



Full wwPDB EM Validation Report ⓘ

Dec 1, 2025 – 12:15 PM EST

PDB ID : 9PNW / pdb_00009pnw
EMDB ID : EMD-71774
Title : N4 vRNAP gp50 bound to P1 promoter - closed complex
Authors : Bellis, N.F.; Lokareddy, R.K.; Cingolani, G.
Deposited on : 2025-07-21
Resolution : 2.90 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.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

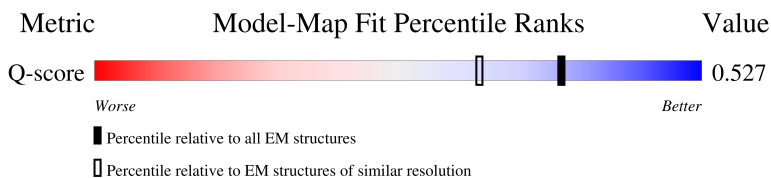
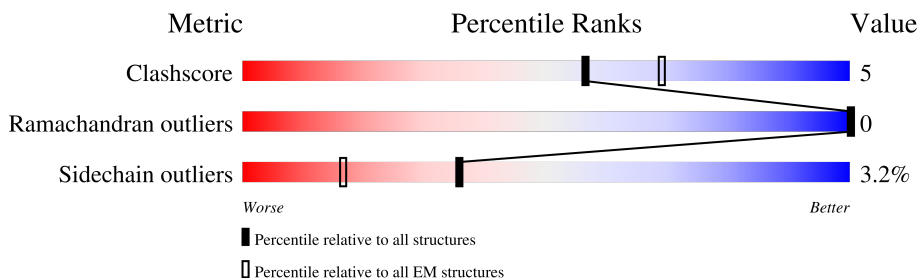
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	B	34	
2	A	3500	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19392 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 DNA chain called N4 P1 DNA Promoter.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	19	Total	C	N	O	P	0	0
			392	186	78	109	19		

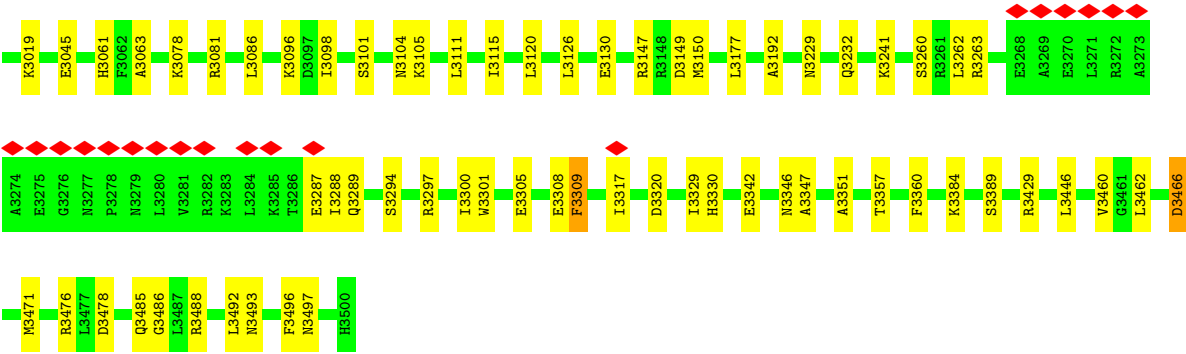
- Molecule 2 is a protein called Virion DNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	2443	Total	C	N	O	S	0	0
			19000	11931	3297	3681	91		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	3218	ALA	SER	conflict	UNP Q859P9





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	128569	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)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	0.306	Depositor
Minimum map value	-0.126	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0431	Depositor
Map size (\AA)	389.44, 389.44, 389.44	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.217, 1.217, 1.217	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	B	0.14	0/441	0.26	0/678
2	A	0.08	0/19302	0.23	0/26087
All	All	0.08	0/19743	0.23	0/26765

There are no bond length outliers.

There are no bond angle outliers.

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	B	392	0	213	1	0
2	A	19000	0	19100	182	0
All	All	19392	0	19313	182	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (182) 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)
2:A:2223:MET:HA	2:A:2223:MET:HE2	1.74	0.68
2:A:3007:ARG:NH2	2:A:3460:VAL:O	2.26	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2141:ILE:HG22	2:A:2142:ARG:HH21	1.62	0.65
2:A:3192:ALA:HB2	2:A:3330:HIS:HB2	1.81	0.62
2:A:2529:THR:HG23	2:A:2531:LEU:H	1.65	0.61
2:A:3466:ASP:O	2:A:3485:GLN:NE2	2.34	0.61
2:A:2012:ASP:N	2:A:2012:ASP:OD1	2.34	0.61
2:A:3262:LEU:HD21	2:A:3317:ILE:HG12	1.83	0.61
2:A:3301:TRP:NE1	2:A:3305:GLU:OE2	2.33	0.61
2:A:2012:ASP:HB2	2:A:2272:SER:HB3	1.82	0.60
2:A:2196:GLU:H	2:A:2199:GLU:HB2	1.66	0.60
2:A:2210:ASN:ND2	2:A:2213:ASP:OD1	2.34	0.60
2:A:3263:ARG:NH2	2:A:3287:GLU:OE2	2.34	0.60
2:A:1179:THR:HA	2:A:1256:MET:HE3	1.84	0.59
2:A:3471:MET:SD	2:A:3476:ARG:NH2	2.76	0.59
2:A:1358:LEU:O	2:A:1524:LYS:NZ	2.36	0.59
2:A:1431:GLN:HG2	2:A:1946:ILE:HG23	1.85	0.59
2:A:3493:ASN:O	2:A:3497:ASN:ND2	2.36	0.59
2:A:1566:MET:O	2:A:1570:THR:OG1	2.20	0.58
2:A:1417:THR:HG23	2:A:1419:VAL:H	1.67	0.58
2:A:3493:ASN:HB3	2:A:3496:PHE:HB3	1.85	0.58
2:A:2909:ASP:HB3	2:A:2912:THR:HG22	1.86	0.57
2:A:2213:ASP:OD1	2:A:2213:ASP:N	2.34	0.57
2:A:2556:LYS:HA	2:A:2559:LYS:HG3	1.86	0.56
2:A:2267:ARG:HD2	2:A:2267:ARG:H	1.70	0.56
2:A:3300:ILE:HD12	2:A:3309:PHE:HE2	1.70	0.56
2:A:2180:VAL:HG11	2:A:2219:VAL:HG22	1.86	0.56
2:A:1235:MET:O	2:A:1235:MET:HE3	2.06	0.56
2:A:2498:ASP:OD1	2:A:2498:ASP:N	2.36	0.55
2:A:2197:MET:O	2:A:2201:GLN:NE2	2.40	0.55
2:A:2351:GLN:NE2	2:A:2352:ALA:O	2.39	0.55
2:A:2174:TYR:HB2	2:A:2221:PRO:HG3	1.89	0.54
2:A:1179:THR:O	2:A:1263:ASN:ND2	2.40	0.54
2:A:2374:GLN:HG2	2:A:2375:PRO:HD2	1.90	0.54
2:A:1183:GLN:HA	2:A:1186:LEU:HD22	1.88	0.54
2:A:2678:GLN:NE2	2:A:2680:GLU:OE2	2.37	0.54
2:A:3096:LYS:HA	2:A:3096:LYS:HE2	1.90	0.54
2:A:1750:ARG:O	2:A:1751:LYS:HD2	2.08	0.53
2:A:1513:VAL:O	2:A:1517:ASN:ND2	2.42	0.53
2:A:2993:ASP:OD2	2:A:2996:THR:OG1	2.26	0.53
2:A:1112:ASP:HB2	2:A:1115:LYS:HB2	1.90	0.53
2:A:3460:VAL:HG23	2:A:3462:LEU:HG	1.91	0.53
2:A:2694:LYS:HE3	2:A:2694:LYS:HA	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:3147:ARG:NH2	2:A:3149:ASP:OD2	2.32	0.53
2:A:2137:SER:OG	2:A:2138:ALA:N	2.42	0.53
2:A:1124:ASN:OD1	2:A:1133:ASN:ND2	2.42	0.52
2:A:2491:GLU:OE2	2:A:2505:ARG:NH2	2.42	0.52
2:A:2730:ASP:OD2	2:A:3078:LYS:NZ	2.35	0.52
2:A:1017:VAL:O	2:A:1029:ASN:ND2	2.42	0.52
2:A:3342:GLU:OE2	2:A:3346:ASN:ND2	2.43	0.52
2:A:2182:GLU:OE2	2:A:2186:GLN:NE2	2.39	0.52
2:A:2494:MET:HE2	2:A:2497:PRO:HA	1.91	0.52
2:A:2786:SER:O	2:A:2790:LYS:NZ	2.43	0.52
2:A:2371:MET:O	2:A:2372:ARG:NH1	2.43	0.51
2:A:1750:ARG:C	2:A:1751:LYS:HD2	2.36	0.51
2:A:1056:ALA:HA	2:A:1090:MET:HE1	1.91	0.51
2:A:1371:ASP:O	2:A:1375:LYS:NZ	2.40	0.51
2:A:2362:ASN:O	2:A:2362:ASN:ND2	2.44	0.51
2:A:1781:ALA:O	2:A:1785:ASN:ND2	2.44	0.51
2:A:2921:ILE:HG13	2:A:2922:PRO:HD2	1.93	0.51
2:A:3007:ARG:HD3	2:A:3045:GLU:HG2	1.93	0.51
2:A:2761:GLY:O	2:A:2765:THR:OG1	2.21	0.51
2:A:1041:GLN:NE2	2:A:1043:SER:O	2.44	0.51
2:A:3320:ASP:N	2:A:3320:ASP:OD1	2.37	0.51
2:A:2067:ASN:O	2:A:2067:ASN:ND2	2.44	0.50
2:A:2146:LYS:HD3	2:A:2146:LYS:H	1.75	0.50
2:A:1461:GLN:OE1	2:A:1481:SER:OG	2.27	0.50
2:A:2212:ASP:HB3	2:A:3357:THR:HA	1.94	0.49
2:A:2697:GLN:HB3	2:A:2698:PRO:HD3	1.94	0.49
2:A:1075:ASN:OD1	2:A:1401:GLN:NE2	2.46	0.49
2:A:2347:TRP:CD1	2:A:2350:LYS:HE3	2.47	0.49
2:A:2396:GLU:OE1	2:A:2400:GLN:NE2	2.46	0.49
2:A:1170:LYS:HD3	2:A:1194:PHE:HD1	1.78	0.48
2:A:1391:LEU:HD13	2:A:1436:VAL:HG13	1.94	0.48
2:A:1062:ARG:NH2	2:A:1075:ASN:O	2.46	0.48
2:A:1668:ASN:HB3	2:A:1671:THR:HG22	1.96	0.48
2:A:1160:ARG:HD2	2:A:1272:ILE:HD11	1.95	0.48
2:A:1607:ASP:OD1	2:A:1607:ASP:N	2.35	0.47
2:A:2069:LYS:HD3	2:A:2069:LYS:HA	1.64	0.47
2:A:2143:ASN:HA	2:A:2146:LYS:HZ3	1.79	0.47
2:A:2153:THR:HG23	2:A:2154:GLN:HG3	1.95	0.47
2:A:2982:LEU:O	2:A:2983:GLN:HG3	2.14	0.47
2:A:3485:GLN:HE22	2:A:3488:ARG:HD3	1.79	0.47
2:A:2273:LYS:HZ3	2:A:2329:SER:HB3	1.77	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1480:MET:HE2	2:A:1480:MET:HB3	1.81	0.47
2:A:1487:LEU:HB3	2:A:1492:LEU:HD12	1.97	0.47
2:A:1786:MET:HE2	2:A:1786:MET:HB2	1.76	0.47
2:A:2071:ASP:OD1	2:A:2073:SER:OG	2.32	0.47
2:A:2641:SER:O	2:A:2641:SER:OG	2.33	0.47
2:A:1108:LEU:HD11	2:A:1142:PHE:HB2	1.97	0.47
2:A:3232:GLN:HG3	2:A:3492:LEU:HD11	1.97	0.47
2:A:3289:GLN:HA	2:A:3289:GLN:OE1	2.14	0.47
2:A:2418:VAL:HG11	2:A:2605:MET:HG2	1.97	0.47
2:A:2485:MET:HE1	2:A:2515:ILE:HG22	1.96	0.47
2:A:3241:LYS:HD3	2:A:3241:LYS:HA	1.65	0.47
2:A:3384:LYS:HE2	2:A:3384:LYS:HB2	1.83	0.47
2:A:2052:LEU:N	2:A:2066:ASN:OD1	2.48	0.46
2:A:1028:LYS:HE3	2:A:1028:LYS:HB3	1.74	0.46
2:A:2414:ARG:NH1	2:A:2598:ASP:OD1	2.48	0.46
2:A:2010:GLU:HG3	2:A:2279:ARG:HH21	1.80	0.46
2:A:1636:GLN:NE2	2:A:1785:ASN:OD1	2.37	0.46
2:A:1820:GLN:NE2	2:A:1867:ALA:O	2.49	0.46
2:A:1052:LEU:HD13	2:A:1094:GLU:HG2	1.98	0.46
2:A:1260:ASP:OD1	2:A:1260:ASP:N	2.48	0.46
2:A:1359:MET:HB3	2:A:1659:LEU:HD21	1.98	0.46
2:A:2150:LEU:HD12	2:A:2154:GLN:HB2	1.98	0.46
1:B:9:DA:H62	2:A:1174:ASP:HB3	1.81	0.45
2:A:1491:ASN:N	2:A:1491:ASN:OD1	2.49	0.45
2:A:3357:THR:HG23	2:A:3360:PHE:H	1.81	0.45
2:A:1256:MET:HG3	2:A:1259:ILE:HD11	1.98	0.45
2:A:2149:ASN:O	2:A:2149:ASN:ND2	2.49	0.45
2:A:1468:LEU:O	2:A:1523:ARG:NH1	2.49	0.45
2:A:2057:MET:HE2	2:A:2057:MET:HB3	1.75	0.44
2:A:2700:HIS:HE1	2:A:3081:ARG:HH11	1.65	0.44
2:A:2560:LYS:HE3	2:A:2560:LYS:HB2	1.81	0.44
2:A:1835:LYS:HA	2:A:1835:LYS:HD2	1.79	0.44
2:A:2271:ILE:HD12	2:A:2271:ILE:N	2.33	0.44
2:A:2737:HIS:O	2:A:2740:THR:OG1	2.35	0.44
2:A:2197:MET:H	2:A:2197:MET:HG2	1.62	0.44
2:A:1948:ASP:N	2:A:1948:ASP:OD1	2.50	0.44
2:A:1057:GLN:OE1	2:A:1064:ARG:NE	2.50	0.43
2:A:1085:ARG:HA	2:A:1085:ARG:HD2	1.63	0.43
2:A:1200:LEU:HD21	2:A:1900:MET:HB2	2.00	0.43
2:A:2556:LYS:HE3	2:A:2556:LYS:HB2	1.56	0.43
2:A:1597:ASN:OD1	2:A:1597:ASN:N	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2086:LYS:NZ	2:A:2090:GLU:OE2	2.51	0.43
2:A:1582:ILE:HD12	2:A:1582:ILE:HA	1.90	0.43
2:A:2146:LYS:H	2:A:2146:LYS:CD	2.32	0.43
2:A:2615:TYR:O	2:A:2616:ASP:HB3	2.18	0.43
2:A:2559:LYS:HE3	2:A:2559:LYS:HB3	1.86	0.43
2:A:1301:PHE:HB2	2:A:1411:HIS:HB2	2.00	0.43
2:A:1841:LYS:HE2	2:A:1841:LYS:HB3	1.81	0.43
2:A:2996:THR:HG22	2:A:3126:LEU:HD13	2.00	0.43
2:A:1042:LYS:HD2	2:A:1042:LYS:HA	1.83	0.43
2:A:2589:LYS:HB2	2:A:2589:LYS:HE2	1.76	0.43
2:A:3149:ASP:OD1	2:A:3150:MET:N	2.51	0.43
2:A:2409:VAL:HA	2:A:2584:MET:HE1	2.01	0.42
2:A:2615:TYR:C	2:A:2617:ALA:H	2.27	0.42
2:A:3476:ARG:NH1	2:A:3478:ASP:OD1	2.51	0.42
2:A:1945:LYS:H	2:A:1945:LYS:HG2	1.70	0.42
2:A:2423:ARG:NH2	2:A:2602:GLU:OE1	2.35	0.42
2:A:3229:ASN:OD1	2:A:3429:ARG:NH2	2.43	0.42
2:A:3347:ALA:HB3	2:A:3351:ALA:HB2	2.00	0.42
2:A:3485:GLN:NE2	2:A:3486:GLY:H	2.17	0.42
2:A:1543:ASP:OD1	2:A:1545:SER:OG	2.37	0.42
2:A:3111:LEU:HD23	2:A:3111:LEU:HA	1.85	0.42
2:A:1016:LEU:HD23	2:A:1016:LEU:HA	1.89	0.42
2:A:1475:MET:HE2	2:A:1475:MET:HB3	1.76	0.42
2:A:1764:LYS:HD2	2:A:1764:LYS:HA	1.80	0.42
2:A:2953:TYR:HB3	2:A:2964:LYS:HB2	2.01	0.42
2:A:1084:LYS:HD3	2:A:1084:LYS:HA	1.79	0.42
2:A:2760:THR:HG23	2:A:2764:LYS:HD3	2.02	0.41
2:A:3098:ILE:HD13	2:A:3098:ILE:HA	1.87	0.41
2:A:1163:ALA:O	2:A:1167:THR:HG23	2.20	0.41
2:A:3101:SER:OG	2:A:3104:ASN:OD1	2.38	0.41
2:A:3471:MET:HB2	2:A:3476:ARG:HH21	1.85	0.41
2:A:2902:GLU:OE1	2:A:2990:GLY:N	2.41	0.41
2:A:2960:ARG:HB2	2:A:2960:ARG:CZ	2.50	0.41
2:A:2981:ILE:CD1	2:A:2983:GLN:HB3	2.51	0.41
2:A:1170:LYS:HD3	2:A:1194:PHE:CD1	2.56	0.41
2:A:1575:THR:HG22	2:A:1577:ASP:H	1.85	0.41
2:A:1430:PRO:O	2:A:1437:ARG:HD3	2.20	0.41
2:A:2333:GLN:NE2	2:A:2337:ASP:OD1	2.46	0.41
2:A:2360:PHE:HB2	2:A:2363:LEU:HB2	2.01	0.41
2:A:1052:LEU:HD23	2:A:1052:LEU:HA	1.93	0.41
2:A:1293:LEU:HD12	2:A:1293:LEU:HA	1.82	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2519:ASN:HD22	2:A:2519:ASN:HA	1.69	0.41
2:A:3086:LEU:HD23	2:A:3446:LEU:HB2	2.03	0.41
2:A:1648:LEU:HD12	2:A:1648:LEU:HA	1.93	0.41
2:A:2771:ARG:HD2	2:A:2771:ARG:HA	1.71	0.41
2:A:3061:HIS:CE1	2:A:3063:ALA:HB3	2.56	0.41
2:A:3115:ILE:HG21	2:A:3120:LEU:HD12	2.02	0.41
2:A:3263:ARG:HD2	2:A:3263:ARG:HA	1.86	0.41
2:A:3288:ILE:H	2:A:3288:ILE:HG12	1.73	0.41
2:A:1417:THR:HG22	2:A:1421:ARG:H	1.87	0.40
2:A:1567:MET:HE3	2:A:1567:MET:HB3	1.87	0.40
2:A:2101:LYS:HE3	2:A:2101:LYS:HB3	1.72	0.40
2:A:2796:LEU:HD12	2:A:2796:LEU:HA	1.94	0.40
2:A:3294:SER:HA	2:A:3297:ARG:HH11	1.86	0.40
2:A:1711:ILE:H	2:A:1711:ILE:HG12	1.68	0.40
2:A:1511:ASN:OD1	2:A:1511:ASN:N	2.50	0.40
2:A:3262:LEU:HD23	2:A:3262:LEU:HA	1.83	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	
2	A	2435/3500 (70%)	2395 (98%)	40 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	A	2047/2874 (71%)	1982 (97%)	65 (3%)	34	69

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	1089	LEU
2	A	1135	VAL
2	A	1190	LEU
2	A	1283	SER
2	A	1297	THR
2	A	1309	VAL
2	A	1322	THR
2	A	1339	VAL
2	A	1450	SER
2	A	1491	ASN
2	A	1549	THR
2	A	1553	VAL
2	A	1597	ASN
2	A	1601	SER
2	A	1667	LYS
2	A	1688	SER
2	A	1852	THR
2	A	1871	GLU
2	A	1900	MET
2	A	1929	MET
2	A	1933	LEU
2	A	1971	SER
2	A	2018	THR
2	A	2053	SER
2	A	2073	SER
2	A	2099	VAL
2	A	2153	THR
2	A	2160	GLU
2	A	2176	THR
2	A	2190	THR
2	A	2197	MET
2	A	2205	ILE
2	A	2210	ASN
2	A	2213	ASP
2	A	2257	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A	2321	LEU
2	A	2328	THR
2	A	2344	LYS
2	A	2373	SER
2	A	2420	GLU
2	A	2507	TYR
2	A	2549	ILE
2	A	2554	VAL
2	A	2570	THR
2	A	2602	GLU
2	A	2616	ASP
2	A	2620	THR
2	A	2716	VAL
2	A	2723	VAL
2	A	2787	LYS
2	A	2816	LYS
2	A	2868	LEU
2	A	2886	GLU
2	A	2964	LYS
2	A	3009	THR
2	A	3019	LYS
2	A	3105	LYS
2	A	3130	GLU
2	A	3177	LEU
2	A	3260	SER
2	A	3308	GLU
2	A	3309	PHE
2	A	3329	ILE
2	A	3389	SER
2	A	3466	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	1158	GLN
2	A	1263	ASN
2	A	1333	GLN
2	A	1381	ASN
2	A	1853	GLN
2	A	1973	GLN
2	A	1979	ASN
2	A	2056	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	A	2065	GLN
2	A	2258	ASN
2	A	2325	GLN
2	A	2402	ASN
2	A	2581	ASN
2	A	2697	GLN
2	A	2737	HIS
2	A	2807	ASN
2	A	3232	GLN
2	A	3255	ASN
2	A	3277	ASN
2	A	3396	GLN
2	A	3403	ASN
2	A	3485	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

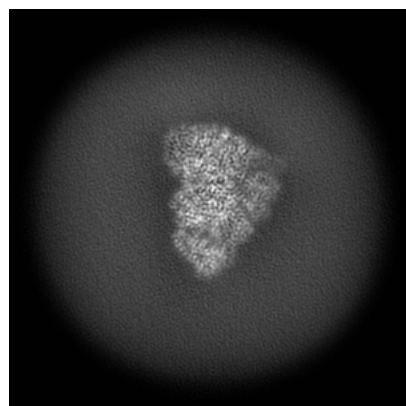
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71774. These allow visual inspection of the internal detail of the map and identification of artifacts.

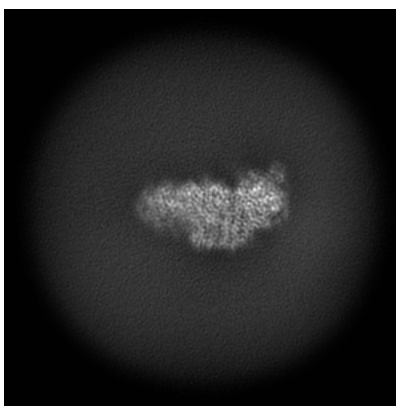
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

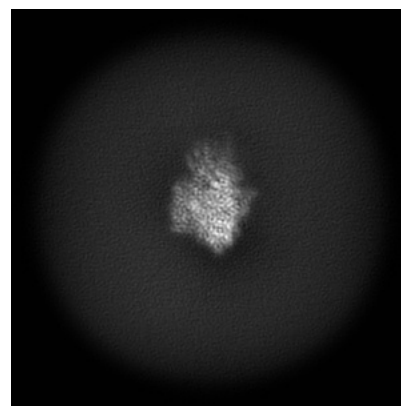
6.1.1 Primary map



X

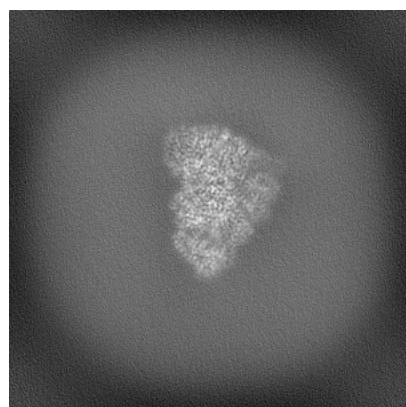


Y

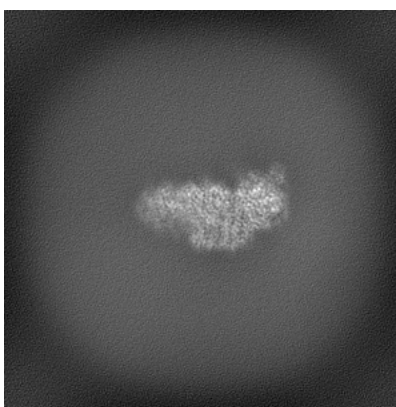


Z

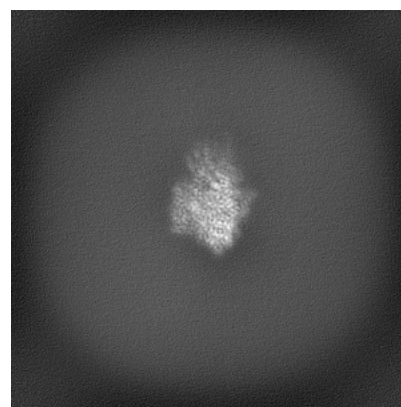
6.1.2 Raw map



X



Y

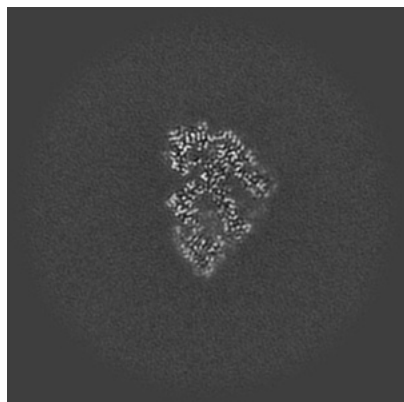


Z

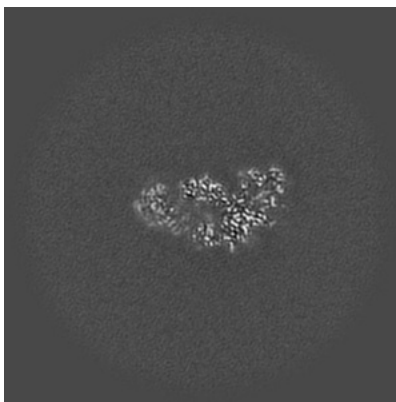
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

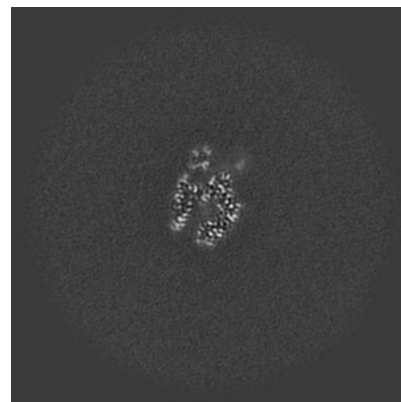
6.2.1 Primary map



X Index: 160

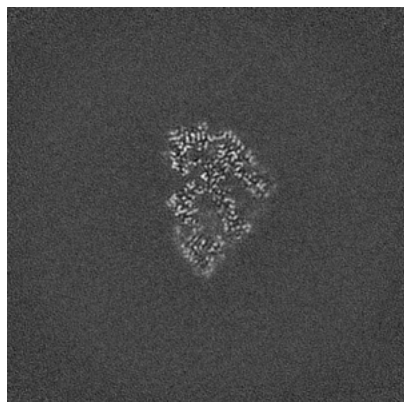


Y Index: 160

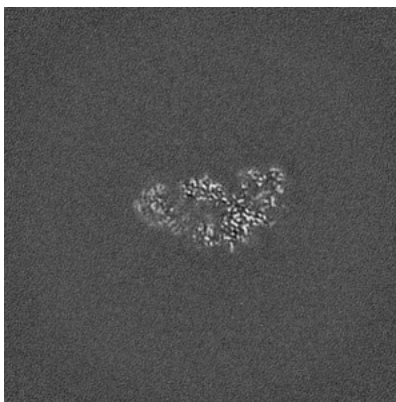


Z Index: 160

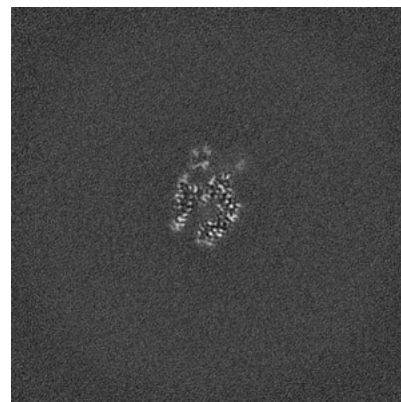
6.2.2 Raw map



X Index: 160



Y Index: 160

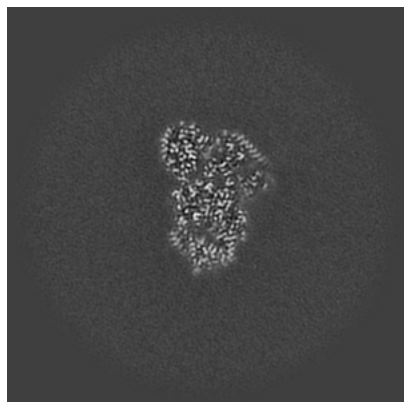


Z Index: 160

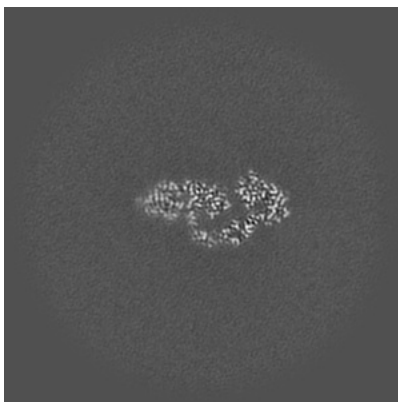
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

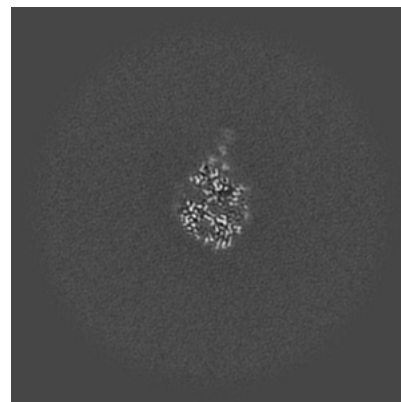
6.3.1 Primary map



X Index: 166

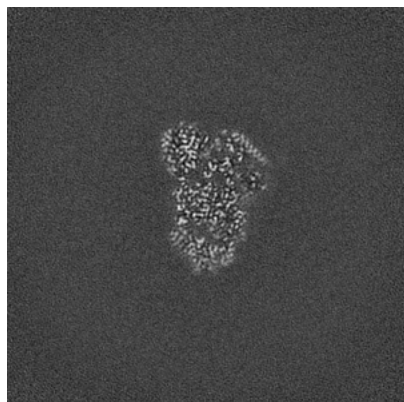


Y Index: 149

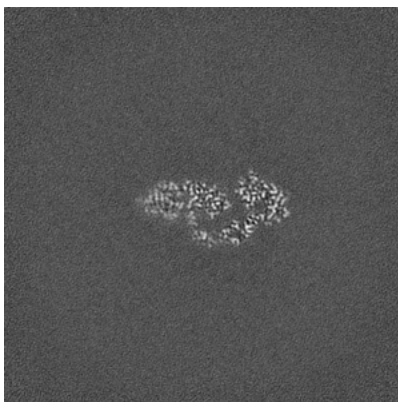


Z Index: 195

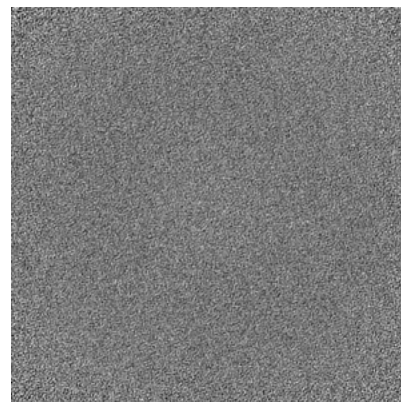
6.3.2 Raw map



X Index: 167



Y Index: 149

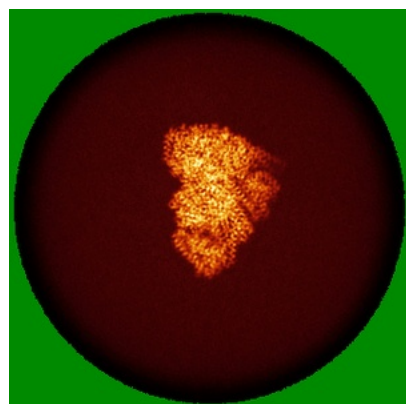


Z Index: 0

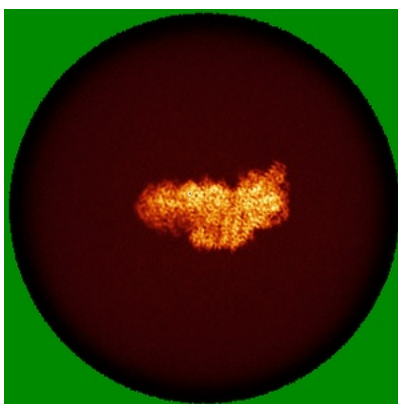
The images above show the largest variance slices of the map in three orthogonal directions.

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

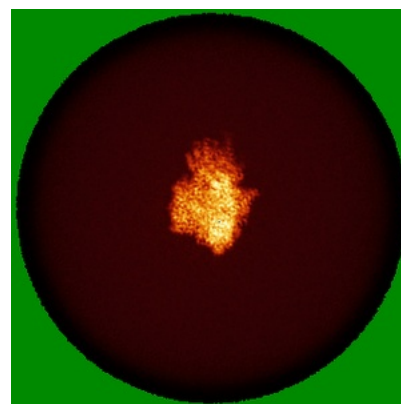
6.4.1 Primary map



X

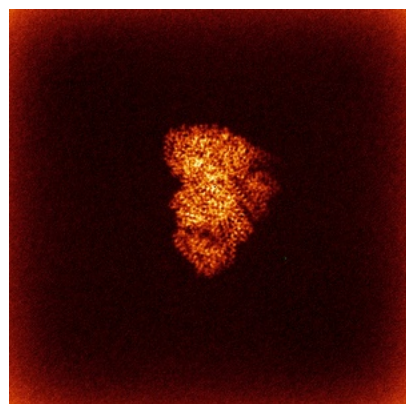


Y

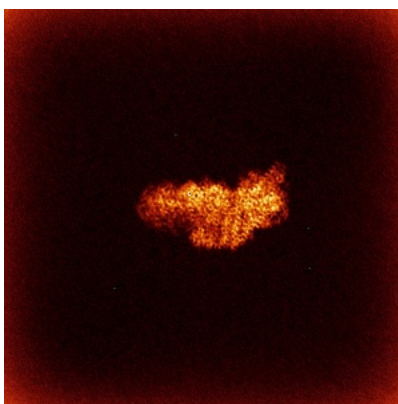


Z

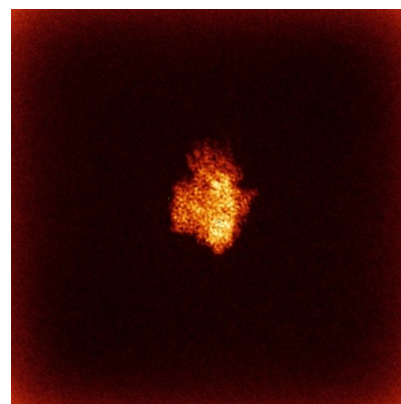
6.4.2 Raw map



X



Y

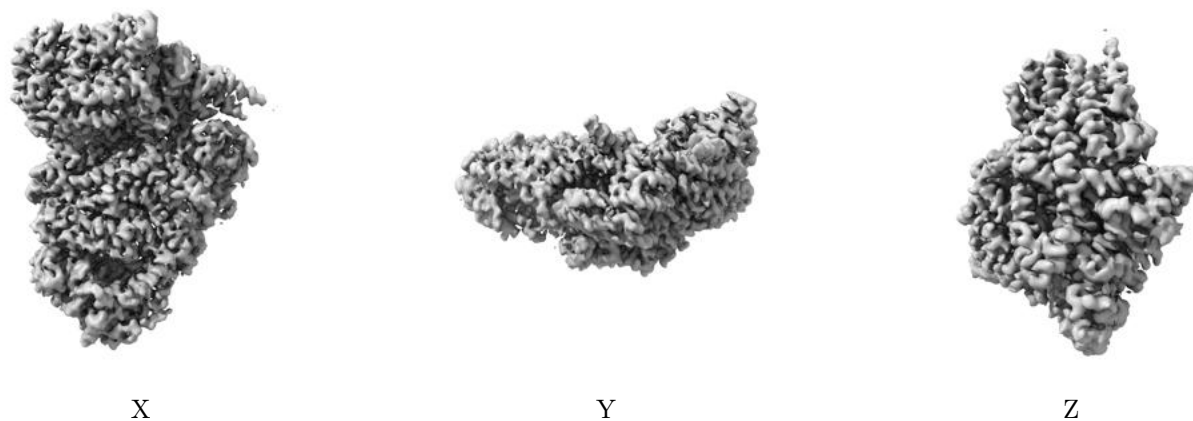


Z

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.

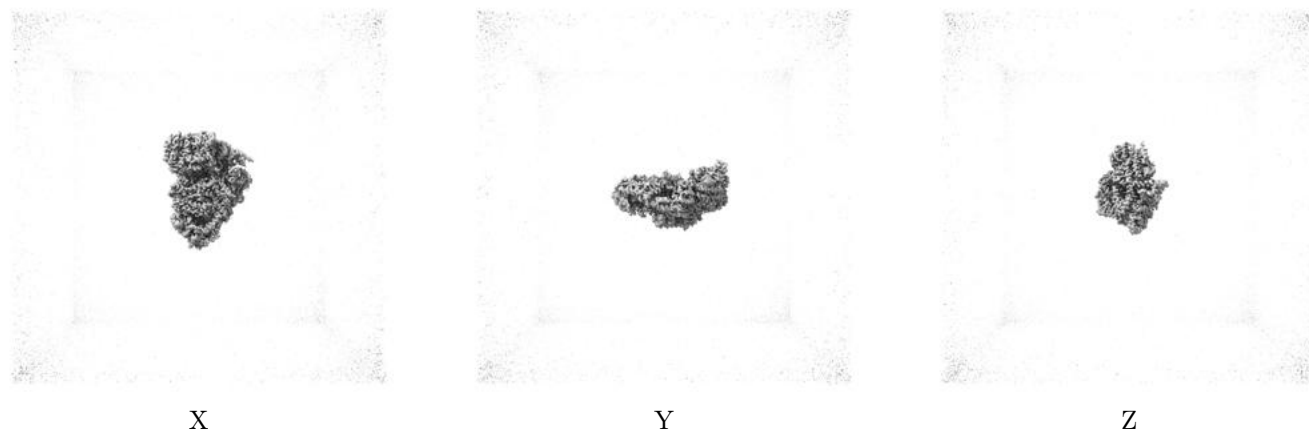
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0431. 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.

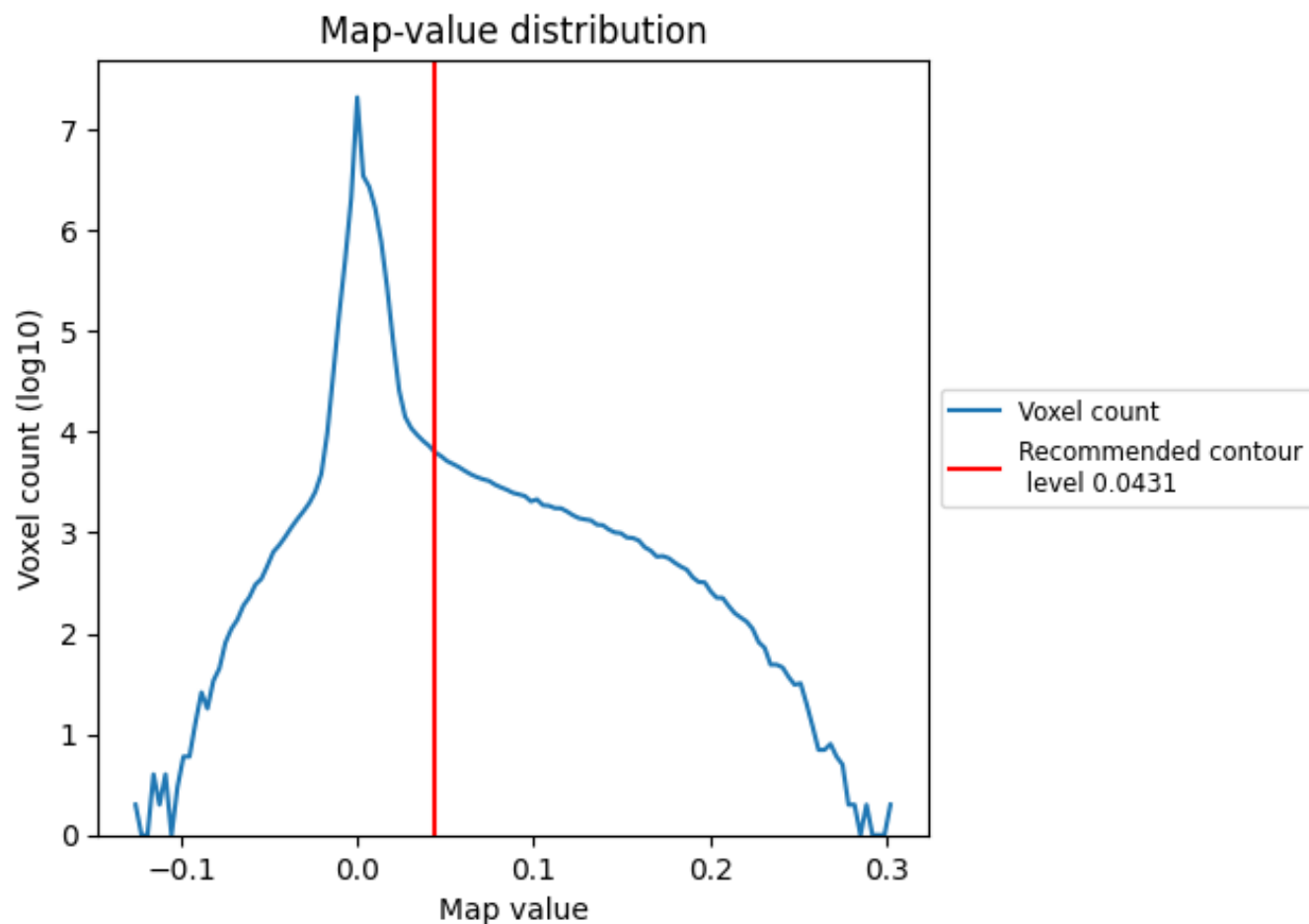
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

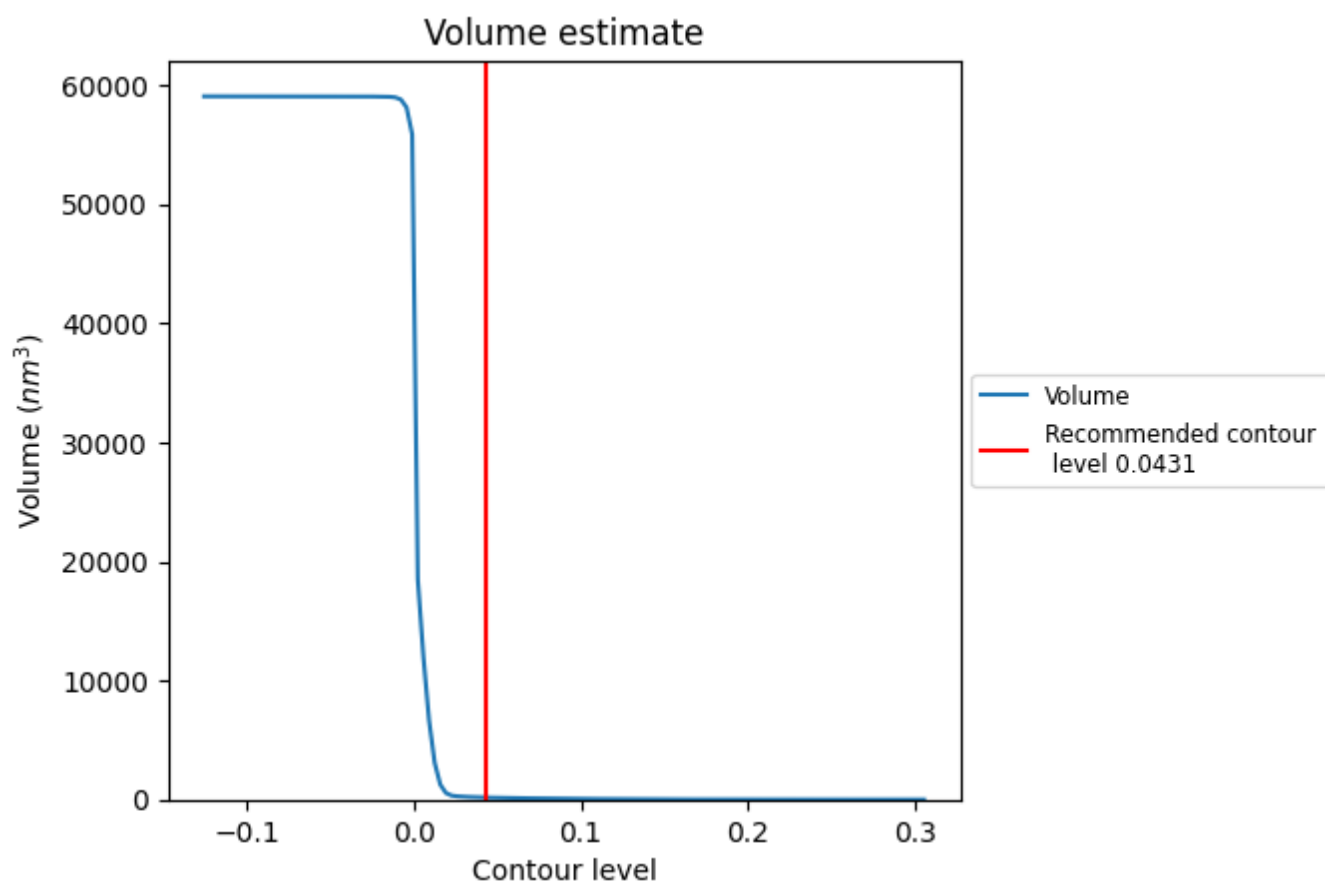
This section contains the results of statistical analysis of the map.

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.

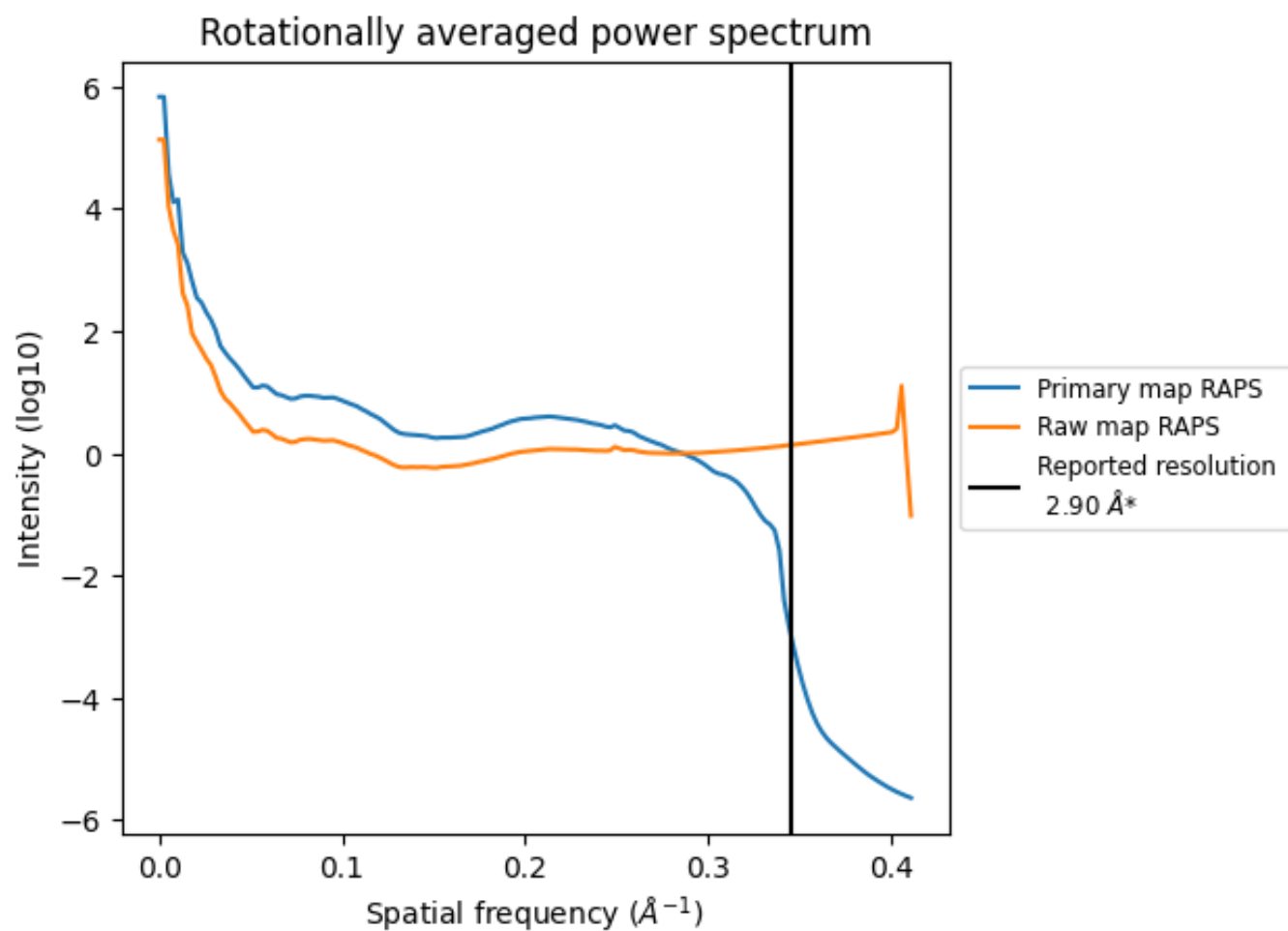
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 173 nm³; this corresponds to an approximate mass of 157 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 ⓘ

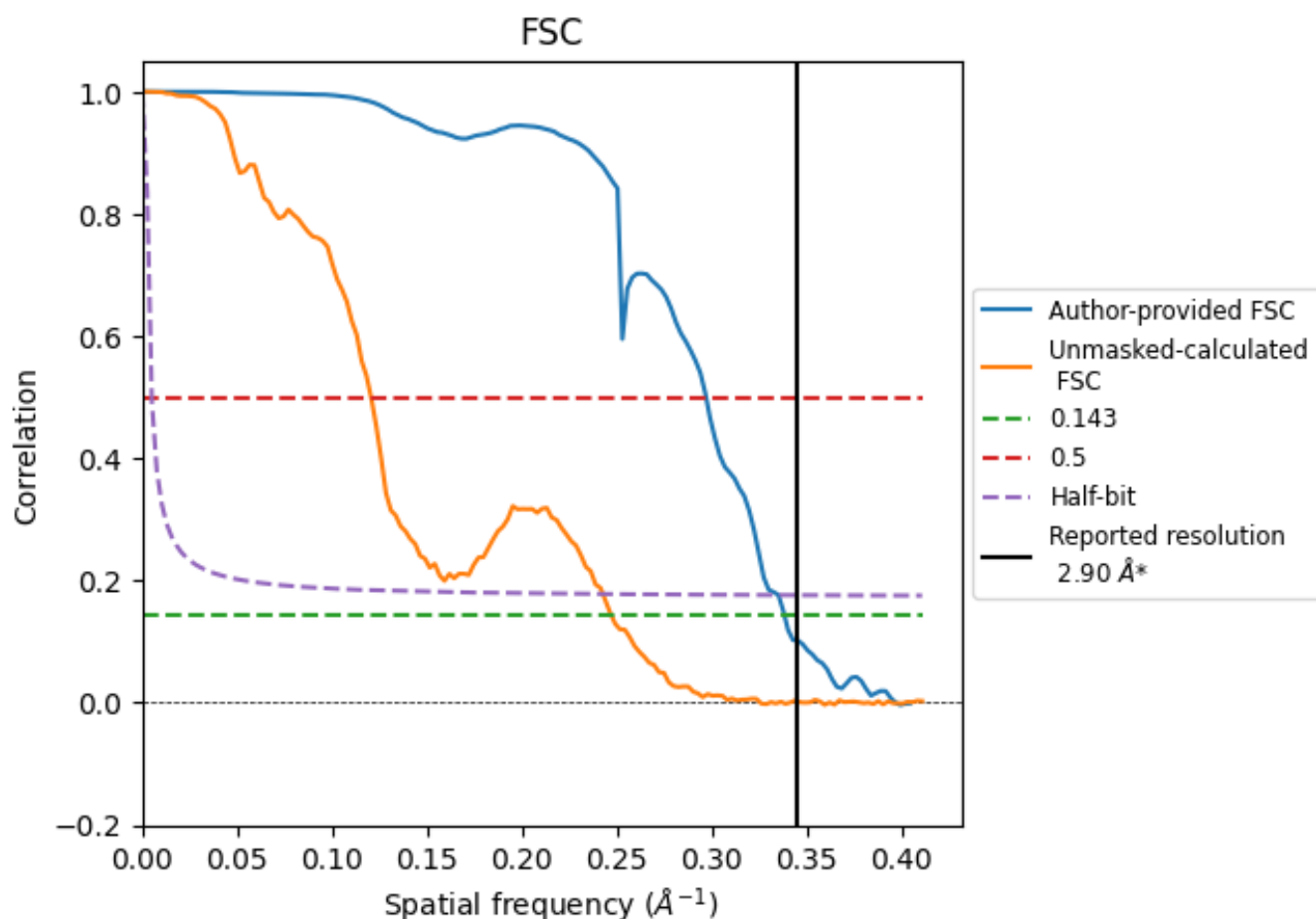


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 \AA^{-1}

8.2 Resolution estimates [i](#)

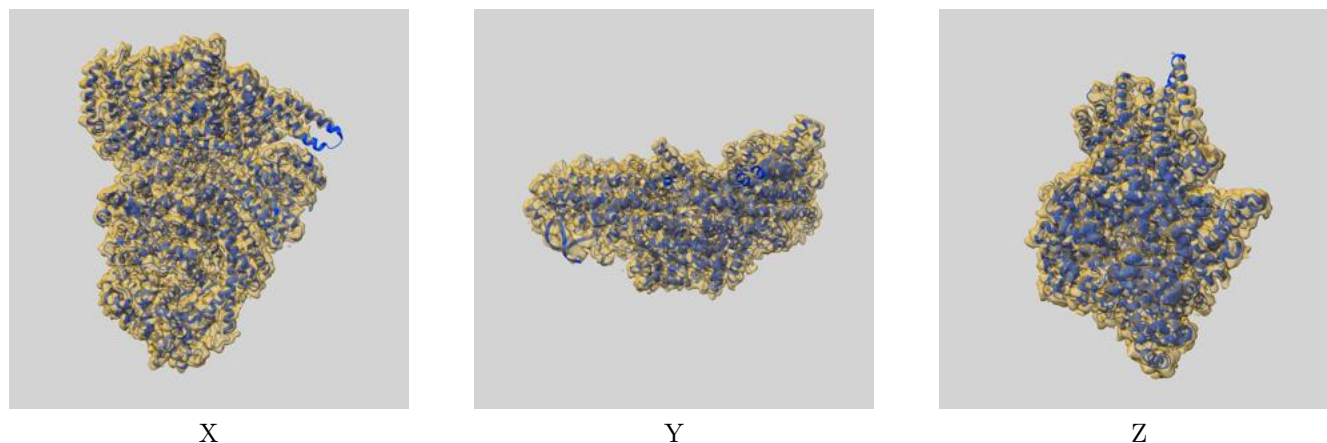
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.96	3.37	2.98
Unmasked-calculated*	4.05	8.30	4.12

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.05 differs from the reported value 2.9 by more than 10 %

9 Map-model fit [i](#)

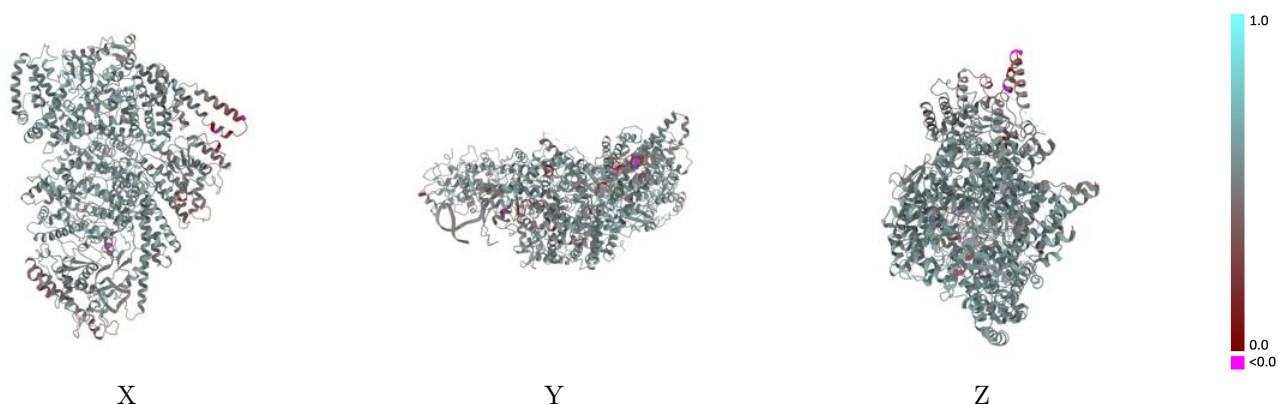
This section contains information regarding the fit between EMDB map EMD-71774 and PDB model 9PNW. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



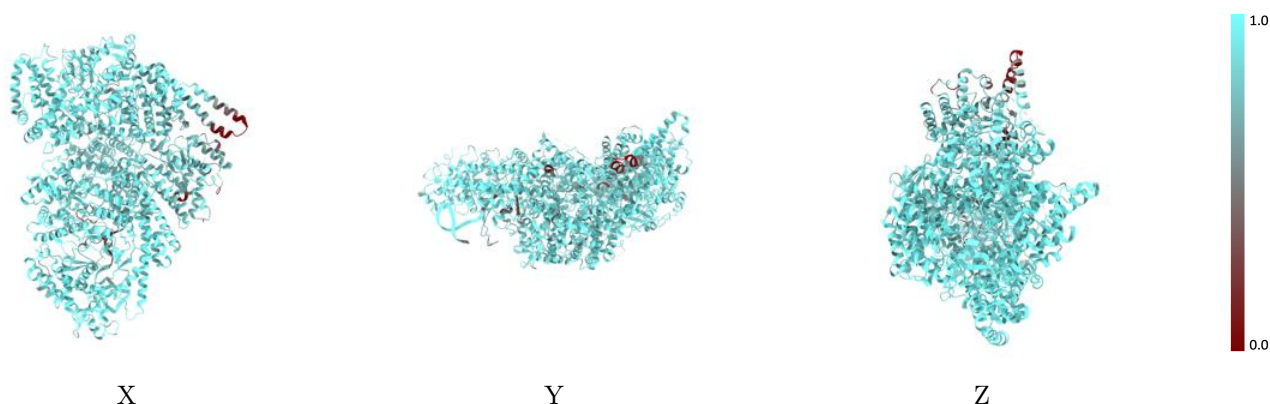
The images above show the 3D surface view of the map at the recommended contour level 0.0431 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



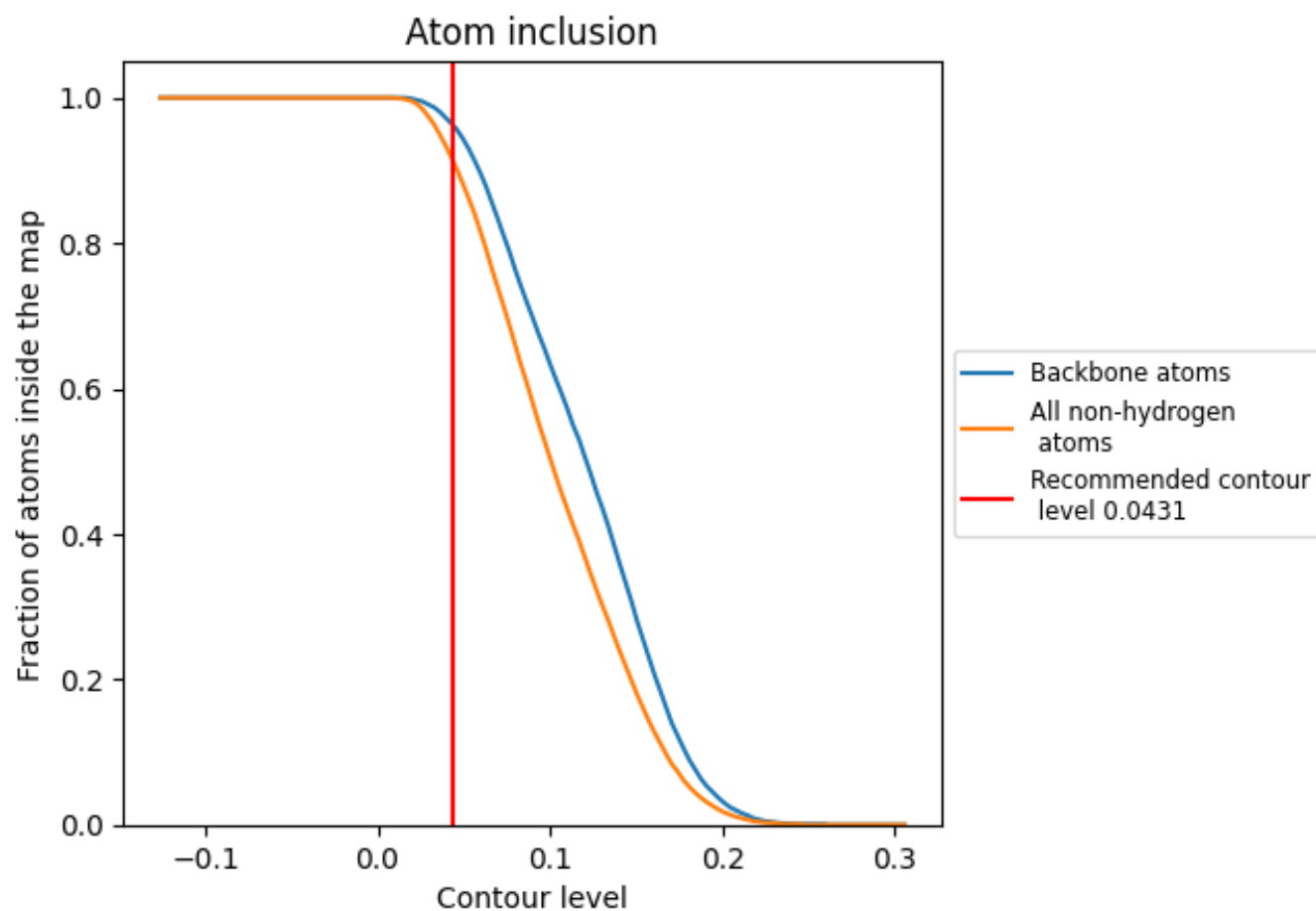
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0431).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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 (0.0431) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.9170	<div></div> 0.5270
A	<div></div> 0.9210	<div></div> 0.5290
B	<div></div> 0.7170	<div></div> 0.4330

