



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 06:39 AM UTC

PDB ID : 6EZ8 / pdb_00006ez8
EMDB ID : EMD-3984
Title : Human Huntingtin-HAP40 complex structure
Authors : Guo, Q.; Bin, H.; Cheng, J.; Pfeifer, G.; Baumeister, W.; Fernandez-Busnadi
ego, R.; Kochanek, S.
Deposited on : 2017-11-14
Resolution : 4.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

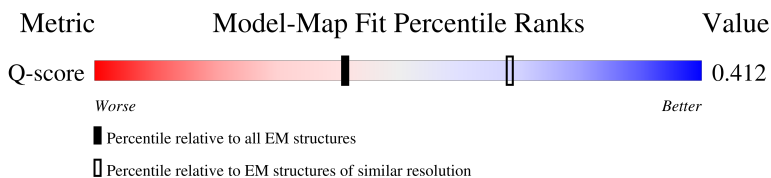
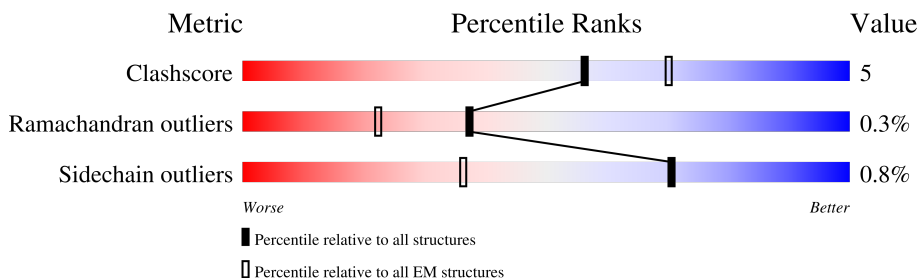
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	7587 (3.50 - 4.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	3138	14% 65% 10% 25%
2	B	371	8% 56% 16% 28%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20491 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 Huntingtin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2353	Total	C	N	O	S	0	0
			18458	11839	3157	3343	119		

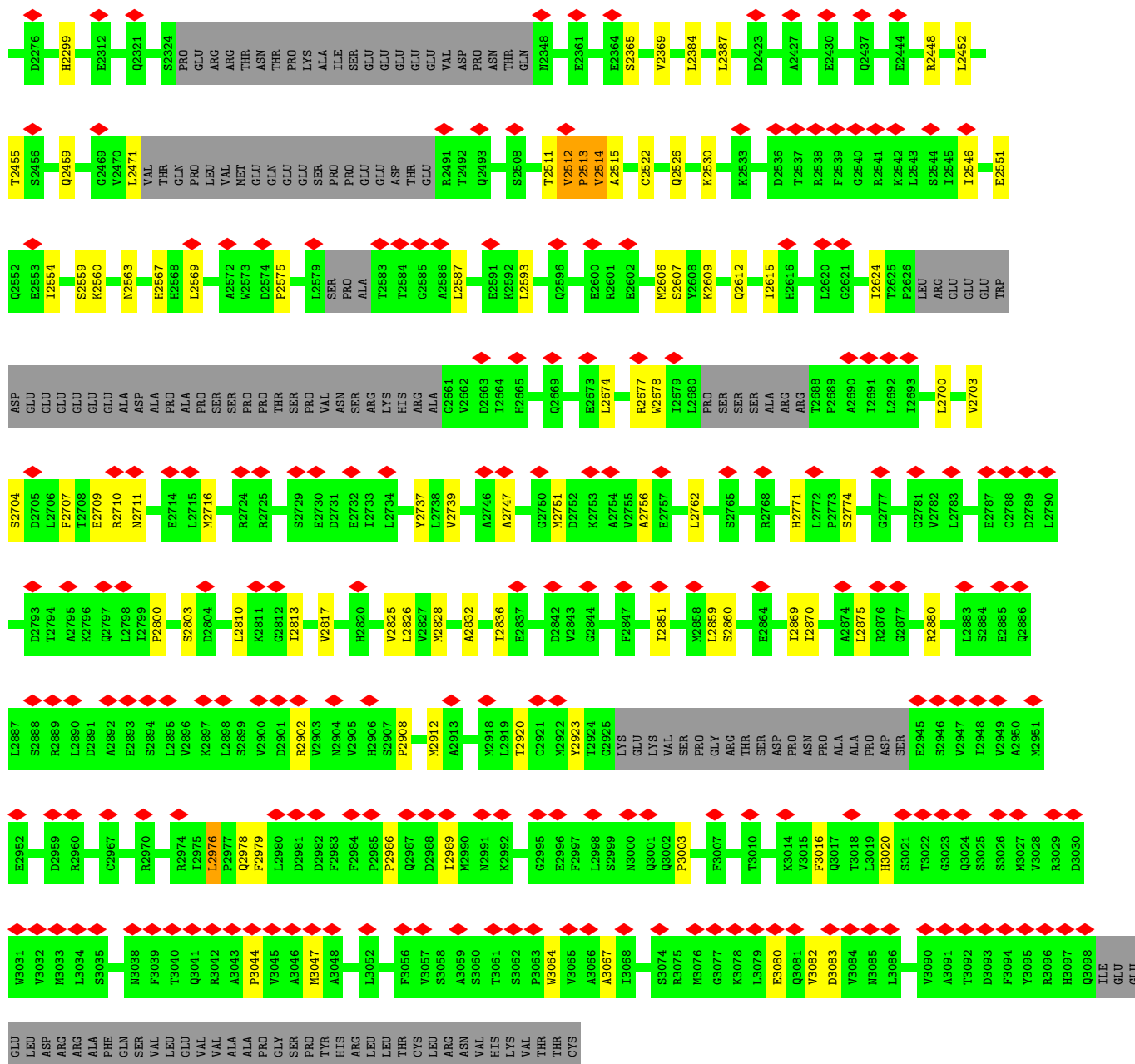
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P42858
A	?	-	GLN	deletion	UNP P42858
A	?	-	GLN	deletion	UNP P42858
A	?	-	GLN	deletion	UNP P42858
A	1234	ARG	LYS	conflict	UNP P42858
A	1716	ASN	THR	conflict	UNP P42858
A	2305	HIS	TYR	conflict	UNP P42858

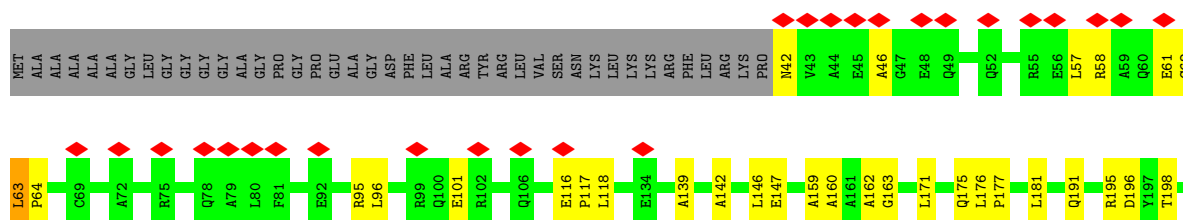
- Molecule 2 is a protein called Factor VIII intron 22 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	268	Total	C	N	O	S	0	0
			2033	1290	367	366	10		





● Molecule 2: Factor VIII intron 22 protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98310	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	32	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.475	Depositor
Minimum map value	-0.388	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	216.0, 216.0, 216.0	wwPDB
Map dimensions	160, 160, 160	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	0.31	0/18818	0.75	7/25566 (0.0%)
2	B	0.35	0/2067	0.79	0/2808
All	All	0.32	0/20885	0.75	7/28374 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
2	B	0	3
All	All	0	8

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1645	VAL	N-CA-C	-7.28	105.43	111.91
1	A	670	THR	N-CA-C	-6.98	105.96	114.75
1	A	2703	VAL	CA-C-N	5.64	129.62	120.60
1	A	2703	VAL	C-N-CA	5.64	129.62	120.60
1	A	1259	PHE	N-CA-C	-5.61	106.37	113.43
1	A	2593	LEU	CA-C-N	5.45	129.00	120.82
1	A	2593	LEU	C-N-CA	5.45	129.00	120.82

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1045	VAL	Peptide
1	A	1314	THR	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	1838	LEU	Peptide
1	A	2268	SER	Peptide
1	A	296	VAL	Peptide
2	B	162	ALA	Peptide
2	B	259	LEU	Peptide
2	B	63	LEU	Peptide

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	18458	0	18894	178	0
2	B	2033	0	2074	39	0
All	All	20491	0	20968	205	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 (205) 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:1076:PRO:HB2	1:A:1235:LEU:HD21	1.74	0.68
1:A:308:LEU:HD21	1:A:368:VAL:HA	1.80	0.63
1:A:2219:ARG:HH21	1:A:2269:LEU:HD11	1.65	0.61
1:A:2832:ALA:HB1	1:A:2851:ILE:HD13	1.82	0.61
1:A:1369:ALA:O	1:A:1682:GLN:NE2	2.34	0.61
1:A:2522:CYS:SG	1:A:2563:ASN:ND2	2.74	0.60
1:A:928:ILE:HD11	1:A:1027:LEU:HB3	1.84	0.60
1:A:2233:SER:HA	1:A:2236:HIS:HD2	1.66	0.59
1:A:1666:GLN:HE21	1:A:1767:PHE:HD2	1.49	0.59
1:A:173:ASN:OD1	1:A:215:ARG:NH2	2.36	0.59
1:A:861:ARG:NH1	1:A:914:ASP:OD1	2.36	0.59
2:B:268:ARG:NH1	2:B:351:GLU:OE1	2.36	0.59
1:A:2448:ARG:O	1:A:2452:LEU:HB2	2.04	0.58
1:A:978:ARG:O	1:A:1313:LYS:NZ	2.35	0.58
2:B:62:CYS:SG	2:B:63:LEU:N	2.77	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:920:ARG:HD2	1:A:1020:GLY:HA3	1.86	0.57
1:A:2624:ILE:HG21	1:A:2710:ARG:HB2	1.86	0.57
1:A:1489:ILE:HG12	1:A:1493:ILE:HG13	1.86	0.57
1:A:199:ARG:NH2	1:A:238:PHE:O	2.38	0.56
1:A:1783:PHE:HB3	1:A:1838:LEU:HD22	1.87	0.56
1:A:2256:LEU:HD13	1:A:2266:PRO:HG2	1.87	0.56
1:A:2365:SER:O	1:A:2369:VAL:N	2.37	0.56
2:B:271:VAL:HG13	2:B:322:LEU:HD11	1.87	0.56
1:A:2214:LEU:HD22	1:A:2252:THR:HG22	1.86	0.56
1:A:1974:GLU:O	1:A:2011:ARG:NH1	2.39	0.56
1:A:2511:THR:HB	1:A:2515:ALA:HA	1.87	0.55
1:A:2272:GLN:HE21	1:A:2387:LEU:HD11	1.71	0.55
1:A:689:LEU:HB2	1:A:752:TYR:HE2	1.71	0.55
1:A:857:TYR:HD2	1:A:860:VAL:HG23	1.71	0.55
1:A:1704:CYS:O	1:A:1708:ASN:ND2	2.40	0.54
2:B:58:ARG:HH21	2:B:96:LEU:HD11	1.72	0.54
1:A:1733:GLU:HG2	1:A:1790:ARG:HB3	1.89	0.54
1:A:293:GLY:HA2	1:A:296:VAL:HB	1.90	0.54
2:B:208:GLN:NE2	2:B:270:GLU:OE2	2.41	0.54
1:A:934:LEU:HD12	1:A:997:ASN:HB3	1.90	0.54
1:A:1044:GLY:HA3	2:B:177:PRO:HD2	1.90	0.53
1:A:2836:ILE:HD11	1:A:2851:ILE:HD12	1.89	0.53
2:B:273:ARG:HH22	2:B:294:THR:HG21	1.72	0.53
1:A:1275:GLU:OE2	1:A:1310:GLN:NE2	2.42	0.53
1:A:2709:GLU:HG2	1:A:2711:ASN:H	1.74	0.53
1:A:686:ALA:HB2	1:A:730:LEU:HD11	1.90	0.53
2:B:191:GLN:HB3	2:B:196:ASP:HB3	1.91	0.52
1:A:1900:ASP:HB2	1:A:1931:PRO:HB3	1.89	0.52
1:A:1975:GLY:HA2	1:A:2011:ARG:HH12	1.75	0.52
1:A:1997:PHE:HB2	1:A:2000:LEU:HB2	1.90	0.52
1:A:2551:GLU:HA	1:A:2554:ILE:HD12	1.92	0.52
1:A:2817:VAL:HG11	1:A:2870:ILE:HG21	1.91	0.52
1:A:205:LEU:O	1:A:209:LEU:N	2.43	0.51
1:A:2615:ILE:HD13	1:A:2747:ALA:HB1	1.92	0.51
1:A:1998:ARG:H	2:B:324:SER:HB2	1.76	0.51
1:A:3080:GLU:H	1:A:3083:ASP:HB2	1.76	0.51
2:B:57:LEU:O	2:B:61:GLU:N	2.44	0.51
1:A:1077:LEU:HD21	1:A:1234:ARG:HB3	1.92	0.51
1:A:1799:PHE:HD2	1:A:1839:VAL:HG11	1.75	0.51
1:A:291:LEU:HB3	1:A:310:VAL:HG13	1.94	0.50
1:A:354:TYR:OH	1:A:680:CYS:SG	2.65	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1749:GLU:O	1:A:1753:THR:OG1	2.28	0.50
1:A:356:LEU:O	1:A:360:HIS:ND1	2.39	0.50
1:A:1906:LEU:HD12	1:A:1942:ASN:HD21	1.77	0.50
1:A:2384:LEU:HD23	1:A:2387:LEU:HD12	1.93	0.50
1:A:2005:ASP:OD2	1:A:2048:HIS:ND1	2.44	0.50
1:A:2704:SER:HA	1:A:2707:PHE:HD2	1.76	0.50
1:A:1689:LEU:HB3	1:A:1732:PRO:HB2	1.94	0.50
2:B:58:ARG:HG2	2:B:63:LEU:HD21	1.93	0.50
1:A:1610:ILE:HG13	1:A:1619:MET:HE3	1.94	0.50
1:A:1078:ASP:OD1	1:A:1078:ASP:N	2.44	0.49
2:B:350:ALA:HA	2:B:353:ASN:HB2	1.93	0.49
1:A:944:ASP:HB2	1:A:947:VAL:HG23	1.94	0.49
1:A:1083:GLN:HB3	1:A:1262:PHE:HD1	1.77	0.49
1:A:2365:SER:HB2	1:A:2369:VAL:HB	1.95	0.49
1:A:1589:GLN:HE21	1:A:1636:ILE:HD13	1.78	0.49
1:A:1531:VAL:HA	1:A:1535:ILE:HD12	1.95	0.49
1:A:2751:MET:HE3	1:A:2756:ALA:HA	1.94	0.49
1:A:395:GLY:HA3	1:A:399:GLN:HE22	1.76	0.48
1:A:2039:LEU:HB3	1:A:2045:ALA:HB2	1.95	0.48
1:A:2530:LYS:O	1:A:2880:ARG:NH2	2.35	0.48
1:A:2813:ILE:HG22	1:A:2817:VAL:HG22	1.95	0.48
1:A:1305:THR:O	1:A:1309:GLN:N	2.47	0.48
1:A:1921:GLN:HG3	1:A:1956:ARG:HH11	1.79	0.48
1:A:275:GLN:HE21	1:A:320:LEU:HD21	1.79	0.48
1:A:296:VAL:HG22	1:A:297:PRO:HD3	1.96	0.48
1:A:145:GLU:HB3	1:A:1248:VAL:HG13	1.95	0.48
1:A:2737:TYR:HE1	2:B:116:GLU:HG3	1.77	0.48
1:A:2121:ARG:HH11	1:A:3067:ALA:HB2	1.79	0.47
1:A:3044:PRO:HG2	1:A:3047:MET:HB3	1.96	0.47
1:A:167:TYR:CZ	1:A:204:ASN:HB3	2.49	0.47
1:A:1259:PHE:O	1:A:1263:LEU:N	2.44	0.47
2:B:142:ALA:HB2	2:B:171:LEU:HB2	1.95	0.47
1:A:252:ILE:HA	1:A:255:LEU:HD23	1.97	0.47
2:B:181:LEU:HD21	2:B:210:LEU:HD12	1.95	0.47
2:B:275:LEU:HD22	2:B:356:LEU:HD23	1.97	0.47
1:A:991:ASP:HB3	1:A:994:MET:HB3	1.97	0.47
1:A:1015:ARG:HG3	1:A:1074:TRP:HZ2	1.80	0.47
2:B:328:ALA:O	2:B:332:LYS:N	2.48	0.47
1:A:166:LEU:HB3	1:A:186:PHE:CE1	2.50	0.47
1:A:350:LEU:HB3	1:A:387:LEU:HD12	1.95	0.47
1:A:691:THR:O	1:A:744:GLN:NE2	2.48	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2471:LEU:HD22	1:A:2678:TRP:HH2	1.79	0.47
1:A:2559:SER:O	2:B:195:ARG:NH1	2.43	0.47
1:A:675:ALA:HB3	1:A:678:VAL:HG23	1.97	0.47
1:A:931:VAL:HG11	1:A:998:LEU:HD23	1.97	0.46
1:A:2704:SER:HA	1:A:2707:PHE:CD2	2.51	0.46
1:A:1421:PHE:O	1:A:1425:VAL:N	2.43	0.46
1:A:194:ARG:NH2	1:A:196:GLN:OE1	2.48	0.46
1:A:198:CYS:SG	1:A:199:ARG:N	2.89	0.46
1:A:2607:SER:O	1:A:2612:GLN:NE2	2.49	0.46
1:A:2976:LEU:HA	1:A:2979:PHE:HB3	1.97	0.46
1:A:3080:GLU:HG3	1:A:3082:VAL:H	1.81	0.46
2:B:95:ARG:NH1	2:B:147:GLU:OE1	2.49	0.46
1:A:163:GLN:HE21	1:A:189:LEU:HB3	1.80	0.46
1:A:836:SER:OG	1:A:837:SER:N	2.49	0.46
1:A:1461:LEU:HD11	1:A:1467:PHE:HB3	1.98	0.46
1:A:2093:LYS:HG2	1:A:3064:TRP:HE1	1.80	0.46
1:A:2567:HIS:HD2	2:B:361:GLN:HE22	1.63	0.46
1:A:2800:PRO:HA	1:A:2803:SER:HB3	1.97	0.46
1:A:1448:LEU:HD23	1:A:1451:LEU:HD12	1.97	0.46
1:A:2526:GLN:N	1:A:2612:GLN:O	2.47	0.46
1:A:2123:PRO:HG3	1:A:3064:TRP:HH2	1.80	0.46
2:B:274:VAL:HG21	2:B:298:TYR:HE2	1.81	0.45
1:A:1999:VAL:HG11	2:B:323:GLN:HB3	1.98	0.45
1:A:2739:VAL:HG22	1:A:2762:LEU:HD21	1.98	0.45
1:A:2231:LEU:HD13	1:A:2235:LEU:HB3	1.96	0.45
1:A:187:ALA:HB1	1:A:230:LYS:HB2	1.99	0.45
1:A:227:ALA:O	1:A:231:ILE:N	2.40	0.45
1:A:1042:HIS:HB2	1:A:1059:THR:HG21	1.97	0.45
1:A:1819:ARG:HD2	1:A:1849:GLU:HG2	1.98	0.45
1:A:2826:LEU:HD12	1:A:2870:ILE:HD13	1.99	0.45
1:A:2986:PRO:HA	1:A:2989:ILE:HG12	1.98	0.45
1:A:667:GLY:O	1:A:679:HIS:ND1	2.49	0.45
1:A:1997:PHE:HD2	1:A:2000:LEU:HD22	1.82	0.45
1:A:1595:ASN:OD1	1:A:1595:ASN:N	2.50	0.45
1:A:2127:MET:O	1:A:2131:MET:N	2.50	0.45
1:A:1438:VAL:HG21	1:A:1485:GLU:HB2	1.98	0.45
1:A:1685:GLU:HG3	1:A:1788:PHE:HA	1.99	0.45
1:A:3016:PHE:O	1:A:3020:HIS:ND1	2.47	0.45
1:A:1888:GLU:OE1	1:A:1891:ARG:NH1	2.47	0.45
2:B:63:LEU:HD22	2:B:96:LEU:HD22	1.98	0.45
1:A:999:SER:HB2	1:A:1040:GLY:HA2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1659:MET:HB2	1:A:1665:VAL:HG22	1.99	0.45
1:A:2250:VAL:HG21	1:A:2299:HIS:HB3	1.99	0.45
1:A:2810:LEU:HG	1:A:2828:MET:HE1	1.98	0.44
1:A:1891:ARG:NH2	1:A:1922:ASP:OD2	2.50	0.44
1:A:2771:HIS:HB3	1:A:2774:SER:HB3	1.99	0.44
1:A:378:GLN:NE2	1:A:382:THR:OG1	2.50	0.44
2:B:298:TYR:HA	2:B:323:GLN:HG2	1.99	0.44
1:A:712:LEU:HD13	1:A:764:THR:HG23	2.00	0.44
1:A:815:SER:HB2	1:A:818:THR:HG23	1.98	0.44
2:B:355:LEU:HD23	2:B:355:LEU:HA	1.83	0.44
1:A:2860:SER:HA	1:A:2902:ARG:HD2	1.98	0.44
1:A:2920:THR:HA	1:A:2923:TYR:HB2	1.98	0.44
1:A:2859:LEU:HD13	1:A:2875:LEU:HD12	1.98	0.44
1:A:1068:THR:HG21	2:B:139:ALA:HB3	1.99	0.44
1:A:1293:LEU:HA	1:A:1296:CYS:HB3	2.00	0.44
1:A:2455:THR:OG1	1:A:2459:GLN:OE1	2.31	0.44
1:A:2513:PRO:O	1:A:2515:ALA:N	2.51	0.44
1:A:2700:LEU:HD21	1:A:2716:MET:HG3	2.00	0.43
2:B:198:THR:HG22	2:B:280:LEU:HD22	2.00	0.43
1:A:2674:LEU:HD23	1:A:2677:ARG:HH21	1.82	0.43
1:A:752:TYR:HB2	1:A:764:THR:HG21	1.99	0.43
1:A:2575:PRO:HA	1:A:2587:LEU:HD21	2.00	0.43
1:A:1783:PHE:HA	1:A:1792:THR:HG22	2.00	0.43
1:A:1011:THR:HG22	2:B:146:LEU:HD13	1.99	0.43
1:A:1830:LEU:HD21	1:A:1890:VAL:HA	2.01	0.43
1:A:2908:PRO:O	1:A:2912:MET:N	2.51	0.43
1:A:107:VAL:HA	1:A:112:ARG:HH22	1.83	0.43
1:A:2168:THR:HG23	1:A:2220:ALA:HB1	2.00	0.43
1:A:1524:MET:HE3	1:A:1524:MET:HB2	1.86	0.42
2:B:278:LEU:HD11	2:B:326:VAL:HG22	2.01	0.42
1:A:1738:ARG:HH21	1:A:1798:LEU:HD13	1.84	0.42
1:A:295:LEU:HD22	1:A:356:LEU:HD11	2.00	0.42
1:A:1245:ASN:O	1:A:1249:THR:OG1	2.31	0.42
2:B:101:GLU:HG3	2:B:117:PRO:HG2	2.01	0.42
1:A:1311:LEU:HD12	1:A:1421:PHE:HZ	1.84	0.42
1:A:1850:VAL:HG13	1:A:1851:GLN:HG3	2.00	0.42
1:A:2563:ASN:HD21	1:A:2606:MET:HG3	1.85	0.42
1:A:2869:ILE:HD11	2:B:159:ALA:HB3	2.01	0.42
2:B:318:LEU:HD12	2:B:347:LEU:HB3	2.00	0.42
1:A:391:LEU:HB3	1:A:677:LEU:HG	2.02	0.42
1:A:1367:ALA:O	1:A:1370:SER:OG	2.36	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1999:VAL:HG22	2:B:324:SER:HB3	2.01	0.42
1:A:2559:SER:OG	1:A:2560:LYS:N	2.53	0.41
1:A:2817:VAL:HG13	1:A:2825:VAL:HG11	2.01	0.41
1:A:2869:ILE:HD12	2:B:160:ALA:HB2	2.01	0.41
1:A:215:ARG:HD2	1:A:220:VAL:HG11	2.03	0.41
1:A:308:LEU:HD23	1:A:308:LEU:HA	1.85	0.41
1:A:2126:ASP:OD1	1:A:2126:ASP:N	2.53	0.41
1:A:1680:ILE:HA	1:A:1788:PHE:HZ	1.85	0.41
1:A:1796:THR:HG22	1:A:1839:VAL:HG23	2.01	0.41
2:B:175:GLN:HB3	2:B:176:LEU:HD12	2.01	0.41
1:A:779:SER:O	1:A:781:PHE:N	2.54	0.41
1:A:1128:ARG:HE	1:A:1131:VAL:HG21	1.84	0.41
2:B:42:ASN:O	2:B:46:ALA:N	2.53	0.41
2:B:325:LEU:HD11	2:B:356:LEU:HD21	2.02	0.41
1:A:2171:ARG:HG3	1:A:2217:LEU:HD11	2.03	0.41
1:A:2546:ILE:HG12	1:A:2978:GLN:NE2	2.35	0.41
1:A:1421:PHE:HB3	1:A:1425:VAL:HG23	2.03	0.41
1:A:2512:VAL:HG13	1:A:2513:PRO:HD2	2.03	0.41
1:A:3003:PRO:HB3	2:B:284:PRO:HD2	2.02	0.41
1:A:388:LEU:HD21	1:A:721:LEU:HD22	2.03	0.40
1:A:2513:PRO:HB2	1:A:2514:VAL:H	1.74	0.40
1:A:1828:LEU:HD23	1:A:1828:LEU:HA	1.88	0.40
1:A:907:VAL:O	1:A:911:LEU:N	2.42	0.40
2:B:282:PRO:HG2	2:B:287:LEU:HD12	2.03	0.40
1:A:1419:ARG:HB3	1:A:1422:GLU:HG3	2.04	0.40
1:A:1851:GLN:HA	1:A:1891:ARG:HG3	2.02	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	2313/3138 (74%)	2162 (94%)	146 (6%)	5 (0%)	43	75
2	B	262/371 (71%)	248 (95%)	12 (5%)	2 (1%)	16	52
All	All	2575/3509 (73%)	2410 (94%)	158 (6%)	7 (0%)	37	70

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2514	VAL
1	A	277	SER
1	A	2513	PRO
1	A	1046	PRO
1	A	2266	PRO
2	B	163	GLY
2	B	64	PRO

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	2075/2763 (75%)	2057 (99%)	18 (1%)	70	76
2	B	202/274 (74%)	201 (100%)	1 (0%)	81	82
All	All	2277/3037 (75%)	2258 (99%)	19 (1%)	70	77

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	LEU
1	A	183	LEU
1	A	240	ASN
1	A	255	LEU
1	A	388	LEU
1	A	705	VAL
1	A	989	ILE
1	A	1045	VAL
1	A	1263	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1702	ILE
1	A	1743	LEU
1	A	1838	LEU
1	A	2201	LEU
1	A	2253	LEU
1	A	2512	VAL
1	A	2569	LEU
1	A	2609	LYS
1	A	2976	LEU
2	B	118	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	ASN
1	A	240	ASN
1	A	281	GLN
1	A	377	GLN
1	A	399	GLN
1	A	722	HIS
1	A	844	GLN
1	A	906	ASN
1	A	953	GLN
1	A	1091	ASN
1	A	1146	ASN
1	A	1310	GLN
1	A	1364	GLN
1	A	1443	GLN
1	A	1492	ASN
1	A	1563	GLN
1	A	1589	GLN
1	A	1605	GLN
1	A	1666	GLN
1	A	1682	GLN
1	A	1693	GLN
1	A	1742	GLN
1	A	1942	ASN
1	A	2019	ASN
1	A	2040	GLN
1	A	2133	ASN
1	A	2236	HIS
1	A	2272	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2305	HIS
1	A	2555	GLN
1	A	2563	ASN
1	A	2590	HIS
1	A	2771	HIS
1	A	2809	ASN
1	A	2872	HIS
1	A	2909	HIS
1	A	2978	GLN
1	A	3071	HIS
1	A	3085	ASN
2	B	106	GLN
2	B	119	GLN
2	B	172	GLN
2	B	191	GLN
2	B	291	HIS
2	B	352	GLN
2	B	361	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 ⓘ

There are no chain breaks in this entry.

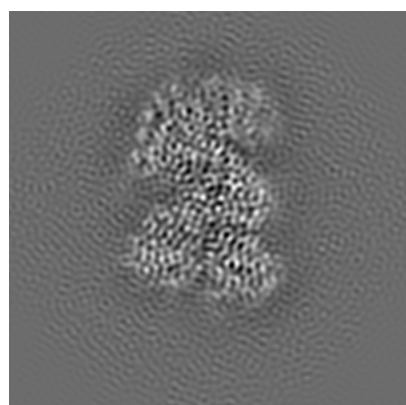
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3984. These allow visual inspection of the internal detail of the map and identification of artifacts.

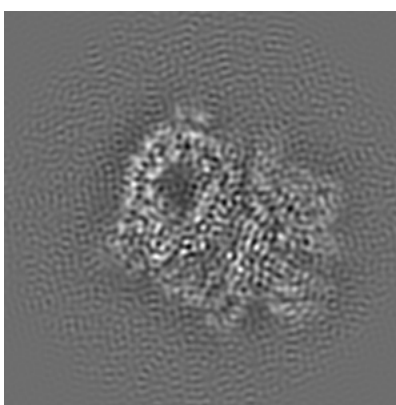
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

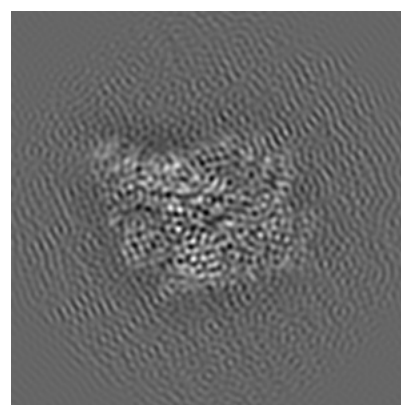
6.1.1 Primary map



X



Y

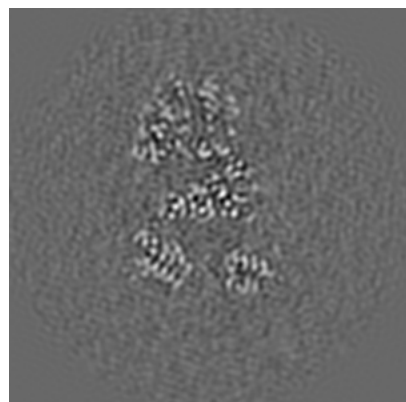


Z

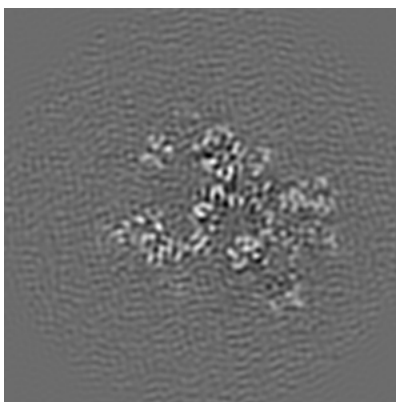
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

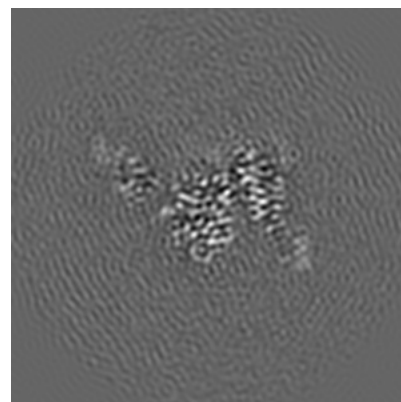
6.2.1 Primary map



X Index: 80



Y Index: 80

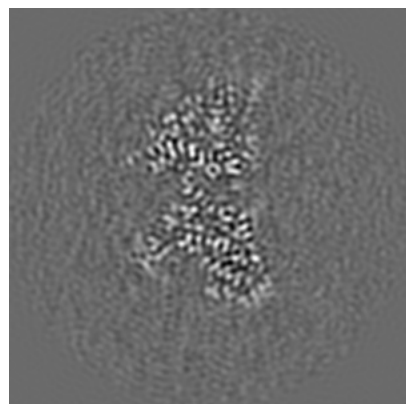


Z Index: 80

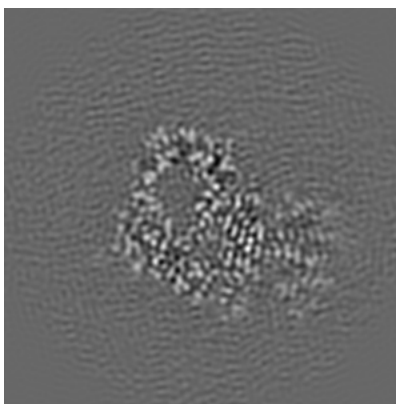
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

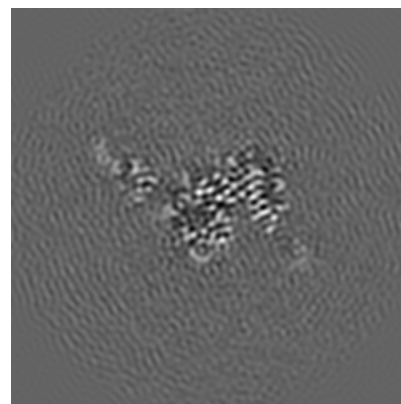
6.3.1 Primary map



X Index: 66



Y Index: 90

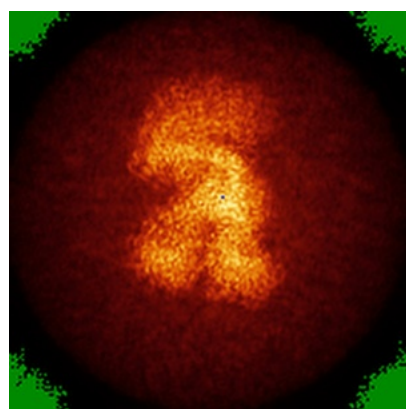


Z Index: 81

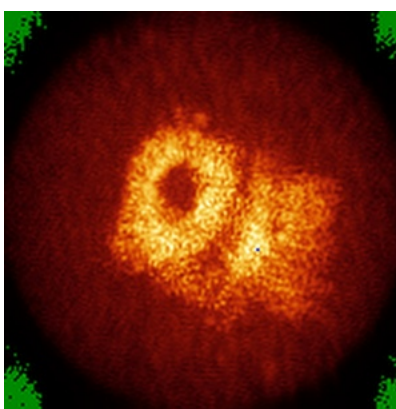
The images above show the largest variance slices of the map in three orthogonal directions.

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

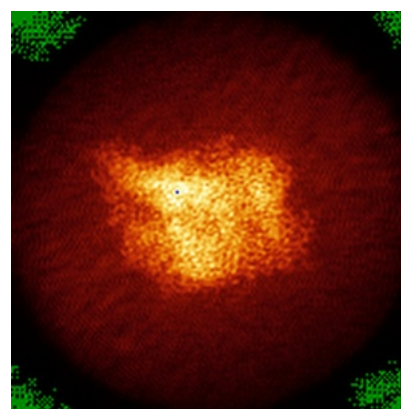
6.4.1 Primary map



X



Y

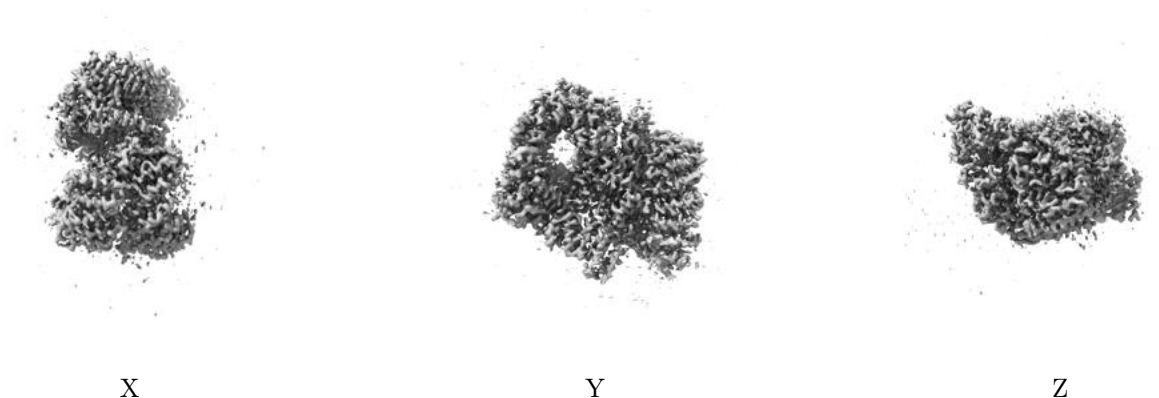


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

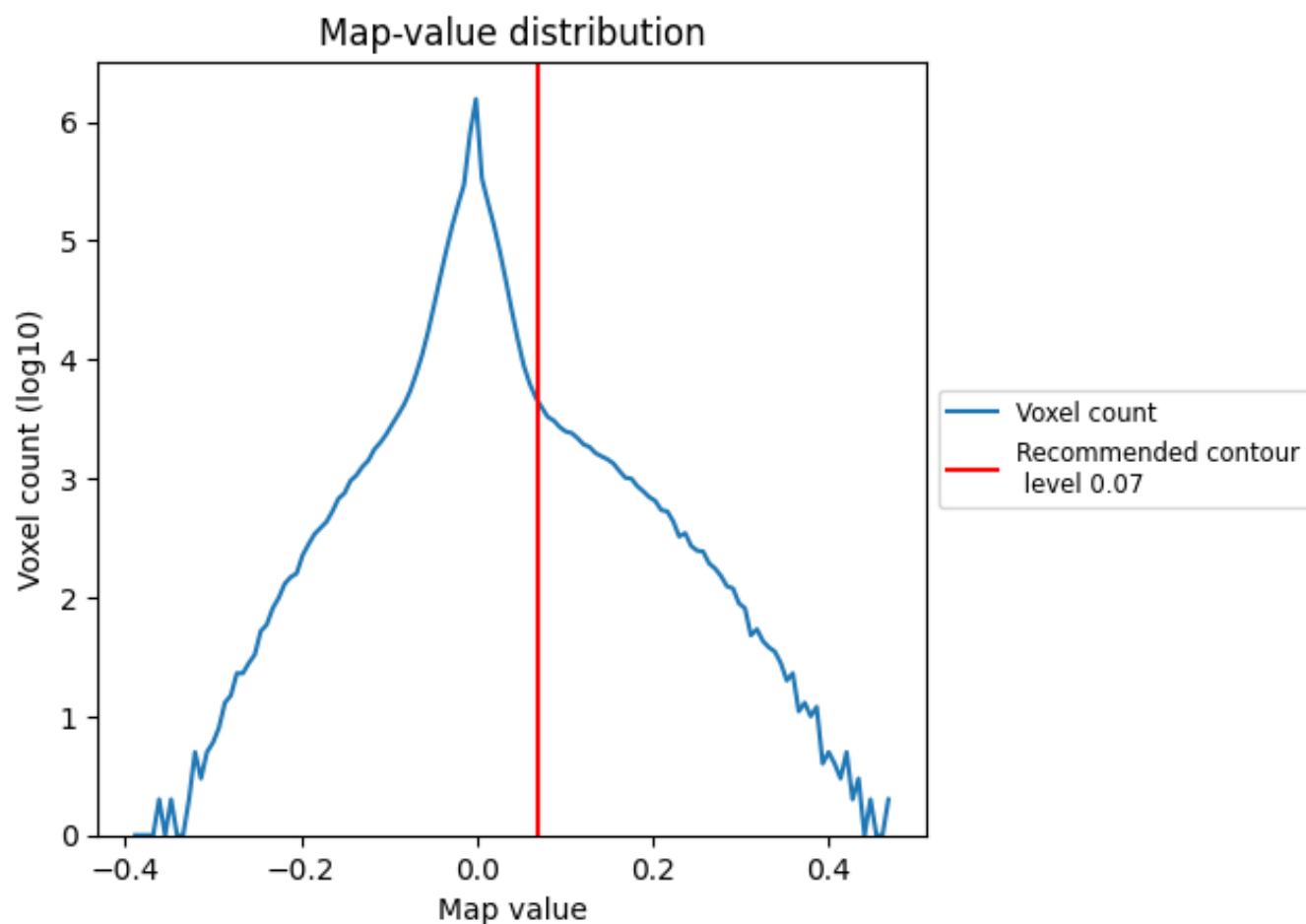
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

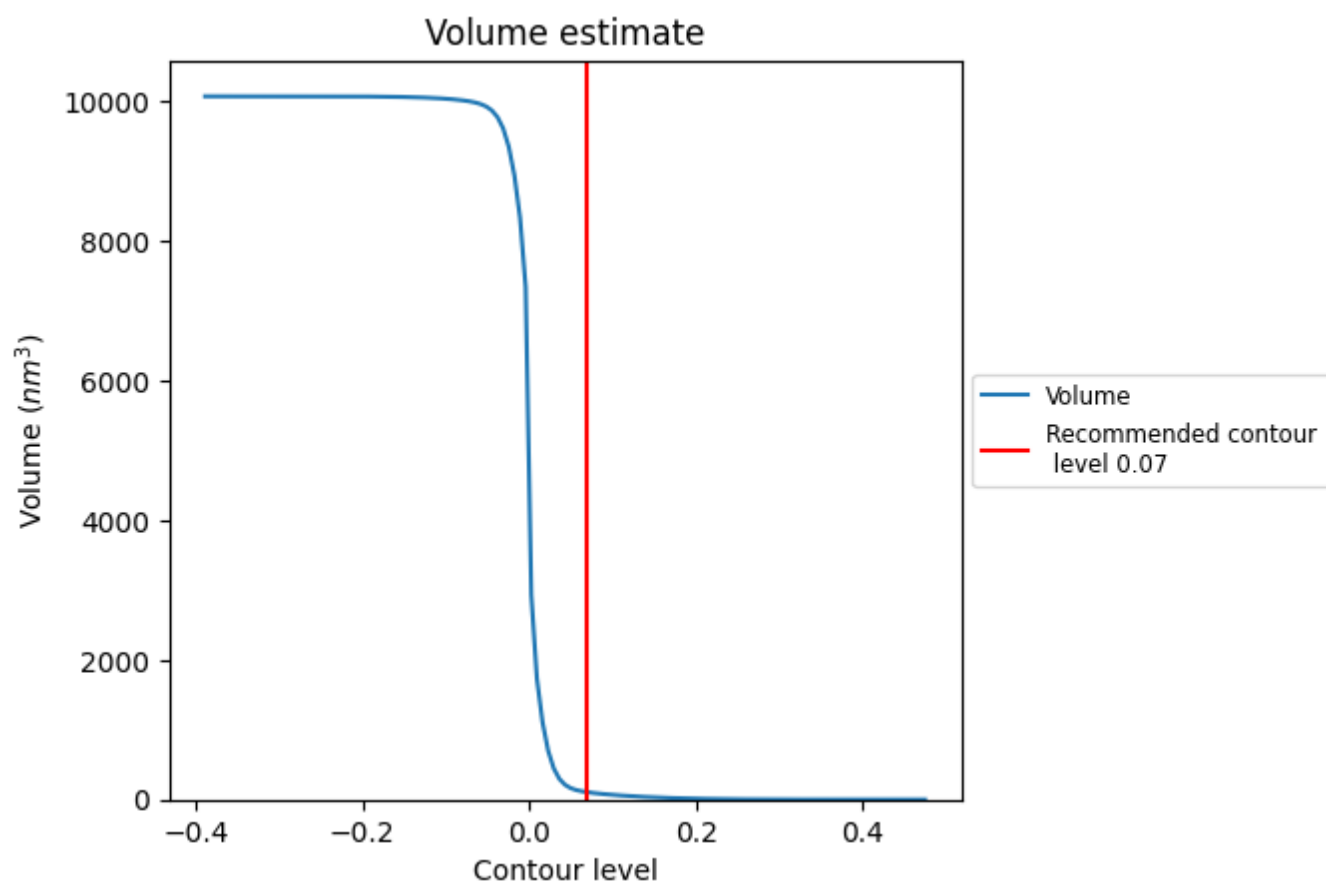
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

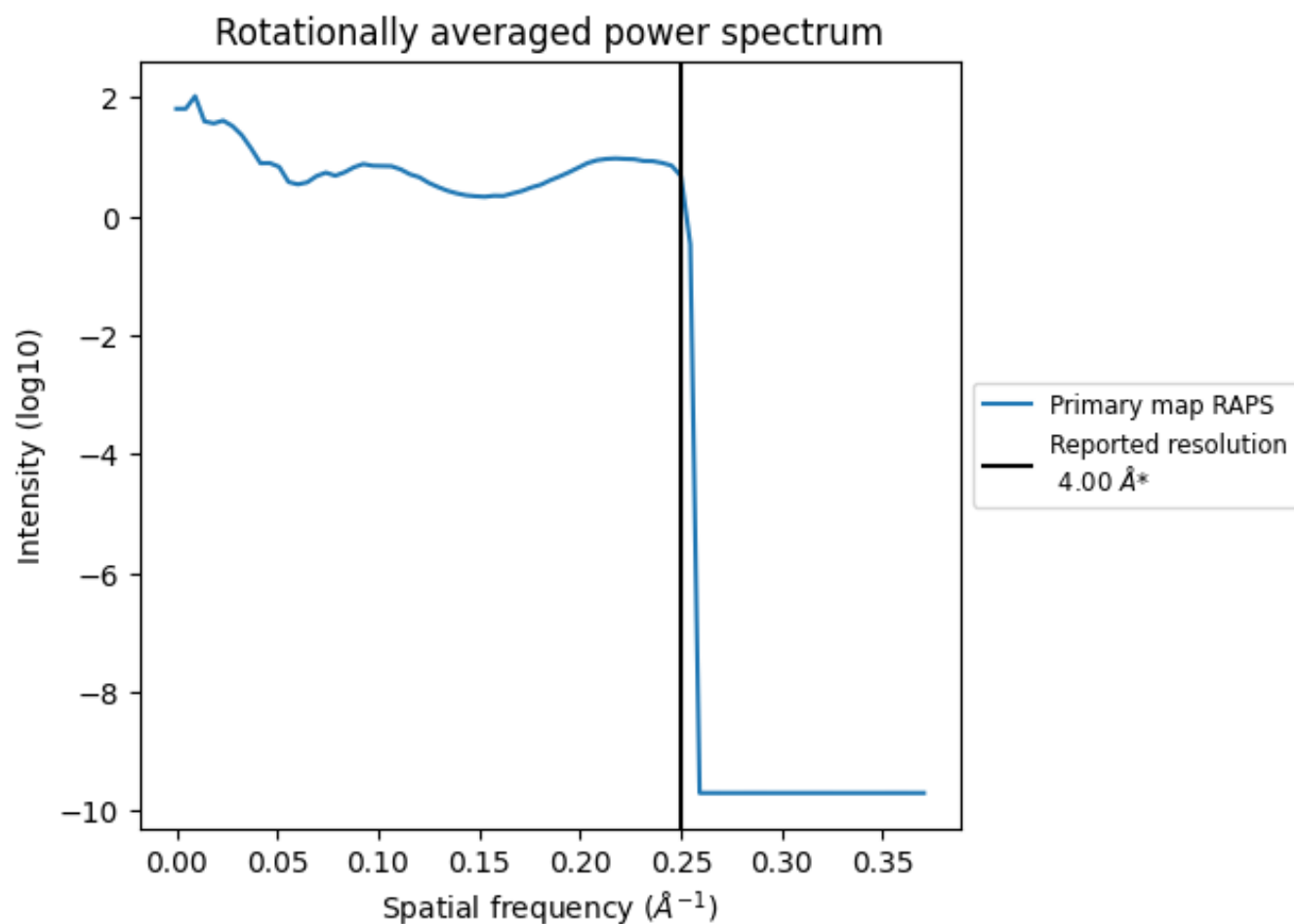
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 105 nm³; this corresponds to an approximate mass of 95 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 0.250 Å⁻¹

8 Fourier-Shell correlation

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

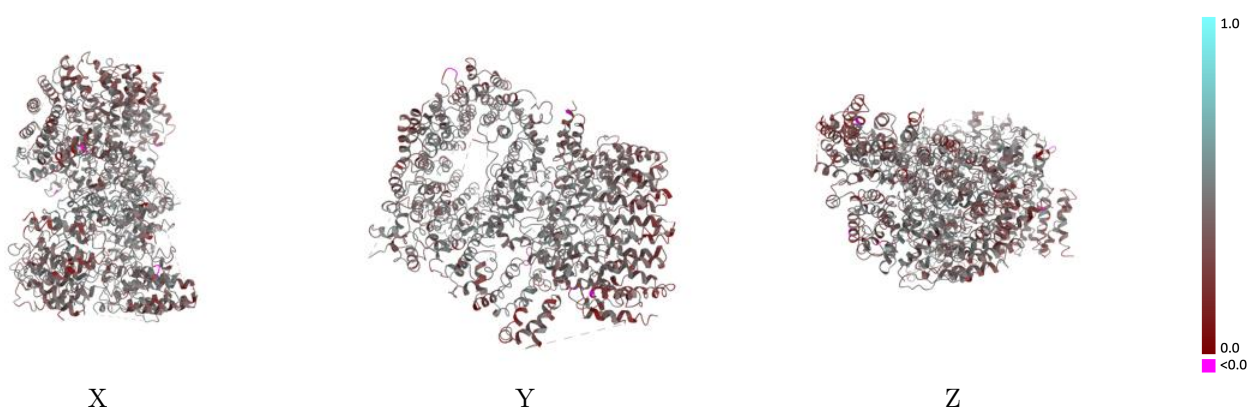
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3984 and PDB model 6EZ8. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

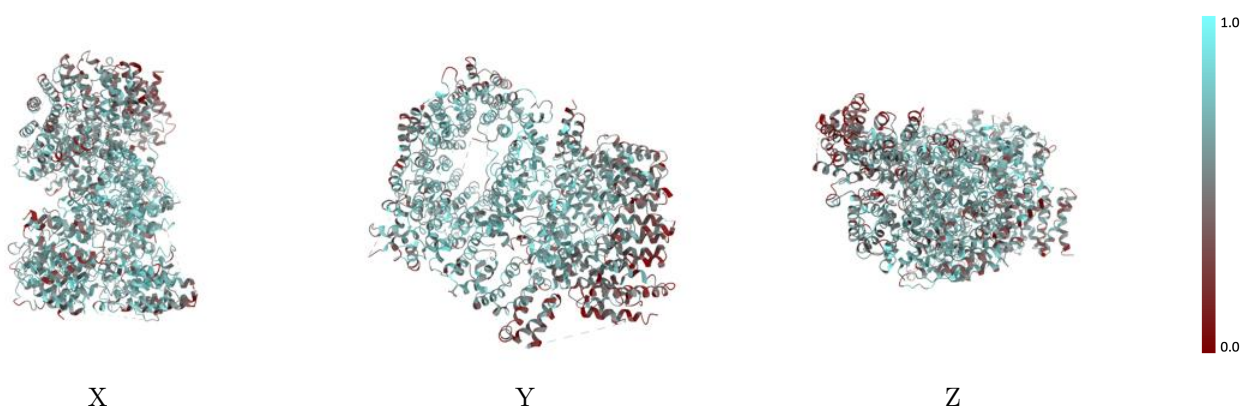
This section was not generated.

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



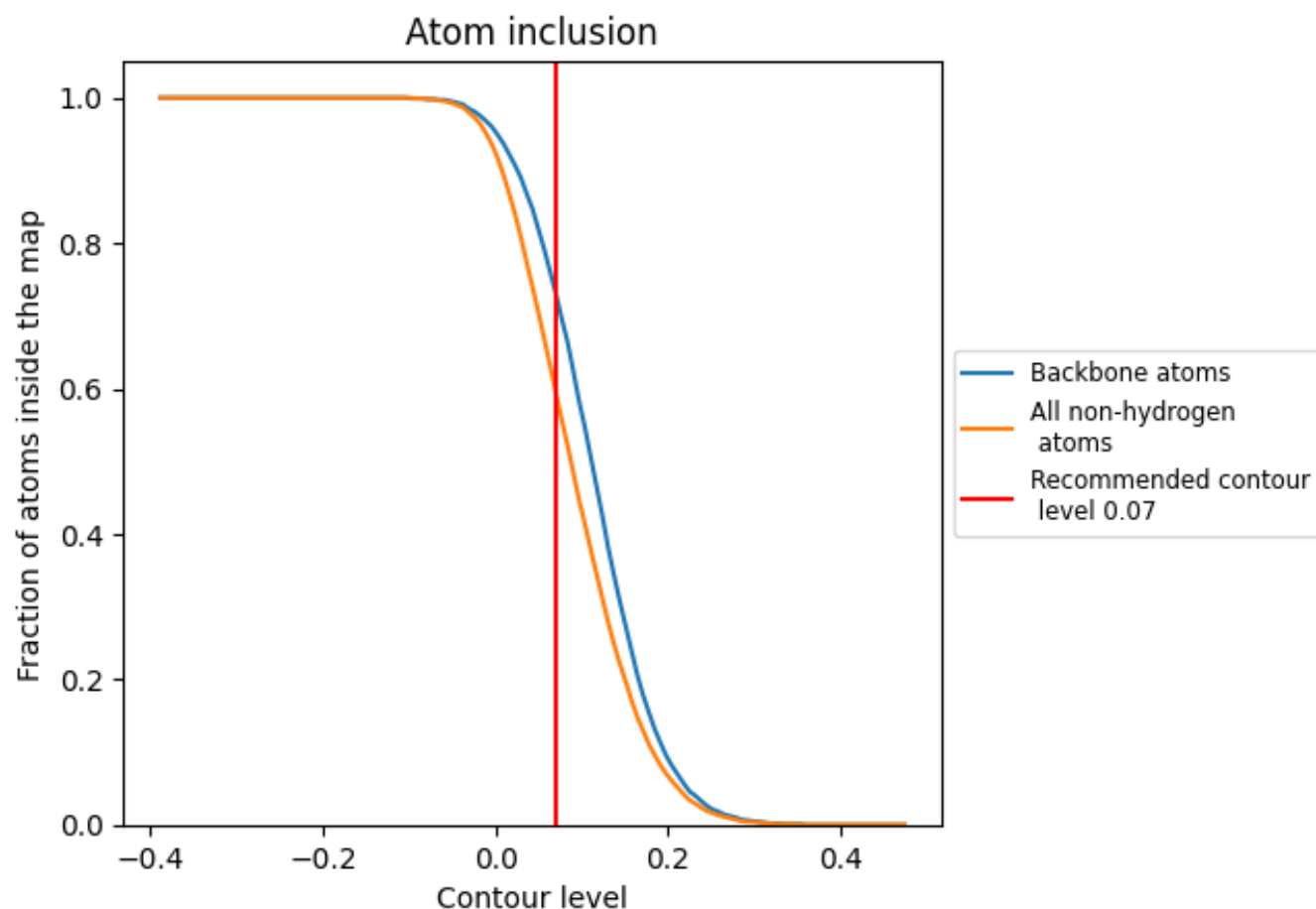
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion ⓘ



At the recommended contour level, 73% of all backbone atoms, 60% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5950	0.4120
A	0.5900	0.4110
B	0.6440	0.4270

