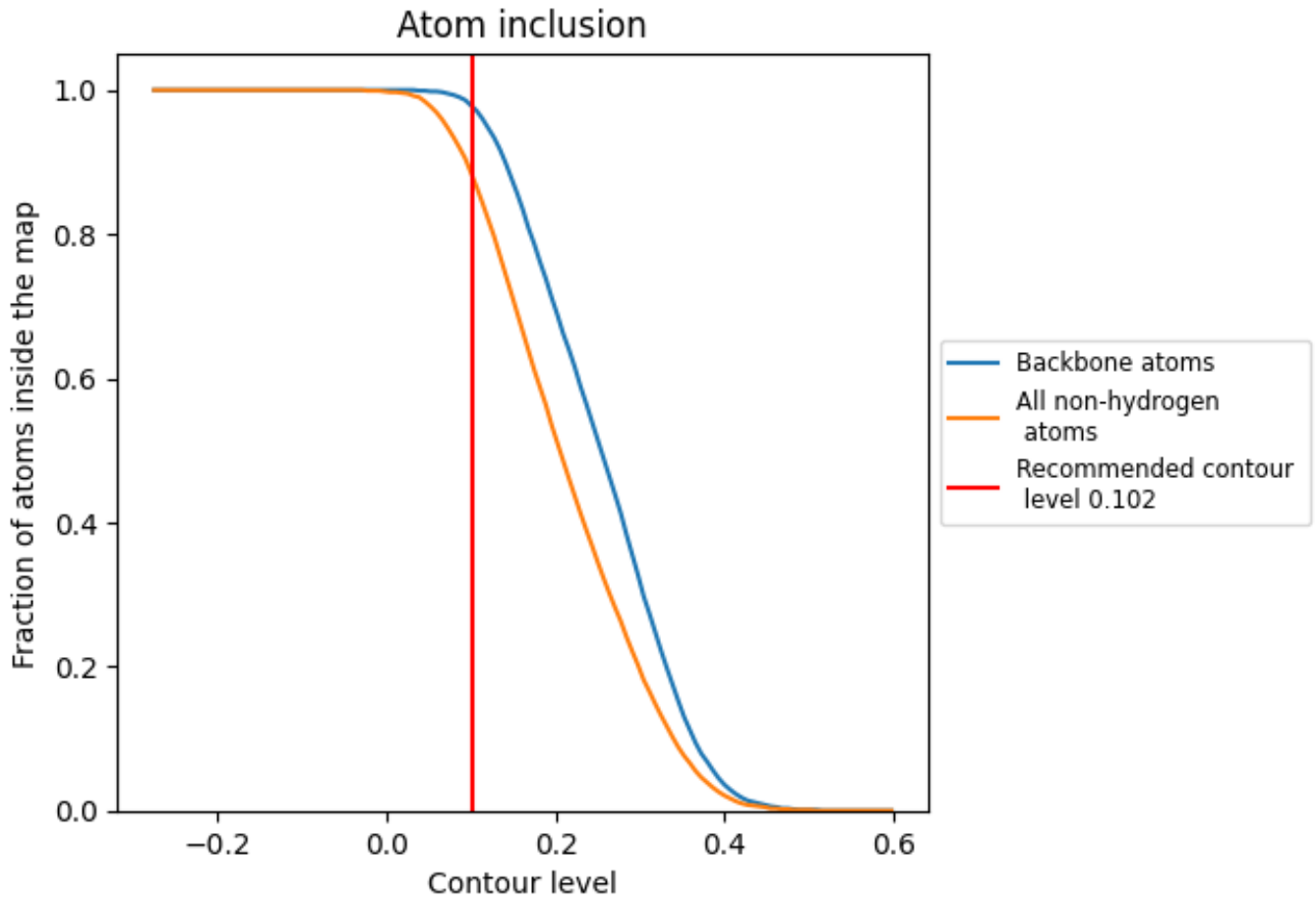
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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