



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 03:00 AM UTC

PDB ID : 6Z6F / pdb_00006z6f
EMDB ID : EMD-11092
Title : HDAC-PC
Authors : Lee, J.-H.; Bollschweiler, D.; Schaefer, T.; Huber, R.
Deposited on : 2020-05-28
Resolution : 3.11 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:

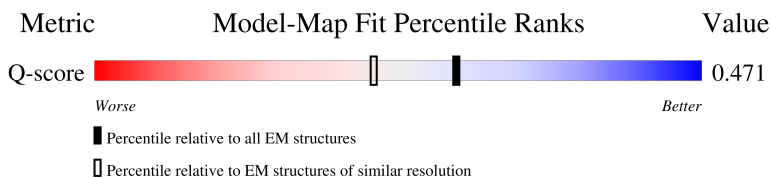
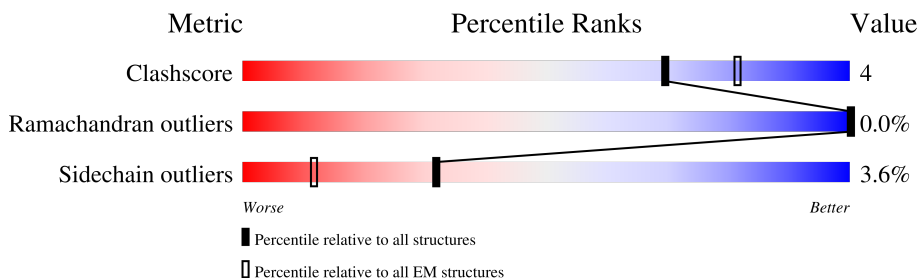
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.11 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	14465 (2.61 - 3.61)

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	661	88% 10% .
2	B	672	89% 9% .
3	D	543	8% 84% 13% ..
4	C	629	72% 13% . 14%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 19217 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 Histone deacetylase HDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	651	Total	C	N	O	S	0	0
			5178	3303	876	972	27		

- Molecule 2 is a protein called Histone deacetylase HDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	661	Total	C	N	O	S	0	0
			5245	3339	883	995	28		

- Molecule 3 is a protein called HDA1 complex subunit 3,HDA1 complex subunit 3.

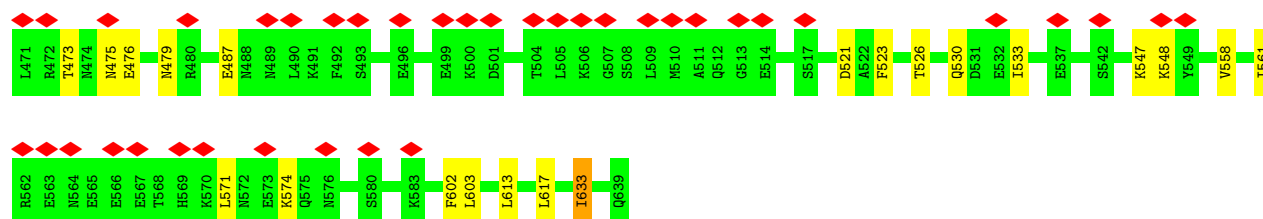
Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	534	Total	C	N	O	S	0	0
			4376	2765	737	854	20		

- Molecule 4 is a protein called HDA1 complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	541	Total	C	N	O	S	0	0
			4416	2801	759	843	13		

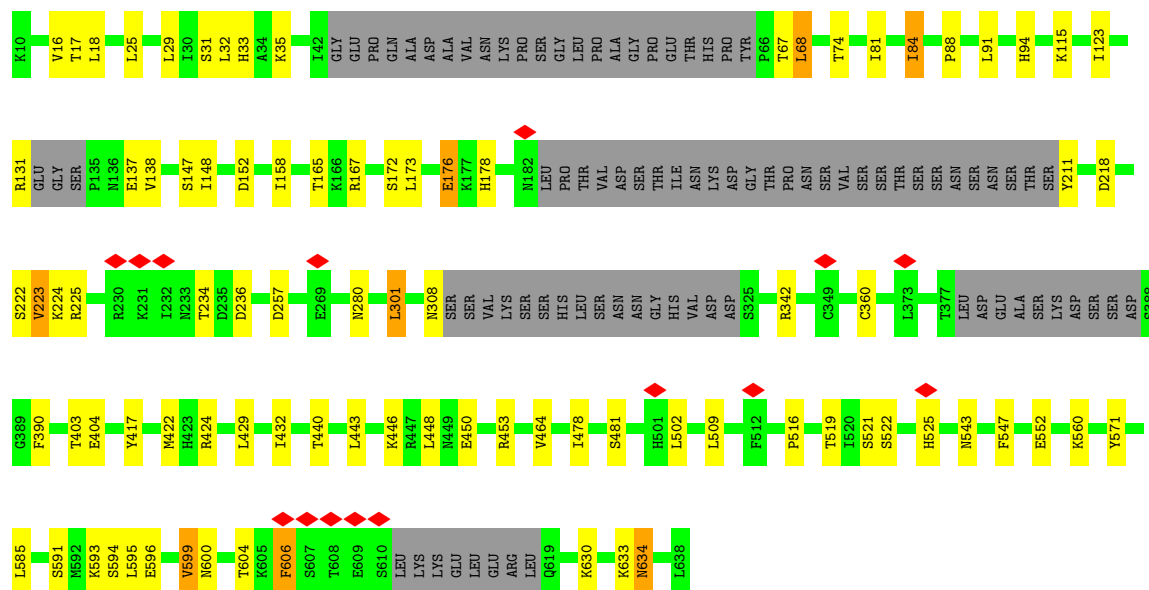
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	A	1	Total	Zn	0
			1	1	
5	B	1	Total	Zn	0
			1	1	



• Molecule 4: HDA1 complex subunit 2

Chain C: 72% 13% 14%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	466972	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	62.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.904	Depositor
Minimum map value	-0.272	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	377.91998, 377.91998, 377.91998	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.181, 1.181, 1.181	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.29	0/5301	0.63	0/7189
2	B	0.28	0/5366	0.63	0/7277
3	D	0.30	0/4449	0.61	0/5997
4	C	0.30	0/4486	0.63	0/6037
All	All	0.29	0/19602	0.62	0/26500

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	1
2	B	0	2
4	C	0	1
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	54	SER	Peptide
2	B	32	LEU	Peptide
2	B	54	SER	Peptide
4	C	634	ASN	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	5178	0	5104	37	0
2	B	5245	0	5155	29	0
3	D	4376	0	4380	41	0
4	C	4416	0	4493	42	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	19217	0	19132	139	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 4.

All (139) 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:B:620:ASN:HD21	2:B:622:LEU:HD13	1.60	0.65
4:C:502:LEU:HB3	4:C:522:SER:HB2	1.82	0.62
4:C:464:VAL:HG22	4:C:560:LYS:HB3	1.83	0.60
3:D:156:HIS:HB2	3:D:177:THR:HB	1.84	0.59
3:D:422:ILE:HG13	3:D:617:LEU:HG	1.83	0.59
4:C:31:SER:OG	4:C:424:ARG:NH1	2.36	0.59
3:D:166:LYS:HD2	3:D:168:LYS:HE3	1.83	0.59
4:C:147:SER:OG	4:C:148:ILE:N	2.36	0.59
4:C:521:SER:O	4:C:525:HIS:ND1	2.35	0.59
1:A:644:LYS:O	1:A:671:ARG:NH2	2.38	0.56
2:B:480:LEU:HD21	2:B:572:VAL:HG13	1.87	0.56
3:D:259:SER:OG	3:D:260:ARG:N	2.38	0.56
1:A:578:ASP:OD2	1:A:609:ARG:NH2	2.38	0.56
4:C:342:ARG:NH2	4:C:390:PHE:O	2.39	0.56
4:C:67:THR:OG1	4:C:68:LEU:N	2.37	0.56
2:B:96:ILE:HG13	2:B:384:ALA:HB1	1.87	0.55
1:A:150:SER:OG	1:A:151:ARG:N	2.39	0.55
1:A:310:GLU:HG3	1:A:409:PRO:HB3	1.87	0.55
1:A:468:TYR:OH	1:A:532:ASP:OD2	2.23	0.55
1:A:250:ASN:OD1	1:A:250:ASN:N	2.40	0.55
1:A:457:LEU:O	1:A:460:ALA:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:455:PHE:HB3	2:B:530:ILE:HG23	1.88	0.55
3:D:58:ARG:NH2	3:D:64:HIS:O	2.40	0.55
3:D:523:PHE:HA	3:D:526:THR:HG22	1.90	0.54
4:C:16:VAL:HG11	4:C:115:LYS:HG3	1.90	0.54
1:A:583:TYR:HB3	3:D:408:VAL:HG11	1.91	0.53
4:C:443:LEU:HD22	4:C:585:LEU:HD23	1.91	0.53
3:D:198:ARG:HB3	3:D:223:LYS:HB2	1.90	0.53
4:C:218:ASP:N	4:C:218:ASP:OD1	2.42	0.52
1:A:453:LYS:NZ	2:B:536:ASP:OD1	2.42	0.52
1:A:486:PRO:O	1:A:489:THR:OG1	2.27	0.52
4:C:33:HIS:HE2	4:C:417:TYR:HH	1.52	0.52
3:D:41:GLN:HG2	3:D:88:PRO:HG3	1.92	0.52
4:C:432:ILE:HG21	4:C:595:LEU:HD23	1.92	0.52
4:C:481:SER:OG	4:C:543:ASN:ND2	2.41	0.52
1:A:527:SER:HB2	2:B:558:PHE:HB2	1.92	0.51
4:C:593:LYS:O	4:C:593:LYS:NZ	2.37	0.51
4:C:403:THR:OG1	4:C:404:GLU:N	2.44	0.51
4:C:450:GLU:OE2	4:C:453:ARG:NH1	2.44	0.51
4:C:84:ILE:HG13	4:C:91:LEU:HD13	1.93	0.50
1:A:651:ASN:HD21	1:A:679:GLY:H	1.60	0.50
2:B:146:THR:HA	2:B:149:MET:HG3	1.93	0.50
3:D:113:SER:OG	3:D:114:GLY:N	2.45	0.49
2:B:510:SER:OG	2:B:511:ASP:N	2.45	0.49
3:D:571:LEU:HA	3:D:574:LYS:HD3	1.95	0.48
1:A:80:ILE:HD11	3:D:92:ILE:HD12	1.95	0.48
3:D:521:ASP:OD2	3:D:521:ASP:N	2.46	0.48
4:C:429:LEU:HD22	4:C:599:VAL:HG11	1.95	0.48
3:D:433:CYS:SG	3:D:437:GLN:NE2	2.87	0.48
2:B:444:GLU:HB3	2:B:452:SER:HB2	1.96	0.48
4:C:152:ASP:OD1	4:C:167:ARG:NH2	2.47	0.48
1:A:169:ASP:O	1:A:173:SER:OG	2.30	0.48
1:A:364:SER:HB2	2:B:360:HIS:CD2	2.49	0.48
1:A:513:TRP:HB3	1:A:529:VAL:HG22	1.95	0.48
4:C:222:SER:O	4:C:225:ARG:HB3	2.13	0.48
1:A:360:HIS:CD2	2:B:364:SER:HB2	2.49	0.47
2:B:592:PHE:HB2	2:B:618:VAL:HG12	1.96	0.47
1:A:158:THR:HG22	1:A:166:PHE:H	1.79	0.47
2:B:150:SER:OG	2:B:151:ARG:N	2.47	0.47
4:C:176:GLU:OE1	4:C:178:HIS:NE2	2.41	0.47
1:A:223:VAL:O	1:A:227:ASN:ND2	2.35	0.47
2:B:309:ALA:HB1	2:B:409:PRO:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:538:ILE:HG23	2:B:548:ILE:HG21	1.95	0.46
4:C:17:THR:OG1	4:C:18:LEU:N	2.49	0.46
4:C:422:MET:HE2	4:C:606:PHE:HB2	1.96	0.46
3:D:475:ASN:O	3:D:479:ASN:ND2	2.49	0.46
1:A:84:PRO:HA	1:A:378:TYR:HE1	1.81	0.46
2:B:481:VAL:O	2:B:575:TYR:OH	2.26	0.46
1:A:503:ILE:HB	1:A:548:ILE:HD13	1.97	0.45
1:A:647:LEU:HD23	1:A:647:LEU:HA	1.86	0.45
4:C:509:LEU:HD11	4:C:519:THR:HB	1.98	0.45
1:A:269:ARG:NH2	1:A:271:GLU:OE2	2.43	0.45
4:C:633:LYS:H	4:C:633:LYS:HG2	1.64	0.45
3:D:150:LEU:HD23	3:D:178:VAL:HG21	1.97	0.45
4:C:509:LEU:HD13	4:C:516:PRO:HD2	1.98	0.45
3:D:34:PRO:O	3:D:288:TYR:OH	2.31	0.45
4:C:301:LEU:H	4:C:301:LEU:HG	1.64	0.45
3:D:165:ILE:HD12	3:D:165:ILE:HA	1.86	0.45
3:D:436:LYS:HA	3:D:603:LEU:HD23	1.98	0.45
1:A:624:ASP:OD1	1:A:624:ASP:N	2.50	0.44
2:B:505:VAL:HG12	2:B:507:HIS:HB3	1.99	0.44
2:B:677:THR:OG1	2:B:678:ASP:N	2.51	0.44
4:C:35:LYS:HA	4:C:35:LYS:HD2	1.76	0.44
2:B:83:HIS:CD2	2:B:85:GLU:H	2.35	0.44
3:D:602:PHE:HD2	3:D:603:LEU:HD12	1.83	0.44
3:D:296:VAL:HA	3:D:299:LEU:HD12	1.97	0.44
3:D:28:SER:OG	3:D:29:GLY:N	2.49	0.44
3:D:135:ILE:HG21	3:D:146:LEU:HD21	2.00	0.44
3:D:613:LEU:HD23	3:D:613:LEU:HA	1.86	0.44
3:D:633:ILE:HD13	3:D:633:ILE:HA	1.84	0.44
1:A:307:GLY:N	1:A:310:GLU:OE1	2.40	0.44
4:C:223:VAL:HG13	4:C:224:LYS:HD2	2.00	0.44
1:A:302:PRO:HG2	1:A:412:GLU:HB3	1.99	0.43
1:A:462:ARG:O	1:A:465:GLN:HB3	2.18	0.43
1:A:172:ALA:HB1	2:B:30:ASN:HD21	1.82	0.43
4:C:29:LEU:HD23	4:C:29:LEU:HA	1.85	0.43
2:B:195:ASN:OD1	2:B:195:ASN:N	2.51	0.43
3:D:487:GLU:OE1	3:D:547:LYS:NZ	2.51	0.43
4:C:123:ILE:HD13	4:C:158:ILE:HD12	2.00	0.43
4:C:172:SER:OG	4:C:173:LEU:N	2.52	0.43
2:B:88:ARG:O	2:B:91:TYR:HB3	2.18	0.43
3:D:530:GLN:HA	3:D:533:ILE:HG22	2.01	0.43
3:D:83:LEU:HD23	3:D:83:LEU:HA	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:646:SER:OG	1:A:670:GLY:O	2.36	0.42
3:D:476:GLU:HA	3:D:479:ASN:HD22	1.84	0.42
3:D:558:VAL:HA	3:D:561:ILE:HG22	2.02	0.42
2:B:462:ARG:HA	2:B:462:ARG:HD2	1.86	0.42
4:C:25:LEU:HD23	4:C:25:LEU:HA	1.88	0.42
4:C:257:ASP:OD2	4:C:257:ASP:N	2.50	0.42
3:D:306:TRP:HA	3:D:307:PRO:HD3	1.93	0.42
2:B:90:ILE:HD11	2:B:201:ARG:HG2	2.02	0.42
3:D:333:LYS:HD2	3:D:333:LYS:HA	1.82	0.42
1:A:230:LYS:HE3	1:A:230:LYS:HB3	1.84	0.42
1:A:85:GLU:OE2	1:A:201:ARG:NE	2.45	0.42
1:A:542:LEU:HD23	1:A:542:LEU:HA	1.89	0.42
2:B:343:ASP:OD1	2:B:344:THR:N	2.45	0.42
4:C:596:GLU:O	4:C:600:ASN:HB2	2.20	0.42
1:A:511:ASP:OD1	1:A:511:ASP:N	2.53	0.41
3:D:407:ASN:OD1	3:D:407:ASN:N	2.52	0.41
4:C:478:ILE:HD11	4:C:547:PHE:HD1	1.84	0.41
2:B:652:ASN:ND2	2:B:676:ASP:O	2.43	0.41
3:D:469:THR:O	3:D:473:THR:OG1	2.29	0.41
4:C:131:ARG:NH2	4:C:137:GLU:O	2.50	0.41
2:B:237:ARG:NE	4:C:634:ASN:OD1	2.46	0.41
3:D:548:LYS:HA	3:D:548:LYS:HD3	1.87	0.41
4:C:236:ASP:OD1	4:C:236:ASP:N	2.53	0.41
1:A:382:ALA:O	1:A:386:SER:OG	2.32	0.41
2:B:582:LYS:HE3	3:D:453:LEU:HD11	2.03	0.41
1:A:675:CYS:SG	1:A:687:ARG:HD2	2.61	0.41
2:B:470:SER:HA	2:B:475:PHE:H	1.86	0.41
3:D:49:VAL:HG11	3:D:271:VAL:HG13	2.03	0.41
3:D:306:TRP:NE1	3:D:308:LEU:HB2	2.36	0.41
4:C:591:SER:O	4:C:594:SER:OG	2.30	0.41
3:D:204:CYS:HB2	3:D:237:ARG:HG2	2.03	0.41
4:C:29:LEU:HD12	4:C:84:ILE:HD12	2.03	0.40
4:C:446:LYS:HE3	4:C:446:LYS:HB2	1.86	0.40
1:A:522:THR:OG1	1:A:523:ILE:N	2.54	0.40
3:D:57:LEU:HD23	3:D:57:LEU:HA	1.93	0.40
3:D:156:HIS:CD2	3:D:174:PHE:HB2	2.56	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	645/661 (98%)	593 (92%)	52 (8%)	0	100	100
2	B	655/672 (98%)	602 (92%)	53 (8%)	0	100	100
3	D	526/543 (97%)	505 (96%)	21 (4%)	0	100	100
4	C	527/629 (84%)	484 (92%)	42 (8%)	1 (0%)	43	71
All	All	2353/2505 (94%)	2184 (93%)	168 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	88	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	575/585 (98%)	561 (98%)	14 (2%)	43	67
2	B	586/596 (98%)	569 (97%)	17 (3%)	37	63
3	D	504/511 (99%)	482 (96%)	22 (4%)	25	54
4	C	504/582 (87%)	480 (95%)	24 (5%)	23	52
All	All	2169/2274 (95%)	2092 (96%)	77 (4%)	32	59

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LEU
1	A	80	ILE
1	A	90	ILE
1	A	228	ILE
1	A	258	GLN
1	A	315	PHE
1	A	364	SER
1	A	374	LEU
1	A	386	SER
1	A	481	VAL
1	A	490	VAL
1	A	508	ASP
1	A	581	ILE
1	A	645	ASN
2	B	34	THR
2	B	64	VAL
2	B	114	LEU
2	B	134	VAL
2	B	146	THR
2	B	164	VAL
2	B	195	ASN
2	B	197	LEU
2	B	199	VAL
2	B	200	VAL
2	B	246	ILE
2	B	315	PHE
2	B	374	LEU
2	B	381	ASP
2	B	400	ASP
2	B	450	ILE
2	B	633	LEU
3	D	36	THR
3	D	69	VAL
3	D	70	ILE
3	D	95	TYR
3	D	105	VAL
3	D	113	SER
3	D	150	LEU
3	D	161	ASP
3	D	177	THR
3	D	216	ILE
3	D	239	VAL
3	D	271	VAL

Continued on next page...

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Mol	Chain	Res	Type
3	D	274	ARG
3	D	284	LEU
3	D	304	VAL
3	D	327	LEU
3	D	407	ASN
3	D	422	ILE
3	D	453	LEU
3	D	459	GLU
3	D	470	VAL
3	D	633	ILE
4	C	32	LEU
4	C	68	LEU
4	C	74	THR
4	C	81	ILE
4	C	84	ILE
4	C	94	HIS
4	C	138	VAL
4	C	165	THR
4	C	176	GLU
4	C	211	TYR
4	C	223	VAL
4	C	234	THR
4	C	280	ASN
4	C	301	LEU
4	C	308	ASN
4	C	360	CYS
4	C	440	THR
4	C	448	LEU
4	C	552	GLU
4	C	571	TYR
4	C	599	VAL
4	C	604	THR
4	C	606	PHE
4	C	630	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	135	HIS
1	A	139	HIS
1	A	167	ASN
1	A	195	ASN

Continued on next page...

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Mol	Chain	Res	Type
1	A	286	GLN
1	A	349	HIS
1	A	464	GLN
1	A	465	GLN
1	A	488	ASN
1	A	651	ASN
2	B	220	ASN
2	B	253	GLN
2	B	286	GLN
2	B	296	ASN
2	B	357	HIS
2	B	454	ASN
2	B	466	GLN
2	B	620	ASN
2	B	681	ASN
3	D	156	HIS
3	D	179	HIS
3	D	213	GLN
3	D	316	GLN
3	D	404	ASN
3	D	419	HIS
3	D	437	GLN
3	D	458	ASN
3	D	479	ASN
3	D	512	GLN
3	D	572	ASN
3	D	575	GLN
3	D	576	ASN
3	D	611	ASN
4	C	87	HIS
4	C	295	ASN
4	C	423	HIS
4	C	497	ASN
4	C	505	ASN
4	C	543	ASN

5.3.3 RNA ⓘ

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	334:LYS	C	404:ASN	N	82.37

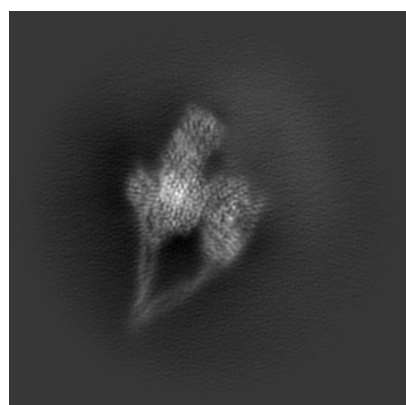
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11092. These allow visual inspection of the internal detail of the map and identification of artifacts.

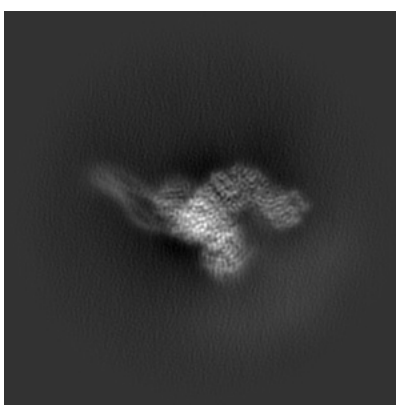
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

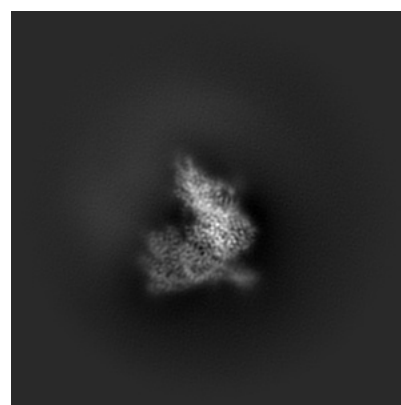
6.1.1 Primary map



X



Y

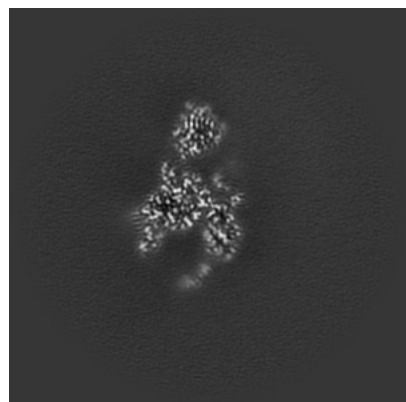


Z

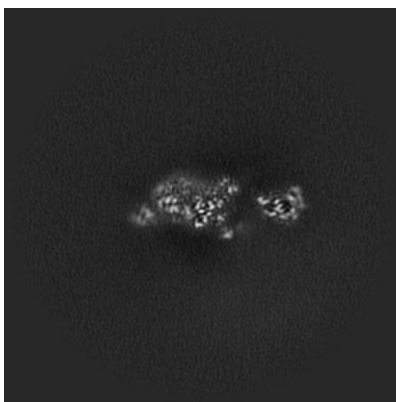
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

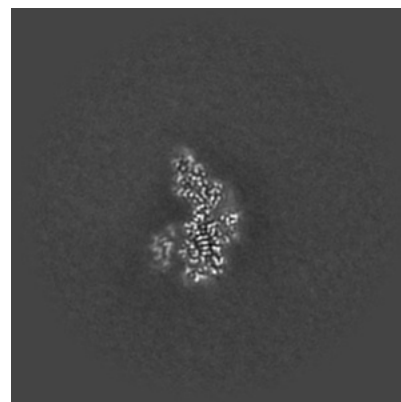
6.2.1 Primary map



X Index: 160



Y Index: 160

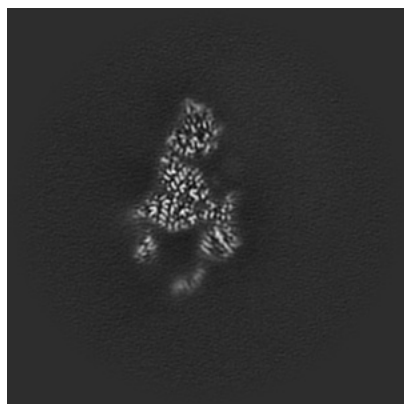


Z Index: 160

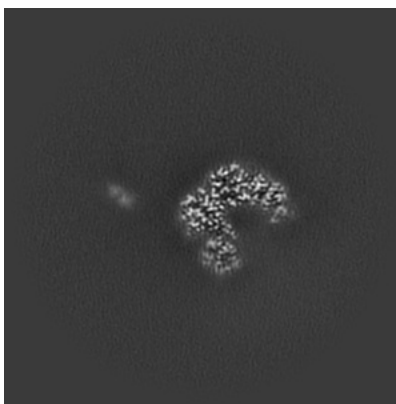
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

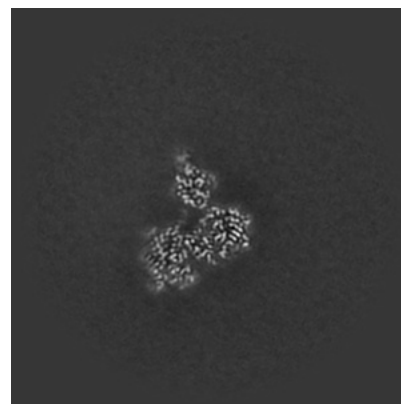
6.3.1 Primary map



X Index: 164



Y Index: 135

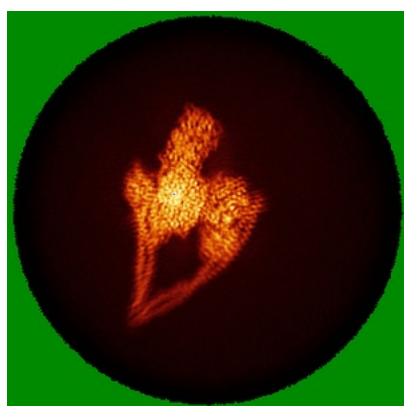


Z Index: 171

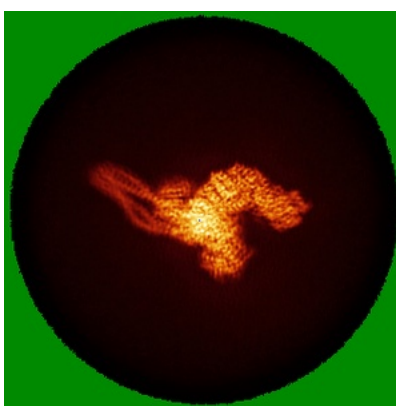
The images above show the largest variance slices of the map in three orthogonal directions.

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

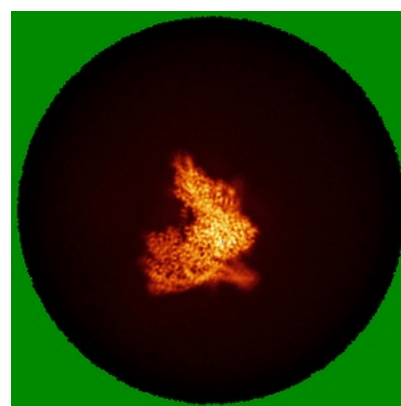
6.4.1 Primary map



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

This section was not generated.

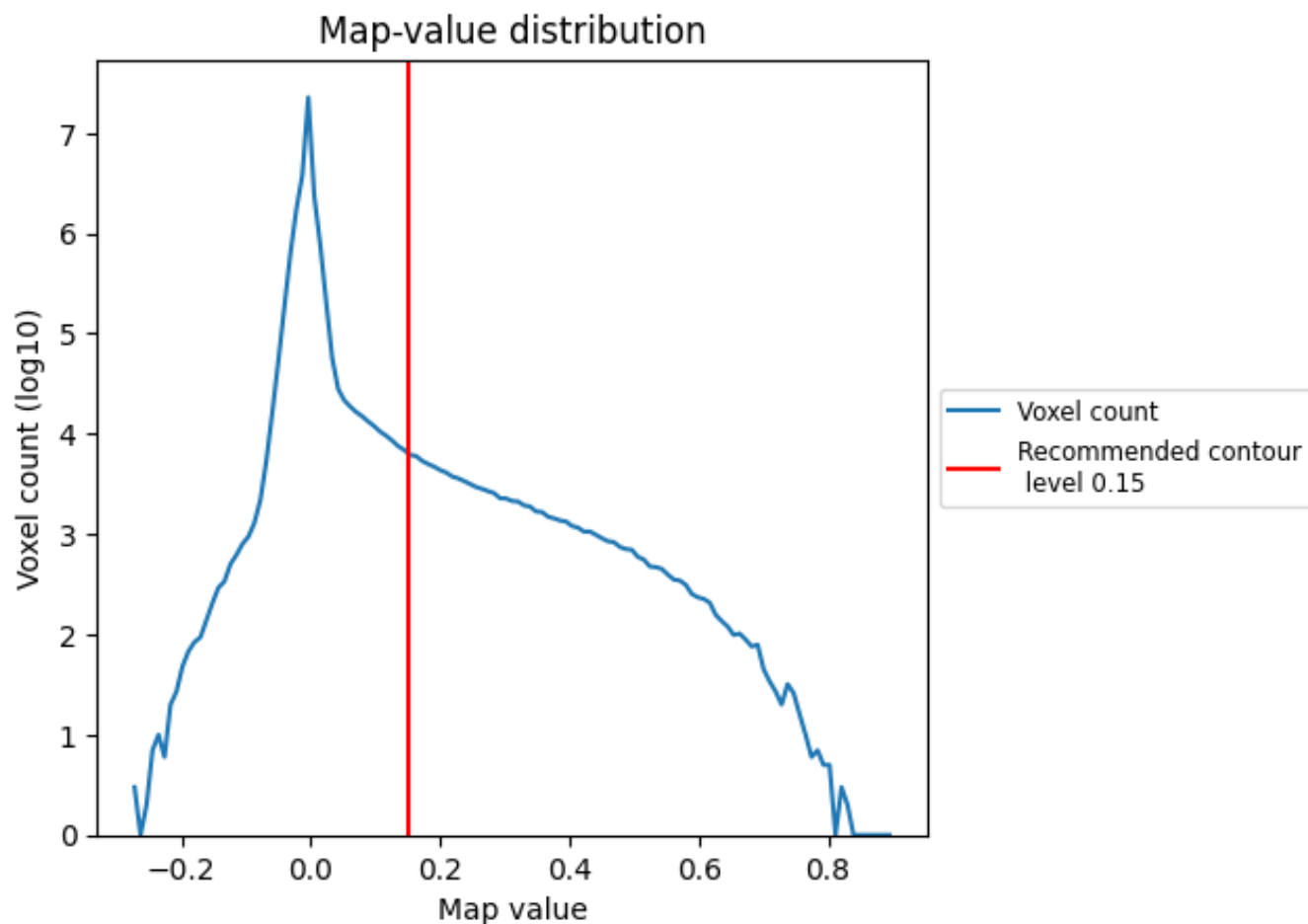
6.6 Mask visualisation

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

7 Map analysis [i](#)

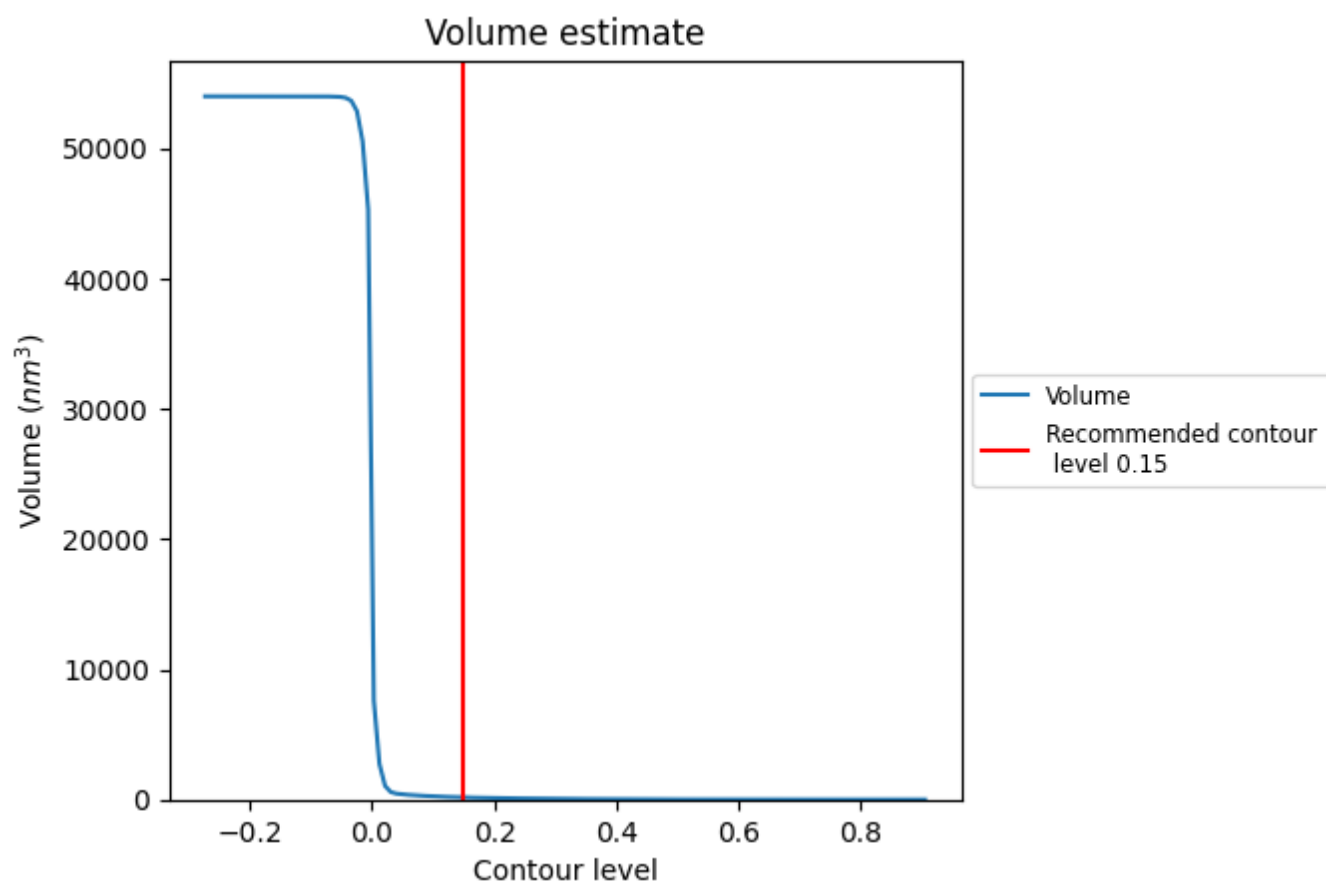
This section contains the results of statistical analysis of the map.

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.

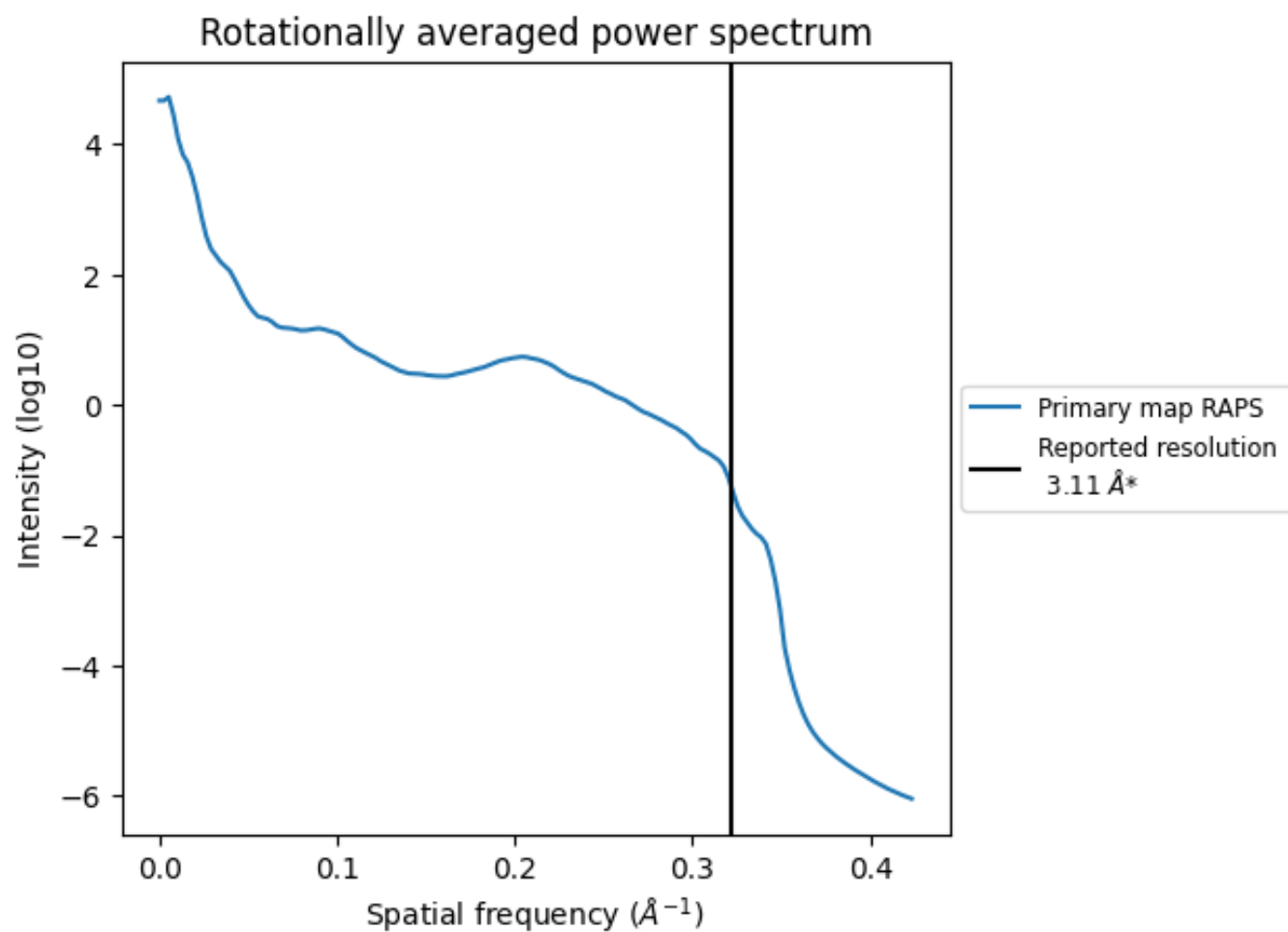
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 167 nm³; this corresponds to an approximate mass of 151 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 0.322 Å⁻¹

8 Fourier-Shell correlation

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

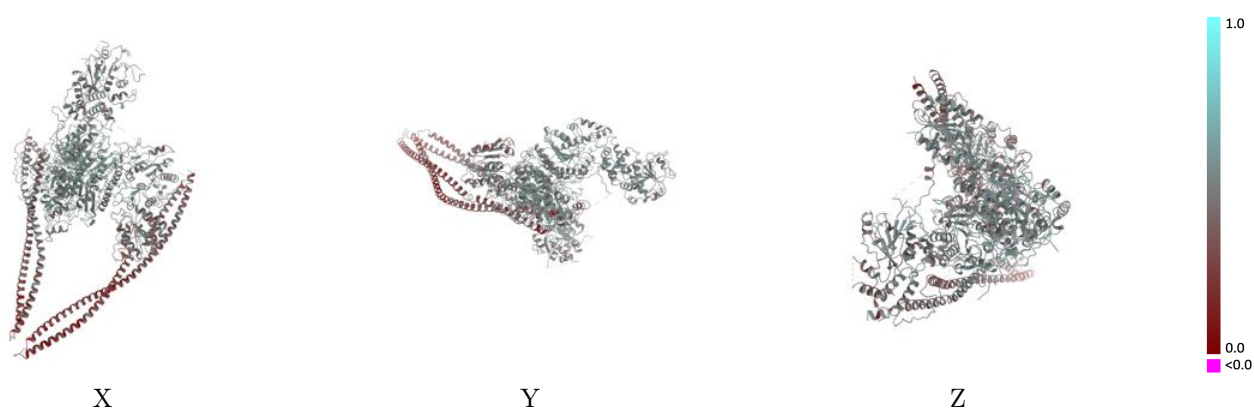
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11092 and PDB model 6Z6F. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

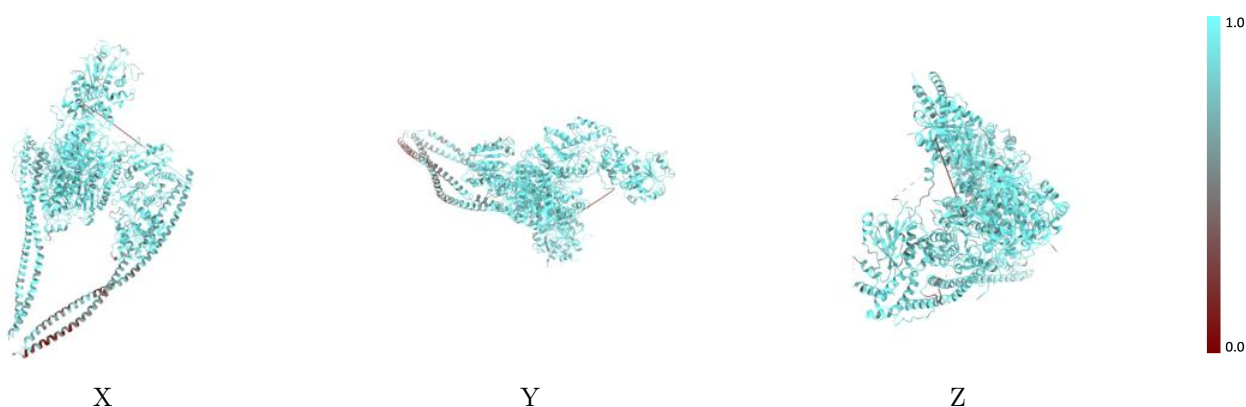
This section was not generated.

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



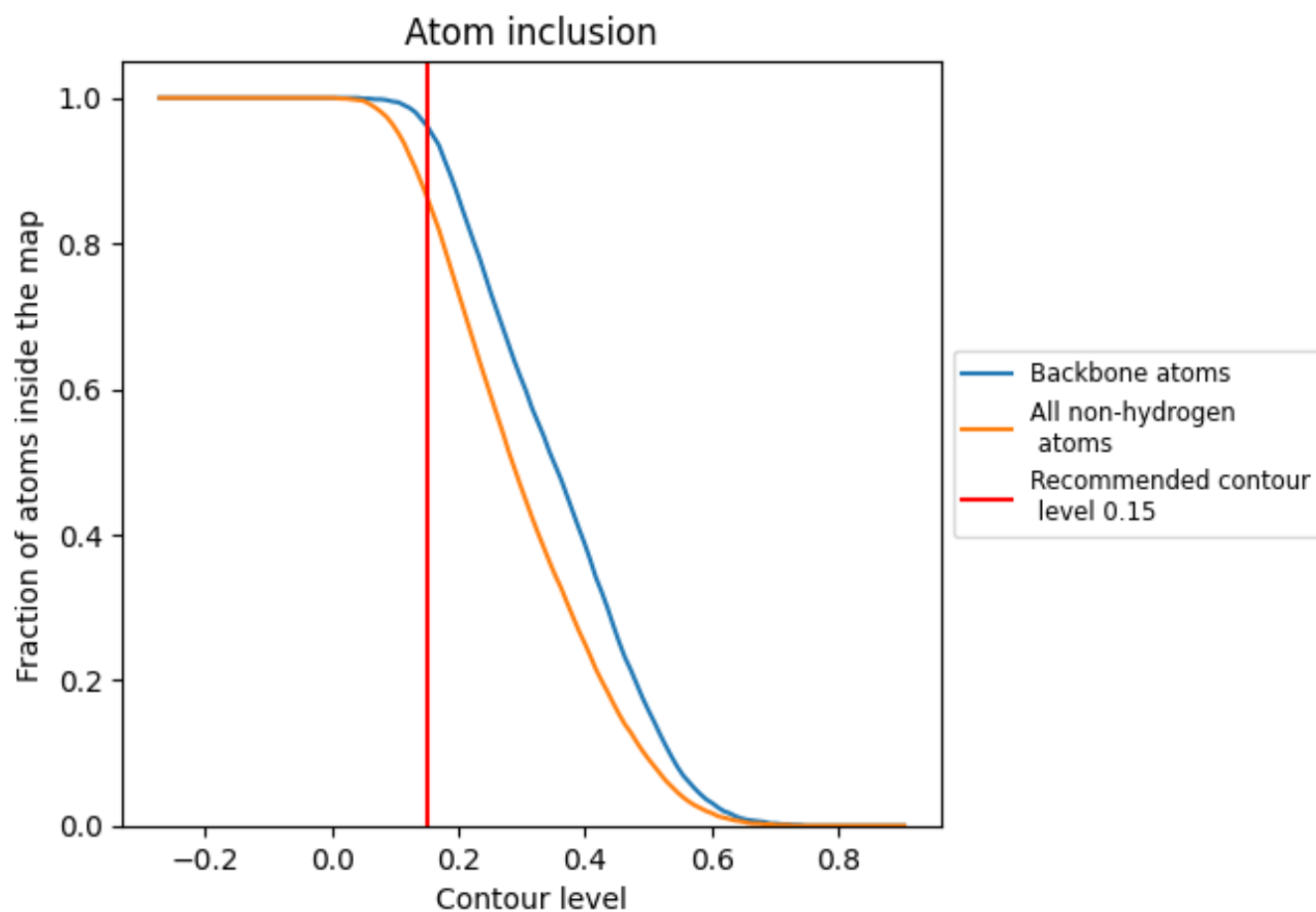
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 86% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8650	0.4710
A	0.9270	0.5240
B	0.9110	0.5050
C	0.8330	0.4380
D	0.7670	0.4020

